

Supplementary information, Table S1

Table S1 Summary statistics of the exome sequencing data from all the five individuals

Sample	Total number of reads	Non-duplicated reads	Unique reads	Unique reads overlapping targets	Average depth	% of bases covered by $\geq 8\times$
III:6	85,036,326	82,330,594	72,023,420	31,538,343	58.77	90.18%
II:5	71,656,536	69,266,558	61,586,102	35,294,824	65.77	90.62%
III:4	89,366,250	85,976,316	75,521,976	43,940,097	81.88	91.47%
IV:1	76,794,072	74,548,742	66,226,045	37,366,255	69.63	91.11%
IV:2	138,144,520	130,365,202	108,589,044	56,288,187	104.89	86.25%