Total reads	48,370,376
Total yield (bp)	4,885,407,976
Read length (bp)	101
Target regions (bp)	51,189,318
Average throughput depth of target regions	95.4
Initial mappable reads (mapped to human genome)	48,226,494
% Initial mappable reads (out of total reads)	99.70%
Non-redundant reads (de-duplicated by Picard tools)	40,185,068
% Non-redundant reads (out of initial mappable reads)	83.30%
Non-redundant unique reads (uniquely mapped to human genome)	39,499,130
% Non-redundant unique reads (out of non-redundant reads)	98.30%
On-target reads (mapped to target regions)	33,227,086
% On-target reads (out of non-redundant unique reads)	84.10%
% Coverage of target regions (more than 1X)	98.80%
Number of on-target genotypes (more than 1X)	50,588,994
% Coverage of target regions (more than 10X)	95.60%
Number of on-target genotypes (more than 10X)	48,939,557
Mean read depth of target regions	56.8
Number of SNPs	65,425
Number of coding SNPs	20,088
Number of synonymous SNPs	10,575
Number of nonsynonymous SNPs	8,999
Number of Indels	5,739
Number of coding Indels	450