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:

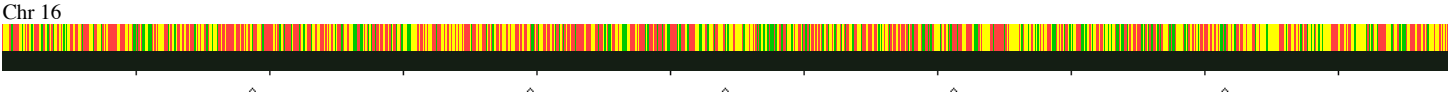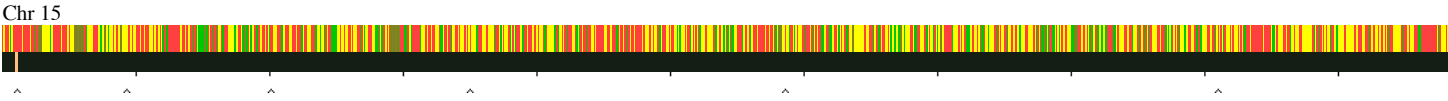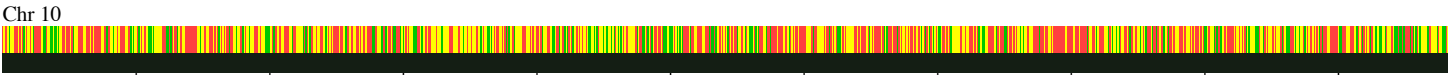|	
Significant	
Moderate	
Low	
Insignificant	
Large gap between adjacent SNPs	
No Match	
Centromere	

Comparing Kit ▆▆▆▆▆ (*target.stripy.genome.1) [23andMe] and ▆▆▆▆▆ (*22stripy.genome.1) [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 1

Image size reduction 1/2   K--10M

Chr 2

Image size reduction 1/2

Chr 3

Image size reduction 1/2

Chr 4

Chr 5

Chr 6

Image size reduction 1/2

Chr 7

Chr 8

Chr 9

Chr 10

Chr 11

Chr 12

Chr 13

K--20M

Chr 14

K--20M

Chr 15

Chr 16

Chr 17

Chr 18

Chr 19

Chr 20

Chr 21
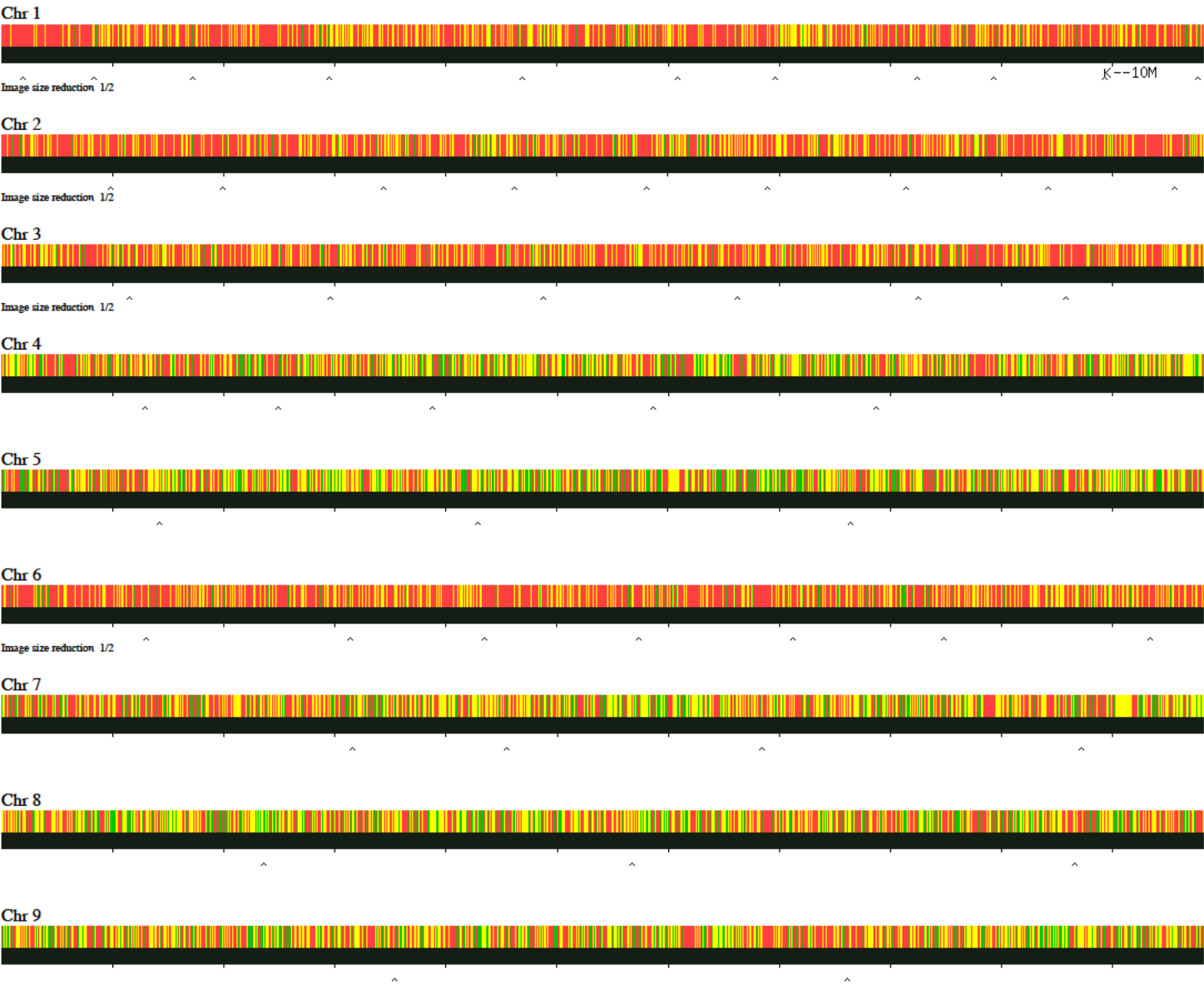
Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
22	27,427,698	27,680,780	1.3	47
22	33,771,672	34,328,741	0.8	45
22	37,519,864	37,827,711	1.1	42
22	40,054,428	43,112,674	1.2	40

Chr 22

K--20M
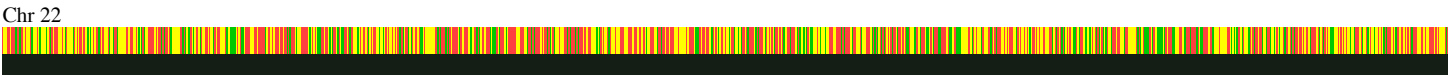
Largest segment = 1.3 cM

Total Half-Match segments (HIR) = 4.3 cM (0.120 Pct)

4 shared segments found for this comparison.

514763 SNPs used for this comparison.

18.393 Pct SNPs are full identical

Comparison took 0.411 seconds.
CPU time used: 0.181 cpu seconds.

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K--20M