Table S1 Observed and expected genotype association

Matrices showing the number of mites we observed (top) and expected (bottom) for each of the ten most prevalent genotypes combinations (G1–G10) and combinations with other genotypes (Others). *F* represents the overall frequency of each genotype sampled in the colonies. The *F* was used to calculate the expected frequencies of each genotype association and overall. Recombinant genotypes are italicized.

Observed	**G1**	**G2**	**G3**	**G4**	*G5*	*G6*	**G7**	**G8**	**G9**	**G10**	**Others**
G1	47	49	22	8	13	9	7	3	2	4	54
G2		12	8	5	10	7	5	5	3	1	27
G3			4	3	2	1	1	2	5	1	13
G4				2	0	4	0	1	0	0	11
G5					0	1	0	0	1	0	10
G6						0	1	1	0	0	2
G7							0	0	0	0	7
G8								0	1	0	5
G9									0	0	0
G10										0	3
Others											10

Expected		**G1**	**G2**	**G3**	**G4**	*G5*	*G6*	**G7**	**G8**	**G9**	**G10**	**Others**
	F	0.336	0.183	0.084	0.046	0.046	0.033	0.028	0.023	0.015	0.013	0.193
G1	0.336	44	48	22	12	12	9	7	6	4	3	51
G2	0.183		13	12	7	7	5	4	3	2	2	28
G3	0.084			3	3	3	2	2	2	1	1	13
G4	0.046				1	2	1	1	1	1	0	7
G5	0.046					1	1	1	1	1	0	7
G6	0.033						0	1	1	0	0	5
G7	0.028							0	1	0	0	4
G8	0.023								0	0	0	3
G9	0.015									0	0	2
G10	0.013										0	2

Others	0.193		15