Recursion

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Hannah Adeoye: Hi, everyone. Thank you so much for joining us here today. My name is Hannah Adeoye. I'm an Associate Biotech Analyst here at J.P. Morgan. Today, we are pleased to have Recursion with us today. Here to present and tell you guys a little bit about their company is Chris Gibson and some other members of the management team.

Just want to say before we move into Q&A, we're going to have some runners here with mic, so if you have any questions during the Q&A section, just raise your hand and they'll bring the mic over to you. With that, Chris, take it away.

[applause]

Chris Gibson: Thanks so much, Hannah. Thanks everybody for joining on a rainy day here in San Francisco, but excited to be back in-person. I'm going to tell you today about how at Recursion we are decoding biology to radically improve lives.

Before I do that, I do want to share that I'm going to be giving some forward-looking statements, so please treat appropriately. Here we are at the end of a 60-year decline in biopharma efficiency. Despite the incredible efforts of hundreds of thousands of scientists over this last 60 years, this trend continues.

In the same period of time, we've seen a dramatic shift in another industry, the technology industry, where we've seen rapid improvements across a wide variety of technology tools that are creating step-function changes in industry after industry.

Recursion was founded back in 2013, before ML and AI became a cool part of biopharma, to take advantage of the opportunity at the arbitrage of these two slopes. Why is it that we're seeing this declining efficiency in biopharma?

It's our belief that it's because biology is so massively complex. That's probably a pretty easy answer to take away, but what I have to share with you is probably too complex for us to understand as humans.

I want to give you some evidence for this. This is a set of genes that are described in every textbook as being related at the intersection of these five well-known pathways that you see at the bottom, [inaudible] , TGF-beta, etc.

The relationships you see here in red, these red lines, indicate positive relationships between genes. Blue lines indicate negative relationships between genes. When we applied our platform, which I'll tell you about in a few more minutes, to this set of pathways, what we actually found was extraordinary complexity. This is what it actually looks like.

There's over 350 genes that are interacting with these pathways in a way with the same strength as the 50 genes I showed you at the beginning.

This is far too complex, with thousands of interactions and nodes, for us to understand as humans, and so we have to start leveraging new technologies in order to make more progress more quickly, bring better medicines to patients more quickly, in the context of biology, given its complexity, and that's what we're here to do at Recursion.

Our map-based approach is designed to set the standard for drug discovery in the 21st century. What's philosophically different about Recursion is that compared to traditional approaches, we're leveraging our platform to drive discovery in an unbiased and target agnostic way. We're not leveraging the literature to drive our initial target hypotheses.

What's more in traditional approaches, data tend to be treated as an exhaust. They're a byproduct of testing hypotheses, where at Recursion data are the beginning of every hypothesis. They shape every hypothesis that we generate, and these are data generated at scale.

In traditional approaches, there tends to be learning in iteration, but it tends to happen mostly within individual programs.

At Recursion, all of our data generated to be relatable over time, data we generate this week relatable to data we generated two or three years ago, allowing us to create virtuous cycles of atoms and bits that allow us to learn and iterate not only within a program but between programs as well.

Data generation in traditional approaches tends to be siloed. It tends to rest with individual teams. It tends to be generated for individual projects where at Recursion, our data is connected across programs.

Finally, in a traditional approach bespoke assays are built early to try and uncover exciting hypotheses and relationships in biology taking extraordinary efforts. At Recursion, we've automated industrialized and standardized assays at scale, generating omics data, a small number of assays at massive scale that broadly gives insight across hundreds of thousands of different areas of biology.

Let me show you a little bit about what we've delivered in 2022 with this approach. I'm excited to share that we initiated four clinical trials in the first three quarters of 2022. Additionally, we're planning a fifth clinical trial that we just shared a couple of months ago in an indication in oncology.

Beyond that, we have a number of additional oncology programs moving towards IND-enabling studies. What's more, we have more than a dozen projects coming behind those that we're really excited to start taking towards the clinic.

In addition, we've announced significant collaborations with Bayer in fibrosis, and Roche Genentech in neuroscience in a single oncology indication. We've made compelling advances in both of those partnerships. I'll be able to talk a little bit more about that soon.

Finally, we built what we believe to be one of the largest relatable data sets, proprietary data sets, in all of biology. What we've learned from the technology industry is that machine learning by itself often becomes commoditized, but machine learning with the definitive data set, that's where the true power exists. That's where you can build a moat.

I think Recursion extraordinarily well positioned to continue leading this space of tech enabled drug discovery. We have five clinical stage programs in our pipeline today, as well as a number of other programs that we're advancing towards the clinic.

We have multiple simultaneous programs we're advancing with our partners. As I mentioned before, more than a dozen additional programs in the early discovery stage that we're advancing. We're very excited about all of these. What's exciting to us today at Recursion is that we're trying to leverage technology to reshape the funnel of biopharma.

Rather than a V, I would argue that the idealized shape of the funnel should be a T, one where you can leverage technology to broadly explore every possible combination of biology and chemistry, identify the molecule with the highest probability of success, and advance it all the way to the market with no attrition.

Now, of course, anyone who's been in the industry knows that's impossible to achieve, but if we can drive technology to make that funnel look more like a T where failure happens early when it's less expensive and we can go faster.

I think today, Recursion, with our pipeline, you're starting to see that T shape start to show up in our own data across more than a hundred programs we've run at recursion. That means that we're spending less and going faster.

I've told you a bit about our broad philosophy. I want to share with you a little bit about how we build and navigate maps of biology and chemistry to turn drug discovery into a search problem. I really mean that. Our scientists begin programs today from a web app, using proprietary data that we've generated at Recursion.

Then, I'll talk a little bit about our clinical programs. To talk about our platform, I'm going to begin with an analogy. Biology is massively complex. If we want to understand a system as complex as biology, I liken it to trying to understand our entire planet and everything that's happening on the planet right now.

You can imagine that if the only insight you have was at a street level, like you can see in this street map, there's a lot you can learn. This is a little bit like specific assays that people are

building to look at very niche parts of biology. We can tell that there's palm trees here. We're probably in somewhere relatively tropical.

As you start to zoom out, perhaps adding additional data sets, you can create relationships across these data and between these data to add more context.

This is exactly what we're doing at Recursion with scaled transcriptomics, exploring areas like proteomics, excited one day to explore metabolomics, and even moving massive quantities of data week over week into our data set using phenomics, which is microscopy imaging of human cells.

We're doing up to 2.2 million of these experiments every week at Recursion, giving us broad context at an orthogonal, high level cellular state.

All of these data, by themselves, insufficient to really advance drug discovery development, but if you start putting them together and you create the software systems that allow you to see relationships between and among each of these layers, we're really excited about the potential to transform drug discovery and, as I mentioned before, turn it into a search problem just like exploring our Earth using Google Maps.

Let me show you what it actually looks like. The Recursion OS is our software platform, our process platform that we use to build these data sets and explore them. It begins with a massive automated laboratory where we have robots that are doing the equivalent of my entire PhD every 15 minutes, which is relatively humbling. All five years' worth.

Up to 2.2 million experiments a week at Recursion. From this automated lab and other labs that

we've now automated and continue to automate, we're able to generate massive data set, more than 21 petabytes of proprietary biological data.

To put that in perspective, that's more than every feature length film in human history in every language in 1080p five times over. This is on par with the data sets of some of the largest pharma companies, but what's different about our data set it was all built for the purpose of machine learning. It's built to be relatable It's built to train neural nets.

To do training of neural nets on this quantity of data, you need sophisticated computational tools. At Recursion, we actually operate one of the 500 fastest supercomputers on Earth, allowing us to dive deep in this data and from that data to start to see relationships that no human could ever pull out of this quantity of data.

Today, we've made over three trillion predictions about relationships across biology and chemistry. Those sit in a web app and our scientists begin their programs by looking for novel insights across that map of biology and chemistry.

When we find interesting insights, we have to validate them. One of the things we've been doing over the last two years is scaling transcriptomics to allow us to use an orthogonal, high-dimensional assay not based on images, based on transcription that allows us to validate these interesting hypotheses.

We can now do this at scale. 15,000 samples a week near whole exome levels. Super excited about that. We're not just doing this across a single cell type. At Recursion today, we've worked on more than 48 human cell types, including primary cells.

Most recently, excited to share that over the last 12 months, we have scaled iPSC-derived neurons at an extraordinary level, half a trillion of these neurons having been generated at Recursion at incredibly high levels of quality control.

To give you a sense of relative scale, if you were to go buy these from some of the large suppliers, this is a nine-figure investment to get this number of neurons. We believe we're on par, if not exceeding the largest producers in the world.

All of that work simply to allow us to build maps of neuroscience with our partners at Roche Genentech. This is what the future looks like. It looks like massive scale data sets and computational systems to help explore them.

Let me show you what one of the maps actually looks like. Now what I'm showing you here are millions of interactions. We're not going to be able to go through the whole thing, unfortunately, today. I'm showing you in one human cell type, every human gene across the rows and the columns.

What you can see in red along the diagonal is the cell similarity in dark red between every gene and itself. That's good to see. What you can also start to see as you go along the diagonal is these dark red clusters. These represent areas of biology with similar function.

If we dive in on one little tiny piece of this, you can see, for example, the JAK/STAT pathway. You can see in the bottom left, JAK is clustered with IL-6, STAT3, IL-6 receptor, just like you'd expect. If we were to take a tour down this diagonal, you'd identify thousands of examples of known biology that you can rediscover using these maps.

What's most exciting to us is when you see among this known biology, novel biology as well, potentially novel targets that one can exploit. I'll give you an exciting example that we just shared at a poster at NeurIPS, which is one of the premier machine learning conferences just a couple months ago as part of our partnership with Genentech.

We took one of these maps. Our partners at Genentech had an interest in the integrator complex. We were able, from this map that I just showed you, to pick up almost all of the components of this very, very complex integrator complex.

What was interesting, as you see highlighted in orange, we picked up chromosome 7 open reading frame 26 as clustering very, very nicely with the rest of the integrator complex. As we were doing that work, a paper was published, demonstrating that this particular gene is actually a part of the integrator complex.

There are thousands of examples at Recursion of novel biology sitting in these maps, waiting for us or us with our partners to exploit them and, hopefully, to turn them into exciting new medicines for patients at scale.

Now that I've told you a bit about the platform, I want to share a little bit about our partnerships' clinical and preclinical programs. At Recursion, we've taken sort of a bimodal approach, a hybrid approach to discovering biology. We want to turn latent data in our map, latent value into tangible value. We know that we cannot do that alone.

We want to partner with the very best companies to go after some of the most intractable areas of biology. That's why over the last two years, we've signed a very exciting collaboration with Bayer in fibrosis and an exciting collaboration with Roche Genentech in neuroscience and a single oncology indication.

We're going to build maps and explore maps to find novel targets with our partners that, together, we can translate. Then we can leverage our partners to help develop those through the clinic in these very, very difficult areas of clinical development.

We also believe it's important, especially in this field of tech bio, to not just believe in your platform but to believe yourself in the programs that come out of it. That's why we have our own pipeline at Recursion, five assets, five programs at the clinical stage.

I'll talk a little bit more about those in a minute. They're really focused in oncology and rare disease, where we believe we can rapidly translate these programs potentially to fast approvals. Before I do that, a little bit more on our two partnerships.

We signed our first major collaboration with Bayer about two years ago. Just last year, we expanded this collaboration to take advantage of some of our newer technologies and to add additional programs in fibrosis. What I can share is that we are simultaneously advancing multiple programs.

We love working with our colleagues at Bayer. It's been a fantastic collaboration so far. I'm hopeful we'll be able to share much more very soon.

Of course, just about 12-1/2 months ago, we signed one of the largest blue sky discovery collaborations in biopharma history with Roche and Genentech to go after the whole of neuroscience, 40 programs and up to a decade of work together and a single oncology indication.

What's exciting about this partnership to us is the breadth of vision of our partners at Roche and Genentech, where we're going to be building massive maps with neural iPSC cells and other sorts of cell types to look for completely novel targets in some of the hardest areas of biology.

Now I want to talk a little bit about our own pipeline. As I mentioned before, we have five programs at the clinical stage. I'm going to walk through each of those briefly. Then I'm also going to talk about a couple of our most exciting preclinical programs.

The first program we put into a Phase II trial last spring is REC-994 for cerebral cavernous malformation. I think this is an incredibly important program for Recursion because it represents exactly what we built this operating system to do.

Cerebral cavernous malformation affects five times as many patients as cystic fibrosis. Yet, very few people have heard of it. These patients develop focal neurologic deficits. They develop epilepsy, hemorrhagic stroke. Essentially, these patients are getting small aneurysms growing in the capillaries of their central nervous system.

For decades, we have understood that mutations in CCM1, CCM2 and CCM3 lead to this disease. Unfortunately, we haven't understood the downstream pathophysiology that would allow us to identify or execute against a really exciting target.

In fact, Recursion was born out of a traditional molecular biology approach I took with my dissertation advisor to try and target this disease, where we failed. Ultimately, using an early version of the Recursion OS, we were able to identify a surprising target.

By targeting superoxide, we were able to create a dramatic rescue of cellular systems, animal

systems. We've now taken a molecule through IND-enabling studies, Phase I and now into Phase II exploratory safety and efficacy studies.

It's important to note we are the first company and only company in the clinic for this disease that represents a huge area of unmet need. Very excited about this program. We're excited to soon be able to give some guidance around readouts.

We also started last summer a Phase II/III adaptive trial in neurofibromatosis type 2. Now in this particular indication, we're looking at meningiomas driven by the NF2 syndrome or by somatic mutations in NF2 that drive these meningiomas in a sporadic way.

We used our platform to identify a surprising interaction of a subset of HDAC inhibitors with loss of function of NF2. Now HDAC inhibitors and cancer-like biology, maybe not that surprising.

What I can tell you is that this subset of HDAC inhibitors was interacting deeply with NF2 and very few other oncogenes or tumor suppressors that we modeled. There's a specific interaction of HDACs, a subset of them with merlin and the NF2 system.

We were able to turn that into an exploration of HDACs more broadly and identified a former clinical-stage molecule that was orally bioavailable and blood-brain barrier penetrant. We were able to take that molecule, license it and drive it into this exciting new indication, where we're running this Phase II/III study, which again, I mentioned we started last summer.

The third trial in Phase II right now is REC-4881 for familial adenomatous polyposis. This is another example of how we used our platform to find a surprising interaction. We knocked down APC and identified, unlike other tumor suppressors or oncogenes, that a subset of MEK inhibitors

was having a very, very pronounced effect.

In fact, this was part of a very small collaboration with Takeda. They were excited enough about the data. They actually optioned that and shortly thereafter they made a strategic shift away from rare disease internally and we were able to pull the program back into recursion and then drive it into this Phase 2 trial where we're trying to treat patients who have familial adenomatous polyposis.

As many of you know these patients, it's a cancer predisposition syndrome. They get hundreds of polyps in their colon and their bowel. They typically have to have a colectomy in their late teens or early 20s. It has a profound impact on quality of life.

It's our hope that we can prevent the high levels of cancer or delay the high levels of cancer in these patients after colectomy and that's what we're looking to evaluate in this particular study. Eventually, one day, if we have enough efficacy and safety, we'd love to see if we can push back or delay colectomy for these patients to really move that important life event outside of that prime part of life.

We're also excited to share that our first new chemical entity where we weren't just identifying chemical matter that others had developed in ways we could use it against novel insights in biology has just started a Phase 1 trial in the fall.

This particular program is recurrent C. diff and our internal chemistry team was able to take this small molecule all the way through and we're now excited to demonstrate our ability to execute not only in the clinic, but to create that pipeline for all the other NCEs that we have following behind this one in oncology.

While I've shared a little bit about our clinical programs, I do just want to briefly talk about...Sorry, one more clinical program. Got to keep them all straight. Just a few months ago, we announced AXIN1/APC mutant cancers. We're using REC-4881 again here.

In this particular contact we used our map to identify a strong effect of this molecule in the context not only of APC but of AXIN1 as well. We're very excited to drive this program.

We're still planning the trial and we're doing a lot of PDX modeling because we want to go after a basket trial looking at a lot of different tumor types that could be driven by mutations in either AXIN1 or APC outside of colorectal cancer. Very excited about that as well.

Now, let me transition to two of our most advanced NCEs in the preclinical space in oncology. I'm excited about these because they represent the Recursion Operating System starting to run at full gait not only novel biological targets but novel chemistry as well.

The first of these is target alpha, and the TPP for this program was can we find a molecule that can modulate not only an increase in the sensitivity of a tumor to anti-PD-L1, but can actually decrease systemic inflammation? That's what we were looking for.

We started by taking hundreds of known genes from large population studies that have been published, that either up- or downregulate their response to anti-PD-L1. We clustered these hundreds of genes in our map, and we identified subsets and families of these that were surprising. The one I'm showing you here is clustered around BERC 2.

We identified two genes, gene A and gene B that we're not sharing the names of here -- they

were surprisingly clustered next to BERC 2 -- as well as a chemical compound, REC-648918, that was also clustering here.

We took this insight and went straight into a CT-26 animal model, which you can see on the bottom left. You can see that in this model, as expected, vehicle and anti-PD-L1 have very little effect. No effect essentially.

With monotherapy of a REC-648918, which we believe targets both gene A and gene B, we were able to have a significant decrease in tumor growth, and in combo with anti-PD-L1 we had 40 percent complete responses.

What I think is most interesting is what you see on the right though. The interferon gamma as well as a number of other cytokines that we measured you can see intratumorally that the combo therapy increases the level of expression of interferon gamma, the level of secretion of interferon gamma, whereas in the plasma in these mice you see a marked decrease in inflammation.

This is important because while only a subset of patients respond to anti-PD-L1, that subset is further reduced by the patients who have essentially too much inflammation as a response to the therapy. If one could mitigate that systemic inflammation while also increasing the inflammation within the tumor, we think that that's a very important potential innovation.

Again, this is a poly-pharmacological approach identified using our map going after two different unrelated targets that are differently expressed both in the tumor and in the systemic biology.

Lastly, I want to talk about target gamma. This is one of my favorite programs because the team took some known biology. We know that CDK-12 is an interesting potential target in the context of

homologous recombination deficient negative ovarian cancer that's resistant to PARP inhibitors.

CDK12 is challenging to go after because it's very closely related to CDK13, and you don't want to go after CDK13 for a variety of reasons related to toxicity. What you can see in our map is that CDK13 looks nothing like CDK12.

Functionally very different. You can also see that we identified a compound 65029 that was clustering with CDK12, as well as a gene, gene A, which was also clustering with CDK12.

Gene A has not been reported to have anything to do with CDK12 biology, but our map is telling us that functionally, it's extraordinarily closely related. We were able to validate biochemically that REC-65029 potently inhibits the protein product of gene A, but has no effect on CDK12 activity. We really have a gene A inhibitor here.

We were able to take that molecule and go straight into a bracket proficient ovarian cancer PDX model. It's important to know, this is a log two tumor volume scale. What you see is that this particular molecule by itself has a profound effect on mitigating tumor growth in this PDX model.

In combination with a PARP inhibitor, olaparib, you see that it's a more pronounced effect. On the right, you can see that we have complete responses more quickly with this combination. This is our ability to identify novel biology, novel targets.

To take those targets and act on them with chemistry, we predict from our maps of biology and chemistry could be active, and then to drive it straight into animal models that read out six months after we initiated this trial. I'm really excited about this program as a prototype for what many of the programs Recursion will deliver in the future.

Finally, before I end, I want to talk a little bit about value-driven by our team and our milestones. Our team is extraordinary. We have about 500 people. What's very different about Recursion is we don't look like the typical biopharma company. We have almost equal weighting of biologists, and chemists, and data scientists, and software engineers.

I think in the next decade, that's what all companies in this space must look like if they want to be competitive. There's an inevitability to the creep of technology into this space and the impact that we're going to have.

I'd ask a colleagues from Recursion just to stand briefly. I didn't tell you I was going to do that. Just in case afterwards, anybody has questions. We have Mike Secora, our CFO, Gerald Albak, head of IR, and Ryan, from chief communication officer. Very excited for you to spend time with each of them or with myself after the discussion.

What's next for Recursion? We've talked about the milestones we've hit. In the near-term, we expect the potential for option exercises, for assets in our partnerships with Roche or with Bayer.

We have the potential for option exercises for map building. As you'll recall earlier, there's up to half a billion dollars of milestones in our Roche, Genentech collaboration. Set aside not for programs, but for us building maps of neuroscience and oncology and then potentially optioning some of the underlying data to our partners.

We have the potential for additional INDs and clinical starts, the potential for additional partnerships, and the potential for consolidation of the best technologies teams and assets in the tech biospace, as many of the later stage private companies face really strong economic

headwinds.

I think Recursion positioned better than any other company in the tech biospace to continue leading this sector. We're very, very excited about the future, because if we can achieve these things, Recursion has the potential to create enormous impact. With that, we should probably transition over to questions. Thank you so much.

[applause]

Hannah: Thanks Chris, for the presentation. I just want to remind everyone that if you want to ask a question, feel free to raise your hand and one of our mic runners can bring a mic over to you. For our online listeners, if you would like to ask a question, you can ask via the Ask a Question button on the portal.

Eric: Hey, Chris, great presentation.

Chris: Thanks.

Eric: One of the opportunities with the map platform was the potential to repurpose existing chemical matter, perhaps approved or evaluated chemical matter to other ends. That being said, some of the new programs that you're unveiling are with NCEs. This novel [inaudible] .

I guess at this point in time have you...Where is the company in having screened existing chemical matter against the battery of biological assays? How should we be thinking about the

balance or the origination of new programs going from either existing chemical matter versus NCEs going forward?

Chris: Thanks so much, Eric. I think this is one of the places we were most wrong in the early days of Recursion. It turns out there's lots of opportunities to repurpose shelved assets in the context of biology, but there's not a pervasive set of incentives that make that likely to happen in this industry.

There are dozens of examples of medicines that we might be able to develop, but we were unable to get our colleagues at a variety of biotech and pharma companies to externalize those assets. There's not structures that are set up well. Doesn't mean we won't take those opportunities when we see them, and we reach out to pharma companies all the time when we identify opportunities like that.

That said, we shifted to NCE focus over the last two or three years to take advantage of all the opportunities where we're not able to license an asset. The other thing I'd point out, we did some interesting work, and we haven't published it yet.

At a high level, when we look across the genome, and we look across not only the 10,000 molecules we have that are FDA-approved or bioactive or potentially shelved, we start looking across hundreds of thousands, near now a million new chemical entities. Only a minority of genes have a small molecule that is replicating the knockout of that gene.

There's a ton of functional biology that none of the small-molecule chemistry, even in a large library, a pharma-scale library, none of it is being touched by these small molecules, and so, for us, an opportunity, not only to use machine learning to expand our small-molecule library to go after those targets, but potentially to use other modalities in the future with partners to go after them as well, when we find that they're important.

Eric: How are you expanding the breadth of chemical matter going into your screenings? Can you talk a little bit, how it's sourced, perhaps some of it via partnerships? How much of it is also being broadened out internally?

Recursion Representative: Yeah, thank you. We have half a million compounds from our partners at Bayer. We're expecting hundreds of thousands of compounds from our partners at Roche Genentech. Then internally, we have about a million compounds that our team has sourced. We source these from NME, WuXi, a variety of other suppliers.

What is exciting about our work is that as we generate omics data at multiple concentrations for each of the molecules in our library, now 1.7 million molecules in total, it sets up the opportunity for us to use ML to predict what molecule we should order next, and not only in terms of building out the library, but perhaps in the future, investing in what we describe as automated microsynthesis.

Today, running an SAR cycle for our chemists means you have an interesting insight, now, you want to improve that molecule. It requires a whole bunch of iterations of 8 to 12 weeks of us sending out a list of molecules that are synthesized by our partners, shipped back to us, and we then put them through the platform.

My hope is in three to five years down the street from recursion, we will have an automated platform.

We are site-acceptance testing the first piece of this for predictive ADMET that will allow us to not only evaluate tens of thousands of molecules every week in a variety of predictive ADMET

assays, but synthesize, in very small quantities in-house, molecules that our generative AI or AI systems suggest we should explore next.

If we could decrease that 8 to 12 weeks down to 2 to 4 weeks across 10, 12 cycles of SAR, you could dramatically shorten the period of time that one invests in translating each of the molecules from our platform. What's more, all of that data becomes an important input for training new machine learning models that eventually can help reduce the number of cycles one needs across SAR as well.

All of this compressing our programs, ideally to the shortest time possible, scaling with automation and standardization so we can work on many projects simultaneously, and hopefully increasing the probability of success as we start to predict early in a program, right after we get a hit.

For example, which chemical series should we take forward? Perhaps, if we can predict there's going to be an ADME issue with one of these series, we cannot prioritize that for further work.

Eric's going to keep rolling with the questions.

[laughter]

Eric: Of the programs that are in the clinic currently, how are things progressing in terms of enrollment? Give us some brief vignettes for several of them. Any further color in terms of site-activation, patient enrollment, those kind of metrics? How will you be updating them over time?

Chris: We are really excited to give concrete guidance on that really soon, in the next two or three weeks, I would say.

Eric: OK. [laughs]

Chris: Not yet ready to give it today, but in late January, we'll be giving guidance now that we have a sense of the enrollment rates.

Eric: Great.

[pause]

Eric: By way of additional, or perhaps a business development which has been part of the business model over the past couple years, how to think about additional partnering activity and where the focus might be placed, whether it's with some of the existing programs within your pipeline or outside that scope?

Chris: Yeah, thanks Eric. We'll be opportunistic with programs in our pipeline. Target Alpha would be a really good example of a program we could externalize early in the clinic.

Certainly in the IO space, it could behoove us to be partnered with a larger pharma who has the resources to drive a program like that, while a program like Target Gamma in HRD-negative ovarian cancer might be one that we would drive ourselves later through the clinic.

From a platform perspective, last year we were really focused on setting up the Roche Genentech collaboration for success. When you sign up to work with a partner for over a decade, with a partnership the scale of the one that we signed, we wanted to really focus there.

We have delivered across all expectations in that partnership today, and we are well positioned, if we wanted to, to do another partnership now. What would that look like, where would it be focused? I would say probably in large, intractable areas of biology.

Perhaps areas like cardiovascular metabolism, where I don't think Recursion wants to drive our programs all the way through the clinic given some of the challenges in that space, the resources that one needs, and where there are companies very well positioned with extraordinary teams, resources and expertise to help us execute in those areas.

I wouldn't also rule out the potential for large technology partnerships. If you look at some of the large tech companies, they have been marching towards this industry for the past 10 years, and people are finally starting to see this with DeepMind and Isomorphic. You're even seeing Amazon with PillPack, and then...What's...

Eric: One Medical.

Chris: One Medical, and then more recently starting to design clinical trials. You see these companies starting to converge around biopharma. They're going to provide services for companies in this space, but I wouldn't be surprised if components of these entities start to try to develop medicines.

Recursion, perhaps, could be well positioned to partner with a company in that kind of space as well. What we're really looking for is transformative partnerships. A big upfront in all of that is exciting, but it's about, "What can we deliver value-wise to patients over five or six years?"

That's what we want to set ourselves up with with any partner that we consider this year.

Eric: Maybe it was contained within the answer you gave there, but thinking about what lab modeling with the clinical experience, some of which...I'm thinking of Flatiron, for example, where they're gathering all kinds of outcomes from clinical data.

Any kind of integration opportunities there going from the in vitro modeling that you're doing to the clinical?

Chris: Yeah, absolutely. There's two big pieces we are still yet to build. One is digital chemistry. We've built some of that, but there's a lot more build for us to do. The second is integrating population-scale genomics data, or other sorts of data like that.

Those could be integrated not only in our clinical-development stage to help drive our programs, but as an input to our discovery engine. There's a number of companies we could consider partnering with in that space.

We're leading that field, and certainly something Recursion will consider as we start to get our feet under us on the digital chemistry side as well. Thank you, Eric. Appreciate it.

Audience Member: Hi. Hi Chris. Yeah. First of all, congratulations. This is incredible. I had a question. It's a bit of a loaded question because I know you've made some investments in this space. How do you feel about functional technologies that are predicting beyond genetics and how that fits into this space?

Are you bullish in this space? What are your thoughts on some challenges ahead?

Chris: What do you mean by functional technology?

Audience Member: Like phenotypic screens. Known medicine, for example.

Chris: Yeah, no, absolutely. We actually acquired a company two years ago called Vium that had put cameras in the cages of animals -- in rodents. Now we've entirely shifted our ovarium to that technology, enabling us to use machine learning to extract much better signals of efficacy.

You can imagine the rotor rod test. Where you put a mouse on the wheel and it spins. It's 80 years old. We use machine learning to just watch the mouse in its cage, interacting with its wheel, interacting with its neighbors, and extract much better sensitivity and specificity to also detect toxicity.

We see the same thing being true across many levels. Not only phenotypic screens where we've done a lot of investment, but transcriptomics and maybe even organoid work, complex cell types as we're starting to build now. Very bullish in that space generally.

I think the next five years at Recursion will see us starting to integrate some of those types of technologies at real scale, which is something I think we're very good at.

Audience Member: OK, thank you.

Audience Member: Just want to talk a little bit about your new indication that you're looking into with REC-4881. Wondering about how that inference was made. If it was a result of you seeing activity in FAP and thinking, "Oh, perhaps there might be efficacy in AXIN1/APC mutant cancers." Or if that was an inference derived from the platform you're on.

Chris: Yes. Certainly there's a known relationship between AXIN1 and APC, but there's lots of known relationships. What we saw from the map was that there was a very tight functional relationship between AXIN1 and APC, and that led a map-based insight like that, led us to focus on AXIN1 and not some of the other genes there up or downstream of APC?

Hannah: For the design of that study, can you just talk a little bit about how you're thinking about the design of that phase two study?

Chris: Yeah, absolutely. There's a number of tumor types that are driven by mutations in AXIN1 or APC. I think we're still early in the process, but we would imagine designing a basket trial that would allow us to explore a wide variety of tumors that are driven by mutations in either of these genes.

What I think is interesting to note, if you look at the bottom left here you can see these are

different tumors that are injected into mice. You can see in green are wild type tumors that are wild type for AXIN1 and APC. You can see in orange are tumors that are mutant in either AXIN1 or APC.

What's interesting to note is that you see with this particular MEK inhibitor that we're driving for FAP, you actually see tumor growth inhibition for all but one of the tumors that we profiled. We're not looking to just bring a sledgehammer. We're looking for a real precise relationship.

What you see in Orange is a strong, I would say, index of really significant tumor growth inhibition above 60 percent, which is the most meaningful for those tumors that are AXIN1 and APC mutant. This is really a precision oncology play.

It's not just a MEK inhibitor in oncology. It's a MEK inhibitor where we see a really strong biological interaction with these particular pathways that we don't see in other tumor suppressors or oncogenes.

Hannah: Great. Thank you so much.

[crosstalk]

Hannah: It looks like we're at time, but I just want to thank Chris and the Recursion team so much for joining us here today, and thank everyone for joining us.

Chris: Thank you.

[applause]