Supplementary Table S1. GotCloud parameters for initial hard-filtering used in the experiments.

Filter Type		Low-pass			Deep Exome		
		10	100	1000	10	100	1000
Variant Quality	Min	5	5	5	20	20	20
Overall Depth	Min	10	100	1K	20	200	2K
	Max	200	2K	20K	5K	50K	500K
Call Rate	Min	0.5	0.5	0.5	0.5	0.5	0.5
Allele Balance	Max	67	67	67	65	65	65
Strand Bias (z-score)	Min	-5	-5	-5	-10	-10	-10
	Max	5	5	5	10	10	10
Strand Bias (correlation)	Min	-0.2	-0.15	-0.15	-0.2	-0.15	-0.15
	Max	0.2	0.15	0.15	0.2	0.15	0.15
Cycle Bias (z-score)	Max	5	5	5	10	10	10
Cycle Bias (correlation)	Max	0.2	0.15	0.15	0.2	0.15	0.15
Inbreeding Coefficient	Min	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
Non-ref/non-alt allele inflation	Max	3	3	3	3	3	3
Distance to closest known Indel (1000G pilot)	Min	5bp	5bp	5bp	5bp	5bp	5bp
% Mapping Qual.<20	Max	30	30	30	30	30	30
% Low Quality Bases	Max	20	20	20	30	30	30
# Failed Filters for SVM	Min	3	3	3	3	3	3