

BCG Susceptibility Panel for NMIBC

This test combines the results for relevant single nucleotide variants, methylation variants, and immune infiltrate prediction to reach a final score for prediction of BCG treatment success for NMIBC.

Panel name BCG on NMIBC

URL: https://github.com/lucy924/nanopore_multiBM_pipeline

Clinical Details

Sample Name: test4predict

Bladder lesion, transurethral resection:

Papillary urothelial carcinoma, high grade (grade 3/3 - WHO 1973)

Noninvasive, pTa

Specimen: TURBT biopsy

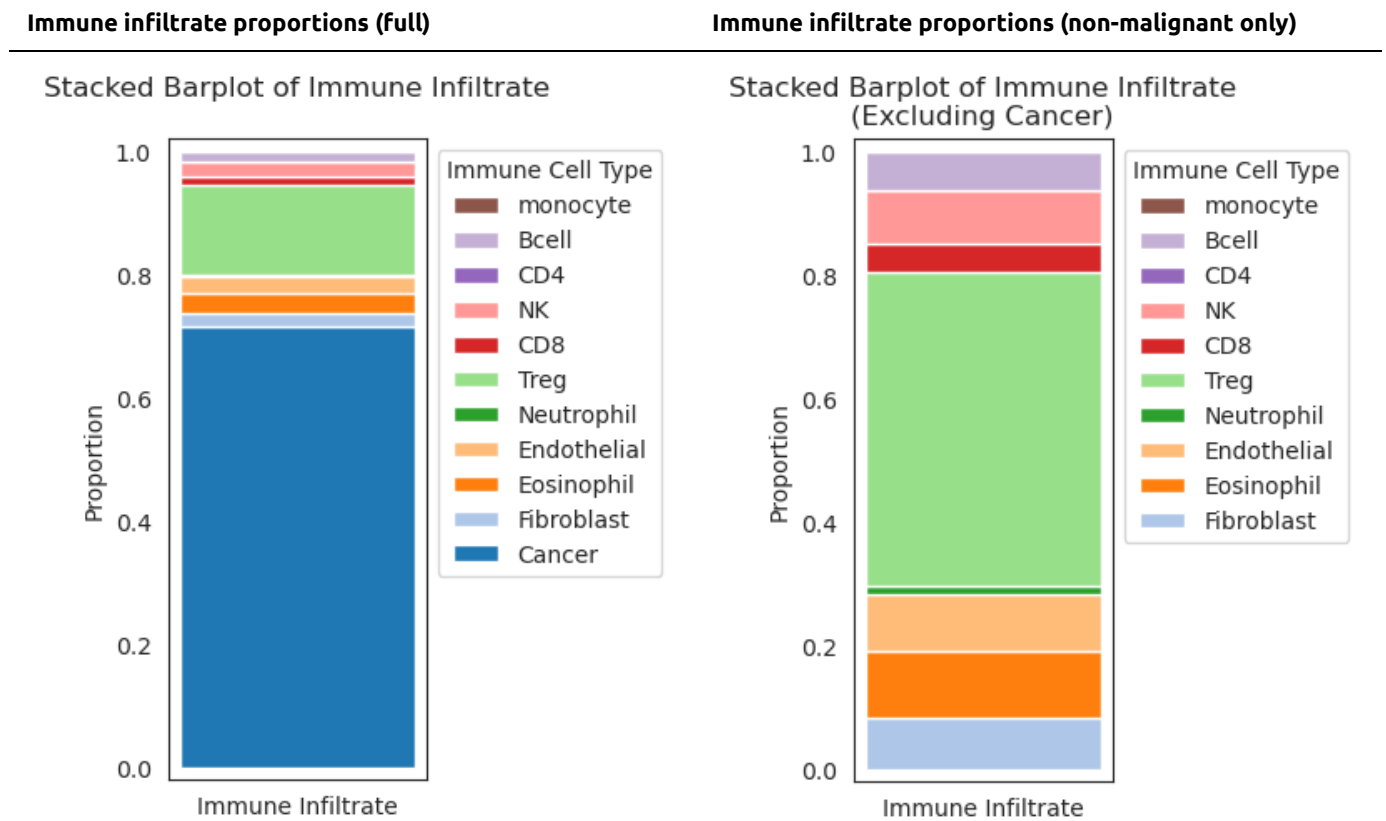
Overall Result and Interpretation

Tumour is **Somewhat Likely** to respond to treatment.

Guidance: Result is out of Highly Unlikely, Somewhat Unlikely, Somewhat Likely, Highly Likely

Comments: The result is an aggregate score obtained by combining the scores of biomarkers that reach read depth threshold and fall within respective scoring parameters.

Immune infiltrate results



Raw results

Guidance: Total (normalised) Score is a scale of 0% – 100%. 0% will respond and 100% will not respond to BCG treatment. Most results will fall between 25% and 75%. We recommend treatment with BCG when the result is <50% for patients who are otherwise healthy, and <40% for all other patients.

ID	Biomarker name	Biomarker type	Result Options	Result	Score
004	NOS3	snv	T T/T A/T G/A A/A G/G G	G G	0.16
005	NOS3	snv	C C/C T/T T	T C	0.53
009	CHST11	mod	0.0-1.0	0.1202386872202884	2.63118846345102
010	KLF8	mod	0.0-1.0	0.2421676545300592	1.6798814563928874
011	GPR158	mod	0.0-1.0	0.2618603411513859	2.9289312366737743
012	C12orf42	mod	0.0-1.0	0.2392036753445635	1.781592649310873
013	WDR44	mod	0.0-1.0	0.6964944649446494	1.1329889298892988
014	FLT1	mod	0.0-1.0	0.0413255360623781	1.5478070175438603
022	PMF1	mod	methyated/unmethyated	0.7149390243902439	1.21
025	IL1B	snv	G G/G A/A A	0.7149390243902439	1.0
026	IL1RAP	snv	G G/G A/A A	0.7149390243902439	1.0
027	IL1RAP	snv	G G/G C/C C	0.7149390243902439	1.0
028	IL1RAP	snv	T T/T A/T C/A A/A C/C C	0.7149390243902439	1.0
029	IL1RAP	snv	G G/G A/A A	0.7149390243902439	1.0
030	IL18R1	snv	C C/C T/T T	T T	0.16
031	IL18R1	snv	G G/G C/C C	T T	1.0
032	IL18R1	snv	C C/C A/A A	T T	1.0
033	IL18R1	snv	C C/C T/T T	T T	0.16
035	IL18R1	snv	G G/G A/A A	A A	0.16
036	IL18R1	snv	G G/G A/A A	A A	1.0
037	IL18R1	snv	C C/C T/T T	T T	0.16
038	IL18R1	snv	G G/G A/A A	T T	1.0
401	LMR	immune_ratio	0.0-10.0	2.973359663832316	4.946719327664632
402	NLR	immune_ratio	0.0-10.0	0.3423641081742103	1.6576358918257903
403	monocyte_inf	immune_inf	0.0-1.0	nan	nan
405	Bcell_inf	immune_inf	0.0-1.0	0.9044892569439369	1.7155914055551502
406	CD4_inf	immune_inf	0.0-1.0	0.851659066167062	0.336663626466825
408	CD8_inf	immune_inf	0.0-1.0	0.0668717129484986	0.0798769722309009
409	Treg_inf	immune_inf	0.0-1.0	0.7722534591745389	1.5218027673396315
Total (raw)	nan	nan	nan	nan	33.500679744344644

ID	Biomarker name	Biomarker type	Result Options	Result	Score
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Total (normalised to 0.0 - 100.0)	nan	nan	nan	nan	47.05501206028529
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Methodology

Nanopore sequencing was used to detect single nucleotide variants, methylation status and immune status (by methylation) of the tumour sample.