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2	U.S. FOOD AND DRUG ADMINISTRATION
3	CENTER FOR DRUG EVALUATION AND RESEARCH
4	AND
5	INTERNATIONAL SOCIETY OF PHARMACOMETRICS
6	PUBLIC WORKSHOP ON
7	Model Informed Drug Development for Oncology Products
8	FDA White Oak Campus
9	10903 New Hampshire Avenue
10	Building 31, Room 1503 & (Great Room)
11	
12	
13	Thursday, February 1, 2018

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PROCEEDINGS

2 WELCOME AND WORKSHOP OBJECTIVES

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3 Dr. Zineh: We are going to start now. Please take your seats.

4 Well, good morning everyone. I would like to welcome you all 5 to this workshop on Informed Drug Development in Oncology 6 jointly convened by FDA and the International Society of 7 The organizers have put together Pharmacometrics. an 8 excellent program that promises to an important launch point 9 for further discussions on the role of how to inform 10 strategies in oncology drug development and regulatory evaluation. My name is Issam Zineh. I am the director of 11 the Office of Clinical Pharmacology in FDA and it's my 12 pleasure to open the workshop. I've been asked to discuss 13 14 the objectives for today and I also want to place this 15 workshop in a larger regulatory and scientific context. The 16 explicit objective of the workshop is laid out here: to 17 discuss best practices in integrating PK/PD efficacy and 18 safety data into the models; to best inform oncology drug 19 development; evaluate disease and mechanisms specific early 20 endpoints to predict long term safety; and discuss potential 21 regulatory implications with these decisions. I have also 22 listed the specific aims of the workshop that are also in the 23 Federal Register note and so I won't read those. Many of the 24 folks here are not surprised I am sure about the impact that 25 MIDD has had when it is successfully applied in drug There are many definitions for model based or 26 development. 27 model informed drug development. I personally gravitate 28 towards this modification of the one put forward by 29 Rick Lalonde and his colleagues about 10 years ago where they 30 defined model-based drug development as the "development and 31 application of pharmacostatistical models of efficacy and 32 safety from preclinical and clinical data to improve drug 33 development knowledge management and decision-making" and 34 what I particularly like about this definition is its 35 emphasis on application and as a lifecycle approach. In 36 impact, the literatures terms of were replete with documentation from FDA and other scientists on the role of 37 38 modelling, for example, pharmacometric modelling on a variety 39 of decisions made as well as efficiencies gained in drug 40 development. This is a nice schematic from the FDA MIDD 41 working group that provides an overview of various internal 42 company decisions and regulatory applications for which MIDD 43 has been particularly helpful. And as you can see, it ranges 44 from target selection and validation. It is in preclinical 45 and early clinical development to late development and

regulatory decision-making on issues of improvability, labeling, just to name a few. So it is really not surprising that MIDD has brought about these efficiencies given that they were models focusing on sources of variability and I think Dr. Woodcock will have something to say about that in a little bit.

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7 This slide emphasizes the MIDD based approach as we have 8 experienced with to varying degrees. On the left, this is on 9 the FDA side, and on the right, I have boxed the regulatory 10 applications with which we have had extensive experience and this includes these modelling-formed strategies for dose 11 12 optimization for the general population as well as sub-groups. In terms of efficacy, we are talking increased access for 13 14 patients in the form of population #4:47 bridging and 15 extrapolations as well as supportive evidence of 16 effectiveness. There is an extensive body of work on 17 exposure safety analyses as well as classification of toxic compounds based on chemical structure. We are seeing more 18 activity in the trial design space and IND space as well as 19 using these approaches to inform policy change. 20

21 drug development academic and regulatory community The 22 communities have been working on the science underpinning MIDD for decades now, and at the same time, regulatory 23 24 science provisions in the last two reauthorizations of PDUFA 25 signal a recognition by all involved—the FDA, the advocacy 26 groups, industry, political leadership—that integrating new 27 science into regulatory review and policies is of significant importance. This is just a high level of what is laid out in 28 29 PDUFA VI under the regulatory decision tools: Provisions and 30 namely there will be mechanisms for drug developers to engage 31 directly with subject matter experts inhouse here on complex 32 innovative designs, all informed drug development where we 33 tend to bring more formality to the biomarker qualification 34 process and faster discussions around real world evidence, 35 real world inference, more structured transparent benefit-36 assessment, and of course, best practices risk for 37 incorporating patient voice into drug development and 38 regulatory decision-making.

On the MIDD front, I have laid out sort of the specific 39 40 things that we have committed to under PDUFA VI. These increasing our 41 include regulatory science and review expertise in capacity in MIDD both through training as well 42 43 as raising the level of the workforce. We have committed to 44 convening a series of workshops to identify best practices in

1 MIDD. This is the first in the series. This one is on, of 2 course, dose exposure, response and other quantitative 3 aspects of MIDD related to oncology, but we have also 4 PBPK best practices, convened workshops on disease 5 progression, and model development We have also • 6 committed to starting up a pilot program on MIDD approaches 7 where sponsors could engage directly with subject matter 8 experts on product-specific issues and add a prominent MIDD 9 component. And we will also either revise or develop new 10 guidances, manuals on policies and procedures and standard 11 operating procedures to advance the science and ensure 12 consistency in the application of these strategies in 13 development and in review.

14 efforts are intended to advance the field These and 15 integration of the science into our work. There are, of course, enablers and challenges in the application of MIDD 16 17 approaches. Based on discussions with our stakeholders as 18 well as our own senior leadership, we feel MIDD is enabled by 19 a variety of factors including environment that fosters 20 collaboration using information from a variety of sources 21 which I am sure we will hear about today, acceptance of 22 model-based approaches by multidisciplinary teams, 23 organizational alignment, prioritization and support, methodological advancement and a variety of other factors. 24 25 There are also recognized challenges and I have raised some 26 these in a slide here including an absence of best of 27 practice for determining a model is fit for its intended 28 the need for identification and transparent purpose, 29 communication of assumptions and knowledge gaps, the need for 30 integration of data from multiple sources, a recognition that 31 there is varying degrees of comfort in adoption of these 32 approaches by end-users and decision makers, clarity on 33 regulatory expectations, and from the Oncology context, a bit 34 of a catch-22 situation. An argument could be made that Oncology is one of the therapeutic areas for which MIDD can 35 36 have the most impact because the pace of Oncology development 37 is moving so fast that there are knowledge gaps around 38 therapeutic individualization and use that could be filled by 39 At the same time, because it is moving so the strategies. 40 fast, oftentimes we do not have the data that we need in 41 order to fill those knowledge gaps, and so there is clearly a 42 situation to be considered here. Notwithstanding those 43 challenges, of course, there is reason for excitement. There 44 is a global convergence of interest, investment and effort in 45 the MIDD space, and so there is global health authorities, drug developers, academic consortia. They are all actively 46

promoting and developing the science of MIDD. We anticipate significant progress in the field, and in fact, there is support for MIDD at the leadership level at FDA. Of course, this is just a blog that was put out last summer by the commissioner highlighting the various ways in which in-silico approaches are being used in drug development and in review, and a call really to increase innovation around these tools and their application. And, of course, in a moment you will hear from Dr. Janet Woodcock who has been a longtime proponent of these strategies at the center and at the Agency level.

12 So with this, I just want to thank the many people that were 13 involved in putting together this workshop. You see these 14 names on the left hand side as well as the speakers and 15 panels in advance. I would like to thank the attendees. At 16 last count, there are nearly 1200 registrants for these 17 meetings. I think that signals a tremendous amount of interest in this space. I would like to also acknowledge the 18 names on the right column. There are many people working on 19 20 the strategic front here at the FDA both in our center as 21 well as the Center for Biologics in ensuring the success of 22 the provisions that we have committed to go under PDUFA and 23 as well. So, again, I extend my welcome on one 24 behalf of the organizers, and I look forward to a very 25 productive day.

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With that, I would like to introduce Dr. Janet Woodcock.

27 [APPLAUSE]

28 Challenge and Opportunity of MIDD in Oncology

29 Dr. Woodcock: Thanks Issam and good morning everyone. Thanks for 30 showing up bright and rolling for this very technical topic. 31 I think there is a lot of excitement in the room and possibly 32 around the world about the potential here. Now, when I took 33 over CDER for the first time, it was at 1994 and mv 34 predecessor Carl Peck who is clinical pharmacologist had been 35 advocating for this type of approaches back in the '80s, and 36 I think he is probably somewhere watching this. To Carl, we 37 are finally getting there. In the intervening years, though, 38 there has been a great deal of effort, I think, built up in 39 experience, building a world class staff at FDA. I just 40 cannot tell you the expertise that we have here. Ι am 41 constantly blown away by this. And, of course, industry with 42 experience in using models of different types in drug 43 development and gradual acceptance of this. So I think the

time is right now, as Issam said, with the PDUFA agreement. We have put a stake in the ground. We said we're going to do this. Ι believe there is a lot of acceptance and understanding in the _____ community which really also had to catch up and we all have to be in this together. So now is really I think the time for us to really informed drug development transform drug development through use of more quantitative information during the preclinical and clinical phases and after marketing.

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10 And why Oncology? How do we find ourselves here this morning talking about oncologic drug development? 11 As you 12 know, the history of oncologic drug development and the theme has been very simple over the years, and this is a very 13 simple approach which is kill the tumor and don't kill the 14 15 patient. Right. [Laughs] And that was the objective and 16 that was the straight line objective-we find the maximum 17 tolerated dose that would not kill patients and then you try to kill the tumor. And because of the desperate situation in 18 19 Oncology where we have people often with untreatable or 20 poorly treated diseases, there are really very few chances 21 and really little room for refinement, and we will still find 22 ourselves in this situation to some extent where the pressure 23 will be to move forward as quickly as possible. But Issam 24 mentioned the patient voice. We have heard from the patients 25 and we know the suffering they undergo not only from their 26 diagnosis but also from their treatment and we can do better 27 in many ways, and I believe that this type of - applying this type of knowledge and information to oncology drug 28 29 development will really help. We know that we have oncology drugs onto the market and they are used without optimization 30 Now it is true for all drugs [laughs], but these are 31 dose. 32 especially toxic drugs, all right? The individualization of 33 dose without optimization of regimen and for combo, the combo 34 therapy, we are not really sure because there are so many multiple ways we might use these drugs together and the 35 36 situation is so dire, and frankly it is true for all drug 37 development. There simply is not enough time and resources to answer these questions through empirical kind of trials. 38 39 We need to have better methods. Now in Oncology, though, we 40 have a changed situation. We have many candidate drugs and 41 we have many approved drugs often for various tumors, and 42 there are many combinations that can be put together and that 43 is a tremendous opportunity for people with cancer and for 44 people who treat cancer it is a stone that there is still 45 this unmet medical need. There is still this sense of

urgency. And so how do we combine these two things? We need 1 2 to have answers to these questions. How do we construct the 3 optimal region for outcomes? How do we construct the optimal 4 exposure patient exposure that will kill most tumors but not 5 cause short term and long term dire adverse consequences? And so we really have to face the fact that what we have done 6 7 is we just do not answer these questions, and so modelinformed drug development offers us a pathway to answer 8 9 perhaps less conventionally than we have answered questions 10 through empirical clinical trials, but to give us answers 11 that are quite convincing and that can guide therapy in ways 12 that we have not realized before. opportunities So 13 include-and Issam has gone through some of these, but I 14 particularly germane to this discussion think today-modelling before and during early clinical development, 15 16 exposure, and exposure response. If we can begin to do that 17 in a much more quantitative manner, figuring out how to 18 manage these combo regimens, figuring out how to do a regimen 19 in general. There are vast amounts of information available from previous experiences in these tumors and in these trials. 20 21 And often in other diseases, we have begun pooling this 22 information to make the same disease models and response 23 models and so forth. There is a tremendous opportunity there, I think, that Oncology to do this. 24

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26 So can we really optimize exposure response on both efficacy and toxicity for cancer drugs? And can we figure out ways to 27 28 do that so that when we get the recommendation for dosing on 29 market it is backed up by quantitative information that we 30 Can we achieve more integration of different understand. 31 levels of knowledge? We have tremendous amount of basic 32 science knowledge right now about tumors based on the war on 33 cancer for the last 50 years, right? And so we have 34 tremendous amount of molecular information, target 35 information, all these sorts of things-tumor behavior and so 36 one—but we are still, I see some printout, we are still 37 using the RECIST criteria. [Laughs] We are still in the 38 translational space. In the clinical space, we are still 39 using the tools that we have used for a very long time. So 40 we may need to keep using these tools, but we can re-inform 41 them better with much more of the scientific information. 42 Can we construct models that bring this information together 43 and give us a more global understanding of both behavior of 44 the tumor and then the pharmacology of the drug overlaid on that? We recently had a sort of workshop here within the FDA model-informed drug development to inform the staff on basically of how far we have come and what the opportunities And really in many other disease settings, we have had are. tremendous, I think, real breakthroughs in understanding for specific drug development programs and also for how we handle a certain approach to the disease based on these models that had been degenerated. They just add tremendous richness when you are able to make these connections. So I think even new end-points that we are considering such as There are a lot of people who are looking residual disease. at circulating tumor cells and how they might be used. There is a lot of biology underlying that. We are still not there There is a lot we can learn. If we can pull that yet. knowledge SO that we can learn faster through the quantitative models, I think we can get to a better level of understanding. So it is not going to be an easy journey.

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Drug development to a great extent likes to travel well-worn 18 Why is that? 19 pathways. Because there is so much risk for 20 whomever the drug developer is. There is a tremendous amount 21 of financial risk and company risk and all sorts of things in 22 pursuing a drug development program, and so people like to do 23 what has been done before and has been successful because 24 trying other things often as perceived at least adding 25 additional risk to the equation. But we have to take some risks here to get to a better place, and I do not think these 26 27 risks have to be to a drug development program. They just ---28 we all have to stretch ourselves a little bit and figure it 29 out. You know, how can we incorporate this knowledge and 30 make decisions based on broader input in something what we 31 find from the empirical trials. I think this is the future. 32 We always hope that we at some point will have enough 33 knowledge of the science of human variability of response to 34 And in this case, the tumors' variable response to drugs. 35 drug as well as the patient's variable response to drug that 36 can predict the influence of all these factors and we 37 actually can predict what the response will be. We are far 38 away from that , but the only way we are going to get there 39 is to incrementally add those pieces of knowledge together and yet our predictions become better and better and better 40 41 over time. This actually eventually will *de-risk* as they 42 call it drug development considerably because our predictive 43 power which is now pretty poor will become better and we will 44 be able to say with some confidence after we have gained a 45 lot of knowledge about a drug, not necessarily just clinical 46 experience. We will be able to say with some confidence what

we think that last trial will be. In fact, you know, I think 1 2 today we are talking a bit about the Learn and Confirm model 3 and learn and confirm, learn and confirm. My hope is sometime in the future we will learn and then the clinical 4 5 clinical trial will be the peak, and the trial 6 trial will be the confirmatory trial. Right now, the 7 have a single construct is we can combo trial and 8 confirmatory model which might from a model from other 9 scientific information, mechanistic information. The future 10 needs to be that we have learned enough mechanistically from Pharmacology and other understandings that we have that when 11 12 we do the clinical trial we are confirming the prediction 13 that we have made. And confirmation hopefully should be more and more and more predictable overtime. 14 This is for the future, okay? But we are here now taking some of the first 15 16 steps to that. In Oncology, the complexity of the disease as 17 well as the complexity of the interventions, for example, the immunotherapies and other types of interventions are being 18 19 It is getting to an extraordinarily high level. conflated. So every tumor-we used to have several tumor breaks-each 20 21 tumor is its own tumor really, and as far as the 22 interventions, we have only begun to sort of plug the science 23 of what we are actually doing to the immune system and how 24 these things are actually playing out overtime. And of 25 course we have new unanticipated side effects of the 26 immunotherapies. All of these things, at least in theory, 27 are mechanistically predictable if we have enough knowledge, 28 and we have to keep that in mind. We cannot become sort of 29 nihilistic empiricists who believe that, you know, this is so complex that we will never understand it. We have to believe 30 31 we can understand enough of it to get there, that we will get 32 to a point where our predictions will become stronger and 33 stronger and more reliable. And frankly for handling the 34 complexity of Oncology in the future, there is probably no 35 other choice and to connect all that basic science 36 understanding of tumor, biology in tumor and so forth and 37 begin to connect it up with the pharmacology of the drug that 38 we understand the toxicity and then get to the next level of 39 what is going to happen in that individual patient who has 40 shown that each one of them has so many different factors 41 including their tumor.

42So I commend our Clinical Pharmacology Office and the43Oncology Center of Excellence for putting all this and our44co-sponsors for this. It is a really fantastic starting45point. It is a long journey, but that first step is usually46the hardest. So good luck on the workshop and I think this

will be the start of something that will really benefit 1 2 patients in the long term. 3 Thank you. 4 [APPLAUSE] 5 Session I NON-CLINICAL MIDD IN ONCOLOGY 6 Dr. Jin (Moderator): Good morning everyone and good afternoon for those on the line calling in. I know some of you guys I know 7 it is a good afternoon or good evening. Please join me in 8 9 thanking Dr. Woodcock and also Dr. Zineh again for setting up 10 a great context and painting us a bright future as a 11 wonderful kickoff of today's workshop. 12 13 [APPLAUSE] 14 15 I am Jin Jin from Genentech. I also represent the 16 International Society of Pharmacometrics as the current 17 president. It is our great privilege to co-sponsor today's workshop with FDA, and I will also act as a moderator for our 18 19 first scientific session. 20 21 Drug development starts in the nonclinical space and our 22 first session will showcase some modelling applications in 23 the preclinical space, and we will have three speakers 24 covering multiple aspects ranging from using assessment 25 pharmacology modelling approach, the informed immuno-oncology , use of in-silico 26 therapy authorizations of modelling to help design up bispecific antibodies, and also 27 28 use of preclinical to clinical translation and modelling to inform and further optimize the advocacy and the safety 29 30 balance for combination therapies. We will take a couple of 31 brief clarification questions at the end of each talk, and at 32 the very end, we invite all the speakers to come to the panel joined by a couple of FDA colleagues with the general panel 33 34 discussion at the very end. 35 36 So now, I will introduce the first speaker for this session 37 Dr. Sergey Aksenov. Dr. Aksenov is a pharmacometrics lead in 38 Quantitative Clinical Pharmacology Division at AstraZeneca. 39 Given the interest of time, I will not read through the detailed bios and this will be posted online afterwards. 40 41 Now, Sergey please come over. 42 43 Dr. Aksenov: Thank you, Jin. Good morning everyone. First of all, 44 I would like to thank the organizers for giving me this 45 opportunity to speak here today. I speak on behalf of my 46 many colleagues in office at AstraZeneca and all the

partnership. The topic for my talk today is

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modelling that we are doing to support evaluation of drug combinations through clinical models and data.

Well, first of all, I would like you to ______ from this, to walk you through the framework that we are using to evaluate potential drug combinations. The approach that we use integrates the PK/PD data, pathophysiology both animal and human. Eventually we use this to make predictions for ______ drugs in humans, and then I will talk about the quantitative systems for oncology model for the immune cycle in mouse, and you will see how we use that model to understand the dynamics of the immune cycle and how it well describes the type of radiation and anti-PDL1 antibodies tumor cycle _____.

So this a general outline of the whole framework. So it consists of two parts: the first part is the QSP quantitative systems pharmacology model. That is the one from the left. The second part of it is what we call a joint It is a model that links the output from the QSP model. . So what is a QSP model in this sort model to the of framework? It consists of three modules. The PK module that describe the pharmacokinetics of drugs, concentration of drugs at the test site. The biology module describes the drug targets and the signaling pathways where this drug was designed, and it also describes the way drugs do that biology of signalling there. And finally, the physiology module describes the context for the drug, the Eventually one of the targets, the pathways • outputs from the variables from this physiological framework links up to the clinical input and that is the joint model of that. I will not spend too much time talking about it, but that is where we — just to give you an idea of the thread that pass through all of this clinical work to the post clinical especially the _____ in patients.

Okay, so for the immune cycle, this is what that annual QSP model looks like. This is again as an _____, the PK/PD module here containing PK of the anti-PDL1 antibodies in mouse, other compounds, and how the concentration of these drugs and the effect of these treatments act on the interaction between the immune components of the system. So that is the PK/PD part of it. The biological part of it is again the interactions between the immune components but also the immune system itself and the whole body of the mouse. And finally the physiological part is where the immune cycle, the immune system links up to what we care about which is the wall of every tumor, the tumor size of the mouse. That is the readout for all of our prediction efforts given.

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Again, just to show you how this would look like eventually in this framework that we are using. The annual model that I have talked about today is here on the left and the output as well tumor size, tumor girth. So if you will click this, it would re-circle here. So one thing that we are working is an effort to translate this mouse tumor model to human. That is necessary because what we will want to understand is how combinations of drugs affect tumors in humans. In that what we will do is we will develop a joint model of tumor cells progression-free survival and overall survival. And the joint model here—It is a technical term statistically. Ιt just means that we will be modeling multivariable divisions , variable for tumor size and progressions and deaths. And so the way we will do it is we will link up predictions from the human #QSP model in which tumor cell response to this joint model that we can build using all the information that is available to us cancer—clinical information, about the clinical trial data-and be able to predict the effect of the combinations on progression free survival and overall survival, so in that way we will be able to make the combinations.

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Okay so now about the mouse models. This is a diagram of the model and the key component, the centerpiece is-I have highlighted this with my mouse-the effector cells in the tumor environment, right here in the middle of the cyan blue box. And what these effector cells do is they promote increased death rate of tumor cells, and that is why they are centerpieces. Now, there are three feedback ropes here in the model that together determine the complex that mimics the immune system response through interventions involving tumor cell response interactions. And the first feedback rope downregulation of differentiation describes the and activation of effector cells through the PDL1 axis or pathway. It is right here. The second that we will describe is the role of the systemic antigens in, again, promoting the infiltration of the effector cells into the tumor. Right here. And finally, the third feedback rope here is the antigen, the effect of the antigens on the immunosuppressive components of the tumor environment which would self-inhibit the differentiation of the effector cells. Ultimately these antigens come from the tumor itself. The tumor in the model here—it is an empirical model describing logistic growth of the tumor and exponential death. In wanting to have the effect of anti-PDL1 antibodies through depletion of the PDL1 that is available to act through the components Last month, the model was estimated — the parameters here. of the model were estimated with using mouse data in syngeneic tumor mouse models. And there were tumor sizes

in response to different treatments, and I will show you this on the next slide. But what I wanted to emphasize is one parameter, one ______ that is circled here on the left. It is the ability of the T-cells to infiltrate the tumor microenvironment. It turns out that that is a very critical parameter in the process in the model, and the ______ was modeled — the parameter that described this interaction was modeled as a distribution across all subjects. In technical jargon, it is the random effect in the population model, and the purpose was to be able to describe the variability of the variation of tumor responses in individual mouse and the model did this very well.

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So these six graphs show you the that were used to estimate the parameters in the model as well as model predictions. So model predictions are the red lines. The red lines are predicted • Individual mouse profiles of tumor cell versus time are the gray lines, and the median of those is that dash black line. So the vertical axis is the tumor size. The horizontal axis is the time since inoculation end-points with the tumor cell. So what you see when you look in the control mice, the tumor growth has been watched exponentially and once you apply anti-PDL1 antibodies to mice or radiation treatment with x-rays, you see that the growth, the overall growth rate of the tumor decreases but then it starts regrowing. The bottom row of graphs show you the combination treatments, radiation plus . And you see the dramatic effect on the anti-PDL1 tumor size. On the average, the tumor size growth is completely suppressed. Of course, there is some variability between here. What is interesting is that the importance that this model was also validated using external data. So these graphs show you predictions in data for a different set of mice. Draw your attention to the rightmost So that is the graph where the combination of graph. radiation and anti-PDL1 was given together with anti-CD8 antibodies. So these antibodies deplete CD8+ effector cells from the body, and so when mapped to a parameter in the model, it is aligned with predictions with the data as well.

So given all these, we are confident that the models qualify to spread the immune cycle directions in the mouse. That was really the goal. And just to expand on this a little bit, we can do two things with this model. We can address mechanistic questions and try to understand exactly what underpins the response of the tumors to these therapies as well as to make predictions. So in terms of mechanistic understanding, recall where the parameter of that image

probably describes the infiltration of T-cells into the tumor 1 2 environment. So that parameter it turns out differentiates 3 the quick responders-mice responders-versus nonresponders. 4 So these are the _____ values of that parameter. So remember it was — how we were computing the values for every 6 And the low values of the parameter right here mouse. 7 corresponding to high ability to infiltrate the environment 8 of the tumor correspond to responders and nonresponders 9 have a wider distribution, larger values of the 10 parameter, lower ability to infiltrate the tumor. Then if we follow through this insight to the different components of 11 12 the model, the variables of the model, you will see a very consistent picture. Responders, quick responders with high 13 ability to infiltrate the tumor also have-I would note the 14 15 second term here on the top-also have the larger number of dendritic cells that are activated. The same for the overall 16 of the effector cells in view of the response, as 17 larger values for tumor effector cells in 18 well as 19 the environment and . So overall, the systemic 20 consequences are the biological differences between 21 responders and nonresponders which should make sense. And to 22 follow through on this element, we also simulated the 23 dynamics of all of these components with two different types 24 mice, ones with a low ability to infiltrate the of 25 T-cells-these are the red rows-and mice with high ability to 26 infiltrate the environment of T-cells. And if you look in 27 the rightmost column, the top _____ that is the tumor 28 size mice with high ability to infiltrate and suppress the tumor very well to 0, and really we 29 30 get this sort of dynamic insight as to how this happens by 31 looking at the dendritic cells overtime. They reach their 32 maximum sooner than mice that do not respond, stay there for 33 a little bit, as well as here in the fourth panel from the 34 top, the T-cell infiltration happens to a great extent in 35 this mice responders.

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36 And the real purpose of this model was to make predictions, 37 and so what you see here are heat maps of efficacy response 38 in mice treated with radiation plus anti-PDL1. The heat map on the left corresponds to radiation treatment started on day 39 40 5 since inoculation of mice and the panel on the right is day 41 12. These are older which are more established tumors on the 42 right. The color corresponds to the degree of 43 The moss green is 100%. The red is 0, no response: 44 response. The rows in this graph correspond to the dose of 45 radiation from 0 to 10 gray at the top, and the

Page | 21

columns correspond to the day when anti-PDL1 treatment was 1 2 started, again, relative to the evacuation of the tumors. 3 And so the pattern that you see here is that response with a 4 combination is most pronounced when radiation and anti-PDL1 5 are given close together. So if you focus on the third row 6 from bottom, you see that this green higher indication 7 response where PDL1 was given 3, 5, 7 days with 5 days of 8 radiation. But then it starts to kind of thin out when PDL1 9 was given much later with day 12 and 19, and this is more 10 dramatic on the right where the tumors are more established. So timing is key and the modelling is for the purpose of 11 12 identifying the sweet spot for scheduling and dosing of the 13 different combinations or in this case radiation and PDL1. Well, the other thing that you see is that older tumors, more 14 15 established tumors in the graph on the right day 12 since 16 evacuation. They have a more established immunosuppressive 17 environment. The model captures that and that is reflected 18 in general in the fact that these treatments are not able to 19 induce a good response except with some very specific 20 combinations here. The maximum dose of radiation was 21 very close to that.

22 So this diagram shows you - this is a diagram of the more 23 immune cycle model of the mouse that we general are 24 developing. So from the on the model I just told 25 you about, it includes more components, more granularity in 26 the immune components. For example, it does include a myeloid-derived suppressor cells, includes deregulatory cells 27 28 exclusively. And the purpose really was to be able to start predicting the effect of many different combinations 29 of 30 targeted treatments that we can think of. So in red you see 31 all these different targets that have been considered in drug cycle 32 development, impacting these different immune 33 directions, and that is what we are starting to do here.

34 So what I will show you next is a prediction from this more 35 general model for some of these combinations. But before 36 that, I am sorry I forgot to say that the one key component 37 is here again the pharmacokinetic models of the drugs and the 38 reason is because you want to be able to make predictions 39 specifically about dosing stages, sequencing of the 40 components of the combinations. That is a very important 41 issue.

42So this table shows you predictions with the version of the43more general model I showed you for two different types of44murine tumors, so two rows in the table. The first row

1 both have developed immunosuppressive environment. 2 So the tumors in the top row are distinguished by the fact 3 that these myeloid suppressor cells, and 4 that the combination of anti-PDL1 and CXCR2 is 5 predicted to be most efficacious compared to other 6 combinations, again, using the same metric that we have used 7 for the radiation tumor model. And that in some way is so 8 surprising because CXCR2 is infiltration of 9 myeloid-derived suppressor cells. The second type of tumor 10 cells is distinguished by having a large number of deregulatory cells in the environment, and springing through 11 12 the combinations with the model, we see that the combination 13 of anti-PDL1 and CTLA-4 is predicted to have the most effect. 14 Again, this can be understood given the role of CTLA-4 in the 15 infiltration of deregulatory cells. We summarize by saying that the first thing that we did 16

17 is-what I have told you about-we built this QSP model, a 18 quantitative systems for oncology model that predicts the 19 effects of dosing and sequencing in mice. The 20 therapies at first radiation but now we are expanding to a 21 large amount of targets, and the important thing about this 22 first attempt to use this QSP model is that we used radiation 23 and the anti-PDL1 just to make ropes, to move the system in 24 different ways. And if you think of radiation actually,

25 framework of hammering the system in different 26 ways and see what moves that allowed us to understand the key interactions in cycle and have a reasonable concise model 27 28 that is predictive. Again, one insight here is that we would 29 translate this model to human and then use it in a joint 30 modeling framework to predict progression free survival 31 effect and overall survival effect for the different 32 combinations, and thereby, we will be able to prioritize very 33 early preclinical efforts on all combinations in terms of 34 their likely effect in tumors.

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Thank you.

36 [APPLAUSE]

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2 Audience: My question is how do you model the effect of radiation, 3 which parameters of the model, which _____?

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Aksenov: Right, right. So the radiation effect was modeled through introduction of double-strand breaks in the DNA and then those were impacting the death rate of the tumor cells.
So the model was breakthrough like I said in terms of logistic growth, exponential death rates, but the death rate was enhanced by the radiation.

- 10 Audience: Do you recommend the QSP model that you had built could be 11 used to differentiate nonresponders from responders and 12 applied to predicting ?
- Aksenov: Yeah, absolutely. So, in fact, we tried this as an example 13 14 in what I talked about, so the beauty of systems for oncology 15 model is that it represents the key systems parameters that 16 presumably mapped to the differences between individuals mice 17 or humans, and so in principle, you would build a population a systems population model and then look at the 18 model, 19 distributions of — how distributions of various population parameters is different between 20 and try to 21 understand what distinguishes responders to nonresponders.
- 22 Jin: Are there any more questions? Please introduce yourself with 23 name and affiliation.
- 24Audience: Okay. I am
previous question. So in terms of understanding the effect25previous question. So in terms of understanding the effect26of dose and sequencing of radiation followed by PDL1, what27kind of input data was used as leading to in order to28build the effect of dosing regimen? You perhaps need some29input data to sort of quantify it
- 30 Aksenov: Right. So the data that we used to develop this model 31 consisted of responses of mice to different regimens, to 32 different combinations of PDL1 and radiation. So radiation 33 and PDL1 were given at different times, at different 34 sequences. First radiation and then PDL1 together and then 35 mice got also PDL1 right after the radiation. So we actually moved the system dynamically in different ways to see how 36 37 radiation and PDL1 affected the system.
- 38 Brown: Anthony Brown from Merck. So in terms of mouse model, we 39 know that there are anti-PDL1 resistant mouse models as well. 40 Have you looked out which components are actually functional 41 in those mechanisms as to what makes it resistant?

Aksenov: Right. But not at this time. So, at this time, we modeled 1 2 mice that have a functional _____ component. If there are no more questions, please join me by thanking 3 Jin: 4 Sergey. 5 [APPLAUSE] 6 Our next speaker is Dr. Armin Sepp. Dr. Sepp is a scientific 7 leader and associate fellow in System Modeling and 8 Translational Biology Division at GlaxoSmithKline. 9 Dr. Sepp: Good morning everyone. Many thanks to Dr. Jin. What I present today is also the work we have carried out at GSK. 10 To start with, when people speak about bispecific antibodies 11 and we have been following on the _____ what happened to 12 an antibody when it sees that target cell, and _____ in 13 brief and what should work about an experimental 14 experience we have seen at GSK. So targeting many different 15 targets at the same time is getting more and more fruitful 16 both in and elsewhere. Target selection is not 17 18 the topic of this talk, but that is obviously the key term. 19 Just a few years ago, there was a nice summary made as to the 20 state of bispecific antibodies that has been developed mostly 21 in Oncology and mostly targeting antigens expressed in 22 different cells but very often also expressed on the surface 23 of the same cell. So we graphed the target we are using here and all the limits with simulation to try to rate 24 25 evaluated in different approaches available at that time. So 26 in a number of different bispecific antibody formats which 27 had been proposed during that time is just demonstrated by 28 adding on additional domains to existing antibody, chopping 29 it down is a little bit as possible and many of 30 those have been obviously evaluated through _____ please.

31 Audience: _____.

32 . Often the question is do we need a bispecific Sepp: 33 antibody or we will have just a combination of tumor-specific 34 antibodies to work just as well and that is what we are 35 trying to answer here because we cannot think to replace this 36 with plus the time and effort and so on. So we 37 will be using experimental data. We will be using 38 mechanistic mathematical modeling. We will be using 39 parameters with and other tools to make meaningful 40 predictions about the system, how it might behave in slightly 41 different conditions. So in the first instance, it is fairly 42 straightforward. If we have both targets in solution, then

from the mechanism point of view, it really does not make any difference if we have bispecific antibody or a combination of tumor-specifics. If one of the targets becomes at this point we can argue that a combination dose with two different antibodies might be more efficacious. That is the one therapy that the surface expressed target could connect it from directly the effect. But the most interesting situation on this space where we have the antibody expressed on the surface of the same cell, and if you look at the literature, you can see quite a few different approaches taken. We have some papers taking the approach that we have taken that targets are all well expressed in solution with the insoluble. We have what you see models when they are postulated to be immovable on cell surface, and this presentation actually will be about the approach which takes into account the lateral mobility of targets in cell surface. Right.

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Well, every model starts from good experimental data and this 18 19 model was introducing excerpt computations from Mazor and 20 _from ____. This was two years ago. They 21 looked at bispecific antibody which was monovalent for either 22 antigen, and the target cell either expressed both CD4 and 23 CD70 or just CD4 or just CD70. We assumed that antibody is 24 in solution stock that targets human trait and symptoms that 25 are on the cell surface. At the end of the day, what we see 26 is that antibody cross-links targets on the cell surface, and 27 in the experimental, it was shown that every target gets 28 cross-linked no matter what consequence they are basically in, 29 and so on and so forth. But trimolecular reactions do not 30 happen in reality, so they are sequentials. So at first, the 31 antibody binds with one or the other arm and that is called 32 cross-linking on cell surface, and cross-linking is very 33 rapid. Here, we are actually modelling this using the 34 Brownian dynamic simulation. We have the cell surface with just a small cube on top of it. 35 It is on the surface 36 . It rarely gets around. When the antibody hits 37 and binds the target, it turns into a big and both 38 arms are cross-linked in terms where each step is a few 39 microseconds along, but this can be more than that. We can 40 figure out what happens over a period of time, and just as a 41 surface infusion can be quite a bit rapid in just about a 42 second, a typical surface protein travels above 200 mm. Ιf 43 it was going in a straight bind, it can circumnavigate, 44 descending about 2 minutes. That is plenty of time for the 45 to get cross-linked. And in the model, over a 46 time from the simulated experiment, period of the

concentration of three targets is exponentially reduced. There is no accumulation of monovalent-attached species. What we do see is exponentially increased drug cross-linked species and that was in perfect fit with the experimental data for double-positive cells or single-positive cells, and we have high affinity for CD4 for single-positive cells. With the CD70, the affinity were much better.

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went on to optimize the system. They really Mazor wanted to have an antibody which would bind just dualpositive cells so that _____ have gone unchanged and then started to compromise the affinity of the CD4 arm, and eventually they raised the situation where there was hardly any binding to single-positive cells, but there was an almost unchanged binding to double-positive cells. We can capture this also in the in silico, and as I have mentioned, there was no caretaking involved. All the in different and experimental measurements of their mistake. So out of curiosity, in planning experimental with , and what we can see here that the end-point reached about 1 hour is actually kinetically limited. There is no equilibrium at very low antibody concentrations, and there is no way that one can actually stand an incubation time much longer than 1 hour that was used, but we can do it easily in silico, and we would actually see increased binding at very low concentration if we put in cells, . And from that, we can actually figure out what is the so-called approach. It turns out to be somewhere around 1000 to 10,000 fold when both arms of the antibody did reach the target at the same time, and it rate constant manifested itself through reduced from the ternary complex. Even if one of the arms becomes detached to re-bond _____, the ternary complex just does not fall apart from practical criticism. In real life, it is more likely it would be generalized . Looking at it with more thought, we can understand a little better how antibody might interact with cells of these antigens in general, and we think about the conventional antibody monospecific. It has known anti-self-symmetry undertaking Fab rotation which means the fragment sides were unable to opposite directions. If we could turn it on the target in the same orientation, the antibody needs to be stronger for a time so that we compromise the avidity over . While in the case of bispecific against a different type _____ on the same molecule, we get a biparatopic kind of antibody that compromise the as well. Anyway that could be likewise with dimerizing

targets on the cell _____. It is unlikely an antibody 1 2 will be able to engage in a dose on the same dimer. Its 3 problem might be it would actually cross-link with different 4 dimers, and I very much hope that one day we will be able to 5 check out _____ cell that is a resistant cell ___ 6 microscopic cell. It really does not matter. It does not need to be an 7 8 antibody which cross-links the cell surface 9 antigen in a sense that if there are any tumor that is 10 screened _____ on the cell surface can bind with the antibody as was shown experimentally and that can 11 be laid out _____ binding. _____ these two targets, 12 we can think of an EGF and INFy . In the former 13 point of view, it is the same approach as we just saw with 14 15 bispecific antibody. It really does not matter if that on the surface of different cells and 16 17 work in the same cellular immunology TCR-pMHC complex, and there are attached three-dimensional kinetics. 18 19 the work is two-dimensional, and two-dimensional kinetics 20 cannot be deduced directly from being around the different work. And obviously we have bispecific antibodies 21 22 which can cross-link, again, in all points of the CD5 23 framework and of how to express that mechanistic requirement 24 _____ expect this to _____. 25 Finally, with all those _____ is taken from the mouse 26 plan. Across the species, we can put a target and compartment modeled with what is the penetration 27 28 rate of the antibody? How much is the target ? 29 How much documented investigation we might encounter? And 30 that is our GSK experience inhouse with mAb-dAb where you have a collision antibody with domain antibody of 31 32 the heavy chain, and we have seen a significant enhancement 33 trait in the binding potency on the antibody side, but it is somewhat unpredictable. Sometimes it is there; sometimes it 34 35 is not. If it is there, it can be actually fantastic. And we have also learned that we have made constant 36 37 benefits hugely the . PK-wise, again, there is a 38 degree of concern that we have that the leads which have 39 antibody-like PK which are compromised PK 40 and it is not necessary — we have not really like managed the _____ that was the image depicted. It still 41 did not really _____ correct. It is not there. 42 The 43 . It very much aligns with our operation from 44 in that there is a similar constant and . 45 Such proteins tend to accumulate _____.

Well, just to sum it up, most of the work was done in 1 2 collaboration with GSK and also with the workshop in silico. For the , we have not - we will publish 3 4 everything later including the . The bottom line is that bispecific antibody can be treated as cell specific. 5 6 It can be very useful. It helps antibody , and in 7 models to device, it can at least guide us to optimize things 8 regarding target expression on double-positive cells and 9 single-positive cells. So the challenge is that in 10 experimental protein engineering, linkers, that really 11 everything actually works on paper, but when it comes to real life, the expression of PK does not _____ surprises. 12 13 Well, more than anything, looking into the results how to understand scenario in terms of let's say what is 14 15 known best affinities for each other and so on and so forth, I could ask _____ prove it. If they approve _ 16 17 parameters , some for small molecules, 18 but antibody would be slightly different, so that is a reason for Genentech _____ 19

20 21 And that's it. _____ colleagues from GSK and academics from _____.

22 [APPLAUSE]

23 Jin: Are there any questions from the audience? I will ask a 24 question. Do you guys have any experience for the bispecific 25 antibodies in the PBPK space, especially for immuno-oncology service, especially when you have bispecific antibody linking 26 27 with one targeting new cell, one targeting on the tumor cell, 28 trying to link them together in the PBPK space that hopefully 29 will help the migration and concentration of the immune cells 30 into the tumor? Do you guys have experience with using any approach capturing that aspect? 31

_____ in the PBPK space, Well, when you look at the __ 32 Sepp: there is to look at _____ that might make 33 such a similar kind of situation where we have target cells 34 35 expressing, let us say PDL1 and we have lymphocyte cell expressing something different and how might 36 37 behave, and one can situations where either one can easily eat up everything there is, and because of the 38 39 large number of cells there are that , and let's 40 it can define what kind of systemic say, 41 concentrations would need to be maintained in circulation, 42 for example, to have any chance to improve their chances thereof for _____ engagement in the PBPK _____ we 43 need _____. Regarding T-cell infiltration, infiltration 44

_____ so the antibody can promote, perhaps 1 probably 2 stabilize cell complex towards at least a sense of where we 3 are making tumor and will they actually T-cells towards tumor 4 If there are no more questions, please join me in thanking 5 Jin: 6 the second speaker. 7 [APPLAUSE] 8 9 Jin: Our last speaker for is Dr. Dean Bottino. Dr. Bottino is a senior scientific director in quantitative 10 clinical pharmacology fact data. 11 12 13 Dr. Bottino: Thank you Jin and thank you to the other organizers for inviting me to today's presentation. I'm going to stop 14 15 . Okay, I just wanted to thank the other people who worked on this very collaborative effort ____ 16 pharmaceuticals _____ a little bit _____ techniques 17 and I'm going to show you _____ original concept around 18 this was built _____. So, the current paradigm of at 19 20 least the way I see it combination that sometimes 21 they just _____. If the X axis here is drug A mg or 22 drug A per day, the Y axis is mg for drug B per day and this 23 is just a drawing and you'll see the real data later. You 24 might escalate drug A where the pipe charts here represent the percent of the patients that have dose-limiting toxicity 25 26 in red or do not in green and maximum tolerated 27 dose or MTD of 8 mg for the first drug, drug A and then drug 28 B study might escalate and get a maximum tolerate 29 dose of 800 mg and then _____ one dose from MTD and 30 started titrating in for example drug A added to a lower dose 31 of drug B and and for your recommended drug A you have another MTD. And you have a question which 32 33 MTD do you go forward for your recommended phase 2 dose. 34 Well, the bad news is that not every clinical team 35 realize this at first glance but when you find it in this 36 axis of this, you can see the maximum tolerated dose for a 37 combination is actually many doses of the curve 38 and those X and Y phase here, so the question then becomes 39 along this curve, what is the recommended phase 2 dose or 40 RP2D and we proposed that the recommended phase 2 dose is a 41 dose that gave you the maximum antitumor effect along this 42 constraint curve. In this case, it would be that 110% growth 43 rate inhibition would be around this dose combination here

would be the recommended phase 2 dose. The maximum growth 1 2 rate inhibition predicted along this curve would be either 3 done from clinical observations if you have the maximum 4 genius phase 1 population which you often do in an 5 phase 1 study or you can use frequent exposures 6 from the frequent clinical species to the clinical situation 7 and I'll show you with justification for that in the next 8 slide. So it turns out for this set of compound study that 9 most models do predict the human tumor response rates when 10 you match the free-fraction exposures to what you can so you have to simulate down months to 11 12 the exposures that you would have attain if they have been 13 constrained by clinical toxicity. This is something that you 14 can only do once. You have the clinical toxicity data but it 15 is predicted once you do that. As you can see here, if you 16 don't match the exposures and then you just the 17 tumor growth inhibition at the maximum tolerated dose for the mice then you correlation with clinical response 18 19 rate. Over here, and this is probably internal 20 growth inhibition at the matching clinical exposure, 21 attainable clinical exposure has a nice correlation to the overall response rate in the clinic. So from this point on 22 23 the presentation, we can use exposures to try both efficacy 24 and toxicity and we are going to eventually at the end of the 25 we can convert this recommend phase 2 exposure 26 back to combination dose _____. If you had noticed this is just a 2D constrained optimization problem. 27 If you remember from those sort of things, the 28 29 branch multipliers and all that stuff. Basically, what you 30 have is an efficacy service and it is a function with the 31 concentration of drugs X and Y and then you have a toxicity 32 constraint curve here in that X, Y space and then you ask you 33 want to find the point and the probable combination region 34 that maximizes the efficacy service location and for 35 I would say most pharmacologically realistic 36 efficacy services and toxicity curve, the maximum 37 that is somewhere around this constraint curve. So, like 38 this specific case study, this is TAK-117/TAK-228 or 39 sometimes we called the paper combination because it combines 40 the inhibitor which you'll see in this 41 presentation. I used the old names, MLN1117 interchangeably 42 for TAK-117 or TAK-228 which also interchangeably called MLN0128. Anyway, MLN1117 is a PIKTOR and then 43 44 MLN0128 is a TORC1/TORC2 inhibitor and that here is that you 45 can get a compensatory reactivation _____ that can reactivate the cancer cells and so _____ MLN0128 46

that, so that's the biological rationale for the 1 2 combination. _____ from magazines but it helps suppress reactivation last about two years. So the first 3 4 step in the technical part once we get the data is to start with _____ the tumor growth inhibition data reverting 5 6 exposures to free-fraction human exposures. So 7 basically what we do is we just . We get growth 8 rate for control, growth rate for treated mice and then we 9 use the transformation, we call growth rate inhibition or GRI 10 which is just the transformation over here and then basically just to calibrate your intuition on what GRI means. GRI of 0 11 12 means you're doing no better than control. GRI above 200 13 means you're slowing down the tumor but not causing 14 regression. GRI of 100 corresponds to tumor spaces and 15 greater than 100% GRI is tumor regression. If you remember 16 from the Harvey Wong's slide before, it takes about 60% GRI 17 approximately to cause any kind of response rate . 18 The next step is we do this for every single dose combination 19 that we try in the mouse free-fraction exposure in 20 the mouse and what we get is a grade of about 910 points in 21 the points for GRI as the function of 117 monotherapy, as a 22 function of 128 monotherapy, and then the combination space 23 . Once we have those points, we use a simple 24 . You can pick whatever models you want just fit 25 the monotherapy. So, GRI of drug A on 117 turns out to be 26 linear function and GRI of drug B which is 128 is a 27 saturating function of concentration. So the next step is to 28 use this equation here. Basically, the percent growth 29 is taking to be the growth rate inhabitation due 30 to each of the two growths added together plus the 31 the two monotherapy, there's only one additional 32 that I need to estimate to get the surface which is this 33 and basically what this shows is that there's a 34 slight synergy between 117 and type 228 which is one of the 35 combination into the clinic and so the next step 36 will be to try to determine its maximum tolerated exposure 37 curve. The first step is to figure out what is the PK driver 38 of toxicity and so we considered maximum concentration 39 and was a good predictor for 228 TAK-117 _____ better predicted for toxicity _____ as 40 41 the toxicity predictor. So these are toxicity, red or patients with those progression. So we use 42 43 concentration from this point forward. Then the 44 next step is to look at the combination. So this is once we have the phase 1 data _____ represents the average 45 46 exposure for type 228 and type 117 for each patient in the

combination study. These ones along the axis are of course 1 2 all the monotherapy patients from the phase 1 studies in the 3 228 and 117 respectively and again green is the patients dose having toxicity _____ toxicity. Red are 4 patients who do. So then two-dimensional logistic 5 6 regression on this data. So this is the equation here. It 7 basically just have ______ slow term for S, slow term for Y and then an interaction _____ concentrations of S and 8 9 Y multiplied together and you get this brown surface where 10 lighter colors are higher probabilities of having toxicity then the maximum tolerated dose is defined to be 11 12 just the lever curve of this probability surface where 13 probability _____ toxicities are 25% which is more or less what a standard _____. When we the MTE 14 15 of the maximum tolerated exposure and just for reference, 16 this is what ______ is the straight line here. So you 17 can see that the maximum tolerated exposure curve, like the 18 efficacy curve synergy and both toxicity and 19 efficacy. So going back to this theoretical drawing first. 20 The question you can think of it is if you're _____ here 21 where an X is longitude and Y is latitude then as you walk 22 along this fence, the question is this fence was on the map and latitude and longitude ______ where do you 23 24 reach your highest point and what latitude and longitude you reach your highest point as _____ phase 2 dose 25 combination. So to animate this, you have-you're moving 26 27 along and what we do is we basically cut the surface along 28 this edge here, well we cut it vertically on this edge here 29 and you get a profile of efficacy as a function-as you _____ basically and moving _____ you recommend 30 phase 2 dose rather than _____ doses that give you this 31 32 optimum efficacy value. So we tried this with our drugs, X 33 and Y, TAK-117 and TAK-228 and this is just a reminder the we used for this efficacy surface and then we had 34 35 to change the color coding to red for the exposure curve so that you could see them on the spot but the maximum 36 37 tolerated exposure from mouse to humans and what that means is when we slice the surface from the side, it 38 39 looks this. Unfortunately, instead of going 40 upward, what if there were combination, this curve 41 goes downward which means that once you take toxicity into 42 consideration, you are actually better off with 43 all TAK-117 and no TAK-228 is you're better off with 44 monotherapy. We try this with all the different mouse models that were tested and basically one product _____. So we 45 46 are going to revisit these predictions once we have-so this

```
was done as a proof-as a _____ of the methodology by
1
2
             using growth clinical data but the move forward
3
             while we are working on this and so we do have the
4
             opportunity to test these predictions once the phase 2
5
                      for this combination. . It's very
6
             interesting.
7
    [Laughs]
             This is like a memo where _____.
8
    Bottino:
9
    [Laughs]
10
11
    Bottino:
             So in terms of the general methodology if we propose this
12
             in the context of a simple problem and phase 1
13
             study with combination, we might want to take this
14
                     efficacy surface and goes straight up
15
             if we don't want to escalate over drugs at the same time or
16
             some other sufficient conservative. The idea is to try to
17
             get this to the _____ efficacy and _____ so you go
18
             up and then actually cohort you could try to
19
             refund with uncertainty bands or exposure curve
             and then ultimately _____ recommended phase 2 dose or
20
             expansion for phase 2 _____. To summarize, ______ in those aspects.
21
22
             So recommended phase 2 dose finding _____ efficacy
23
24
             optimization problem and we have successfully
                                                                 and
25
             the model in this case PIKTOR combination would
26
             not do as well as the monotherapy once you dosing.
27
             We recommend further validation on another combinations. We
28
                       . So we're trying to find other ways to
             try to
29
             validate some of the other combinations. Finally, in
30
             addition to all the authors, co-authors
                                                    , thank
                       and Brian Cooper for other contributions
31
             you.
32
             that you made on these related projects. Thank you for your
33
             time.
34
    [Applause]
35
    Bottino: Come in.
    Audience: Good morning. This is . Nice presentation. So
36
              my question as I remember on the beginning of the
37
38
              presentation, this is a ?
39
    Bottino:
              Yes.
40
    Audience: Okay. So what kind of that has been observed in
41
              the clinic and how do you use this information because
                 any correlation ?
42
43
    Bottino:
                       I don't remember the exact nature of the safety
              events. They were _____ one of the other drug and I
44
              don't remember. Anyway, if you look at the
45
```

1 2 3 4		which ones were drivers. We did test the events and for the there was no predicted volume Cmax with the toxicity but for the monotherapy 117 of Cmax for the toxicity.
5 6 7	Audience:	So, considering the to see how those downstream markers of the PK matrix and how to use that with the model?
8 9 10 11	Bottino:	Yeah, what we did was efficacy surface with the and still with the clinical toxicity constrain, there was no anterior sweet spot or pharmacodynamic effect. The biggest pharmacodynamic effect would be
12	Audience:	·
13	Bottino:	Thanks.
14	Audience:	Can you show the slide which shows that
15	Bottino:	This one?
16 17	Audience:	I wonder if you look like—it looks like most of the combination but it looks like
18		
19 20 21 22 23 24 25 26 27	Bottino:	Yeah. So if we cut the surface here. That's a good question. And there's something-if you notice-and then I'll explain what this lighter was as the 5% and you might ask where's the 95%. The 95% could be calculated because they're just weren't enough samples on the outside and that's because of the nature of how we do those Once we have the tolerability issue exploring in the highest dose so there's- here's a sampling
28 29 30	:	horizontal and vertical line kind of region which is still There are no samples on the diagonal region
31	Bottino:	·
32	Audience:	·
33 34 35 36 37 38 39	Bottino:	Yeah, that's true. There's relatively little support there and you're touching on actually of the darker secrets of MTD finding to begin with and the way we sample, and the way we escalate. If you go back actually a couple of slides here. If you look at even for the monotherapy or the exposure of TAK-117 giving you 25% probability. So we really, in general, across the board

1 _____ patients if you _____. If you believe that 2 there's even one dose that works for everybody. We're just 3 not sampling enough to really have any confidence in maximum tolerated dose. We did find that 4 maximum tolerated dose and that's . 5 6 thanks for your talking. . I would : 7 suggest that the one that-that the key problem here is you 8 try to solve the . shifting to the next paradigm which I told 9 10 . Are there any more questions? I have a question. 11 Jin: the common challenge of limited sample size and limited dose has _____. One 12 common challenge we have faced _____ we work in 13 similar phase on combinations and optimizing 14 phase 2 dose. It's actually more than 15 tolerability _____ within the short-term tolerability 16 is basically more limiting and more 17 18 concerning in longterm clinical development actually not exist from the . So you guys have 19 20 any experience in that phase and how do you ? 21 Bottino: We do. We do. Not in this particular model effort, but in 22 this particular combination developing toxicities to make _____ phase 2 and yeah, there's 23 24 this unfortunate convention of only _____ and so even 25 if you have longer term _____ phase 1 data, they are not actually called first cycle and we have to 26 27 events if we're going to use this simple 28 . The other approach that is not shown here, we have ways measuring all the grades of toxicity model of 29 30 toxicity. It's a method. It's not regression _____ pharmacologically inspired but anyway 31 you could have ______ toxicity and then you would have 32 based on certain grades that you don't want to 33 34 see _____. It hasn't been brought in to this 35 framework. It has been brought into the toxicity framework. We did some work combining toxicity measurement 36 37

38 PANEL DISCUSSION

39Jin:Thank you. Now I will invite all the _____. We also40welcome additional panelist, Dr. Haleh Saber. Dr. Saber is41deputy director for division of hematology, oncology and42toxicology as part of office of hematology and oncology at43FDA.

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1	Jin:	So now, floor is open for more general questions
2		especially for using MITD in the non-clinic
3	Audience:	Actually, I have a question for Dr
4	Jin:	Get closer to the microphone.
5 6 7	_:	Yeah. Sure. Can you hear me now? Dr. Aksenov. Very interesting presentation. The general focused on the mouse size?
8	Aksenov:	·
9	_:	·
10	Aksenov:	Use the microphone.
11	Jin:	Closer to the microphone.
12	Audience:	
13	Jin:	You just need to get closer.
14 15 16	_:	Yes. So I think affecting tumor growth, right? You always see a change in growth size. You don't see a change I don't believe that
17 18 19 20 21 22 23 24 25 26 27 28	:	This is This is more general questions. So there's a couple of presentation this morning with a different tumor models in animals. So my questions to the panel is whoever want to answer the question is, moving to the phase 1, we used the data from what is the exposure either 60% tumor regressions or 90% tumor regressions. So, if we have to predict the exposure based on the, where we should focus on using the tumor model or now we are talking immunotherapy or, how we use versus all those modeling when we move to the phase 1 trial? This is a general question so anybody want to answer.
29 30 31 32 33 34 35 36 37 38 39	Dr. Saber:	I would like to give a long answer to that, just go back to history starting with small molecules where actually animals a good job predicting toxicities in humans and so human dose. So in terms of small molecules, we do the toxicology in the animals on toxicities and then the non-clinical animal adults are used with a disease used for and activity as a very good place to start to understand activity, etc. However, there are limitations always in animal models and just giving you some examples if—this is xenograft model and you're looking at

antitumor activity and you're proposing to give a drug 1 2 _____ to the lymph nodes and you're giving that in the 3 subcu efficacy in humans. To me, activity is 4 not the same as efficacy. Efficacy to me is a meaning to have a clinical benefit. So animals are very 5 6 good place to know the activities, schedule , 7 etc., but it's not efficacy in humans. If you 8 have an antifolic-your drug is an antifolic, how 9 is not the same as in humans. If you have a growth 10 esterases, there's a lot of esterases in a growth so that does not equal to that in humans. So, I 11 12 guess that's a place to have it educated and understanding 13 of activity in humans and then go to humans, study that in 14 humans, and then use the animals to go back for a more 15 tailored question. If you're going to a phase 1 and you see that some _____ patients are responding 16 17 to go back to your abnormal models and with specific 18 questions you have. So it would be an interaction going 19 into the clinic and then back into the animal. That is the 20 best scenario. Now, going to immunotherapy. That is a 21 more complicated challenge in area. If you think about 22 antibodies, inhibitors and simulators where most 23 of this actually animals tolerating the dose very well. So, 24 we don't have actually a good place for selecting the start 25 dose in humans and then you go into your animal models, you 26 have to think about the differences does it bind 27 to targets in the animals. Even if you use a tumor from 28 the humans or patients, you're still dealing with 29 differences in the FC domain and binding to the FC receptor 30 and differences in IGG isotypes. An IGG1 is not the same as IGG1 ______ surrogate in the animals and if 31 32 you have a surrogate in the animals, candidate. 33 You need to characterize it. So these are all these complications. Fortunately, _____ is moving towards 34 35 having better models for these types of clinical candidates 36 and I encourage you to attend our workshop in March 9th 37 because we want to assess these models that are being 38 developed. We attended a workshop in September with the 39 NCI and many academic centers now have very nice or seems 40 to be very nice candidates. industry 41 together. If we can start with the CD models and throw it 42 some safety end points on my markers of activity that is of interest to the regulators and see if uses it. 43 44 So, the _____ workshop will be March 9th. _____. Audience: Thank you for the long explanation. So, model 45 to go to the phase 1. Now, looking to your phase 1 data, 46

1 2		clinical data and to I would say we optimize the is that correct?
3 4 5 6 7 8 9	Saber:	Yes. Do a good job starting with your non-clinical, but There are-at some point, you would probably say, okay I know the dose, I move it to the clinic, but if there are questions to be answered to the lab and study with a more questions.
10	Audience:	Thanks.
11 12 13 14 15 16 17 18 19 20 21 22 23	Bottino:	, I think we need to start thinking about doing a way with the phase 1 is for MTD, phase 2 is for efficacy So, ultimately, we wanted to continually learn about both as but right now are being used in phase 1 is answering the question how but still using the same number of patients and the question is how before investing in the next level of development and that's a very different question but you might be to properly define the dosing strategy but at the same time, you should be learning about efficacy as well. So this idea of phase 1 and phase 2 when you have more patients you could be testing different doses but
24 25 26	Audience:	University. I have a question for When you are presenting your How much of that was because I'm sure you can sort that out.
27 28 29 30	Bottino:	Yeah, yeah efficacy was ultimately less than just toxicity so then when move along so you get an effective loss of efficacy just because you can't get to the doses you need to
31	:	So for sure, there was
32	Bottino:	toxicity. Yeah.
33 34 35 36 37	_:	single mouse you can find the synergy but there has been when you get the benefit from combining two doses is because maybe some patients will respond to drug A and some will respond to drug B you get the response
38 39 40	Bottino:	Yeah Yes So the findings of the model that is shown is continued on the fact that patient tumors are like seen in rats when really they could be

mixtures of multiple tumors. In this case you might get 1 2 benefit from the combination. It would seem 3 model and I'm trying to remember the name of the presenter 4 who showed exactly that a lot of clinical 5 studies that in all synergy can actually be explained 6 _____ patients. 7 8 : Adam . Adam _____. Right, right. Yeah, _____. But 9 Bottino: ultimately I believe, the finding ______ started 10 wondering whether we were doing the wrong thing by chasing 11 down synergy exactly for that reason. I always 12 13 proof of that. ____ paradigm. What is the MTD to how confident do I 14 _: 15 . As a model and that's the concept, need to 16 that's intriguing to me and that fits in with 17 about deviating from those and seeking towards more individualized therapy so we can actually have optimal 18 19 therapies at the time of approval ______ studies. paired with clinicians and regulatory scientists 20 21 who might say, oh, we can do it just by using the MTD 22 approach where we can actually be answering in 23 our clinical studies. 24 Bottino: That's a nice question. So my first answer will be 25 at the right time. We have to start 26 This is our confidence region around the declared MTD. 27 Let's call probability of phase 3 success. If 28 you starting as early as possible and this is 29 really hard because phase 1 is _____, but if it could 30 be done, you of this is a spread of possible 31 phase 3 outcomes and it goes from _____ 1.4 because we 32 only have 17 patients so far, but as we find-we'll keep 33 looking at this dashboard to see if our certainty increases. 34 That's _____ right now. And it would seem that we would need to have more advanced 35 __: 36 models to put into that dashboard so that we can have 37 in relationship of the changes we're seeing 38 in patient and how that relates to the ultimate 39 outcome that _____. 40 I think someday _____ and things like that. If there Bottino: 41 were some would be relevant in driving tumor size changes 42 and that if you have a strong dedication, that dedication

1 2 3 4 5 6 7 8 9 10 11 12 13	: : Bottino:	<pre>that you believe is and overall survival or benefit, then even with those first two patients, you can start making those projections Okay. I will answer that it's a financial-type modeling on how much delay can you tolerate in a program if it means 2% increase in probability and it turns out to be greater than 0 and I think the in phase 3 but a few months in phase 2 or 1 in terms of value can be very much if you increase the probability came up with this</pre>
14	T i m u	
15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34	Jin: Audience:	Maybe a last question from the audience? Can you hear me? Okay. Thank you. My name is we do provide companies. My question is similar to some of the previous questions and may need to I think for a fixed combination even from the small molecules fixed suggesting one single fix. So again if some patients, if we need to or some other patients we need to How in your early research and you know phase 1 given clinical work through simulation modeling. You can generate sufficient data and insight to support the flexibility to get to phase 3 or If you have only one fix, you need to be very careful with the patients, but if you have, you know, combo versus combo, you maybe targeting two, somehow, different segment patients. That means a lot, right? So I think this is If you have a combo submission another type of the combo by differently component A versus component B. Thank you.
35 36 37 38 39 40 41 42 43	Bottino:	Alright. Thank you in terms of predicting one-time baseline factors are predictive of response to that and if you you can start considering the effects of combinations and basically what baseline are predicted of what kind of combination of particular patient needs and then look it up in a table or something and say whether or not the patient dose combination for which dose combination is best for the

1 2 3 4 5		patient. I think it could be done right and I do not know patient's data based on simulations of which those combinations are best and then of whether or not a patient responds to modified data
6	:	for visualization.
7 8 9	Bottino:	That's another on baseline when really you should be refining your predictions based on initial response
10	:	·
11 12 13 14 15 16 17 18 19 20 21 22 23 24	Saber:	We don't have a requirement for pharmacology-what type of pharmacology studies you need to do. You just tailor it based on what you want to show, to prove. So if you believe that those pharmacology combination, pharmacology studies will help you to convince our physicians regarding certain schedule or adjusting the doses up and down , sure, go ahead. That's to decide. But again I want to mention that, when it comes to biologics, combo studies are very tricky even if they have monotherapy, it's not that easy. Sometimes the only species is the and you're talking about modeling in the rodent species so that means you will have surrogate probably in the rodent and how of the clinical candidate is that. Thank you.
25 26 27 28 29 30 31 32 33	Jin:	For the rest of 10 minutes, I would like to ask a general question, hoping for some additional panel discussion especially we are at FDA and we are kicking off to start initiatives. So I would like to hear some thoughts from all panels. Any idea how, especially drug develop regulators better work together. We help each other. FDA helps also help FDA initiatives tackling especially some other challenges we have
34 35 36	:	safety. So with that degree, there is a way to to help correct to make those models a success studies.
37 38 39 40 41 42	Saber:	So we also recognize that there are gaps and we do drug development and patients. We don't want to expose patients to some therapeutic doses and this is what, I think we're actually doing with some of our specifics and that's why we felt that there was a need to collect data to guide us to see how we can do

1		drug development better and if you from 2016,
2		2017 and based on that, there has been actually
3		some adjustment in phase 1 clinical trial design that is
4		therapeutic doses dose is so low.
5		Also in addressing the representatives from
6		industry from NCI March 9th is an
7		attempt to address some of these gaps by bringing every one
8		together in these models. It seems to me that
9		they were not talking to each other and certainly industry
10		was not aware of these models. NCI is funding these
11		programs but they do not know what their regulators need.
12		So discussion to see how we can address some of
13		these gaps.
1 4		
14		
15	Bottino:	different institutions within the larger
16		industry in academic and regulatory environment is that it
17		helped offset what something like that and then
18		you know So we need to identify that when it
19		happens I like your idea with the clinic.
20		Clinical team wont' go for it you have to
21		restrict objections to new ideas to people who can actually
22		speak for who they are and not
23	Jin:	In addition to the cross-institution collaborations,
23 24	Jin:	In addition to the cross-institution collaborations, is the importance of new are
23 24 25	Jin:	is the importance of new are
24	Jin:	is the importance of new are developing minimal models. At the same time
24 25	Jin:	is the importance of new are developing minimal models. At the same time to
24 25 26	Jin:	is the importance of new are developing minimal models. At the same time to hear there is a coming workshop in March
24 25 26 27	Jin:	is the importance of new are developing minimal models. At the same time scientists are developing modelsto hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can
24 25 26 27 28	Jin:	is the importance of new are developing minimal models. At the same time scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm
24 25 26 27 28 29 30	Jin:	is the importance of new are developing minimal models. At the same time scientists are developing modelsto hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can
24 25 26 27 28 29	Jin:	is the importance of new are developing minimal models. At the same time scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm
24 25 26 27 28 29 30	Jin: Saber:	is the importance of new are developing minimal models. At the same time scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm
24 25 26 27 28 29 30 31		is the importance of new are developing minimal models. At the same time scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 32		is the importance of new are developing minimal models. At the same time to scientists are developing models to hear there is a coming workshop in March to attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 31 32 33		is the importance of new are developing minimal models. At the same time to scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 31 32 33 34		is the importance of new are developing minimal models. At the same time to scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious will not have a kind of attendance but the first set I think is to make sure you do have the right model before we how to use those models. Yes,
24 25 26 27 28 29 30 31 31 32 33 34 35		is the importance of new are developing minimal models. At the same time to scientists are developing models to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 31 32 33 34 35 36		is the importance of new are developing minimal models. At the same time to hear there is a coming workshop in March to hear there is a coming workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 31 32 33 34 35 36 37		is the importance of new are developing minimal models. At the same time to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39		is the importance of new are developing minimal models. At the same time to hear there is a coming workshop in March to hear there is a coming workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 31 32 33 34 35 36 37 38		is the importance of new are developing minimal models. At the same time to hear there is a coming workshop in March attendees of the workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious
24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39		is the importance of new are developing minimal models. At the same time to hear there is a coming workshop in March to hear there is a coming workshop. Do you foresee anything we can do I don't know workshop. I'm actually curious

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1	_:	Any audience would like to comments?
2 3	_:	with Dr. Saber that there are some reviewers who?
4 5 7 8 9 10 11 12 13 14 15 16 17	Saber:	No, it's not really It depends on the toxicities or expected toxicities and where the dose is in your phase 1 trial. If this is very low minimally anticipated biological effect level, I believe, indeed, is subtherapeutic and patient will not benefit then the trend is do an but if the toxicities are such as there might be a benefit from a pre-design because you want it better access, those toxicities, and your dose is not too low than that's really for the to decide but what I'm trying to say is that once we put the out, the clerical team actually realizes how low we are with some of these when it comes to the actual dose and that's when started on dose escalation.
18 19	Audience:	Is there somebody at the FDA are being responsible for?
20	Saber:	I think
21 22 23 24 25 26 27 28 29 30 31 32	:	There were concerns about biologic products, of the fact that often the toxicities maybe delayed and then somebody said there's really no reason to be working toxicity products or the flexibility there. If it's not necessary in order to assess of some toxicity over multiple cycles, dose escalation has been permitted. However, because in that previous treatment and particular dose level made altered with responsiveness to a higher dose, we would not use that data for to get a higher dose in cycle 2 or 3 or 4. That data could not support a dose inhalation because of that
33	Saber:	·
34 35 36 37	Jin:	Okay. We are few minutes ahead of schedule. This will end our session. We will take a break, 20 minutes break. So I'll ask everyone, please come back at 10:35 for our start Thank you.
38	SESSION II	CLINICAL MIDD IN ONCOLOGY
39 40 41	Dr. Dutta(Mc	oderator): Good morning. My name is Sandeep Dutta. I am from Amgen and I have the privilege of moderating the next session on the Model-Informed Drug Development

in the clinical phase. We have a ______ session of ______ type of treatment in patients followed by ______ and then come back for six short presentations on examples of ______ of MIDD in ______ development which will be followed by panel discussion on ______ speakers and ______ panelist from FDA. I would like to remind all the speakers to use a mouse because of ______ and not use a laser pointer. Our first speaker is Dr. Stuart Bailey who is Vice President of Biostatistics and ______ on Novartis and he will be presented on Beyond MTD Integrating Non-safety Endpoints into Oncology Dose-finding.

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14 Dr. Bailey: Thank you Sandeep.______. This is a joint15presentation on our team. We are presenting ______ team statisticians _____. Dr. _____ that _____ we need to ______ annual mentioned 16 17 transition ______ presentation ______ I began with 18 the presentation presentation as well. 19 20 Certainly is that better? Fantastic. Okay. Please _____ before _____ that again. I asked you about 21 22 these questions _____ just to let you know that some of the details _____ will be _____ office and 23 24 _____ represent _____ specific _____ and rather than _____ my presentation _____ red flag 25 . I think it is actually be _____ if we do 26 27 not forget the studies of the first drug for combinations into patients so what we think about 28 29 how we should optimize the endpoints we will use translating activity into efficacy. _____ we must not 30 forget that _____ so they are still _____ safety 31 32 of the patients. However, we should think about designing 33 studies in a much more detailed way, learning from what we 34 see . To me, it is about, on the preclinical 35 side, understanding what we believe the drug do and then 36 generating data to try to validate what we have seen 37 _____ look for difference between _____ and _____. Now, you could imagine _____ mentioned 38 having ______. I think we struggle with that. I would 39 like to see _____ just between what we have seen 40 the ability to validate translation of that 41 information. _____ gained information and _____ 42 which means having real time _____ use for decision-43 making _____ and not specifically try to _____ 44 design _____ retrospective use that data to answer 45 different questions. We should have _____ mind those 46

1	questions There is a lot that should and could
2	be done to incorporate data either from taking
3	preclinical human but human
4	into combinations, translate data from the
5	information with preclinical synergy
6	translate that into what we expect to see in
7	combinations. We also need to think a little bit better
8	how we translate data between patient populations
9	Often we think of studies only once
10	we determine that activity of the drug in adults,
11	and I think that tends to and we need to be a
12	little bit more considerate about how we can potentially
13	generate activity generate data
14	populations and how to translate that
15	to across regions. There is a lot of discussion
16	between Western and Japanese running
17	studies out there go to specific region in
18	diversity giving way between Western
19	Japanese concept. We do not understand
20	diversity to predict the differences in how patients
21	differ . Additionally the use of
22	volunteers, we are moving into area where
23	drugs developing may not have the same level of
24	toxicity that in the past and there are
25	questions as to how use potentially healthy
26	volunteers information regions. I
27	think additional thinking is as well as
28	translation between and this is just
29	that increase interactions between statisticians
30	and not just the interaction of
31	oncologists It is no longer how the
32	statistician forward that every
33	time trials, we are using information
34	as well as to understand the information
35	make the best decisions so
35 36	make the best decisions so
	make the best decisions so traditional challenges. This is why people elect to
36	make the best decisions so traditional challenges. This is why people elect to drug determine Hopefully
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36 37 38 39 40	make the best decisions so traditional challenges. This is why people elect to drug determine Hopefully wise people from that safety has been used some studies using, but it is still important that we do consider safety as controlling I do not see the previous approaches were safety potential so you wanted to be able to
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36 37 38 39 40 41 42 43 44	make the best decisions so traditional challenges. This is why people elect to drug determine Hopefully wise people from that safety has been used some studies using, but it is still important that we do consider safety as controlling I do not see the previous approaches were safety potential so you wanted to be able to avoid overdosing, but there are complications

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1 fashion. because it goes to why we want to maximize the use of information _____. 2 that we should not be introduce with 3 4 the same number of patients. We should be looking at the 5 designs that we have put in place, understanding the value 6 that that would bring, the data that we will generate from, 7 so I think we need 50 or 100 patients within the study that 8 would learnings that we understand the value of 9 the data it will bring back to us, so to me it is about finding the best doses and not just necessarily 10 for _____ we talk about that _____, so we need to 11 12 have studies that allow flexibility in _____ patients into , so again, just to look back, generally we 13 have to toxicity data. We use that to establish 14 a starting dose. We have estimated exposure 15 16 that we expect to see . There is discussion 17 about of the preclinical trials and negative 18 predictive value, positive predictive value and they tend 19 to be a little bit of negative _____ some toxicities _____ everything, but we may _____ information 20 _____ dose toxicity relationship. 21 Sometimes _____ sometimes not, but _____ convert it into 22 predefined dose range so you do not have 23 ______ sequence or organizations move to less 24 _____ 100% _____ steps _____ toxicity _____. ___, so if _____ be able to use it 25 26 27 , then you can do much better than to simply say , so relationships, 28 29 commented on the fact that these were traditionally introduced _____ you could still apply _____ and 30 31 the goal is to really try to target MTD introduced is kind of _____ challenges 32 qualifications. _____ going back a little bit to this 33 discussion around the fact, for example, _____, it is 34 interesting to know that _____ approach introduces 35 36 _____, so it is not any _____. It actually is . We do not _____ specific in making ecision _____ and I think that one of the big 37 38 decision 39 differences is the fact how we integrate with clinical we investigate _____ patients. _____ helps to 40 define this window potentially _____ doses that 41 minimize the risk of _______ to _____, so ______, but we actually use _______ from within that range _______, so I may have ______ 20. The ones in 42 43 44 the 20 _____ acceptable. I then used my assessment 45 _____those levels from the _____the view of the 46

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PK related to _____ where the preclinical data was 1 2 indicating exposures to toxicity _____, so actually in as to whether we should make this _____ 3 4 whether we should investigate . I of that, but the nice thing around this is that 5 6 you can incorporate _____ if you have differences 7 between species in terms of the projections for MTD. We incorporate _____. You can allow for a 8 9 variety of to allow you to slow down to approach as long as you have _____ you 10 11 are not specifically defining upfront every single dose 12 that you will define maximum steps because we do not want to encourage undue _____ so you would not be 13 dose, but then you have this window _____ 14 data. We have the flexibility to incorporate 15 16 between populations, so if I have some understanding from 17 the differences between populations or if I want to study differences between the same trial, I 18 19 believe that maybe some differences _____ I can incorporate _____ data ____ difference _____ demonstrate _____ and this can also then 20 incorporate 21 instead of being used as _____ study ____ 22 optimize MTD ______ to integrate with the other data 23 24 that you have _____ make a decision which dose to use. drug _____ case of an antibody _____, 25 26 the weight of that other data will then transition as to _____ about _____ if I reached an area of 27 28 _____, so I would not make _____ 29 away I expect to see activity. There are additional approaches that integrate 30 _____ we can incorporate _____. We can do 31 _____ and then _____ approaches I have seen 32 recently _____ extensions of that 33 _____ extensions again. The paper talked about the 34 ability to _____ MTD, so _____ with this is it is 35 a very nice approach to use, but to use it _____ 36 increasing our _____ between _____ safety but 37 then not necessarily _____ a decision and then 38 _____ do this so _____ we have in our team who 39 _____ combination approach. _____ combination 40 safety _____ with _____ exposure relationships based on the ______ interaction between 41 42 the two and then counting for that within the _____ 43 , so _____ have to augment 44 decision _____ left-hand side which is the case where we have 45 studied a few different dose. We have not seen 46

1	any and potentially increase up to
2	potentially control to some level,
3	but when we actually for platelets
4	and we are platelet counts over time, so you can
5	imagine we may have seen some changes in
6	platelets. Actually using platelet.
7	We can actually now look at the risk of within a
8	specific time You can potential
9	, so if we are to make this slight
10	higher risk of and we get this risk
11	At least, it will be incorporated in the
12	decision making. It may tell us overall, so
13	that is safety assessment with other data.
14	actually not expecting to see, so
15	therapy, so examples based on the
16	study safety issues with this
17	patient to 15 from Really it is a question
18	here that it is not just, but we may see events
19	later and how to deal with this when we are
20	making decision from, but we are
21	, so there are a few different form of approaches
22	to do that. We could incorporate data
23	further and then we have an internal
24	reference what we go by cycle the other end, so
25	and it is still introduces the
26	ability to look at those changes that occur within the
27	as well, but it is very challenging when you are
28	in a situation escalation is that
29	developing to keep the patient long enough on
30	that treatment to be able to see investigated in
31	terms of pushing to try to escalate because they
32	do not see, and these patients how to
33	be , so this formal approach is
34	changes that still have information,
35	so another topic around this will be the studies when we
36	are designing a clinical trial, we should be designing it
37	in a framework that allows us to change into
38	reactions of information trial without the need
39	for mention to around the estimate
40	, but to perform, the number of people
41	the number of so it is a custom to
42	to the time the patients have to wait
43	to get this, but the companies decide to do, so
44	that is the smart design to allow to make these changes and
45	this goes back again to the work that should be done
46	preclinical cases only,

but we already have studied _____. We should be able to incorporate within _____ flexibility to switch to 1 2 _____ reaction and example _____ the compound 3 4 thrombocytopenia and we are able because of the 5 way we approach _____ to introduce treatments _____ because we have not _____ told 6 7 us _____ at the same time inform us that we should not see any change at least in the activity _____ sense to 8 how about we translate _____, so we know _____ we 9 have that we have exposures related to 10 . We know that we also have models that will 11 help us understand _____ changes, the dynamic changes _____ or ____ that would be related to clinical 12 13 events, so _____ presentation _____. 14 presentation _____ talks about the assessment of 15 16 finding an optimal efficacy outcome when I am on my safety 17 boundary. We have to understand that safety boundary 18 changes over time, but the challenge can come if the safety 19 endpoint _____ is also related to the clinical outcome, so _____ this case, the _____ also affected by 20 these treatments and we see changes in _____ we may 21 see the occurrence of _____ and there is _____ to 22 be able to look at the relationship between 23 potential and there is also assessment of the 24 that predict patients _____, so how do you 25 26 look at trying to optimize the outcome, whether going back 27 to investigate treatment to mitigate some of the _____ treatments if that is what is _____ because 28 we do not want patients having _____ but still 29 _____, so understanding _____ to go back to the 30 _____ trials _____ on how to change the frequency 31 and it should not be seen 32 of dose event that we go through _____ should be able to 33 34 integrate to effort within a company or organization as we 35 are collecting data _____. Just to if that is okay. This was an example for a 36 compound where we had multiple _____. We integrated ______ three different ______ platelets. You can 37 38 39 see the reference , but this we used within the study to help us understand how to _____ integrated by 40 41 study design and this also goes how we could 42 consider to support those selections in safety efficacy _____ on assessing the relationship between 43 circulating necessity and ability to inhibit the 44 target with certain _____ within the _____ based 45 on what we can measure in the circulating _____, so 46

just the same, _____ safety _____. We should 1 2 design trials that _____ support decision making while safety is in control, but we should not try to assume we 3 4 could design _____ discussion is that I think we may need to look at ______ studies _____ 5 6 not just looking at how but . Thank 7 you. 8 [APPLAUSE]

- 10Moderator: So, we _____. If there is one more question? Or11questions? If not, thank you. We'll move on to the next12speaker. It is Dr. Tito Fojo. He is a professor of13medicine, Columbia University , and he will be presenting14on _____.
- 16 Dr. Fojo: Thank you. Thank you very much and thank you for the 17 invitation. So, basically what I'm going to describe to 18 you today is a novel method _____ analyzing tumor 19 kinetics and this is the summary of it. It actually rose 20 from a disagreement that Dr. Bates and I were having, and we turned to ______ and we resolved it in her favor, and basically what you see here is in blue, what we 21 22 23 generally measure in the clinically arena. The patient's 24 tumor regresses and they eventually cannot be 25 achieved in the majority of patients with a solid tumor. 26 What is truly happening during that period of time is that 27 the fraction of tumor here shown by the red dotted line, it 28 is regressing in size here and it is gonna disappear 29 . The fraction of tumor which is shown by the 30 green dash line which is the persistent fraction of tumor 31 which is ... 32

33 Audience: would you please speak into the mic...

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35 Dr. Fojo: Okay?...and the green which is the green fraction of...it is 36 the resistant or relatively resistant fraction of tumor 37 which is gradually growing. At any point of time which you see in the clinic, this is a combination of the sensitive 38 39 fraction, and this is gonna disappear, and the resistant 40 fraction that's gonna grow. This could all be described by 41 this equation down here at the bottom where the fraction of tumor at the time it's seen, is the exponential of the 42 growth rate times the _____. The exponential result is negative if _____. This is exponential. If you go on 43 44 Google, what you find is that exponential growth and this 45 is mostly _____ population kinetics. Exponential growth 46 47 is by Ex and decay by E-x and that is exactly 48 what we are using in our analysis. And we know that tumors 49 grow exponentially and regress exponentially. We're doing

that since the late 1950s. _____ paper by Howard Skipper describing the exponential growth without fault. 1 2 3 But we come back in this situation. What you have then is 4 the basic formula, a basic equation which we've shown here. 5 In some cases, you end with a situation where there is no 6 growth at all regression. In that case, the formula's simplified for this. In other cases, you end up 7 8 with a situation where there is no regression at all, you 9 get only growth. In that case, the formula is simplified 10 again. And some of you may be saying you know we've made 11 it something which is very important when you talk about 12 the fraction of tumor that is sensitive and the fraction of tumor that is resistant but is not here. Actually you can 13 describe a formula which takes that into consideration, 14 15 where phi is the fraction of tumor that is sensitive, where 16 the sensitive fraction is decaying at this rate, your 17 resistant fraction which is minus phi is growing at this rate, and so, you can better define and incorporate 18 19 tumor fraction you feel that is sensitive and the 20 The problem is that this has resistant. 21 unknown which is phi. You, therefore, need more data or 22 more robust data, and this we know in clinical trials 23 oftentimes that amount of data is not available. I can't 24 tell you why. I think that a lot of very, very, very smart 25 people think about this. In turns out that knowing phi or 26 not has very little impact on knowing the precise growth of 27 regression. You can get comparable lesson in this, of 28 growth and regression, but the simple formula doesn't 29 incorporate phi. Now, some of you might be thinking, no, 30 that tumors don't grow exponentially. They do, and it's 31 not only the exponential equations that we have looked at. 32 We've looked at countless numbers of other equations. Some 33 of your papers are probably in here and some example of 34 tumor that might be growing exponentially on the surface, 35 is not growing in the center or any model that you might 36 have, we'll be happy to derive an equation, and we'll be 37 happy to put all of our data into it and see how much 38 effective your equation. All of these equations, usually 39 about 1% to 3% of the clinical data will fit any one of 40 these equations, whereas in excess of 90% of the clinical data fit the exponential equations. I've no doubt in my 41 42 mind the tumor's growth will regress exponentially when treated with essentially any therapy. So this is from 43 , and this is from a clinical trial. 44 It's called 45 the Velour clinical trial that used aflibercept in 46 combination with Folfox to determine the efficacy of 47 aflibercept. As you all probably know, aflibercept 48 based on this clinical trial. improved The 49 overall survival had increased 1.4 months. I point that 50 out here because I will show you a lot of data based on this, and so you know I've not picked any sample that had an amazing result. I've actually picked that have a very, very, very modest result, and whatever I show you works . I'm gonna be working for everything else. So here are three examples to treat patient 1, 2 and 3. Their data has been measured using . What you see here in red defines the natural measurements generated by the group. Blue or black in this case is a pick of the data to the best . We used to take this data and wait to let it have the opportunity to fit Dd formula, the Gx formula, the Dx formula and the Gd prime formula, and the program that helps you which was the best fit. Sometimes you should fit to more than one formula or program that helps you provided the best fit, and what you see here, additional randomly selected and wee picked the better ones to show you here today. This is the amazing tips that you can get for today. It is not that we chose to draw these lines, so we're gonna go through all these points as well as the test. Every point of this line, not just the ones. Every point in this line is defined by a G, and a D and a phi. In this case, it was best that you define the equation at the number of days here. As you can see, the actual measurements adhere to that quite closely. Here's another set of examples, another three individuals. Again, you need dimensional measurements by dimension level. Oftentimes what you see is the fit of the biometric data is the best, in which we end up with a lot of key values. You might ask how well does it fit, how well these data fit with this G value and we basically cover the key value the best. Initially we could start _____ with a phi value of less than 105 which was pointed by ______ talk about data from one individual patient, not from many patients, but in any case, as you can see here, the fit of the value • is incredibly, incredibly So this is the summary of the data from this Velour trial as performed in collaboration with the group. In this initial look at the data immediately indicates to you that, in fact, aflibercept was an effective addition. Actually what did is, we experimental arm and which was the We figured out that the D was the experimental control. better or the fact it was. What you see here is the percent of the data applied from the file. This is the _____ dimension and the volumetric measurements. unit I'm gonna show you as we go along, the volumetric is a superior measurement. I'm not proposing it be used in the white robe of Oncology, but it is for research purposes, and I think that drug development will probably be the optimum way to assess tumor measurements. So, what you see here is the percent of the data which is usually 10% or less, and this is true regardless of which they present

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. While we can't get meaningful data, sometimes it's just one point beyond studying data. Sometimes, it's just two points, and in those two points are more than 20% difference. We all consider them meaningful, and we chose this over a decade ago when we started doing this, so that we would be accused of taking data that we since might think was inaccurate in measuring data. I think with our more sophisticated measurements that . What you really want to know is once you've eliminated the data that does not exist, 1% of the data does not fit any of the month, and that usually is something between 5% to 10%. The rest of the data fits something. The rest of the data fits 1 of 4 of Dx, Gd, Gd5 or Gx. You could see by looking at this, with gray representing the bars, the distribution of the rate of models _____ what's happened to the experimental arm, and immediately you begin to see this . Specifically, engraved here at the percent of samples that fit the Gx model the best. This is actually the one you don't want to fit in the drug which has exponential growth, but you can see the pattern of growth percent in green. Regardless of how they're measuring, there are fewer fits to that model, and what you see in red is that there are more fits to models that have a decay rate as part of the equation, so what we're seeing here is that we've taken it away from tumors which are growing to tumors that are now "growing and depressed". When you look at the G-values and this is the median values, you can see here the G-values for the experimental arm and the G-values for the control arm. You can see the ratio of the experimental control. As we go to the volumetric, you can see that that ratio is much less. The volumetric is in fact able to detect the differences between these two experimental...between the experimental and the control arms much better. Now here is a depiction that I like but not everyone likes it, but what you see here is to the left are the slower G-values and to the right are the faster Gvalues. In blue or teal is the control arm. In pink here is the experimental arm. What you can see is that the experimental therapy has in effect brought in all of these tumors that were misbehaving in the past three values and reduced their rate and as a whole made it for the entire arm to have a lower G-value. Again, as you can judge from that, the experimental arm isn't the performing value. Here you can see the median key value and you can see that there is basically no difference between the D-value and This is what we see time and time the experimental arm. again. Experimental therapies, the ones that we use today, did not accelerate the rate of tumor decay. Now, remember this is a rate. I'm not saying that they don't kill more tumor, but the rate at which tumor decay occurs is not

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being impacted in the experimental therapy. Here, it is 1 rapidly depicting, in this case _____ description of 2 it, just so you can do it _____. You can see the 3 4 experimental in pink and the control in teal are actually 5 comparable in terms of the distribution of the D-value. So 6 what does this type of analysis allow us to do? If it 7 could allow us to do all of this, then the answer is yes, 8 and I'm sure that these months at a time. Does it 9 discriminate between two arms? Absolutely. What you see 10 here is a depiction of the rate of growth for the control 11 arm and for the experimental arm. _____. You can see 12 that the median for the experimental arm is less than the 13 median for the control arm. This is unidimensional data. 14 Bidimensional data, instead of seven zeros for the key 15 value, it's now nine. The volumetric data is seven. The 16 key value is eleven. What you're seeing is volumetric 17 actually magnifies the differences between the two arms and 18 that's why I think this would be a valuable way to measure 19 clinical data so that we can move forward even faster in 20 the development of drugs. Theirs is a correlate with PFS. 21 What I've done here for you is we've taken the D-value for 22 the entire data set and divided it into four types, and 23 then passed as a correlate with PFS. There is some pink 24 here. It's the G-value of the slowest growing tumors. 25 This is the G-value of the next slowest. This is the G-26 value of the next slowest. Over to the left, you have the 27 fastest growing G-values. As you can see, a remarkable 28 correlation with PFS. This is the unidimensional 29 measurements, cleaned it up a little bit more. We go to 30 the five dimensional and even more we go to the volumetric. 31 Now I know what you're all thinking. You say, boy, that sounds really good correlation of G with PFS. Actually 32 33 you're wrong. PFS actually correlates really well with G. The gold standard here is G, not PFS, and I have a bias. 34 There is a correlate with all this. At the 35 • 36 end of the day, that's what you really want to know. Again 37 here are the . That's the slowest 38 the next slowest. That's the unit measurement, gives the 39 biodimensional. You can see a remarkable correlate. Again 40 this is data that was obtained exclusively while the 41 patient has been enrolled in the clinical trial and we 42 captured the data that was obtained at the time and only 43 during the period that the patient is in the process and we're able to remarkably predict the overall survival for 44 these patients. Now you want to say, okay, so maybe the 45 46 Volpak people are really good. You don't have to mention 47 it, they know very well. This is true anywhere else. What about comparison to PFS? We tried to do the same with PFS 48 49 and it was very difficult. Actually you can get pretty 50 good regression between PFS and OS and when you get it down

to about 150 patients and you've eliminated data from PFS 1 2 or OS, PFS and OS are the same. As you can see, this is 3 just a few hundred patients and the data that I have shown 4 you had over 500 patients in analysis. Is this something 5 that is unique to Volpak or unique to colorectal cancer? 6 No. We had shown this previously in prostate cancer and we 7 published it last year. If you go the Project Data Sphere 8 where a lot of data is housed, they have a warehouse, you 9 see the correlation in pancreatic cancer between the G and 10 the overall survival. The key here is that this is data 11 from three separate files and it has been blended 12 altogether. You get a G-value in pancreatic cancer. It 13 doesn't matter which trial you were on. It correlates with 14 overall survival. This transcends clinical trials. What 15 about breast cancer? . Not only does it 16 transcend clinical trials, here you have a combination of 17 both control and the experimental arm. prediction of overall survival. This is renal cell cancer. 18 19 This is Sunitinib and interferon combined. You need to see 20 that it doesn't matter whether it is a targeted agent or 21 immunotherapy. It all combines to give you robust data. 22 Here's Sunitinib alone, and here as a surrogate for immuno-23 oncology products. On Project Data Sphere and certainly 24 with the Volpak group especially, we'd be delighted to get 25 immuno-oncology data analyzed. You can see again a 26 remarkable correlation between G and overall survival. So 27 the one last point. We use it to decide which phase to 28 study to move forward. Could we benchmark other clinical 29 trials with the use of guide therapy? And the answer for 30 that is yes. What we have done here is we have taken the 31 data from the control arm as the reference or as the 32 We have been taking the data from benchmark. the 33 experimental arm and gradually pulled up one at a time, at 34 which point that commonly patients, the data from having 35 patients have been pulled, doing a thousand resamplings 36 and the number of patients with with 37 unidimensional data is four. If you take the data from the 38 bidimensional measurements, you only need 33 patients. Ιf 39 you take data from the volumetric analysis, you only need 40 27 patients. What I'm telling you here is active into this 41 clinical trial that had a 1.4-month survival advantage. We 42 used a benchmark, 27 patients, this was the 43 superior treatment than the control arm. And then finally 44 this is the last _____. Does this apply in the real 45 world? Absolutely. So ______ also worked at the VA in the Bronx in New York where we have our laboratories. And 46 47 actually you can go into the VA data which is called 48 It's the largest free source of data in the • 49 world. This is just a small portion of it. This is in 50 prostate cancer, and I will just tell that this is one

therapy and this is another, and what you can see here is 1 that by just looking at 36 patients who seek one therapy, I 2 3 can tell you that it is statistically inferior because it has a faster growth rate than this patient over here. The 4 5 reason is because we have 928 patients in this patient 6 population in this comparison, and that becomes such a 7 large robust and reliable dataset that you can benchmark 8 against it, so soon, when we get around the publicists, 9 we'll be able to tell you an individual, for example, how well the patients did. I could probably be able to tell 10 11 you how well patients that are 85 years old did compared to 12 the rest of the population because we are going to have a 13 dataset that is several thousand, actually over 5000, and 14 you can ask any question that you want for any small set of 15 patients. So you can see the benchmark, you don't need 16 So finally what we plan to do in collaboration 17 with the Volpak group is to make this even better by 18 incorporating _____, and then here at the end, at the 19 top or five of us who have been fanatical about this for the last decade and poured blood on it, and then at the 20 21 bottom highlighted in red, new colleagues in Volpak who are 22 incredible and whom I'm delighted to be working with, and 23 all the other people _____. I want to thank you for 24 your attention. 25

26 [APPLAUSE]

- 27 _____: You kind of assume that you have resistant and susceptible 28 cells initially. Does it make sense to incorporate and 29 plot the distance? Have you tried that and need it?
- 30 _____: _____ after some time in some patients.

31 Fojo: So sometimes the data, we analyze and form data when they 32 actually get cured, then you find that there's no existent 33 population. That sort of data fits the DX model, , so otherwise you will find that there's a 34 35 growth rate in every model that you mentioned with 36 detection very early on, and it is a constant that you 37 emphasize, so it's the same growth rate , but 38 what you are really measuring is the growth rate of that 39 . You don't have the resistance. I'm sorry?

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- 41 _____: _____.

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1 Fojo:

Yeah, so what you're asking is...right, so what you're asking is could we see emergence of resistance? And the answer to that is that the data suggests that they're pre-existing, so yeah, it might a very very small fraction.

6 Audience: Answer to your question. So thank you so much 7 for the last ... the first question is, what do you think about 8 the duration of the tumor band? Does it mean we're getting 9 actually a decline in the tumor's anatomy and we're 10 retaining that duration, so can we summarize, you know, the complex tumor dynamic with a single parameter which is the 11 12 slope of the growth? That's my first question. Because it 13 does not actually capture the duration of response. My 14 second question is going to the premise about using our model for the growth. We know eventually things plateau 15 16 off, so the best answer is maybe plateauing off or an e-max, 17 so maybe a more appropriate model would be better than 18 growth of the tumor and how can you handle the 19 lack of measurement, because after BFS, there is, you know, 20 patients actually switched and we're not tracking them for 21 but tracking them for progression, survival. So 22 measurement is actually a sensor in solid tumor.

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24 Fojo: . We only use the data that's available from the 25 frontal product, and yet we're able to the 26 overall survival. So with regards to your company, I'm not 27 quite sure I understood either of your questions, to be 28 honest, but how I understood it. So, I mean the rate of 29 growth is a constant and it continues, continues, continues, 30 continues, and in fact, we have data on some patients 31 especially for example the Sunitib trial where they stayed 32 on that study for years until they had progression and I'm 33 talking over a thousand cases, taken over a thousand cases. The rate of growth remained constant. 34 What that says, 35 which is why I thought you were going with your first 36 question. In fact, maintenance therapy seems to be 37 effective with some growth in some cancers because it 38 maintains the rate of growth intact.

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40 Audience: So clinically you think that the tumor dynamic can be 41 summarized using a single parameter.

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Absolutely. Well, it can't be summarized using a single 1 Fojo: 2 parameter. You need a growth and you need a regression 3 rate constant, but clinically for patients, the only one 4 that's important is the rate of growth. 5 tomorrow, next week, next month, or next year. As long as 6 it stays the same. All you care about is how fast is the 7 one who has had benign growth. 8 9 : So if the tumor is not growing, you know, which means the duration of response is prolonged, that actually can give 10 benefit in terms of rate of survival. 11 12 13 Fojo: Absolutely. 14 15 : What I'm trying to say is, these models are not capturing 16 the duration of the response but actually the depth and the 17 growth rather than maintaining ... 18 19 Fojo: Except that the growth predicts overall survival. Actually 20 we've done that, but we have very granular data. We can 21 actually predict an individual's overall survival with 22 uncanny accuracy actually, to be honest. 23 24 : Thanks. 25 26 Dr. Roy: Amit Roy from Bristol-Myers Squibb, thank you very much for 27 your very nice talk and also for the decades of work that 28 we've all followed with you. 29 30 Fojo: Thank you. 31 32 Roy: I had a couple of questions as well. One relates to the 33 use of all the data. In the example that you showed, the 34 percentage of subjects who only baseline measurements were 35 there were roughly the same. I am surprised they balanced 36 But I just wanted to sort of make the point that out. 37 oftentimes data, only baseline measurements are available

in patients who progress very very rapidly, and then there's an imbalance between the two arms, so there is informative censoring, if you like, so that might be important to take into account in particular. That's the first question. The second one is, I was wondering if you'd look to see how sensitive the growth estimate was to the number of data points that you actually have because especially in early-phase medical trials, there is a lot of very very ______ patients have grown sequentially. The estimate of the growth may depend or may change as you get more and more data, so how reliable is that estimate based on how many samples are there?

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14 Fojo: Alright, to answer your first question, so fortunately the majority of trials have equal number of patients who have 15 16 data that is inadequate, but obviously there is a greater 17 balance here and we have to take that into consideration. 18 To answer your second question, so, you know, if you give 19 us two parts, we'll draw a straight line for you, so that's 20 that. So you need a minimum of three points really. And 21 by four points, usually you've nailed the growth rate. 22 Actually what you've done is basically have enough up to 23 three, up to four, up to five, up to six, usually up to 24 three and for sure after four, the confidence interval of 25 that fully encompasses the confidence interval of the more _____. So with three or four parts, you 26 mature data 27 can do it. You know, it's actually ... if you really want to 28 do this and do it quick, you just need to get points a 29 little more frequently, you know. You don't have to say, 30 well, I think if four points are two months apart, it's 31 going take me eight months. If you get 12 points a month 32 apart, that's good. You know, you need to see how noisy 33 your data is basically, about three to four months.

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: Thank you.

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37 Dr. Zheng:This is Jenny from Pfizer.I really like the topic.38_________ is that the three-dimension measurement of the39tumor size is important.My question actually is related40to the previous question.Your model _______ clinical41trial actually more frequent than tumor size is actually42measured, _______ so basically all information is unable43for you to define rather than the tumor growth as seen in a

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1 2 later time. So I'm just wondering, theoretically speaking, knowing the trial, knowing a lot of data, there is supposed to be better measurement and more precise measurement than seen. How do you explain which is actually better?

So I think, to answer your question, so there's two things. 7 Fojo: 8 One, the rate of decay is always much faster than the rate 9 of growth by several fold. That's why we're concerned that 10 the tumor has regressed. Actually we can calculate a rate of growth before there's growth of the tumor, and you know, 11 12 if you think that three points, the first one's here, the 13 second one is here, you draw a straight line, the third one 14 should be where that straight line goes down. The fact that that third one isn't and has veered away from the 15 16 trajectory that it should have been following is because 17 there's a hidden component to the tumor that is growing and 18 pushing that out, so usually by the third time point, even 19 if it's declining, we can calculate already the growth and 20 We actually compare it to prostate cancer advances. 21 How mature if you do this would there be PSA quickly. 22 growth, PSA velocity? It's basically eight months on average if you can do this or calculate the growth rate 23 24 . It is faster in decay.

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26 Zheng:information, in my experience. I think that27maybe that primary care needs more information about the28people. Maybe that's why youbut from an29observation perspective, I think it would probably be a30small precise estimate. Thank you.

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32 Fojo:So I'm not quite sure what you were saying, so the G-value33actually has information about the drug effect ______,34so you do get a lot of feedback, which is why I think it's35overall fine.

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37 Zheng: Thank you, thank you.

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1 Turner:David from MerckQuick question for you. Do2you use these G-values in care of an individual patient?3Would you ever tell a patient his or her G-value?

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5 Fojo: I would be willing to do that and I think we're going to 6 get at that point. You know, I mean, we tell patients a 7 couple of times, you know, and so PSA velocity, and really 8 discuss these things. Not really, but, you know, we factor 9 them. We start to tell patients what your CA 19-9 or your 10 CA 125 is growing, so we're trying to show you data in pancreatic cancer and showing the same thing, so patients 11 12 put a lot of faith in them. At some point, we're going to 13 have to tell them not only, you know, it's going up, but 14 what is the rate it is going up. Eventually it'll be less 15 about telling the patient than about knowing it, and the 16 decision of benchmarking it with what will become an enormous amount of data that we'll have as a reference. 17

20 Moderator: If you can hold your questions because we are 21 There is a panel discussion at the end. Please do come 22 back for questions. It is generating a lot of questions, 23 that's great. Our next speaker before we break for lunch 24 is Jeremie Guedj. He is a research scientist with the 25 French National Institute of Health and Medical Research, and he will be presenting on . 26

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28 Dr. Guedj: So thank you first to the organizers for giving me the 29 opportunity to present today. So let me start first with a 30 sum ... short terminology of what we call survival analysis or 31 time to event analysis. So what is a time to event? So 32 even some things that happened at about a long time ago 33 , it can be the appearance of new lesions, or it 34 can be also a positive, even like a cure. The main 35 methodological issue that comes back to the question that 36 was in the audience is that of course this event is 37 sometimes observed, but it can also be sometimes not 38 observed in many contexts that we are interested in. That's what we call the absence of it. It means that no 39 40 patient lived until a certain time. , but we 41 don't know what happened after that, okay. So that's the 42 main methodological hurdle that we have in this sort of survival analysis. So in survival analysis, the instrument 43

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tool that we are using is the hazard function, okay, so 1 2 that the function H(t) that defined the instantaneous rate 3 of experiencing even a time t, knowing that the patient has not experienced yet even the x t. So from that function 4 5 H(t), one can derive the survey mode and one can 6 also adjust the variables to evaluate the effect of the 7 baseline covariant on the hazard function and basically how 8 covariant affects the hazard function and that's what it's 9 used in proportional hazards and Cox's function. So we 10 have typically in our framework longitudinal and survival 11 data. So we have time to event data and we have 12 longitudinal measurements. Typically the longitudinal 13 measurements that we have are PSA ... excuse me, I'm sorry. So 14 we have longitudinal measurements. It's typically tumor 15 size or PSA. I'm sorry, I don't know where they have it. 16 Give me five minutes.

17 Moderator: I think while we wait because it's a little past...maybe we 18 can take some questions for the previous speaker, if you 19 don't mind.

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21 Moderator: argue within the audience.

22____:

23 Moderator: How about then in this case let us break for lunch and we 24 start—

25 I am sorry. I think that with the jetlag - I got some Guedj: 26 charts. I am sorry. So let me resume my presentation. So 27 we have longitudinal measurements. Typically it is the 28 tumor size, but now in this presentation what I will focus 29 on is the PSA. Okay? And typically what we are interested 30 to know about kinetics, PSA kinetics that is nonlinear. 31 And you know that in pharmacometrics, we like nonlinear 32 models which are defined by ordinary differential equations 33 because we believe that these models carry all better 34 representation of the biological mechanism that we try to 35 So we have basically longitudinal measurements address. 36 any time it will be needed. And we can have two slightly 37 different objectives that sometimes people do not really 38 distinguish. So the first objective is how can I 39 characterize my nonlinear kinetics, my PSA kinetics, my 40 tumor size kinetics in the presence of a time-to-event? 41 Okay? How can I characterize the fact that I have this PSA 42 kinetics that I want to attempt to model, but I know that

there is also time-to-event data that I need to take into account. And we will come back to that issue that is informative setting. The other objective that can exist and that we can have which is often the most important is how can I characterize the impact of this kinetics on my time-to-event? How can I characterize how the effect of my PSA kinetics, of my tumor size kinetics on the risk of experiencing the event and especially survival time and time to death.

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10 So the easiest and crudest approach to do that is to use a 11 Cox Model with a time-dependent covariate. Okay? That is 12 something that you can already do, easily do. In our 13 package, we can — we have software to do that, and 14 basically you incorporate, you plug — in your survival 15 model, you plug the observed PSA value and you make the assumption that the PSA is a piecewise constant function. 16 17 The problem is that — this approach posts two problems. 18 The first one is that theoretically it is problematic in a 19 Cox model to incorporate an endogenous variable. So a 20 variable that is virtually in the individual and that is 21 directly dependent on the time-to-event because basically 22 if the is patient experiencing event then you will not 23 observe this variable anymore. So it is an endogenous 24 variable. The other more technical issue is that as I have 25 said you assume constant, piecewise constant function and 26 you do not characterize really what happens between 27 different time points, and second, if you want to make a 28 proper estimation, you need to have a lot of data and you 29 need to make sure that you have data for the measurements 30 in all the patients at all event times. Okay? So that is 31 often incorporated. And it is not for very long, actually 32 since the '80s that this approach can lead to spurious 33 parameters to it. Another more sophisticated approach is 34 to use what we call *two-stage* approach. So basically in 35 two-stage approach, if we come back to this #3:43 36 symbol of PSA kinetics. You can fit the PSA kinetics of 37 the patients for instance using a nonlinear mixed effect 38 model, and now what you really plug into the hazard 39 function is directly the prediction from your model in the 40 So that reduce the values, but it does hazard function. 41 not enumerate all the values that comes, that you could 42 have in the Cox analysis, and that again is not for quite 43 some period of time. Actually to be a little bit more balanced, I would say that this approach works pretty well 44 45 when you do not have much missing data. But the problem as

again was submitted in the previous talk, comes from the 1 2 fact that — actually in #4:33 you have missing 3 data and you have informative missing data. And what I 4 mean by that is that the probability to not observe the 5 biomarker directly depends on the truant biomarker value. 6 So let me try to exemplify that a little bit more clearly. Okay, we have this #4:53 _____ patient. 7 Typically the 8 PSA declines and then regrows its condition. In that phase 9 of regrowth, it is very likely that the condition of the 10 patient deteriorates or that he experienced directly the 11 event or that he is considered as nonresponder to the 12 treatment anymore and then he decides or it is decided that he has to drop out of the study. So for one reason or the 13 14 other, the probability that you will not to follow this patient probably now is high. On the contrary, to compare 15 16 with the patient right here in green that starts with a 17 much lower PSA and let us say responds much better to the 18 treatment, the PSA entity remains low, and in that case, it 19 is much more likely that you will follow this patient for 20 longer period of time. So what that means in practice is 21 that poor responders are more likely to drop out of the 22 even while good responders will study become 23 overrepresented as time goes by which means at the center 24 of which you are doing your two-stage estimation becomes 25 less and less representative as time goes by.

26 So basically, the problem is that as I have said some 27 parameters in two-stage of kinetics will be identified only 28 in survivals or at least will be precisely identified I 29 should say only in survivals and that may create a bias in 30 survival parameters and what we will try to bring forth in 31 general in my opinion is that it tends to underestimate the 32 impact of the dynamics of interest, the PSA, the tumor size 33 on the survival. Okay? So there are some other issues 34 that — we can keep them for the other panel later. Now, 35 again, regarding the other objective which is what about 36 just characterizing my longitudinal kinetics? What about That is what I am 37 just characterizing my PSA kinetics? primarily interested in. I do not want too much to 38 39 understand the impact of this kind of things on my survival. 40 Here, I would be careful, but when I try to look into the examples two-stage 41 different comparing versus more 42 sophisticated approach, it seems to me that again some people may comment on that, but in my opinion, I could not 43 44 find convincing examples of the very strong bias that would 45 be induced by two-stage analysis on the longitudinal

parameters. Okay? So I am not talking about the survival parameters but longitudinal parameters. But again, be careful when you are doing two-stage because the typical diagnostic plot that we can make like typical VPC are of course misleading because of this informative censoring.

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6 So what I would like to introduce in the talk is a joint 7 model. So basically in a joint model, we try as indicated 8 by the way to combine together the longitudinal part and 9 the survival part. So we have the longitudinal part a 10 nonlinear mixed effect model, okay? — this random effect and the survival part. The most simple combination that we 11 12 can think about-we can imagine more complicated stuff-but 13 just for the sake of simplicity, I kept the same framework We have the hazard function, baseline hazard 14 as before. 15 function, and then here, we have a function that-[all right. 16 Sorry.]—and then directly Please. Please. Okay. 17 incorporate in the hazard function the prediction from your 18 longitudinal model. Is this better, Jin? Okay. So here, 19 you really can have the longer PSA for instance or you 20 could have the AUC or it could be the derivative of your 21 PSA, whatever function related to the PSA. So what has 22 long limited the use of joint model in pharmacokinetics is 23 the difficulty to estimate the parameters. So, again, I 24 will not go into the details, but when you calculate a 25 likelihood of a joint model, you can see here the 26 contribution of the longitudinal and the survival part, and 27 And then if you both share the same random effects. Okay? 28 want to calculate the likelihood that means that you have 29 to calculate this complicated integral whose dimensions 30 directly equal to the number of random effects. Okay? And 31 the main difficulty is that for long we did not have really 32 qood numerical tools that is able to calculate and 33 therefore to maximize this likelihood. So in the recent 34 years, there has been an extension of the SAEM algorithm in 35 Monolix that allows now to do that, but there are also some 36 ways to do that in NONMEM. Some people can comment on that. 37 And that's the approach that we used into that project.

38So for the sake of illustration, we have 600 — we have 60039patients from the phase 3 clinical trial in prostate cancer40treated with docetaxel. So we split the sample in two:41first 400 patients that will be used as training dataset to42concentrate in our model and then the validation that I43said on 200 patients that will be used for individual44dynamic prediction, #10:13effect

So you can see here the two startup data that we have in 1 2 the longitudinal measurement. Patient increased before in black and then declined initially under 3 treatment 4 treatment in red and then they stopped treatment, but in 5 that the starting PSA continue to endure, and we can see 6 the increase in PSA on the time started. In here, you see 7 the survival in the Kaplan-Meier curve in that population. 8 So in the Infectious Disease model - I do not have much experience in Oncology #10:46 , so when I was 9 10 asked to supervise the project and to analyze its data, 11 well actually I used what we do typically in Infectious 12 Disease when we want to model the effect of treatment. We 13 have two populations: those that are sensitive to 14 treatment and those that are resistant to treatment. So I 15 have tried to apply the same concept to PSA kinetics, and 16 so we have cells that are sensitive to docetaxel and cells 17 that are resistant to docetaxel. So when you start a 18 treatment, the treatment will block the proliferation of 19 the cells, but it will not act on the resistant cells. 20 And what you measure — the PSA that you measure in Okay? 21 the blood — is the sum of the PSA produced by those that 22 are sensitive and those that are resistant. So I will not 23 enter into the mathematical model that is pretty standard 24 in the field. I am just going back to the question that 25 was asked before. Here, we have some carrying maximum 26 capacity precisely to avoid that the PSA kinetics will try 27 to interfere with as time goes by. So the survival part, 28 as I have said, we have a baseline function at 0 which is 29 called the Weibull function, and then we tried several link 30 functions, so several possible ways by which the PSA can 31 have impact on the survival. So we can assume no link or 32 that just the initial PSA really matters or determined PSA 33 or the slow growth in PSA or the area under PSA or 34 something a little bit more interesting which is the sum of 35 the sensitive and the resistant cells. And, again, that 36 comes back to the previous talk where the previous speaker 37 nicely illustrated that probably when we look at treatment 38 sensitive cells, the impact of treatment sensitive cells 39 and treatment resistant cells on survival that might be 40 very different, and that is exactly what this model tells 41 basically when the PSA will regrow after the end of the 42 treatment that will be treated by this R cells. So we 43 expect this beta prime to be larger than the beta, okay, to 44 be consistent with the previous presentation. So what I 45 think of this joint model is that actually it does not 46 complicate much the approach. I mean once we have the good

software, we can choose to more or less reuse the same 1 2 methodology that we are used to in longitudinal traditional 3 nonlinear mixed effect model. So you can calculate the BIC 4 of your different model, look at which one provides you 5 with the best fit. And here, we could find that the model 6 providing you with the best fit was the one considering a 7 differential effect from treatment sensitive cells and 8 treatment resistant cells on the PSA, on the PSA kinetics. 9 So basically that is how the prediction would look like. 10 The gray area is the parameter during — is the parameter of 11 treatment, and before treatment, you can see the PSA 12 increased. Then the PSA starts to decrease when treatment is initiated, and there is in some patients an escape from 13 14 the treatment that leads to an increase in the PSA. And the nice thing with joint model is that you can directly 15 16 predict the hazard function of your patient from time's 17 view to the initiation of the treatment. Okay? And you can see here the decrease in the current capacity. In fact, 18 19 at some point, the PSA would stop increasing exponentially 20 and will start to plateau.

21 So then, if you remember, we had split the samples in two: 22 one for the training and one for the validation. So now 23 what we said is okay, we fixed the joint model. We fixed 24 the population parameters, and we just looked at the PSA in 25 my validation sample. So patients that we have not used up 26 to now, and just using the PSA of these patients, can I 27 reconstruct the survival of these patients without looking 28 So that is what we did, and we predicted the PSA at it? 29 and used this PSA into joint model to calculate the 30 survival that we predict for these 200 patients. And what 31 you can see here is that this red prediction nicely 32 overlays with the Kaplan-Meier in this population. So, 33 again, I mean let us not be too over optimistic. It is an 34 internal validation and it is clear, but at least it 35 illustrates how a joint model when it is working allows you 36 to actually reconstruct the survival just by looking or 37 just by analyzing the longitudinal kinetics. So now, the 38 last couple of slides, we are interested in dynamic 39 prediction. So what we mean by dynamic prediction is this 40 difficult situation where we have the new patient that 41 enters the study. We have our joint model. We have an 42 idea of how PSA and survival interact or how PSA impacts on 43 survival. We have a model of PSA kinetics, and now we ask, 44 Okay, I'm following this patient for a certain period of 45 time. I have three PSA measurements, and now what can I

1 see from this patient? How — what can I predict after the 2 three observations for the survival of my patient? So 3 basically what we are interested in is to calculate the 4 probability #16:16 of survival in that patient 5 individually. So to do that, we used the same approach. 6 We fit all the parameters on the joint model and then try 7 to calculate the individual parameters of this new patient. 8 To do that, we do not want just to have one estimate. We 9 do not want just to have the EBE, the empirical Bayes 10 estimate of that patient. We do not want to have a median 11 prediction for that patient. We want to take into account 12 uncertainty and the fact that if the patient just entered 13 the study there is probably a lot of anxiety that needs to 14 be taken into account while we make the prediction for that 15 patient and that on the contrary over time when we 16 incorporate more and more data, this uncertainty will 17 shrink. Okay? So we need to take this uncertainty into 18 account and that is what we did here by calculating the 19 full a posteriori individual parameters of this patient 20 using Hamiltonian Monte Carlo in STAN. Okay? So basically that is how you — let us compare these two patients. Okay? 21 22 This patient will die in month 24 and this patient will be 23 censored in month 24. Okay? That means he is alive month 24 24 at the end of the study. So we find that just to 25 include the initial measurements, we can see that in 26 predictions for the PSA are roughly the same. That makes 27 sense because the only information that I have included is 28 the usual PSA. In survival, they are very similar. There 29 is some difference, of course, because they do not have the 30 same initial values and so that impacted the information. But more or less it is the same. Now if I incorporate more 31 32 information, you can see that the fit of my PSA improves 33 and that the interval, the prediction interval tends to 34 shrink over time. And if I am following this patient for a 35 sufficient amount of time, what we call the landmark, at 12 36 months here you can see that I make a very strong 37 prediction of what will happen one month later on. 38 At month 24, for that patient, we predicted the survival 39 will be very low while for this patient the survival is 40 much higher. So again that is example that shows how that 41 could be used in practice that we need to take into account absolutely the uncertainty that we have and the fact that 42 43 this uncertainty depends very much on the amount of data 44 that we have accumulated. It is a very simple idea, but we 45 need to keep that in mind. So now, what we need to 46 evaluate with the predictability — that is just an example.

We need to have the metrics to evaluate really the 1 2 prediction and the capability of this model. So to do that, 3 again, there is nothing really new with that, but 4 statisticians have developed tools for decades. One — and 5 it distinguished generally the capability of the model for 6 discrimination and the capability for calibration. So what 7 we call by discrimination or what we call the area under 8 the ROC curve is the capability of the model if we have two 9 patients that one that will experience the event during a 10 certain window of time and one that will not experience 11 this event during the same period of time. Is the model 12 capable of saying which one is at risk and - which one is 13 the more at risk and which one is less at risk. So that is 14 the discrimination and that is something that we need to 15 quantify if we really want to evaluate the model 16 capabilities. The other one is slightly different. It is 17 what we call the calibration. To do that, we can use the 18 Brier score. So that is entirely different. Now we do not 19 try to really discriminate and compare the ability of 20 making the good prediction between two patients, but we 21 would like to evaluate the capability of the model to 22 really predict the event. Okay? And to really predict 23 when the event will conclude. Okay? And so that is a 24 blind spot and no way to detect. And now what you can do 25 is evaluate the property of your model. And again, the 26 property of that model depends now on two parameters. It 27 depends on the long MAC and so how much information you 28 accept to completing the model and your #20:27 29 how much into the future you want to make your model to be able to make a prediction? So if we stick to AUC to keep 30 31 things simple — here, if I just incorporate the initial PSA, 32 you can see that the AUC for short period of in time, so 33 very rapidly after the initiation of treatment is pretty 34 But very rapidly, the AUC reduce and gets to a very high. 35 low levels, so close to 0.5 which means in a single — if I 36 only have the initial regimen of my patient where really 37 the ability of my model to make this connection is 38 extremely small unless I am really focusing on a very short 39 period of time at the very beginning of treatment. However, 40 if I incorporate more information, if I have the 6 months 41 or the first 12 months of treatment, then you can see here 42 that the AUC tends to be much higher and is close to 0.7. 43 So if I incorporate the year of treatment, now I Okay? 44 start to have good capability for discrimination.

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So just to finish, on the use of joint models, we can see 1 2 this recent review that was published in BMC. It is clear 3 that, I mean, it starts to grow. I am not sure that we can 4 really talk about an exponential growth in the place, but 5 there is more and more interest from the industry and from 6 the academy. I wanted also to have like that — cancer is 7 not, I mean it is one area of research for a joint model, but there are others like HIV, transplant, or cognitive 8 9 decline where it is also used, and the reason for joint 10 modeling — again, there are different processes for joint 11 modeling even though I focused here on how to characterize 12 the impact of my kinetics on the time of treatment. There 13 can be other interests for doing joint models.

14 So in conclusion I hope — at least I have tried to convince 15 you that joint models are needed for two purposes: to 16 characterize the longitudinal process, increase 17 #22:32 informative dropout, to assess the 18 relationship between the longitudinal process and a time 19 treatment data. Okay? And it has long been limited to do in our models, but we now have the tools to use it in 20 21 pharmacometrics even if there are still some technical 22 difficulties that you will face if you use it. There are 23 you could see that there are still some 24 difficulties sometimes to calculate the likelihood when we 25 are working with models that are too much complicated or 26 defined by the length of time it is used. Also there is an 27 order — I mean joint model as I have presented here has 28 also the drawback of its virtues. It is a fully parametric 29 model and we need now to really evaluate different 30 parametrization, how the parametrization impacts on the 31 prediction that we make and so on. Okay?

32 So what is the future of joint models? I think that we 33 need now, now that we have to choose, we really need to 34 evaluate that properly. There is a lot of expectation that 35 joint models can be used to improve and to optimize drug 36 development. I think there is a lot of interest in 37 particular on how we can make the best use of phase 2 to 38 optimize swift phase 3 trial, in particular probably 39 increase the #23:50 of phase 3. Can we early 40 demonstrate that phase 3 trials are in danger or on the way 41 of a failure? So there are a lot of descriptions about 42 that, but now we need to address that properly and really 43 evaluate if joint models bring something and to what extent 44 it brings something. I think also that we will need also 45 to be more realistic, to take into account the fact that in

general there are not only one-time treatment but there are 1 2 several. I did not talk here, but you could also think about new lesions from #24:28_____ modeling, treatment 3 approach whereby you can after dropout, after 4 change of treatment. So a lot of these things need to be 5 6 taken into account, and again, there are also things to do 7 outside drug development. It is the benefit in the 8 treatment individualization outside any issue of drug 9 development of therapeutics. It is how we can really use 10 this kind of dynamic prediction to help distinguishing in the patient to early detect the patients that are the most 11 12 at risk, those that would really benefit from change of 13 treatment. Okay? And again, to do that, we believe - I 14 think just you know make a risk evaluation and the best way 15 to make a realistic evaluation is to make a randomized 16 clinical trial in which you will evaluate whether this sort of dynamic prediction will really bring something. 17

18 And with that, I would like to thank my former PhD student 19 who collated all that work Solène Desmée who is now an 20 assistant professor in France and this work was supervised 21 by myself and France Mentré, and it was funded by Sanofi 22 France.

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Thank you very much.

24 [APPLAUSE]

- 25 Moderator: Alright, please take your seats. We have a really tight 26 session. We have six speakers in 90 minutes. In this 27 session, we are going to talk about some inspiring examples of MIDD clinical development. We are going to kick off. 28 29 Every speaker has 15 minutes, so if you can keep your 30 thoughts down to 10 to 12 minutes, then you can entertain a 31 Otherwise, please hold any questions question or two. 32 until the panel discussion at the end. So we will kick off 33 the session with Dr. Michael Maitland from Inova, and he's 34 going to talk about ... give us a clinical perspective, which 35 will be followed by case examples.
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37 Dr. Maitland: Thank you. So, to help ease you back from lunch, we're 38 going to give you a presentation that's a little less heavy 39 on the quantitative analysis and instead focus on clinical 40 perspective. The title of the talk is bringing the 41 community fair setting into the learning versus confirming 42 paradigm. I have to thank the meeting organizers, most 43 specifically Rene Bruno and Yanan Zheng. Arguably Dr.

Zheng's paper at VIA in 2007 is the inciting event of being 1 2 here today. We were wrestling at that time with ways to 3 shrink the size, shrink the timeframe of phase 2 clinical 4 trials, and it was his modeling analysis suggesting that 5 change in tumor size in lung cancer patients at the 6 earliest time of assessment on clinical trial might be a 7 quantitative marker to be used to predict whether drugs 8 would ultimately improve progression to create overall So that was the inspiration. Then what kept me 9 survival. 10 going in this field was Dr. Bruno approaching me at ASCPT 11 several years back and saying, you know, conditions don't 12 really understand what all of us are doing in the modeling 13 space and we had a few ambassadors to sort of preach to 14 So I've been converted, and here I your community. am 15 today to give you some insights on perhaps some new ways. 16 Apropos Dr. Woodcock's comments at the beginning of the 17 session, we might bring about this new paradigm of not just 18 incorporating fully into drug development but actually 19 directly into patient care with greater effect. So I came 20 up with all these lofty ideas when I was in the ivory tower 21 of the academy at University of Chicago, but two years ago, 22 our team took a leap of faith to come here and work at a 23 place most of you have never heard of, the Inova Health 24 System, so now when I give these talks, I have to introduce 25 you to Inova. We are a hospital and health system. You 26 are here today at the FDA in the state of Maryland. You 27 likelv flew in through Reagan National Airport in 28 Alexandria or Dulles Airport in Loudoun County, and our 29 Inova Fairfax Hospital flagship is located right here, 30 about a 30-minute car ride from FDA. Each of these green 31 pins represents either one of our major community hospitals 32 or a major ambulatory care center. The relevance of this 33 increasingly we find if is we want to personalize 34 therapeutics and have real impact on patients over time, we 35 need to get away from our drug development and clinical trials paradigm into a more of a real-world evidence and 36 37 implementation paradigm. Inspired by that, the leadership of Inova committed nearly eight years ago to building up 38 39 its own translational medicine institute, to beefing up the 40 heart, vascular and cancer institutes by recruiting several 41 of my senior colleagues away from major academic 42 institutions that represented these. Most recently, the 43 health system has established its own strategic initiative 44 and brought on site its own venture capital team to function as an accelerator of technology-enabled health 45 46 care services as well as devices and other methods of

trying to improve the care of patients in our system. 1 Not 2 coincidentally, this great opportunity arose in 2014 when 3 an Exxon Mobile, which had been directly across the street 4 from Inova Fairfax Hospital, decided they were moving back 5 to Houston and left this 120-acre campus and about 2 6 million square feet of office space available for some 7 buyer. The Commonwealth of Virginia along with Inova 8 Health System purchased the property and has begun to fill 9 it with plans that included our having an ambulatory cancer 10 care center, a laboratory building directly adjacent that 11 now committed to being cohosted by Inova and is the 12 University of Virginia, and then to have next door to that 13 this facility for biotech and health IT. In the meantime, since that's due to open in 2019, I moved my practice to 14 15 this rather humble-looking community medical office 16 building across the street from the hospital. It's here 17 over the past year and a half that I've had the opportunity 18 to practice in a less academic, more community-oriented 19 Related to the request of the meeting hosts environment. 20 today, I now will just address for you some real-world 21 examples of a couple of patients who I actually interacted 22 with in clinic this week. So patient 1 is an approximately 23 30-year-old woman who presented in 2014 with prolonged 24 She underwent an endometrial biopsy menses. which 25 unfortunately revealed endometrioid adenocarcinoma. Patient 2 is a woman in her 30s who also presented with 26 27 similar symptoms after she initially had an abnormal 28 screening cytology. She underwent her D&C in January 2014, 29 also with a diagnosis of endometrioid adenocarcinoma. Thev 30 gynecologic oncology both sought surgeons to have unfortunately at such a young age hysterectomy. 31 Patient 1 32 proved to have stage IIIC2 disease. Patient 2 had stage 33 IIIC1 disease. Given the high likelihood that those 34 diseases would recur, both patients underwent standard of 35 adjuvant therapy, patient 1 with cisplatin care and doxorubicin followed by radiation therapy with progesterone, 36 37 patient 2 with adjuvant carboplatin and paclitaxel followed Both had no evidence of disease for more 38 by radiation. 39 than a year during routine surveillance. Patient 1 in 40 March 2016 had recurrent disease and received carboplatin 41 and paclitaxel, patient 2 in October 2015 with carboplatin, 42 letrozole and doxorubicin, etc. Both patients again had 43 some evidence of disease control. Patient 1 in August 2017 44 was found on CT surveillance imaging to have recurrence in 45 the retroperitoneal lymph nodes. Patient 2 had been 46 chronically on bevacizumab through September 2017 and now

is having some bleeding problems and is definitely in need 1 2 of change of treatment. As it is not 100% common in our 3 community environment but increasingly so, both patients 4 now have access to relatively full molecular testing. This 5 patient's tumor sample notably returned with an MLH1 6 nonsense codon leading to full stop of MLH1 expression. In 7 fact, interestingly at the time of resection in another 8 country, the patient had had immunohistochemical testing that showed MLH1 deficiency, but in the United States, I 9 10 would not be able to get her insurance to approve treatment 11 deficient disease without having a US CLIAfor MLH1 12 certified laboratory identify this molecular variation. 13 Patient 2 also had some molecular determinants suggesting a particular treatment strategy. However, in her case, the 14 15 clinical trial that was open most oriented to her disease 16 which has this known functional mutation PIK3CA R88Q as 17 well as apparent deficiency biologically so of PTEN would 18 likely benefit from a PI3K inhibitor, but the clinical 19 trial that we were running at Inova through the GOG NRG 20 with copanlisib was on hold to further accrual. She did 21 not have her MSI testing. Her overall mutation burden was 22 determined to be intermediate whereas patient 1 was found 23 to have a high tumor mutation burden. So ordinarily we 24 would be thinking about enrolling these patients, for those 25 who might not be familiar, on an innovative trial called 26 TAPUR, Targeted Agent and Profiling Utilization Registry 27 Study. What's novel about this study is it's sponsored by 28 our professional society, American Society of Clinical 29 Oncology, and not anymore an industry sponsor. The trial 30 facilitates patients who have molecular testing to access 31 what might be appropriate treatment regardless of the organ 32 of etiology of the cancer, provided that as one of the 33 drugs that has been donated to the trial by any of eight 34 industry sponsors. So patient 1 would have been assigned 35 to an arm involving a checkpoint inhibitor, but we didn't need to enroll her on that trial because the FDA a few 36 37 months earlier had approved pembrolizumab for this broad 38 indication of deficiency of mismatch repair proteins. So 39 in August 2017, our team, after applying for some paperwork, 40 to begin treating her with pembrolizumab. was able 41 Unfortunately patient 2 did not have the same experience. 42 Although there are many PI3K inhibitors available, none 43 commercially approved, we know а lot about their 44 pharmacokinetics, we know a lot about their safety profiles, but the only way I would be able to access this compound 45 46 for this patient is either through a clinical trial, all

1 clinical trials that I'm able to open at Inova are not open 2 to accrual, and so the patient proceeded to receive 3 commercially available paclitaxel in September 2017. So 4 patient 1 has had a very good experience so far. Her 5 October 2017 CT imaging revealed decreased retroperitoneal 6 adenopathy. Our team has had some experience managing 7 patients on checkpoint inhibitors, so we are actively 8 monitoring her liver function tests. We found some 9 unexpected elevations, but she was asymptomatic and they 10 resolved. We have been serially monitoring her thyroid 11 learned through stimulating hormone. We years of 12 collaborating with melanoma colleagues our at the 13 University of Chicago that once you see a rise in the TSH 14 followed by a precipitous fall in TSH while the patient 15 is asymptomatic, still it is wise to beqin some 16 supplemental L-thyroxine therapy, expecting that the 17 patient will become hypothyroid as a result of mild 18 autoimmune thyroiditis. The patient continues to work full 19 time and, except for some mild fatigue, is living an 20 optimal quality of life right now for someone with an 21 incurable disease. Contrast that with patient 2. In 22 October 2017, although her vaginal bleeding was controlled, 23 pain persisted. She has developed progressive her 24 manageable peripheral neuropathy on paclitaxel. Her pain 25 and her fatigue continued. Although I am by no means a 26 right to trial law advocate, our team with lots of 27 experience in coordinating with industry to obtain what we 28 used to call compassionate use INDs now called single-29 patient INDs, completed all that paperwork to have a 30 willing partner sponsor, but we still as of January 2018 31 have not had approval to receive an agent ministering to 32 this patient who, by all estimates of her molecular profile, 33 is expected to have some possible opportunity for definite 34 response to those drugs. So it's putting us in this rather 35 awkward era between prior paradigms and the exciting one as implied by this session today and Dr. Woodcock's conference 36 37 this morning. It highlights some problems we have and articulated the positive elements 38 in this 39 editorial a couple of years ago where some of our drugs are 40 being developed so effectively, largely through some use of 41 model-informed drug development, that they're becoming 42 commercially available before we actually know as much 43 about them as could be helpful in the clinic. So this 44 classification certainly had a major influence on many of 45 the clinical pharmacology fellowship graduates at the 46 University of Chicago. You all are familiar with it. Time

is short, I won't go over it, but suffice it to say, this 1 2 paper is 21 years old and a lot has changed since that time. 3 We're getting quite good at characterizing parts of this 4 response surface. We have, therefore, a new set of issues 5 and problems to deal with. So if you look at a pharma 6 foundation brochure from just 2013, this was sort of a sob 7 story for all of us in drug development of how much testing 8 and how many resources are put into the development of a 9 single FDA-approved medicine. My colleague Tina 10 has characterized how in oncology care, we've really 11 benefitted from a lot of new approaches and are rapidly 12 developing agents having a more fluid concept of how to 13 develop drugs for commercial use. I think it's no 14 exaggeration we are quickly getting to the point where this 15 diagram really looks like it's the new paradigm, and that's 16 creating a whole set of new problems. Not to poke fun at 17 any colleagues here, I just highlighted how impactful an 18 drug can be on a patient immunotherapy who is the 19 appropriate match for it, but we are now effectively 20 generating too many slots for too few patients to answer 21 the many good questions we all have. I think here lies the 22 solution, and this is why our team was so willing to take this flying leap to a community health system with these 23 24 ambitions of conducting research lofty because our 25 information technology today is giving us the very real 26 conduct relativelv rigorous capacity to clinical 27 investigations with a very limited description intensity 28 protocol and to then literally within our electronic health 29 record system incorporate this level of data acquisition 30 and have our routine treating clinicians function as 31 effective self-investigators in the new environment. We 32 also had the opportunity to incorporate new technologies in 33 ways that are less and less intrusive to the patient. In 34 the community health system, unlike our clinical trials, we 35 have the opportunity to collect long-term longitudinal data. On one of my lung cancer patients who we've treated at the 36 37 University of Chicago for a span of about five years, we 38 had serially collected her plasma samples over the course 39 of three of those years. We now are able to use some 40 quantitative plasma DNA detection methods and we could 41 trace the concentrations of her mutated PIK3CA and BRAF 42 mutated status DNA in her plasma over the course of 43 different treatments. An interesting thing we found 44 related to what Dr. Fojo was talking about earlier today is 45 when we assess the total tumor burden by taking volume 46 measurements of her many tumors, we have a more reliable

relationship between the imaged sense of the patient's 1 2 tumor burden and her plasma DNA kinetics reflections of the 3 tumor burden compared to if we had stuck to plain old 4 RECIST-based single longest dimensions of a few target 5 lesions which suggested throughout this entire time that 6 she had rock-stable disease when she did not. We have most 7 recently been able to coordinate with one sponsor to try to 8 take these new technologies into a reductionist approach of 9 can we actually do meaningful and novel subject trials? I 10 think this single patient's result on this study where we had this pretreatment tumor growth trajectory, 11 was on 12 treatment tumor growth trajectory, withdrawal of treatment 13 tumor growth trajectory, and his restoration of treatment tumor growth trajectory, to say that we potentially can do 14 15 this and should in the future, but we have a long way to go 16 to treat patients with pancreatic or biliary tumors and 17 none of them survive long enough for us to be able to 18 perform these full assessments. But my case in point in my 19 last slide is that we really need to focus now on this 20 world of a new paradigm on developing the methodology and 21 the resources to perform these types of analyses in this 22 post-marketing post-approval setting. We can access many 23 more patients. We will have better generalized ability as 24 a result of studying patients in this environment. We know 25 we're moving into a new era of life cycle management where 26 increasingly we will be focused on value. This is 27 seemingly impossible to establish that value with the size 28 of the cohorts we are now studying in standard phase 29 We're in this new era of regulatory management studies. 30 where our colleagues here at FDA are going to have to think 31 about ways that they can oversee the data and the conduct 32 of these types of investigations to ensure patient safety. 33 But I think overall we're going to have better capacity to 34 enhance and extend value of these compounds for the folks 35 who manufacture them, for the folks who use them, for the patients who receive them, as well as for those who are 36 37 actually having to foot the bill. So this is really just This is my email. 38 the beginning of a conversation. For 39 many of you who will have much brighter ideas than our team 40 has so far, we want to let you know that we're sort of open 41 for business and collaboration as we all explore the new 42 paradigm together. Thank you for your time.

43 [APPLAUSE]

44 Moderator: Our next set of speakers are from _____. The next 45 speaker is Dr. David Turner from Merck.

Dr. Turner: Thank you very much for the introduction. It really 1 2 is an honor to be here today. I think we have an excellent 3 panel of speakers, and it seems a lot of us are very keenly 4 interested in endpoints that really is a hot topic of, you 5 know, oncology right now. Now, I am indeed from Merck. I 6 am in the quantitative pharmacology department. I am also 7 a member of a cross-functional working group at Merck 8 that's been tasked with better understanding in describing 9 the relationship of surrogate endpoints and overall 10 survival. So today I have the privilege to show you some of those results. So pembro is obviously very important 11 12 for Merck. It is also very important for patients. The 13 early approvals came on the basis melanoma and non-small-cell lung cancer, and we've obviously expanded 14 15 across the many different tumor types and have been in the 16 market since then. So now that we have this data from 17 KEYNOTE-001 we're sort of going back to the well, 18 so to speak, and beginning to query that to better 19 understand some of those relationships. So we have this 20 sort of hierarchy of questions here, starting with ... these 21 all could be the same. Are there subgroups of patients 22 with progressive disease that have different outcomes? And 23 then, as alluded to from previous speakers, we took 24 as an aggregate measure, but in a sense, we're 25 sort of borrowing some of these data from the individual 26 lesions, so there's a question as to whether or not that gray area might add something to our understanding. 27 Then 28 of course most importantly, what does this mean in terms of 29 What's treatment failure and what clinical practice? 30 clicked? And what we do when a patient progresses by 31 RECIST criteria? Do we keep the patient on the drug or do 32 we remove the treatment? So all of these are important 33 questions, I think. So we started this journey with 34 KEYNOTE-001 as sort of a learning analysis and then we 35 expanded this into KEYNOTE-052 that also looked at bladder So I'm showing you here data from KEYNOTE-001. 36 cancer. 37 . You can see This is some lung antagonist. 38 from this clearly that we have a number of patients who 39 have an excellent response to the treatment. There are a 40 number of CRs and PRs, we have those. Look at the tumor 41 shrinkage. These patients are highlighted here, so this is 42 a disease control group. We also obviously have some 43 patients who have regressed who have SLD growth greater 44 than 20%. I think what's interesting is the sort of middle 45 have patients who ground where we are still have 46 progressive disease by RECIST. Again they don't meet the

threshold on an SLD basis for progression, so this suggests 1 2 that they either have growth of a non-targeted lesion or 3 formation of a new lesion, yet still you can see a lot of 4 these patients have shrinkage in their target lesions, so 5 these patients are actually benefiting, and so this really 6 begs the question of how do we treat these patients and 7 should they be labeled the same as the other patients on 8 Now to sort of further complicate matters, if you druq? 9 look at individual lesions, so here, each vertical column 10 represents а single patient, you will see that some patients have a combination of growing and 11 shrinking 12 lesions such that you have patients who actually progress 13 when you have a shrinking lesion and you have some patients who are responding to growing lesions, so there's a lot of 14 15 gray area here. Obviously we sort of reassess them to make 16 sense of all this information. Just to start out, the 17 purpose of this presentation, we came with up а 18 stratification system. I will show you here. So on the 19 far right, we have our typical aggregate growth and these 20 are patients who have SLD growth greater than 20%. Next, 21 the mixed growth are our patients who have single lesion 22 progression, so they have progression of one lesion but not 23 enough to meet the threshold for SLD progression. Then we 24 have patients who regressed with no growth in the target lesions either with or without a mass, so plus and minus. 25 26 Of course, we have our disease control group on the left. 27 We will come to this schematic after a while to look at 28 some of these results. So again we started with 29 KEYNOTE-001. This is our random dataset. We have a fairly 30 large dataset here, and when you go through all the filters, 31 you see that approximately 60% of our patients have 32 progressed prior to treatment discontinuation. When you 33 look at the general breakdown here, you see that we have a 34 fairly good representation across these different subgroups 35 that we define. So after analyzing KEYNOTE-001 would be a fairly perspective analysis to apply the rules to KEYNOTE-36 37 052, again bladder cancer population. When you look at 38 that data, you see generally the same proportion of 39 patients belonging to individual subgroups. So I think, in 40 it of itself, that's an important finding because it is a 41 very different complex and you see that patients are 42 progressing for different reasons and have underlying 43 differences in their disease status, but it really begs the 44 question, what is the outcome of these different subgroups? 45 So here we start with a Kaplan-Meier plot of KEYNOTE-001 46 again and this is our disease control group. You can see

that survival quite great in these patients who belong to 1 2 the disease control group, as you would expect. Now when 3 we layer in patients who progressed via non-drug targeted, 4 you see that there's a slight difference in here. I think 5 it's interesting that the differential between the mets 6 plus and mets minus is not unusual in size, suggesting that 7 formation of new lesions might not be as important for 8 survival, but still reduces some of the survival gap. Now 9 when we go further down inspection in patients who have 10 targeted lesion growth, either at the sort of the net 11 aggregate level or at the signal lesion progression level. 12 You can see that they have significantly more survival 13 compared to our disease control group and high group. So 14 you can see there's sort of a spectrum of outcomes here, 15 and typically when we summarize things like response rate and PFS, we will be grouping all these patients into a 16 17 single measure. Again interestingly when we look at 18 KEYNOTE-052, we see the same pattern of graded response, 19 starting with the disease control group and the patients 20 being targeted with growth kind of the worst outcome. Ι 21 think again, just to emphasize, the patients with single 22 lesion progression are not progressing due to targeted lesion growth, but they still have similar outcomes, 23 24 suggesting that if you have one tumor that escapes, it the survival of your outcomes or more 25 certainly 26 closely resuming in patients with met SLD growth. So I 27 think Kaplan-Meier plots are a great way for visualizing 28 this data, but we're dealing with unsteady phenomenon and 29 we have do things like minus because these events are 30 occurring at different times. We want to ask questions, 31 for instance, what is the impact of treatment 32 discontinuation? So to do so, we put an extended Cox model which is similar to traditional Cox 33 , and yet 34 considered covariants as time varying, so all patients 35 started at baseline at an unknown status, but then after 36 the first progression, we locked their status and then we 37 also accounted for when it was continued, so it's 38 essentially a subgroup of a subgroup. As time progresses 39 on the study, dynamically we allocated to different 40 subgroups, as suggested by the figure on the left. This 41 allows us to tease out the individual impact of either 42 belonging to a group or being on a in that 43 particular subgroup. So when we look at the hazards now 44 associated with being on drug in any of these particular 45 subgroups, it more or less captures the trends that I 46 showed you in the Kaplan-Meier plots, so here, our

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reference hazard is the disease control group, and you can 1 2 see that as we move down this spectrum that patients with 3 no growth mets minus and then mets plus and then to the 4 target lesion, the hazard increases as we move down the 5 table. Now, again, as we look perspectively at KEYNOTE-052, 6 you can see again that the patterns here recapitulate the 7 patterns that we saw in KEYNOTE-001 and also the patterns 8 we saw in the Kaplan-Meier plots, so we see an agreement 9 between the non-parametric and the Cox model results here. 10 Now I think sort of the take home point and more 11 interesting aspect of this is when we estimate the hazard 12 associated with discontinuation and belonging to any of 13 these particular subgroups. We start at the top. You can see that the hazard ratios for each of these subgroups are 14 15 significantly greater than 1, suggesting that there are patients within these groups who stay on drug and there's 16 17 an association, a positive association with survival. We can see the disease control group, the hazard ratios 18 19 , the hazard ratio for our no-growth mets minus 20 group actually more closely resembles the hazard in our 21 disease control group. Then you see a pattern of 22 decreasing hazard such that patients with aggregate growth 23 perhaps a lesser benefit and yet have they still 24 have ... there's still some patients in that subpopulation that 25 could benefit or potentially benefit from staying on drug. 26 Again, as we applied our learnings to KEYNOTE-052, we see 27 the same pattern of hazard ratios where most of the 28 patients show ... some patients who are staying on drug may 29 survive longer. So my quick summary slide here is that in 30 KEYNOTE-001, we showed that there was a difference with 31 survival in lung patients who progressed and so we 32 typically treat these patients as all being a member of the 33 same group, perhaps that's misleading. The perspective 34 would confirm that KEYNOTE-052. The general feeling was 35 that patients who have non-targeted growth tend to survive longer than patients with growth at the targeted lesion 36 37 level, including patients who don't meet the threshold for 38 SLD growth but just growth in a single lesion. I think 39 most importantly we found that there was an association 40 between staying on treatment post progression and survival, 41 and again we confirmed that in KEYNOTE-052. So there's 42 sort of two competing hypotheses here. Either pembro 43 itself is patients or alternatively commissions 44 are selecting patients with better prognostic features to 45 stay on drug. I think if we assume even a sort of worst-46 case second scenario and this suggests that RECIST alone is

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doing a poor job of capturing the disease severity in these patients, so this...I think these are interesting questions. One thing we want to do next is potentially look at these trends and chemo treat patients because we think we could better tease out some of the causality here. So that's all I have. I just wanted to...just a quick acknowledgement. Seth Robey, who is in the audience, was a key in a lot of this work and has been an incredible player here. We have collaborations with our stats colleagues--Robin Mogg, Brian Tomko, and many other people.

Our next speaker is Dr. Yanan Zheng from MedImmune.

11 [APPLAUSE]

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18 19 Dr. Zheng: Thank you for the introduction and it is really an honor to be invited to the ______ workshop and I hope to take this opportunity to talk about our ______ MedImmune in modeling of the tumor kinetics and overall survival but verify prognosis including durvalumab's efficacy for . So as many of you know, durvalumab is an anti-

20 21 PD-L1 monoclonal antibody that has been developed for 22 cancer immunotherapy. Its mechanism of action is to block 23 the interaction between the PD-L1, its effects on both 24 tumor cells as well as immune cells can lead to these 25 factors as described on T-cells. Blocking the interaction 26 between PD-L1 and its receptor will result in enhanced T-27 cell activity as well as T-cell mediated tumor cell killing. 28 Therefore, leading to tumor shrinkage. Just earlier last 29 year, durvalumab has been approved for patients with 30 locally-advanced or metastatic urothelial carcinoma that 31 have progressed following not even maintaining chemotherapy. 32 The approval of durvalumab using the patient, as many as supportive data from the study 1108, which is at 33 34 phase 1/2 dose escalation expansion study in solid tumor 35 which includes using expansion for 10 mg per 36 kilogram Q2W. So in that study, durvalumab has 37 demonstrated favorable efficacy with concurrent objective 38 results with a 17.8 in a total population in 27.6 in the 39 PD-L1 type sub population where the high was 40 defined as greater than 35% of PD-L1 expressions in the 41 tumor biopsy. At this time, it corresponded to a median 42 survival of about 18.2 in the overall population and 20 43 months in the PD-L1 type population. Now, the question 44 about we would like to address is how can we further 45 improve the efficacy, how we will benefit and impact 46 patients who are likely to respond to durvalumab treatment

so that we can use that to greater _____ and also to 1 2 quide the physicians' decision to identify who are the best 3 patients to treat. So to answer this question a 4 pharmacologic modeling approach is because 5 better than the traditional approach which looks at 6 dichotomized response to date, the pharmacologic modeling 7 focused on the entire longitudinal tumor responses to each 8 individual patient which contains a lot more to each 9 information and also it allows us to evaluate the 10 biomarkers in a continuous fashion rather than looking receptors. Further it is a powerful tool to 11 12 have a systematic way to evaluate the multi-13 variant/covariant analysis. So, using the pharmacologic modeling approach, we developed a tumor kinetic and overall 14 15 survival modeling framework for immuno-oncologic therapy. So first, we developed a tumor kinetic model to describe 16 17 the longitudinal tumor response over time which enhances 18 the tumor growth as K_{α} as well as the tumor 19 killing in response to immunotherapy which is 20 $K_{\rm kill}$ and then we then developed an overall survival model 21 which uses the predictive tumor dynamics from the tumor 22 kinetic model as the input function and predicts the survival from over time. In addition, we also 23 24 developed a dropout model to describe the relationship 25 between the tumor response and the likelihood of patient 26 dropout from the study. Lastly, we performed a multi-27 variant/covariant analysis on all of these models to 28 identify significant factors not only for tumor growth but 29 also for tumor killing, the dropout as well as survival. 30 So, using this modeling framework we have analyzed data from using patient in the study in _____. So, here on 31 32 the left-hand side you can see only a third of individual 33 tumor kinetic from the study. Here, the tumor 34 size is defined as the sum of the longest parameter. So 35 you can see that there is a modeling agent 36 individual responses and when you look at each individual 37 responses closely, that is the essentially three different type of tumor dynamic profiles. So the first 38 39 type is one that has continued tumor progression whereas 40 the second one shows that the last tumor shrinkage rather 41 than and then reaches a steady state over time as opposed to and the third type is 42 43 characterized by initial increase in tumor size. So, 44 has little progression and then followed by 45 tumor shrinkage which suggests a delay in the tumor 46 response in these patients. So in order to describe these

1 different types of tumor kinetic responses, we developed a 2 model that describes the tumor growth as first 3 models and K_{α} here and then the tumor killing in response to 4 anti PD-L1 treatment and the scores as added killing rate 5 constant K_{kill} and here the growth rate is modeled as first 6 order kinetics as done in the standard models and the 7 killing rate is modeled as the same order kinetics to 8 represent reaction which will be the immune 9 cells and the tumor cells and also allows the system to 10 reach input again over time as consistent with 11 data. Also, in order to describe the delay in tumor 12 response in some of the patients, we also incorporated a 13 delay in the immune response which is modeled using a 14 transit compartment model, a model rate with K_{kill} so that in 15 some patients the killing rate increases from zero is 16 maximum value over time and allows to delay tumor response. 17 So with these structural model with each individual the 18 ability in incorporating the population to the tumor 19 kinetic model, we are then able to describe all the 20 different types of tumor kinetic in the study. 21 And another important aspect in the tumor response is that 22 there is a strong relationship between the tumor response 23 and the dropout. As you can see from the individual 24 profiles, the patients who do not respond and progress with 25 the study tend to drop out of the study early. So very 26 limited data from these subjects, whereas the patient who 27 responded to the drug tend to stay in the study for a 28 longer period of time. Therefore, we needed to develop a 29 dropout model to track the range _____. So here, it 30 shows the different tumor kinetics in the study using the 31 final tumor kinetic model coupled with the dropout model. 32 Again we can see that the model is finally 33 fairly well, both in terms of mean response as well as the 34 durability among individual patients. So with the model, 35 we can then perform model-based covariant analysis to 36 identify significant covariates for a tumor kinetic 37 . Specifically, with both the tumor growth rate 38 constant K_{q} as well as the tumor killing rate constant K_{kill} . 39 So data in gathering action of anti-PD-L1 40 therapy is to induce the T-cell mediated tumor killing. 41 Therefore, the factors that impact the tumor growth rate 42 are considered as prognostic factors as those who even have 43 another treatment whereas the factors that affect tumor 44 killing are computed as related factors because those 45 should be related to the treatment effect. So for the K_{α} , 46 the growth rate we evaluated around the potential

prognostic factors as you can see here. For example, neutrophil ______ standard ratio, ______ spaces, line of therapy, the ECOG's health performance fitness as well as the baseline levels of LDH, hemoglobin and albumin which have been reported in the literature as potential prognostic factors ______ types. So the model as in the ______ spaces as the most significant factor for K_g where the patients with liver metastasis are associated atypically with greater than 50% increase in their tumor growth rate.

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On the other hand for the tumor killing rate, we evaluated 11 the PD-L1 expression as specifically in the 12 13 type two different scores here, one is the TC score 14 representing the PD-L1 expression in the tumor cells. The 15 other one is IC score which represents the PD-L1 expression 16 in the immune cells. So the model actually estimated that 17 the IC score is the significant factor while the TC score 18 or the tumor killing and increased IC score into increased 19 killing rate which leads to greater tumor shrinkage as 20 consistent with what was found in the data. 21 Also the model predicted the baseline tumor size as the 22 significant factor where a smaller baseline tumor size are 23 associated with a great killing rate which the definite 24 smaller tumor is easier to treat. So more interesting is 25 how we translate to the tumor response rate in 26 we used the models in remission to predict the tumor 27 response rate by various groups and then you can see here that model predicts a high response rate in 28 29 patients with higher IC scores or with baseline tumor size 30 as well as the liver metastasis, without liver 31 metastasis compared to those with the liver metastasis. We 32 can also use the model to predict the response with 33 different cutoff values for PD-L1 expression 34 PD-L1 high population is defined as either TC or IC greater 35 than 25%. So here, using the model simulation, we 36 predicted that increasing the IC count to 25% to 50% and 37 further to 75% will lead to increase the response rate and 38 the TC score does not have the obvious impact. So of 39 course this is based under the result of one study and we 40 will continue to validate this in future trials and once 41 this is confirmed, this could help in improving the patient using 42 in terms of clinical application of PD-L1 43 patients with durvalumab treatment. So then, we want to 44 see how the tumor kinetics is linked to the overall survival. So here this graph shows you curves 45 46 expected survival from the study type and the last tumor

response. You can see that as a clear separation between 1 2 these which suggests that there is a strong 3 relationship between the two where the patient who has 4 better tumor response had a longer survival compared to 5 those who have poor tumor results. So given that we 6 further have to balance the overall survival model where 7 the hazard of survival is modeled as a function of the 8 predicted tumor dynamics from the tumor kinetic model as 9 well as other baseline factors and predictive survival 10 probability over time. So on the model actually you can see that it captured the observed monitored the 11 12 survival very well with regards to the overall population 13 as well as the sub-group of patients by various response 14 types. So you can see that the model predicts the 15 responders, either with delay or no delay has the longest 16 survival, followed by the non-responder and non progressors 17 and the progressors have the worst survival which is consistent with its . And finally, similar to 18 19 the tumor kinetic model, we also performed model-based 20 covariate analysis using the survival model to evaluate the 21 significant factors for survival after the tumor kinetic 22 has been accounted for. So we identified a number and 23 various of TC and IC score, liver metastasis, 24 hemoglobin as well as albumin as significant features and 25 here it shows several examples of the simulated overall 26 survival occurrence, like covariance interest. So for 27 example you can see that similar to tumor kinetics response, 28 the increase in immune cell PD-L1 expression of these two 29 increased probably besides survival but not the tumor cell 30 PD-L1 expression. And in addition, we also showed that the model also predicted increase for _____ survival for 31 32 patients with a higher baseline albumin levels as well as those without different metastasis compared to those with 33 the metastasis. So with _____ these prognostic 34 35 factors can also be used in addition to PD-L1 expression to 36 help select patients for future clinical trials and also 37 help the physicians to identify the likely responders in 38 the clinic. So in summary, we developed a relation in 39 tumor kinetics for overall survival and dropout modeling 40 input to describe both the longitudinal change in the tumor 41 size as well as survival in cancer patients treated with 42 durvalumab and as a modeling framework as a useful tool to 43 study the tumor cells in combination with as 44 well as the fact of multiple prognostic factors in the multi-variant analysis and ultimately, the results 45 46 from this type of modeling can be used to try patients with

and enrichment strategies and to optimize clinical trial designs for our therapies plus various responses in patients. With that, I would like to thank everybody who have contributed to this ______ including entire financing and ______ and last but not the least, all the patients and investigators who have participated in the development of the trials.

- Thank you.
- 10 [APPLAUSE]

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11 Moderator: Okay. Our next speaker is Amit Roy from BMS.

13 Dr. Roy: Let me start by thanking the organizers for inviting me and let me say some of the role that we have been doing at BMS 14 15 along the lines of . I would like to start by stating somewhat more explicitly the role in dose 16 selection that had been alluded to in some previous talks 17 18 where we had been talking about using tumor response in 19 making decision on dose selection and why that is really, so unlike any other therapeutic area, the oncology endpoint in 20 21 the early phase of a trial is different from the phase III 22 ipilimumab trial anywhere in most cases where the endpoint is 23 somewhat single-based, either it is tumor response rate or 24 its PFS at baseline research whereas its is based oftentimes 25 on survival. It has also been alluded to you like the 26 necessity being pointed out by Dr. Woodcock the assessed 27 number of ORR. Our research actually does not use all 28 available data. Usually, it requires a minimum new recent 29 followup, let us say, for six months, let us say, and they have before that ipilimumab use and this is , so 30 31 you have duration of followup with every situation response 32 More of our... And there is also exponential • 33 study in a limited number of subjects that we have, so the 34 point being that what we want to do is ... This is actually 35 what is reasonably well despite all the talks starting, you 36 know, this morning, but I think there is a lot more that we 37 can do due to university setting of necessity and data are so 38 precious and only fragment use of all the available data. We 39 will disclose selection becomes more complicated overall 40 honestly.

42 So the proposed approach that we have been following is very 43 much along the lines from the other speakers here. We got 44 across the tumor growth dynamics and overall survival for 45 tumor genotype. Maybe the assumption that these tumor growth 46 dynamics and overall survival is more agnostic with 47 nivolumab. That is to say, the more you characterize the

tumor response profile, and I am going to talk about it very generally, does not necessarily mean someone is dying with it over time. It could mean other things as well. Only that is what we should look at. That once you characterize the tumor response over time that essentially represents an official efficacy for the effect of drug. Ready to press now which drug which may induce that response once you characterize the response which you are going to do pretty similar as to . And then once you have this, the more something you characterize the tumor genotype it is going to reflect to the clinical data that you might have from other phase trials with limited number of subjects with new followup to be able to make predictions of survival and make judgments on whether that overall survival you would like to be further detailed So you can form both no-go decisions or go . decisions as that is the informed dosage.

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So that I can motivate these concepts with every case done and effectively with this, quite recently, it was published with utilizing a few number of TGD-OS model on nivolumab applied to break overall survival with ipilimumab. So the advantage, these are both immunecheckpoint inhibitors, but actually, the mechanism of action actually complementary. Ipilimumab is stimulates the activation of and proliferation of T-cells whereas nivolumab primarily reactivates quiescent T-cells in the tumor microenvironment, and there is evidence that these mechanisms of action are complementary comes from a peripheral file we have regarding advanced metastatic melanoma which shown that complementing the two is better than having it alone, so somewhat they are adding something to each other. We actually have a very interesting set of data set within inhouse to evaluate this because what happened was that ipilimumab was approved for 3 mg/kg once every two weeks for four doses, and other than from the basis of a phase III study that was initiated prior to BMS becoming involved in the development of the drug and then in the end we got involved in the development of the drug, there were several phase II studies that were conducted, one of which was of two-ranging phases. In these two-ranging phases of the study, we found that the 10-mg/kg dose given once every two weeks had better tumor response, RECIST response, than the 3-mg/kg dose. Soon after that, the phase III study led up. It was positive for ipilimumab solely received , but we also have a postmarketing commitment to the phase III study to evaluate free-growth system, free-growth study Subsequently in the meantime, nivolumab came along and it has a short benefit in overall survival for metastatic melanoma as well as other genotypes. This is an aside to those that were initiated for three weeks of the nivolumab versus the

once in two weeks with a flat dose of 240 mg. So the essence of it, it is unusual to have phase III data from two different agents with the same treatment effect which can actually do this

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We now address to the approach to tumor growth dynamic We have decided to sort of move to an initial modeling. model for describing profile, and it was shown over here significant loss from ipilimumab and what you can see usually are three distinct profiles, types of packet of response, and these had been classified based upon initial model approach that had been given nivolumab. And what you can see clearly is that ... Okay. I think I said that. Just to make sure, the tumor growth dynamic model was based upon a model that was published by Young some years ago. We did some modification to actually make sure the model had one component that has no growth at all because otherwise everyone has growth with this that has been present over time. And that was not the fact that we had seen. We had enough stable tumor growth that we had seen. And also as an aside, we make a point that in this case tumor shrinkage model was exponentially decreased. The linear increase. tumor growth is of We also think exponential increase to growth rate models that we have taken very comparable. And as you can see given the limited amount of data that we have for patients who are progressing, a linear growth model recently discussed that recently at least after that.

29 Into the view of looking at this, maybe you can say, "Okay. 30 The subjects in this no-growth group of subjects are lacking 31 growth better in terms of overall survival" whereas the progression-free overall survival 32 we have linear 33 growth survival. So a few points to make over here, we 34 decided to use that data profile because again 35 even though we may not get a deep response we have a long 36 durable response and this is a thing. A single fine-point 37 example, we can get tumor shrinkage and maximum tumor You might get some subjects who have high 38 shrinkage. 39 shrinkage that involve generally overall survival. So that is the reason why we chose the shrinkage model. 40

42 So here are some key results from this long study. 43 Interestingly, the progression-free survival was very similar 44 for the three . I am showing the reference that 45 whereas there was a highly significant difference in overall survival. So there was about 6% to 7% difference in maximum 46 47 survival at one year. So the approach that we have taken 48 actually is to accumulate a setback. So the approach that we 49 have taken in terms of overall survival modeling is to 50 include all the baseline prognostic factors that can include

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all the features of a tumor profile to include the shrinkage rate, growth rate and time key to include baseline to include absolute and relative tumor sizes as well as include new lesions that may appear at times, so from time to time, the model... Importantly, we also recognize that there are subjects who drop out early. That is the highest factor that has been included in the model as well as in the... That is it. I mentioned that one.

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10 So here are the results of the study, a complete list of study, a completely different drug. We did in 11 12 describing the 3-mg/kg dose and the 10-mg/kg dose. 13 The effectiveness had turned out very good. Despite this, 14 the model has captured some of the benefit, additional 15 benefit, with the 10-mg/kg dose. So what we are showing here 16 is how can we actually use this model to limit the data and 17 how can we actually do. So if you take a limited data from this phase III study with ipilimumab, 35 subjects turnout 18 19 with six months' followup and you use the model for free-20 tumor growth survival, can you relate the better overall survival with 10-mg/kg as better treatment for the patient? 21 22 This shows exhaustive direct horizontal line that is showing 23 the observed differential in survival percentage at one year 24 and in two years, and the show the distribution of 25 clinical trials that show an advantage. So approximately between, you know, 70% and 75% _____ would show that the 26 27 10-mg/kg dose has been shown better even though PFS was 28 essentially identical in percentage. 29

So in summary, the TGD-OS model developed with one drug, nivolumab, ______ rate of survival for a different drug, ipilimumab, providing proof principle that this set of approach could be agnostic to the drug in terms of tumor shrinkage and the tumor response profile may be sufficient to break the overall survival on the drug. This set of model can be used to leverage data from all new clinical data from ______ receptors to form a program of ______ modification and several set of improvements to the TGD-OS model can be made and maybe discussed at the

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 Moderator: Alright ______. Our next speaker is Dr. Rene Bruno

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 Dr. Bruno: Thank you, and welcome to the FDA ______. ISOP

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 _______. find interesting ______. So _____.

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 _______. In fact, there is a link between ______. treatment ______.

The beauty of that is that you can develop a model using 1 2 clinical studies, and then you can use is used 3 as a biomarker to capture treatment effect and predict 4 benefit. Then when we have developed this type 5 of model, then we can learn about TGI data and therefore 6 . There is a variation of this where we can 7 apply this type of modeling entering phase 2 studies or in phase 3 studies when we are 8 ______ then we can ______ tumor data _____. 9 So when we are talking _____ and recently we have 10 11 _____ actually today TGI-OS models ______ phase 2 data that have been used _____ phase 3 studies 12 _____. From there, we have two studies. The POPLAR 13 14 study was a phase 2 study for varying dose effects 15 single agent in patient with . Those are the data. You can see that atezolizumab is doing 16 better than docetaxel. _____ is the team that developed docetaxel _____ and I think _____ 17 18 successful phase 3 trial in _____ patients _____. 19 20 So that is very, very interesting. 21 22 Okay so then we developed a model based on those data _____ model _____. The tumor growth inhibition 23 _____ using is _____ that is being presented by 24 except that instead of _____ patients 25 26 depending what you see, we used a population approach with that. Patients ______ we could estimate ______ for 27 28 each of the patients. We then _____ population approach _____ The only thing _____ at least 29 _____ baseline, you can _____ that in the POPLAR 30 31 study, we had 277 patients; and 91% of the 277 patients 32 _____. What I am showing here is the typical profiles of the _____. What you see _____ is docetaxel, 33 and you see that docetaxel _____ initially _____ 34 35 than we would expect; and then there is compared with atezolizumab _____. So if you got any of the 36 matrix overall survival, you will see at least 37 38 that as we are using earlier is not going to 39 predict the benefit from atezolizumab. Same when we have 40 the using in the past. Of course and we want to predict the _____. So you will see that 41 those things . Now let's see what's happening in 42 those patients that we defined as _____ those patient 43 who are _____ right? _____ and here you see that 44 there is _____ between docetaxel and atezolizumab 45

_____ with the atezolizumab _____. Of note, we did not find any evidence of _____ drug effect kind of 1 2 3 ______ studies. We did not find any ______. 4 Now we are going to _____ of the patients, and we 5

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 6 7 not a good assessment _____ patients _____ number 8 9 of sites that are _____. When we use _____ 10 treatment effects _____ but when you _____ explain the _____. 11 12 Now we are _____ model in simulating the POPLAR study, and this _____ here. We are simulating _____ 13 14 study _____ distribution for each of the _____ 15 16 and what you see here is a prediction of we predict the _____ we did that for all of the patients 17 18 and we did that by baseline biomarker expression. So 19 patients that expressed _____ PD-L1 at baseline _____ tumor cells or immune cells _____. Those 20 patients are benefitting a bit more _____ when the 21 22 patient not expressing PD-L1 . In addition to 23 that, we have a marker or a gene expression of the Teffector and interferon _____ genes ____, and we could show _____ predict the model _____ 24 25 26 benefitting the patient with high _____ gene expression _____. Now we can _____ further and 27 28 we predict that in phase 3 studies _____. This study _____ docetaxel _____ but still we can predict 29 30 the phase 3 study based on the tumor dynamic data _____ in patient by data of the biomarkers. Here you 31 will _____ the patient with no expression of PD-L1 32 benefitted. Patient with _____ gene expression benefitted _____. Here we have the _____ here we 33 34 got the phase 2 study _____ when the _____ phase 35 3 _____ comparing atezolizumab to _____ but still 36 we see the same thing in the _____. Here we have the 37 _____. Here it is a qualification of the model 38 39 but we have the two groups of the patients. 40 First group were first-line patients, cisplatin group were second-line patients who _____ and you see 41 that _____ patients _____ first line versus 42 second line= _____. Now we go to that model and we 43 44 predict the _____ that is comparing _____

1		docetaxel this group and we which is
2		comparing atezolizumab with Same thing
3		So now what we do is except the
4		phase 3 studies Let's see what we
5		can do to help selection of combinations
6		Okay, so we know that predicts
7		This is a typical profile. This is the one
8		you have seen in KG growth rate. You see that the
9 10		predictions here. We can see that
10		single agent or even growth rate 20%
12		So then based onyou can
13		show you studies that recently because they can be You have to Here what we are
14		doing is that we are comparing the growth rate estimated in
15		those patients single agent patient
16		characteristics Then we compare what is the
17		difference in growth rates patients. From there
18		growth rate we see that the
19		of the growth rate is According to
20		the OS model, we would expect
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22	[APPLAUSE]	
23	Moderator:	Next to the last presenter is Dr. Jenny Zheng.
23 24		Next to the last presenter is Dr. Jenny Zheng. Yeah, I would like to thank the committee inviting me today
		Yeah, I would like to thank the committee inviting me today approach and to guide in decision
24		Yeah, I would like to thank the committee inviting me today
24 25 26 27		Yeah, I would like to thank the committee inviting me today approach andto guide in decision making So before I give the presentation, I'd like to emphasize that the previous presentation is all
24 25 26 27 28		Yeah, I would like to thank the committee inviting me today approach and to guide in decision making So before I give the presentation, I'd like to emphasize that the previous presentation is all about phase 3 information but here we are
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we can use _____. Secondly _____ we should learn from prior knowledge ______ the quantitative relationship between ______ and long-term 1 2 3 4 clinical endpoint using approach 5 prior data indication. The third is using the 6 relationship from the project the 7 clinical outcome using the data obtained from the early trials. _____ I think the tumor dynamic is a good 8 9 approach to • 10 So I want to talk about _____ tumor size data. Tumor 11 size data actually is _____ trials. Tumor size 12 actually _____ so those information can help us to 13 bring the _____ tumor size _____ contains a lot 14 15 of information the drug effect difference caused by _____ or caused by _____ tumor size _____ 16 information. _____ it has been diagnostic _____ 17 tumor size _____. So that relationship can be 18 quantitative _____ relationship actually _____ to 19 project long-term clinical outcome using the 20 21 tumor size information. So in this aspect, FDA 22 made a huge contribution to _____ this exercise from the FDA _____. So the objective of 23 24 _____ presentation is to present two cases to demonstrate the value of using _____ data and prior 25 knowledge for decision making, and specifically _____ 26 27 first-line treatment for metastatic renal cell carcinoma. This presentation _____ the impact of the proposal so 28 I am not going to go _____. So the new treatment 29 30 assessed here is axitinib plus avelumab. Another _____ combination X+Y which is masked treatment 31 _____ as a first-line treatment of sunitinib. So the 32 first step is to pull _____ data from the new treatment sunitinib and then _____ dynamic model. 33 34 35 Data from axitinib plus avelumab come from patients. This actually is _____ considering this is 36 37 a phase 1b study. Data from combination of X+Y come from 38 data only from 10 patients. For standard of care data, _____ information. So the drug effect, as 39 I said, can be estimated using _____ study; and the 40 and drug effect _____ from the model 41 42 compare the two new treatments versus sunitinib. This comparison _____ focus on two parameters. One is the 43 tumor size which is _____ this presentation. 44 45 Another is drug effect on tumor shrinkage rate. The reason

to _____ tumor size _____ of the treatment so 1 2 that parameter _____ can be estimated _____ much 3 information about the tumor growth. So this is the tumor _• 4 dynamic model we use in _____ proposing _ 5 This model basically has _____ assumptions. The first assumption is that tumor growth _____ growth rate of KL indicated in this equation. The second assumption is 6 7 8 that tumor shrinkage in this equation. The 9 third parameter is about described resistance. Eventually it is assumed that the tumor meaning the tumor 10 will regrow actually describes how . 11 12 This slide shows the tumor reduction after treatment of 13 axitinib plus avelumab patients. As you can see, 14 tumor size shrinkage is quite a lot, and this reduction is 15 good. However, we don't know how good is good enough for combination model. So this slide shows the 16 17 comparison between two treatments off axitinib plus avelumab versus sunitinib. So all the represent 18 19 tumor size reduction from sunitinib, and the right line 20 represents tumor size reduction from combination. So as 21 you can see, combination did cause greater tumor size 22 reduction as compared with sunitinib. However, I think 23 so the tumor size reduction rate is actually compared between the combination versus 24 more 25 standard of care sunitinib. So as you can see, the 26 combination did greater tumor size reduction rate as compared with the sunitinib. The difference 27 28 actually is statistically significant. This slide shows the tumor size reduction _____. So as you can see, 29 30 the combination caused more tumor size reduction and the 31 difference is statistically significant. So the same 32 we will actually apply to treatment X+Y, and this I would say _____ data for the second combination 33 tumor size reduction. When compared with 34 better than 35 sunitinib, the reduction does not 36 the standard of care. For the tumor size reduction rate, this is actually really ______ so no surprise. For the 37 38 tumor size reduction _____, the second combination is 39 sunitinib. So based on that, actually the second combination _____ move forward not only based 40 41 on this exercise but _____ to this agent. So this 42 _____ support _____ of the combination of axitinib plus avelumab for the second 43 44 combination, and I hope the case convinced that a modeling approach can be informative _____ knowledge for that. 45

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So I would like to acknowledge the team _____ without their support, this exercise is not possible. So that's it.

4 PANEL DISCUSSION

5 [APPLAUSE]

6Dutta:Thank you all.We have _____ presentations,7the first few focusing on methodology _____ examples.8I now would like to ask the other speakers to come9_____ to ask questions, as well as _____.

11So I think we are settled. Before we start ______ from12the FDA. Dr. Atik Rahman is the Director of Division of13Clinical Pharmacology, and Dr. Jerry Yu is a team leader in14the Division of Pharmacometrics. Before we entertain15questions, I would like to give the floor a little bit if16Dr. Rahman or Dr. Yu has any _____.

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18 Dr. Rahman: Thank you for giving me an opportunity to say a few 19 words. The first thing I would like to mention about what 20 we have done at the FDA Board with MIDD . The first thing is that we have started to use MIDD drug 21 22 development as well as in drug approval and in drug 23 labelings. We have used MIDD approach for validating the 24 selected dose or approved dose retrospectively through this 25 tool. We have also marketing trials so as you 26 know that most of the data that comes and as you have seen 27 that sometimes the PFS and OS do not have the same outcome, 28 and we have issues related to dosing which is universal not 29 only for Oncology as Dr. mentioned. We have 30 used phase IV approach to PMR post-marketing trials, and we 31 have used modeling to kind of help select dosing comparison 32 in the post-marketing settings. We have also used a community-based modeling approach to informed dosing for 33 34 combinations especially for drug interactions in the labels. 35 So these are just a few examples of modeling approaches we 36 have used in the FDA. All we plan to do is to further help 37 move this bill forward and in order to do that, we need to 38 have training within the FDA to understand how this 39 technology is developing and how we can have early resource 40 have early discussions with allocation to the 41 pharmaceuticals to provide our knowledge to help move their 42 particular drug development program. Also we need to

collaborate internally among our pharmacometericians, 1 2 statisticians and the pharmacogenomic folks as well as the nonclinical scientists to understand how we can approach 3 4 this modeling _____ development from the get-go to the 5 end setting. So these are the few words that I 6 have 7 Moderator: Thank you. Dr. Yu? 8 So I actually have _____ oncology products _ Dr.Yu: delayed effect. So when we _____ an assumption with 9 10 using the model is that the _____. So as we see _____ modeling _____ today, we can use _____ 11 tumor response. _____ is always on tumor, and the 12 if it is tumor and actually contains 13 14 that is when you use all data, tumor sizing data, you can 15 actually get more information. This is important in the 16 early stage because in the early stage when we look at 17 . We look at the detail of tumor size data, it 18 really provides more information tumor modeling 19 will work . 20 Moderator: Thank you. I think Dr. Roy has Thanks, Sandeep. I just wanted to correct an omission I 21 Roy: neglected to advance to the _____ the work was done 22 _____. The tumor marking was done largely by colleagues ______ was done largely by colleagues at 23 24 _____ Research Group, and we _____ collaboration. 25 26 I just want to mention we actually _____. Thanks. 27 Moderator: Thank you. We will take the first question. 28 Audience: Thank you so much. from 29 Pharmaceutical. My first question is for Dr. Amit _____. In your example _____ if PFS was the 30 _____ of the study or overall survival? 31 32 Overall survival. Roy: 33 Audience: Overall survival. So hence I do understand that the goal of this session was to present _____ but I think it 34 35 will be interesting to see something because one of the examples when we presented data for 3 mg and 10 mg $\,$ 36 was _____ to see if _____ the same way _____. 37 This is really what I saw as missing in all of the 38 presentations so I do not see the metrics how 39 this endpoint if we look at the tumor model. So 40 41 what has happened between the time we do the process versus _____ whether or not the clearance has 42

changed overtime, and I think one of the examples is that 1 2 immunotherapy that clearance has changed 3 overtime. How this affects the endpoint of the 4 process. Yeah. So in the we presented, we did not 5 Roy: include the exposure response part. 6 So the doses 7 will be investigated with 3 versus 10 8 increase in dose. The of monoclonal antibodies 9 is quite small in comparison to that full 10 increase in dose. It is still about 20% additional 25% overtime 11 the change in dose. So 12 change coming from the dose is . Our 13 focus here again, as I have mentioned and as Dr. 14 also mentioned, is that dose actually inducing the tumor shrinkage, the idea was let us capture 15 16 tumor shrinkage and _____. If we can capture that, then you can get, as the next step, the ratio of exposure 17 18 and tumor profiles. 19 Bruno: just to comment actually it is _____ I 20 think it is important to realize that exposure 21 So it is not exposure but survival. It is 22 23 Audience: Yeah. Thank you for that response because-or maybe I should... 24 25 Can I add a comment on what you said? I think that the old Guedj: 26 presentations that you see, I think that we are still 27 by the traditional proportional . 28 Therefore, we expect dose. We expect that if 29 the biomarker responds better from the higher dose, let's 30 say, we expect that this should translate into overall 31 survival. I think we need also to be prepared now, maybe 32 in future situations where the higher dose might very well affect the _____ marker that _____ that this 33 marker does not translate differential effect 34 35 even at all in some situation to overall survival. We 36 could very well have a situation where the high dose 37 improved the but does not improve at all the 38 survival. So in that case, what could be the 39 interpretation? We need to think about whether this is due 40 to the way that we modeled the biomarker into survival take into account all the factors such 41 42 as toxicity for instance. So I think there are a lot of 43 things that we need to think about in that area.

2 I'd like to ______ a comment as well. So you mentioned Turner: 3 exposure. We have actually done a lot of work with exposure response and looking at _____ tumor size and 4 5 survival. Just as you mentioned, clearance is really 6 with response so it is not the typical pattern. 7 We think about exposure . It is actually 8 exposure is a trailing effect of disease status where when 9 you look dose, you see a very clear relationship of exposure response, but then _____ this dose ranging, 10 11 you can clearly deconvolute and see that actually clearance 12 for disease status. It is not the typical 13 causal relationship of exposure driving response, so I 14 think we have some _____ of exposure response.

15 Moderator: We'll have the next question.

16 Audience: all the speakers, there's really a neat collection of so many _____ approaches in tumor sizing. 17 18 everything were saying, there is some 19 commonalities but also some differences so I think like in 20 some slides, there were references to new _____ being important for overall survival but then it 21 22 wasn't that important compared to overall change in tumor 23 size. In some talks, there was mechanism tumor size ______ survival ______ like in the first 24 25 assessment, you compare doxy and a little bit. It actually is _____ into account. I guess with so 26 27 much leadership here in terms of ISoP and FDA, I feel like 28 something really useful would be an effort to kind of 29 synthesize all this information into just 30 everything like what are some few _____ we do agree on and ______ states that need more investigation and also 31 32 _____ way to do that .

33 Yu: Just a brief response. I think, I mean the question asked 34 . I think it is the definition of and 35 there is what you call immune-modified disease criteria so 36 we have _____ progression. _____ definition as a 37 new definition specifically for the therapy, kind of implying that _____ it is important _____ 38 39 long-term benefit as _____ said before. So I think also we have modeling _____. There is also _____ 40 41 data so that's •

42Bruno:Just to comment on your comment.I think you're right.We43could may be kind of _____collaboration to see what

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1the best approach is ______
thinking of doing ______
drugs and studies.conception, and we are
collaboration across

If I can also just quickly comment _____ quick. So I 4 Roy: 5 think _____ and clearly the tumor data is much, much 6 greater than that. I think what you saw target 7 lesions is quite different from having it from one large lesion. The will be different. The implication 8 ______ survival will be different. Where the lesion 9 10 occurs _____ some references to liver metastasis, for 11 . So I think new lesions can have example, _____ 12 . I think there is room for improvement and really digging down deeper into aspect of it. 13 _____ actually need more information from _____. 14

Audience: Lily Turner from _____. First, I have a comment on 15 this general discussion on the relationship between 16 17 exposure and response endpoints response and 18 survival. I think it's important to be clear that the 19 comments that were made about the relationship between drug 20 clearance and things _____ tumor burden, that really 21 an antibody or an immunotherapy scenario, you might have 22 other or drug classes where you could have a 23 relationship with the concentration and change in tumor 24 size, and then an independent relationship 25 survival. May be we will hear more about that later, but 26 now I have a specific question for Dr. Zheng from 27 AstraZeneca. In your model, did you test for correlation 28 between the baseline tumor size and the shrinkage or the 29 delay in treatment to see if the reason for the delay is 30 just due to bigger tumor or if there is a delay just based on tumor size? 31

Yes. We did test the baseline tumor size as a 32 Zheng: for the _____ constant, and actually it is a 33 34 significant _____. As I showed in the results, the 35 patient with a smaller tumor to begin with has a higher 36 tumor _____ rate. As far as the delay time, so we did 37 test the _____ for the delay time in a post hoc fashion so after we have accounted for the _____ 38 39 factor from as well as tumor remaining correlation between _____ and delay time, 40 41 and we didn't find any significant _____ at that point.

42 Audience: Thank you.

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_____ I have a question regarding the influence of 1 Audience: 2 post-progression treatment to overall survivor. I think in most cases, the treatment either surgery or 3 4 medication may influence the overall survival especially 5 when overall survival is much longer than the _____. 6 In randomized trials, the post-progression 7 treatment is not always balanced between the control arm 8 and treatment arm. Therefore, in this case, the efficacy 9 and results may be affected by such imbalance. So I just want to clear the panelists' opinion regarding 10 this issue and _____. 11

So I think it _____ presentation material that we saw. 12 Turner: We weren't comparing necessarily the treatment versus 13 14 control. We were comparing treatment versus treatment. So 15 here we see progress discontinuing or they remain on the drug. We are not advocating for a 16 17 causal relationship here because there is clearly an issue 18 of for those patients who do stay on the drug 19 post progression, compared to their peers who received the same treatment but discontinued, it was associated with 20 21 longer survival.

22 excellent presentation. I actually have two Audience: questions, one regarding the which is basically 23 24 we are moving from making an inference personalized medicine, and that's where we want to be in 25 terms of the biomarkers especially for _____ so the 26 27 idea here is how can we do a better job identifying those 28 patients who are responding due to therapy . So 29 my question to the panel is what are we doing about the 30 biomarker? Especially most of the work is more of post hoc, and what we're doing is we have _____ so the 31 32 literature is _____ this is prognostic and it is all over the place as a clinical pharmacologist 33 34 to understand better how these biomarkers behave 35 and how we can

Since no one else is speaking out a comment on that, I 36 Roy: 37 think my sense is that most, if not all responses, have a very active biomarker _____. Unfortunately it is not 38 39 identify biomarkers. So for example, 40 for _____ has a very nice _____. It really activates and proliferates the T cells dose 41 42 response _____ does not always lead to improvement in 43 tumor response or survival. Although we have looked very, very deeply _____ for over a long period of time 44 because there is who likely respond do not even 45

find _____. So it is not always possible to identify 1 2 a biomarker. In addition to that, the notion that we want 3 to have a method that is treatment agnostic to predict 4 survival _____ sort of converge on this tumor response profile _____ talk about it in very general terms, it 5 6 does not . It could be volume. It could account 7 for different number of lesions and so on and so forth, but 8 that ultimately I think has the potential to be agnostic to 9 the drug where as a biomarker is likely to be connected to 10 the of the drug.

11Bruno:Just to comment on biomarkers.We are trained to do12biomarker gene expressions _____, right?When we do13that ______ we can see that some of those biomarkers14are very strongly correlated ______ they would also15have _____

16 Zheng: I would like to comment _____ immune-oncology actually 17 is but in terms of . I think the challenge here, in my experience, is the how we 18 19 biomarker, what biomarker needs to be 20 because in immune-oncology, we work with so many pathways 21 so a single biomarker for prediction of outcome, I think, 22 is _____.

23 Moderator: _____ willing to ask your questions _____ then we
24 will have _____ questions _____.

25 Audience: This is from Genentech/Roche.

26 speakers who are telling us about what they have done and 27 data sets for phase III and so on. We have 28 learned a lot of insights from these data so we can connect tumor growth to survival _____. We heard quite a bit 29 about _____ but _____ actually be able to bring 30 31 this to the table in a tangible way that we are actually 32 helping patients in our clinical trials or ultimately 33 helping patients Dr. Maitland was talking about. So I 34 would like _____ the panel to think about 35 challenges still that what could be some of the things that 36 we could do and whether FDA would help us with 37 because this is part of expediting the development part of 38 using model-based decision making. So what are some of the that you see and what could we do as an 39 40 organization ISoP .

41Audience:Actually I also want to tackle this question42FDA. So thank you for this brief presentation.We saw a43lot of ______ from the industry side ______ and

there are some . A lot of times, you do not have 1 2 clinical data and traditional but why will you use this tumor growth model to address this question, but 3 do you see these kinds of things? So that may 4 affect ______ survival ______ immunogenicity but if 5 6 you have reliable tumor-growth model and you can integrate 7 to that immunogenicity to adjust it can affect 8 the overall survival. So those kinds of 9 questions ______ need to address ______ regulatory 10 agents.

I think those are great points and from the clinician's 11 Maitland: 12 perspective, you asked about low-hanging fruit and 13 collective opportunities. As fantastic modelers with great 14 teams, you are used to doing the most you can possibly with 15 the available data. I think one of the compelling issues I 16 see is we are still collecting data at fixed with regard to tumor burden based on conventions from 17 18 assessing cytotoxic therapy. We have tried to breach this 19 in individual pilot studies at different institutions. It 20 is enormously challenging because ______ appropriately 21 will not allow us to just perform extra CT scans at will, 22 and similarly patients are only so willing to make the 23 extra trips back and forth to a radiology facility, but I 24 think a concerted effort to better define what are the 25 optimum time points of collection to assess tumor burden, 26 even new models to new technologies, there is nothing they 27 could do that might make a difference in the near term.

28Zheng:Yeah. I just want to concur that this is really very29important. I think the example presented here demonstrated30and hopefully convinced ______ tumor size information31could be ______. However, what is the best time to32collect those information ______ they all kind of make33a contribution in the ______ in this area. I think the34important thing ______ information.

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To comment on that as well, in terms of the ____ 36 Bailey: 37 phase how we decide to switch I think one thing is the _____ in the early stage of 38 phase I trials. We intend to actually move and with those _____ exploration with any other 39 40 forward with those trial. So on the slides, I touched on very briefly at the 41 42 very end _____ looking at how to look for _____ when you have no _____ data. It does not really 43 44 target and estimate what is happening in the 1tumor based on what you see on the blood. To be able to2look at simulated predictions or which doses would give you3suspicion _______ under different schedules ______4within that trial. So to be able to _______ and use of5that data _______

6 Guedj: I think we need to have the same systematic approach in survival _____ in clinical pharmacology. 7 That being said, people _____ to come up with 8 alternative models ______ show why they chose this 9 10 model rather than another one or evaluate ways to have a 11 combination of models, so we need to see that and we need to see how _____ to change the assumptions that are 12 made . So I think it is something that needs to 13 14 be done.

Moderator: So I think we are 6 minutes overtime. I just _____. 15 So I think the questions that were raised today _ 16 17 in terms of fixed dose versus doses. There is still a long way to _____. First, I'd like to thank 18 all the organizers for _____ this workshop. It has 19 been _____ interesting _____ and the industry 20 part of this community. Then last 21 22 There has been bias, a lot of bias 23 immuno-oncology presentations, and in order for this to 24 gain wide acceptance, the clinical community has to _____ kind of decisions has to be applied across all 25 _____ therapies that are being ______ Again, they 26 27 could have _____ there is a lot of _____ a lot of 28 data overall survival. There are many reasons 29 for it and we want to reasons, but we need to 30 understand that and apply a concrete this to be applied more frequently _____. With that, I would 31 like to thank all the speakers _____. Thank you. 32

33 [APPLAUSE]

34 SESSION III MIDD BEFORE AND AFTER APPROVAL

35 Dr. Wang (Moderator): Okay thank you for sticking around. This will be our last session of this workshop. As you can see, we 36 37 designed the workshop to cover the entire from 38 preclinical to early clinical, all the way to its approval. 39 That is why the third session today, we will cover when the 40 whole drug in our data are collected and the sources are 41 ready to submit the whole package for review and the 42 financial approval and how model informed analysis can be used by sponsors to support _____ of arguments 43

and how FDA reviewers review this type of analysis or when you apply additional modeling informed analysis to support approval or laboring or potentially towards marketing targets so then we have three speakers to cover this news and our first speaker who is Dr. Kellie Turner-Jones from VIP and that she is a senior research scientist at Eli Lilly where she is the ______ leader for one drug that she will go into details to discuss at the stage of submission, how model informed development, the informed analysis were used to support most of the disease.

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11 Dr. Turner-Jones: Thank you to the moderators for the invitation to 12 speak to you. I am honored to represent the Event Cycle Team. 13 Please shout if you cannot hear me well. Today I will tell 14 the story of abemaciclib and how model informed development 15 and collaboration, computation and communication. So this 16 afternoon, we will release just the tip of the iceberg. There is a whole lot of model stimulation detail that lies at 17 18 the base so briefly I will go through who the team is, some 19 background of abemaciclib and the model informed development 20 and So first off, this work was highly 21 collaborative. You can see a list of cross functional 22 teammates who worked together to tell a story of abemaciclib 23 and ultimately I would like to also extend a special thank 24 you to the patients and their families and the site and 25 clinic staff who participated. Without their devotion and 26 time and samples, we would have nothing to tell you. So 27 abemaciclib is an inhibitor of CDK4 and 6 that was approved 28 hormone-receptor positive HER2 negative advanced in for 29 metastatic breast cancer based on the results of the 30 registration studies of MONARCH 1 and MONARCH 2. Tt is 31 important to remember throughout this talk that abemaciclib 32 is such It is metabolized to the active . 33 metabolites that are equal potent to parent and then 34 represent an approximately 45% of plasma exposure. With the dosing, with the abemaciclib, this is used as single agent. 35 36 This is orally 200 mg twice daily. In a combination setting 37 with fulvestrant, it is dosed at 150 mg orally twice daily 38 and it is also important to know that dose reductions are 39 permitted per individual tolerability at 50 mg units to a 40 dose of less 50 mg twice daily. So when we were building the 41 models to hormone development of abemaciclib, we always have 42 a purpose in mind for the models or a question. The 43 seasonable questions that we would ask that relate to dose 44 justification broadly. We used the models as input or PK/PD 45 models or exposure response models. We want to understand the therapeutic window and ultimately our goal was to justify 46

the starting dose and the dose reductions. So there are four 1 2 types of models that I am going to tell you about today. 3 First a preclinical PK/PD model, next PopPK models then 4 PopPK/PD model and ultimately a PD/PK model as well. So 5 starting off at the early stages of development where in the 6 preclinical phase and we would like to find out what doses we 7 should study in humans and how we should be able to tell if 8 doses are working or they might be active. So we built a 9 model based on data in lines PK/PD data and we were able to 10 link the possible concentration in lines to biomarker model where we incorporated the data from possible RV, temperature 11 12 output and possibility of which we are all downstream of the targets CDK4 and CDK6. 13 We linked those biomarkers to inform the growth of the tumor or 14 15 and also model and there was also a concentration dependent off that was still cytostatic and cytotoxic. 16 So the impact 17 of the preclinical PK/PD model was that we were able to 18 demonstrate its sustained inhibitions required for durable 19 These models supported the plan or the cell cycle arrest. strategy to use a chronic dosing paradigm for patients who 20 21 take abemaciclib daily with no time off or no prescribed time 22 off. It also helped us to select the PD biomarker that we would study in patients, namely that was _____ and then 23 24 it also helped us to identify a target study stage trough 25 concentration that was needed to maintain drug or cell cycle 26 arrest and this was a trough concentration of 200 ng/mL, and 27 again here as a reminder these are the sorts of questions or 28 purposes that the models were built. We are going into dose 29 justification and we have identified the target exposure that 30 we want to achieve in humans. So next, we were first in the 31 human study in cancer patients. This is called JPDA and the 32 question here is what exposures can we achieve in humans and 33 these exposures leading to target inhibition, are and 34 ultimately based on the results of the study, what dose 35 should be carrying forward into registration studies. So we published the results of this publish in PK modeling last 36 37 year in clinical pharmacokinetics. This was collaboratively done by Sonya Tate and Damien Cronier and others so I want to 38 39 show you the results of the PK analysis. On top, we have 40 concentration time profiles for a dose of 150 mg twice daily, 41 on the bottom is 200 mg twice daily and that these results we 42 are seeing that we are achieving at this dose level that 43 targeted trough concentration at 200 ng/mL, and then we were 44 able to get the target phospho-Rb in cancer patients. These 45 were based on skin biopsies taken at baseline and that study 46 state and here we are finding the change in the phospho-Rb

from baseline versus the total daily dose and so I told you 1 2 we have a data at 150 twice daily and 200 twice daily so this 3 300 mg represents the 150 twice daily and then 400 this is 4 the 200 mg twice daily, and so based on this analysis of 5 biomarker data from patients with cancer, we are seeing 6 target inhibition, it is maximized at those levels of 150 or 7 200 mg twice daily and ultimately in this study, the maximum 8 tolerated dose was identified as 200 mg twice daily and that 9 is one of the dose levels that was carried for into the 10 registration study but we also used the dose of 150 mg twice daily and so the modeling and simulation work that we did in 11 12 the study helped to support carrying those doses forward into 13 registration studies. So now we fast forward to the time when we were preparing to see the data from registration 14 15 studies MONARCH 1 and MONARCH 2 and we need to develop a 16 population pharmacokinetic model because we need to do 17 covariant screening to determine if there are any patient 18 level cofactors that would require dose adjustments but we 19 knew that we are going to have a lot of data from a lot of 20 patients because we are incorporating data from that first 21 study I just showed through JPDA. The data from MONARCH 1 22 and an extensive clinical pharmacology package when we have ___ 23 C14 study and data from our study, а 24 clarithromycin interaction and rifampicin interaction study so it is a lot of data and knew it would be a computational 25 26 intensive exercise so we developed an intermediate model and 27 that is the structure of the model I am showing you here. It 28 is a two-compartment model and this is full of 29 only and we used this as a tool to screen the covariants that 30 we were just to see things impact dosing and with this small we screen for those covariants, those that came 31 32 out of it or if we tested in our ultimate model population 33 pharmacogenetics so where we incorporated that in 34 the metabolites as well and here is the structure of that 35 model. It is a mechanistic model and we wanted to be able to 36 describe the exposures not only of the parent but the active metabolites and to _____ and that is important because 37 given their activity, they could be contributing to both 38 39 advocacy and safety, only needed a way to output exposures to 40 determine if anyone was driving either efficacy or 41 safety and we used all of the data and fit this model to it 42 and this is what we used as input for other exposure response 43 analysis and modeling. So the impact of this model, we were 44 able to describe the disposition of the parent and to active 45 metabolites highlights and it was useful for exposure 46 response analysis and it helps to understand the relative

contribution of the parent and the metabolites to respond at length and we were able to understand the covariant effects that could impact those, and one of those is weight. So here we are finding that trough concentrations of abemaciclib M2or M20 versus weight and there is no appreciable impact of weight by any exposures. Therefore we do not need to have dosing based on weight and that supports the paradigm that we have used and these were all we so expect and may need presented last fall at . So one past forward to the time, we have the results from MONARCH 2. This was a phase III study randomized control _____. Patients received either fulvestrant plus placebo or abemaciclib plus fulvestrant and these are the results from a plan _____ analysis. This is the standard analysis we have seen at this time throughout the drugs that we see something that we know FDA might expect to see. The good news from these results are that for any of abemaciclib exposure, there was longer progression for a survival compared to the control group for those who received placebo plus fulvestrant control group is here in the bottom line and here you have the of the abemaciclib exposure, and if you have seen on, we might have already noticed that the lowest _____ of exposure here is on top and there is a miracle tendency towards longer for patients who have the lower exposures. This presented a problem for us because you might conclude that we should not be using that maximum tolerated dose approach and maybe our efforts to achieve that trough concentration of 200 ng/mL were misguided but here one of the challenges we are facing is time because I told you about dose reductions that are permitted for abemaciclib. The longer a patient is on study, the longer PFS they have, will also the longer opportunity to have for dose reduction so we were looking at a single summary metric for exposure and we are calculating that based on average exposure while on study, there is correlation or a confounding between low exposure and long time on the study. So that is one problem with time but this is where modeling has a unique advantage to be able to help us to understand the impact of time because this sort of analysis is really more suited to understanding the impacts of factors that exist before a patient moves on the study, not only suited to address time varying like what we are seeing here with exposure but another problem with time is that we have these top claim results and we need to submit quickly. We would normally like to take three months or so to build the model to help us to

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relationship between 1 understand the abemaciclib 2 concentrations and the response _____ but we do not have It is our own effort we did it quickly and 3 that much time. 4 we got our result. We started off for the change in tumor 5 sites model and we have abemaciclib concentration dependent 6 fact and there is also fulvestrant impact here because we 7 have data, all the patients in the study were receiving 8 fulvestrant. We have a transient compartment model, where 9 ultimately the concentration and impact leads to cell death, 10 and here is a spot of the results from that model. Here we are seeing a positive slope where higher abemaciclib plasma 11 12 concentration results in faster tumor shrinkage so we are 13 starting to trip away at that initial conundrum where we saw 14 the opposite relationship. When we took those step further 15 and we built a model for the hazard of progression and this 16 hazard model includes not only a concentration dependent that 17 directly on the hazard of progression increase survival but 18 there is also that we have that concentration dependent fact 19 of the change in tumor size so progression-free survival 20 versus time in weeks, the abemaciclib plus fulvestrant group 21 is depicted with the gray line, the observations of the line 22 and the shaded areas are the model prediction of the data so 23 you can see that the model that we have built predicts the 24 data well, and here the relationship between concentration 25 and hazard is that higher concentrations lead to a lower 26 hazard so again we tripped away at that initial conundrum and this ultimately supports the dosing paradigm where we need to 27 28 start at the higher dose, in this case it is 150 mg twice 29 daily in combination with fulvestrant and we can lower the 30 dose for patients who needed for individual tolerability and 31 we have simulations that showed the relationship between the 32 median progression groups survival's line and the dose. The 33 simulation was from the model are predicted here in black and 34 there are two groups, two abemaciclib groups, the green 35 represents the patients who started at a dose of 200 and by amendment a short time into the study, we reduced the 36 37 starting dose to 150 mg due to unacceptable fall rates of 38 diarrhea and then the next group of patients started out 150 39 mg twice daily. There was not a significant difference 40 between these two groups but there was a significant 41 difference from the placebo group. So this PK/PD modeling 42 approach where we incorporated individual dosing changes as a 43 concentration change in tumor size and survival confirm the 44 appropriateness at the starting dose reductions that were used in registration study. This is very important and might 45 have the results from the static _____ analysis and this 46

helped us to define efficacy portion of therapeutic window 1 2 which could be used to evaluate scenarios such as the impact 3 of the true defect or drug interactions. So as a safety side 4 of the therapeutic window, neutropenia is one adverse event that we see so we took the neutropenia data and we wanted to 5 6 understand the relationship of abemaciclib exposure on that. 7 We have fit the free bird model to the data and we saw a 8 concentration dependent effect. Here we are seeing the 9 inhibitory effect on neutrophil progenitor cells versus 10 concentration. There is a positive but non-linear relationship and this helped to confirm our understanding of 11 12 the low frequency of this adverse event and how just you 13 define the safety side of the therapeutic window which we could use in evaluation in different scenarios. So finally I 14 15 wanted to tell you just a little bit about the PD/PK model 16 that we developed. Remember that was and its 17 metabolized to the active metabolites M2 and M20 but the 18 of those metabolites are also fraction of the 19 metabolites but the parent has a larger fraction 20 metabolized than the metabolites _____ and so when you have a drug interaction that would _____ 21 for, the effect 22 on the parent is bigger than the effect on the total active 23 So when we built this PD/PK model, we could species. 24 understand the impact of scenarios on abemaciclib and the 25 total active species and that helped us to make dosing 26 recommendations for drug interactions that we have in study. 27 We put that clarithromycin and rifampicin but we were able to 28 make recommendations for the label for drugs like diltiazem 29 and verapamil and . So by way of summary and conclusion, we tabulated the types of models that we used and 30 31 the decisions that we were able to make or how these models 32 have turned informed the development of abemaciclib. It is 33 important the dosing paradigm of continuous twice daily 34 dosing. It helped us to identify and confirm the target 35 systemic exposure. It helped us to figure out which biomarkers we should look at in patients, what does with 36 37 violation in dosing. Very importantly, it helped us to confirm the acceptability of the starting dose which 38 39 started out as a bit of a riddle. It helped us to understand 40 the risks for adverse events that might be associated with 41 changes in exposure and it helped us to note the dose 42 adjustment recommendations that had not been studied in clinical studies but we were able to simulate. Thank you 43 44 very much.

45 [Applause]

Moderator: I think we have time for two questions. 1 2 Audience: Yeah. I wonder . 3 Turner-Jones: So if I understand the question, you're saying here's the model to see if we could reproduce the original 4 5 quartiles from the static analysis when we took the static. 6 That's something that we haven't tried, but it would make 7 sense that it should be predicted-8 Audience: We're not really interested in because here essentially _____ divide into groups and ___ 9 predictions so if you're saying that this model is 10 _____ prediction, it would be able to reproduce the 11 12 Turner-Jones: Yeah, thank you for the suggestion. 13 14 Audience: I was wondering since you modeled _____ whether you tried to incorporate toxicity or at least 15 entities in your model. 16 In terms of if you have a neutropenia event, would 17 Turner-Jones: that then trigger dose adjustment? 18 19 Audience: No, whether that would change this _____ because I 20 mean at the end of the day, the x_____ of the patient 21 is a balance between the efficacy and toxicity so ... 22 That's right. I quess another way to frame that would Turner-Jones: 23 be is it required to dose to neutropenia in order to 24 achieve longer progression-free survival. 25 Audience: Yeah. Just wondering if you could try to model that. Turner-Jones: Yeah, I think it would be we could try it, yeah. 26 Audience: Also a suggestion. When you did the 27 survival analysis, if you remove _____ because it could be that 28 the higher the concentration ______ seeing dropout effect so sometimes when ______ this analysis and then 29 30 remove _____ then we see actually nice curves which by 31 the way _____ because again it is _____. 32 33 Turner-Jones: So one of the details in the we did handle 34 dropout in the model so it should be taken care of here 35 with our dynamic model. 36 37 Moderator: Thank you. Our next speaker is Dr. Chao Liu. He is a 38 current team leader in the Division of Pharmacometrics, and

2 _____ analysis to NDA review. 3 4 Dr. Liu: Thank you. Good afternoon. My name is Chao Liu and I'm from at FDA. It is my great honor to do this 5 6 presentation at this session. Today I would like to talk 7 about models NDA/BLA review for presenting two 8 review cases. Before starting my presentation, I'd like to 9 make a disclaimer that the views in this presentation 10 represent my personal opinion. We are presenting these two review cases. I will show that _____ the analysis of 11 _____ response relationship may ______ assessment 12 of efficacy, safety as well as dose. In addition, 13 modeling-based analysis _____ can be used to 14 15 two cases can provide some insight to in terms of the relevance of the modeling 16 17 analysis for NDA/BLA review. 18 I will start my presentation case of 19 rociletinib, an EGFR inhibitor for treatment of non-small 20 cell lung cancer. The second case is about lenvatinib and 21 everolimus combination therapy for the treatment of renal cell cancer. In this case _____ analysis was used 22 23 trial. It shows of each case. 24 Let me first provide some background in the first case, 25 rociletinib. Rociletinib is an EGF receptor inhibitor that 26 was developed for the treatment of T790M mutation-positive 27 non-small cell lung cancer. The efficacy was primarily assessed by _____ dose levels from two clinical 28 studies. Based on _____ 625 mg b.i.d. for approval. 29 30 Hyperglycemia and QTc prolongation were the two major 31 adverse events of special interest. During the clinical 32 study, patients across different dose levels were not randomized. The pharmacokinetic causes of rociletinib are 33 34 shown here. Rociletinib . Therefore in the 35 clinical studies, rociletinib was administered 36 rociletinib is converted to two major metabolites, M502 and 37 M460. These two metabolites are responsible for hyperglycemia and QTc prolongation. Hyperglycemia is 38 39 primarily attributed to M502, and QTc prolongation is 40 attributed to M460. During review, we 41 relationship over a dose range from 500 to 1000 mg b.i.d. 42 non-compartmental analysis on the left, and the population ______ analysis on the right ______ each 43 44 part represents a steady-state AUC of one individual

he will discuss how we as reviewers apply modeling

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1 patient. The _____ analysis on the left was based on the _____ data collected from a subset of the subject 2 _____ AUC of day 15 of cycle 1 is flat, suggesting 3 over the dose range of 500 to 1000 mg b.i.d. 4 5 The plot on the right shows the dose exposure relationship 6 based on _____ analysis of over 300 patients. The 7 plot represents the distribution of the 8 individual exposures. results from the data. Subjects with 500, 625, 750 and 1000 mg 9 b.i.d. doses showed _____. Thus, based on the 10 11 analysis, we concluded that dose exposure 12 relationship as flat from 500 to 1000 mg b.i.d. We also 13 evaluated the exposure response relationships for efficacy 14 and safety of this drug. Exposure-efficacy relationship 15 between rociletinib response rate was explored using data from patients who were treated _____. The 16 relationship was _____. In the plot, the mean ______ 95% _____ of the observed response rate of 17 95% 18 19 _____ rociletinib exposure _____. The actual plotline _____ represented _____ is 95%. 20 21 represent the distribution of rociletinib 22 steady-state AUC at each dose group. The plot shows that 23 within the smaller range between 500 and 750-mg b.i.d. 24 doses, the effect of the drug exposure to efficacy 25 . Using this model, the predicted ORR for the 26 500, 625 and 750-mg b.i.d. dose _____ risk factors 27 were identified. Based on the exposure-efficacy analysis, 28 the results efficacy across different dose 29 levels. No meaningful different in efficacy would be 30 expected by increasing the dose level about 500 mg b.i.d. 31 M502 is primarily responsible for hyperglycemia. 32 The plot on the left represents the exposure-safety 33 relationship between M502 steady-state AUC and the instance 34 of grade 3 or 4 hyperglycemia as evaluated by the FDA. _____ 95% 35 of grade 3 or 4 hyperglycemia M502 exposure are represented by the 36 represent the _____ incidence of grade 3 or 4 37 38 hyperglycemia represent the distribution of M502 39 steady-state AUC at each dose group. For exposure-safety 40 analysis, there appeared to be a correlation between 41 increasing M502 exposure and the incidence of grade 3 or 4 42 hyperglycemia, suggesting that a patient with high M502 43 exposure has a greater risk of grade 3 or 4 hyperglycemia. 44 M460 is responsible for QTc prolongation. As 45 shown on the right, a model predicted correlation between M460 exposure and QTc prolongation but the _____ 46

1 concentration of M460 and _____ from baseline. The 2 solid _____ represents the predicted change from 3 baseline _____ QTc _____ correlation between 4 prolongation of the QTc interval and the increasing M460 concentration. Finally ______ similar exposure from 500 to 1000 mg b.i.d. ______ from different dose levels will provide ______. In addition, based on the 5 6 7 8 identified exposure response relationship from 500 to 750 9 mg b.i.d., patients with higher rociletinib exposure are 10 unlikely to have further benefit. However, subjects with 11 higher metabolite exposure are at greater risk for QTc elongation and hyperglycemia. Thus we _____ proposed 12 13 625-mg dose was not adequately supported based on available 14 data. FDA's analysis was . Along with other 15 issues approval based on available data. A 16 complete response In the second part of the presentation, I'd like to talk 17 about _____ collaboration with _____ analysis 18 19 marketing trial. In addition, the novel 20 analysis strategy was used so that drug toxicity can be _____. So that _____ tyrosine kinase inhibitor ______ approved as a first-line therapy for 21 22 23 the treatment of differentiated thyroid cancer. In 2016, 24 lenvatinib was approved for the treatment of metastatic 25 renal cell carcinoma as a second-line therapy in combination with everolimus. The approved dose is 18-mg 26 27 lenvatinib plus 5-mg everolimus g.d. In the 28 trial, patients in the lenvatinib/everolimus combination 29 shown here in the shows significant 30 improvement in progression-free survival as compared with arms of lenvatinib or everolimus _____. However, 89% 31 of the patients in the combination arm had dose reductions 32 33 or interruptions due to _____ drug toxicity. Thus, 34 safety was one major concern about the approved dose issues by the FDA to optimize the dose 35 a post-marketing trial. For the selection of an 36 37 alternative dosing regimen to study exposure-38 based model simulation dosing regimens to find out the most promising candidate. _____ analysis at 39 40 each case is how to handle the dosage dose adjustment and one subject trial. In this case 41 overtime. It is challenging to define 42 at the subject level _____ response 43 analysis and _____ representing the drug exposure 44 derived from average dosing intensity over treatment 45 estimate of the E-R relationship. For example, 46

assuming the progression-free survival was used as an 1 2 efficacy endpoint. For a subject who progresses soon, the duration of the treatment will be short. The patient may 3 4 have no chance to experience dose reductions and thus still remains at a higher dose level 5 6 average exposure could then be higher. On the other hand, 7 a subject who progresses later stays longer on the trial 8 and thus has a higher chance to experience more dose reductions and _____ exposure. The _____ average 9 10 exposure and efficacy would be appear to be flat or _____ estimate of the exposure _____ relationship. 11 12 To address these challenges model strategy was 13 adapted. The standard of using a constant exposure matrix 14 subject level exposure matrix was used 15 tumor size was used to assess the drug efficacy. In terms of _____ safety _____ AE was associated 16 with _____ exposure. Finally in the simulation 17 _____ to address the _____ dose adjustment 18 trial to incorporate the dose 19 exposure-safety interaction. The exposure-safety and 20 21 efficacy relationship between lenvatinib and everolimus 22 _____ tumor size was explored _____ trial. tumor growth rate _____ to the natural 23 growth rate minus the suppression effect from lenvatinib 24 25 plus everolimus. _____ from the three arms of the 26 previous study _____ to estimate model parameters. 27 Tumor growth rate was referred study where a placebo arm renal cell carcinoma 28 29 . Meanwhile through communication with FDA, a longitudinal _____ AE ____. AE is ____ 30 dose adjustment were treated _____ and this model will 31 be used to predict the dose _____ regimens to form the 32 dose adjustment cost by _____. So in terms of 33 34 selecting the alternative dosing regimen dosing 35 regimen were simulated to predict the efficacy and safety 36 profile. At each dosing regimen _____ dose adjustment 37 _____ adverse events was _____ overtime based on 38 the E-R of a single-agent dosing 39 history overtime where each dose level is represented by 40 different . Finally based on the generated dosing history, the tumor dynamics was simulated 41 42 efficacy at each dosing regimen. This slide shows the 43 simulated tumor dynamics. At each graph, the X axis is the 44 time of the treatment up to one year, and the Y axis is the relative tumor size compared with baseline. _____ is 45 a single agent _____ values of the tumor dynamics. 46

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The dosing regimen of 18-mg lenvatinib plus 5-mg everolimus 1 2 served as the _____. We first evaluated ____ lowering the lenvatinib dose would provide comparable 3 4 efficacy. Dosing regimens of 14, 12 or 10-mg lenvatinib 5 plus 5-mg everolimus were validated. None of them was able 6 to provide the same magnitude of tumor suppression compared 7 with . Upon further simulation, we found that 8 implementation of . In this scenario, a patient could be uptitrated to a higher dose level _____ if 9 10 the patient did not experience any _____. The dose 11 cap of lenvatinib was set to 18 mg. When up-titration option is provided _____ lenvatinib starting dose 12 13 could provide comparable tumor suppression compared with the control. In terms of _____ lenvatinib, ____ 14 requirement was _____ to optimize the dose, and 14-mg 15 lenvatinib plus 5-mg everolimus was selected as the 16 alternate dosing regimen _____. 17 18 The end of this presentation will just be a revisit of the 19 take-home message. The modeling-based analysis relationship facilitates FDA's assessment of efficacy and 20 21 safety. In addition _____ review, drug exposure-based 22 modeling can be used to form the trial design for the post-marketing study _____ frequent dose reduction 23 ______ should be perfectly incorporated. Last but not 24 25 the least, I'd like to thank my FDA colleagues . 26 I'd like to especially thank Dr. Yaning Wang who led to and Dr. _____ who performed the pharmacometrics analysis _____. Thank you very much. 27 who performed the 28 29 [APPLAUSE] 30 question? If not, we will move to the third one. Moderator: 31 The next speaker is Dr. Daniele Ouellet. She is the Senior 32 Director _____ group leader under the Global Clinical 33 Pharmacology from Janssen, and she will talk about _____ from the post-marketing perspective. 34 35 Dr. Ouellet: Thank you, everyone. Thank you for having me present today and for putting together this workshop. I think everything 36 37 has been really interesting so far. So as Yaning said at 38 the beginning, the purpose of the last session was really 39 to look at model-informed application for late stage 40 it was nice to hear the regulatory perspective, 41 and here it is really post approval so trying to find an 42 example where we use a model-informed decision to support post approval. So the example we are going to 43 44 talk about is with ibrutinib, a BTK inhibitor.

the context of _____ activities that we do also in 1 2 terms of the post-approval stage of what is going on. So 3 most of you are familiar with this figure that comes from the paper that was done by the MID3 workgroup so 4 5 model-informed drug discovery and development 6 and really talking about the impact that it can have at the 7 different stages of development. So we have heard a lot of 8 different case studies, but what is really important is 9 what kind of decision do we make based on that. So really 10 her in development, it is all about selecting 11 the target, selecting the dose, optimizing the study design and things _____ tumor model will be nice ____ 12 13 really start to integrate that and optimize some of those decision we make _____. Then I think Kellie showed a 14 15 nice example of understanding the risk-benefit 16 characterization for when we submit, and then post approval 17 to see here the darker green, the questions are 18 a little bit different, right? So it is about extending to 19 different patient population and it is about 20 drug combination, how do we support the combination after 21 the first approval. So looking at the we have 22 and the activity we spend supporting these projects that 23 have been approved and the idea here is that we 24 are lucky that we have a lot of different information and 25 understanding of those relationship between dose and 26 exposure. We have done a model 27 package and also between exposure and efficacy and safety, 28 and it is really capitalizing on that knowledge to inform 29 and be efficient when we go to this other 30 So part of what we do is really bridging population. 31 and the question we ask ourselves is always, 32 okay, so what do we do when we go to a different tumor type? 33 Should we go with the same dose? And then the question we have to answer upon treating _____ manner is verifying 34 the assumption that we have. Is the patient population 35 really similar to what we have? Is the tumor 36 37 similar to what we have studied or are there any difference there worthy of concern? Is the tumor burden 38 SO 39 thinking about these things and seeing what can we do to 40 leverage the knowledge we have. A lot of the activity post 41 marketing is also on pediatric. I think there has been 42 workshop there to show the value of 43 model-informed drug development in dose-specific indication, 44 and I think it is well accepted in that particular aspect. 45 The other one is really supporting some of the labels. 46 Someone this morning mentioned that especially in oncology,

1 the drug development and approval is really fast and 2 sometimes we do not have as much time to optimize perhaps 3 the formulation that you have to take multiple capsules or 4 tablets, so there is some work being done post approval to 5 do that, and completing sometimes the clinical pharmacology 6 package that there is a little bit of gap there, just given 7 the speed of trying to get the drug to patients as quickly 8 as we can. So again, that is really capitalizing on what we know these other activities. 9 10 So I'll talk a little bit about ibrutinib. So ibrutinib is 11 a BTK inhibitor. So BTK is part of the signaling pathway 12 for the Bruton tyrosine kinase, a part of the B-cell 13 here will stop somewhat the B-cell receptor 14 activation so any B-cell malignancies that 15 abnormal activation of the pathway, it has been found to be really useful and has shown efficacy in those type of 16 malignancy. 17 Ibrutinib is a covalent inhibitor so 18 IC50 less than 0.5 nM, and it binds to the 19 cysteine residue of BTK. If we look at the indications so 20 that in the US, the first time it was approved in late 2013 21 approval there in MCL second line, and then it approval, as I said, in 22 has received several 23 different B-cell malignancies, either combination. The most recent approval is actually in 24 25 chronic graft versus host disease, a little bit different 26 patient type there. 27 28 So specifically for ibrutinib, if we talk about how to use 29 model approach to support different indication, those of 30 you who know a little bit ibrutinib know it is a very 31 sensitive substrate. So as part of the late-32 stage package, a lot of activities that we do are still 33 under using a PBPK model _____ the drug interaction 34 package. When we first submitted, we had a couple of drug interactions with 35 inhibitor, and then we worked 36

interactions with ______ inhibitor, and then we worked closely with the FDA to really understand the different _______ of different ______ inhibitor, different types of inhibitor because we could not study all the different scenarios. With PBPK, it was really ibrutinib to understand some of these effects and estimate those. So I think it is a really nice example the example that I talked about. So we have had to fulfill a couple of PMR and post-approval measure, and we had to a study with omeprazole so that is the example also _______ it is a very specific sample of how we use

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_____ is also around the pediatric model-based 1 2 development using the PBPK model to help with estimating that starting dose versus _____ matrix scaling 3 4 approach, and I think most people will have some model 5 approach with that. So for those _____, bear with me while I explain the _____ study. So really this was a 6 7 study with PPIs or proton-pump inhibitor. Ibrutinib is wheat-based so it has a pH dependence 8 9 high pH. It is a BCS class 2 so high 10 permeability and low solubility _____ with rapid 11 absorption, Cmax within one to two hours. Ibrutinib 12 effect so it is sensitive to blood flow so if 13 you take it with food, it is going to activate blood flow; 14 therefore, you see an increase in exposure with food so 15 Cmax two to fourfold increase and then you see about a 16 twofold increase. It has nice safety so it is still a BTK 17 that can be taken with or without food even with 18 food, it is within the range of what has been studied. So 19 the study objective was really to evaluate the effect of omeprazole given for four days _____ single dose of 20 21 ibrutinib ______ study design, we gave ibrutinib alone 22 first and then a week later gave it after four days of 23 omeprazole, so making sure that the pH was really elevated 24 and we could see the effect of pH elevation. So these are 25 the results. So the concentration, a very different kind 26 of curve. So the open circle here will show the PK profile 27 of ibrutinib alone so you could see how , and 28 then the full circle will show the effect of ibrutinib with 29 omeprazole. So lower Cmax but you could see the profile is 30 a little different and some residual absorption there that the AUC was actually maintained a little 31 32 bit versus ibrutinib alone. If we look at what the PK 33 parameter will look like, on the right for Cmax of about 0.37 _____ AUC was pretty much similar 34 between the two treatments_____ AUC 24, AUC 48, AUC 35 36 _____ there is a little bump in the ibrutinib profile 37 so calculated in enough number of patients. You 38 can see a little bit delay in absorption, two hours versus 39 one hour; and in the half-life, a little longer here, I 40 think just because of that residual absorption. 41 so on the top there so it is Cmax with ibrutinib alone and 42 ibrutinib with omeprazole, and the cartoon below is the AUC. 43 So again, AUC was fairly consistent _____ subject while Cmax, you could see a lot of subject _____. I think we felt fairly confident that _____ probably 44 45 46 would not have an effect on efficacy and safety and we

could recommend to take it with PPI, but we really wanted 1 2 to be able to support the clinical recommendation of what 3 to do with this pH-altering agent. So we understood well 4 the mechanism of action. Again, it is a covalent binding 5 so what we decided to do was really to develop this 6 mechanistic model based on the kinetic of binding and 7 dissociation kinetics and look at the effect on our target engagement, so taking target engagement as a 8 9 surrogate for efficacy. Again, using this mechanistic 10 model, I think somebody asked this morning on how you 11 validate this. So what we did was to do some sensitivity 12 analysis to look at _____ of the model given different 13 assumptions into its parameters. We had some BTK 14 data so we kind of used that to make sure the 15 model was doing, what it was predicting was appropriate. 16 We also had done similar exposure response for efficacy 17 based _____ Cmax and tried to use that also in 18 recommendation. So this is the supporting 19 mechanistic model of BTK. So represent the 20 enzymes with BTK. I represented ibrutinib inhibitor and so 21 you have formulation of the complex here, k_{on} 22 Again, it is a covalent binder; and then your inactivation complex and into degradation that you could see 23 of the complex and also 24 from BTK itself. So what we did was that there was some published 25 26 data that had been done on the association and dissociation for ibrutinib on BTK, so we used these data. 27 28 There was another publication that also had done some time-29 dependent studies BTK half-life to inform that 30 degradation again from another publication that 31 talked about the turnover of the BTK. So we plugged in 32 these different assumptions there, the different 33 the different parameters to try to estimate what would be Then here the concentration 34 the _____ ibrutinib. what the I profile would look like, 35 profile right? So what was the profile _____ omeprazole so we 36 37 can look at what the effect was going to be with the receptor _____. So this is the resulting 38 39 simulation data. So we basically did the simulation up to 40 steady state so the timescale was basically here 41 24-hour profile at steady state, and here represent the 42 receptor occupancy. So for ibrutinib alone, you could see there is still a little bit of variability _____ the 43 44 day but all above 90%. With omeprazole, you can see that the effect, if anything, was just to _____ 45 dose 46 variability. So if we calculate the average receptor

occupancy, it was comparing 94% and 96% so very similar. 1 2 So we felt fairly confident that this was really going to 3 be helpful to make recommendation that no 4 difference. Let me skip to this one. So that is the data 5 that we have following single dose, and single dose really 6 kind of is an agreement with data. So on the open circle 7 here, you got the PK profile _____ as you have seen 8 with the omeprazole study fairly rapidly from 9 circulation; but you can see that the BTK here engagement, 10 we have measured that at 4 and 24-hour that the enzyme, you 11 see the complex formation. Because of the half-life of 24 12 hours for BTK turnover, it is maintained across that dosing. 13 So the results of the simulation were consistent with what we had observed in that study. Again, as I have said, we 14 15 did some sensitivity analysis for the different parameters, 16 and we really stretched some of these . So 17 threefold variation here for the BTK half-life so the 18 24 and then we ranged between threefold higher 19 and threefold lower to see the impact. So the impact was 20 really actually not that much. It was about, at most, 10% 21 on the affected cells; but if you look at the difference 22 between the two treatments, that was also a very small kind The effect of _____ that was really 23 of effect. nothing because the _____ is minus 1 to 1% so a very 24 25 small effect even if you change the value a tenfold factor. Here a little bit more than it packed on $k_{\rm on}$ $% k_{\rm on}$. So if you 26 tenfold down, you can see _____ change, but 27 28 if you increase that tenfold, then you will see a change in 29 the BTK predicted value; but again, the difference between 30 the two treatments was still very similar. So we felt that 31 was really _____ assessment of our assumption there. 32 We also had done some of the efficacy and exposure 33 relationship so looking at just responder rate versus quartile and exposure, on the left, there is 34 Cmax; on the right is AUC. So there was really no 35 36 relationship and you can see there is a fairly high life 37 range and concentration, about a hundredfold there. Again, the drug _____ you are going to see some 38 39 variability; but the dose was selected to make sure that 40 most of the patients would be above that 90% inhibition in 41 90% of your subjects so that kind of supported that as well. 42 So basically the conclusion were this mechanistic model was 43 developed to really support the outcome of this drug 44 interaction study with omeprazole and to be able to provide 45 clinical recommendation adjustment obstruction with the use of ibrutinib with PPI or other pH-altering 46

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The data supported the lack of clinical relevance 1 agent. 2 or changes in Cmax which really _____ AUC that was 3 similar between the two treatments. In terms of these 4 examples, I think it is a nice small example that 5 demonstrates the value of different modeling approaches. 6 This one was a mechanistic model that really supports some 7 of the conclusion that we want to make and some of the 8 questions that we may have. I really want to acknowledge 9 the people who helped and did some of this work, so 10 here is the _____ for ibrutinib worked closely with this _____ and, of course, the one who 11 12 did most of the modeling here and these guys really helped 13 with the omeprazole clinical study; and many more people that I am not mentioning here. That's it. 14

15 PANEL DISCUSSION

16 Moderator: Any questions? We can just invite all the speakers back if 17 you have any questions and can ask them together, and we 18 will also invite two additional panelists to join us to 19 address any questions you have on this late phase 20 just use our own two additional FDA panelists, 21 Dr. Pat Keegan on the far left and the community doctor of 22 the division of oncology department too, and Dr. Lei Nie. 23 She is one of the statistical team leaders covering 24 Again I will give them both an oncology products. opportunity to give some comments, since they have not 25 26 mentioned about this late phase.

27 Dr. Nie: I think in the opening remark is some talk about a Catch-22 28 dynamic. I think the speaker illustrated nice work that 29 could be part of the solution, that is my first comment. 30 My second comment is all the speakers are non-statisticians 31 I'm very impressed and I really hope a 32 statistician can additionally more contribute to that A comment for this session is I would like to 33 aspect. 34 mention that the first speaker and second speaker also 35 mentioned the difficulty of the exposure response, and the 36 first speaker illustrated the dynamic nature, the low dose 37 associated with , the high dose associated with 38 , and the second speaker talked about you really 39 need to see the dose all the time. That is a well-known 40 concept in statistics because dosage is a cause of the 41 efficacy, also in the constraints of the efficacy and 42 safety, so we have to put these relations in the model. Ιt 43 is very complex and rarely in the past that has been considered. Thank you. 44

1 Dr. Keegan: Thank you. So I guess I'm going to start with comments 2 that cover from the opening remarks as well, and I think 3 that Dr. Woodcock is right. There are so many aspects of 4 drug development that really incorporate a lot of knowledge 5 in technology, and clinical trials is a little bit lagging 6 behind here in oncology in terms of addressing new models 7 and incorporating a lot of the really interesting science 8 that we heard today. I would say that it took the rare and 9 the phase 2 meeting where someone walks in with a fully 10 developed pharmacokinetic analysis that says to us based on 11 our review of everything that's happened thus far, we now 12 know so much more about how to dose this drug. I would say 13 I could probably count on one hand how often that happens, 14 so I think that Dr. Woodcock is right that we really do 15 need to use this new information to really inform phase 3 drug development, and so in that sense, I felt that the 16 17 last topics in particular were really interesting and 18 illustrated both how you can use that data to inform as 19 well as what happens when you don't, and then you have an 20 application sitting in front of you and realize that 21 there's big trouble. I think the examples illustrated, you know, in one case, a drug that couldn't be approved because 22 23 there was so much that really wasn't evaluated during the 24 drug development process, critical aspects which may or may 25 not have been addressable but certainly should have been 26 discovered at the time of the marketing application. In 27 other, and this is a situation we found ourselves in for 28 many decades in oncology and should know what we're getting 29 ourselves in, which is approving a dose that we don't feel 30 comfortable with, that we feel that is unlikely to be 31 marketed or accepted by the community, and we shouldn't be 32 at that point anymore. We should actually know more. 33 Another aspect that I think was touched on a little bit 34 that in the morning, when we were having all this 35 discussion about picking doses and looking at dose-limiting toxicity, I think one thing that I didn't hear as much of 36 37 and I would have liked to was that when we talked about dose-limiting toxicity again, we are back at the cytotoxic 38 39 base. People have grade 3 or 4 toxicity, and we're not...it 40 does not fit the current paradigm for cancer development. 41 You either have therapy and usable proteins with prolonged 42 exposure for daily dosing of drugs and we no longer can 43 just consider what's a grade 3 or 4 as we did when we gave 44 cyclical chemotherapy every three or four weeks, and it was 45 only alopecias, nausea, vomiting, and some cytopenia. We 46 have very many different toxicities now, and many of the

grade 2 toxicities are equally intolerable or problematic, 1 2 particularly in patient populations that are going to be 3 taking the drugs for a long time. So as we get to more 4 highly effective drugs and longer exposure and chronic 5 I think we really need to rethink even dosing, the 6 dose-limiting toxicity paradigm. To say that grade 2 7 fatigue is tolerable is kidding ourselves. To say that, 8 you know, grade 2 hypertension over years is a good idea is 9 not getting through. So I do think that we need to, as we 10 look at some of the early models, we need to rethink how we approach dose-limiting toxicity. I think as we go into the 11 12 phase 2, we need to look at a lot of these things like how 13 tolerable were the drugs and what are the toxicities before we enter phase 3, because I think we're missing a lot of 14 15 opportunities for successful drug development. While we'd 16 all like to get to the end as quickly as possible, we'd 17 also like to get there with a satisfactory end. We don't want to have a drug which, once it's out in the market, 18 19 people are still trying to figure out how to use it or 20 still concerned about the dose. I'm not because 21 the statistics are hard and beyond me, but this is a really 22 fascinating presentation.

23 Moderator: Thank you. Any comments or questions from the audience?

So it was a really great day when a lot of case 24 Nie: _____as well as the late phase and the post 25 studies marketing area. I think we all agree that integrating all 26 27 the data will help us to describe, explain and hopefully as 28 well predict better and better what people are going to see. 29 I think what we are today here is also trying to understand 30 how can we move this field forward into good practice, so 31 where ... and I would also like to comment about how can we 32 move this forward into good practice where there is 33 methodologies or the different application areas where there is some points of considerations or guidance. 34 How 35 should we do in order to also from a small track 36 perspective drive this forward.

37 Moderator: Good practice. Yes, that's in our objective.

38 [LAUGHTER]

39 Keegan: So I'll start with one that was started on a little bit.
40 There was concern that, you know, we do these details up in
41 phase 1 and then we don't look at it and we don't consider
42 the phase 2, and some people brought it up that we don't do
43 much dose ranging in phase 2. One of the reasons it was

mentioned was we do have to slow things down. 1 I think 2 we're going about as breakneck speed as we can with a lot 3 of the seamless design trials and I think there's no reason 4 not to take opportunity to continue to do a lot more 5 evaluation in those phase 2 with those ranging in schedule 6 assessment and then getting that data, particularly in 7 those expansion where you remove the variability in patient 8 population and usually focusing on one disease entity. Ιt 9 makes it less problematic and, you know, there's always 10 some variability. I would suggest that I think a lot of my colleagues in pharmacology would suggest that dose ranging 11 12 continues with the phase 2 portion. I don't think it has 13 to slow it up that much if, you know, you build it into most of the trials. I would caution over interpreting that 14 15 data, which I think was part of the strategy, but I think, 16 because they only looked at one aspect and not the whole 17 thing, but I do think that would be the best practice.

18 Nie: I can have statisticians talk about my idea and Okay. 19 using that idea and talk about the life cycle approach. 20 The ideal approach is early phase clinical use data and 21 find a good study. Use a good methodology and find the 22 phase 2 dose. In phase 2 dose, it depends. If it is 23 really efficacious and no toxicity, then go ahead, just a 24 single may be okay. But the drug and find a 25 good dose for phase 3. That is the ideal approach. But if 26 this is not, all of them talk about the life cycle approach 27 You cannot do a profile in phase 1, you try 28 phase 2. If you cannot do phase 2, phase 3. But if you're 29 not happy with the dose, you can go to phase 4 and continue 30 to optimize that. For many cases, going to phase 4, we can 31 find the right dose by going the life cycle approach. 32 Thank you.

33 : The only thing I was going to add in and I don't know if 34 you have somewhere you wanted to go in terms of moving the 35 field, right, so there has been a lot of these tumor modeling approach and obviously you develop this model once 36 37 you get your late stage data and it's how you circle it 38 back to the early data. I don't think we have that many 39 example of applying it for. I think that something is a 40 community that, you know, we can share some of these 41 knowledge and there's always a question that if you go in a 42 population that's a little different that has a different 43 genetic mutation, how are the application of these models? 44 Are they still valid? I think we still have some homework 45 to do, especially in those cases. I think we did good in

- sharing the…publishing these data, but I think to apply and treat it for, it's hard to do within, you know, a company that got to cycle all the time to be able to do that, so there's probably…there's something there that you can put in practice.
- Just some comments in terms of the tumor modeling efforts 6 7 from the community. The things move forward rapidly, 8 especially for the renal palliative therapy where for many 9 cases the drug effect is starting directly on the tumor per 10 se, but we have an immune system. So in terms of that, it 11 a new concept in terms of how do we or drug 12 effect into this kind of a tumor suppression. For some 13 drugs, this is always there and it could extend into effort 14 with it before for four doses, but the tumor 15 suppression is sustainable, which means that the 16 activates some kind of a system, either through 17 or some other system which may not be fully described or based on clinical data, but each will be incorporated to 18 19 sustain the tumor suppression in immune drug use 20 after some kind of period. So I think before we come up with a universal or good practice of this kind of effort, 21 22 right now, still I think the community is trying their best 23 to collect more data and especially in the combination 24 therapy where it may have synergetic effect from both 25 components in oncology which may even more complicate this 26 kind of tumor model. So I would like to see more study 27 results or data collected before we can come up with a good 28 practice to address these clinical complicated issues.
- 29 Audience: I have one question. Is this on?
- 30 Moderator: Closer, closer to the mike.
- 31 Audience: One quick question.
- 32 Moderator: How we're all friends.
- 33 Audience: I did mean to ask a question for that.
- 34 [LAUGHTER]

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35 Audience : Alright, so I'll just speak loudly.

36 Moderator: Why don't you come up, there are people on line.

37Audience__: I'm just wondering if anyone knows this.38How do we go from model-based drug development about 10 or3915 years ago to modeling for drug development? Have we40gone soft over age or is there some other reason for why

it's deformed? Alright, okay, so I'll go to the second question...

3 [LAUGHTER]

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4 : Which is an interesting anecdote and I'm glad there's someone here from the FDA biostat department. So this is 5 6 a...and I don't if this meeting between biostat and clinical 7 pharmacology occurred on the FDA side or the sponsor side, 8 but there was a situation where we had an active dose 9 escalation algorithm in place and the operating 10 characteristics showed to one of the reviewers on the 11 , there was concern that there was too much 12 probability of overdose. On the pharmacology side, there 13 was a request to insert a new second dose, so instead of 14 jumping from, I don't know, say 1 to 10 mg, 1, 5, 10, 15 something like that, so what happened was that the operating characteristics did not get any better when we 16 17 inserted that in intermediate dose because the scenario 18 required that the second dose was toxic irrespective of the 19 magnitude of the dose, so that means there was no 20 inherent ... there was no underlying pharmacology model for 21 probability in toxicity and no concept in pharmacology, so 22 it could have been 1 mg or 1.1 mg. The scenario seemed to require that 1.1 mg _____. I don't know if that's an 23 24 FDA thing or is that just something that happened, I'm just 25 curious, on its own.

26 Nie: We will first try to answer your question. Is that model 27 based that you're modeling from. You know, what 28 we do, we actually do not like model based or 29 have a single-arm trial that's not modeling based. So 30 that's why we promoted to MCT mode approach in phase 2 31 including many doses instead of just a single 32 dose. That's why we right now still promote more model 33 based . Maybe right now, and 34 establish biomarker to simulate the model-based simulator 35 complex design. All of these concepts were not emphasized 36 With the second question, it's a little bit before. 37 difficult to answer because I do not know the context, so a 38 statistician may consider some potential risk. Doctor, do 39 you have any comments?

41 _____: Yeah, I'm also from the Office of Biostatistics. I would 42 say two _____. You got to go back to the FDA and say 43 .

Yeah, actually they may also be looking at these different 1 Keegan: 2 aspects of what happened, right, so the statisticians are 3 saying, just basing on the amount of work, you know, did it 4 all basically, does it look like it's balanced statistics? 5 You know, the clinical pharmacology people may actually 6 have been informing and usually in a phase 1 are also 7 preferably drawing on toxicology data to maybe suggest an 8 intermediate dose. And then I think the third, which is, 9 you know, the clinical people have taken a look at it to 10 say, well, what exactly are we doing when we're exposing the people, you know, and what are the thresholds that are 11 12 being used, because neither the clinical pharmacologist or 13 the toxicologist or the statisticians are going to be able to interpret some of the rules. And I think the last is if 14 15 this happened a couple of years ago, then you should just 16 let it go, okay?

17 [LAUGHTER]

18 Keegan: We now see on a regular basis at least half of the applications coming in with some ______ dose-finding approach. And we've learned, okay, so, you know, if you get a straight answer, yes, ask, but I mean, in general, I think we were just probably gaining familiarity with the approaches.

24 _____: I was mostly just wanting to highlight an opportunity for 25 the statistical side to have more pharmacological concepts 26 for what worst case scenario is, where there might be a 27 certain shape of the dose toxicity is the worst case 28 scenario, not just a particular numbered dose, that's all.

29 Keegan: Oh, okay.

30 Moderator: Thank you. I hear you.

31 [LAUGHTER]

___: I just wanted to follow up _____ the basic approaches 32 33 that are commonly used _____. One thing I really 34 advise is that a lot of the discussion around questions 35 occurs in question, do I understand the question right and 36 send it back to the FDA and understand the response. They 37 sent back a response. It's just as easy for a call to 38 occur to be able to clarify some of the situations. Some 39 of the challenges around some scenarios that are presented 40 in operating characteristics are often scenarios chosen as 41 absolute worst case scenarios that easily could have really 42 possibly occurred. It is also important for those

1scenariosthe likelihood of that scenario even2occurring.So I definitely encourage through a positive3experience the potential for.

If I may, I can add a little bit on the first question, 4 Moderator: model-based versus model-informed. To me, it really 5 6 doesn't matter. In fact, if you look at the history when 7 we were one of the few who were mainly using the model-8 based analysis, I can tell you, we were trying to get some 9 resource from a group of five. We did not get it. Somehow 10 during the PDUFA VI, there was a change in model informed. 11 All of a sudden, industries supported PDUFA VI, and now you 12 look at how much support you get from commissioner from 13 PDUFA VI, I don't care what you call it.

14 [LAUGHTER]

15 Moderator: If I get support, whatever you call it.

16 : Thanks again. I was going to comment that MIDD 17 comment. And I think, you know, with immunotherapies, what we realize quite early on from the experience was that the 18 19 conventional PBPK models don't really hold, because the 20 conventional PBPK model has either a direct effect or an 21 indirect effect. Ultimately even if there's a lag in the 22 effect, the drug you effect is gone. 23 many of these immunotherapies, they are wrapping up the 24 system and just self-perpetuating essentially, so I think 25 the ... so what do we do? I mean, you know, rather than leave 26 it at that, I think the answer to me is coming back full 27 circle in the beginning of today's session where we're 28 talking about, you know, pharmacology markers. I think 29 those are the kinds of models that may be described in 30 situations and eventually may have a perpetuating effect. 31 You know, many companies have now reactive efforts in this 32 area. I have to say, so do we. We have a very compelling 33 example, not in oncology, but a different therapeutic area, give an outline where 34 just to we use the system 35 pharmacology model to select a dose for a phase 2 study for 36 a combination therapy, so I think this is very effective 37 for combination therapy where you have different sort of 38 targets and then is there a synergistic effect and the 39 model predicted the synergy very nicely and the trial was 40 read out and the model-based was spot on, so I think, you 41 know, bringing it back full circle I think will have a lot 42 of potential with pharmacology models .

: I have a question for FDA in the . I think the 1 2 publication of some basis of approvals online including the detailed report summarizing both the sponsor analysis and 3 4 regulator analysis has been also the tremendously 5 insightful and helped really to advance MIDD druq 6 development. As we can see also from different discussions 7 today, there are a lot of application of MIDD 8 addressing PMC/PMR questions or supplementary findings for 9 SND and SPOA. Is there any potential...I know you're already 10 keeping our FDA colleagues there busy, but is there any potential for them to publish basis for approvals for the 11 12 supplementary findings ? We don't need to have 13 an absolute answer.

First, let me clarify that when you say summary basis for 14 Keegan: 15 approval, what you're really talking about are the original NDA and DLA review documents that are around the 16 FDA 17 website. We also publish manuscript primarily for 18 clinicians usually the oncologists or cancer research, and 19 generally those don't have a lot of information. The 20 pharmacokinetics, I mean, it describes it but it doesn't go 21 into as greater detail as looking at the review. The 22 reviews can be all posted for anything that ends up, you 23 know, with a labeling change, but it requires that we receive requests for that, so we would have to have freedom 24 25 of information and request that those be published. 26 although perhaps Dr. McKee can tell us if there 27 is. I think we internally process it. We're frustrated 28 We would like them to put everything on, with that too. 29 and so I'm not sure if that will be happening in the future, 30 but if there is a particular application where you have an 31 interest, I think the rule of thumb is like we get three 32 requests, that's enough for them to trigger. We should put 33 this on the website. So, you know, that's what you should 34

35 [LAUGHTER]

36 Keegan: Also you should make your concerns known to the agency that 37 you would like to see more of that because I think, you 38 know, we're comfortable with doing that, but it's just not 39 our current policy. It might be a manpower issue, but if 40 they heard there was enough demand for it, that might 41 facilitate faster action in that regard.

42 Dr. McKee: I'm Amy McKee. And just to clarify on what Pat said, it is 43 a staffing issue within our division that redacts 44 information that's publicly put on our website. So if you put in enough information requests, eventually it gets put up on the list of things that will be put on the website, so any supplements you're interested, you and all your colleagues keep sending a request for it.

5 : Thank you.

6 Moderator: Doctor, I've heard similar feedback during the reco session. 7 Multiple people ask me, why don't you put the reviews for 8 the supplement online just like the original one? My 9 answer was, I don't know. I should. As long as you 10 request, the FDA will, you know, through the Freedom of Information, will give it to you, but I guess now you heard 11 12 You have to request multiple times, then it can it. 13 potentially be on the website for everyone to review. But 14 I guess it's a staff issue. But in theory, they are all public information once the drug . 15 I think we're...I have to thank my speakers and panelists. 16 We went 17 by 15 minutes because we started late, so I would like to 18 keep this on time. We're exactly on time. I know some of 19 you will catch the airplane, so we will move to the next 20 Once again, I thank our speakers and panelists. one. 21 Thank you very much.

22 [APPLAUSE]

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24 Dr. Jin: I think we have had a very busy day. Thanks for still 25 staying here until the end of the day. I will just give a 26 very brief summary and also share some of the three key 27 points that's touched me during today's workshop. I will 28 try to keep it very brief.

29 I think one thing that's very clearly seen is MIDD oncology 30 is a very fast-evolving area on multiple fronts, including 31 many of the novel immunotherapies, combinations, including many development of ... I don't have any slides, by the way, 32 33 just in case you're looking ... and also a lot of novel 34 evolvement of experimental approaches and also end points, 35 whether it is about a novel annual model to address 36 immunology-related unique questions or autometric 37 measurement for tumor size and novel biomarkers. A lot of 38 these are evolving fast because techniques also offer us 39 novel data versus to gain more scientific insight by 40 analysis. also seen throughout We have today's 41 presentation many novel quantitative approaches, whether it 42 modeling with a different type of is more 43 modifications, whether it is more of a system modeling

approach on the PBPK front or the QSP front. Yeah, they should do that. On the more practical side, it is very exciting to see from Dr. Michael Maitland's presentation that we are also developing novel ways in electronic systems to collect more real-time patient data, whether at that side or even from patients at home, so that will give us also a unique source to understand what's happening both about the disease and also about the therapies in the real-world setting.

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10 not least, hopefully all the totality Last but of 11 information will give us a filter for individualizing 12 therapy oncology as mentioned by both Dr. Jenny Woodcock 13 and also Dr. Michael Maitland. I see practical provision 14 in the field is really the individual patients we are 15 talking about. So with a few of these so fast evolving, I think it's overwhelming for anyone of us to really catch up. 16 17 I think we are always stronger and smarter together, so we 18 really need to work together and also have this real-time 19 merging of the frontier sides. Whether we are talking 20 about the real-time merging of experimental sides and also 21 the quantitative sides, we learn as the model learns from 22 us where all these novel quantitative approaches real time 23 and also for the experimentalists learning from us. What 24 are some of these quantitative approaches? Can we use at 25 fingertip to gain more scientific insights from their new 26 systems? Or it's also a call for merging of even within 27 the quantitative sides. We heard in the last session even 28 aesthetician and also talking between an а 29 pharmaconutritionist, add additional not even to 30 scientists, informatics engineer system pharmacology 31 modelers. So merging of these scientific disciplines, I 32 think, this real-time merging will be very critical. Today 33 we are at FDA, so it's very exciting to see this merging of 34 the scientific approach and also record of the patients 35 because no matter how the size we are doing, we are trying 36 to get approved to help patients. So how to make these new 37 size impact the record of the patient's decision making? 38 We require this real-time dialogue among all of us so that 39 we keep each other informed about these new evolving 40 techniques rather than each one of us struggling by I think this is really a common 41 ourselves. that's also in the spirit of _____, but I just want to 42 43 re-highlight that today.

44The second thing, I think, one thing Dr. Jenny Woodcock45mentioned really resonated with me.She mentioned

sometimes perception of new approaches sometimes will 1 2 actually add risk, especially add risk for drug 3 interactions. However, she is pointing out that we have to 4 try these things in spite of the risk. We can take small 5 incremental steps in reality, but we have to make changes. 6 So how to make that concrete step? Hopefully in today's 7 workshop is a starting point, but I think we really need to 8 have a very concrete path and action pass moving forward, 9 whether under the _____ umbrella, it means some 10 additional followup, probably a workshop on more focused 11 areas or the pilot ideas. I know the pilot is another 12 workscreen for , maybe calling out some specific pilot ideas for areas of interest or it can maybe in the 13 14 non-competitive space as mentioned by Dr. Rene Bruno for 15 CIC or Cancer Immunotherapy Consortium or by Dr. 16 regarding writing some maybe integrating information and 17 knowledge we do that collective intelligence and help each other move forward. I think 18 they are 19 representing the International Society of Pharmacometrics. 20 I think ISOP is a scientific society for including 21 scientists like us really devoting our career for MIDD, so 22 ISOP I think will love to be at least one of the venues to 23 help advance these areas and we would love to hear from all 24 of you guys whether you are online about additional ideas 25 and see what are some of the concrete things we can link 26 Our annual conference will be happening in forward. 27 October in San Diego of this year and the conference theme 28 is modeling without boundary, so it's also focused on 29 of collaboration, promoting the idea especially 30 international collaboration, and also fusion and 31 integration of different approaches. So many of these are 32 overlapping or do they seem, so hopefully we can have 33 multiple fronts and other conferences to help to proceed 34 the field moving forward.

35 Last thing I want to share one observation is today we have 36 speakers from industries from academia and also from FDA, 37 but there's one voice that we are missing. We are missing 38 the voice from patients. Although patients are touched 39 upon by multiple speakers in questions by Dr. Michael 40 Maitland and Dr. , but patients are really what we 41 are all working for. We are working for the patients. For 42 oncology patients, this means survival. And this is about 43 people's lives. So the last thing I would like to call for 44 , so I think we're talking about people's lives 45 here. We really need to work together. They are moving in the field at a very fast speed. Some of us have friends 46

and families who either battled or is battling with cancer 1 2 right now. As Dr. Rene Bruno mentioned, Dr. who 3 is a dear friend for some of us and have worked almost 4 exclusively in tumor dynamics modeling for many, many years, 5 he is unfortunately currently battling this basal cell 6 carcinoma and that is the reason he has to cancel his trip 7 to this specific workshop at the very last minute. The 8 options are running out for him and he is in very desperate 9 need of immuno-oncology therapy. We are struggling with 10 finding him drug access in France for immuno-oncology 11 therapy, so for anyone who is listening in the room or 12 online, please help if anyone of you can provide even 13 remote help because you will be not only helping one real 14 patient, but more importantly, you will be helping someone 15 who is devoting his career and now his life for MIDD 16 oncology. I think this also will be tremendously help to 17 advance our field forward. That's all, thank you.

18 [APPLAUSE]

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20Jin:So now I would like to invite my fellow co-chair, Dr. Amy21McKee from FDA to come over to give the final round of22remark.

23 Dr. McKee: I don't...I don't think I can end with anything better than 24 what's said other than to say thank you for everyone who 25 came and participated. I think this is one of the most 26 lively discussions I've ever seen in this room, and I think 27 the one point that I would take away from this is it is 28 clear that all of us need to have more cross-discipline 29 talk both within our own organizations and between our 30 organizations to use modeling to more prospectively drive 31 drug development, so thank you all for sharing your views 32 and your data and everything that you brought to the table 33 today. Thank you.

34 [APPLAUSE]