Table S1. Summary of the analysis of 23 pairs of sequences.

Class	# of genes	Gene A	Gene B	Significant region(|Z| > 1.96); 1 = detected, 0 = not detected			
				M	I	K	C
A	3	FBP29	FBP26	0	0	0	1
		FBP29	PFG	0	0	1	1
		FBP26	PFG	0	0	0	0
B-AP3	2	Not analyzed					
B-PI	2	FBP1	PMADS2	0	1	0	0
C	2	PMADS3	FBP6	0	0	0	0
D	2	FBP11	FBP7	0	0	0	0
E	5	FBP9	FBP23	0	0	0	0
		FBP9	FBP4	0	0	0	0
		FBP9	FBP2	0	0	0	0
		FBP9	FBP5	0	0	1	0
		FBP23	FBP4	0	0	1	0
		FBP23	FBP2	0	0	1	0
		FBP23	FBP5	0	0	1	0
		FBP4	FBP2	0	0	0	0
		FBP4	FBP5	0	0	1	0
		FBP2	FBP5	0	0	1	0
F	4	FBP20-UNS	FBP21	0	0	0	0
		FBP20-UNS	FBP28	0	0	0	0
		FBP21	FBP28	0	0	1	0
		FBP20-UNS	FBP22	1	0	0	0
		FBP21	FBP22	0	0	1	0
		FBP28	FBP22	0	0	1	0
G	1	Not analyzed					
T	2	FBP13	FBP25	0	1	1	1
Total	23 genes	23 pairs		1	2	11	3
				14 pairs*			

*Some pairs showed significant rate differences in more than one domain.