**Supplementary File 9**. 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 ≥ **0·99** and **0·01** < hSNP < **0·99**

|  |  |  |
| --- | --- | --- |
|  | **cSNPs in all 62 samples** | **hSNPs in all 62 samples** |
|  | **H37Rv reference, n=49965** | **MT-0080 reference, n=361** | **H37Rv reference, n=5819** | **MT-0080 reference, n=129** |
|  | **Median (IQR)** | **Range** | **Median (IQR)** | **Range** | **Median (IQR)** | **Range** | **Median (IQR)** | **Range** |
| Phred  | 25180·77 (15127·77, 29568·77) | 610·77, 55420·77 | 28133·77 (25313·77, 31561·77) | 792·77, 47999·77 | 4457·77 (1338·53, 8490·77) | 50·77, 37538·77 | 157·77 (84·77, 1986·77) | 50·77, 43450·77 |
| RMS-MQ  | 60 (60, 60) | 39·13, 69·31 | 60 (60, 60) | 39·75, 60 | 59·41 (56·64, 60) | 33·81, 69·25 | 60 (60, 60) | 46·61, 60 |
| DP | 676 (415, 787) | 20, 1468 | 759 (683, 844) | 23, 1235 | 664 (233, 1017) | 20, 1500\* | 271 (79, 691) | 32, 1191 |
| ReadPosRankSum | 0·032 (-0·975, 1·09) | -2·898, 2·82 | 0·118 (-0·738, 0·953) | -1·868, 2·71 | 0·628 (-2·273, 4·538) | -7·992, 15·309 | 0·773 (-0·624, 2·475) | -6·366, 4·101 |
| FS | 0 (0, 0) | 0, 9·514 | 0 (0, 0) | 0, 0 | 5·933 (1·018, 22·791) | 0, 59·985 | 1·623 (0, 4·676) | 0, 58·993 |