Resolving the complex genetic basis of phenotypic variation and variability of cellular growth – Supplementary material

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Figure S1

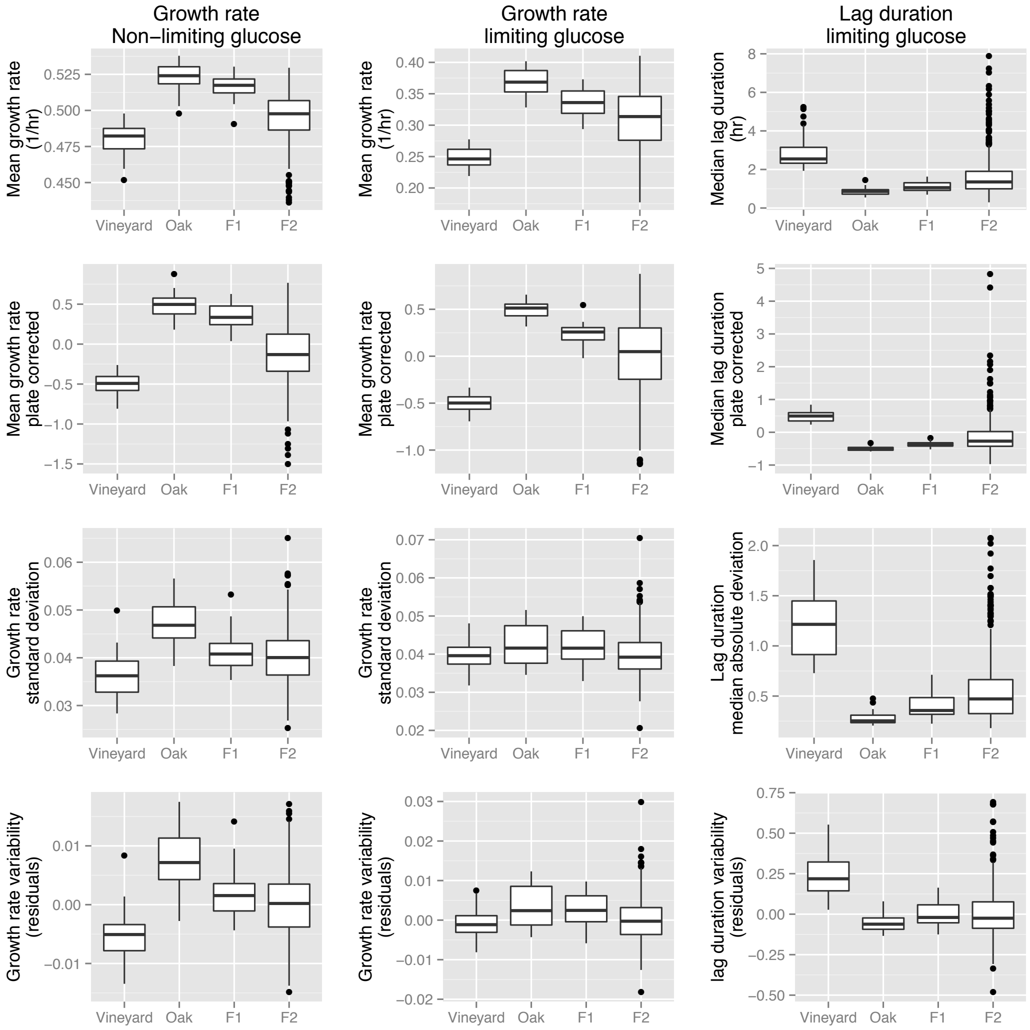


Figure S1 - Cell growth traits for parental, F1 and F2 strains.

Estimates of central tendency and variability for growth rate and lag duration distributions. The parental and F1 strains are represented by 24 values (4 wells X 6 plates) measured in each condition. The 477 F2 strains are represented by one well per strain per condition. The first row of panels displays the original central tendency measurements and the second row displays the plate corrected central tendency measurements, which were used for mapping phenotypic variation. The third row displays the original dispersion estimates and the fourth row displays the residuals from loess regressions, which were used for mapping phenotypic variability.

Figure S2

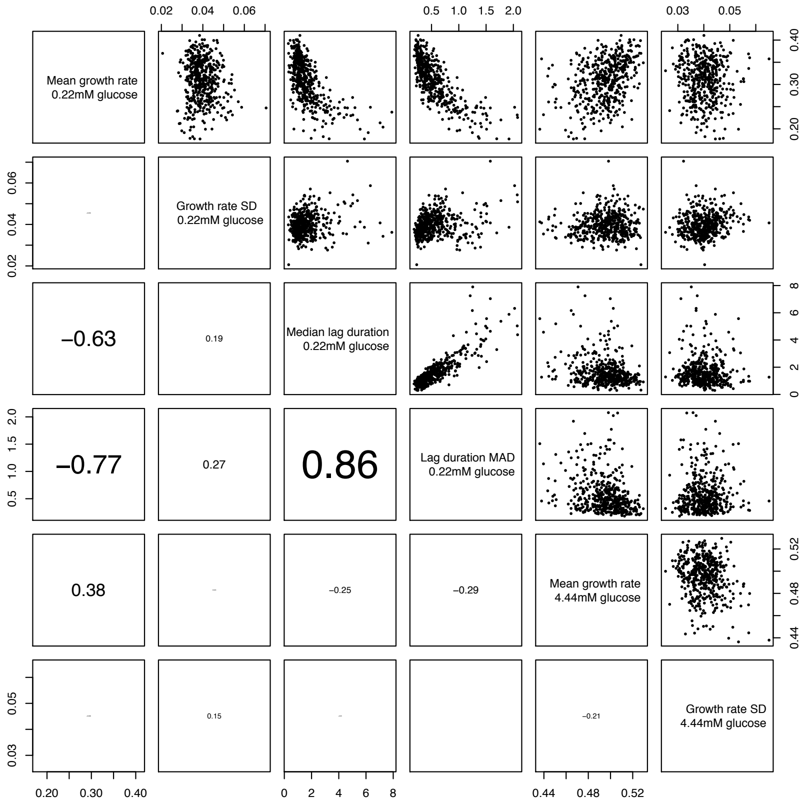
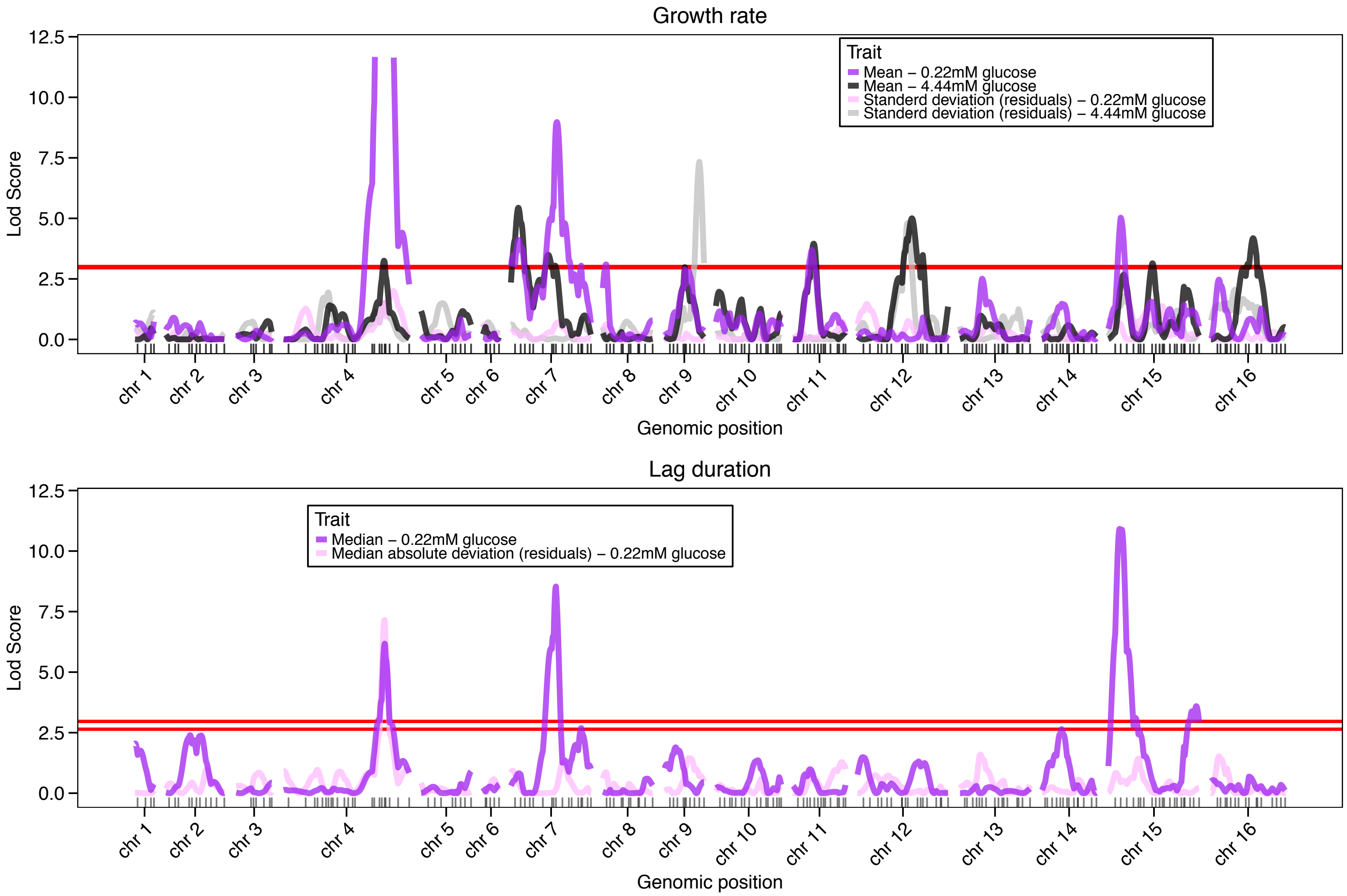


Figure S2 - Correlations between cell growth traits.

Trait values correspond to measurements from each well for all F2 segregants phenotyped. Data are displayed in the upper triangle and the linear pearson correlation values are given in the lower triangle. The size of the text corresponds to strength of the correlation estimate.

Figure S3



LOD profiles using a single-QTL model were determined by performing interval mapping using 374 F2 segregants assayed for growth rate variation and variability (upper panel) and lag duration variation and variability (lower panel) in two different glucose concentrations. The colors represent the combination of trait and environment as specified in the legend. Black tick marks on the x-axes represent marker locations. The y-axes are limited to a LOD score of 12 for clarity. The QTL underlying variation in growth rate in 0.22mM glucose on chromosome IV reaches a maximum value of 41.8.

Figure S4

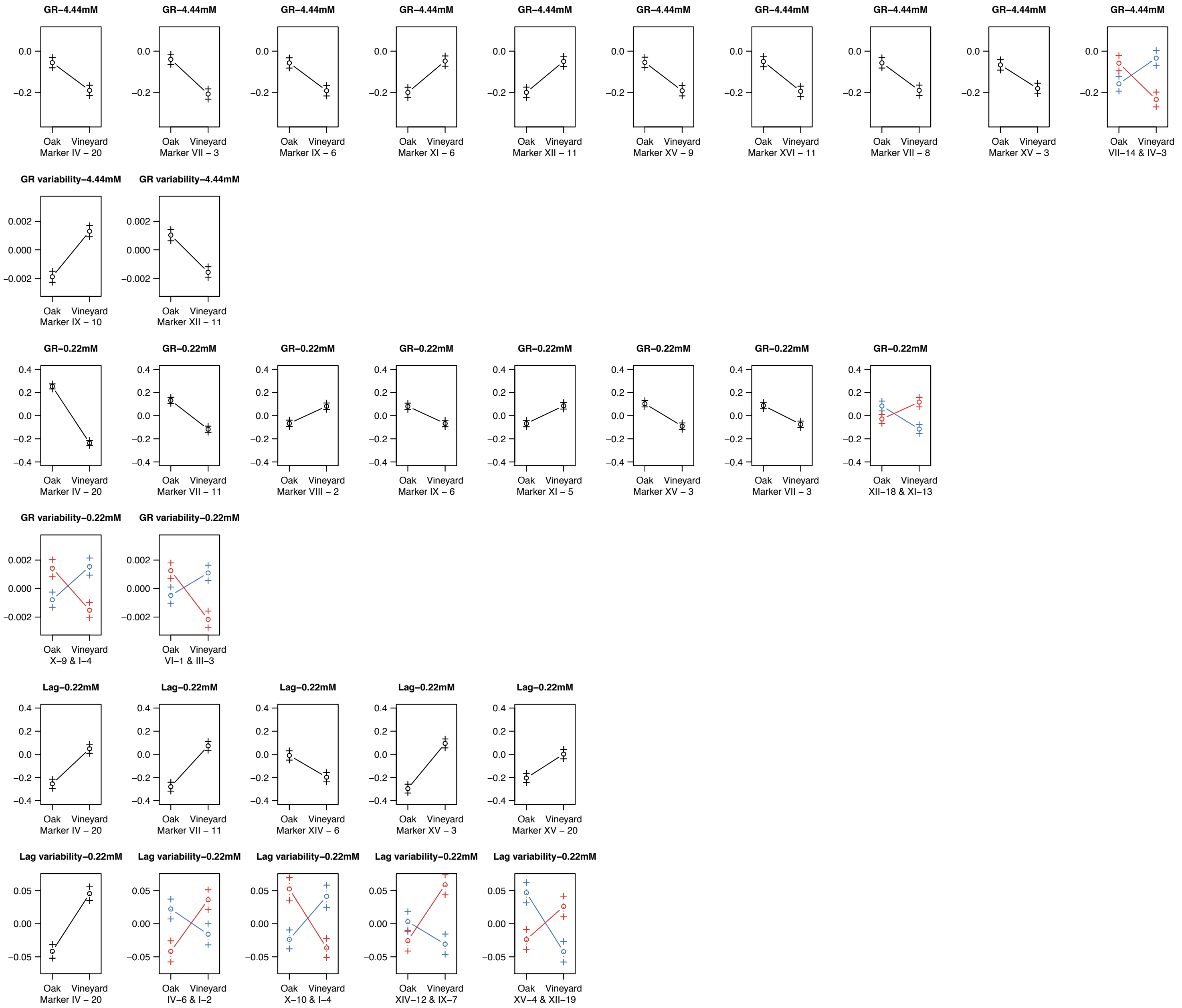


Figure S4 - Effect sizes for additive QTL and genetic interactions.

Each row represents a single trait for either growth rate (GR) or lag variation or variability measured in the specified glucose environment. Plots depicting additive loci correspond to trait means and standard errors for the oak and vineyard genotype class at the closest marker. Plots depicting genetic interactions correspond to trait means and standard errors for the four genotype combinations at closest markers; the x axis corresponds to first marker and colors represent the genotype at the second marker as either oak (blue) or vineyard (red). To interpret the magnitude of effects, consider that for central tendency variation traits, normalization results in a difference of 1 unit between parental genotypes, ranging from -0.5 (vineyard phenotypic value) to 0.5 (oak phenotypic value). For phenotypic variability, trait values represent residuals from a loess regression (see methods).

Figure S5

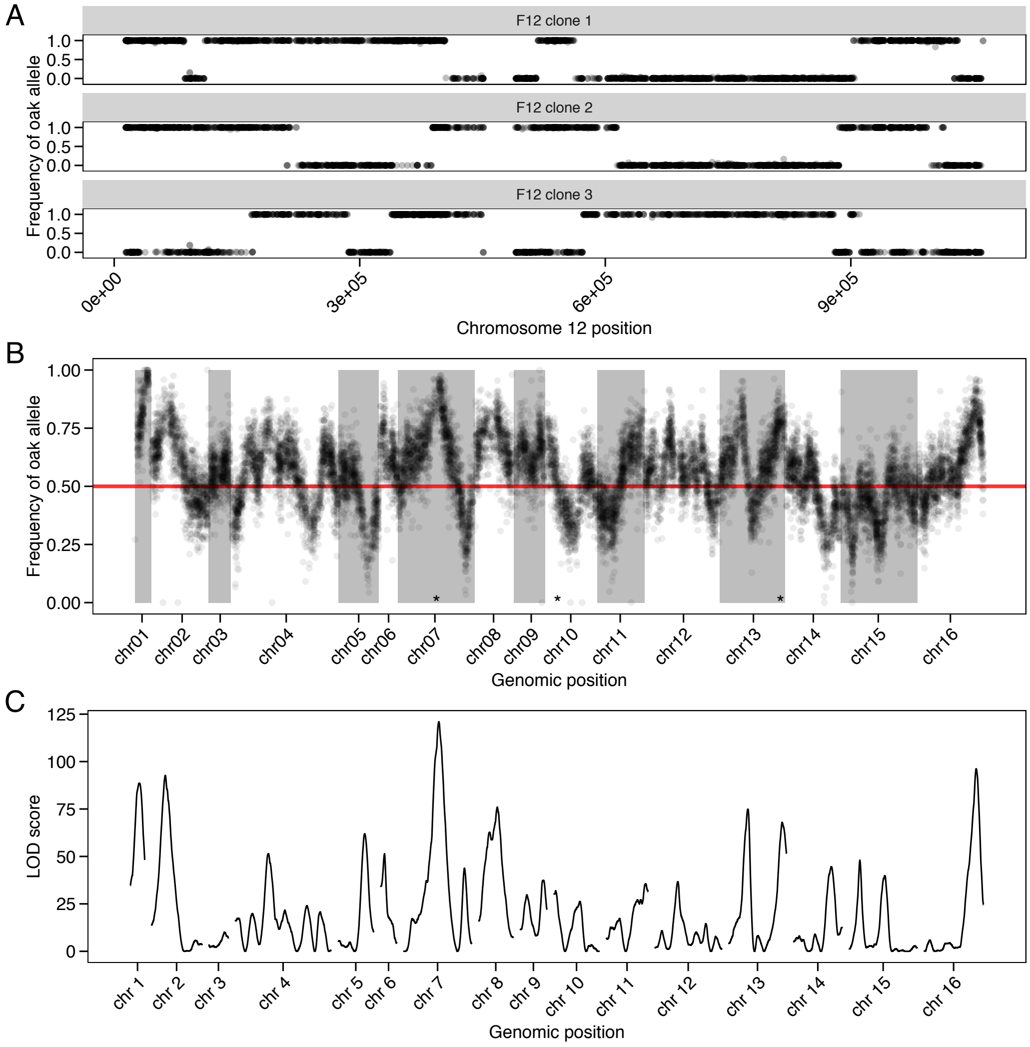


Figure S5 - Allele frequencies and genetic mapping in an advanced intercross population.

(A) Allele frequencies for chromosome 12 in three advanced intercross F12 clones. (B) Allele frequencies in the final advanced intercross population following eleven rounds of random mating. SNPs with minor allele frequencies <10% in the F1 heterozygote were excluded. The three major sporulation efficiency QTL known to segregate in this cross are indicated by asterisks (nearest marker). (C) MULTIPOOL LOD score results for the advanced intercross population determined using parameter values of n=1000 (number of individuals), r=2500 (length of cM) and mode=replicates.

Figure S6

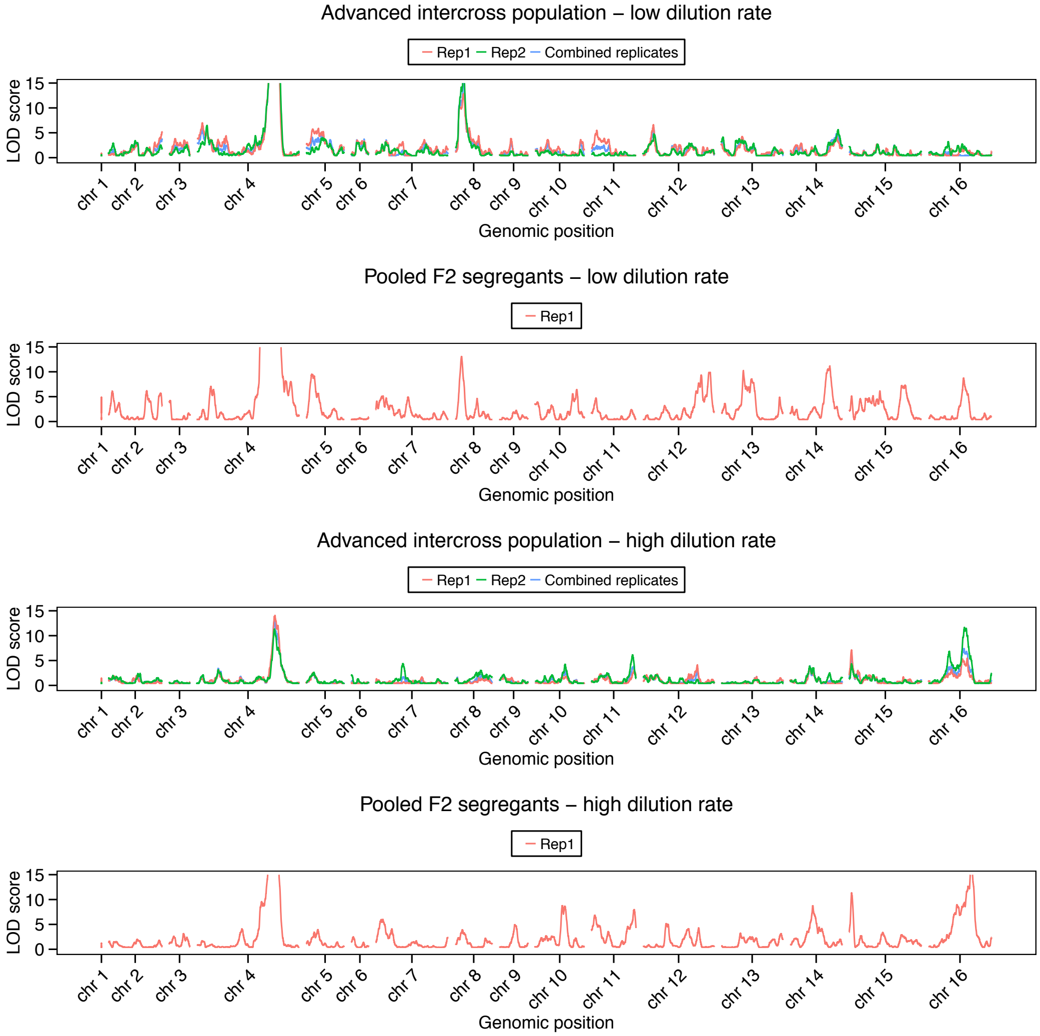


Figure S6 - MULTIPOOL-generated genome-wide LOD profiles.
LOD profiles generated using MULTIPOOL are based on allele frequency differences following selection in chemostats at either a low (0.18) or high (0.35) dilution rate. Panels represent different mapping populations and selective conditions. Individual replicates or combined scores, generated by summing reads per SNP for both replicates, are shown. The y-axes are limited to a LOD score of 15 for clarity. The QTL on chromosome IV for the advanced intercross selected in the low dilution rate reaches a maximum of 54.97. MULTIPOOL results are shown with parameter values of n=1000 and r=1000.

Note on chromosome XVI peaks in the pooled F2 samples: In the high dilution rate, the proportion of oak alleles increased, matching the environmental specific effects seen in the interval mapping and the advanced intercross population. In the low dilution rate, the LOD peak corresponds to increases in the vineyard alleles, not supported by the interval mapping or the advanced intercross population.

Figure S7

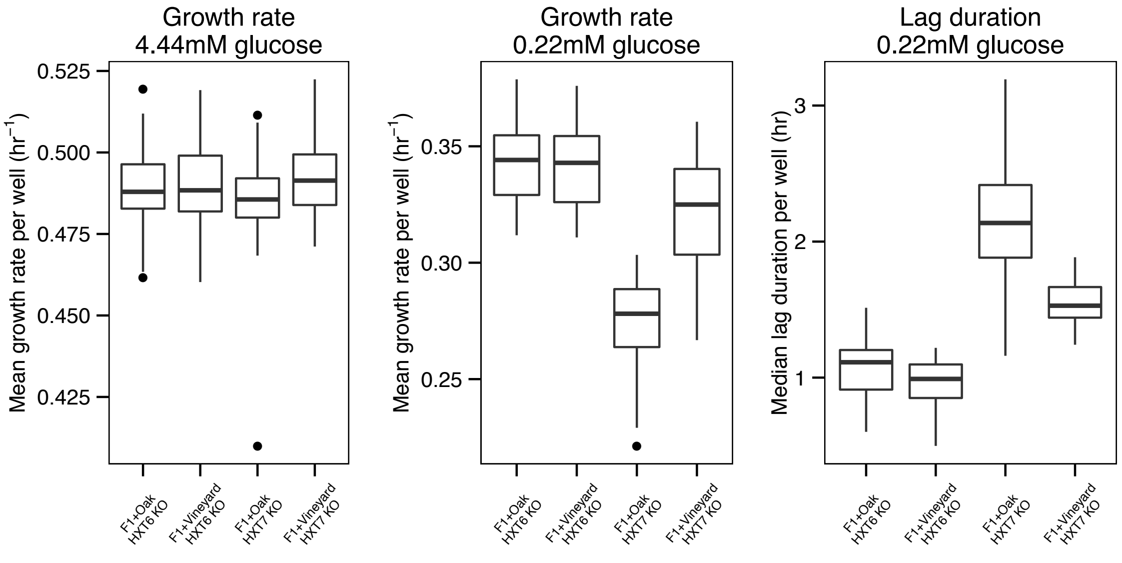


Figure S7 - Phenotypic analysis of HXT6 and HXT7 reciprocal hemizygotes.

Distributions of mean growth rate or median lag duration per well for strains that are hemizygous for just one of the duplicate gene pair, HXT6 and HXT7. Data are from measurement of 34-48 wells (across 4 plates) per strain and condition combination.

Figure S8

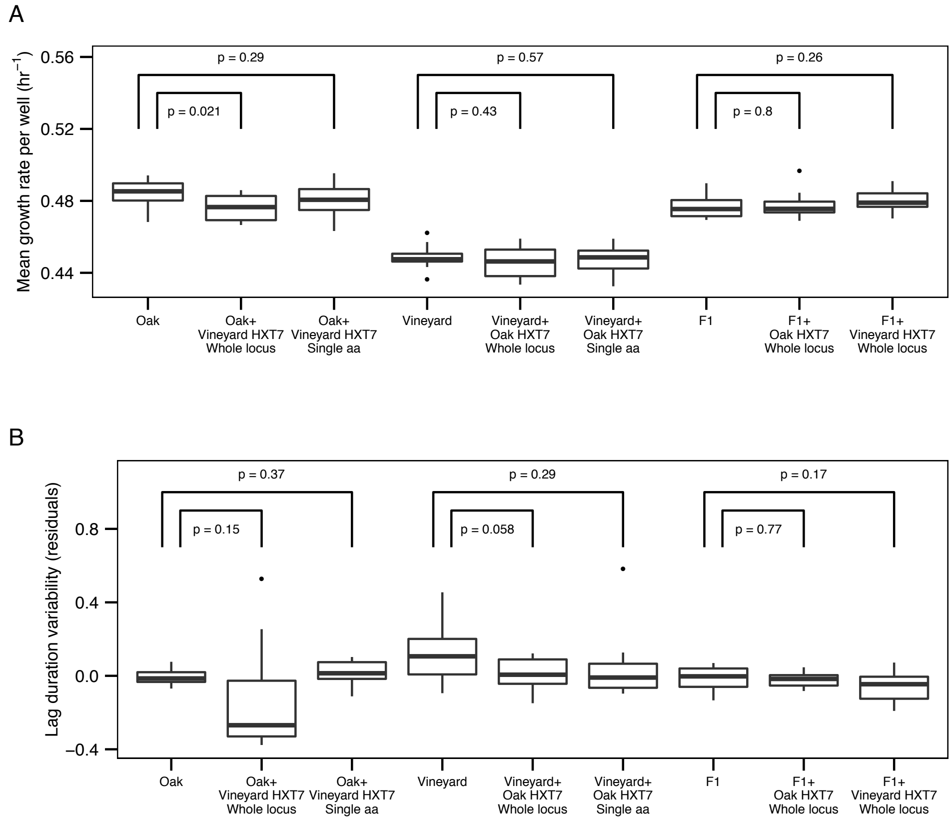


Figure S8 - Growth rate in non-limiting glucose conditions and lag duration variability in limiting glucose condition for HXT7 allele replacement strains.

Distributions of (A) mean growth rate in 4.44mM glucose or (B) lag variability in 0.22mM glucose for HXT7 allele replacement strains. P-values are for two sample t-tests, n=12 (4 wells x 3 plates) for each strain.

Figure S9

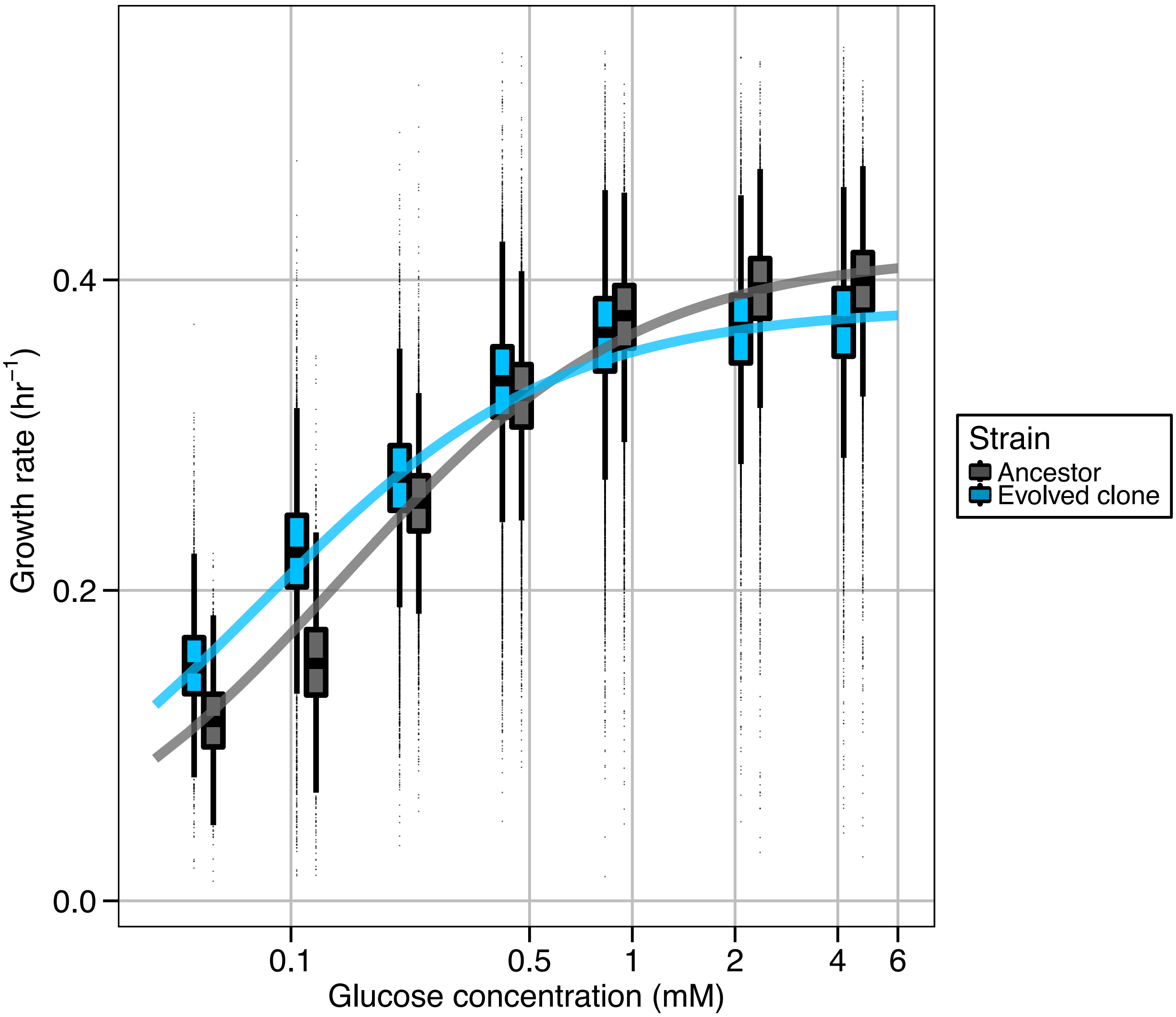


Figure S9 - HXT6/7 amplification confers a growth advantage only at limiting glucose concentrations.

The evolved clone contains a HXT6/7 amplification that is not present in the ancestor. Solid curves depict best fit of the Monod equation to normalized data, see (Ziv et al. 2013). Data are from measurement of 12 wells (across 4 plates) per strain and condition combination. Estimated µMax and KS values are 0.417hr-1 and 0.14mM for the ancestor and 0.38 hr-1 and 0.08mM for the evolved strain.

Ziv N., Siegal M. L., Gresham D., 2013 Genetic and Nongenetic Determinants of Cell Growth Variation Assessed by High-Throughput Microscopy. Mol. Biol. Evol. 30: 2568–2578.

Figure S10

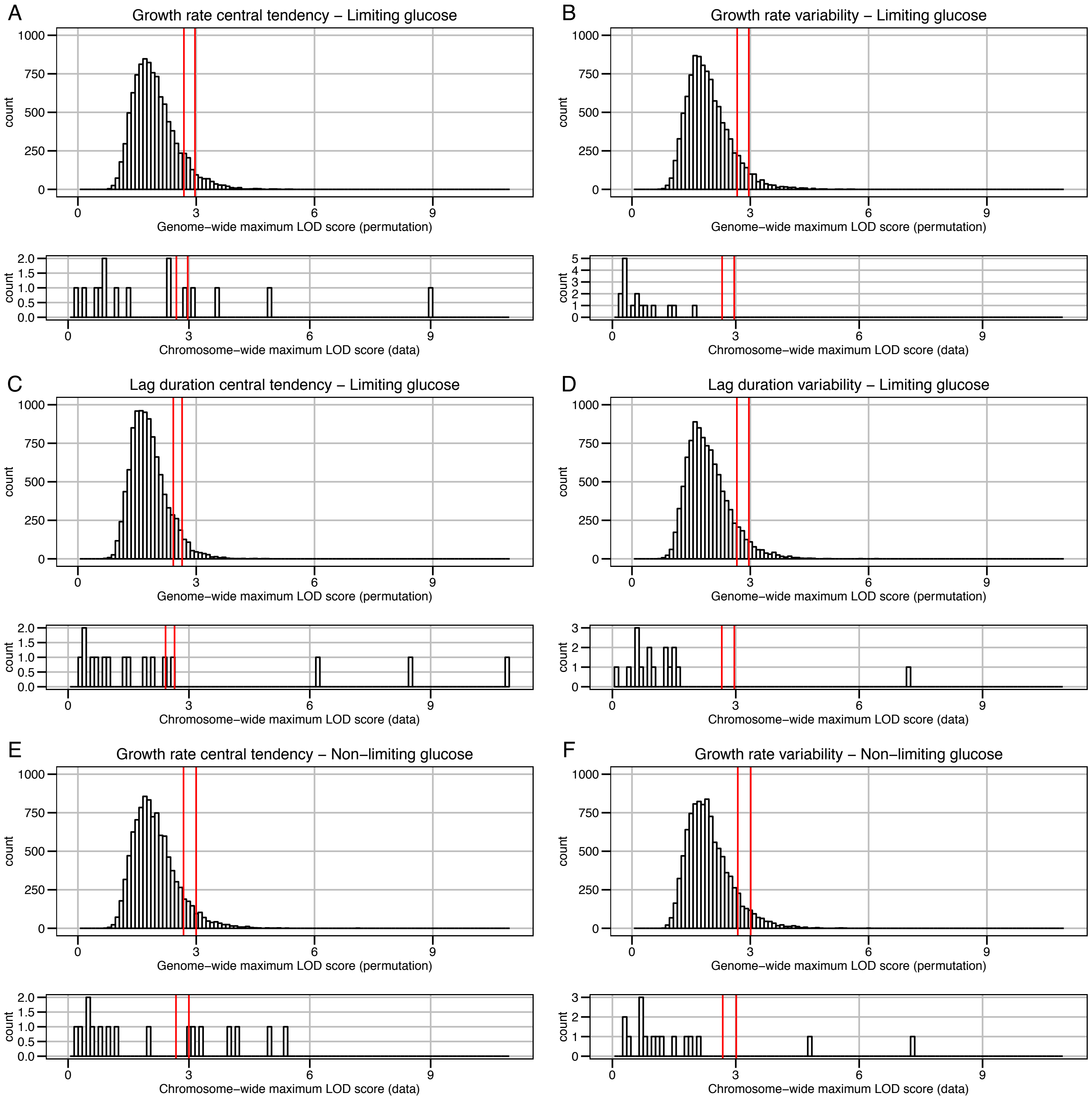


Figure S10 - Permutations for single QTL genome scans.

Empirical null distributions obtained by 10,000 permutations (upper panels) and distributions of chromosome maximums (lower panels). Each permutation retains the maximum LOD score for each trait (upper panels). Red vertical lines correspond to 0.1 and 0.05 significance thresholds. (A) Mean growth rate in 0.22mM glucose, (B) growth rate variability in 0.22mM glucose, (C) median lag duration in 0.22mM glucose, (D) lag variability in 0.22mM glucose, (E) mean growth rate in 4.44mM glucose, (F) growth rate variability in 4.44mM glucose. The x-axes are limited to a LOD score of 11 for clarity. Chromosome IV maximum for mean growth rate in 0.22mM glucose reaches a maximum value of 41.8.

Figure S11

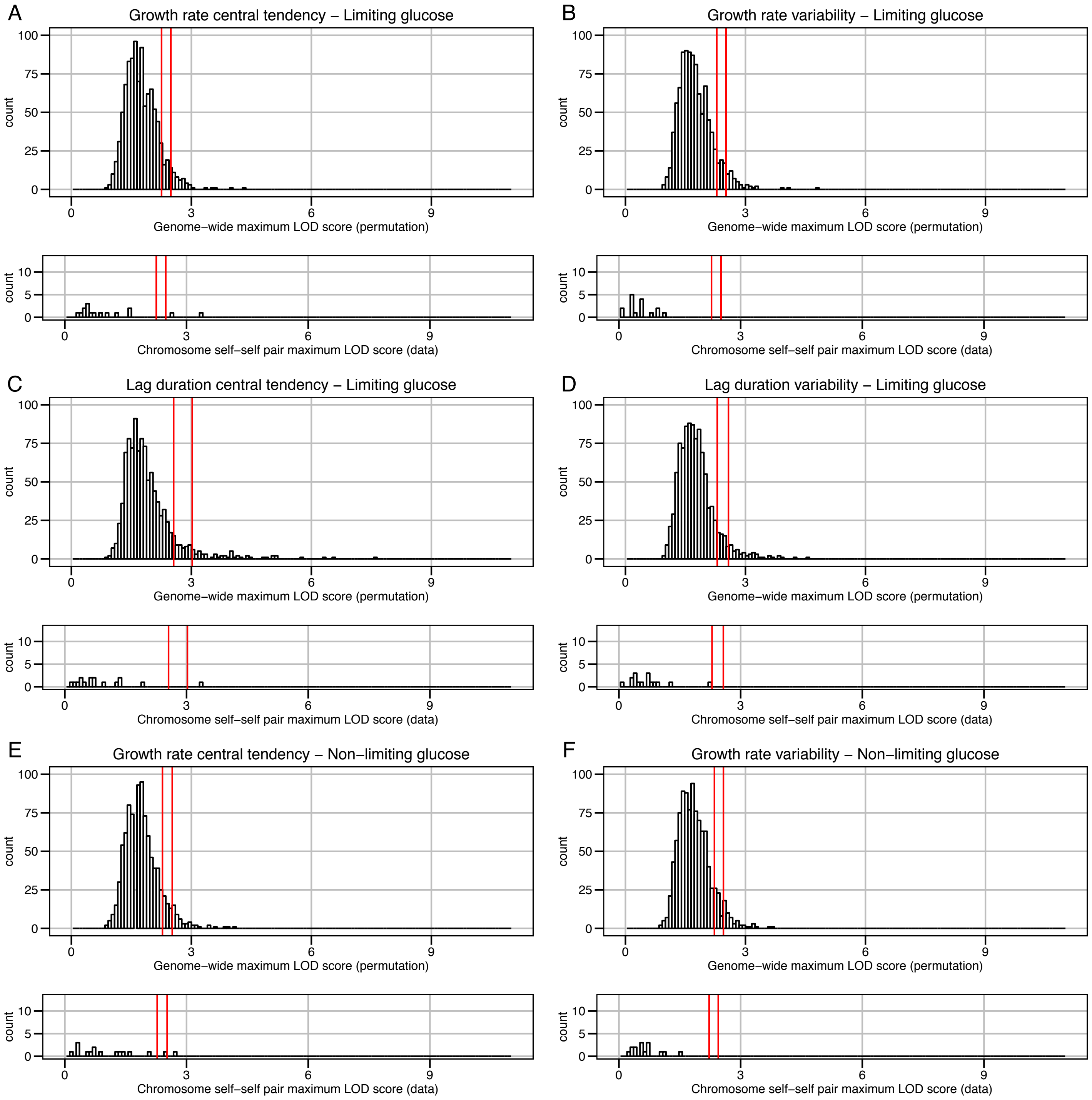


Figure S11 - Permutations for two QTL genome scans: identifying multiple additive QTL on the same chromosome. Empirical null distributions obtained by 1000 permutations (upper panels) and distributions of chromosome self-self pair maximums (lower panels). Each permutation retains the maximum conditional additive LOD score for each trait (upper panels). Red vertical lines correspond to 0.1 and 0.05 significance thresholds. (A) Mean growth rate in 0.22mM glucose, (B) growth rate variability in 0.22mM glucose, (C) median lag duration in 0.22mM glucose, (D) lag variability in 0.22mM glucose, (E) mean growth rate in 4.44mM glucose, (F) growth rate variability in 4.44mM glucose. For mean growth rate in 0.22mM glucose, two chromosomes (VII and X) passed the conditional-additive threshold but only the pair of loci on chromosome VII passed the additive threshold.

Figure S12

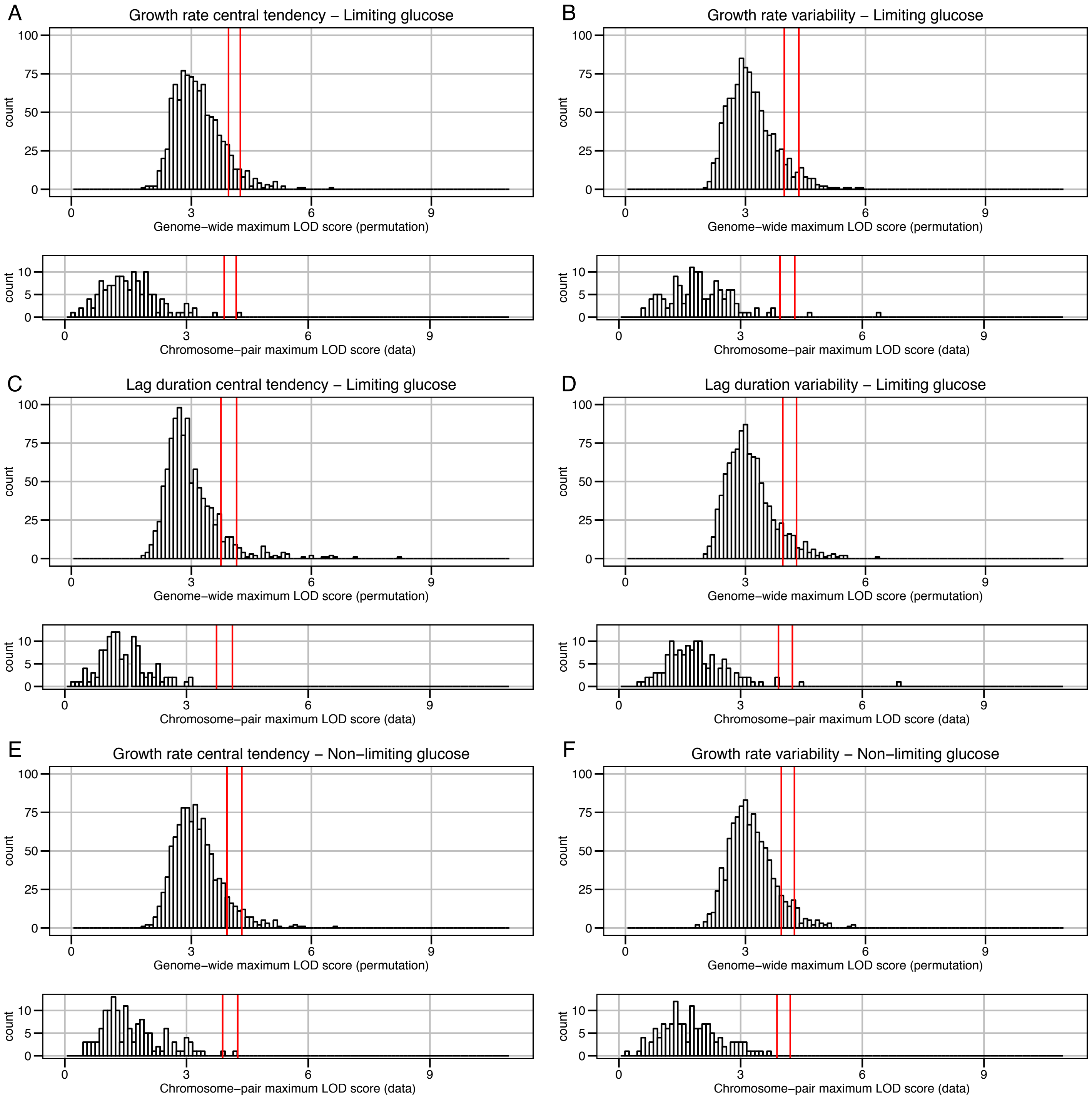


Figure S12 - Permutations for two QTL genome scans: identifying genetic interactions.

Empirical null distributions obtained by 1000 permutations (upper panels) and distributions of chromosome pair maximums (lower panels). Each permutation retains the maximum interaction LOD score for each trait (upper panels). Red vertical lines correspond to 0.1 and 0.05 significance thresholds. (A) Mean growth rate in 0.22mM glucose, (B) growth rate variability in 0.22mM glucose, (C) median lag duration in 0.22mM glucose, (D) lag variability in 0.22mM glucose, (E) mean growth rate in 4.44mM glucose, (F) growth rate variability in 4.44mM glucose.

Table S1. LOD scores for single QTL model determined by genome-wide interval mapping.
LOD scores for all loci identified in this study including additive QTL and genetic interactions. Positions are shown in cM as well as approximate physical location (in bp) based on known genomic location of markers. LOD scores are shown for all traits and are maximum value within 30cM of position. GR-growth rate, GR.V-growth rate variability, Lag-lag duration, Lag.V-lag duration variability, Chr.-chromosome, ‘low’ and ‘high’ correspond to glucose concentration.

Trait	Chr.	Position (cM)	Position (bp)	GR. (low)	GR.V (low)	Lag (low)	Lag.V (low)	GR. (high)	GR.V (high)
GR. (low)	4	421	1160904	41.809	1.84	6.177	7.155	3.251	1.504
GR. (low)	7	194	604096	8.965	0.708	8.535	1.277	3.282	0.048
GR. (low)	8	13	62967	3.098	0.615	0.142	0.864	0.26	0.497
GR. (low)	9	85.209	224632	2.892	0.243	1.764	1.451	2.985	1.927
GR. (low)	11	79	268728	3.691	0.09	0.989	0.891	3.955	0.1
GR. (low)	15	51.783	150756	5.029	0.682	10.916	0.833	2.674	1.781
GR. (low)	7	30	137644	4.101	0.329	0.818	0.93	5.439	0.615
GR. (low)	11	200	588873	0.705	0.752	0.337	1.288	0.176	0.288
GR. (low)	12	360	1002860	0.007	0.008	0.09	0.284	1.354	0.704
GR.V (low)	1	69	162928	0.737	0.142	1.23	0.106	0.468	1.113
GR.V (low)	10	154	412254	1.054	0.086	1.361	0.464	1.171	0.281
GR.V (low)	3	76	141885	0.357	0.273	0.203	0.85	0.367	0.739
GR.V (low)	6	5	119284	0.097	0.606	0.274	0.43	0.516	0.712
Lag (low)	4	424.142	1179958	41.809	1.94	6.177	7.155	3.251	1.504
Lag (low)	7	188.801	594654	8.977	0.708	8.535	1.277	3.475	0.048
Lag (low)	14	82	361686	1.473	0.161	2.644	0.199	0.594	0.944
Lag (low)	15	47	137707	5.029	0.712	10.916	0.833	2.674	1.781
Lag (low)	15	350	974737	1.214	0.224	3.381	0.212	2.049	0.26
Lag.V (low)	4	423	1173031	41.809	1.894	6.177	7.155	3.251	1.504
Lag.V (low)	1	27	88087	0.705	0.297	2.054	0.004	0.17	0.621
Lag.V (low)	4	157	327970	0.349	0.275	0.214	0.537	1.228	1.924
Lag.V (low)	1	67	156762	0.737	0.172	1.319	0.004	0.468	1.113
Lag.V (low)	10	157	417725	1.054	0.129	1.361	0.002	1.242	0.281
Lag.V (low)	9	92	253032	2.892	0.243	1.735	1.176	2.985	2.693
Lag.V (low)	14	160	587945	0.315	0.249	0.329	0.525	0.341	0.105
Lag.V (low)	12	380	1033949	0.194	0.004	0.014	0.003	1.354	0.012
Lag.V (low)	15	77	214637	5.029	0.668	10.909	0.384	2.674	1.781
GR. (high)	4	421	1160904	41.809	1.84	6.177	7.155	3.251	1.504
GR. (high)	7	30	137644	4.112	0.329	0.818	0.93	5.429	0.615
GR. (high)	9	85.209	224632	2.892	0.243	1.764	1.451	2.985	1.927
GR. (high)	11	86	286752	3.691	0.09	0.989	0.891	3.955	0.1
GR. (high)	12	229	609824	0.183	0.76	1.309	0.1	5.003	4.806
GR. (high)	15	185	528176	1.564	1.203	1.525	0.461	3.145	0.621
GR. (high)	16	177	512955	1.018	0.229	0.683	0.247	4.181	1.543
GR. (high)	7	156	466129	8.006	0.596	8.229	0.093	3.496	0.065
GR. (high)	15	63	179172	5.029	0.682	10.916	0.826	2.669	1.781
GR. (high)	4	105	182578	0.251	1.273	0.103	0.844	0.269	0.124
GR. (high)	7	255	763417	4.802	0.434	2	1.194	0.162	0.251
GR.V (high)	9	146.039	361957	2.062	0.08	0.463	1.331	1.753	7.335
GR.V (high)	12	209	550479	0.21	0.76	1.116	0.27	5.003	4.806

Table S2. Two QTL model LOD scores determined by interval mapping for all genetic interaction loci and traits.

Each column specifies one interaction, with position for both loci in cM as well as approximate physical location (in bp) based on position of markers. The additive model and full model LOD scores are shown for the specific pair of positions for all traits. GR-growth rate, GR.V-growth rate variability, Lag-lag duration, Lag.V-lag duration variability, Chr.-chromosome, 'low' and 'high' correspond to glucose concentration.

Trait	**GR. (low)**	**GR.V (low)**	**GR.V (low)**	**Lag.V (low)**	**Lag.V (low)**	**Lag.V (low)**	**Lag.V (low)**	**GR.V (high)**
Chr. 1	11	1	3	1	1	9	12	4
Position 1 (cM)	200	69	76	27	67	92	380	105
Position 1 (bp)	588873	162928	141885	88087	156762	253032	1033949	182578
Chr. 2	12	10	6	4	10	14	15	7
Position 2 (cM)	360	154	5	157	157	160	77	255
Position 2 (bp)	1002860	412254	119284	327970	417725	587945	214637	763417
GR. (low) Additive	0.706	0.279	0.244	0.671	0.308	2.543	2.154	2.577
GR. (low) Full	5.037	1.115	0.326	0.702	1.036	2.931	3.634	3.258
GR.V (low) Additive	0.744	0.198	0.998	0.197	0.182	0.496	0.016	1.29
GR.V (low) Full	0.746	6.627	5.707	2	6.512	0.523	0.037	1.347
Lag (low) Additive	0.029	1.39	0.217	1.97	1.452	0.536	5.936	1.392
Lag (low) Full	1.722	1.45	0.395	1.98	1.478	0.643	5.987	1.875
Lag.V (low) Additive	1.315	0.002	0.708	0.544	0.005	1.665	0.386	0.803
Lag.V (low) Full	2.141	6.538	1.104	4.492	6.879	5.599	4.888	0.913
GR. (high) Additive	0.14	0.447	0.607	0.05	0.5	2.224	3.548	0.424
GR. (high) Full	0.318	1.152	0.668	0.067	1.149	2.31	3.728	4.62
GR.V (high) Additive	0.267	1.123	1.362	1.661	1.098	1.002	1.535	0.053
GR.V (high) Full	0.669	1.265	2.847	1.802	1.312	1.033	1.54	0.348

Table S3. Comparison of QTL mapping approaches.
The list of intervals defined by each pair of adjacent markers used in the interval mapping. Each row specifies an interval that had a maximal LOD score greater than 3 in at least one condition. The data include interval mapping in 0.22mM glucose or 4.44mM glucose, bulk segregant analysis of the advanced intercross grown in low or high dilution rate chemostats (scores are for combined replicate data) and bulk segregant analysis of the pool of F2 segregants grown in low or high dilution rate chemostats. MULTIPOOL results are shown with parameters n=1000 (number of individuals) and r=1000 (length of cM). GR-growth rate, 'low' and 'high' correspond to glucose concentration or dilution rate, AIC-advanced intercross.

Marker 1	Marker 2	Position 1 (bp)	Position 2 (bp)	GR. (low)	GR. (high)	F2 (low)	F2 (high)	AIC (low)	AIC (high)
L1.1	L1.2	32304	65359	0.7	0.01	4.72	1.22	0.54	0.52
L1.2	L1.3	65359	112085	0.67	0.17	4.85	0.66	0.5	0.49
L2.1	L2.2	120437	157331	0.55	0.2	3.57	1.51	0.48	1.31
L2.2	L2.3	157331	232715	0.9	0.07	3.79	0.89	1.43	1.06
L2.6	L2.7	401143	470054	0.26	0.18	0.95	2	3.02	1.9
L2.8	L2.9	502224	575934	0.67	0.04	6.18	0.7	1.66	0.79
L2.9	L2.10	575934	656829	0.17	0.04	6.1	0.5	1.85	0.6
L2.11	L2.12	702460	771102	0.01	0.02	5.49	1.78	3.28	1.24
L3.4	L3.5	188786	225558	0.36	0.54	1.15	3.14	2.61	0.49
L4.1	L4.2	49679	114170	0.01	0.02	2.39	1.69	5.8	1.79
L4.2	L4.3	114170	151239	0.25	0.42	1.56	1.38	5.42	0.68
L4.3	L4.4	151239	246448	0.25	0.42	7.06	0.98	5.6	0.64
L4.4	L4.5	246448	280697	0.01	0.03	6.42	0.66	1.61	1.2
L4.5	L4.6	280697	346360	0.05	0.03	2.83	0.55	2.84	3.41
L4.12	L4.13	635526	696637	0.63	0.99	1.02	4.09	1.65	1.78
L4.15	L4.16	826861	938147	6.44	0.84	15.13	7.44	3.55	1.59
L4.16	L4.17	938147	1005614	9.79	1.04	24.21	9.57	4.95	1.56
L4.17	L4.18	1005614	1071559	20.35	1.55	31.39	16.66	16.07	1.71
L4.18	L4.19	1071559	1105164	30.71	2.49	44.2	21.63	30.66	4.87
L4.19	L4.20	1105164	1179958	41.81	3.25	60.1	21.82	54.97	13.09
L4.20	L4.21	1179958	1230646	40.53	3.19	59.81	18.75	27.15	10.87
L4.21	L4.22	1230646	1264123	34.55	2.61	42.53	13.19	17.25	6.68
L4.22	L4.23	1264123	1362236	15.45	1.11	11.49	4.26	4.57	4
L4.23	L4.25	1362236	1501556	4.41	0.45	8.01	0.85	0.71	0.82
L5.1	L5.2	49043	100056	0.17	1.17	9.51	2.47	4.09	2.25
L5.2	L5.3	100056	158171	0.1	0.1	9.39	3.43	3.73	2.61
L5.3	L5.4	158171	217279	0.1	0.14	5.64	3.94	3.98	1.42
L5.4	L5.5	217279	338773	0.3	0.36	3.09	1.77	4.79	0.72
L5.5	L5.6	338773	399605	0.3	0.36	2.39	0.62	3.58	0.45
L6.3	L6.4	170876	201882	0.04	0.32	0.51	1.37	3.71	0.64
L6.4	L6.5	201882	223558	0.25	0.24	0.49	0.71	3.25	0.48
L7.1	L7.2	44796	96932	3.48	4.11	5.07	5.97	2.2	0.88
L7.2	L7.3	96932	171763	4.11	5.44	5.14	5.99	3.55	0.67
L7.3	L7.4	171763	230207	3.79	4.83	3.66	3.43	2.86	0.7
L7.4	L7.5	230207	284675	2.63	2.97	3.22	4.07	0.53	0.58
L7.7	L7.8	432466	490117	5	3.5	4.91	0.86	0.63	1.35
L7.8	L7.9	490117	545582	5.51	2.96	4.73	1.39	0.53	0.72

L7.9	L7.11	545582	594654	8.84	3.05	1.38	1.49	0.41	0.46
L7.11	L7.12	594654	644097	8.98	2.97	1.46	1.7	1.49	0.46
L7.12	L7.13	644097	726509	4.8	0.75	1.3	0.93	2.85	1.25
L7.13	L7.14	726509	763036	3.26	0.64	0.55	0.55	2.96	0.58
L7.15	L7.16	809363	863960	3.05	0.72	1.61	0.72	1.61	0.51
L7.16	L7.17	863960	892563	3.05	0.89	1.66	0.62	1.36	0.5
L8.1	L8.2	44529	66740	3.1	0.26	8.36	2.33	10.71	0.73
L8.2	L8.3	66740	117292	3.07	0.14	13.06	3.9	13.93	0.51
L8.3	L8.4	117292	153282	0.53	0.14	9.59	3.5	15.54	0.5
L8.4	L8.5	153282	198394	0.15	0.31	3.18	2.95	8.85	0.82
L8.5	L8.6	198394	218718	0.22	0.31	0.9	1.29	4.98	0.96
L8.6	L8.7	218718	256537	0.22	0.08	1.15	1.3	4.41	0.89
L8.7	L8.8	256537	297020	0.21	0.01	2.11	0.42	3.18	0.97
L8.8	L8.9	297020	396688	0.2	0.12	4.62	0.53	3.81	2.17
L9.5	L9.6	201167	224632	2.89	2.99	1.87	4.13	1.93	0.64
L9.6	L9.7	224632	250317	2.89	2.99	2.12	4.94	0.53	0.65
L9.7	L9.8	250317	276759	2.83	2.2	2.24	4.69	0.76	0.66
L10.1	L10.2	37500	66255	1.16	1.97	3.89	1.31	1.47	0.65
L10.5	L10.6	219800	270368	0.58	0.58	3.29	2.63	1.72	1.54
L10.8	L10.9	336551	385727	0.63	0.71	1.49	4.67	1.35	1.26
L10.9	L10.10	385727	444535	0.83	0.64	1.2	8.76	1.28	2.63
L10.10	L10.11	444535	465360	1.05	1.27	0.79	8.63	0.68	2.85
L10.11	L10.12	465360	527586	1	1.27	1.99	6.69	0.45	2.19
L10.12	L10.13	527586	565916	0.51	0.06	5.56	0.69	0.57	0.58
L10.13	L10.14	565916	619631	0.8	0.15	6.27	2.24	0.59	1.14
L10.14	L10.15	619631	660770	0.77	0.26	6.4	1.78	0.91	1.09
L10.15	L10.16	660770	690593	0.68	0.86	1.96	0.42	3.08	0.49
L11.1	L11.2	42555	98234	0.01	0.02	4.73	6.84	2.41	1.12
L11.2	L11.3	98234	153726	1.21	1.44	2.07	4.79	2.25	2.2
L11.4	L11.5	206087	249055	3.32	2.56	1.28	3.55	1.87	1.98
L11.5	L11.6	249055	295134	3.69	3.95	0.49	3.55	2.54	2.35
L11.6	L11.7	295134	350464	3.03	3.9	0.55	1.64	0.79	0.47
L11.11	L11.12	504700	550500	1.02	0.16	0.86	4.57	0.61	0.94
L11.12	L11.13	550500	575225	0.94	0.09	1.49	4.35	0.43	2
L11.13	L11.14	575225	611629	0.71	0.18	2.37	5.65	0.41	3.61
L11.14	L11.15	611629	637800	0.52	0.18	1.87	7.97	0.41	3.92
L12.2	L12.3	89702	154678	0.34	0.05	0.52	0.84	4.99	2.04
L12.3	L12.4	154678	213608	0.17	0.11	0.73	1	5.96	2.2
L12.6	L12.7	311265	367241	0.33	1.07	3.18	5.15	0.86	0.66
L12.7	L12.8	367241	451216	0.33	2.54	2.11	5	2.37	1.03
L12.9	L12.10	492640	518152	0.21	3.64	1.29	0.65	1.99	0.41
L12.10	L12.11	518152	561785	0.1	4.17	0.84	0.69	2.39	0.66
L12.11	L12.12	561785	672637	0.07	5	2.72	4.01	2.22	1.38
L12.12	L12.13	672637	717712	0.32	3.29	1.28	4.13	2.79	1.54
L12.13	L12.14	717712	755968	0.91	3.49	2.96	2.23	2.76	1.57
L12.14	L12.15	755968	820804	0.91	3.49	6.65	3.55	2.07	3
L12.15	L12.16	820804	881789	0.06	0.87	9.32	4.28	0.81	2.46

L12.16	L12.17	881789	969370	0.06	0.05	7.71	0.51	1.7	0.78
L12.17	L12.18	969370	990749	0.07	0.02	9.87	0.46	1.36	0.81
L12.18	L12.19	990749	1034324	0.19	1.35	9.87	0.68	1.63	1.1
L13.1	L13.2	56276	102221	0.36	0.13	3.62	0.51	1.4	0.71
L13.5	L13.6	244520	308353	1.53	0.88	4.62	3.24	3.65	0.48
L13.6	L13.7	308353	341111	2.51	0.98	10.24	2.39	3.88	0.51
L13.7	L13.8	341111	396424	2.51	0.92	8.93	2.17	2.88	0.62
L13.8	L13.9	396424	502787	1.55	0.63	8.55	2.5	2.16	1.52
L13.9	L13.10	502787	555633	0.82	0.62	5.98	2.25	1.99	1.76
L13.16	L13.17	858414	914425	0.81	0.09	4.86	3.14	1.42	1.38
L14.4	L14.5	231538	288198	1.06	0.02	1.38	4.18	1.43	3.19
L14.5	L14.6	288198	340447	1.36	0.07	2.47	8.73	1.77	3.93
L14.6	L14.7	340447	387811	1.47	0.27	2.93	8.71	1.65	3.07
L14.7	L14.8	387811	437370	1.44	0.55	2.39	5.7	1.07	1.17
L14.8	L14.9	437370	466584	1.06	0.59	1.25	4.22	0.64	1.31
L14.9	L14.10	466584	502292	0.35	0.57	3.76	4.15	0.41	0.45
L14.10	L14.11	502292	558811	0.05	0.28	10.31	2.68	1.45	0.45
L14.11	L14.13	558811	635465	0.31	0.04	11.16	1.08	3.58	0.94
L14.13	L14.14	635465	694158	0.31	0.29	5.32	1.38	4.78	0.61
L14.14	L14.15	694158	745494	0.25	0.29	3.02	2	4.8	0.46
L15.1	L15.2	51154	88251	1.34	0.27	3.19	9.3	0.93	4.09
L15.2	L15.3	88251	150756	5.03	2.22	3.38	1.56	0.5	2.29
L15.3	L15.4	150756	215310	5.03	2.67	4.59	2.69	1.36	2.1
L15.4	L15.5	215310	280789	1.92	2.16	4.64	1.34	1.46	1.71
L15.5	L15.6	280789	346309	0.29	0.13	4.74	0.66	0.64	1.97
L15.6	L15.7	346309	407363	0.21	0	5.16	0.52	2.33	1.89
L15.7	L15.8	407363	454325	0.55	0.27	5.85	1.21	2.69	1.51
L15.8	L15.9	454325	523989	1.56	3.13	6.11	3.37	1.35	0.88
L15.9	L15.10	523989	572941	1.55	3.15	2.77	2.65	1.26	0.93
L15.13	L15.14	693081	747648	1.25	0.72	3.31	1.39	1.77	0.65
L15.14	L15.15	747648	804445	1.25	0.73	7.23	2.9	0.46	1.17
L15.15	L15.16	804445	826784	0.48	0.48	7.23	2.61	0.45	1.32
L15.16	L15.17	826784	870951	0.29	1.05	7.27	2.41	0.46	1.14
L15.17	L15.18	870951	898552	1.44	2.18	4.57	1.72	0.54	0.95
L15.18	L15.19	898552	912655	1.44	2.18	3.46	1.74	1.33	0.91
L16.6	L16.7	266276	324298	0.43	0.7	0.45	3.24	1.16	3.73
L16.7	L16.8	324298	372267	0.05	1.95	1.08	6.32	0.85	4.06
L16.8	L16.9	372267	429004	0.54	2.95	0.75	8.96	0.51	2.91
L16.9	L16.10	429004	482737	0.82	3.12	3.72	8.77	0.59	3.34
L16.10	L16.11	482737	536003	0.85	4.18	8.73	9.38	0.41	7.4
L16.11	L16.12	536003	593104	0.41	3.48	7.92	12.67	0.49	7.26
L16.12	L16.13	593104	648617	1.28	2.91	5.46	16.3	0.68	4.26
L16.13	L16.14	648617	745578	1.28	2.5	0.83	16.16	1.19	2.87

File S1 (uploaded separately). ***HXT6*** **and** ***HXT7*** **sequences in the oak and vineyard strains.**

FASTA file containing Oak and Vineyard HXT6 and HXT7 open reading frames, downstream and upstream sequences determined by cloning the loci and performing sanger sequencing.