

Threshold	Q1	Q2
Minimum reads for top strand and for bottom strand	0	3
Minimum BWA-MEM mapping quality	20	50
Maximum duplex clipping (bp)	0	15
Minimum base consensus	51%	95%
Maximum insert size (bp)	NA	1000
Minimum distance from read base to adapter ligation site (bp)	3	35
Minimum distance to read end (bp)	0	4
Minimum base Phred score	20	30
Minimum Q1/Q2 duplex coverage at same position in sister sample	0	10

Supplemental Table S1. Quality thresholds for mutation calling.

For a *bona fide*, *de novo* mutation candidate to be reported it must meet Q2 thresholds, and wildtype candidates in the sister sample must meet at least Q1 thresholds. Note that the value of 0 for the Q1 threshold in the first row means that a candidate can reach Q1 status even if all of its reads come from the same strand (instead of being contributed by both the top and bottom strands).