|  |  |  |
| --- | --- | --- |
| Terms | Case | Control |
| Number of samples | 54 | 87 |
| Number of sequencing reads (s.d.) | 146919215 (31650649) | 97942689 (13911765) |
| Size of sequencing data (s.d.) | 14760.83 Mb (3087.93 Mb) | 14658.28 Mb (2081.72 Mb) |
| On target rate (s.d.) | 52.62% (10.40%) | 50.52% (3.75%) |
| Genome mapping rate (s.d.) | 99.68% (0.74%) | 99.93% (0.02%) |
| Mismatch rate on target (s.d.) | 0.39% (0.12%) | 0.23% (0.03%) |
| Mean sequencing depth on target (s.d.) | 129.56 (47.13) | 122.09 (17.69) |
| Fraction of target covered >= 4X (s.d.) | 98.57% (5.33%) | 99.10% (0.15%) |
| Fraction of target covered >= 10X (s.d.) | 97.90% (5.58%) | 97.78% (0.38%) |
| Fraction of target covered >= 20X (s.d.) | 95.29% (5.57%) | 94.86% (0.96%) |
| Fraction of target covered >= 50X (s.d.) | 78.59% (9.84%) | 81.90% (3.54%) |
| Coding variants (s.d.) | 20546 (202.6) | 20995 (167.7) |
| Rare coding variants (s.d.) | 578 (28.9) | 587 (27.5) |
| Rare coding variants predicted to be damaging (s.d.) | 26(5.6) | 18(4.1) |

**Table S2**

Sequencing statistics for samples in this study

Abbreviations: s.d., standard deviation.