

Table 2. Comparison of haplotype frequencies.

Haplotype	Homo. Count	Freq. ($\sqrt{\text{Homo. Count}}$)	Freq. (EM)
<i>AAGA AAAG</i>	171	.439	.437
<i>GGAG AAAG</i>	74	.289	.288
<i>GGAG CGGA</i>	66	.272	.269
<i>AAAA AAAG</i>	0	.0	.004
<i>AAGA CGGA</i>	0	.0	.002
Total		1.0	1.0

Observed three major haplotypes and two minor haplotypes are shown on the first column in conjunction with their counts of homozygous pairs on the second column. Relative frequencies of square root of the homozygous counts (the total sum is normalized to 1) and the corresponding haplotype frequencies estimated by using EM algorithm from the same data set are also shown on the third and fourth columns. The square roots of the homozygous counts divided by the total sum are quite similar to the haplotype frequencies estimated by the EM algorithm, although the precise frequency of each minor haplotype cannot be obtained from the textile plot.