

Whole genome and transcriptome-assisted immune profiling of metastatic tumours: a precision medicine approach to immunotherapy trial design

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Disclosure Information



CAPTIV-8 is an investigator-initiated study from BC Cancer, Vancouver that is partially funded by Roche Canada

Whole genome and transcriptome-assisted immune profiling of metastatic tumours:



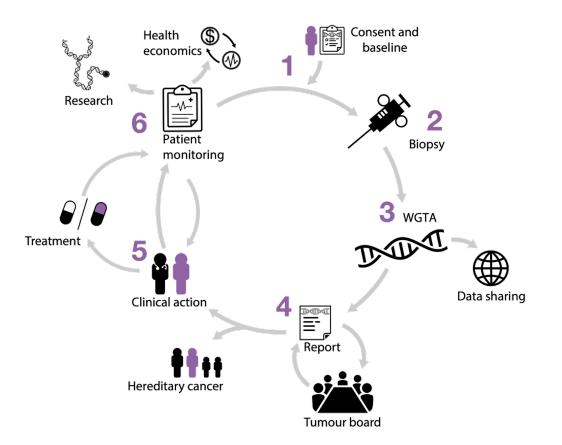
a precision medicine approach to immunotherapy trial design





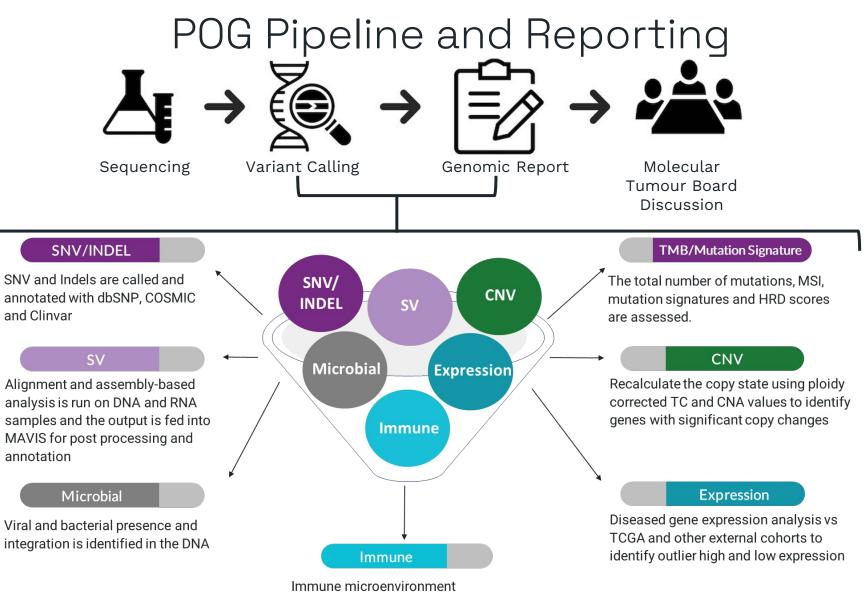
- Whole genomes and transcriptomes (WGTA) short read sequencing from 1668 adult cases and 179 pediatric cases
- Research results are discussed at a molecular tumour board
- **Clinically actionable** findings are identified in 83% of cases
- WGTA-informed therapies are administered in 37% of cases
- **Patients show clinical benefit** in 46% of treated cases

Whole genome and transcriptome-assisted immune profiling of metastatic tumours: a precision medicine approach to immunotherapy trial design Pleasance, Bohm *et al., Annals of Oncology, 2022* Pleasance, Titmuss, Williamson *et al., Nature Cancer, 2020*









Immune microenvironment deconvolution, T- and B-cell clonality, HLA subtyping, and neoantigen expression

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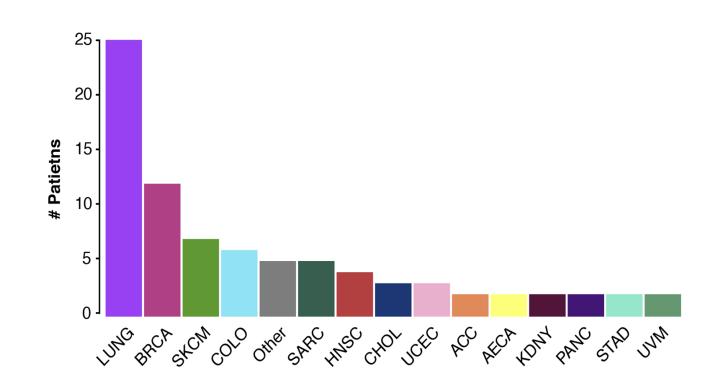
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POG Patients Treated with Immune Therapy





ICI received	n (%)
PD-1	45 (55)
PD-L1	10 (12)
PD-1/IDO1	8 (10)
PD-L1/CTLA-4	8 (10)
NKG2A	2 (2)
CTLA-4	1 (1)
PD-L1/OX40	1 (1)
PD-1/CTLA-4	1 (1)
OX40	1 (1)
PD-1/Chemo	1 (1)
PD-1/LAG-3	1 (1)
PD-L1/CTLA-4/Chemo	1 (1)
PD-L1/HER2	1 (1)
PD-L1/SMAC	1 (1)

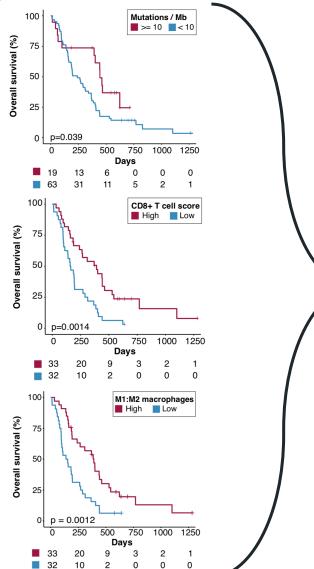
Whole genome and transcriptome-assisted immune profiling of metastatic tumours: a precision medicine approach to immunotherapy trial design Pender, Titmuss *et al., Clin Cancer Res., 2021*

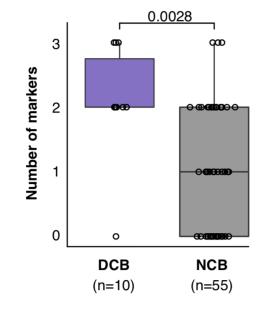


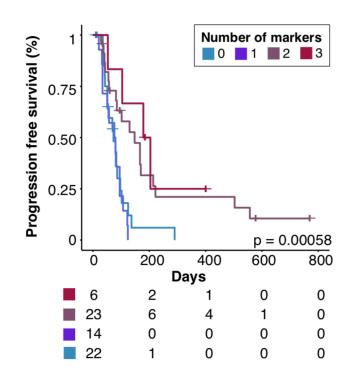


Combinations of Markers are Effective









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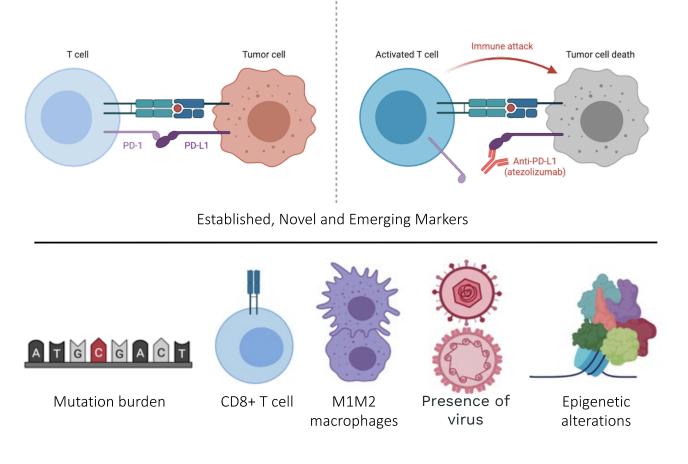




CAPTIV-8 (NCT04273061)



- CAPTIV-8 is an investigator-initiated study from BC Cancer, Vancouver that is partially funded by Roche Canada
- Open label, phase 2 study matching Canadian subjects, who have undergone whole genome and transcriptome analysis (WGTA).
- To date, 31 patients have been enrolled with a target of 50 participants total by April 2026



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- By integrating multiple alteration classes, WGTA can broaden the number of molecularly informed therapies
- Retrospective analysis of immune therapy treated patients revealed integration of multiple biomarkers improved prediction of therapeutic response
- CAPTIV-8 will determine if the information from WGTA-derived biomarkers corresponds with response to atezolizumab





Acknowledgements



<u>POG PIs:</u> Marco Marra Janessa Laskin

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> personalizedoncogenomics.org POG team

https://www.cbioportal.org/study/summary?id=pog570_bcgsc_2020 Searchable POG data for POG570 cohort

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