

A) *D. miranda* - Four-fold degenerate sites for unpreferred codons, XR chromosome arm:

Response: Within *D. miranda* diversity

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			113	189.31		
Gene Density	1	19.3165	112	169.99	14.7325	0.000212*
Mutation	1	4.0318	111	165.96	3.0750	0.082422
Recombination	1	3.6666	110	162.29	2.7965	0.097450
GC	1	12.0835	109	150.21	9.2159	0.003026*
Gene Density*Mutation	1	1.7380	108	148.47	1.3256	0.252209
Gene Density*Recombination	1	2.2921	107	146.18	1.7482	0.188979
GC*Mutation	1	4.1785	106	142.00	3.1869	0.077120
GC*Recombination	1	0.2356	105	141.77	0.1797	0.672503

B) *D. miranda* - Four-fold degenerate sites for unpreferred codons, XR chromosome arm:

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

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			113	150.03		
Gene Density	1	0.4358	112	149.60	0.4091	0.52382
Mutation	1	25.7548	111	123.84	24.1743	<0.00001*
Recombination	1	2.2430	110	121.60	2.1054	0.14976
GC	1	6.2611	109	115.34	5.8769	0.01705 *
Gene Density*Mutation	1	0.0689	108	115.27	0.0646	0.79979
Gene Density*Recombination	1	1.8244	107	113.44	1.7124	0.19353
GC*Mutation	1	1.4378	106	112.01	1.3496	0.24798
GC*Recombination	1	0.1440	105	111.86	0.1352	0.71385

C) *D. pseudoobscura* – Flagstaff- Four-fold degenerate sites for unpreferred codons, XR chromosome arm:

Response: Within *D. pseudoobscura* diversity

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			136	340.12		
Gene Density	1	0.9072	135	339.21	0.4275	0.514404
Mutation	1	13.1025	134	326.11	6.1740	0.014255 *
Recombination	1	16.3881	133	309.72	7.7222	0.006276 *
GC	1	7.8689	132	301.85	3.7079	0.056372
Gene Density*Mutation	1	6.7494	131	295.10	3.1804	0.076898
Gene Density*Recombination	1	2.1753	130	292.93	1.0250	0.313240
GC*Mutation	1	1.9675	129	290.96	0.9271	0.337426
GC*Recombination	1	0.1473	128	290.81	0.0694	0.792639

D) *D. pseudoobscura* – Flagstaff- Four-fold degenerate sites for unpreferred codons, XR chromosome arm:

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

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			136	191.95		
Gene Density	1	0.061	135	191.89	0.0583	0.809536
Mutation	1	37.210	134	154.68	35.5459	<0.00001*
Recombination	1	0.219	133	154.46	0.2096	0.647832
GC	1	10.574	132	143.89	10.1008	0.001858 *
Gene Density*Mutation	1	0.022	131	143.86	0.0207	0.885836
Gene Density*Recombination	1	0.171	130	143.69	0.1632	0.686941
GC*Mutation	1	4.749	129	138.94	4.5362	0.035099 *
GC*Recombination	1	0.014	128	138.93	0.0130	0.909472

E) *D. pseudoobscura* – Pikes Peak- Four-fold degenerate sites for unpreferred codons, XR chromosome arm:

Response: Within *D. pseudoobscura* diversity

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			130	348.84		
Gene Density	1	8.867	129	339.98	4.4927	0.036066 *
Mutation	1	23.251	128	316.72	11.7803	0.000818*
Recombination	1	16.148	127	300.58	8.1813	0.004981*
GC	1	32.477	126	268.10	16.4545	<0.00001*
Gene Density*Mutation	1	19.330	125	248.77	9.7939	0.002191*
Gene Density*Recombination	1	2.887	124	245.88	1.4626	0.228853
GC*Mutation	1	0.916	123	244.97	0.4639	0.497078
GC*Recombination	1	0.000	122	244.97	0.0001	0.993139

F) *D. pseudoobscura* – Pikes Peak- Four-fold degenerate sites for unpreferred codons, XR chromosome arm:

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

	Df	Deviance	Resid.Df	Resid. Dev	F	Pr(>F)
NULL			130	186.13		
Gene Density	1	0.017	129	186.11	0.0172	0.89577
Mutation	1	40.047	128	146.06	40.2343	<0.00001*
Recombination	1	0.094	127	145.97	0.0944	0.75922
GC	1	16.499	126	129.47	16.5766	<0.00001*
Gene Density*Mutation	1	3.239	125	126.23	3.2540	0.07372
Gene Density*Recombination	1	0.130	124	126.10	0.1308	0.71823
GC*Mutation	1	2.508	123	123.59	2.5201	0.11499
GC*Recombination	1	0.086	122	123.51	0.0862	0.76954