

Table S1: Mapped read metrics for all samples.

Sample	Total reads	Total high quality reads	Mapped reads
1	33,303,360	31,688,748	31,559,707 (99.59%)
2	28,269,036	28,097,504	27,855,567 (99.14%)
3	24,420,734	24,306,410	23,934,348 (98.47%)
4	36,382,770	34,652,838	34,418,676 (99.32%)
5	31,209,158	29,498,204	29,211,552 (99.03%)
6	27,715,904	25,793,532	25,702,525 (99.65%)
7	34,142,884	33,219,054	33,042,777 (99.47%)
8	29,136,848	28,075,056	27,552,753 (98.14%)
9	36,906,608	35,271,298	35,040,457 (99.35%)
Control	29,814,074	28,519,194	28,261,262 (99.10%)

Table S2: Depth of coverage summary with total and average bases and the percentage of the exome covered with at least 2x, 5x, 10, 20x and 30x sequence depth read.

Sample	Total	Average	2x	5x	10x	20x	30x
1	2.62 GB	51.80	98.2	97.4	94.9	84.8	70.0
2	2.26 GB	44.74	98.2	97.3	94.3	81.7	64.5
3	1.91 GB	37.65	98.1	96.8	92.3	75.1	54.9
4	2.85 GB	56.26	98.4	97.8	96.0	87.7	75.1
5	2.40 GB	47.39	98.1	97.1	93.9	81.5	65.0
6	2.04 GB	40.26	98.1	96.7	92.5	76.5	57.2
7	2.70 GB	53.30	98.1	97.2	94.7	85.0	70.7
8	1.89 GB	37.40	98.0	96.7	92.5	75.5	55.2
9	2.79 GB	55.07	98.2	97.3	94.9	85.5	71.8
control	2.33 GB	45.93	98.0	97.0	93.9	81.4	64.4