

# 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](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

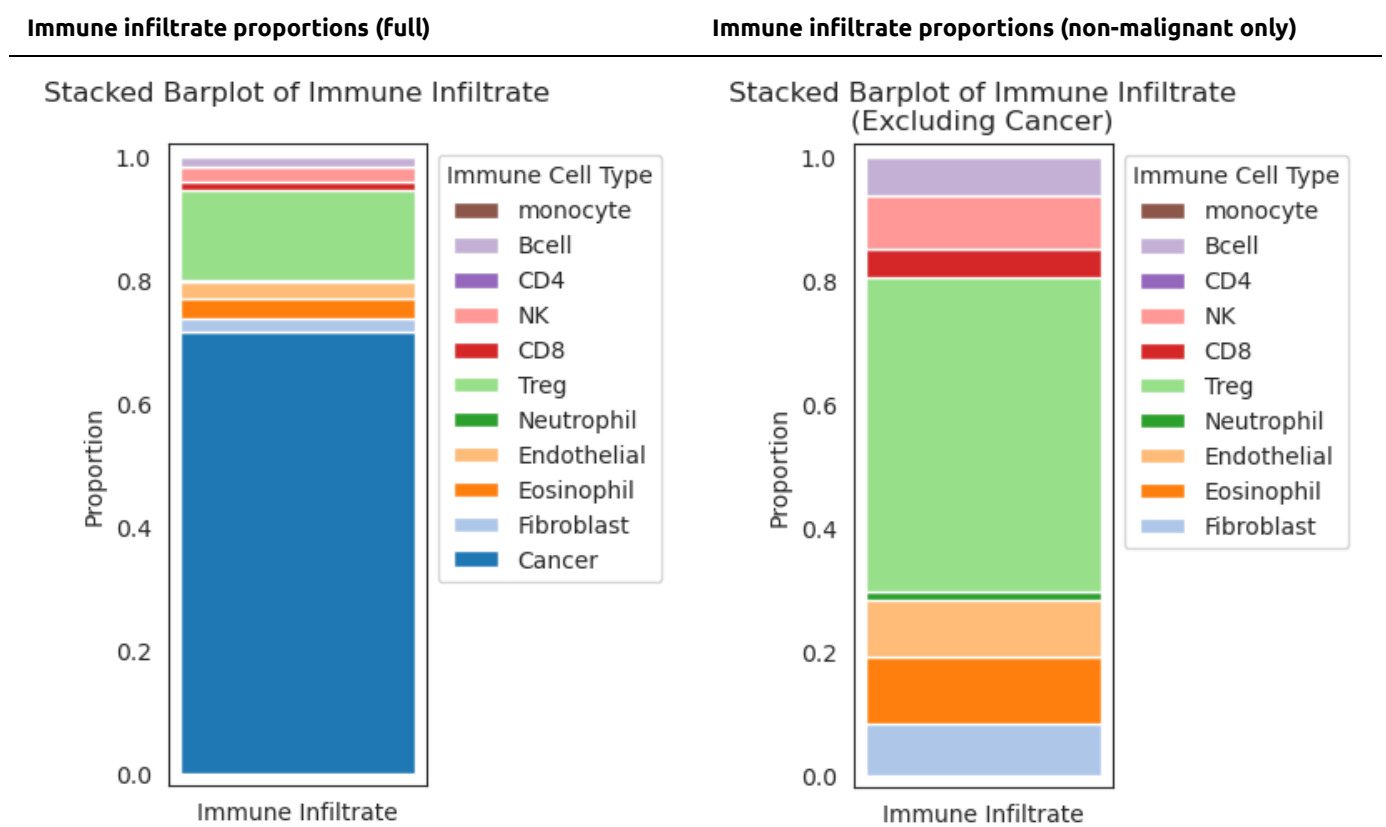
## Overall Result and Interpretation

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
005	NOS3	snv	C	C/C	T/T
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	methyalted/unmethyalted	0.7149390243902439	1.21
025	IL1B	snv	G	G/G	A/A
026	IL1RAP	snv	G	G/G	A/A
027	IL1RAP	snv	G	G/G	C/C
028	IL1RAP	snv	T	T/T	A/T
029	IL1RAP	snv	G	G/G	A/A
030	IL18R1	snv	C	C/C	T/T
031	IL18R1	snv	G	G/G	C/C
032	IL18R1	snv	C	C/C	A/A
033	IL18R1	snv	C	C/C	T/T
035	IL18R1	snv	G	G/G	A/A
036	IL18R1	snv	G	G/G	A/A
037	IL18R1	snv	C	C/C	T/T
038	IL18R1	snv	G	G/G	A/A
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		
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)					33.500679744344644

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

Methodology

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