

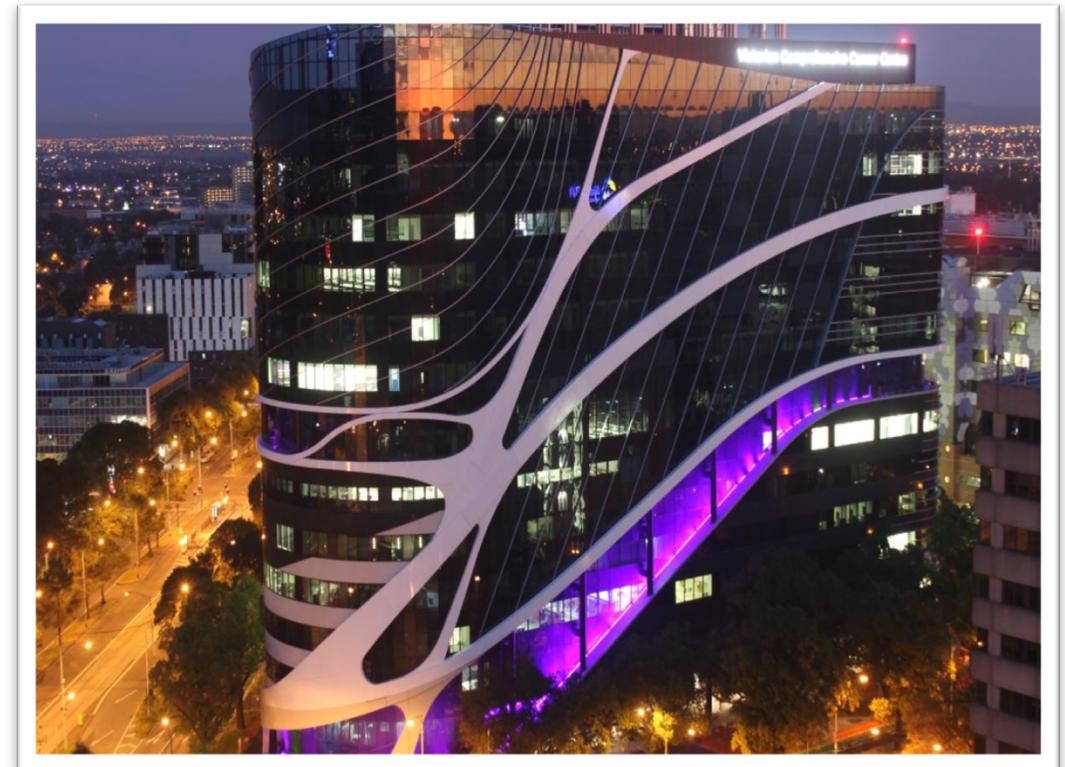
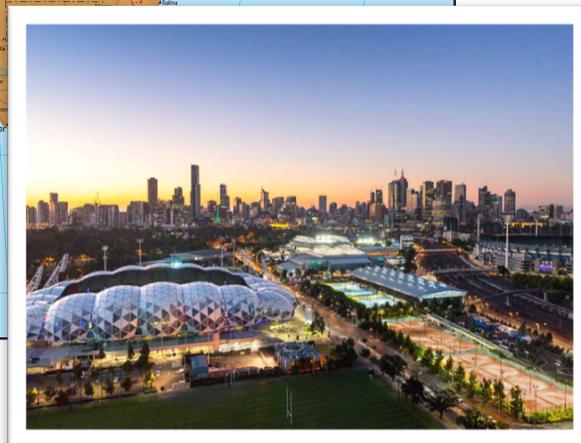
Using advanced R packages for the visualisation of clinical data in a cancer hospital setting

ROXANE LEGAIE

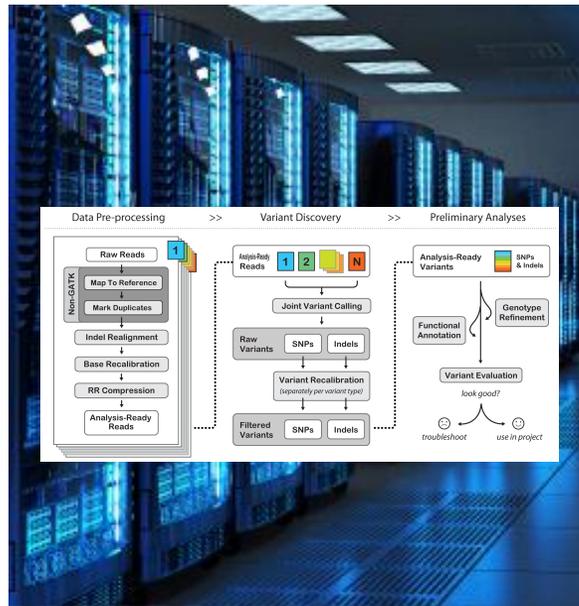
LEAD CLINICAL BIOINFORMATICIAN

PETER MACCALLUM CANCER CENTRE – MELBOURNE, VIC, AUSTRALIA

Peter MacCallum Cancer Centre Melbourne, VIC, Australia



Next Generation Sequencing service Pathology Department



The screenshot shows the PathOS reporting tool interface, which includes a search bar, navigation links, and a detailed view of sequenced variants. The interface is divided into several sections:

- Sequenced Variants List:** Displays sample information, patient details, and analysis parameters.
- Classification:** Shows the variant classification as **Pathogenic**.
- Collected Evidence:** Lists evidence supporting the classification, including in vitro functional studies and case-control studies.
- Pathogenic:** Provides a list of pathogenic variants with columns for Edit, Filter, Flags, Report, Curate, Current, Context, Variant, Alt, Current, Gene, and HCVSig.



Sequencers

HPC & Bioinformatics Pipelines

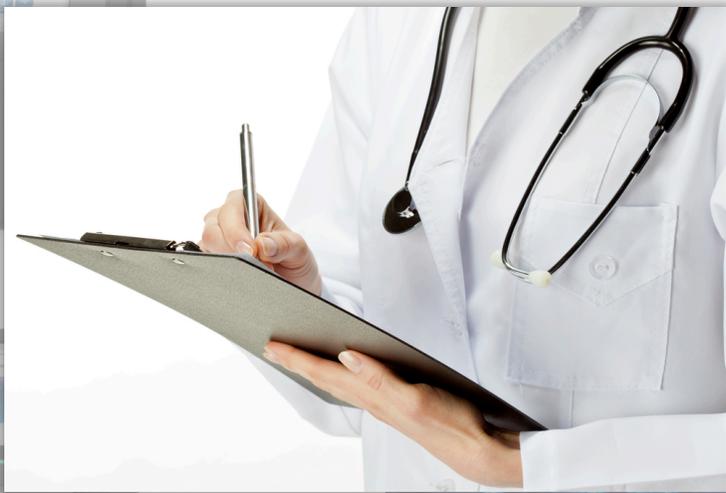
Variants curation & reporting tool

Next Generation Sequencing service Pathology Department

Personalised Medicine



Sequencers



HPC &
Bioinformatics Pipelines



Variants curation &
reporting tool

PathOS Peter Mac

Gene	Variant	Classification	Frequency	Impact	Gene	Variant	Classification	Frequency	Impact
BRCA1	c.11311G>A	Pathogenic	1/1000	Missense	BRCA1	c.11311G>A	Pathogenic	1/1000	Missense
BRCA2	c.11311G>A	Pathogenic	1/1000	Missense	BRCA2	c.11311G>A	Pathogenic	1/1000	Missense
BRCA1	c.11311G>A	Pathogenic	1/1000	Missense	BRCA1	c.11311G>A	Pathogenic	1/1000	Missense
BRCA2	c.11311G>A	Pathogenic	1/1000	Missense	BRCA2	c.11311G>A	Pathogenic	1/1000	Missense
BRCA1	c.11311G>A	Pathogenic	1/1000	Missense	BRCA1	c.11311G>A	Pathogenic	1/1000	Missense
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BRCA2	c.11311G>A	Pathogenic	1/1000	Missense	BRCA2	c.11311G>A	Pathogenic	1/1000	Missense

Pathogenic

Collected Evidence

STRONG

- In vitro functional studies
- Huang Q, Baker AG, Tang PC. Phosphatidylinositol 3-kinase mutations identified in human cancer are oncogenic. Proceedings of the National Academy of Sciences of the United States of America 2005; 102(5): 825-7.
- Class control studies show enrichment in cases (7/9)
- Garnett GJ, Futreal AG, Chong DM, et al. Mutation of the PTEN Gene in Ovarian and Breast Cancer. Cancer research 2004; 64(7): 7978-81.
- Class 5 Cancers pathogenic
- Transition from G to A in exon 10
- Missense substitution
- Gly at position 545 is changed to Lys, Transition from G to A in exon 10
- Known to affect function of highly conserved residue within the helical domain. Genom Res 2004; 14(12): 2110.
- gln1: Reversed scores: 0.58, median: 0.50.
- Multiple/other disease causing: 0 value: 1
- more than 2000 times in COSMIC

Pathogenic

Stand-alone

- Truncating variant (promoter, frameshift, canonical splice site, initiation codon) in a known tumour suppressor gene
- Same missense change as a previously established pathogenic variant

Strong

- Well established in vitro or in vivo functional studies support a deleterious effect on the gene or gene product
- Class control studies show enrichment in cases
- For familial cancer: Proband's family study shows co-segregation with cancer

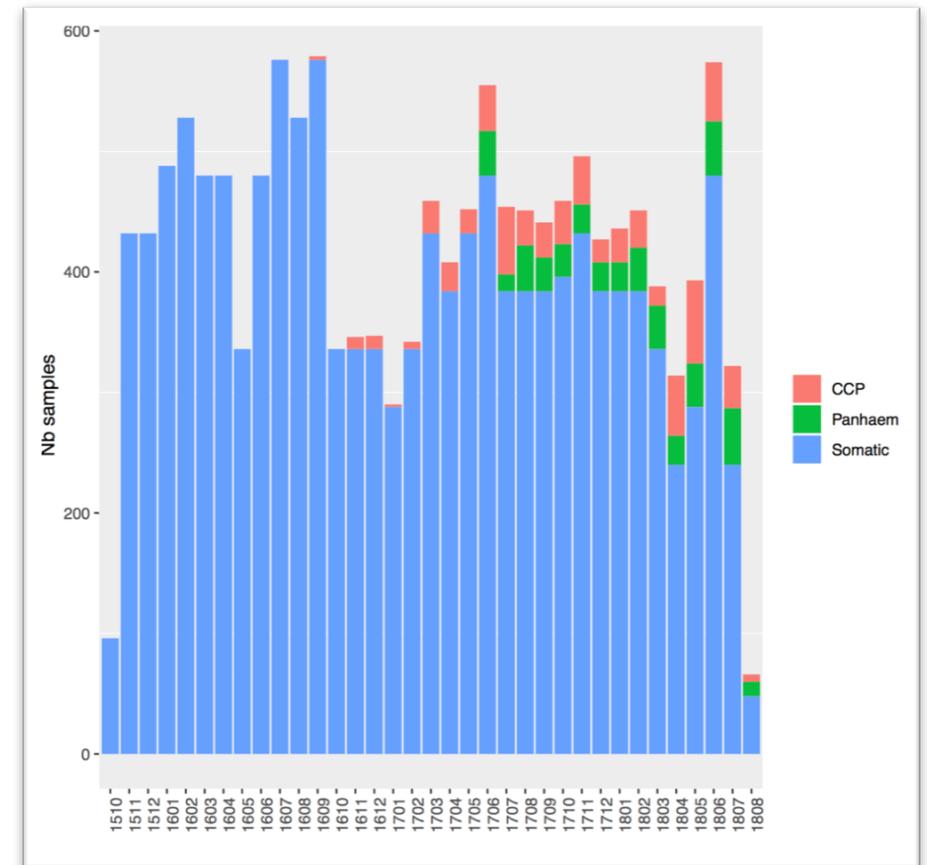
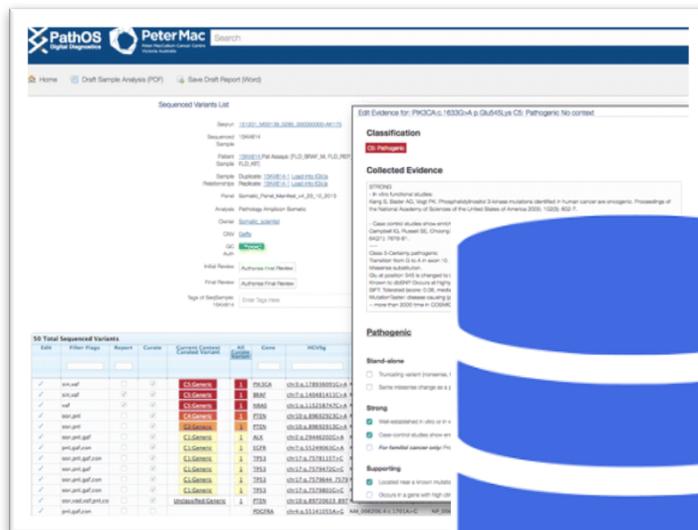
Supporting

- Located near a known mutational hot spot or within a well characterized functional domain
- Occurs in a gene with high clinical specificity and sensitivity for the disease

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
- ...

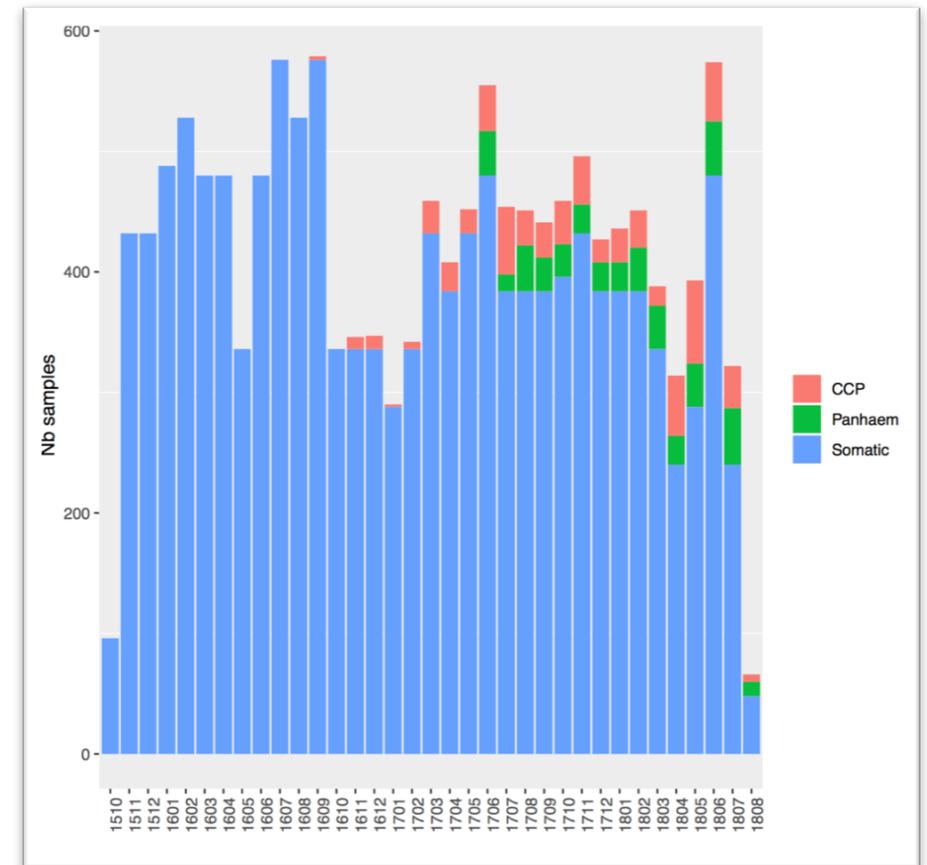
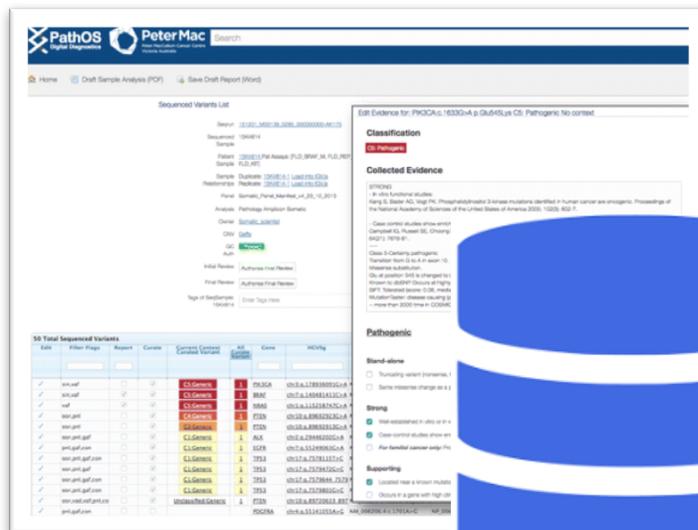


Number of cases per test per month

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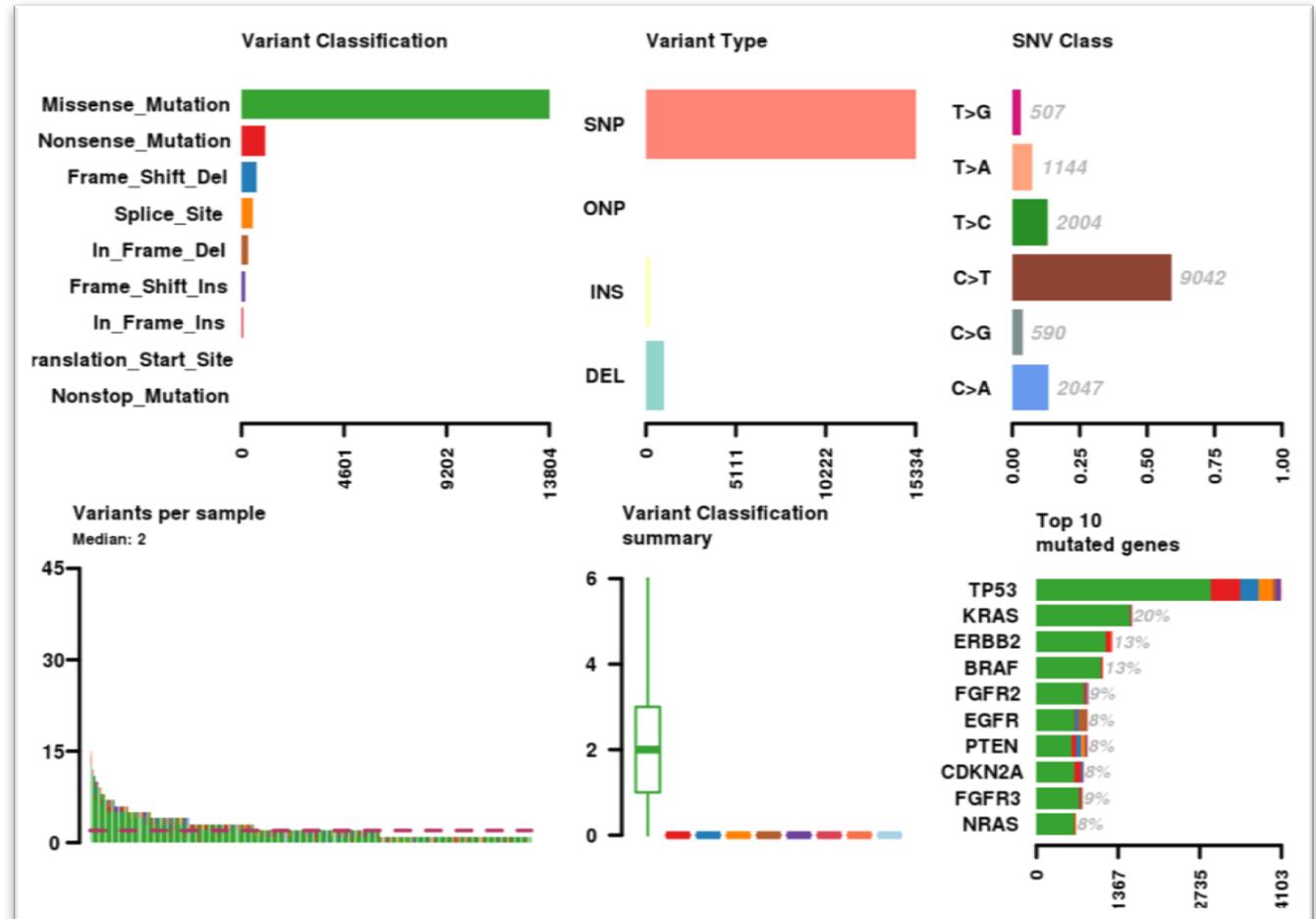
Exploring clinical genomics findings using R & oncoplots

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)



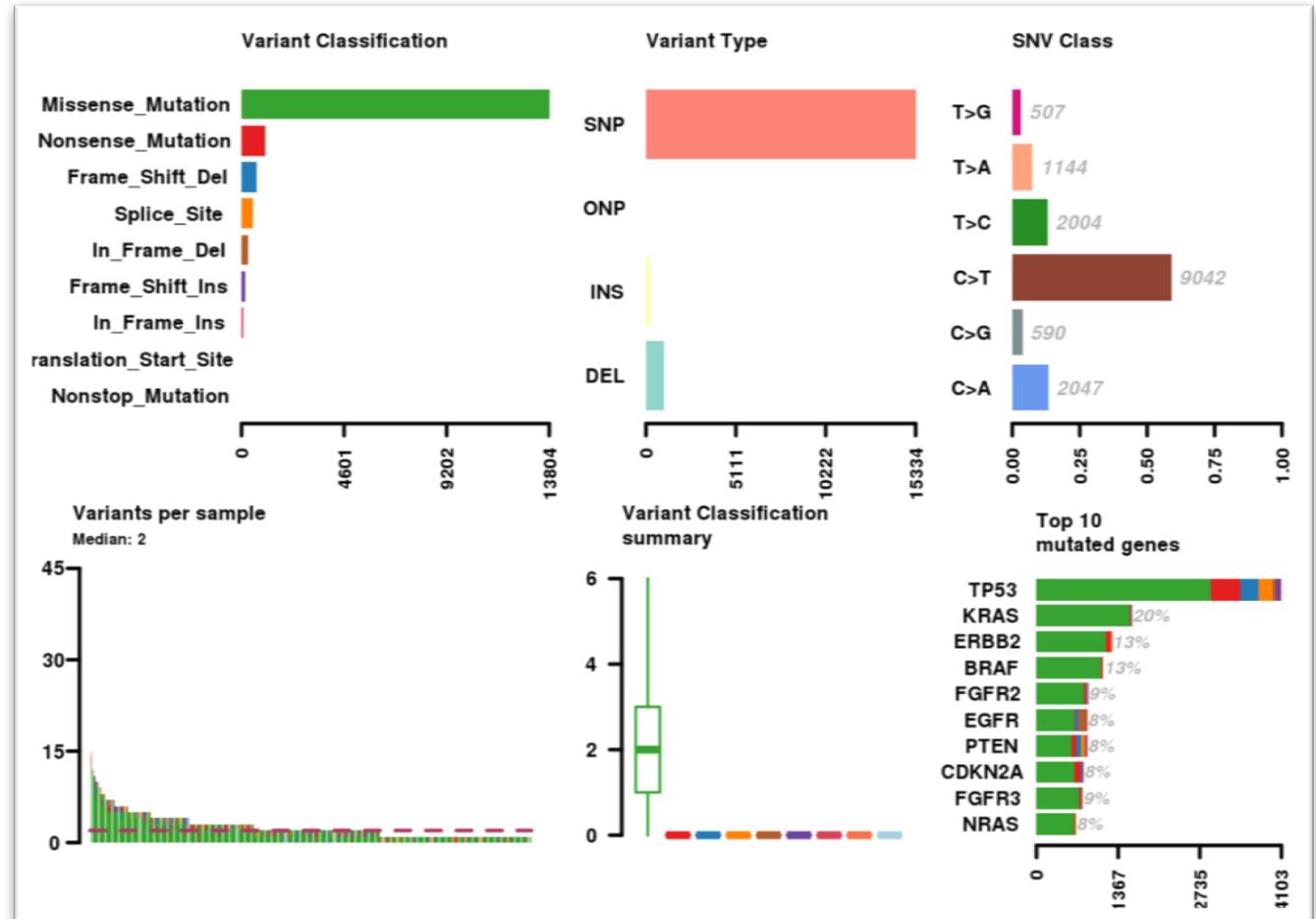
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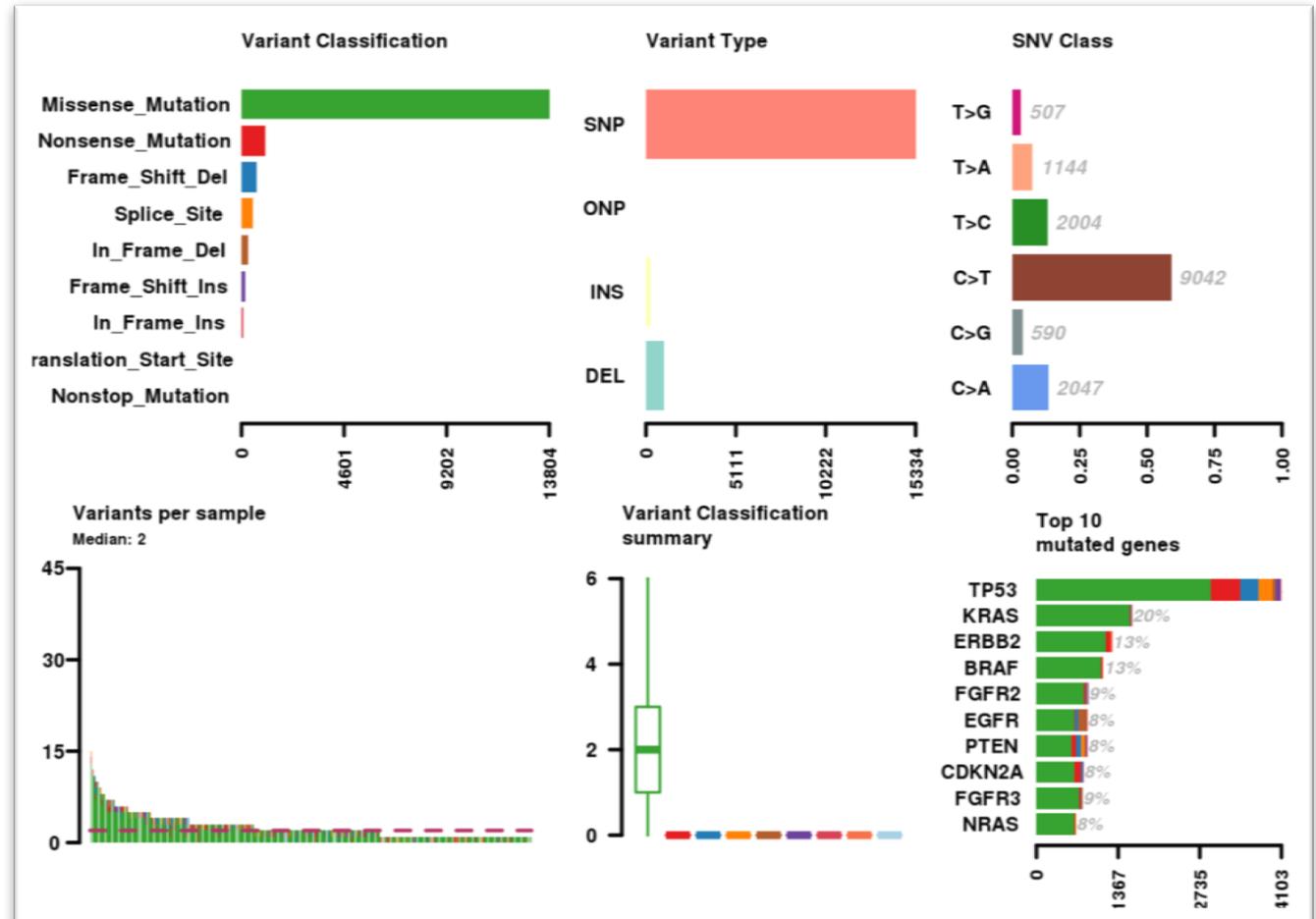
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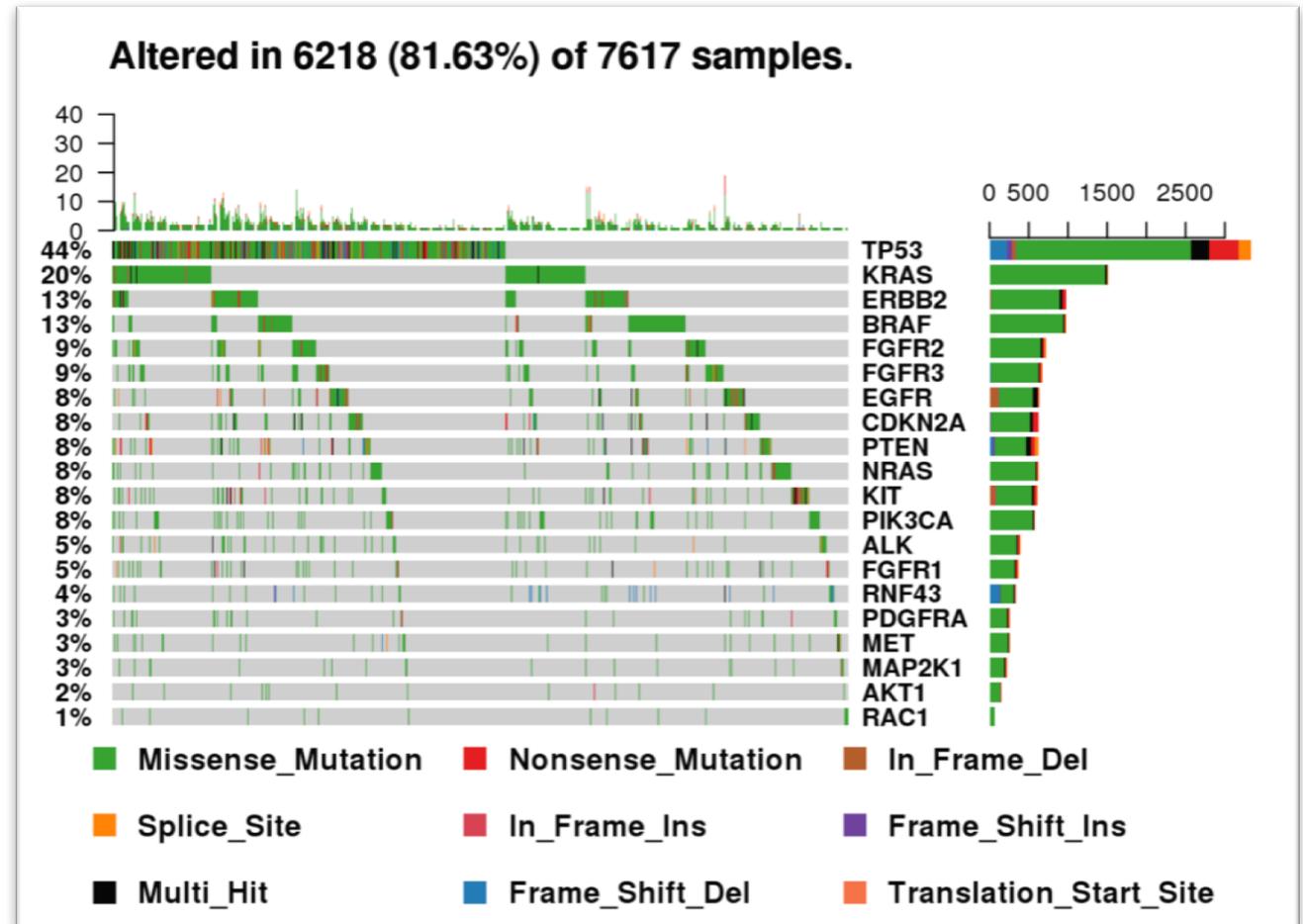


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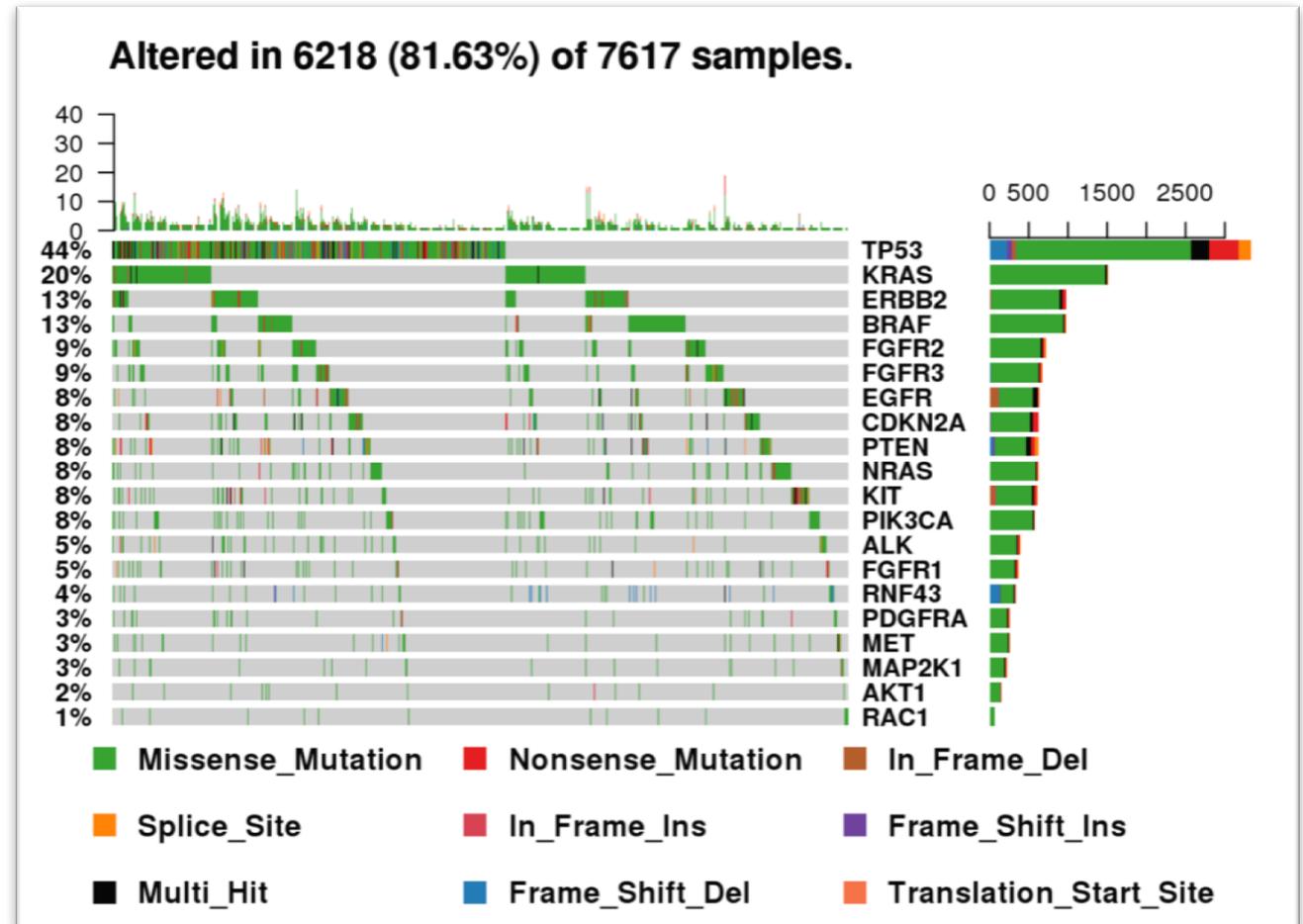


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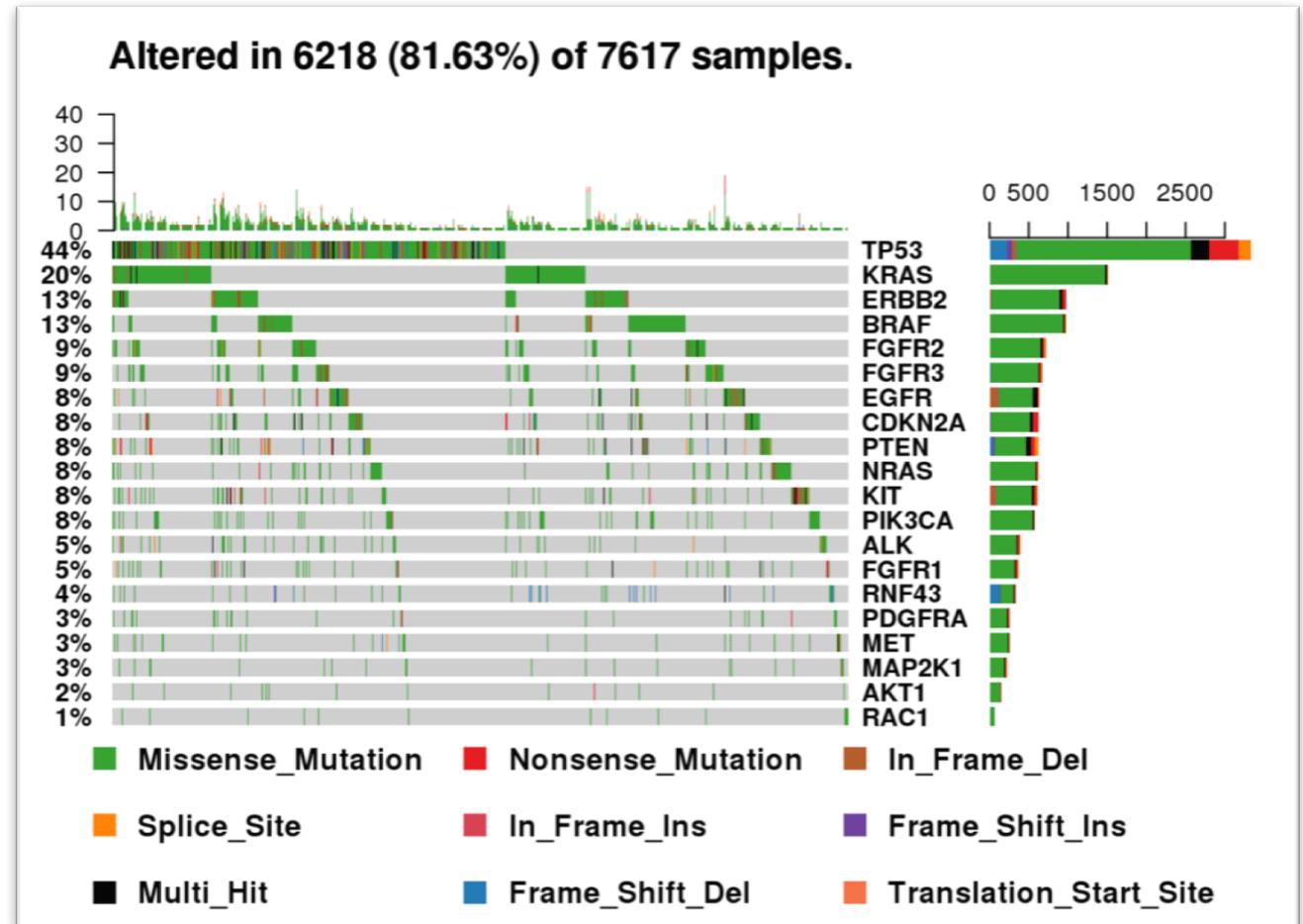


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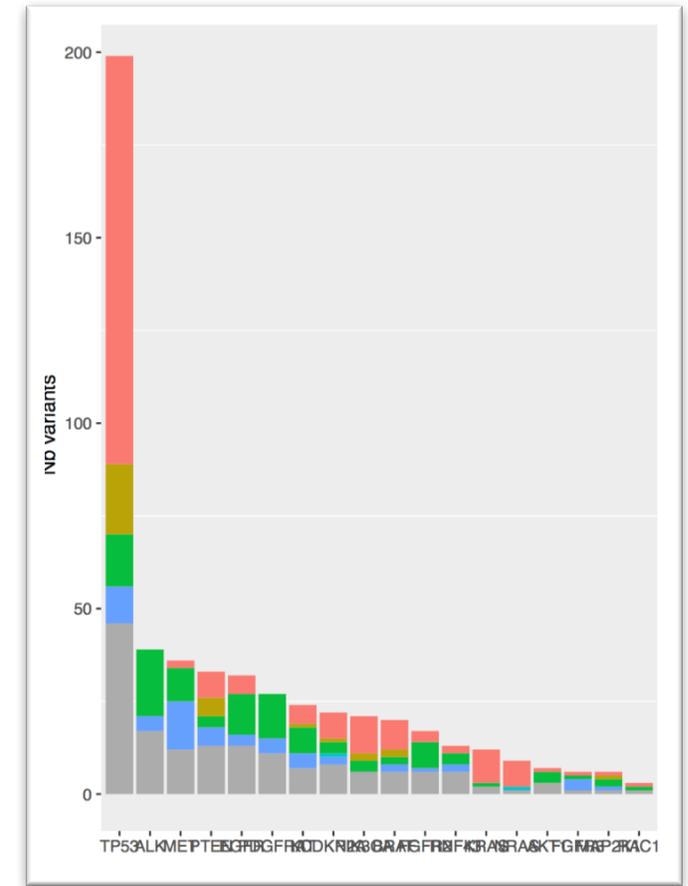
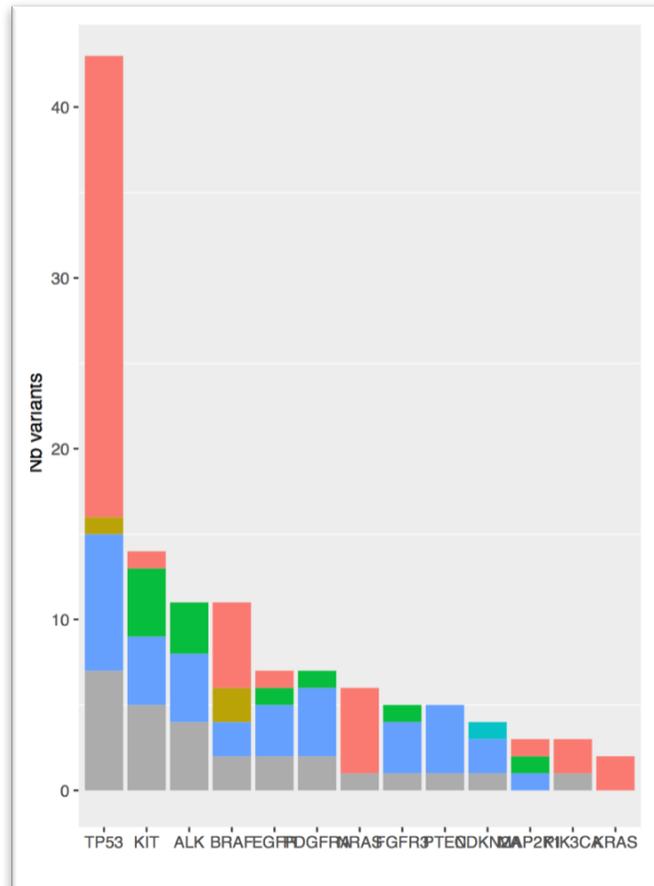
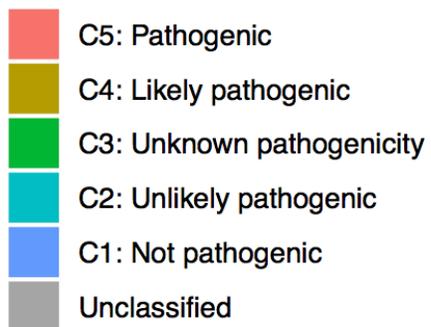


Exploring clinical genomics findings using R & ggplot

Variants pathogenicity per gene:

- PanHaem panel
- Comprehensive panel

Classification

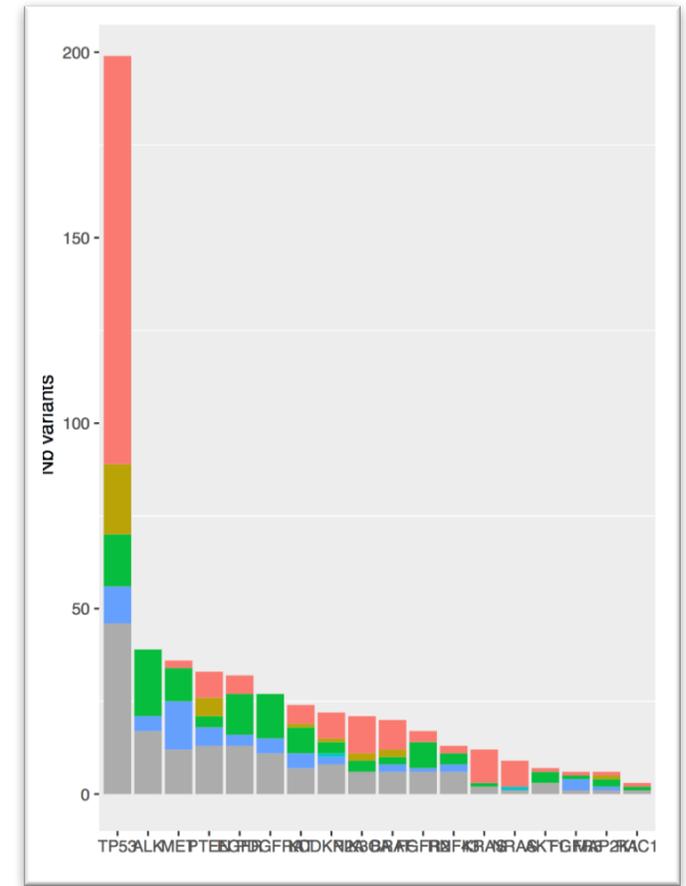
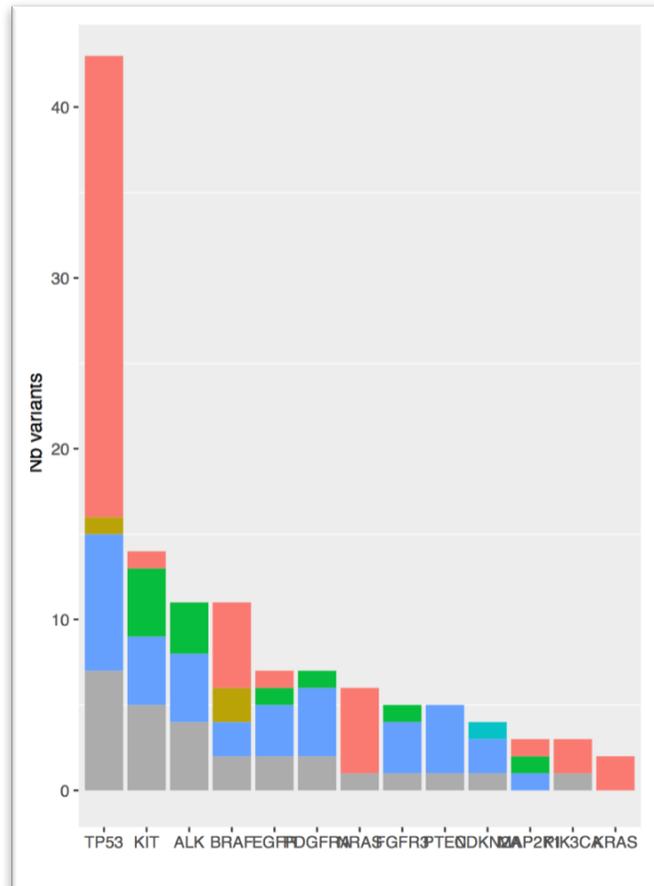
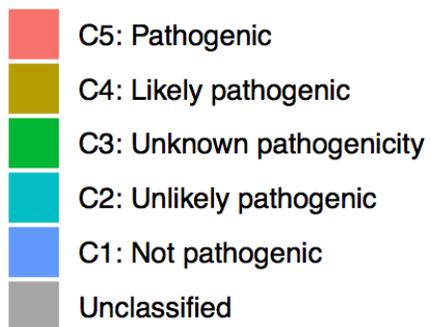


Exploring clinical genomics findings using R & ggplot

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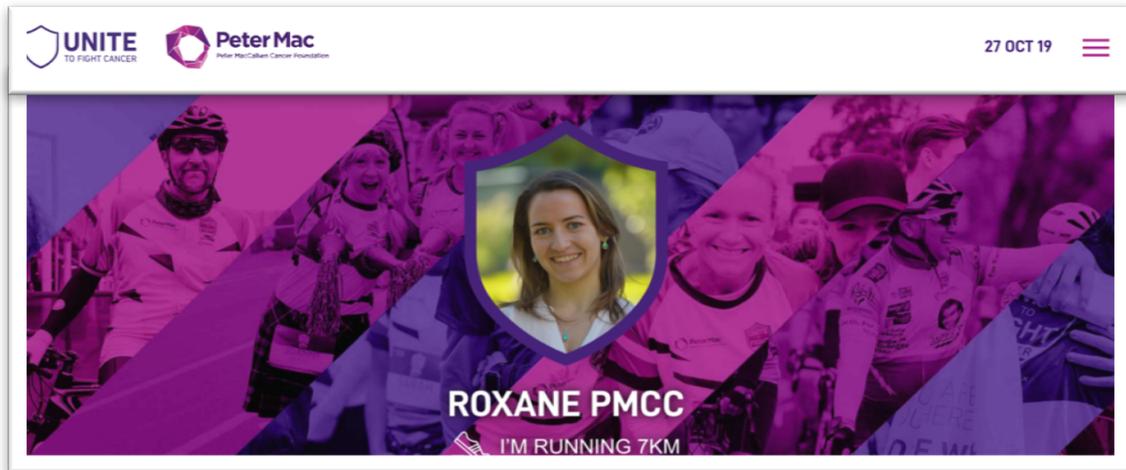
- PanHaem panel
- Comprehensive panel

Classification



Thanks!

Any question:
Roxane.Legaie@pertermac.org



<https://my.unitetofightcancer.org.au/roxane-pmcc>

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

