So, but after I have driven, I am Dr. Darshana.
I am a pathologist with other cancer genetics and I am glad to present our data on lung
cancer here today.
But before I actually run through the all the figures of our experience, I will just
try to briefly introduce about our company.
So, the other cancer genetics we are journey has started in 2013.
We are a molecular diagnostic testing service provider, focusing only on oncology.
While providing the routine diagnostic sequencing solutions on tissue and liquid, we also have
some unique solutions where there is, you know, which are innovative.
And we, I am proud to say that our journey does started in India.
Now we have labs in UK and USA and we currently service over 40 countries.
And this has been, I think, achievable because our sole focus since we began our journey
was has been on quality and I that can be seen with the accreditation that I can show
here, which is NABL cap as well as clear accreditation that our India facility as well
as UK facility boost.
Of course, NABL is only for India.
So now going to the experience.
So first, what when I started data mining for this presentation today, first thought that
as a pathologist obviously came what has been the histopathological subtypes that I observe in my data.
And as you can see here, adenocarcinoma stood out the most common histopathological subtype
at 86%.
Now when I looked up the literature for the incidence rate from India, of course adenocarcinoma
varied from, you know, about 1 third to close to 50 percent of incidence.
But for obvious reason, even though the guidelines like NCCN for example do recommend broad
molecular profiling even in squamous cell carcinoma, but the clinical outcome has not
been great in squamous subtype.
And that's why maybe clinicians to preferred sending only adenocarcinoma or more commonly
the adenocarcinoma are tested.
And that might have been the reason that we see that subtype as the most common one.
The median and mean age between male and female, they had some difference though not
statistically significant.
The presentation or the testing happened in women at slightly earlier age, but of course
not statistically significant at all.
When it came to age distribution of these histopathological subtypes, in this third decade we had very few cases, absolutely few cases.
Adenocarcinoma was most commonly seen in the seventh decade and squamous cell carcinoma
of course was again common in that decade only.
However, adenocarcinoma percentage in the third and fourth decade was not so uncommon.
The early stage presentation is significant in our population.
Now when looking at the gender wise comparison of incidence versus the molecular testing,

we know the incidence in female statistically for lung cancer is less.
They comprise only about one fourth of the cases.
But if we see the comparative prescriptions for molecular testing, female had more commonly
tested for molecular testing.
Again for maybe obvious reason that non-smoker people are known to have higher incidence
of diveraltations.
And most of our Indian women being non-smokers, again, clinician tend to do molecular testing
more diligently in women maybe.
And also maybe with a female present at advanced stage.
But my data set, I did not have much information on staging for majority of the cases.
Hence, I am not presenting on the staging difference between the genders.
So what are the panels that we provide?
It is a kind of disclaimer also that whatever data I am presenting is not uniform.
I have some small panel testing data which is focusing only on the 12-gen panel, where
there is some data is from comprehensive genomic profiling.
So most common diveraltation of course the denominator is uniform, but when I go to certain
unique non-microslic microsatellite instability, the denominator is much less.
So when coming to the actionable drivers, of course the EJFAR stood out and I tried to compare it with the TCGA incidence.
I think it is a well proven fact now our Indian especially, and also the South East Station,
we see much higher percentage of EJFAR and that also was seen in our data set.
We had close to 39% incidence of EJFAR alterations.
The K-A-RAS or ALC was more or less similar.
One important point here that I felt was quite clinically relevant would be the incidence
of hardware amplification and alfusion in neuroendocrine.
We do know that neuroendocrine morphology also has EJFAR quite significantly, even though
the outcomes are not great, we see EJFAR.
But in our data set I saw that hardware amplification and the ALC fusions were also quite significantly
present in the neuroendocrine subtype.
In the neuroendocrine I have data of small cell as well as the large cell neuroendocrine
and other low-grade neuroendocrine tumors, although of course their percentage is less.
So this is what I was referring to.
And the squamous morphology, the met amplifications were quite common and significantly if we compare
the percentage were more common compared to adenos called carcinoma.
I think this is a unique finding.
I haven't been really, maybe I missed, I don't know, I didn't see any literature citing
that squamous morphology had more common met amplification or met exone skipping rotation,
but our data set clearly showed higher incidence of these metaltation in squamous as compared
to adeno.
And again comparing these rival rotation gender-wise.
So EJFAR of course was significantly more common in women, so was the alcultation.
Men of course because of maybe the smoking had the k-raz alteration more common compared

to women.
And also the hurtumutations because now there is significant options for even hurtumutations
in lung cancer.
The hurtumutations were also more commonly seen in men and I think that is relevant and
they also had higher incidence of red fusion.
EJFAR, alcros1 were of course more common in the women.
So was the B-Rath.
Now comparing the incidence of EJFAR variants or the subtypes in tissue versus liquid, of
course the exone 19 was the most common whether it was tissue or liquid and next was exone 21.
And as maybe the earlier talk of liquid-wise they did refer to that liquid-wise Cesar Farmour
sensitive for acquired resistance mutations.
Aligning with that I had T79KM more common in liquid versus tissue because of course it
is a resistance mechanism.
And so was the okay.
And now coming to the coexisting alterations in EJFAR positive cohort.
So here the denominator is only those patients who had one sensitizing EJFAR mutation and
I tried to look at what were the other alterations that I could see.
Concurrent EJFAR alteration the resistance alteration like T79KM or C797S of course were more commonly seen when it was a liquid sample that I was using.
So was the Keras and B-Rath mutations.
So these mutations which are known diver for the resistance acquired resistance to EJFAR
tyrosine kinase therapies were more commonly seen on the liquid data.
Coming to distribution of Keras variant because now we have option for Keras G12c I thought
that I should really look into its incidence.
In our data also Keras G12c was the most common orientation and which is targetable now and
the next common were I think this is a pretty known fact but the data did concord with whatever
information is out there already.
For the immune checkpoint in a bit of biomarkers I think already discussed micro satellite instability
high status is not very common in lung and that same was the finding in our data.
We had only 0.5% of the patients of lung cancer who had micro satellite instability high status.
The TMB high was when I said TMB high I am referring to 10 mutes per MB.
The TMB high was seen in close to 33%.
Now TMB high and the PDL1 positive status was relatively less common compared to the
literature evidence that I saw.
So our data sets the Indian patients I did not find equivalent TMB high status as well
as PDL1 positivity.
So now this was about the data.
I also wanted to take this opportunity to enlist some challenges which we face as a lab.
So when I was doing this data analysis so much demographic information was missing because
whenever we get a sample patients or clinicians are not really focusing because it is more
private laboratory testing we do not have access to the hospital records and

patient
records but when we are publishing data regularly it would be more meaningful if we have insight
to that the data being shed.
Of course not details but you know the prior smoking is too many a times and I think clinicians
here can play rope patients are more proactive to share that data if they clinicians sound
them months otherwise they feel it not if you push them, they will push them, they will
push them, they will be able to have that data.
Another aspect that is very critical is the tissue quality that we receive.
The majority of the times by the time we receive the tumor blocks that tumor is used
up in the immunostrochemists analysis it is a point of debate whether now I do not know
versus commerce really matters or not of course it still matters but I think that the tissue
utilization has to be done judiciously even in pathology laboratories and so it is a
fixation.
So many patients who can really benefit from this targeted therapist do not achieve that
because the nucleic acid quality is so degraded by the you know the block is made
and there are certain various challenges I will just take 30 seconds when it comes to
the data that is turned out in the report.
There are so many variants which may have conflicting interpretation across databases
they may have conflicting interpretation for somatic versus germline and when the report
is floating around there might be you know you might refer to one database and feel
okay this report may be done it may not be so because there is a lot of effort and
experience of you know 13 years going into there or for any laboratory it is but I would
request to really discuss what is the evidence that led a particular lab to classify and
give a particular interpretation for the variant because that is something may impact the patient
management as well.
Yes sorry so that is all thank you so much for your time.