S2 Table. Whole exome sequence metrics, PREDICTION-ADR

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Centre Average | Total number of reads | % mapped (with duplicates) | % at 20x coverage | % on target reads | % duplicates | No of variants |
| Liverpool  (356 samples) | 75,289,026 | 98.36 | 89.85 | 56.59 | 23.98 | 44,372 |
| Uppsala  (349 samples) | 45,766,833 | 97.17 | 93.71 | 58.05 | 20.31 | 44,041 |
| Dundee  (336 samples) | 64,325,883 | 96.68 | 90.22 | 66.76 | 16.38 | 43,880 |