Table S1. Sequencing, mapping, and normalization factors for the experimental populations A and B and the respective offspring populations A' and B'

	A	B	A'	B'
sequence reads	44,860,778	45,748,016	39,701,327	38,515,061
uniquely mapped reads	27,210,806 (60.66%)	27,901,537 (58,80%)	28,562,044 (71.94%)	28,479,574 (73.94%)
unalignable reads	9,580,791 (21.37%)	10,096,077 (22.07%)	3,882,210 (9.78%)	2,710,235 (7.04%)
reads suppressed by uniqueness command	8,069,181 (17.99%)	8,750,412 (19.13%)	7,257,073 (18.28%)	7,325,252 (19.02%)
normalization factor "housekeeping genes"	1	1.012	0.655	0.907