**Supplementary File 2**. Comparison of consensus single-nucleotide polymorphisms (cSNPs) and heterogeneous alleles (hSNPs) in all samples aligned to H37Rv versus MT-0080\_PB, after initial filtering with Allelic Fraction for cSNPs ≥ **0·95** and **0·05** < hSNP < **0·95**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **cSNPs in all 62 samples** | | | | **hSNPs in all 62 samples** | | | |
|  | **H37Rv reference, n=51430** | | **MT-0080 reference, n=365** | | **H37Rv reference, n=4897** | | **MT-0080 reference, n=125** | |
|  | **Median (IQR)** | **Range** | **Median (IQR)** | **Range** | **Median (IQR)** | **Range** | **Median (IQR)** | **Range** |
| Phred | 24922·77 (12084·77, 29426·77) | **596·85,** 55420·77 | 28115·77 (25306·77, 31561·77) | 792·77, 47999·77 | 3820·76 (1065·77, 8864·77) | 50·77, 37538·77 | 136·77 (84·77, 1872·77) | 50·77, 26808·77 |
| RMS-MQ | 60 (60, 60) | **39·13**, 69·42 | 60 (60, 60) | 39·75, 60 | 58·91 (56·62, 59·95) | 33·81, 65·42 | 60 (60, 60) | 46·61, 60 |
| DP | 670 (322, 783) | 20, 1468 | 758 (683, 844) | 23, 1235 | 801 (421, 1056) | 20, 1500\* | 256 (78, 687) | 32, 990 |
| ReadPosRankSum | -0·064 (-1·093, 1·043) | **-5·269**, 3·735 | 010 (-0·783, 0·913) | -2·84, 2·71 | 1·383 (-2·691, 5·418) | -7·992, 15·309 | 0·892  (-0·501, 2·502) | -6·366, 4·101 |
| FS | 0 (0, 0) | 0, **45·053** | 0 (0, 0) | 0, 2·28 | 9·28 (1·979, 26·173) | 0, 59·985 | 1·723 (0·685, 4·69) | 0, 58·993 |