Extra from Homework 3, Q1:

B-locus	A-locus A_1A_1	A_1B_1	B_1B_1
A_2A_2	143	17	2
A_2B_2	35	(5)	0
B_2B_2	3	0	0

If there are any B_1B_2 they will most likely show as double-heterozygotes, as A_1A_2 is the common haplotype.

#(A_1A_2) = 2*143 + 35 + 17 + 5x = 338 + 5x; $q_1 = (338+5x)/410$
#(A_1B_2) = 35 + 2*3 + 5(1-x) = 41 + 5(1-x); $q_2 = (46-5x)/410$
#(B_1A_2) = 17 + 2*2 + 5(1-x) = 21 + 5(1-x); $q_3 = (26-5x)/410$
#(B_1B_2) = 5x

If $x = 0$, $2q_2q_3 = 0.014$ and expected double-hetzs is 2.9.

The fact that we see 5 is some (slight) evidence that there is maybe at least one B_1B_2 haplotype in the sample:
EM estimates q_4 as about 0.005, so expected #(B_1B_2) is $410q_4 \approx 2$.