**Supplemental Table S1: Sequencing metrics for targeted capture libraries.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Total sequenced read pairs** | **Adapter trimmed reads (%)\*** | **Median insert size (bp)** | **Duplicate rate (%)** | **Mapped reads†** | | | ***SMAD4* mean read depth‡** |
| **Whole genome** | **Panel only** | **Proportion on-target (%)** |
| 1 | 20,304,004 | 2.96 | 233 | 70.86 | 4,466,309 | 3,773,441 | 84.49 | 3,866 |
| 2 | 7,298,993 | 3.29 | 194 | 16.29 | 6,018,425 | 5,106,264 | 84.84 | 2,312 |
| 3 | 5,433,758 | 3.50 | 184 | 6.52 | 4,144,379 | 3,506,463 | 84.61 | 1,662 |
| 4 | 9,265,458 | 1.24 | 176 | 10.09 | 7,610,364 | 6,487,338 | 85.24 | 3,043 |
| 5 | 8,340,941 | 1.26 | 192 | 9.02 | 8,226,145 | 7,022,509 | 85.37 | 2,231 |

\*As a proportion of the total reads processed.

†Following raw read processing and duplicate removal.

‡Calculated for the coding sequence defined by transcript NM\_005359.5 (<https://www.ncbi.nlm.nih.gov/nuccore>). The sequenced read length for the reported libraries was 101-bp.