

Supplemental Results Table 1. Sequencing summary statistics

Percentage of bases mapping to the human genome	Percentage of reads mapping to the human genome	Percentage of reads mapping uniquely to the targeted regions	Percentage of the Nimblegen targeted exons with coverage/ covered across entire length	Percentage of the target nucleotides covered at 1x, 5x and 10x	Number of contigs	Mean, min, and max depth of coverage of the target region
99.61%	98.75%	76.16%	97.36%/95.95%	99.1%, 95.7%, 85.9%	170,642	34x, 1x, 621x