

| | Chromosome 21 | | Chromosome 22 | |
|-------------------------|---------------|--------------|---------------|--------------|
| | Batch | Serial | Batch | Serial |
| % Identity Align | 98.51 | 98.37 | 98.51 | 98.28 |
| Alignment Length | 439.11 | 416.00 | 395.98 | 373.99 |
| Query Length | 500.00 | 500.00 | 450.00 | 450.00 |
| Query Sequences | 65,413 | 65,413 | 71,870 | 71,870 |
| Query Hits | 57,560 | 65,413 | 64,087 | 71,870 |
| Hit Frequency | 87.99 | 100.00 | 89.17 | 100.00 |
| Query Identity | 86.51 | 81.84 | 86.68 | 81.68 |
| Overall Identity | 76.12 | 81.84 | 77.29 | 81.68 |

Table 1 – Comparison of results where queries are submitted in batch mode rather than serial mode. Note the significant increase in hit frequency, and decrease in alignment length.

| | Chromosome 21 | | Chromosome 22 | |
|-------------------------|---------------|--------------|---------------|--------------|
| | Ungapped | Gapped | Ungapped | Gapped |
| % Identity Align | 98.27 | 97.86 | 98.28 | 97.66 |
| Alignment Length | 416.01 | 496.46 | 373.99 | 441.23 |
| Query Length | 499.99 | 501.50 | 450.00 | 451.47 |
| Query Sequences | 65,413 | 65,413 | 71,870 | 71,870 |
| Query Hits | 65,413 | 65,413 | 71,870 | 71,870 |
| Hit Frequency | 100.00 | 100.00 | 100.00 | 100.00 |
| Query Identity | 81.76 | 96.88 | 81.68 | 95.44 |
| Overall Identity | 81.76 | 96.88 | 81.68 | 95.44 |

Table 2 – Comparison of results where insertions and deletions are accounted for. Note the significant increase in alignment length.

| pident | nident | length | qlen | Similarity |
|---------------|---------------|---------------|-------------|-------------------|
| 97.56 | 240 | 246 | 300 | 80.00% |
| 97.67 | 293 | 300 | 300 | 97.67% |
| 97.07 | 298 | 307 | 300 | 97.07% |
| - | - | - | 300 | 00.00% |
| Total: | 831 | 1207 | | 68.85% |

Table 3 – Examples of calculation methodology; for illustrative purposes only.

| Chromosome | Sequenced (Mb) | Identity | SEM |
|------------|----------------|----------|--------|
| 1 | 230.0 | 97.22% | ±0.18% |
| 2 | 239.6 | 97.07% | ±0.20% |
| 3 | 196.3 | 97.16% | ±0.19% |
| 4 | 188.2 | 96.98% | ±0.19% |
| 5 | 180.7 | 97.22% | ±0.17% |
| 6 | 169.1 | 97.38% | ±0.17% |
| 7 | 156.8 | 95.91% | ±0.32% |
| 8 | 143.3 | 96.93% | ±0.20% |
| 9 | 120.3 | 97.14% | ±0.19% |
| 10 | 132.0 | 97.16% | ±0.18% |
| 11 | 132.5 | 97.07% | ±0.21% |
| 12 | 131.6 | 97.13% | ±0.19% |
| 13 | 97.8 | 97.09% | ±0.19% |
| 14 | 90.3 | 97.21% | ±0.19% |
| 15 | 82.5 | 96.97% | ±0.21% |
| 16 | 80.2 | 96.49% | ±0.22% |
| 17 | 80.1 | 96.78% | ±0.22% |
| 18 | 76.2 | 97.07% | ±0.21% |
| 19 | 58.3 | 95.77% | ±0.25% |
| 20 | 62.2 | 96.96% | ±0.20% |
| 21 | 39.9 | 97.28% | ±0.16% |
| 22 | 39.0 | 96.53% | ±0.22% |
| X | 151.6 | 96.79% | ±0.23% |
| Y | 23.1 | 87.11% | ±0.58% |
| Total | 2,901.7 | 96.90% | ±0.21% |

Table 4 - Comparison of Chimpanzee slices to Human genome. The total result is a weighted average of all the chromosomes.