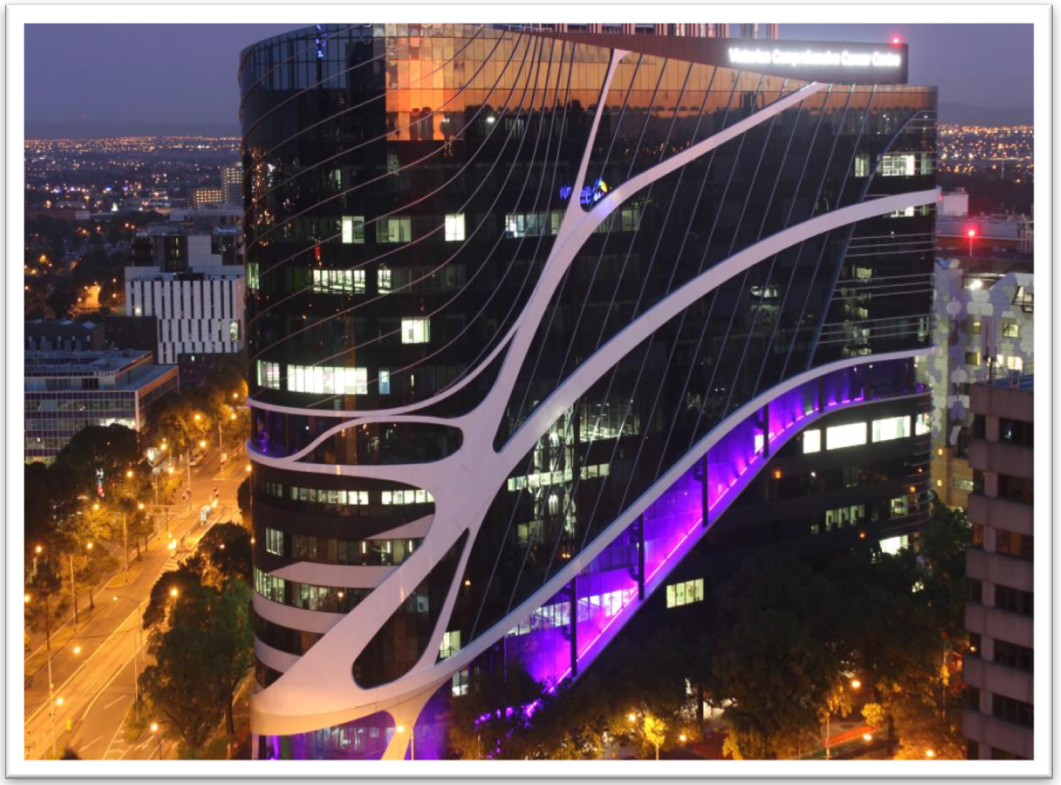
Using advanced R packages for the visualisation of clinical data in a cancer hospital setting

ROXANE LEGAIE

LEAD CLINICAL BIOINFORMATICIAN

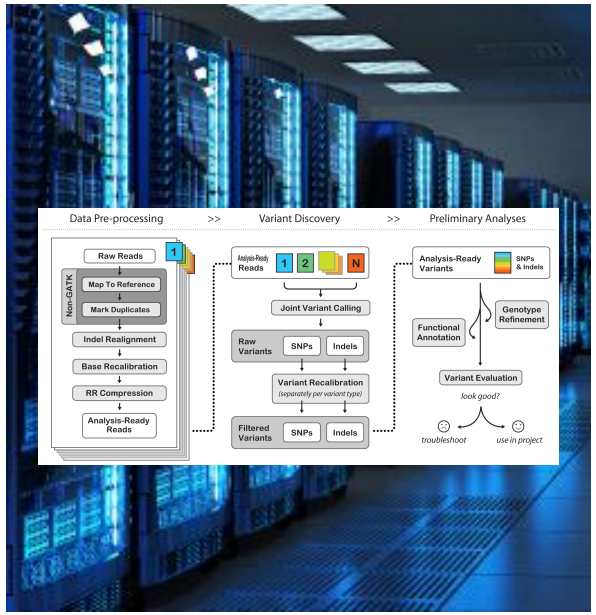
PETER MACCALLUM CANCER CENTRE – MELBOURNE, VIC, AUSTRALIA

Peter MacCallum Cancer Centre Melbourne, VIC, Australia

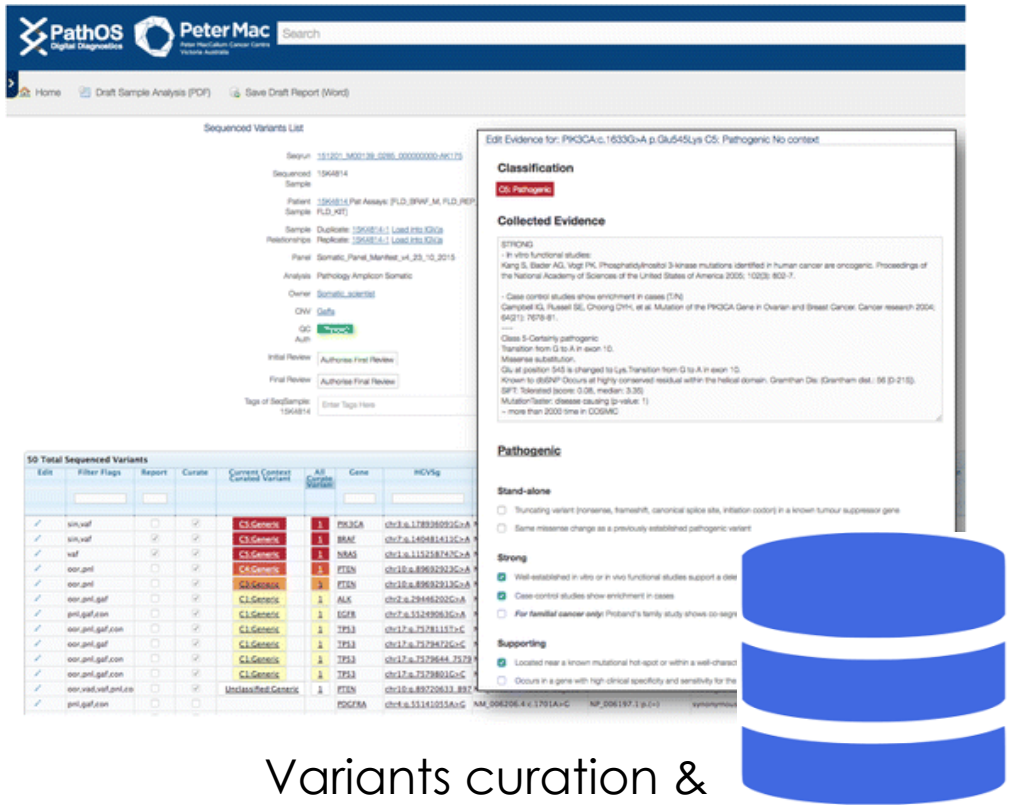


Next Generation Sequencing service
Pathology Department

Sequencers



HPC &
Bioinformatics Pipelines



Variants curation &
reporting tool

Next Generation Sequencing service
Pathology Department

Personalised Medicine

Sequencers

HPC &
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Variants curation &
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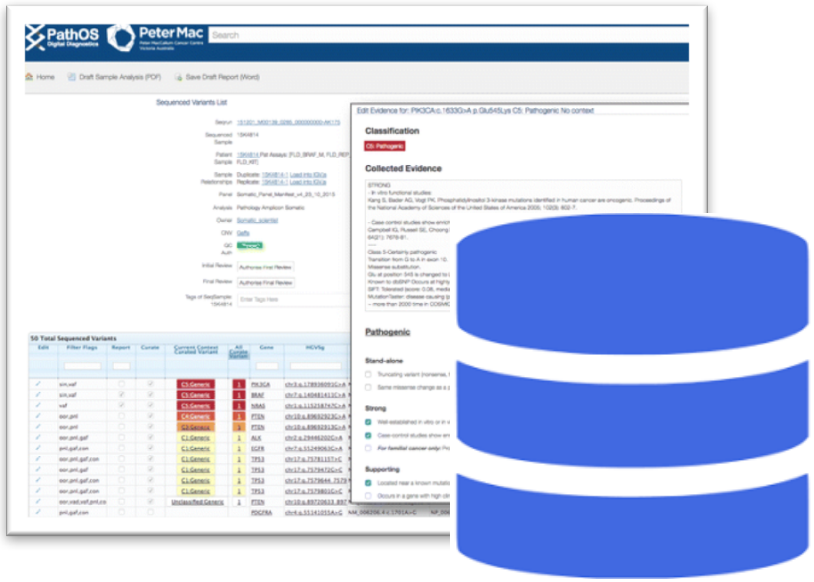
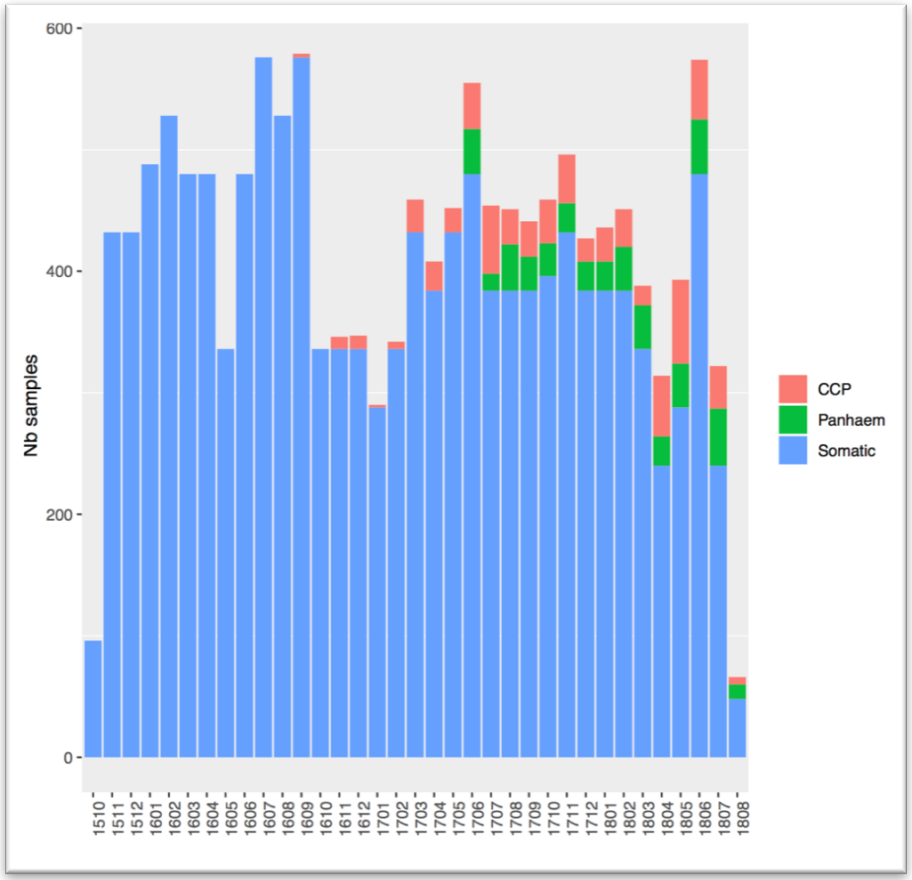
Monitoring a sequencing service using R & ggplot

Various gene panels based on the clinician's request:

- Somatic amplicon panel
- Panhaem Hybrid Capture Panel (*blood cancers*)
- Comprehensive Capture Panel (*solid tumours*)
- Familial Risk Cancer Panel
- …





Number of cases per test per month

Monitoring a sequencing service using R & ggplot

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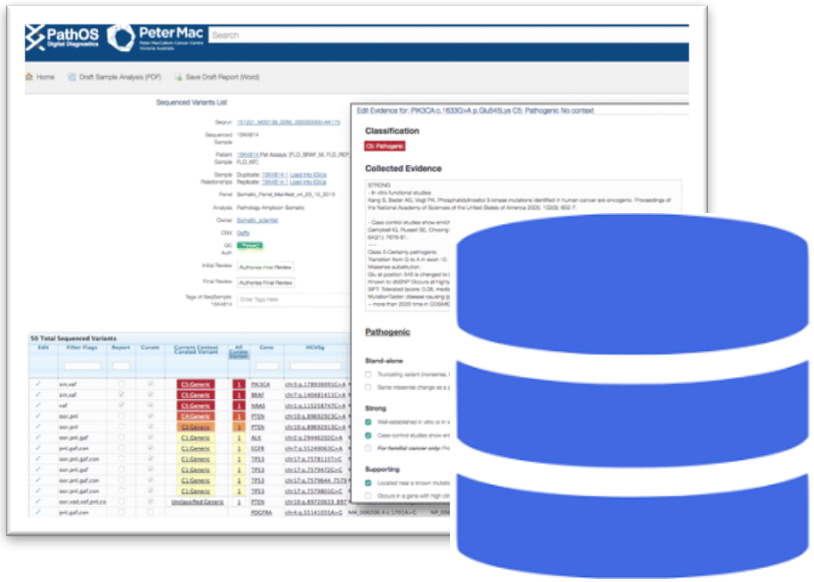
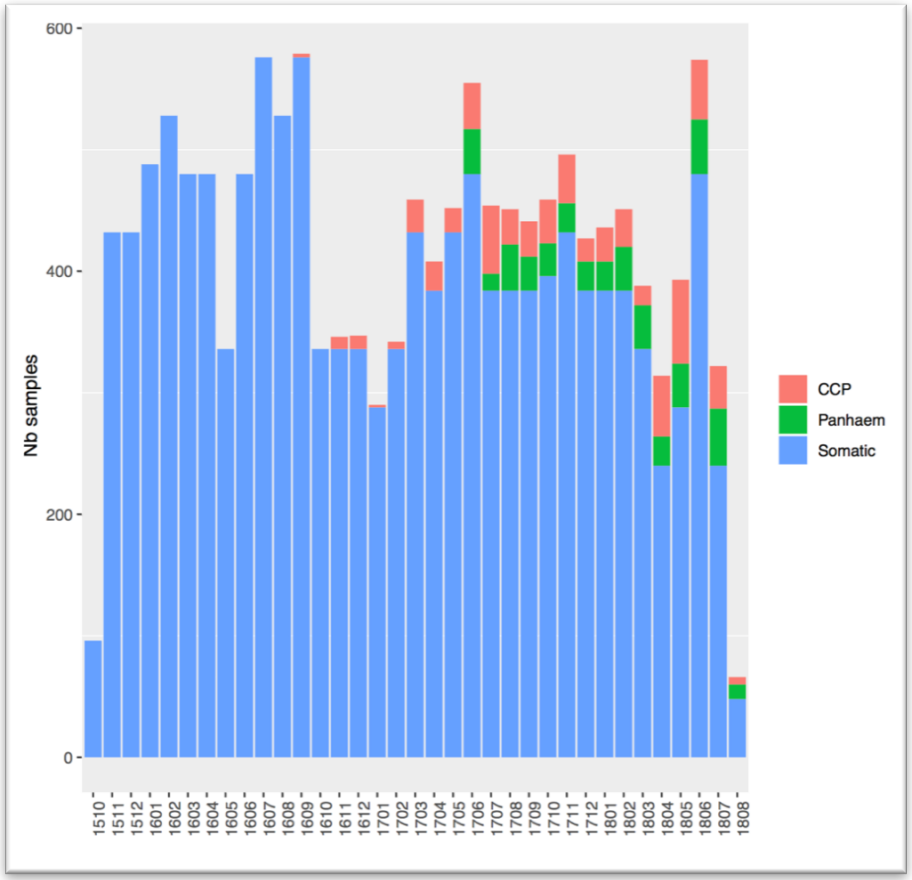


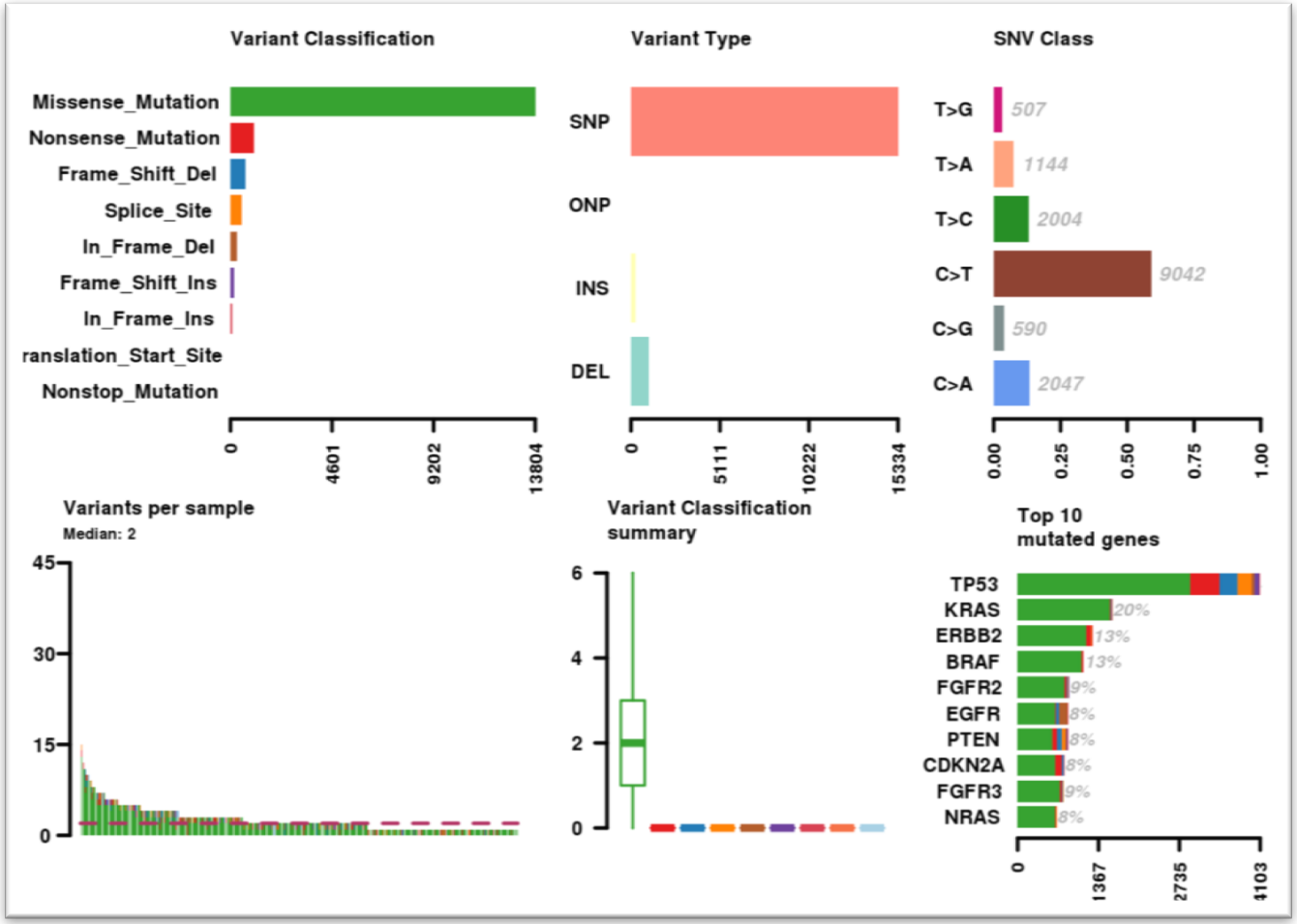


Number of cases per test per month

Exploring clinical genomics findings using R & *oncoplots*

Variants frequency & type:
- Somatic amplicon panel

Excluded variants:
- Variants with ExAC_AF > 0.01
- Variants with with high freq in dataset (>35% cases)
- Variants with low confidence (t_vaf < 20% & t_depth < 500x)



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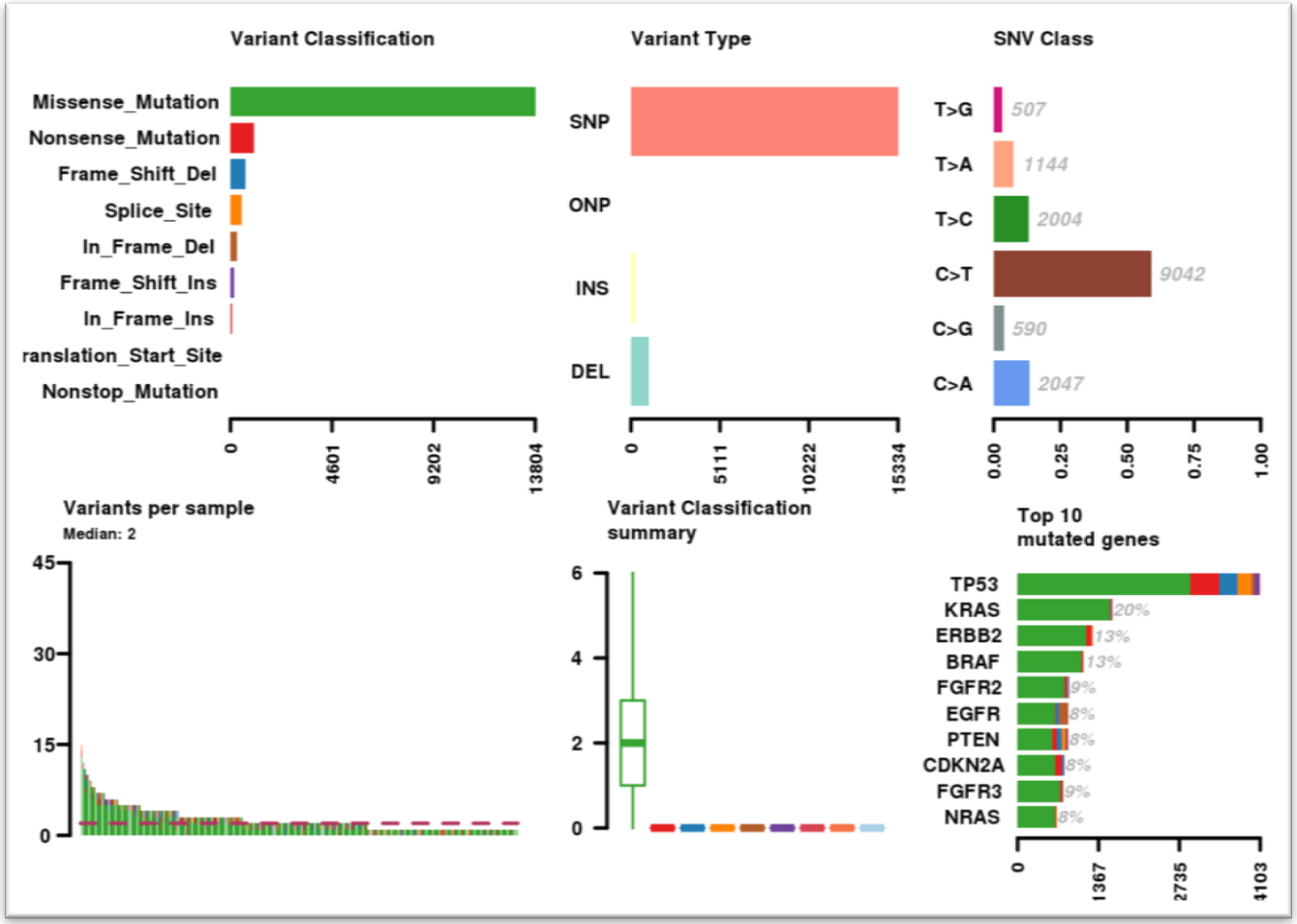

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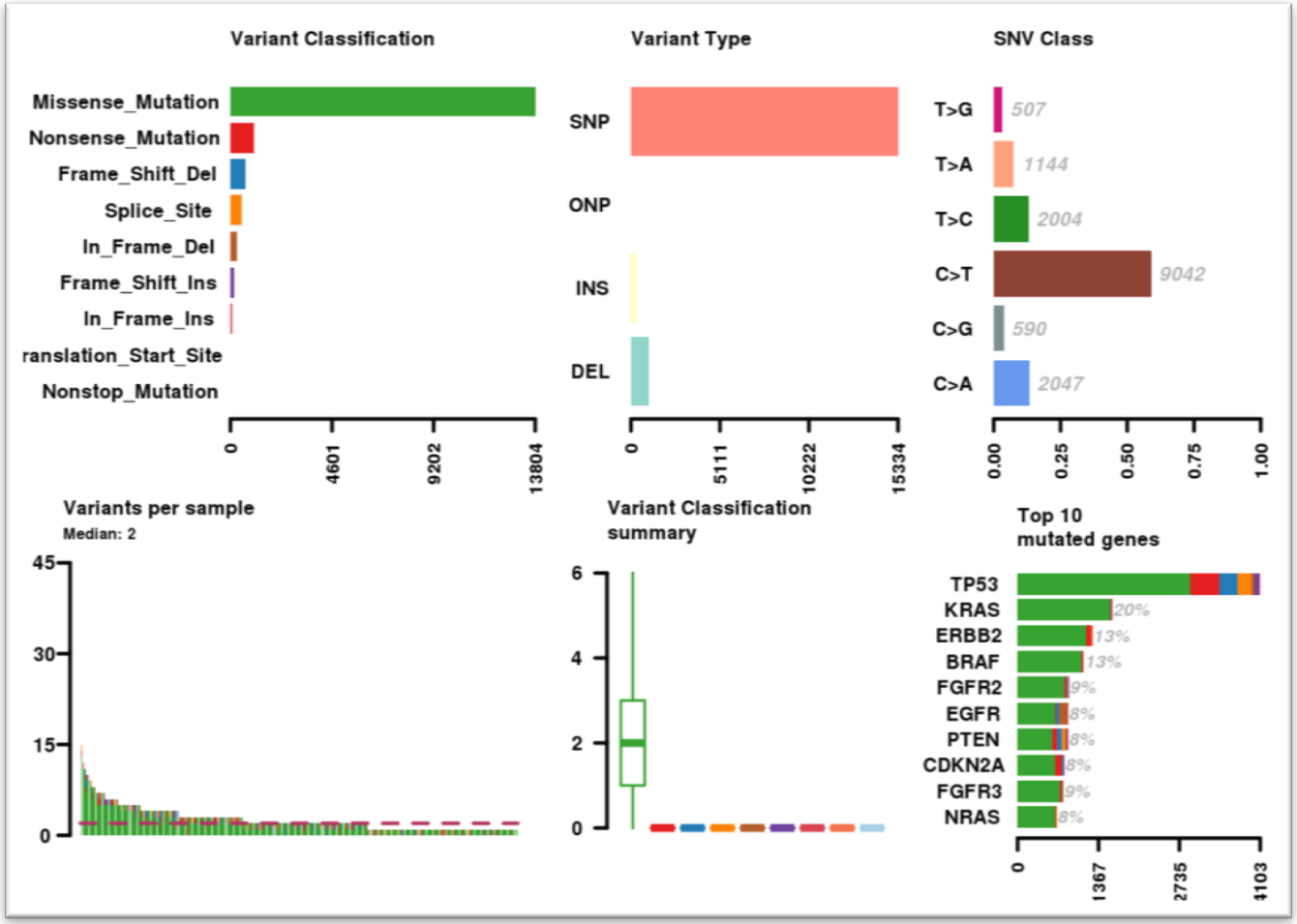

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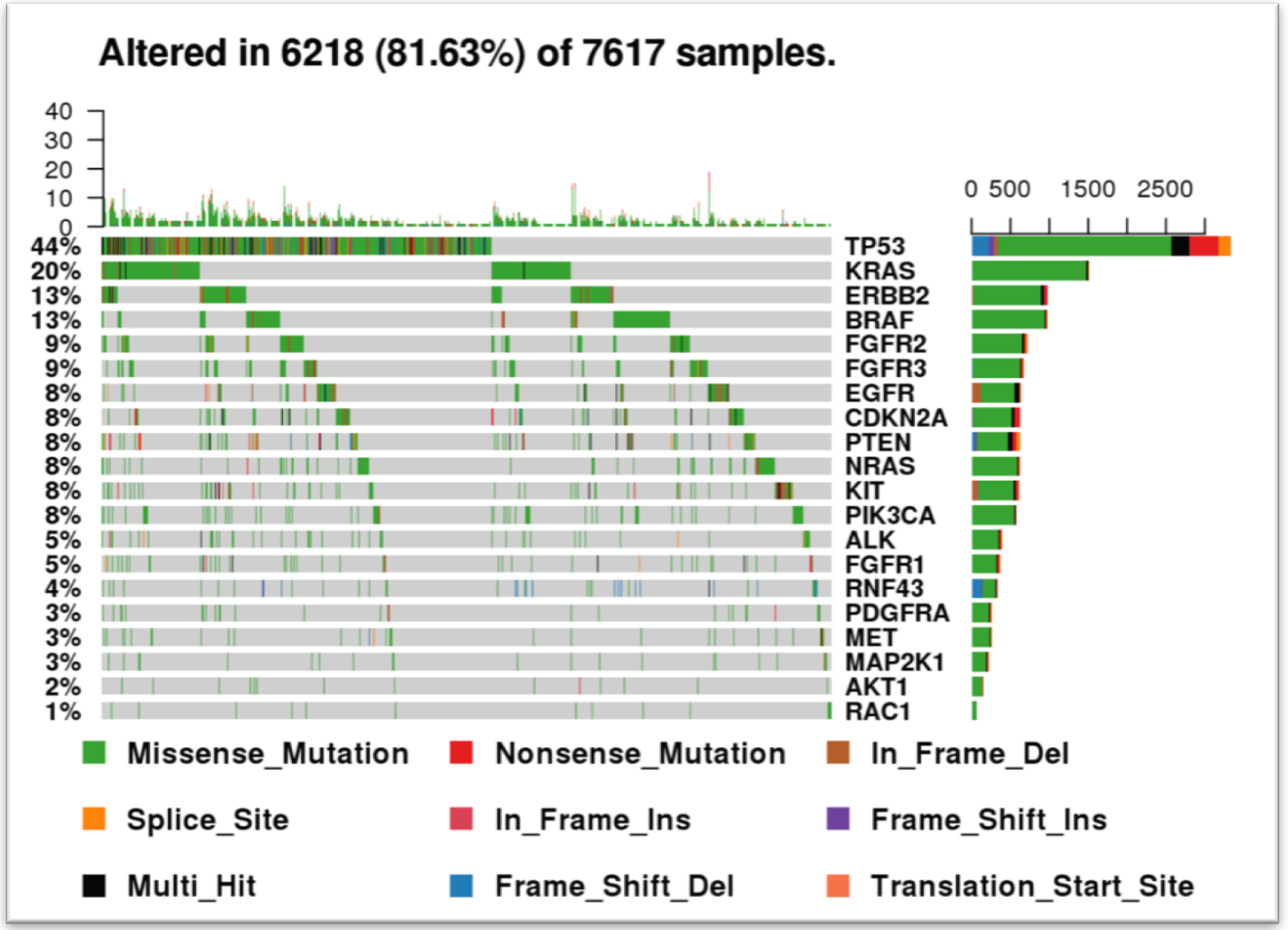

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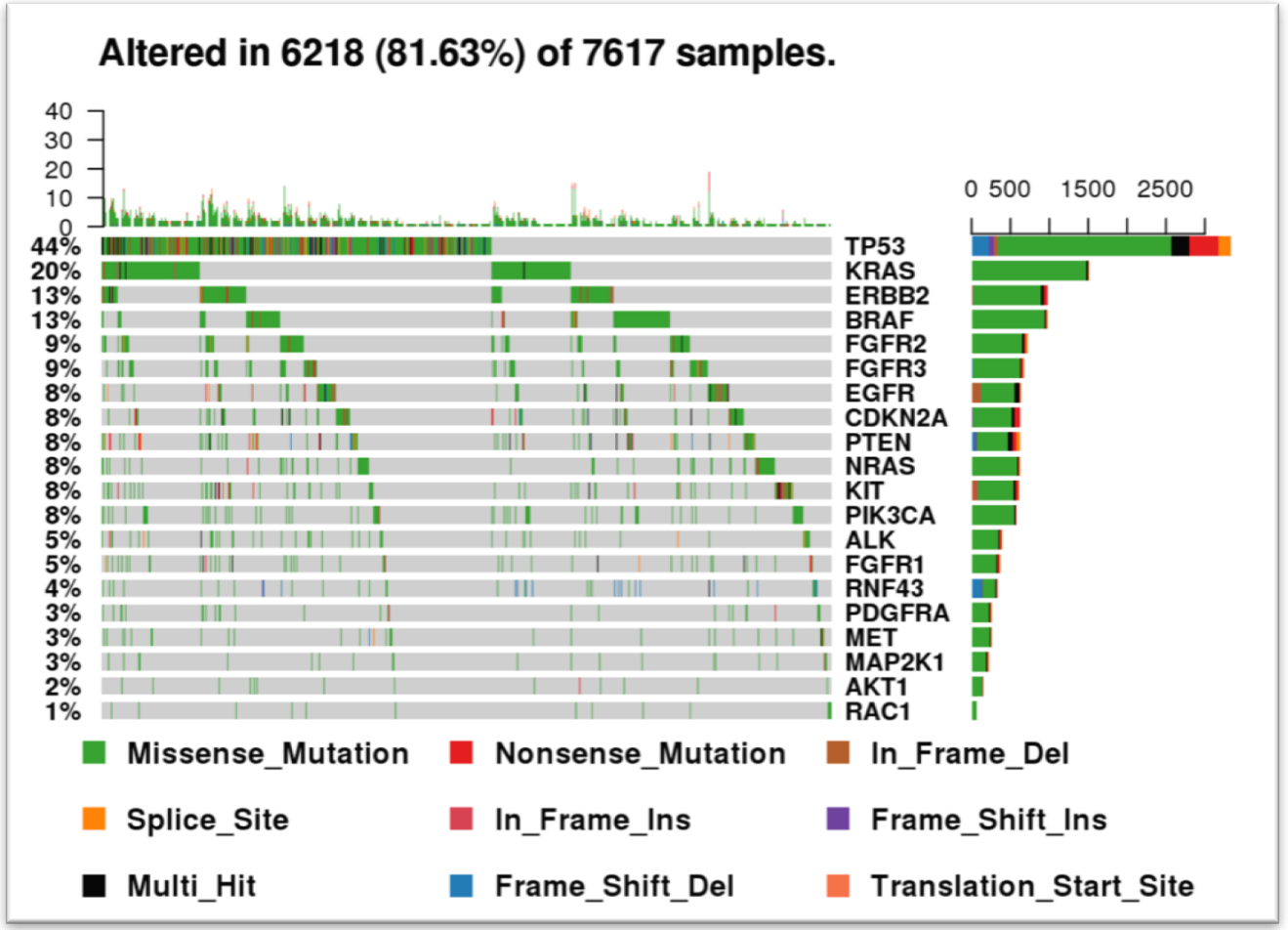

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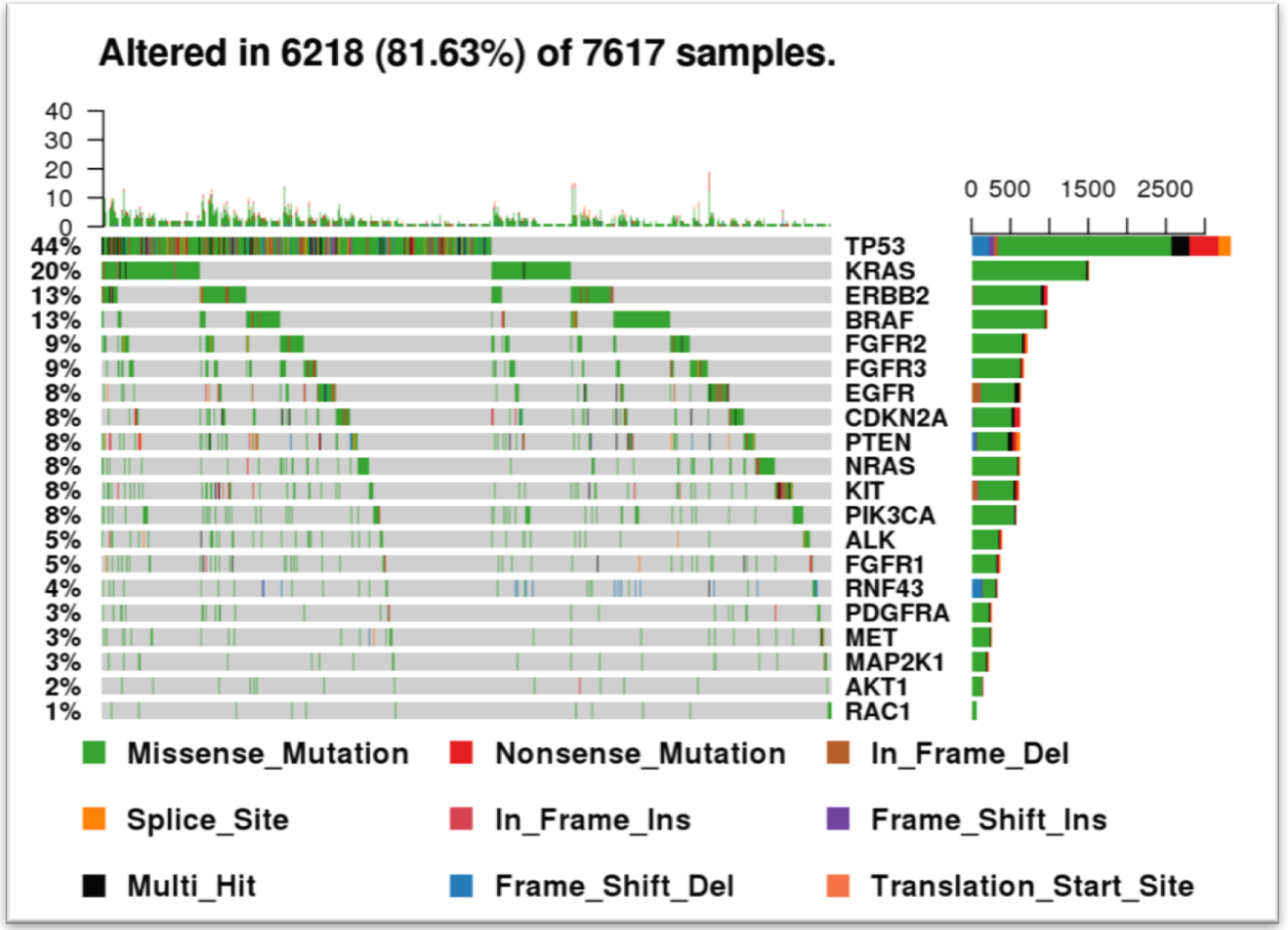
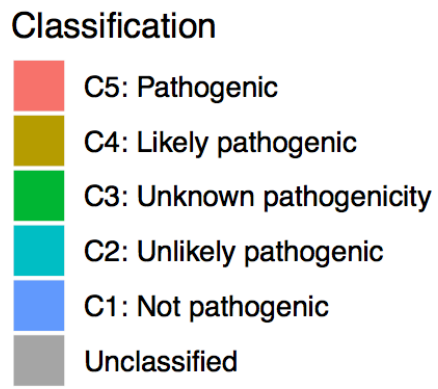
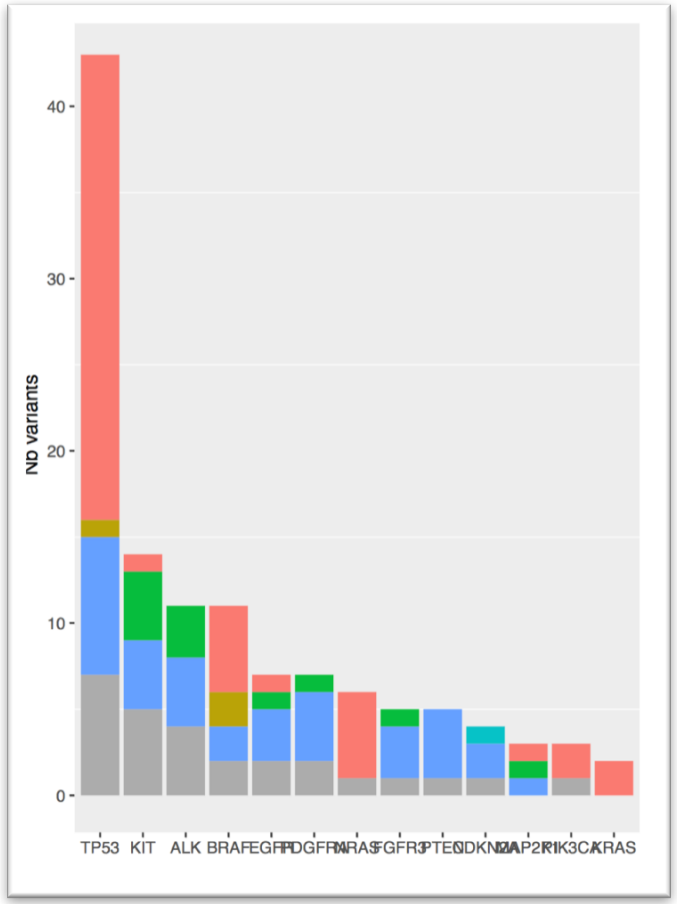


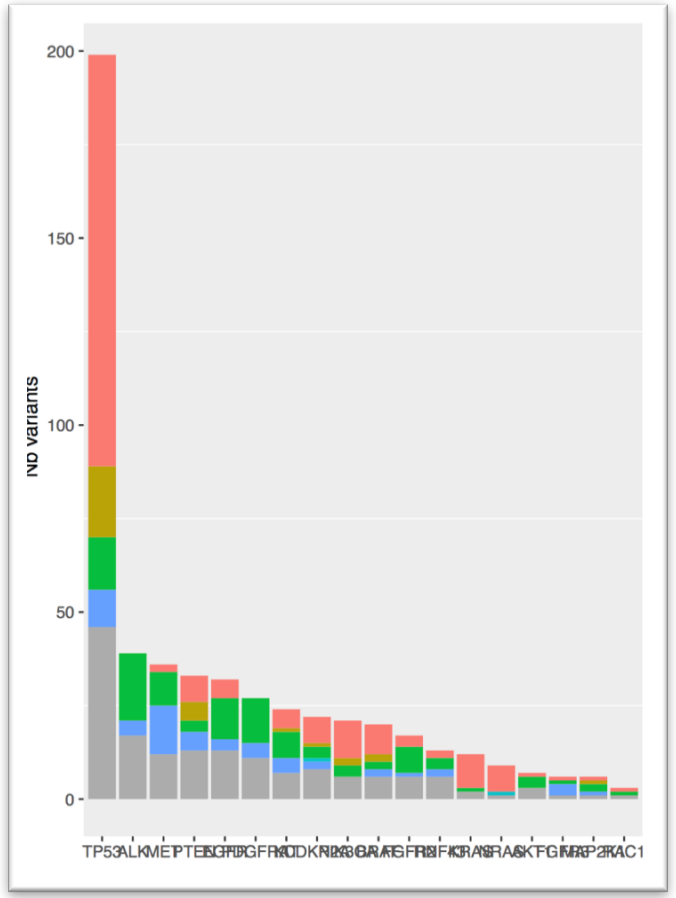
Exploring clinical genomics findings using R & ggplot

Variants pathogenicity per gene:

- PanHaem panel
- Comprehensive panel







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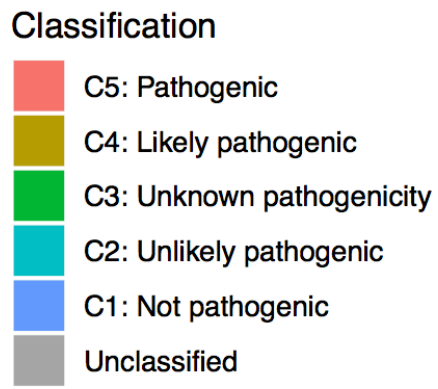
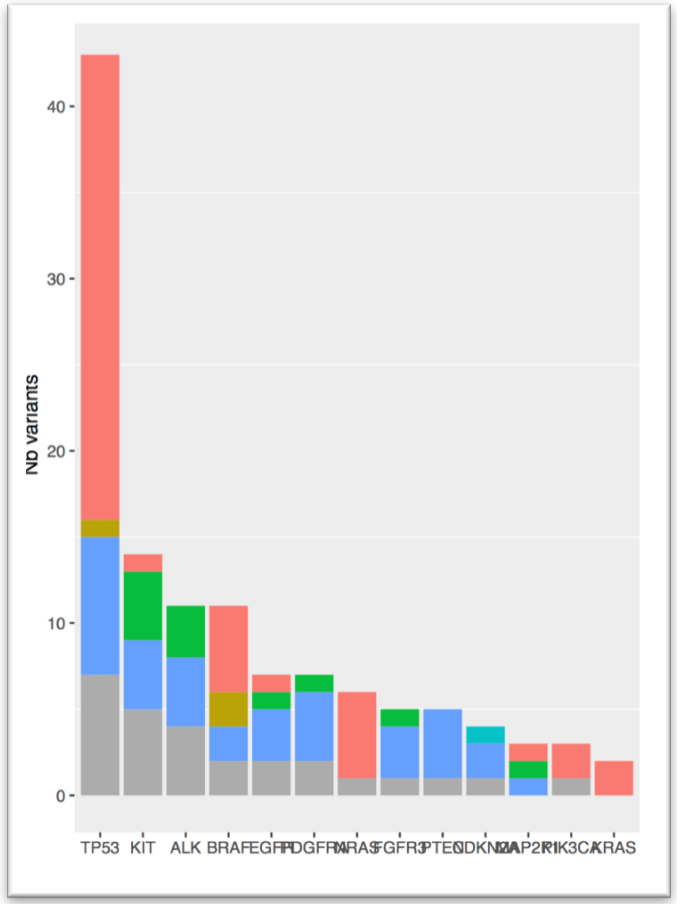
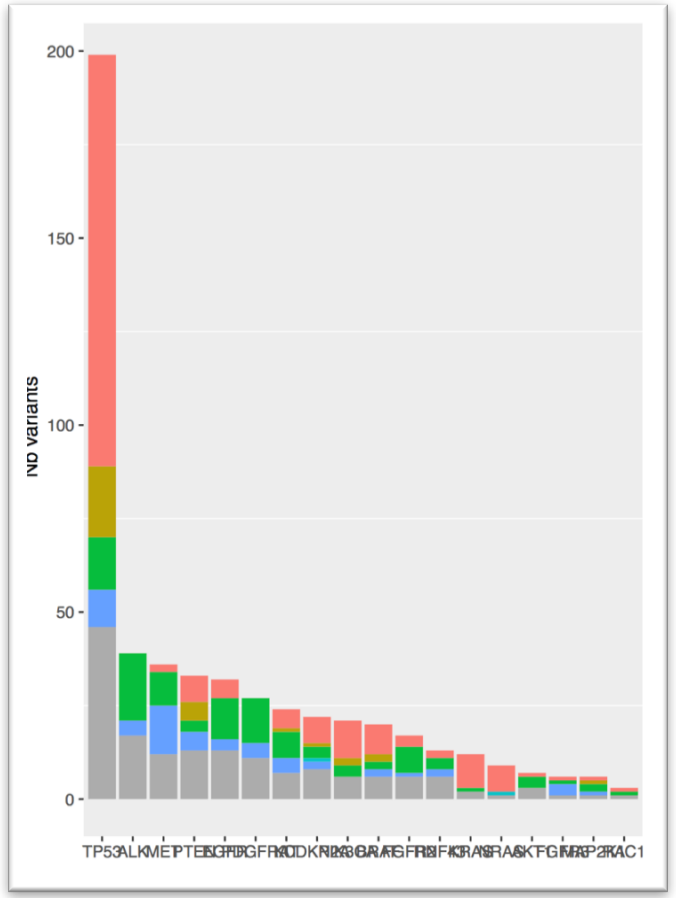


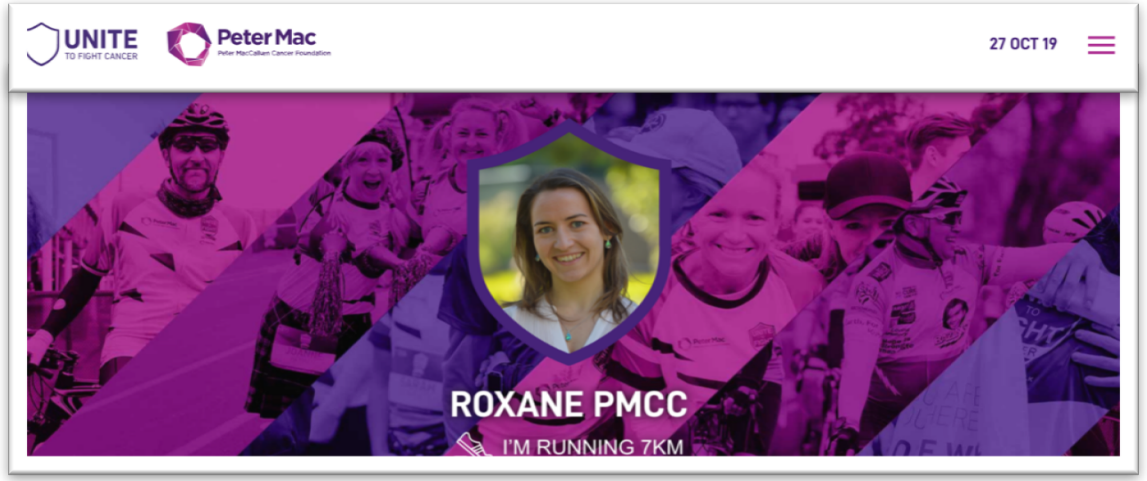




Thanks!

Any question:
Roxane.Legaie@pertermac.org

https://www.linkedin.com/in/roxane-legaie



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