

Sahraeian et al. Achieving robust somatic mutation detection with deep learning models derived from reference data sets of a cancer sample

Supplementary Tables

Table S1 -Trained Network models used in this study

Model	Training Dataset	Somatic mutations	Region Trained	# of T/N replicates	Coverage of samples	Somatic mutations AF	# of somatic mutations in all replicates	# of total candidate variants used for training
DREAM3	DREAM3 WGS	<i>In silico</i> spikes	50% of genome	5	30x	5-50%	450K	29.2M
WES-TCGA	TCGA	<i>In silico</i> spikes	exome	12	45x-185x	0.5-100%	1.5M	5.9M
SEQC-WGS-Spike	SEQC2 WGS	<i>In silico</i> spikes	genome	20	40x-170x	0.3-90%	2M	272M
SEQC-WGS-GT-50	SEQC2 WGS	Real GT mutations in SEQC2	50% of genome	24	40x-390x	0.5-100%	416K	137M
SEQC-WGS-GTS0-SpikeWGS10	SEQC2 WGS	Real GT mutations in SEQC2 + <i>in silico</i> spikes from 10% of WGS	genome	44	40x-390x	0.3-100%	574K	164M
SEQC-WES-Spike	SEQC2 WES	<i>In silico</i> spikes	exome	7	60x-550x	0.1-100%	755K	3.7M
SEQC-FFPE-Spike	SEQC2 WGS-FFPE	<i>In silico</i> spikes	genome	16	54x-77x	0.5-83%	1.7M	191M
SEQC-FFPE-WES-Spike	SEQC2 WES-FFPE	<i>In silico</i> spikes	exome	14	70x-90x	0.1-88%	1.4M	9.6M
SEQC-WES-SpikeWGS10	SEQC2 WES/WGS	<i>In silico</i> spikes	exome	27	40x-550x	0.1-100%	963K	30.9M
SEQC-FFPE-SpikeWGS10	SEQC2 WGS-FFPE/WGS	<i>In silico</i> spikes	genome	36	40x-170x	0.3-90%	1.9M	218M
SEQC-FFPE-WES-SpikeWGS10	SEQC2 WES-FFPE/WGS	<i>In silico</i> spikes	exome	47	40x-170x	0.1-90%	1.6M	36.8M

Table S9 - F1-score (%) performance for the SEQC-WGS-Spike model and two sample-specific network trained models

Sample						
	NeuSomatic-S			NeuSomatic		
	SEQC-WGS-Spike	Sample	Sample+10%WGS	SEQC-WGS-Spike	Sample	Sample+10%WGS
SNVs						
WGS-NovaSeq	89.9	91.4	90.7	94.2	94.7	94.4
Titration-50%T-30X	77.1	74.9	75.4	83.1	82.7	82.0
Titration-10%T-100X	45.2	46.0	46.1	63.8	64.4	62.3
Library-prep-1ng-Nextera	88.5	86.3	86.9	90.3	91.9	91.4
WGS-FFPE-24h (FFPE-normal)	82.9	83.7	81.2	84.8	86.0	85.8
WGS-FFPE-24h (Fresh-normal)	81.8	80.1	80.8	84.1	85.9	86.2
WES	97.1	82.7	97.6	97.1	96.4	97.5
WES-FFPE-24h (FFPE-normal)	86.2	53.3	84.9	83.2	82.7	87.0
WES-FFPE-24h (Fresh-normal)	86.8	54.9	82.3	86.9	86.3	86.6
Average	81.7	72.6	80.7	85.3	85.7	85.9
INDELS						
WGS-NovaSeq	75.8	78.5	77.3	82.0	81.8	85.3
Titration-50%T-30X	66.5	65.0	68.0	74.4	74.2	67.6
Titration-10%T-100X	46.2	43.1	45.6	56.9	54.2	56.3
Library-prep-1ng-Nextera	59.8	67.3	67.1	60.2	79.6	78.1
WGS-FFPE-24h (FFPE-normal)	68.6	66.1	66.9	74.3	78.4	77.6
WGS-FFPE-24h (Fresh-normal)	64.2	65.7	64.3	63.8	78.8	78.6
Average	63.5	64.3	64.9	68.6	74.5	73.9

Table S10 - Computational complexity comparison of different somatic mutation detection algorithms. CPU time (hours) and maximum memory (GB) are shown for NA12878.BRCA sample with 220x tumor coverage and 75x normal coverage

Tool	CPU time (hours)	Maximum Memory (GB)
NeuSomatic	785	44
NeuSomatic-S	153	44
Strelka2	55	1
Lancet	5014	85
MuTect2	168	5
Octopus-hard	7150	24
Octopus-RF	7500	24
MuSE	170	0
SomaticSniper	16	7
VarDict	161	3

* DRAGEN spent 1.4h on FPGA to finish for this sample. Since DRAGEN ran on FPGA and does not use memory the same way as a CPU the CPU time and maximum memory usage are not comparable with other techniques.