

# GEDmatch.Com Autosomal Comparison

Base Pairs with Full Match =	
Base Pairs with Half Match =	
Match with Phased data =	
Base Pairs with No Match =	
Base Pairs not included in comparison =	
Matching segments greater than 3 centiMorgans =	

Comparing Kit A241640 (\*BillH) and F266907 (Jeffrey Wayne Waugh)

Minimum threshold size to be included in total = 500 SNPs

Mismatch-bunching Limit = 250 SNPs

Noise Reduction Threshold = 0.80

Minimum segment cM to be included in total = 3.0 cM

Chr 1



Image size reduction: 1/55

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
2	133,532,954	138,070,206	4.2	1,139

Chr 2



Image size reduction: 1/54

Chr 3



Image size reduction: 1/44

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
4	56,474,015	111,255,851	46.4	9,989

Chr 4



Image size reduction: 1/38

Chr 5



Image size reduction: 1/40

Chr 6



Image size reduction: 1/45

Chr 7



Image size reduction: 1/36

Chr 8



Image size reduction: 1/35

Chr 9



Image size reduction: 1/31

### Chr 10



Image size reduction: 1/37

### Chr 11



Image size reduction: 1/34

### Chr 12



Image size reduction: 1/33

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
13	32,349,662	59,800,118	26.8	6,684
13	81,975,705	100,391,674	20.4	4,654
13	107,506,505	108,867,738	3.1	530

### Chr 13



Image size reduction: 1/26

### Chr 14



Image size reduction: 1/22

### Chr 15



Image size reduction: 1/21

### Chr 16

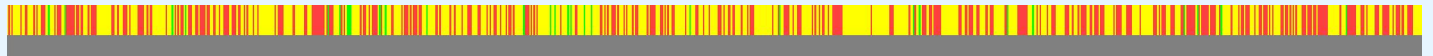


Image size reduction: 1/22

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
17	70,144,818	72,550,890	4.5	612

### Chr 17

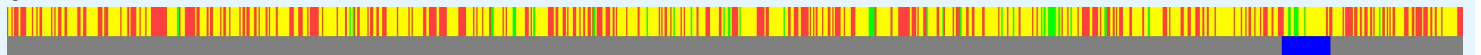


Image size reduction: 1/19

### Chr 18

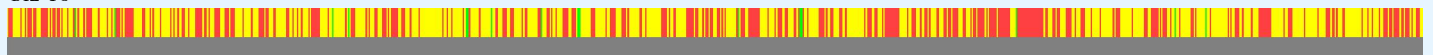


Image size reduction: 1/21

### Chr 19

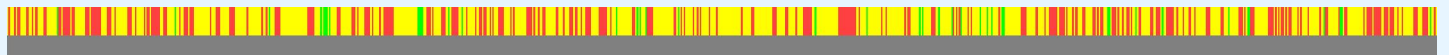


Image size reduction: 1/14

### Chr 20



Image size reduction: 1/18

### Chr 21



Image size reduction: 1/10

### Chr 22



Image size reduction: 1/10

Largest segment = 46.4 cM

Total of segments > 3 cM = 105.3 cM

Estimated number of generations to MRCA = 3.5

Comparison took 0.44814 seconds.