









## GWAS activities

1. In the following table, identify which genotypes correlate with coat color. Are the SNPs that are close to the most strongly correlated gene also correlated to coat color? Why?

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
	CC	AT	CC	GG	AA	TC	TT	CC	GG	AA	TT	GT	AG	AA	CC	GG	AT
	CC	AT	AC	GG	GG	TT	TT	CC	GG	AG	TT	GG	AG	AG	CC	GG	AT
	CC	AA	AC	CG	GG	TT	TT	CT	GG	AA	TT	GT	AG	AG	CC	TT	AT
	CC	AA	AC	GG	AG	TT	TT	CT	GG	GG	TT	GG	AG	AG	CC	GT	AT
	CC	AT	CC	CG	AA	TT	AA	CT	GG	AA	TT	GT	AA	AA	CC	GT	AT
	CC	AT	CC	GG	AA	TT	AA	TC	GG	AA	TT	GG	AG	AA	CC	GG	TT
	CC	AT	CC	GG	AA	TT	AA	CC	GG	AA	TT	GG	AA	AA	CC	GT	AT
	CC	AA	CC	GG	AG	TT	AA	TC	GG	GG	TT	GG	AA	AA	CC	TT	AT

**Table 1. Nucleotides at 17 Different Loci in Two Groups of Dogs.**

2. In the envelope, you will find a series of strips that are the genotypes of dogs. You should use these strips to identify the gene locus that you think correlates most strongly with long/short difference. The following table might help you identify the locus

<b>Locus</b>	<b>Allele</b>	<b>Short Coat</b>	<b>Long Coat</b>	<b>Difference</b>
				Total number of differences

Then, determine the  $\chi^2$  of this locus. Please calculate by allele, not genotype (1 not 2 df). The following tables may be helpful.

<b>Allele</b>	<b>Short</b>	<b>Long</b>	<b>Expected</b>

Given this  $\chi^2$ , is this significant?

	P										
<b>DF</b>	<b>0.995</b>	<b>0.975</b>	<b>0.20</b>	<b>0.10</b>	<b>0.05</b>	<b>0.025</b>	<b>0.02</b>	<b>0.01</b>	<b>0.005</b>	<b>0.002</b>	<b>0.001</b>
<b>1</b>	0.0000393	0.000982	1.642	2.706	3.841	5.024	5.412	6.635	7.879	9.550	10.828
<b>2</b>	0.0100	0.0506	3.219	4.605	5.991	7.378	7.824	9.210	10.597	12.429	13.816
<b>3</b>	0.0717	0.216	4.642	6.251	7.815	9.348	9.837	11.345	12.838	14.796	16.266
<b>4</b>	0.207	0.484	5.989	7.779	9.488	11.143	11.668	13.277	14.860	16.924	18.467
<b>5</b>	0.412	0.831	7.289	9.236	11.070	12.833	13.388	15.086	16.750	18.907	20.515

If you have time, do it for the curly/strait phenotype.

3. Why do GWAS usually find common variants with moderate to large effects?