Subsets		T.TOTAL	F1_Score.mean		Precision.mean			Recall.mean			Frac_Assessed.mean			
V 4 V	Size (kb)	N variants	BWA-GATK	NSv4	NSv4/BWA-GATK	BWA-GATK	NSv4	NSv4/BWA-GATK	BWA-GATK	NSv4	NSv4/BWA-GATK	BWA-GATK	NSv4	NSv4/BWA-GATK
× *		3641960	96.12	95.73	0.9959	97.43	97.52	1.0009	94.85	94	0.9911	95.03	95.35	1.0034
hgnc_exons	63626	49749	97.66	97.43	0.9977	98.36	98.58	1.0022	96.96	96.31	0.9933	95.1	96.19	1.0115
hgnc_genes	63626	49749	97.66	97.43	0.9977	98.36	98.58	1.0022	96.96	96.31	0.9933	95.1	96.19	1.0115
3WA-		612157	91.8	90.63	0.9872	92.41	92.78	1.004	91.2	88.56	0.9711	68.14	69.92	1.026
hgnc_exons	63626	6425	94.39	93.64	0.992	94.69	95.22	1.0056	94.1	92.11	0.9788	75.5	77.01	1.0199
hgnc_genes	63626	6425	94.39	93.64	0.992	94.69	95.22	1.0056	94.1	92.11	0.9788	75.5	77.01	1.0199