

GEDmatch® Autosomal One-to-one Comparison - V1.0

Software Version Nov 12 2019 14:54:30

[Here](#) is a link to a useful YouTube video on using the One to One DNA comparison tool.

Individual marker indications:

| | |
|----------------------------|--|
| Base Pairs with Full Match | |
| Base Pairs with Half Match | |
| Match with Phased data | |
| Base Pairs with No Match | |

Validity of segments:

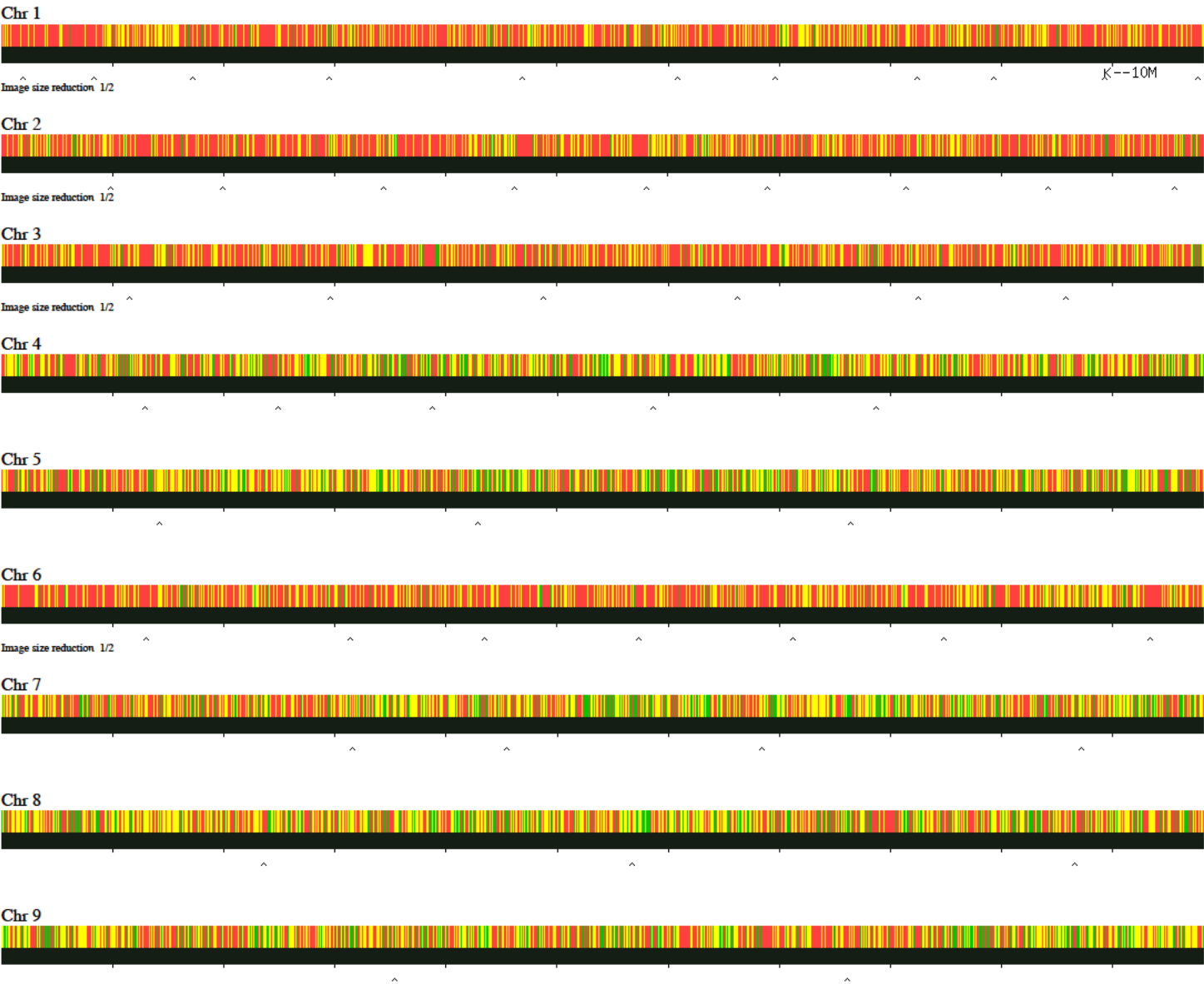
| | |
|---------------------------------|--|
| Significant | |
| Moderate | |
| Low | |
| Insignificant | |
| Large gap between adjacent SNPs | |
| No Match | |
| Centromere | |

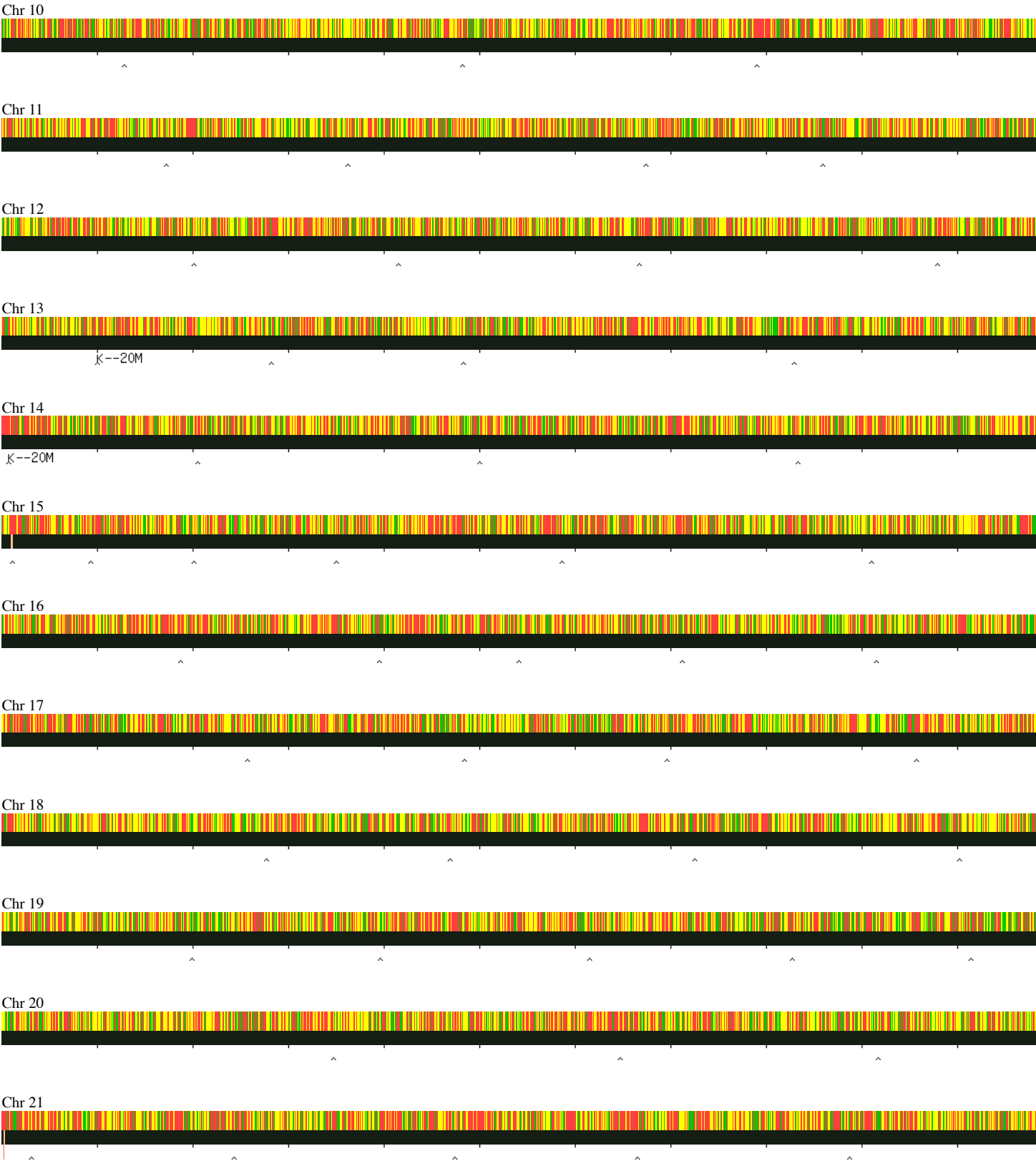
Comparing Kit [redacted] (*target.stripy.genome.3) [23andMe] and [redacted] (*22stripy.genome.2) [23andMe]

Minimum segment threshold size to be included in total = 25 SNPs

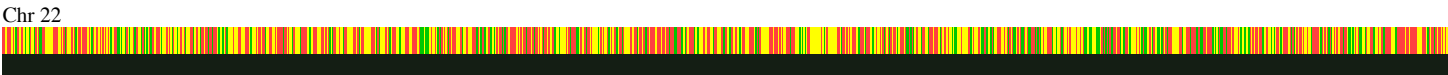
Minimum segment cM to be included in total = 0.7 cM

Mismatch-bunching Limit = 25 SNPs





| Chr | B37 Start Pos'n | B37 End Pos'n | Centimorgans (cM) | SNPs |
|-----|-----------------|---------------|-------------------|------|
| 22 | 27,433,179 | 27,680,780 | 1.3 | 45 |
| 22 | 33,771,672 | 34,328,741 | 0.8 | 45 |
| 22 | 37,519,864 | 37,827,711 | 1.1 | 42 |
| 22 | 40,357,667 | 43,112,674 | 0.9 | 32 |



Largest segment = 1.3 cM

Total Half-Match segments (HIR) = 4.1 cM (0.113 Pct)

4 shared segments found for this comparison.

514763 SNPs used for this comparison.

18.391 Pct SNPs are full identical

Comparison took 0.345 seconds.

CPU time used: 0.159 cpu seconds.

Ver: Nov 12 2019 14:54:30