All supplementary plots and tables show results for the following 7 sets of parameter values:

A) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 2 dimensions. This is identical to the figures in the main text

B) $\mu = 10^{-4}$, $\theta = 1$, $\lambda = 1/2$ and 2 dimensions

C) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 2$ and 2 dimensions

D) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/4$ and 2 dimensions

E) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 3 dimensions

F) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 4 dimensions

G) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 7 dimensions

Figure S1. Phenotypic distribution of homozygous alleles as in Figure 1 for all sets of parameter values. For simulations containing more than two dimensions (plots E-G), only the first two dimensions are shown.

Figure S2. Epistasis as a function of overdominance as in Figure 3 for all sets of parameter values.

Figure S3. Maximum pairwise distance statistic as in Figure 4 for all sets of parameter values.

Figure S4. Maximum distance from optimal trajectory statistic as in Figure 5 for all sets of parameter values.

Figure S5. Effective number of paths statistic as in Figure 6 for all sets of parameter values.

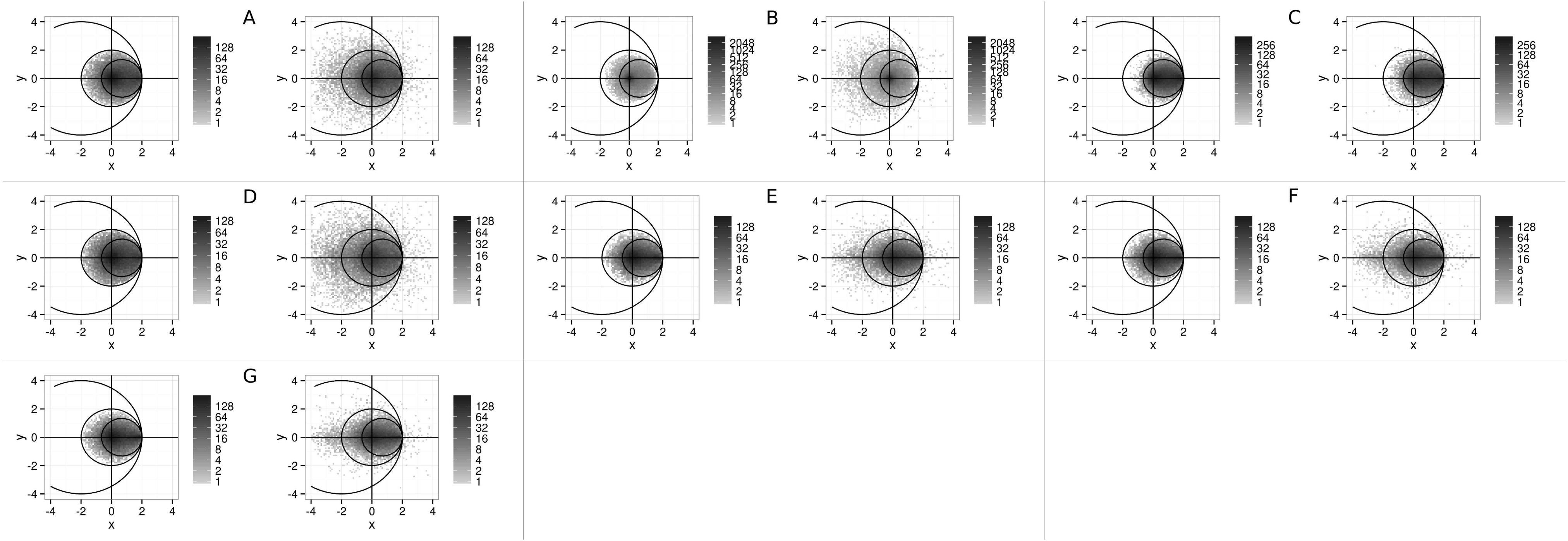
Figure S6. Mean path divergence statistic as in Lobkovsky et. al. (2011) for all sets of parameter values.

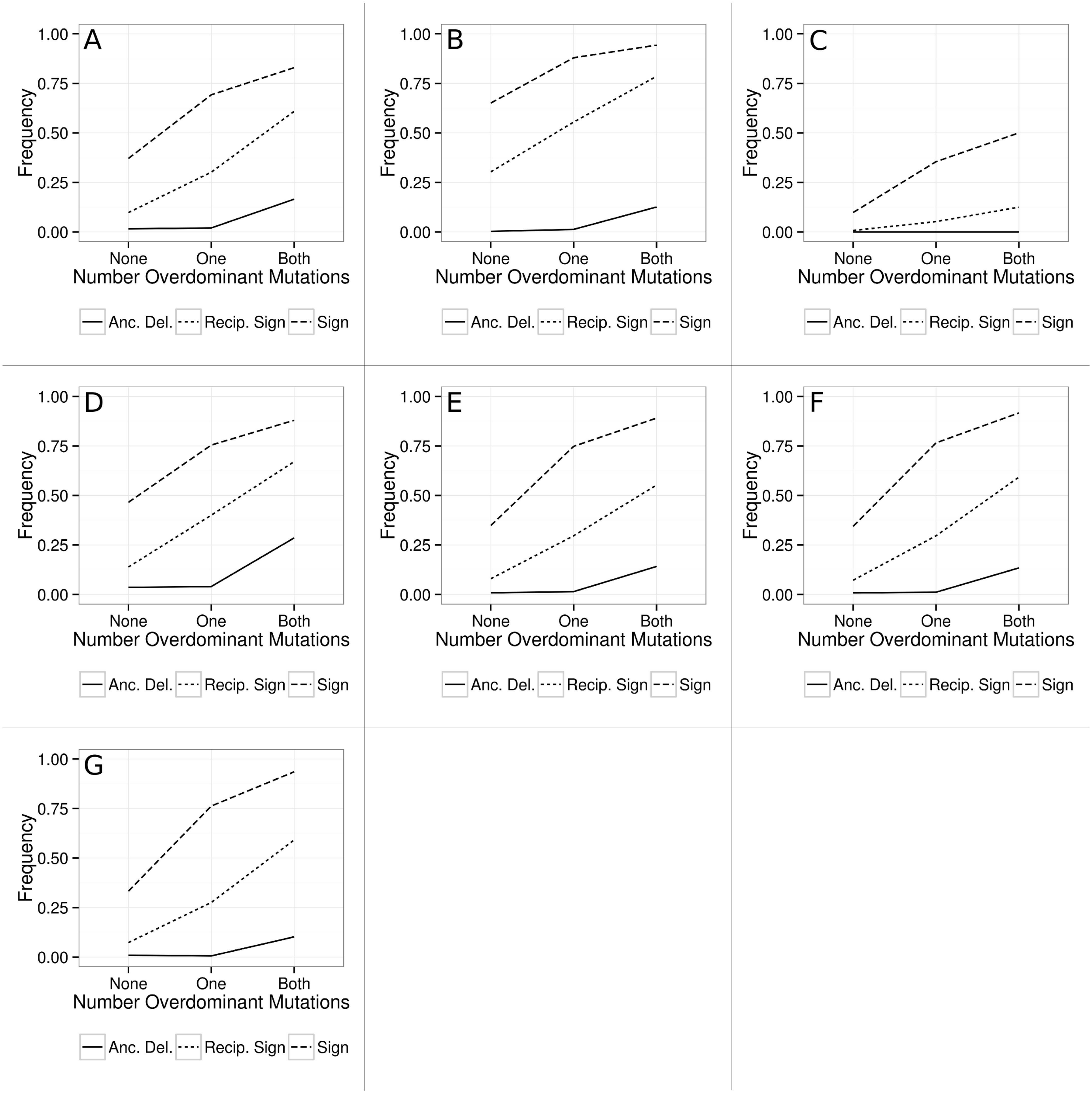
Table S1. Pairwise Epistasis (n=5,000)

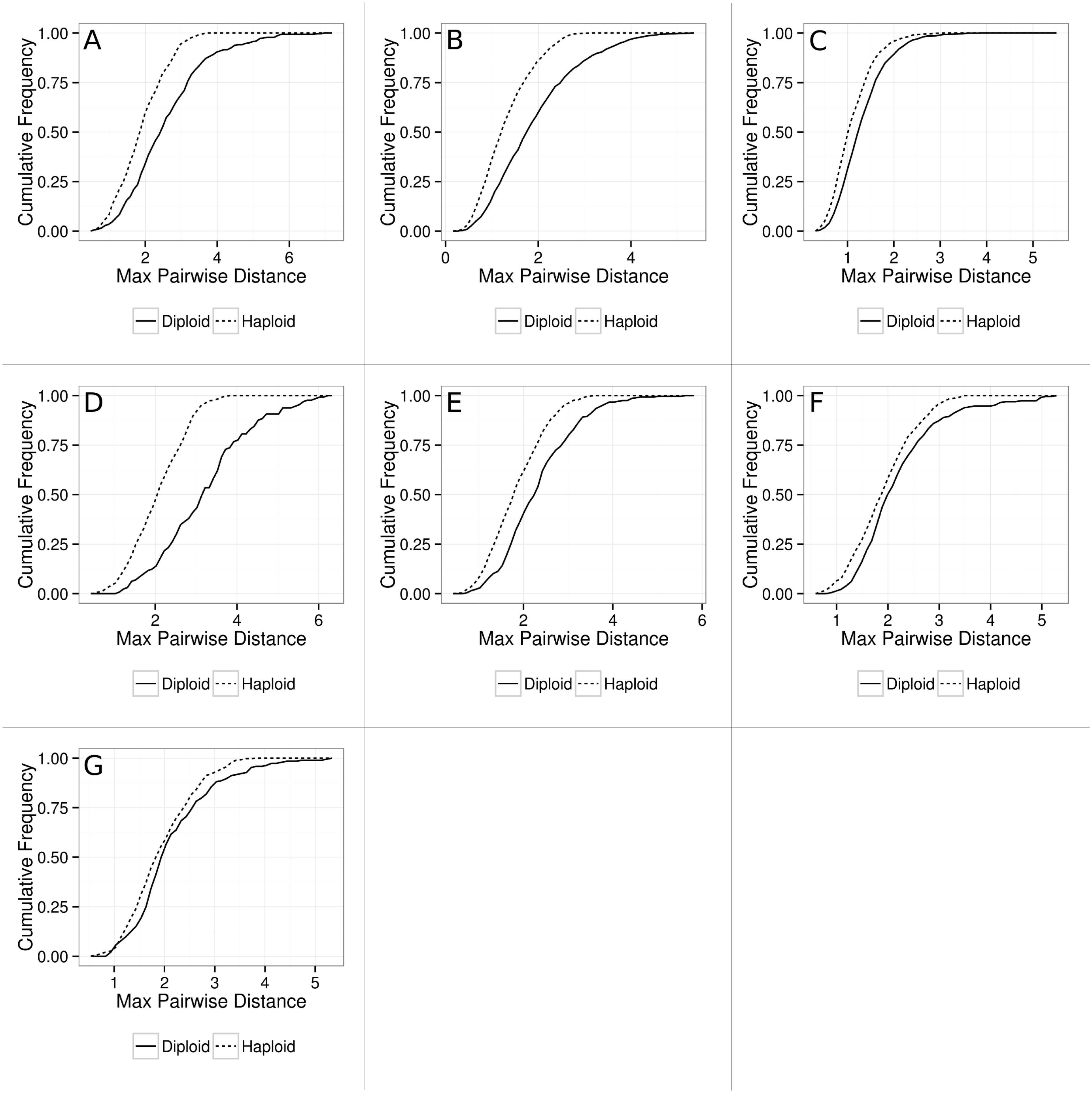
Table S2. Conditional Mutations

Table S3. Backwards Predictability P Values

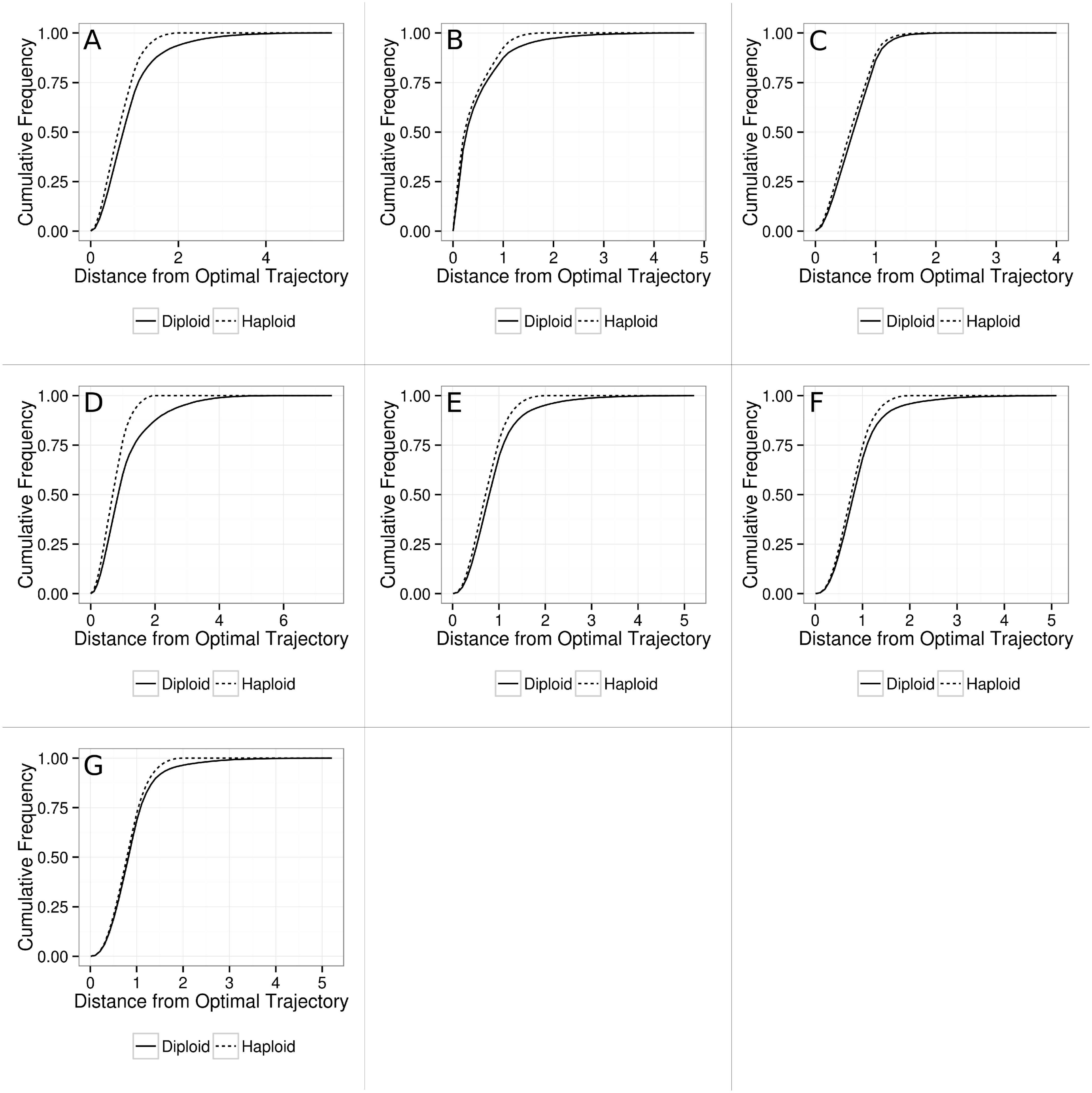
Table S4. Epistasis and Predictability P values

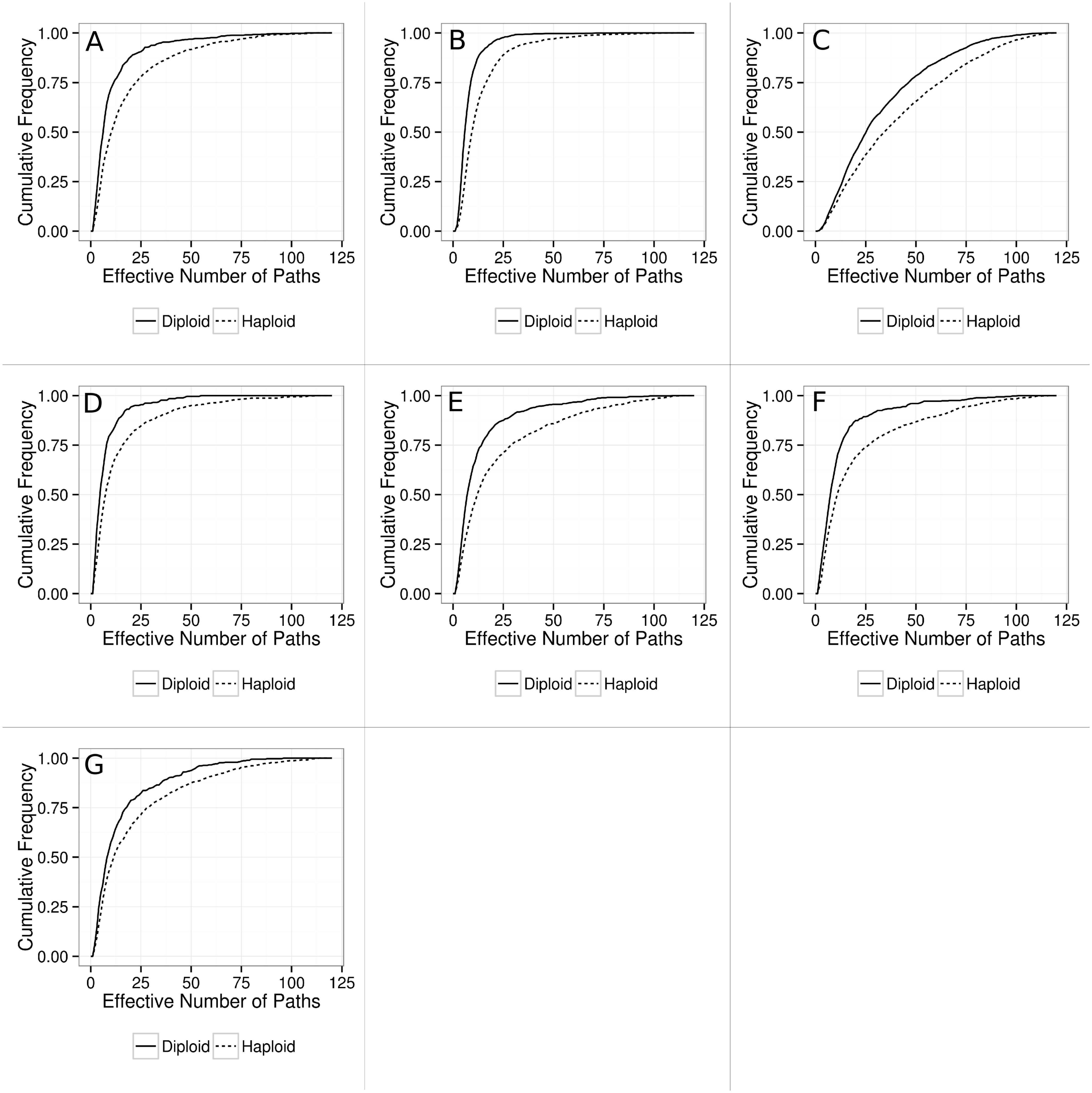

A
B
C
D
E
F
G
x
y


A
B
C
D
E
F
G
Frequency
1.00
0.75
0.50
0.25
0.00
None
One
Both
Number Overdominant Mutations
Anc. Del.
Recip. Sign
Sign



A
B
C
D
E
F
G
Cumulative Frequency
Max Pairwise Distance
Diploid
Haploid


A
B
C
D
E
F
G
Cumulative Frequency
0.00
0.25
0.50
0.75
1.00
Distance from Optimal Trajectory
0
1
2
3
4
5
6
Diploid
Haploid



A
B
C
D
E
F
G
Cumulative Frequency
Effective Number of Paths
0.00
0.25
0.50
0.75
1.00
0
25
50
75
100
125
Diploid
Haploid

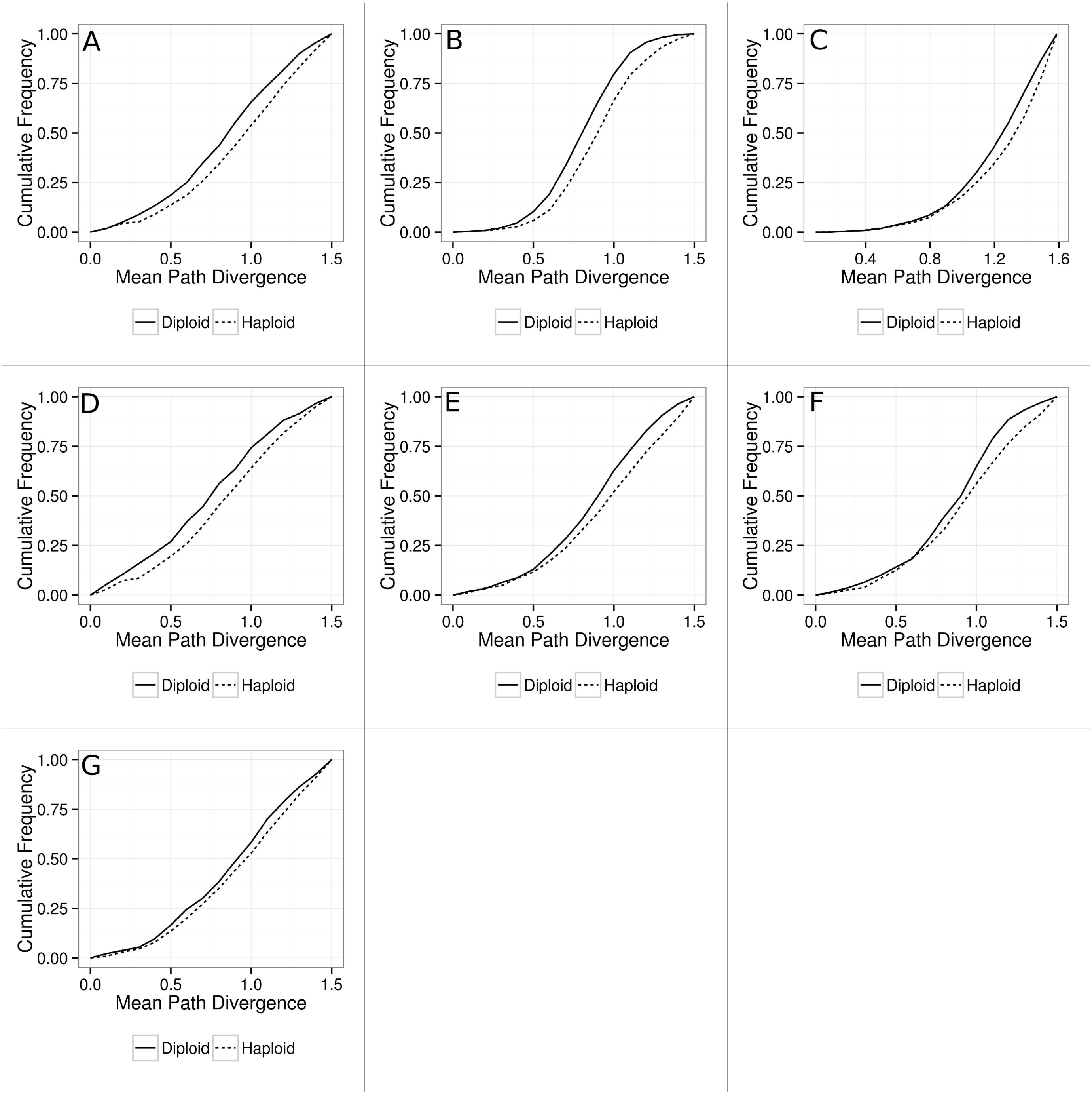

A
B
C
D
E
F
G
Cumulative Frequency
Mean Path Divergence
0.00
0.25
0.50
0.75
1.00
0.0
0.5
1.0
1.5
0.4
0.8
1.2
1.6
Diploid
Haploid

Table S1

Parameter	χ^2 p-value	Ploidy	Sign	Reciprocal Sign	Ancestral Deleterious
A	8.8E-128	Haploid	52.30%	31.00%	16.00%
		Diploid	53.00%	21.40%	2.80%
B	5.8E-252	Haploid	74.70%	68.80%	47.20%
		Diploid	76.40%	65.10%	6.20%
C	1.3E-015	Haploid	12.60%	3.50%	0.80%
		Diploid	12.00%	1.30%	0.00%
D	2.8E-151	Haploid	61.40%	51.00%	38.00%
		Diploid	65.80%	49.40%	17.20%
E	7.7E-125	Haploid	53.20%	38.10%	23.00%
		Diploid	51.40%	26.70%	3.30%
F	3.3E-139	Haploid	52.90%	38.00%	23.80%
		Diploid	50.60%	25.40%	2.90%
G	2.5E-145	Haploid	54.20%	38.90%	24.50%
		Diploid	48.80%	23.20%	2.20%

Table S2

Parameter	χ2 p-value	Ploidy	All	Initial Mutation Overdominant	Initial Mutation Not Overdominant
A	1.50E-14	Haploid	21.4%	NA	NA
		Diploid	26.3%	62.4%	18.2%
B	1.30E-79	Haploid	48.1%	NA	NA
		Diploid	40.8%	82.9%	30.4%
C	4.50E-06	Haploid	3.4%	NA	NA
		Diploid	4.6%	27.2%	3.7%
D	2.80E-34	Haploid	27.4%	NA	NA
		Diploid	36.1%	65.5%	28.0%
E	1.40E-07	Haploid	18.3%	NA	NA
		Diploid	21.5%	61.4%	14.0%
F	8.20E-05	Haploid	17.4%	NA	NA
		Diploid	19.7%	61.9%	12.1%
G	9.46E-01	Haploid	17.6%	NA	NA
		Diploid	17.5%	60.9%	10.3%

Table S3

		N	extra mutations	final homozygote advantageous	observed path viable	other paths viable	observed path top 50% most likely	observed path most likely
A	Diploid	645	57.98%	99.53%	92.87%	98.91%	80.78%	16.74%
	Haploid	1220	7.54%	100.00%	100.00%	98.44%	69.75%	14.10%
B	Diploid	2031	99.90%	100.00%	97.49%	99.75%	93.30%	38.70%
	Haploid	2295	91.94%	100.00%	99.56%	99.78%	96.47%	34.77%
C	Diploid	2286	45.98%	99.96%	99.34%	100.00%	71.39%	3.85%
	Haploid	2627	12.18%	100.00%	100.00%	100.00%	67.34%	4.76%
D	Diploid	263	48.67%	98.10%	90.11%	98.10%	80.23%	20.91%
	Haploid	679	3.68%	100.00%	100.00%	97.50%	67.16%	17.38%
E	Diploid	555	64.86%	99.46%	91.53%	97.84%	76.58%	12.97%
	Haploid	1283	6.31%	100.00%	99.92%	98.99%	66.17%	10.44%
F	Diploid	456	63.82%	99.78%	93.42%	98.90%	75.00%	12.28%
	Haploid	1164	5.50%	100.00%	100.00%	99.23%	66.41%	12.63%
G	Diploid	388	62.11%	99.48%	93.04%	98.97%	74.23%	11.60%
	Haploid	1008	5.56%	100.00%	100.00%	99.31%	64.29%	10.71%

Table S4

P values from chi-square contingency table tests

	Hap vs Dip across all 4 levels of Epistasis	Diploid Sign Epi. One overdom vs no overdom	Diploid recip sign epi one overdom vs no overdom	Diploid anc del epi one overdom vs no overdom	Diploid sign epi two overdom vs no overdom	diploid recip sign epi two overdom vs no overdom	Diploid anc del epi two overdom vs no overdom	conditional mutation haploid vs diploid	initial mutation vs diploid not overdom initial mutation
A	8.84E-128	2.03E-103	6.20E-70	3.20E-01	2.37E-61	2.02E-137	4.75E-49	1.52E-14	2.09E-290
B	5.80E-252	2.23E-71	1.50E-66	2.36E-04	3.93E-28	2.55E-69	5.87E-59	1.28E-79	0.00E+00
C	1.34E-15	5.72E-54	6.21E-16	0.00E+00	1.31E-03	7.47E-02	0.00E+00	4.53E-06	1.15E-100
D	2.75E-151	8.36E-85	1.42E-80	4.95E-01	3.50E-77	6.26E-155	1.11E-76	2.80E-34	1.90E-177
E	7.71E-125	3.76E-157	1.70E-86	5.70E-02	1.29E-56	5.26E-101	2.28E-46	1.39E-07	0.00E+00
F	3.27E-139	6.21E-168	1.17E-94	2.66E-01	1.43E-62	4.06E-127	1.22E-44	8.25E-05	0.00E+00
G	2.51E-145	6.20E-171	2.71E-80	2.99E-01	1.99E-61	5.47E-114	4.87E-24	9.46E-01	0.00E+00

p values from two-tailed t tests

	max pairwise dist p value	max dist from optimal p value	Dip vs Hap Effective num paths p valuje	cor dip effective num paths and num overdom	cor p value dip effective num paths and num overdom	mean path divergence p value
A	9.97E-22	0.00E+00	4.06E-20	-0.345	1.40E-19	4.89E-10
B	1.36E-66	7.66E-220	1.38E-79	-0.302	2.15E-44	3.45E-40
C	4.98E-27	4.21E-91	5.12E-31	-0.425	4.52E-101	5.11E-12
D	6.42E-21	0.00E+00	3.31E-15	-0.282	1.86E-06	4.42E-06
E	4.42E-17	0.00E+00	2.15E-23	-0.393	6.80E-22	5.63E-09
F	9.75E-07	3.71E-196	6.41E-19	-0.331	2.68E-13	1.63E-07
G	3.94E-04	7.81E-111	3.86E-09	-0.287	4.68E-09	9.85E-04