Parameter	Patient sample	Reference average
Total reads	20,094,270	14,851,242
% mapped to genome	94.80%	94.0%
% mapped on target	75.88%	48.5%
On target reads	14,455,272	6,622,724
% of on target that are unique	52.95%	87.9%
Unique on target reads	7,654,306	5,796,593
Mean mapping quality	69.99	69.98
% positions ≤ 50x unique	99.56%	99.6%
% positions ≤ 400x unique	97.41%	93.4%
% positions ≤ 1000x unique	35.27%	59.2%
Average unique coverage (across full capture region)	1560.0	1135

All SNV calls were reported only when depth of coverage >= 50x, and Fisher strand bias <= 75, and VAF > 0.1 OR VAF between 0.03-0.1 and strand bias not 0 or 1
All indel calls were reported only when depth >=50 and Fisher strand bias <= 75, and no adjacent homopolymer run longer than 7bp.