

Supplementary Table 2. Somatic high-stringency parameters used during the analysis of next-generation sequencing data for the liquid biopsy part of OncoSTRAT&GO™

Torrent suite variant caller parameters			
Parameter	SNP	INDEL	Description
min_allele_freq	0.001	0.001	Minimum allele frequency
min_variant_score	6	6	Minimum quality
min_coverage	100	100	Minimum coverage
min_cov_each_strand	3	3	Minimum coverage on either strand
strand_bias	0.95	0.9	Maximum strand bias
data_quality_stringency	10		Minimum relative read quality
filter_unusual_predictions	0.12		Maximum common signal shift
filter_insertion_predictions		0.2	Maximum reference/variant signal shift (insertions)
filter_deletion_predictions		0.2	Maximum reference/variant signal shift (deletions)
Torrent suite variant caller advanced parameters			
Parameter	Value		
snp_strand_bias_pval	1		
position_bias	0.75		
mnp_min_allele_freq	0.001		
mnp_min_variant_score	6		
hp_max_length	8		
heavy_tailed	3		
outlier_probability	0.005		
mnp_strand_bias_pval	1		
indel_strand_bias_pval	1		
indel_as_hpindel	0		
mnp_strand_bias	0.9		
position_bias_ref_fraction	0.05		
hotspot_strand_bias_pval	1		
sse_prob_threshold	0.2		
do_mnp_realignment	0		

downsample_to_coverage	2000
do_snp_realignment	0
mnp_min_cov_each_strand	3
mnp_min_coverage	100
prediction_precision	1
realignment_threshold	0
suppress_recalibration	0
position_bias_pval	1
use_position_bias	0
min_indel_size	4
short_suffix_match	5
min_var_count	5
min_var_freq	0.07
output_mnv	1
max_hp_length	8
relative_strand_bias	0.8
kmer_len	19
gen_min_coverage	20
allow_mnps	1
allow_complex	0
min_mapping_qv	4
read_snp_limit	10
allow_indels	1
read_max_mismatch_fraction	1
gen_min_alt_allele_freq	0.001
allow_snps	1
gen_min_indel_alt_allele_freq	0.035

OncoDNA parameters

output_filtered	TRUE
filter_splice_variant	TRUE
filter_synonymous	TRUE
min_variant_frequency	0.1
minimum_coverage	100

minimum_variant_coverage	30
minimum_variant_strand_frequency	5
minimum_InDel_strand_frequency	1
