Supplementary Table 1. Variation within and between runs in the elements of the **M**-matrix. This table shows estimates of the mutational variances, covariance and correlation from four randomly chosen runs with parameter values equal to those used for the top panel of Figure 2. For each run, we show the single-generation **M**-matrix every 1000 generations. Each run was entirely independent of the other runs, with unique starting conditions and epistasis parameters. These runs used a selection surface with positive correlational selection, and the data show that the tendency to evolve a positive mutational correlation is quite robust. Within a run, the **M**-matrix tends to be stable, but different runs do show some variation in their average **M**-matrices, likely due to differences in the extent to which their randomly chosen epistatic parameters facilitate the evolution of mutational variances and covariances. Regardless, the evolution of triple alignment, as shown in Figure 2, occurs in nearly all runs. The last two rows show the means over all runs and the standard deviation of the within-run means across 20 independent runs.

Run-Generation	M_{11}	M_{22}	M_{12}	r_μ
R5-G1000	0.089	0.075	0.012	0.143
R5-G2000	0.101	0.080	0.016	0.192
R5-G3000	0.099	0.081	0.015	0.170
R5-G4000	0.094	0.080	0.015	0.177
R5-G5000	0.099	0.075	0.015	0.180
Run Mean	**0.095**	**0.079**	**0.014**	**0.164**
Run St. Dev.	**0.005**	**0.003**	**0.002**	**0.020**
R6-G1000	0.084	0.080	0.004	0.066
R6-G2000	0.081	0.080	0.006	0.084
R6-G3000	0.087	0.081	0.006	0.082
R6-G4000	0.087	0.079	0.008	0.099
R6-G5000	0.096	0.090	0.012	0.120
Run Mean	**0.086**	**0.083**	**0.007**	**0.091**
Run St. Dev.	**0.004**	**0.004**	**0.003**	**0.024**
R11-G1000	0.095	0.092	0.024	0.247
R11-G2000	0.103	0.096	0.025	0.241
R11-G3000	0.103	0.093	0.032	0.287
R11-G4000	0.098	0.093	0.026	0.242
R11-G5000	0.095	0.086	0.024	0.238
Run Mean	**0.099**	**0.093**	**0.026**	**0.254**
Run St. Dev.	**0.004**	**0.004**	**0.003**	**0.017**
R16-G1000	0.089	0.098	0.028	0.276
R16-G2000	0.093	0.100	0.028	0.272
R16-G3000	0.110	0.104	0.038	0.336
R16-G4000	0.102	0.099	0.033	0.336
R16-G5000	0.098	0.106	0.037	0.350
Run Mean	**0.099**	**0.103**	**0.033**	**0.313**
Run St. Dev.	**0.006**	**0.003**	**0.005**	**0.033**
Overall Mean	**0.089**	**0.090**	**0.016**	**0.169**
St. Dev. Run Means	**0.009**	**0.006**	**0.008**	**0.076**

Supplementary Table 2. Evolution of the additive genetic variances, additive genetic covariances, and **M**-matrix under different orientations of the selection surface and various population sizes. In these simulations, the selection surface retains the same shape but is oriented differently in phenotypic space for different sets of runs. Note, however, that within a run the individual selection surface does not change. Both the **M**-matrix and the **G**-matrix (the additive genetic variance-covariance matrix) tend to evolve to align with the individual selection surface. The parameter values used to generate this table are identical to those used for Table 2, except as indicated. The first four columns describe the individual selection surface, as described in Table 1, where $\angle_\omega$ is the angle of its leading eigenvector. The additive genetic variances and additive genetic correlation are given by $_{11}V_A$, $_{22}V_A$, and r_A, while M_{11}, M_{22}, and r_M represent the mutational variances and the mutational correlation for the two traits. The angles of the leading eigenvectors of the **G**-matrix and **M**-matrix are given by $\angle_A$ and $\angle_M$, respectively.

ω_{11}	ω_{22}	r_ω	$\angle_\omega$	N	$_{11}V_A$	$_{22}V_A$	r_A	$\angle_A$	M_{11}	M_{22}	r_M	$\angle_M$
93	5	0	0	256	0.451	0.144	0.005	0.2	0.271	0.216	0.008	2.0
88	10	0.69	13.8	256	0.469	0.161	0.283	13.4	0.298	0.237	0.078	17.1
82	16	0.80	20.6	256	0.407	0.187	0.380	21.8	0.284	0.259	0.078	29.4
71	27	0.87	30.0	256	0.403	0.223	0.469	28.7	0.327	0.285	0.042	15.7
60	38	0.89	37.7	256	0.333	0.259	0.500	38.0	0.254	0.234	0.112	35.0
49	49	0.90	45.0	256	0.321	0.298	0.562	43.1	0.269	0.264	0.170	43.3
93	5	0	0	1024	0.305	0.097	-0.006	-0.3	0.130	0.094	0.007	1.2
88	10	0.69	13.8	1024	0.296	0.110	0.301	15.1	0.124	0.097	0.084	17.5
82	16	0.80	20.6	1024	0.287	0.122	0.385	20.6	0.125	0.097	0.085	17.0
71	27	0.87	30.0	1024	0.254	0.155	0.472	31.1	0.117	0.108	0.135	36.8
60	38	0.89	37.7	1024	0.227	0.167	0.482	36.2	0.115	0.104	0.114	33.4
49	49	0.90	45.0	1024	0.207	0.198	0.532	43.9	0.112	0.108	0.157	41.6
93	5	0	0	4096	0.262	0.079	0.000	0.0	0.103	0.072	0.002	0.4
88	10	0.69	13.8	4096	0.258	0.090	0.264	12.9	0.100	0.074	0.062	11.0
82	16	0.80	20.6	4096	0.239	0.102	0.382	20.5	0.098	0.075	0.093	18.0
71	27	0.87	30.0	4096	0.210	0.123	0.460	29.8	0.094	0.081	0.129	29.7
60	38	0.89	37.7	4096	0.186	0.145	0.505	38.2	0.091	0.083	0.148	36.4
49	49	0.90	45.0	4096	0.174	0.175	0.551	45.1	0.089	0.090	0.183	45.9

Supplementary Table 3. An analysis of the response to selection in the presence of epistasis. The values in this table were generated by allowing populations to evolve under individual selection surfaces shaped like those in Supplemental Table S2. Every 100 generations, we made a copy of the entire population and imposed directional selection on trait one by culling all individuals below the mean. The value of the selection gradient on trait one, β_1, is then the slope of the least-squares regression of relative fitness on trait values. There is no selection on trait two (i.e., $\beta_2 = 0$). Results for population sizes of 128, 512, and 4096 are shown here. We report the total genetic variances and covariance ($_{11}V_G$, $_{22}V_G$, and $_{12}V_G$), the additive genetic variances and covariance ($_{11}V_A$, $_{22}V_A$, and $_{12}V_A$), and several quantities related to the response of the population mean to selection. The values Exp. $_{11}R_G$ and Exp. $_{22}R_G$ are the responses to selection that would be expected if all genetic variance were additive, whereas Exp. $_{11}R_A$ and Exp. $_{22}R_A$ are the expected responses to selection for trait one and trait two based on the observed additive genetic variances and covariance and the magnitude of β_1. Note that the absence of selection on trait two means that the response to selection for this trait is due entirely to a correlated response to selection. Obs. $_{11}R$ and Obs. $_{22}R$ are the observed responses to selection in the simulated population. We also relaxed selection for two generations after the single generation of strong directional selection. The remaining responses to selection after this two-generation relaxation of selection are shown in the last two columns. The standard errors of the means for the values in this table are much, much smaller than the means reported here.

N	β_1	$_{11}V_G$	$_{22}V_G$	$_{12}V_G$	$_{11}V_A$	$_{22}V_A$	$_{12}V_A$	Exp. $_{11}R_G$	Exp. $_{22}R_G$	Exp. $_{11}R_A$	Exp. $_{22}R_A$	Obs. $_{11}R$	Obs. $_{22}R$	$_{11}R$, relaxed	$_{22}R$, relaxed
128	0.657	0.567	0.182	-0.001	0.531	0.155	-0.001	0.372	-0.001	0.349	0.000	0.317	-0.002	0.313	-0.003
128	0.660	0.508	0.201	0.079	0.474	0.175	0.079	0.335	0.052	0.313	0.052	0.299	0.047	0.298	0.050
128	0.672	0.471	0.225	0.105	0.441	0.199	0.103	0.317	0.070	0.296	0.069	0.276	0.066	0.274	0.068
128	0.674	0.446	0.266	0.151	0.413	0.240	0.149	0.300	0.102	0.278	0.100	0.269	0.090	0.264	0.089
128	0.693	0.373	0.311	0.154	0.344	0.281	0.151	0.259	0.106	0.239	0.105	0.228	0.096	0.225	0.096
128	0.700	0.327	0.312	0.149	0.297	0.283	0.145	0.229	0.104	0.208	0.102	0.201	0.090	0.199	0.092
512	0.669	0.431	0.168	0.005	0.373	0.118	0.005	0.289	0.004	0.250	0.003	0.257	0.004	0.245	0.003
512	0.672	0.416	0.183	0.072	0.360	0.132	0.069	0.279	0.048	0.242	0.047	0.249	0.045	0.239	0.047
512	0.677	0.396	0.202	0.090	0.339	0.150	0.088	0.268	0.061	0.230	0.060	0.239	0.061	0.227	0.060
512	0.679	0.388	0.236	0.119	0.330	0.182	0.116	0.264	0.081	0.224	0.079	0.236	0.078	0.223	0.079
512	0.694	0.323	0.275	0.125	0.265	0.216	0.123	0.224	0.087	0.184	0.085	0.196	0.084	0.186	0.085
512	0.705	0.283	0.286	0.121	0.229	0.232	0.119	0.199	0.085	0.161	0.084	0.177	0.083	0.165	0.084
4096	0.684	0.354	0.166	0.000	0.262	0.079	0.000	0.242	0.000	0.179	0.000	0.205	0.000	0.181	0.001
4096	0.688	0.343	0.174	0.041	0.258	0.090	0.040	0.236	0.028	0.177	0.028	0.203	0.029	0.185	0.025
4096	0.692	0.326	0.185	0.061	0.239	0.102	0.060	0.226	0.042	0.165	0.041	0.190	0.040	0.170	0.042
4096	0.700	0.295	0.207	0.076	0.210	0.123	0.074	0.207	0.053	0.147	0.052	0.173	0.050	0.152	0.051
4096	0.707	0.273	0.203	0.086	0.186	0.145	0.083	0.193	0.061	0.131	0.059	0.159	0.060	0.138	0.057
4096	0.710	0.260	0.263	0.100	0.174	0.175	0.096	0.185	0.071	0.124	0.068	0.152	0.068	0.132	0.068

Supplementary Table 4. The effects of the mutational variance for reference effects on the evolution of the genetic variance and the **M**-matrix in the multivariate model of epistasis. The parameter values used to generate this table are identical to those indicated in Table 1, except as noted. Variables and symbols are described in Table 2.

r_ω	$\alpha_1^2 = \alpha_2^2$	$_{11}V_G$	$_{22}V_G$	r_G	$_{11}V_A$	$_{22}V_A$	$_{12}V_A (r_A)$	$_{11}V_{AA}$	$_{22}V_{AA}$	$_{12}V_{AA}$	M_{11}	M_{22}	r_M
0	0.01	0.43	0.45	-0.01	0.40	0.41	-0.004 (-0.01)	0.034	0.032	0.000	0.051	0.054	-0.002
0.50	0.01	0.37	0.36	0.11	0.34	0.32	0.043 (0.13)	0.030	0.030	0.001	0.046	0.045	0.012
0.75	0.01	0.30	0.27	0.29	0.27	0.25	0.090 (0.35)	0.025	0.024	0.001	0.041	0.037	0.095
0.90	0.01	0.20	0.21	0.37	0.18	0.19	0.080 (0.43)	0.017	0.017	0.001	0.035	0.037	0.116
0	0.02	0.54	0.56	0.02	0.47	0.49	0.008 (0.02)	0.067	0.066	0.000	0.098	0.106	0.017
0.50	0.02	0.49	0.48	0.14	0.43	0.42	0.075 (0.18)	0.059	0.058	-0.001	0.099	0.094	0.027
0.75	0.02	0.42	0.40	0.32	0.37	0.35	0.138 (0.38)	0.044	0.044	0.001	0.091	0.090	0.108
0.90	0.02	0.25	0.27	0.40	0.22	0.23	0.114 (0.51)	0.030	0.031	0.002	0.068	0.072	0.136
0	0.05	0.78	0.70	0.01	0.63	0.56	0.013 (0.02)	0.134	0.132	0.001	0.275	0.245	-0.007
0.50	0.05	0.63	0.64	0.21	0.49	0.49	0.132 (0.27)	0.133	0.132	0.004	0.227	0.222	0.077
0.75	0.05	0.49	0.48	0.32	0.40	0.39	0.164 (0.42)	0.081	0.079	0.004	0.209	0.201	0.114
0.90	0.05	0.30	0.30	0.41	0.24	0.24	0.126 (0.53)	0.049	0.048	0.002	0.159	0.156	0.131
0	0.25	0.79	0.82	-0.01	0.50	0.52	-0.013 (-0.03)	0.260	0.272	0.007	0.912	0.956	-0.007
0.50	0.25	0.67	0.66	0.16	0.44	0.43	0.103 (0.24)	0.211	0.214	0.005	0.867	0.856	0.041
0.75	0.25	0.46	0.46	0.23	0.31	0.31	0.104 (0.34)	0.134	0.135	0.006	0.695	0.740	0.054
0.90	0.25	0.28	0.28	0.33	0.20	0.20	0.092 (0.46)	0.071	0.074	0.006	0.595	0.597	0.076
0	1.00	0.87	0.86	0.02	0.47	0.47	0.011 (0.02)	0.330	0.328	0.001	3.536	3.596	0.010
0.50	1.00	0.72	0.74	0.15	0.39	0.42	0.101 (0.25)	0.273	0.258	0.007	3.241	3.341	0.039
0.75	1.00	0.55	0.55	0.25	0.33	0.32	0.128 (0.39)	0.174	0.172	0.010	3.097	3.101	0.052
0.90	1.00	0.35	0.34	0.35	0.21	0.20	0.114 (0.56)	0.094	0.098	0.008	2.581	2.471	0.067
Ave	**SEM**	0.016	0.015	0.020	0.015	0.014	0.011	0.004	0.004	0.001	0.03	0.03	0.02

Supplementary Table 5. The effects of the strength of stabilizing selection on the evolution of the genetic variance and the **M**-matrix in the multivariate model of epistasis. The parameter values used to generate this table are identical to those indicated in Table 1, except as noted. Variables and symbols are described in Table 2.

r_ω	$\omega_{11}=\omega_{22}$	$_{11}V_G$	$_{22}V_G$	r_G	$_{11}V_A$	$_{22}V_A$	$_{12}V_A (r_A)$	$_{11}V_{AA}$	$_{22}V_{AA}$	$_{12}V_{AA}$	M_{11}	M_{22}	r_M
0	9	0.18	0.18	0.00	0.14	0.14	-0.001 (-0.01)	0.034	0.034	0.000	0.138	0.127	0.008
0.50	9	0.15	0.15	0.18	0.12	0.12	0.027 (0.23)	0.028	0.027	0.001	0.119	0.120	0.051
0.75	9	0.12	0.12	0.29	0.09	0.10	0.035 (0.37)	0.022	0.021	0.001	0.107	0.103	0.079
0.90	9	0.09	0.09	0.39	0.08	0.08	0.036 (0.45)	0.014	0.014	0.001	0.093	0.093	0.095
0	29	0.45	0.46	0.00	0.35	0.36	0.003 (0.01)	0.095	0.096	-0.001	0.189	0.195	0.011
0.50	29	0.41	0.43	0.20	0.32	0.34	0.087 (0.26)	0.076	0.081	0.004	0.185	0.206	0.087
0.75	29	0.31	0.33	0.33	0.25	0.26	0.108 (0.42)	0.055	0.058	0.003	0.166	0.168	0.113
0.90	29	0.21	0.20	0.43	0.17	0.17	0.092 (0.54)	0.035	0.033	0.002	0.131	0.120	0.134
0	49	0.72	0.73	0.01	0.57	0.58	0.007 (0.01)	0.141	0.140	0.002	0.255	0.270	0.003
0.50	49	0.62	0.61	0.17	0.49	0.48	0.114 (0.24)	0.119	0.120	0.002	0.231	0.215	0.043
0.75	49	0.50	0.49	0.31	0.40	0.39	0.159 (0.40)	0.086	0.085	0.003	0.218	0.200	0.085
0.90	49	0.31	0.30	0.41	0.26	0.24	0.133 (0.53)	0.048	0.050	0.003	0.170	0.166	0.110
0	89	1.19	1.22	-0.01	0.95	0.98	-0.010 (-0.01)	0.219	0.214	-0.002	0.309	0.324	-0.004
0.50	89	1.03	1.02	0.18	0.83	0.83	0.185 (0.22)	0.189	0.179	0.007	0.299	0.311	0.040
0.75	89	0.79	0.76	0.29	0.63	0.61	0.235 (0.38)	0.142	0.143	0.003	0.249	0.247	0.102
0.90	89	0.46	0.46	0.39	0.38	0.38	0.194 (0.51)	0.075	0.077	0.006	0.193	0.189	0.105
0	149	1.88	1.96	-0.02	1.56	1.63	-0.044 (-0.03)	0.290	0.312	0.002	0.427	0.440	-0.023
0.50	149	1.56	1.53	0.13	1.28	1.26	0.214 (0.17)	0.256	0.256	0.006	0.392	0.384	0.026
0.75	149	1.18	1.19	0.29	0.98	0.99	0.368 (0.37)	0.191	0.192	0.005	0.313	0.324	0.088
0.90	149	0.72	0.72	0.40	0.59	0.59	0.299 (0.51)	0.118	0.120	0.006	0.238	0.230	0.113
Ave	**SEM**	0.021	0.023	0.019	0.020	0.023	0.015	0.005	0.005	0.002	0.011	0.011	0.019

Supplementary Table 6. The effects of the mutation rate (μ) on the evolution of the genetic variance and the **M**-matrix in the multivariate model of epistasis. The parameter values used to generate this table are identical to those indicated in Table 1, except as noted. Variables and symbols are described in Table 2.

r_ω	μ	$_{11}V_G$	$_{22}V_G$	r_G	$_{11}V_A$	$_{22}V_A$	$_{12}V_A (r_A)$	$_{11}V_{AA}$	$_{22}V_{AA}$	$_{12}V_{AA}$	M_{11}	M_{22}	r_M
0	0.0001	0.16	0.16	0.01	0.15	0.15	0.004 (0.03)	0.014	0.014	0.001	0.171	0.175	0.000
0.50	0.0001	0.13	0.13	0.19	0.12	0.11	0.026 (0.23)	0.012	0.011	0.001	0.137	0.135	0.028
0.75	0.0001	0.11	0.10	0.24	0.10	0.09	0.034 (0.36)	0.009	0.008	0.000	0.133	0.124	0.005
0.90	0.0001	0.06	0.06	0.35	0.06	0.06	0.027 (0.45)	0.005	0.005	0.000	0.096	0.089	0.013
0	0.0002	0.30	0.29	0.00	0.26	0.25	-0.001 (0.00)	0.033	0.034	0.000	0.203	0.210	0.009
0.50	0.0002	0.24	0.25	0.11	0.21	0.21	0.033 (0.16)	0.029	0.031	0.001	0.169	0.176	0.004
0.75	0.0002	0.20	0.20	0.29	0.17	0.18	0.063 (0.36)	0.024	0.024	0.002	0.164	0.168	0.063
0.90	0.0002	0.12	0.11	0.35	0.10	0.10	0.043 (0.43)	0.013	0.013	0.001	0.119	0.112	0.042
0	0.0005	0.75	0.75	0.04	0.59	0.58	0.029 (0.05)	0.149	0.149	0.002	0.234	0.242	0.036
0.50	0.0005	0.67	0.65	0.21	0.54	0.52	0.145 (0.27)	0.120	0.116	0.002	0.255	0.243	0.074
0.75	0.0005	0.46	0.45	0.28	0.37	0.36	0.129 (0.35)	0.089	0.085	0.006	0.195	0.185	0.072
0.90	0.0005	0.29	0.30	0.40	0.23	0.24	0.122 (0.52)	0.051	0.050	0.001	0.153	0.160	0.129
0	0.001	1.34	1.35	-0.03	0.90	0.91	-0.035 (-0.04)	0.407	0.400	-0.007	0.255	0.256	-0.022
0.50	0.001	1.17	1.15	0.18	0.81	0.80	0.207 (0.26)	0.329	0.326	0.009	0.251	0.241	0.062
0.75	0.001	0.91	0.93	0.35	0.64	0.66	0.322 (0.50)	0.247	0.251	0.012	0.209	0.216	0.170
0.90	0.001	0.58	0.61	0.46	0.44	0.46	0.273 (0.61)	0.132	0.131	0.007	0.178	0.184	0.201
0	0.002	2.37	2.37	0.01	1.23	1.21	0.014 (0.01)	1.067	1.073	0.001	0.271	0.268	0.006
0.50	0.002	2.09	2.14	0.18	1.12	1.17	0.376 (0.33)	0.896	0.896	0.018	0.255	0.260	0.090
0.75	0.002	1.67	1.61	0.34	1.00	0.95	0.546 (0.56)	0.609	0.611	0.020	0.237	0.230	0.188
0.90	0.002	1.08	1.06	0.44	0.70	0.68	0.460 (0.67)	0.340	0.346	0.020	0.196	0.191	0.225
Ave	**SEM**	0.018	0.019	0.021	0.017	0.018	0.013	0.006	0.005	0.003	0.008	0.008	0.020

Supplementary Table 7. Evolution of the additive genetic variances, additive genetic covariances, and **M**-matrix under different types of epistasis. As in Supplementary Table 2, the selection surface retains the same shape but rotates in the two-dimensional parameter space. The parameter values used to generate this table are identical to those indicated in Table 1, except as noted. The first four columns describe the individual selection surface, as described in Table 1, where $\angle_\omega$ is the angle of its leading eigenvector. The next two columns indicate the variances for the distributions from which the epistatic parameters were drawn. In the first six rows of the table, the within-trait epistasis parameters (i.e., $_1\varepsilon_{11}$ and $_2\varepsilon_{22}$) were drawn from a distribution with a variance of one, while all other epistatic parameters (i.e., $_1\varepsilon_{22}$, $_2\varepsilon_{11}$, $_1\varepsilon_{21}$, and $_2\varepsilon_{12}$) were set at zero. In the last six rows of the table, the within-trait epistasis parameters (i.e., $_1\varepsilon_{11}$ and $_2\varepsilon_{22}$) were set at zero and the remaining epistasis parameters were drawn from a normal distribution with a variance of one (i.e., $_1\varepsilon_{22}$, $_2\varepsilon_{11}$, $_1\varepsilon_{21}$, and $_2\varepsilon_{12}$). The additive genetic variances and additive genetic correlation are given by $_{11}V_A$, $_{22}V_A$, and r_A, while M_{11}, M_{22}, and r_M represent the mutational variances and the mutational correlation for the two traits. The angles of the leading eigenvectors (in degrees in two-dimensional trait space) of the **G**-matrix and **M**-matrix are given by $\angle_A$ and $\angle_M$, respectively.

ω_{11}	ω_{22}	r_ω	$\angle_\omega$	Var. $_1\varepsilon_{11},_2\varepsilon_{22}$	Var. other ε parameters	$_{11}V_A$	$_{22}V_A$	r_A	$\angle_A$	M_{11}	M_{22}	r_M	$\angle_M$
93	5	0	0	1	0	0.625	0.098	-0.004	-0.1	0.166	0.071	0.000	0.0
88	10	0.69	13.8	1	0	0.530	0.106	0.186	5.9	0.146	0.074	0.000	0.0
82	16	0.80	20.6	1	0	0.392	0.119	0.215	9.4	0.138	0.082	0.000	0.0
71	27	0.87	30.0	1	0	0.270	0.135	0.266	18.5	0.105	0.084	0.000	0.0
60	38	0.89	37.7	1	0	0.226	0.155	0.308	29.1	0.101	0.083	0.000	0.0
49	49	0.90	45.0	1	0	0.181	0.201	0.325	49.7	0.088	0.108	0.000	90.0
93	5	0	0	0	1	0.371	0.125	0.001	0.1	0.161	0.128	0.011	7.5
88	10	0.69	13.8	0	1	0.384	0.142	0.291	14.6	0.160	0.125	0.048	7.9
82	16	0.80	20.6	0	1	0.361	0.149	0.374	19.6	0.160	0.125	0.094	20.5
71	27	0.87	30.0	0	1	0.337	0.202	0.508	31.4	0.157	0.141	0.121	33.9
60	38	0.89	37.7	0	1	0.306	0.221	0.527	36.3	0.163	0.141	0.140	31.4
49	49	0.90	45.0	0	1	0.273	0.275	0.553	45.2	0.143	0.150	0.161	48.2