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Title	Recombination and purifying and balancing selection determine the evolution of major antigenic protein 1 (map 1) family genes in Ehrlichia ruminantium
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Table S1. Primers used in the present study.

Primer name	Direction	Sequence (5' to 3')	Position[a]
map_75F	Forward	TGCATTTTCATCACCACTTCC	75-95
map_675R	Reverse	TTGACCTATGCCAATGCAAA	675-656
map_897F	Forward	TGGTGGTGAAGTTGGTCTTAGAT	897-919
map_2265R	Reverse	GCTGATCTTGCTAACGCAAA	2265-2246
map_2976F	Forward	AACAGCACTCCCAATCCAT	2976-2994
map_3299R	Reverse	CAGCTGCTTGGAAAAACTCA	3299-3280
map_5516F	Forward	TCTGTCGGGTACTCGTCTCT	5516-5535
map_5775R	Reverse	TCTCCACCAATTCCTGTGC	5775-5757
map_6862F	Forward	TCGGATATTTTGGAGGAGAAG	6862-6882
map_7393R	Reverse	CTTTGGTCATACTGCGTGCT	7393-7374
map_8064F	Forward	CAGATTTTCAAGACAGCAGCA	8064-8084
map_8244R	Reverse	CCGCGTCTACCTACGGATCT	8244-8225
map_8390F	Forward	GACTTTTTCGATGCTACACATATCA	8390-8414
map_8459F	Forward	CCTGATGTTACATTATTTGTTGATGG	8459-8484
map_9239R	Reverse	TTGTGATGTAGAAAACTGATAGCAA	9239-9215
map_9315F	Forward	AAACTTGCGTGCCAAGTTAAA	9315-9335
map_9887R	Reverse	TCATAGCTGATATCATAGACATTCG	9887-9863
map_9968R	Reverse	ACACACAGCTCTGAAAAATTCTTAT	9968-9944
map_9945F	Forward	TCAGAATTTTTCAGAAATGTGTGTAT	9945-9970
map_10518R	Reverse	TGAAATTGTGCATGATATGGTGT	10518-10496
map_10538F	Forward	AGTGGCACTATYGGACAGTATYTG	10538-10561
map_10613F	Forward	AAAAACCCTGGATATTACGATG	10613-10634
map_10947F	Forward	TTGCAGATGGGTACTATCACAAA	10947-10969
map_11639R	Reverse	TCCAGTTCACGTGCTAATGC	11639-11620
map_11652F	Forward	TGAGCCAAAACCATATCAAYTAGAC	11652-11676
map_12037F	Forward	GGAGCCGAAGTTGGAATAAG	12037-12056
map_12538F	Forward	TCGGTCATAAACTACACGATGC	12538-12559
map_13045F	Forward	CTGGTAAATAAAATTTAGCTTAATGGA	13045-13071
map_13142R	Reverse	GTATACCAGTACCATTAGAATACTG	13142-13118
map_13134F	Forward	CTGGTATACATCATATGGTACATAC	13134-13158
map_K13209F	Forward	AGAAAACACTGTGATTAAACCAAATA	K13209-13234[b]
map_13699R	Reverse	GATGTTTTGTTTTTAATGTTGTTT	13699-13676
map_14198F	Forward	TAGCTTCCATACCTAAAAACAACAG	14198-14222
map_14209F	Forward	CCCAAAAACAACAGTATAGACTAGG	14209-14233
map_14431F	Forward	TCGTAAGAAGTGCGTTAATCTCAT	14431-14454
map_14491R	Reverse	GGTTCTGCAAAAGACTGATATGG	14491-14469
map_14767F	Forward	GAGTAGAGATTGAAGCTGCATAC	14767-14789
map_15197R	Reverse	GGAAGTGCTTTGAGGAGCAT	15197-15178
map_15186F	Forward	CAAAGCACTTCCGCTTCAGT	15186-15205
map_15315F	Forward	CGTAYATAAYAGGGAAAACATAGAG	15315-15339
map_15762F	Forward	TACATGCCAACTGCTTCACAT	15762-15782
map_15769F	Forward	CAACTGCTTCACACTTTGGTAAA	15769-15791
map_15945F	Forward	TTAGGTTTCGCTGGAGCAAT	15945-15964
map_16438F	Forward	GCTTTGCATCAGCAACACTT	16438-16457
map_16911F	Forward	TCTATGGTTCATCAGAATATAAACGTG	16911-16937
map_17223R	Reverse	TTCCTCTAGTATTATAGCAATAAAAAGC	17223-17196
map_17623R	Reverse	CATGTTTTGAGCTAATACATGTAATG	17623-17598
map_17867F	Forward	GACATCACAATAAAAACACACCTG	17867-17890
map_17890R	Reverse	CAGGTGTGTTTTTATTGTGATGTC	17890-17867

map_18281R	Reverse	TGCTATTTGGTGGTGGGTATT	18281-18261
map_18598R	Reverse	TTTCGGAGTTGAAAGGCAGT	18598-18579

[a]Conting from 3' end of the *map1-14* of Welgevonden (Erwo) strain. [b]Conting from 3' end of the *map1-14* of Kerr Seringe strain.

Table S2. The results of the test of goodness-of-fit and selective neutrality tests and their associated *p*-values.

gene	SSD (*p*-value)	"r" (*p*-value)	Tajima's *D*	Fu's
HG	0.081 (0.01)	0.166 (0.05)	0.65249	2.989
map1	0.025 (0.05)	0.037 (0.05)	0.46226	2.243
map1-1	0.086 (0.05)	0.145 (0.05)	0.26555	0.370
map1+1	0.034 (0.10)	0.067 (0.00)	1.03057	2.362
map1-2	0.050 (0.00)	0.082 (0.00)	1.85858	5.276
map1-3	0.061 (0.05)	0.109 (0.00)	-1.28350	1.752
map1-4	0.019 (0.55)	0.046 (0.35)	-1.25604	-1.091
map1-5	0.028 (0.60)	0.039 (0.50)	1.14465	1.826
map1-6	0.043 (0.00)	0.077 (0.05)	1.47022	3.577
map1-7	0.092 (0.30)	0.114 (0.10)	0.07468	2.085
map1-8	0.042 (0.20)	0.043 (0.45)	0.21759	0.437
map1-9	0.043 (0.20)	0.043 (0.30)	0.27100	-0.303
map1-10	0.089 (0.25)	0.126 (0.20)	0.08336	2.662
map1-11	0.037 (0.50)	0.025 (0.80)	0.40045	0.247
map1-12	0.892 (0.00)	0.102 (1.00)	0.09657	1.540
map1-13	0.048 (0.10)	0.077 (0.05)	0.70184	4.177
map1-14	0.020 (0.25)	0.037 (0.15)	0.08688	0.540

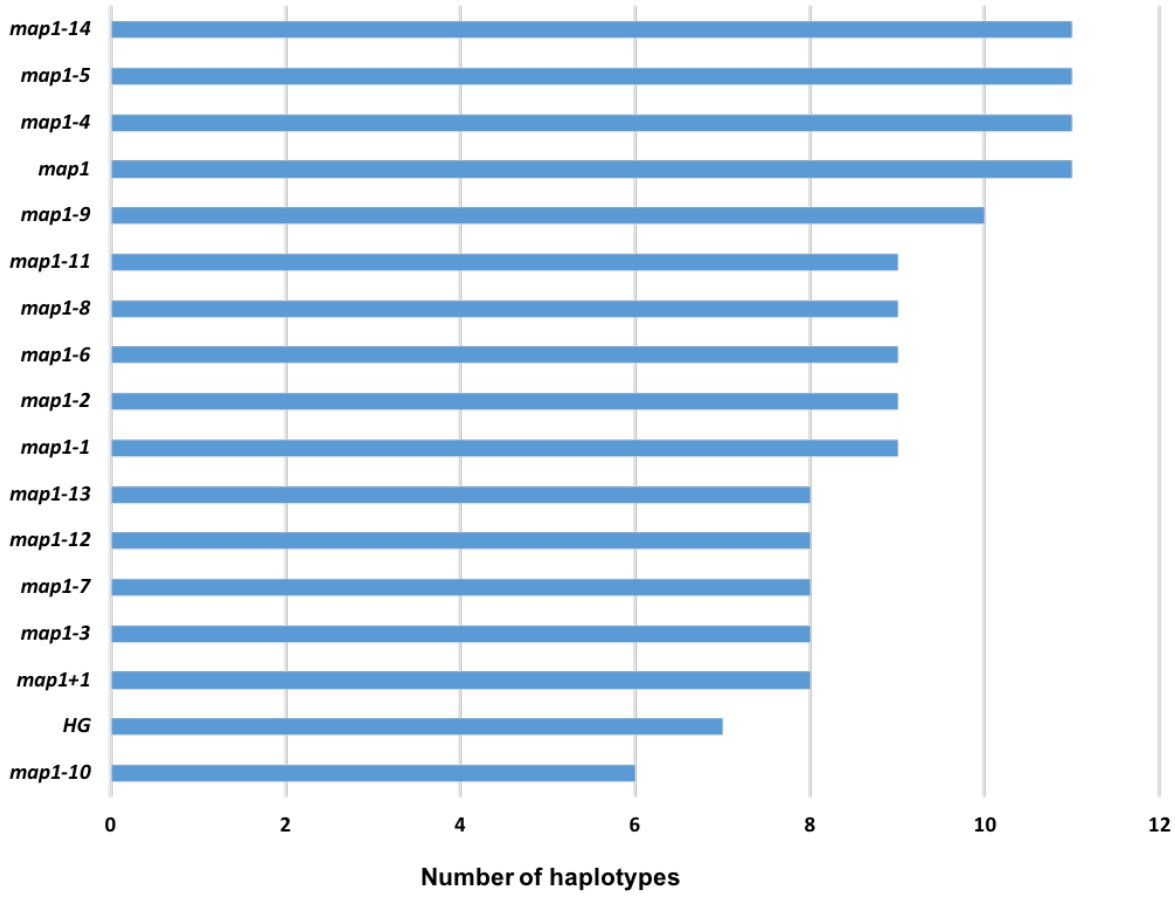


Figure S1. Number of haplotype of *map1* family genes.

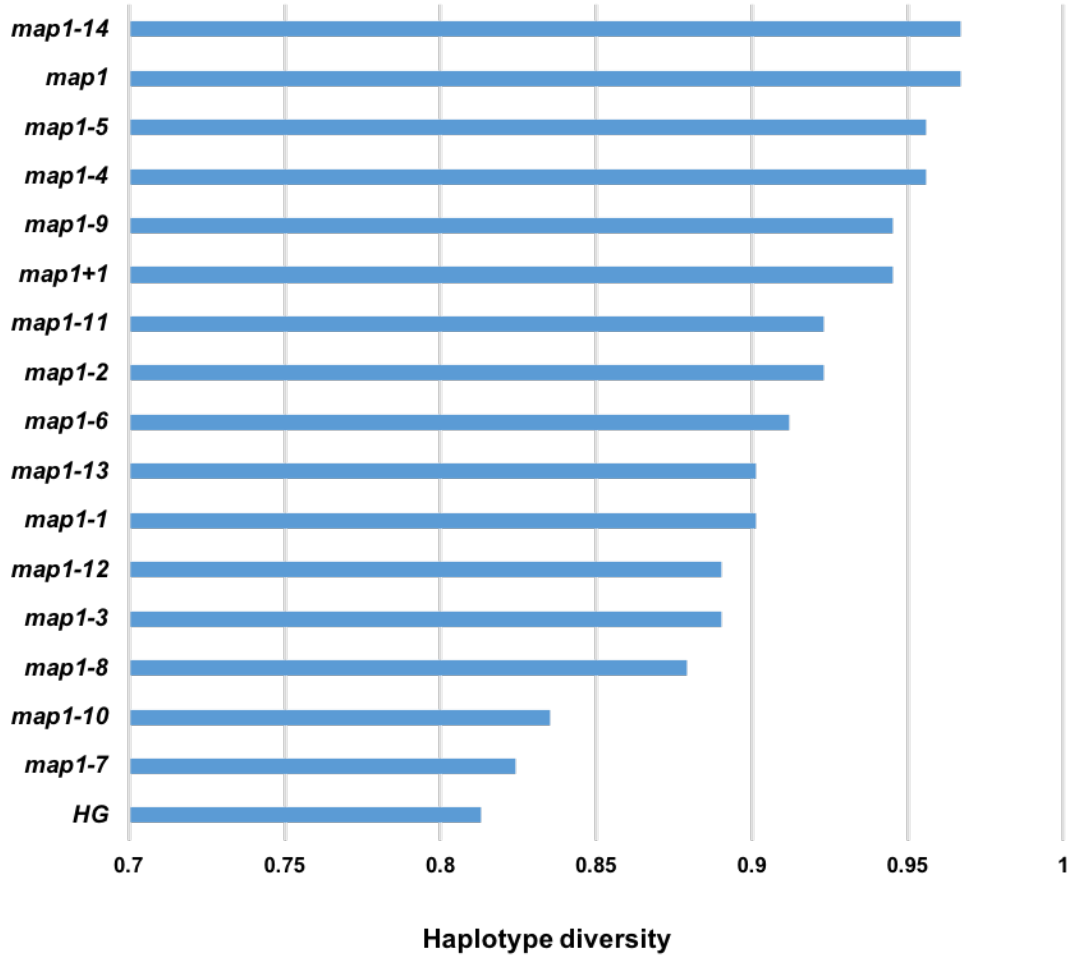
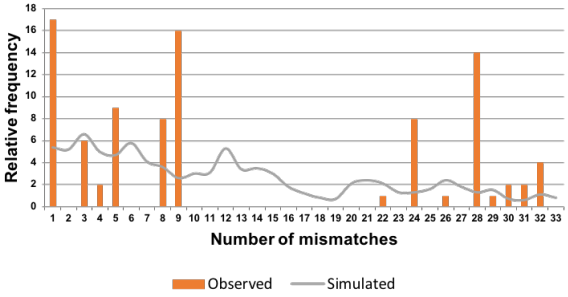
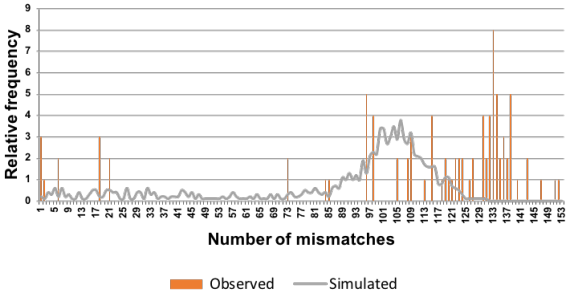


Figure S2. Haplotype diversity of *map1* family genes.

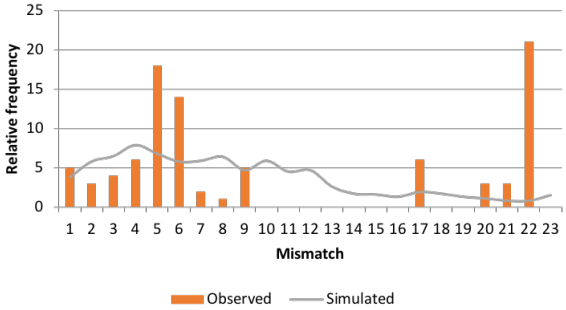
A: *HG*



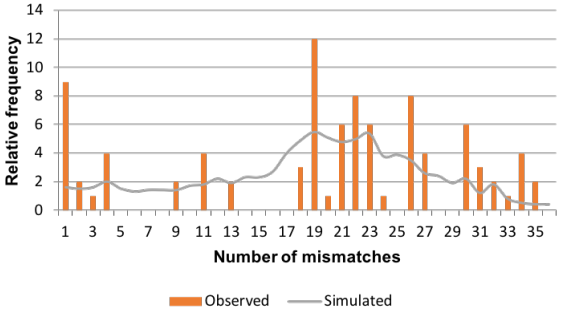
C: *map1*



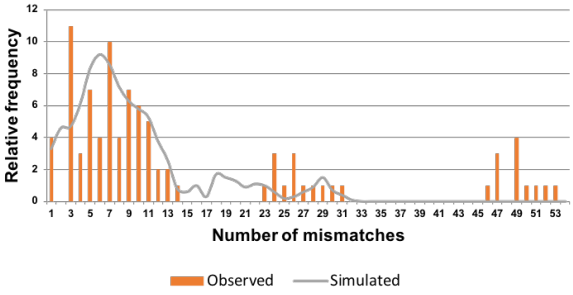
B: *map1-1*



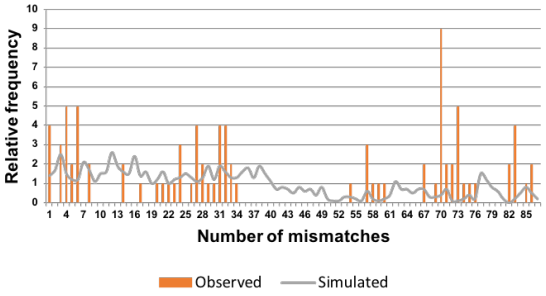
D: *map1+1*



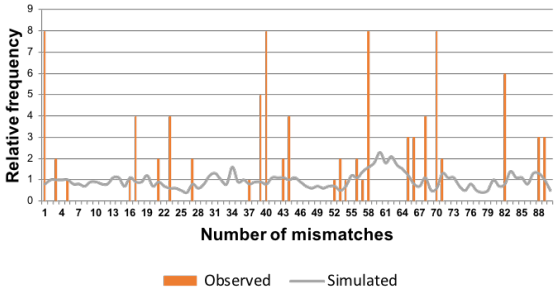
E: *map1-4*



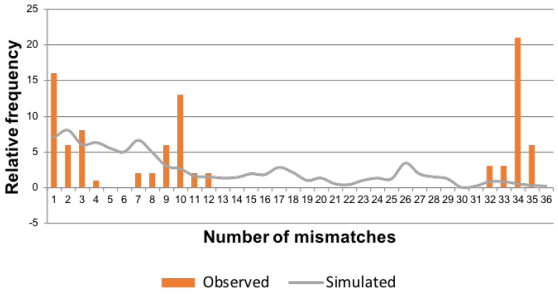
G: *map1-5*



F: *map1-6*



H: *map1-7*



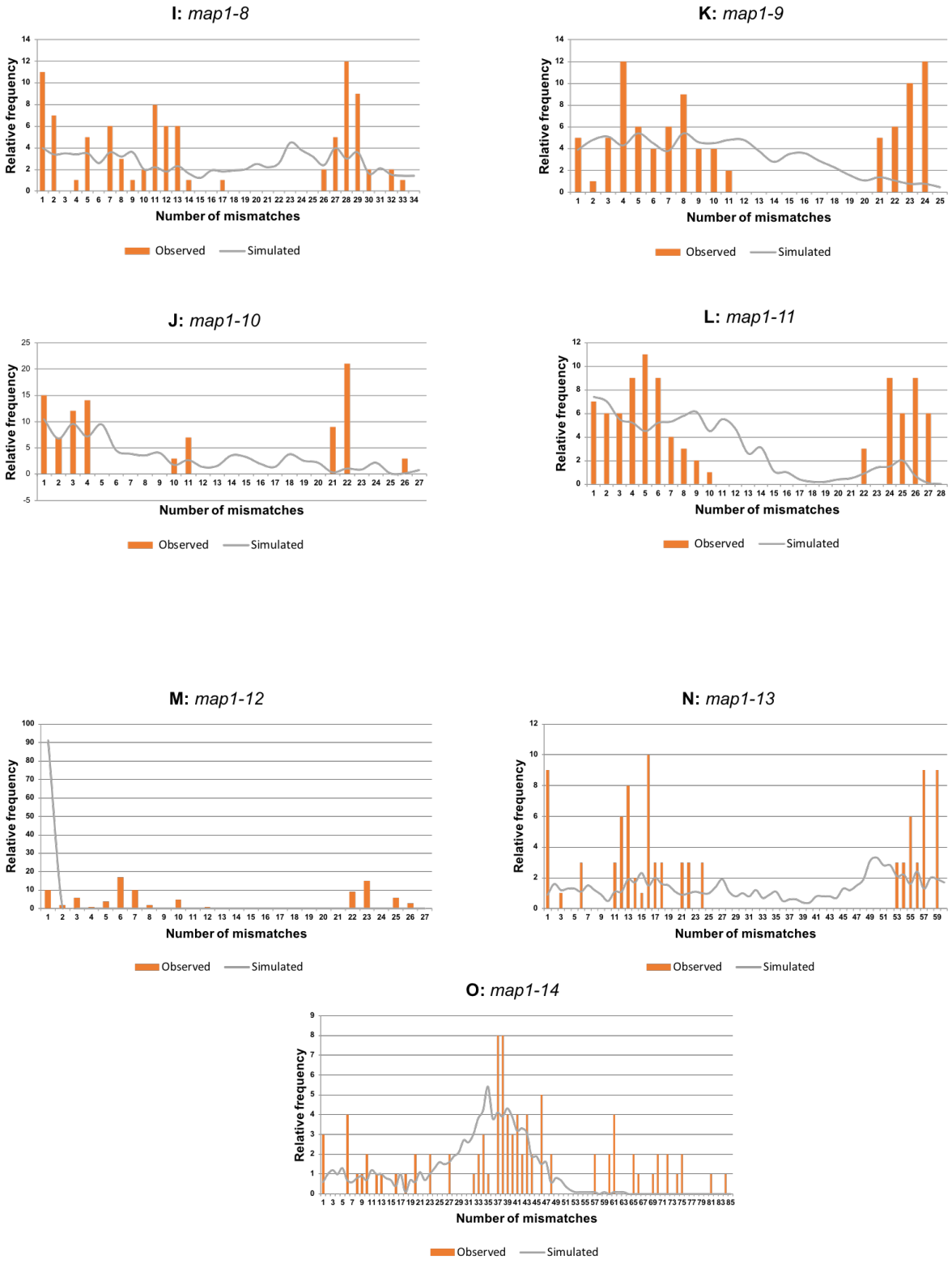


Figure S3. Mismatch distribution pattern of pairwise differences between sequences of *map1* family genes. The goodness-of-fit measures quantified the smoothness of the observed mismatch distribution and a non-significant result indicates an expanding population. But these results revealed the opposite as multimodal as is dominated.

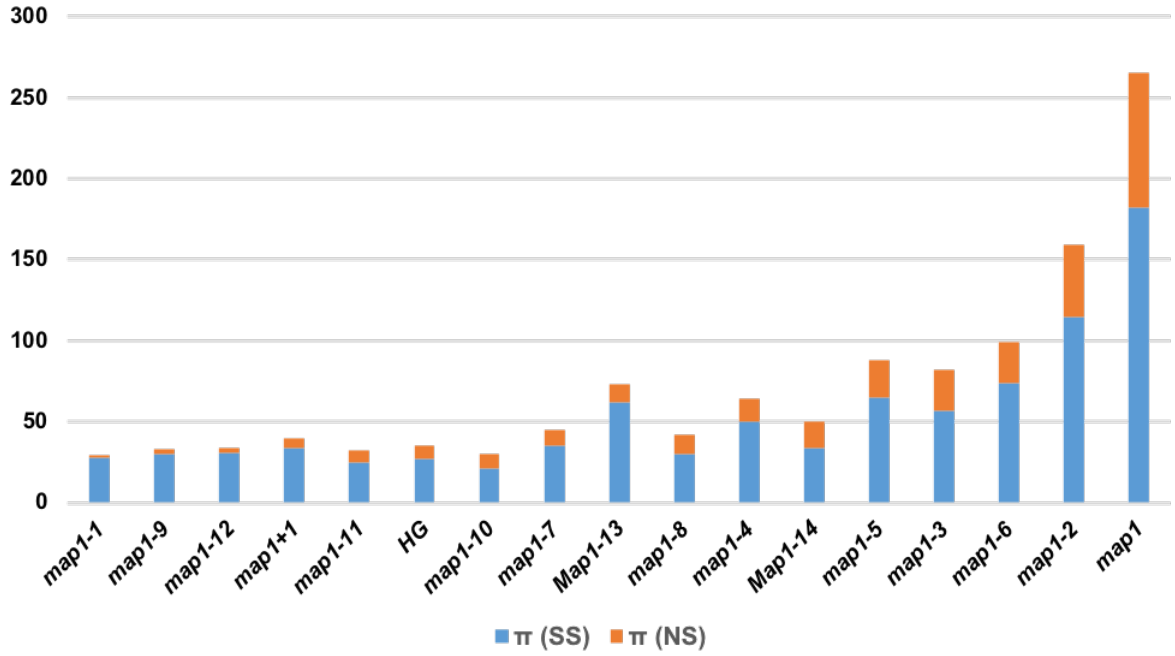


Figure S4. Synonymous and nonsynonymous nucleotide substitutions of *map1* family genes.