









## Worksheet for GWAS lab

### Part 1: Mapping Genes to Traits in Dogs Using SNPs:

A particular SNP is 100% associated with coat color when *all* dogs with white fur have the same nucleotide at a particular position, while *all* dogs with black fur have another nucleotide.

SNPs are not associated to fur color, when they occur with about equal frequency in dogs with black fur and dogs with white fur.

**Table 1. Nucleotides at 17 different loci in two groups of dogs.**

	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

1. Draw a circle around the SNP(s) in Table 1 that are 100% associated with coat color. What is the locus number(s) for the 100% associated SNP(s)? \_\_\_\_\_.
2. Draw a rectangle around the SNP(s) in Table 1 that are “somewhat associated” to coat color. What is the locus number(s) for the somewhat associated SNP(s)? \_\_\_\_\_.
3. What is the locus number(s) for the SNP(s) that are not associated to fur color? \_\_\_\_\_.

### Part 2: Mapping coat and hair type traits

You will be provided with either coat length cards or hair type cards. Organize your cards (there are two different sets: short vs. long coat, or curly vs. straight hair).

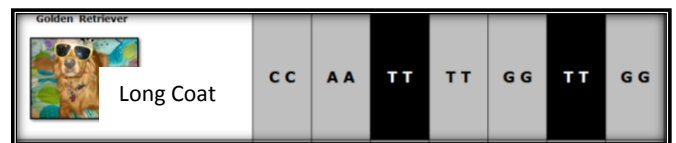
- Place the loci strip at the top.
- Make a pile for each card type (short vs. long or curly vs. straight) - you should have two piles.
- Line the cards up below the loci strip.

Example:

Loci strip:

Dog	Coat Length	chr32 7420804	chr32 7472206	chr32 7473337	chr32 7479580	chr32 7482867	chr32 7490570	chr32 7492364
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Two card types:



4. Count the number of nucleotides for each type and record on the following charts (the first loci is an example):

SNP locus	Allele	Trait 1	Trait 2	Difference
		Short Coat	Long Coat	
Chr32 7420804	T	4	4	0
	C	8	8	0
			Total number of differences	0

SNP locus 1	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

SNP locus 2	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

SNP locus 3	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

SNP locus 4	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

SNP locus 5	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

SNP locus 6	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

SNP locus 7	Allele	Trait 1	Trait 2	Difference
			Total number of differences	

- Which SNP (or SNPs) is most strongly associated with the trait you are exploring? (Write the SNP locus or loci in the space.) \_\_\_\_\_.
- Which SNP (or SNPs) is least associated with the trait you are exploring? \_\_\_\_\_.

**Part 3: Chi-Square Analysis (Short Coat vs. Long Coat; Curly Hair vs. Straight Hair)**

$$\chi^2 = \sum \frac{(o - e)^2}{e}$$

Example:

Coat Length, SNP Locus: 7473337

Total # of alleles	Expected # of alleles
G=9	9/2 = 4.5
T=15	15/2 = 7.5

SNP/Allele	Short	Long	Expected
G	9	0	4.5
T	3	12	7.5

Short:  $\frac{(9-4.5)^2}{4.5} + \frac{(3-7.5)^2}{7.5}$       Long:  $\frac{(0-4.5)^2}{4.5} + \frac{(12-7.5)^2}{7.5}$        $\chi^2 = 4.5 + 2.7 + 4.5 + 2.7 = 14.4$

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

Chi square = 14.4  
p value < 0.001

7. Complete the table below for the SNP with the strongest association for the trait you are exploring.

SNP/Allele	Trait 1	Trait 2	Expected

8. Use the space below to show your calculations of the expected allele distribution for this SNP:

9. Calculate the chi-square value (show your work):

10. Record the chi-square value\_\_\_\_\_.

11. Using the chi-square distribution table above record the  $p$ -value for the SNP with the strongest association: \_\_\_\_\_.

12. What does this  $p$ -value tell you?