



Supplementary Material

File S1. Pipeline used to analyze sequencing data starting from fastq generated after Illumina run:

- Sickle (sequence quality filter)

```
sickle pe -f <name>_R1.fastq -r <name>_R2.fastq -t sanger -o <name>_F_trimmed -p <name>_R_trimmed -s <name>_trimmed
```

- BWA (mapping against reference genome H37v_NC_000962.3)

```
bwa index -p H37Rv_NC_000962.3_index -a is H37Rv_NC_000962.3.fasta
```

```
bwa mem / H37Rv_NC_000962.3_index ../<name>_R1.fastq ../<name>_R2.fastq > -o <name>_alin_vs_lin.sam
```

- Sam to bam (transformation of bwa output to analyze SNP)

```
samtools view -S -b <name>_alin_vs_lin.sam > <name>_alin_lin.bam
```

```
samtools sort -o <name>_sorted_alin_lin.bam <name>_alin_lin.bam
```

```
samtools index -b <name>_sorted_alin_lin.bam <name>sorted_alin_lin.bam.bai
```

- bcftools mpileup (SNPs analysis)

```
bcftools mpileup -O b -o <name>.bcf -f /gen_lineage.fasta <name>_sorted_alin_lin.bam
```

- Variant calling (Identification of SNPs)

```
bcftools call -o <name>.vcf -mv <name>.bcf
```

```
bcftools filter --exclude "QUAL < 30" <name>.vcf > <name>_filtered.vcf
```

```
bcftools view -v snps <name>_filtered.vcf | more
```

```
ls | less -S <name>.vcf | grep -v "##" | cut -f1,2,3,4,5,6,10 | sed '/^#{x;p;x}' > snp.txt
```

Table S1: Sample information. Age, Gender and bacterial culture results, previous culture (relapse) and HIV information were recorded. Reclusion Center: N°4 (-34.8036113,-56.3547671), N°5 (-34.791844, -56.230891), N°6 (-34.8363927,-56.092903), N°7 (-34.5270384,-56.2663051), N°18 (-33.379260, -56.521940). * Detected at Entry Center, then transferred to N°4.

| ID | Age | Sex | Bacterial culture | Relapse | HIV | Reclusion Center |
|----|-----|-----|-------------------|---------|-----|------------------|
| 1 | 25 | M | Positive ++ | 0 | 0 | N°4* |
| 2 | 28 | M | Positive ++ | | | N°6 |
| 3 | 20 | M | Positive + | 0 | 0 | N°4* |
| 4 | 31 | M | Positive ++ | | | N°4* |
| 5 | 35 | M | Positive <20 | 0 | 0 | N°4* |
| 6 | 43 | F | Positive <20 | 0 | 0 | N°18 |
| 7 | 60 | M | Positive +++ | 0 | 0 | N°4* |
| 8 | 24 | M | Positive ++ | 0 | 0 | N°4* |
| 9 | 23 | M | Positive + | 0 | 0 | N°4* |
| 10 | 46 | M | Positive <20 | 0 | 0 | N°4* |
| 11 | 54 | M | Positive + | 0 | 0 | N°4* |
| 12 | 33 | M | Positive <20 | 0 | 0 | N°4* |
| 13 | 27 | M | Positive +++ | 0 | 0 | N°6 |
| 14 | 26 | M | Positive <20 | 0 | 0 | N°4 |
| 15 | 26 | M | Positive ++ | 0 | 0 | N°4* |
| 16 | 30 | M | Positive + | | | N°4* |
| 17 | 22 | M | Positive <20 | 0 | 0 | N°4* |
| 18 | 28 | M | Positive +++ | 0 | 0 | N°4* |
| 19 | 40 | M | Positive <20 | 0 | 0 | N°4* |
| 20 | 39 | M | Positive <20 | 0 | 0 | N°4* |
| 21 | 73 | M | Positive <20 | 1 | 0 | N°4* |
| 22 | 37 | M | Positive + | 0 | 0 | N°4* |
| 23 | 25 | F | Positive <20 | 0 | 0 | N°5 |
| 24 | 48 | F | Positive <20 | | | N°5 |
| 25 | 21 | M | Positive +++ | 0 | 0 | N°6 |
| 26 | 43 | M | Positive <20 | 0 | 0 | N°4* |
| 27 | 46 | M | Positive +++ | 0 | 0 | N°4* |
| 28 | 24 | M | Positive ++ | 0 | 0 | N°4 |
| 29 | 25 | M | Positive + | 0 | 0 | N°4* |
| 30 | 41 | M | Positive <20 | 0 | 0 | N°4* |
| 31 | 32 | M | Positive <20 | 1 | 0 | N°7 |
| 32 | 31 | F | Positive ++ | 0 | 0 | N°5 |
| 33 | 27 | M | Positive + | 0 | 0 | N°7 |
| 34 | 30 | M | Positive <20 | | | N°6 |
| 35 | 23 | M | Positive +++ | 0 | 0 | N°4* |
| 36 | 35 | M | Positive +++ | 0 | 0 | N°4* |
| 37 | 34 | M | Positive <20 | 0 | 0 | N°6 |
| 38 | 38 | M | Positive +++ | 1 | 0 | N°6 |
| 39 | 29 | M | Positive <20 | 0 | 0 | N°4* |
| 40 | 36 | M | Positive +++ | 0 | 0 | N°4* |

| | | | | | | |
|----|----|---|--------------|---|---|------|
| 41 | 19 | M | Positive <20 | 0 | 0 | N°7 |
| 42 | 29 | M | Positive <20 | 0 | 1 | N°4* |
| 43 | 41 | M | Positive <20 | 0 | 0 | N°4* |
| 44 | 32 | M | Positive +++ | 0 | 0 | N°6 |
| 45 | 35 | M | Positive + | 0 | 0 | N°4 |
| 46 | 31 | M | Positive <20 | 1 | 0 | N°4 |
| 47 | 39 | M | Positive <20 | 0 | 0 | N°4* |

Table S2: Lineage Region information. The table indicates the lineage, the name or denomination it receives, the gene and the position of the mutation with respect to the reference genome. Additionally, the base change, the codon number where it occurs, is indicated. They are all silent substitutions so there is no amino acid change.

| Lineage | Sublineage | Position* | Gen coord. | Allelic change | Codon number | Codon Change | AA change | ID Locus | Gen name |
|----------------|------------|-----------|------------|----------------|--------------|--------------|-----------|----------|----------|
| lineage7 | Lineage 7 | 1137518 | 543 | G/A | 181 | AAC/AAT | N/N | Rv1018c | glmU |
| lineage6 | Lineage 6 | 1816587 | 399 | C/G | 133 | GTC/GTG | V/V | Rv1617 | pykA |
| lineage5 | Lineage 5 | 1799921 | 339 | C/A | 113 | GGC/GGA | G/G | Rv1599 | hisD |
| lineage4.4.1.1 | S | 355181 | 684 | G/A | 228 | AAG/AAA | K/K | Rv0291 | mycP3 |
| lineage4.3 | LAM | 764995 | 1626 | C/G | 542 | GCC/GCG | A/A | Rv0668 | rpoC |
| lineage4.1.2.1 | Haarlem | 107794 | 195 | C/T | 65 | GCC/GCT | A/A | Rv0098 | fcoT |
| lineage4.1.1 | X | 514245 | 1077 | C/T | 359 | GTG/GTA | V/V | Rv0425c | ctpH |
| lineage4 | Lineage 4 | 931123 | 171 | T/C | 57 | TAT/TAC | Y/Y | Rv0835 | lpqQ |
| lineage3 | Lineage 3 | 3273107 | 894 | C/A | 298 | GCC/GCA | A/A | Rv2936 | drpA |
| lineage2 | Lineage 2 | 497491 | 810 | G/A | 270 | GAC/GAT | D/D | Rv0411c | glnH |
| lineage1 | Lineage 1 | 615938 | 1104 | G/A | 368 | GAG/GAA | E/E | Rv0524 | hemL |

*According to the reference genome NC_000962.3

Table S3: Region information. Genes associated with resistance to anti-tuberculosis drugs

| Gene | Resistance | Position* |
|-------------|------------------|-----------------|
| <i>eis</i> | Kanamycin | 2714124-2715332 |
| <i>embB</i> | Ethambutol | 4246514-4249810 |
| <i>gyrA</i> | Fluoroquinolones | 7302-9818 |
| <i>gyrB</i> | Fluoroquinolones | 5240-7267 |
| <i>inhA</i> | Isoniazid | 1674202-1675011 |
| <i>katG</i> | Isoniazid | 2153889-2156111 |
| <i>pncA</i> | Pyrazinamide | 2288681-2289241 |
| <i>rpoB</i> | Rifampicin | 759807-763325 |
| <i>rrs</i> | Streptomycin | 1471846-1473382 |

*According to the reference genome NC_000962.3

Table S4. Primers designed for lineage pool

| <i>Gene</i> | <i>Lineage</i> | <i>Fwd/Rev</i> | <i>Sequence 5'-3'</i> | <i>Amplicon size (bp)</i> |
|--------------|----------------|----------------|-----------------------|---------------------------|
| <i>ctpH</i> | X | Fwd | GGAAAAGTGCCTCGACTGC | 374 |
| | | Rev | GTTTCGCGCTGATCCAAG | |
| <i>mycP3</i> | S | Fwd | TGACGGCTTCTCTGGTGTG | 400 |
| | | Rev | GCCACCGACAACACGTAG | |
| <i>fcoT</i> | Haarlem | Fwd | GGTTCCGATCGCAGAGGA | 320 |
| | | Rev | TTGATCGCCGGGAGTTGTAA | |
| <i>rpoC</i> | LAM | Fwd | CGCCGGAAATCATCGTCAAC | 648 |
| | | Rev | TCGGTGGTCAGGTAGTACAG | |
| <i>hemL</i> | Lineage 1 | Fwd | GAAGTGGTTGGTACGGAATC | 372 |
| | | Rev | ATGGCATGAAAGAACGCTGG | |
| <i>glnH</i> | Lineage 2 | Fwd | GATACAACGTGTTCCAGGTG | 356 |
| | | Rev | GTCTACCTCGACGCCAAC | |
| <i>drpA</i> | Lineage 3 | Fwd | TGAAGGATCTGGACGCTATC | 201 |
| | | Rev | TCAGAGACTCGGTGGGATC | |
| <i>lpqQ</i> | Lineage 4 | Fwd | GATCAGTCGTGTGTTGCTCC | 269 |
| | | Rev | TACGGAACTCTGACCAGTCG | |
| <i>hisD</i> | Lineage 5 | Fwd | TCTGGGAGAATGGTCTACGTG | 435 |
| | | Rev | CACCACGTTTCATCACCAC | |
| <i>pykA</i> | Lineage 6 | Fwd | ACAAGGTCGCCTATGAGC | 364 |
| | | Rev | GAGATCCTCGATGTCCTTC | |
| <i>glmU</i> | Lineage 7 | Fwd | CTGGCATGTACGGTCTGG | 212 |
| | | Rev | GATGATCCCTTCGGCTAC | |
| <i>alkA</i> | Bovis | Fwd | GGCCTTCGTCGATACCTG | 732 |
| | | Rev | AATGGAATGTGCGTAGTGAC | |

Table S5. Primers designed for resistance pool

| <i>Gen</i> | <i>Resistance</i> | <i>Fwd/Rev</i> | <i>Sequence 5'-3'</i> | <i>Amplicon size (bp)</i> |
|-------------|-------------------|----------------|-----------------------|---------------------------|
| <i>eis</i> | Kanamycin | Fwd | AAAGCCCGTCAGCCTAGC | 1280 |
| | | Rev | ATCGCGTGATCCTTTGCC | |
| <i>embB</i> | Ethambutol | Fwd1 | GGATCGGTGGAGCAGTACC | 1281 |
| | | Rev1 | GTTGTTGAACGGCATCCAC | |
| | | Fwd2 | TACCGCCGCATTCACACT | 1080 |
| | | Rev2 | GGCTGGTTGGGTTTCATCACG | |
| | | Fwd3 | GAGTCCTGGCATCAATGGTT | 978 |
| | | Rev3 | CCAACACCCCTGCGCCGAC | |
| <i>gyrA</i> | Fluoroquinolones | Fwd | AAACGAGGAATAGATGACAG | 2588 |
| | | Rev | CACCCCGACTCCTAACACTC | |
| <i>gyrB</i> | Fluoroquinolones | Fwd | GGGTAAAAACGAGGCCAGA | 2114 |
| | | Rev | CAGGGTTGCGTTAGACATCC | |
| <i>inhA</i> | Isoniazid | Fwd | GGCCACTGACACAACACAAG | 825 |
| | | Rev | CAGCAGGACGGCATCAAATTG | |
| <i>katG</i> | Isoniazid | Fwd1 | CGATCAACCCGAATCAGC | 1141 |
| | | Rev1 | GGTGGATCCGATCTATGAGC | |
| | | Fwd2 | GTCAGTGGCCAGCATCGTCG | 1044 |
| | | Rev2 | GATCACAGCCCGATAACACC | |
| <i>pncA</i> | Pyrazinamide | Fwd | AACAGTTCATCCCGGTTCG | 575 |
| | | Rev | GTCGCCCGAACGTATGGTG | |
| <i>rpoB</i> | Rifampicin | Fwd1 | GATTCCCGCCAGAGCAAAAC | 1281 |
| | | Rev1 | TAGTCCACCTCAGACGAGGG | |
| | | Fwd2 | CCCTCGTCTGAGGTGGACTA | 906 |
| | | Rev2 | GTCGAGCACGTAACTCCCTT | |
| <i>rrs</i> | Streptomycin | Fwd | TCCAAAGGGAGTGTTTGGGT | 1594 |
| | | Rev | CAGTTGGGGCGTTTTCTGTG | |



Table S6. Coverage by sequenced resistance regions.

| Coverage (resistance regions) | | (nreads x reads length/amplicon length) | | | | | | | |
|-------------------------------|-------|---|------|------|-------|-------|-------|--------|--------|
| | rrs | embB | gyrA | gyrB | inhA | eis | katG | pncA | rpoB |
| Sample/amplified length | 1594 | 3339 | 2588 | 2114 | 825 | 1280 | 2185 | 575 | 2187 |
| 1 | 1277 | 11 | 204 | 34 | 2445 | 1379 | 988 | 896 | 1712 |
| 2 | 5113 | 29 | 941 | 384 | 11444 | 5261 | 6633 | 29057 | 10846 |
| 3 | 13470 | 11 | 2703 | 719 | 19518 | 8582 | 7318 | 5516 | 15117 |
| 4 | 7484 | 7 | 1045 | 197 | 10479 | 6986 | 5178 | 4056 | 10509 |
| 5 | 147 | 8 | 23 | 14 | 37089 | 14779 | 11925 | 2100 | 32776 |
| 6 | 14669 | 4 | 1243 | 246 | 21347 | 13840 | 9432 | 665 | 18266 |
| 7 | 7101 | 105 | 1244 | 251 | 10634 | 6756 | 5674 | 43491 | 9637 |
| 8 | 8801 | 146 | 1393 | 205 | 16456 | 7895 | 9688 | 0 | 13179 |
| 9 | 3330 | 7 | 275 | 33 | 9335 | 5278 | 5308 | 24 | 25953 |
| 10 | 2749 | 20 | 446 | 52 | 6077 | 3609 | 3003 | 175831 | 4459 |
| 11 | 1530 | 28 | 273 | 41 | 4131 | 1709 | 1594 | 40 | 2715 |
| 12 | 1463 | 2 | 221 | 35 | 8100 | 3442 | 4409 | 892 | 7912 |
| 13 | 446 | 6 | 133 | 6 | 672 | 390 | 335 | 1857 | 18610 |
| 14 | 2468 | 0 | 141 | 11 | 858 | 137 | 121 | 2637 | 102603 |
| 15 | 3753 | 25 | 377 | 140 | 5306 | 3160 | 3636 | 17333 | 6100 |
| 16 | 527 | 1 | 5 | 8 | 160 | 5 | 65 | 1339 | 22455 |
| 17 | 1143 | 9 | 137 | 24 | 3189 | 1896 | 974 | 4223 | 2297 |
| 18 | 5603 | 75 | 910 | 104 | 14057 | 7944 | 5940 | 1796 | 11903 |
| 19 | 7520 | 38 | 1466 | 128 | 31330 | 17092 | 10301 | 18286 | 22489 |
| 20 | 874 | 1 | 57 | 10 | 756 | 12 | 69 | 3083 | 21432 |
| 21 | 4768 | 223 | 1151 | 349 | 16081 | 7098 | 9274 | 1624 | 11306 |
| 22 | 567 | 3 | 115 | 7 | 699 | 215 | 147 | 2477 | 30185 |
| 23 | 5 | 1 | 2 | 1 | 7005 | 45 | 7 | 116578 | 183 |
| 24 | 789 | 10 | 87 | 2 | 2383 | 1111 | 537 | 7297 | 38689 |
| 25 | 274 | 9 | 41 | 1 | 404 | 195 | 96 | 1028 | 21205 |
| 26 | 31 | 7 | 2 | 0 | 2427 | 52 | 22 | 12796 | 23015 |
| 27 | 6 | 2 | 6 | 1 | 10 | 13 | 3 | 18 | 15 |
| 28 | 28 | 22 | 33 | 19 | 61 | 56 | 26 | 45 | 81 |
| 29 | 1341 | 4 | 5 | 31 | 47 | 12 | 159 | 1538 | 25590 |
| 30 | 732 | 4 | 2 | 1 | 1976 | 67 | 12 | 7846 | 12746 |
| 31 | 8 | 5 | 7 | 2 | 144 | 31 | 13 | 144772 | 57 |
| 32 | 2008 | 2 | 45 | 32 | 608 | 8 | 181 | 5346 | 50573 |
| 33 | 607 | 1 | 2 | 12 | 54 | 47 | 107 | 1379 | 19825 |
| 34 | 767 | 5 | 2 | 1 | 1394 | 32 | 151 | 7022 | 15031 |
| 35 | 369 | 5 | 55 | 2 | 560 | 217 | 120 | 1722 | 14412 |
| 36 | 650 | 2 | 100 | 5 | 795 | 306 | 200 | 1846 | 19495 |
| 37 | 289 | 3 | 47 | 2 | 279 | 169 | 102 | 830 | 12641 |
| 38 | 4 | 3 | 18 | 1 | 3670 | 30 | 154 | 888442 | 166 |
| 39 | 2 | 1 | 1 | 1 | 58 | 3 | 2 | 7 | 10 |
| 40 | 1501 | 2 | 124 | 31 | 1321 | 17 | 208 | 3713 | 49336 |
| 41 | 249 | 2 | 16 | 4 | 241 | 6 | 47 | 707 | 7932 |
| 42 | 606 | 1 | 106 | 2 | 781 | 226 | 91 | 2673 | 31688 |
| 43 | 412 | 2 | 81 | 3 | 527 | 181 | 85 | 1541 | 17231 |
| 44 | 824 | 1 | 82 | 12 | 786 | 51 | 119 | 1858 | 18655 |
| 45 | 1053 | 2 | 2 | 10 | 100 | 6 | 118 | 2322 | 31257 |
| 46 | 365 | 5 | 11 | 10 | 168 | 9 | 53 | 603 | 11972 |
| 47 | 1158 | 9 | 67 | 4 | 1960 | 221 | 545 | 8136 | 9567 |
| H37 | 850 | 1 | 161 | 4 | 793 | 369 | 183 | 1849 | 29213 |
| Mean | 2286 | 18 | 325 | 67 | 5390 | 2520 | 2195 | 32065 | 17980 |
| SD | 3357 | 41 | 552 | 133 | 8281 | 4233 | 3431 | 131229 | 17489 |

Table S7. Coverage by sequenced lineage regions.

| Coverage | (nreads x reads length/amplicon length) | | | | | | | | | | |
|-------------------------|---|-----------|-----------|-----------|---------|-------|-------|-------|-----------|-----------|-----------|
| | Lineage 1 | Lineage 2 | Lineage 3 | Lineage 4 | Haarlem | LAM | S | X | Lineage 5 | Lineage 6 | Lineage 7 |
| Sample/amplified length | 372 | 356 | 201 | 269 | 320 | 648 | 400 | 374 | 435 | 364 | 212 |
| 1 | 174 | 868 | 238 | 350 | 3535 | 824 | 609 | 801 | 229 | 772 | 342 |
| 2 | 1224 | 5248 | 3133 | 2409 | 22272 | 2222 | 2377 | 3345 | 1087 | 3748 | 2760 |
| 3 | 1726 | 8318 | 2399 | 3156 | 34521 | 6668 | 5019 | 6290 | 1650 | 6665 | 3189 |
| 4 | 260 | 5229 | 1735 | 2054 | 22810 | 4582 | 3278 | 4074 | 239 | 4307 | 2128 |
| 5 | 647 | 18396 | 4995 | 7320 | 82917 | 8169 | 8108 | 12748 | 657 | 13087 | 6669 |
| 6 | 1358 | 7909 | 2322 | 3123 | 41447 | 4628 | 4595 | 6268 | 1352 | 6412 | 3178 |
| 7 | 2076 | 5759 | 1756 | 2323 | 19187 | 5956 | 4225 | 6189 | 2447 | 6307 | 2228 |
| 8 | 2496 | 6016 | 2446 | 3174 | 30906 | 4149 | 5025 | 6650 | 2420 | 6237 | 3059 |
| 9 | 1192 | 3421 | 1045 | 1400 | 27144 | 1306 | 1382 | 2259 | 1047 | 1927 | 1496 |
| 10 | 808 | 2341 | 641 | 811 | 9275 | 1396 | 1425 | 1914 | 856 | 1720 | 753 |
| 11 | 37 | 1759 | 502 | 583 | 4748 | 1272 | 898 | 943 | 16 | 1188 | 516 |
| 12 | 913 | 2814 | 990 | 1148 | 18359 | 735 | 971 | 1727 | 897 | 1604 | 1462 |
| 13 | 1 | 1455 | 1040 | 701 | 12 | 564 | 323 | 10 | 12 | 933 | 763 |
| 14 | 6 | 1753 | 1029 | 1233 | 47 | 646 | 699 | 43 | 9 | 1101 | 763 |
| 15 | 531 | 1613 | 687 | 653 | 11508 | 819 | 632 | 913 | 517 | 916 | 763 |
| 16 | 18 | 943 | 726 | 650 | 70 | 342 | 93 | 89 | 14 | 32 | 420 |
| 17 | 373 | 1275 | 385 | 380 | 3899 | 938 | 583 | 864 | 459 | 880 | 354 |
| 18 | 1967 | 5352 | 1120 | 1539 | 20963 | 3770 | 2728 | 4159 | 2170 | 3932 | 1563 |
| 19 | 5021 | 16342 | 3670 | 5885 | 36205 | 12799 | 11506 | 14317 | 5532 | 14619 | 5110 |
| 20 | 1 | 1896 | 969 | 1094 | 141 | 539 | 534 | 2 | 16 | 289 | 509 |
| 21 | 2934 | 9737 | 2319 | 3086 | 24336 | 4247 | 3683 | 5923 | 3144 | 5679 | 3410 |
| 22 | 3 | 2287 | 1405 | 1306 | 152 | 695 | 759 | 8 | 20 | 249 | 919 |
| 23 | 13 | 48031 | 2596 | 14442 | 59 | 644 | 3779 | 30 | 9 | 2105 | 1768 |
| 24 | 4 | 5211 | 3638 | 2929 | 23 | 1036 | 1361 | 3 | 2 | 1148 | 2387 |
| 25 | 1 | 862 | 510 | 535 | 13 | 292 | 275 | 2 | 2 | 466 | 432 |
| 26 | 2 | 5543 | 992 | 2805 | 2 | 191 | 851 | 7 | 1 | 261 | 611 |
| 27 | 49 | 715231 | 6081 | 81443 | 2 | 201 | 6795 | 107 | 37 | 1395 | 7015 |
| 28 | 577 | 2120666 | 24266 | 147839 | 54 | 4011 | 18322 | 505 | 350 | 10916 | 35571 |
| 29 | 6 | 2236 | 1514 | 1418 | 16 | 50 | 29 | 8 | 3 | 6 | 756 |
| 30 | 17 | 7238 | 4677 | 4212 | 41 | 1912 | 938 | 2 | 4 | 215 | 3105 |
| 31 | 18 | 35250 | 1182 | 6502 | 37 | 25 | 465 | 88 | 16 | 225 | 1533 |
| 32 | 6 | 4896 | 3208 | 3292 | 12 | 351 | 153 | 10 | 17 | 19 | 1710 |
| 33 | 2 | 1071 | 649 | 598 | 20 | 330 | 254 | 12 | 27 | 66 | 400 |
| 34 | 1 | 4835 | 2761 | 3031 | 30 | 896 | 473 | 1 | 20 | 80 | 1499 |
| 35 | 4 | 1566 | 1091 | 1032 | 21 | 538 | 552 | 40 | 19 | 120 | 764 |
| 36 | 11 | 1900 | 1482 | 1197 | 75 | 677 | 689 | 8 | 24 | 213 | 1040 |
| 37 | 6 | 830 | 701 | 603 | 411 | 30 | 17 | 32 | 7 | 2 | 463 |
| 38 | 23 | 71 | 42 | 51 | 203 | 21 | 31 | 28 | 13 | 40 | 104 |
| 39 | 4 | 126803 | 2770 | 20566 | 119 | 26 | 595 | 18 | 8 | 215 | 2217 |
| 40 | 26 | 3364 | 2374 | 2095 | 59 | 1129 | 978 | 0 | 1 | 306 | 1563 |
| 41 | 3 | 471 | 260 | 247 | 94 | 132 | 153 | 7 | 1 | 267 | 211 |
| 42 | 2 | 2136 | 1146 | 1272 | 57 | 663 | 928 | 6 | 34 | 526 | 753 |
| 43 | 5 | 1279 | 872 | 833 | 47 | 495 | 438 | 1 | 7 | 167 | 550 |
| 44 | 10 | 1434 | 890 | 949 | 47 | 535 | 617 | 7 | 2 | 668 | 726 |
| 45 | 1 | 1191 | 593 | 843 | 11 | 251 | 393 | 18 | 16 | 60 | 339 |
| 46 | 3 | 508 | 375 | 280 | 1 | 221 | 190 | 1 | 19 | 101 | 230 |
| 47 | 1 | 8099 | 5800 | 4189 | 15 | 1812 | 1929 | 8 | 2 | 1921 | 3933 |
| H37Rv | 3 | 1750 | 1207 | 1025 | 47 | 744 | 298 | 20 | 11 | 47 | 789 |
| Mean | 512 | 66942 | 2234 | 7263 | 8666 | 1760 | 2103 | 1677 | 530 | 2170 | 2350 |
| SD | 991 | 320060 | 3556 | 23912 | 16115 | 2517 | 3354 | 3226 | 1063 | 3423 | 5143 |