**Appendix Table A1.** General information on the exome sequencing output.

| Categories | Count |
|---:|---|
| Raw data (G) | 5.34 |
| Clean reads | 35,312,448 |
| Mapped reads | 35,237,849 (99.8%) |
| Effective yield on target (Mb) | 5,236.87 |
| Average sequencing depth on target | 56.25× |
| Fraction of target covered with at least 10× | 98.0% |
| Exonic SNVs | 22,779 |
| Splicing SNVs | 2,443 |
| Exonic Indels | 601 |
| Splicing Indels | 386 |

SNV = single nucleotide variant, Indel = insertion-deletion.