A) *D. miranda* – Four-fold degenerate sites for unpreferred codons, Chromosome 2:

Response: Within *D. miranda* diversity

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			153	281.46		
Gene Density	1	2.426	152	279.04	1.6283	0.20397
Mutation	1	7.209	151	271.83	4.8394	0.02940 *
Recombination	**1**	**33.149**	**150**	**238.68**	**22.2531**	**<0.0001***
GC	1	8.832	149	229.85	5.9286	0.01611*
Gene Density*Mutation	1	5.595	148	224.25	3.7558	0.05457
Gene Density*Recombination	1	2.018	147	222.23	1.3544	0.24642
GC*Mutation	1	4.324	146	217.91	2.9025	0.09058
GC*Recombination	1	1.527	145	216.38	1.0254	0.31294

B) *D. miranda* - Four-fold degenerate sites for unpreferred codons, Chromosome 2:

Response: *D. miranda-D. pseudoobscura* divergence

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			153	291.64		
Gene Density	1	0.1275	152	291.52	0.0797	0.778150
Mutation	1	30.0005	151	261.51	18.7390	<0.00001*
Recombination	**1**	**0.0879**	**150**	**261.43**	**0.0549**	**0.815105**
GC	1	12.7503	149	248.68	7.9641	0.005442*
Gene Density*Mutation	1	2.6918	148	245.99	1.6813	0.196807
Gene Density*Recombination	1	0.1692	147	245.82	0.1057	0.745599
GC*Mutation	1	3.5827	146	242.23	2.2378	0.136846
GC*Recombination	1	2.3182	145	239.91	1.4480	0.230811

C) Flagstaff recombination map- Four-fold degenerate sites for unpreferred codons, Chromosome 2:

Response: *D. pseudoobscura-D. pseudoobscura* diversity

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			139	365.73		
Gene Density	1	1.203	138	364.53	0.6368	0.42630
Mutation	1	41.299	137	323.23	21.8673	<0.00001*
Recombination	**1**	**37.580**	**136**	**285.65**	**19.8980**	<0.00001*
GC	1	17.212	135	268.44	9.1136	0.00305*
Gene Density*Mutation	1	5.129	134	263.31	2.7159	0.10175
Gene Density*Recombination	1	0.767	133	262.54	0.4060	0.52512
GC*Mutation	1	1.163	132	261.38	0.6160	0.43397
GC*Recombination	1	0.334	131	261.05	0.1769	0.67477

D) Flagstaff recombination map- Four-fold degenerate sites for unpreferred codons, Chromosome 2:

Response: *D. miranda-D.pseudoobscura* divergence

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			139	279.92		
Gene Density	1	2.028	138	277.89	1.3105	0.254400
Mutation	1	48.277	137	229.61	31.1908	<0.00001*
Recombination	**1**	**0.175**	**136**	**229.44**	**0.1131**	**0.737167**
GC	1	11.796	135	217.64	7.6212	0.006596 *
Gene Density*Mutation	1	6.257	134	211.39	4.0424	0.046423*
Gene Density*Recombination	1	0.205	133	211.18	0.1326	0.716290
GC*Mutation	1	1.228	132	209.95	0.7935	0.374677
GC*Recombination	1	2.246	131	207.71	1.4510	0.230544

E) Pikes Peak recombination map-- Four-fold degenerate sites for unpreferred codons, Chromosome 2:

Response: *D. pseudoobscura-D. pseudoobscura* diversity

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			157	403.80		
Gene Density	1	0.747	156	403.05	0.3962	0.53000
Mutation	1	40.007	155	363.05	21.2219	<0.00001*
Recombination	**1**	**42.366**	**154**	**320.68**	**22.4733**	**<0.00001***
GC	1	17.237	153	303.44	9.1433	0.00294*
Gene Density*Mutation	1	1.485	152	301.96	0.7875	0.37629
Gene Density*Recombination	1	7.733	151	294.23	4.1022	0.04461*
GC*Mutation	1	1.479	150	292.75	0.7845	0.37719
GC*Recombination	1	0.154	149	292.59	0.0816	0.77548

F) Pikes Peak recombination map-- Four-fold degenerate sites for unpreferred codons, Chromosome 2:

Response: *D. miranda-D. pseudoobscura* divergence

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			157	315.47		
Gene Density	1	2.392	156	313.08	1.5127	0.220672
Mutation	1	47.810	155	265.27	30.2330	<0.00001*
Recombination	**1**	**1.010**	**154**	**264.26**	**0.6389**	**0.425380**
GC	1	12.046	153	252.22	7.6172	0.006508*
Gene Density*Mutation	1	5.578	152	246.64	3.5274	0.062317
Gene Density*Recombination	1	0.362	151	246.28	0.2292	0.632844
GC*Mutation	1	1.433	150	244.84	0.9065	0.342596
GC*Recombination	1	7.712	149	237.13	4.8770	0.028744 *