

S1 Table

DCB AUC	p-value	Filters	With BQSR?	IMPACT Precision	IMPACT Recall
0.65, 95% CI (0.43, 0.85)	n=25, Mann-Whitney p=0.22	Tumor/Normal Depth \geq 7, Tumor VAF > 0.1, Normal VAF < 0.03	Yes	0.72	0.49
0.61, 95% CI (0.35, 0.85)	n=25, Mann-Whitney p=0.41	Tumor/Normal Depth \geq 30, Tumor Alt Depth \geq 5	Yes	0.68	0.52
0.63, 95% CI (0.36, 0.86)	n=25, Mann-Whitney p=0.29	No Depth/VAF Filters	Yes	0.68	0.63
0.72, 95% CI (0.51, 0.90)	n=25, Mann-Whitney p=0.075	Tumor/Normal Depth \geq 7, Tumor VAF > 0.1, Normal VAF < 0.03	No	0.63	0.5
0.63, 95% CI (0.38, 0.86)	n=25, Mann-Whitney p=0.29	Tumor/Normal Depth \geq 30, Tumor Alt Depth \geq 5	No	0.68	0.52
0.72, 95% CI (0.48, 0.90)	n=25, Mann-Whitney p=0.084	No Depth/VAF Filters	No	0.53	0.65

Choice of depth and VAF filtering, as well as whether or not to run Base Quality Score Recalibration (BQSR), resulted in differences in predictive value for mutation load. We chose to optimize for precision, choosing the highlighted set of filters/BQSR. Precision is defined as the fraction of filtered missense mutations in IMPACT genes that were actual IMPACT panel variants. Recall is defined as the fraction of actual IMPACT panel variants that were found in the filtered missense results.