Supplement Table S3. Quality control of the whole-exome sequencing.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Yield**  **(Gbases)** | **Mean**  **Depth** | **Coverage**  **10x (%)** | **Coverage**  **25x (%)** | **Clusters**  **(millions)** | **Align**  **(%)** | **Mismatches**  **Rate Read1 (%)** | **Mismatches**  **Rate Read2 (%)** | **≥ Q30**  **bases (%)** | **Quality**  **Score** |
| I-1 | 11.067 | 113x | 92 | 88 | 73.8 | 96.85 | 0.2 | 0.29 | 96.62 | 39.5 |
| I-2 | 10.242 | 106x | 92 | 88 | 68.3 | 96.91 | 0.19 | 0.28 | 97.09 | 39.6 |
| II-2 | 10.709 | 109x | 92 | 88 | 71.4 | 96.94 | 0.19 | 0.28 | 97.09 | 39.6 |