Data	P1	P4
Total number of reads	506,703,008	2,101,160,202
Trimmed reads	420,926,397	1,718,944,763
Reads mapped	419,160,298	1,710,162,053
Percentage mapped	99.58%	99.49%
Coverage	21 X	86 X
Total variants	4,905,687	4,904,615
Merged variants	6,517,075	
Rare variants (MAF < 5%)	890,387	
Common homozygous Variants	27,236	
In-silico prediction (CADD >15)	4	
Phenotype associated variant	0	
Machine Used	NovaSeq6000	NovaSeq6000
Library Used	TruSeq PCR free	TruSeq PCR free

S2 Table: Whole genome sequencing data summary for P1 and P4.