

PRACTICE ANALYZING DELETION MAPPING

D.B. Fankhauser, revised 18 Feb 2009

Strains 1 through 5 carry mutations in a gene and were mapped using deletion mapping by transduction. The mutants were crossed times the known mutants (a through g) carrying deletions as indicated (xxx means the material has been deleted). If wild type recombinants appear, it is scored +; if none are produced it is scored 0.

On the dotted lines below the deletions, indicate with an "H" bar the limits of the region in which the point mutation is located relative to the various deletion mutations. Be certain to line up the limits correctly with the deletion mutations above.

Mutants:						Del :	
samp	1	2	3	4	5		
+	+	+	+	+	+	a	XXXXXXXX-----
+	+	+	0	0	+	b	-----XXXXXXXXXXXXXXXXXXXX
+	0	+	0	0	+	c	-----XXXXXXXXXXXXXXXXXXXXXXXXXXXX
0	+	+	+	+	0	d	-----XXXXXXXXXXXXXXXXXXXX-----
+	+	+	0	+	+	e	-----XXXXXXXX-----
0	+	0	+	+	+	f	XXXXXXXXXXXXXXXX-----
0	0	0	0	+	0	g	---XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-----

mutant: Draw your "H" bars here:

Sample
 1
 2
 3
 4
 5

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0	+	0	+	+	+	f	XXXXXXXXXXXXXXXX-----
0	0	0	0	+	0	g	---XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-----

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