Supporting Information

Table S1. Tukey test results following ANOVA tests to examine the influence of environment and strain on the rate of genome size change.

Haploids

Environment	Change	Group
SDC	98.0 ± 40.0	a
SD	3.5 ± 6.2	c
Pdep	10.5 ± 21.6	c
Ndep	63.3 ± 25.2	b

Diploids

Environment	Change	Group
SDC	-3.5 ± 9.5	b
SD	-0.9 ± 4.0	b
Pdep	12.6 ± 37.5	a
Ndep	-4.1 ± 3.4	b

Line	Change	Group
2N1	9.8 ± 32.6	a
2N2	-5.3 ± 9.0	b
2N3	-1.1 ± 3.4	b

Tetraploids

Environment	Change	Group
SDC	-42.2 ± 50.4	a
SD	-79.4 ± 45.0	c
Pdep	-77.1 ± 64.1	bc
Ndep	-58.5 ± 61.6	ab

Line	Change	Group
4N1	-126.9 ± 34.1	b
4N2	-35.9 ± 51.7	a
4N3	-44.5 ± 45.7	a
4N4	-49.3 ± 44.9	a

Supporting Information

Table S2. Least square means pairwise posthoc tests to determine the influence of evolutionary environment on change in growth rate. Degree of freedom was 342 in all tests.

Haploids

SE = 0.0142

Contrast	estimate	t ratio	p value
Ndep-Pdep	0.0460	3.236	0.007
Ndep-MM	0.0462	3.250	0.007
Ndep-SDC	-0.083	-5.855	< 0.0001
Pdep-MM	0.0002	0.014	1.000
Pdep-SDC	-0.129	-9.091	< 0.0001
MM-SDC	-0.130	-9.105	< 0.0001

Diploids

SE = 0.0112

Contrast	estimate	t ratio	p value
Ndep-Pdep	-0.041	-3.537	0.003
Ndep-MM	-0.053	-4.536	< 0.0001
Ndep-SDC	-0.037	-3.203	0.0081
Pdep-MM	-0.012	-0.999	0.750
Pdep-SDC	0.004	0.334	0.987
MM-SDC	0.016	1.334	0.541

Polyploids

SE = 0.0101

Contrast	estimate	t ratio	p value
Ndep-Pdep	0.1000	9.912	<0.0001
Ndep-MM	0.0838	8.326	< 0.0001
Ndep-SDC	0.0988	9.817	< 0.0001
Pdep-MM	-0.0159	-1.585	0.388
Pdep-SDC	-0.0010	-0.095	1.000
MM-SDC	0.0150	1.490	0.444

Supporting Information

Table S3. Least square means pairwise posthoc tests to determine the influence of evolutionary environment on change in yield. Degree of freedom was 342 in all tests.

Haploids

SE = 0.0142

Contrast	estimate	t ratio	p value
Ndep-Pdep	0.301	6.213	<0.0001
Ndep-MM	315	6.502	< 0.0001
Ndep-SDC	-0.371	-7.650	< 0.0001
Pdep-MM	0.014	0.289	0.992
Pdep-SDC	-0.672	-13.863	< 0.0001
MM-SDC	-0.686	-14.152	< 0.0001

Diploids

SE = 0.0112

Contrast	estimate	t ratio	p value
Ndep-Pdep	-0.003	-0.033	1.000
Ndep-MM	-0.025	-0.636	0.920
Ndep-SDC	-0.105	-2.645	0.042
Pdep-MM	-0.024	-0.603	0.931
Pdep-SDC	-0.103	-2.613	0.046
MM-SDC	-0.080	-2.009	0.187

Polyploids

SE = 0.0101

Contrast	estimate	t ratio	p value
Ndep-Pdep	0.252	7.375	<0.0001
Ndep-MM	0.190	5.551	< 0.0001
Ndep-SDC	0.211	6.155	< 0.0001
Pdep-MM	-0.062	-1.824	0.264
Pdep-SDC	-0.042	-1.220	0.615
MM-SDC	0.021	0.603	0.931

Supporting Information

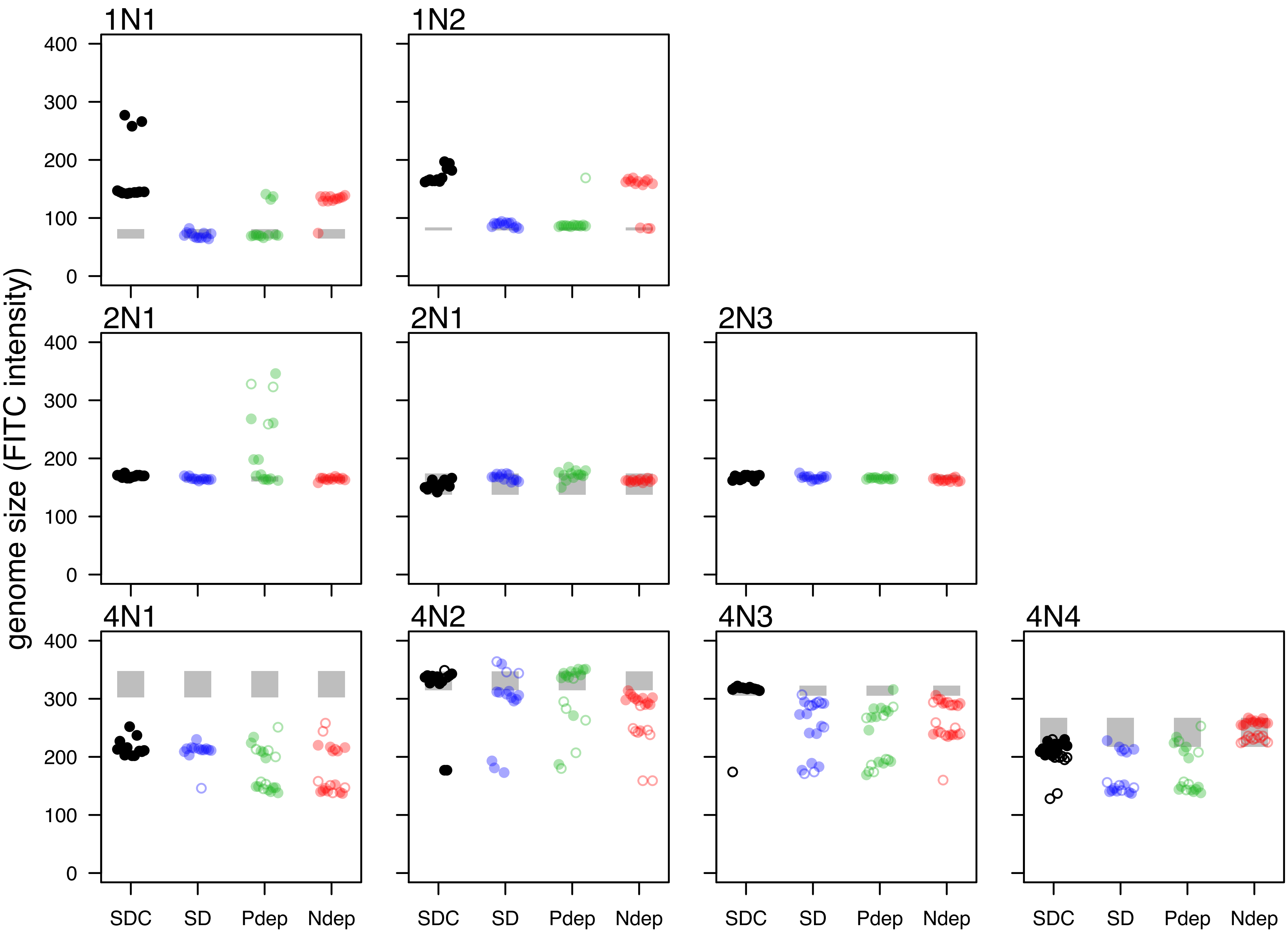

Figure S1. Strain background and environment influence genome stability. Twelve lines of each ancestral strain were evolved in complete (SDC, black points), minimal (MM, blue), phosphorus-deprivation (Pdep, green) and nitrogen-deprivation (Ndep, red) medium. Filled points represent the major peak and hollow points indicate the minor peaks in FITC intensity (see Figure 1) after ~140 generations of evolution. Top row = initially haploid lines; middle row = initially diploid lines; bottom row = initially polyploid lines. Grey boxes indicate the genome size range measured from twelve ancestral replicates for each strain.

Supporting Information

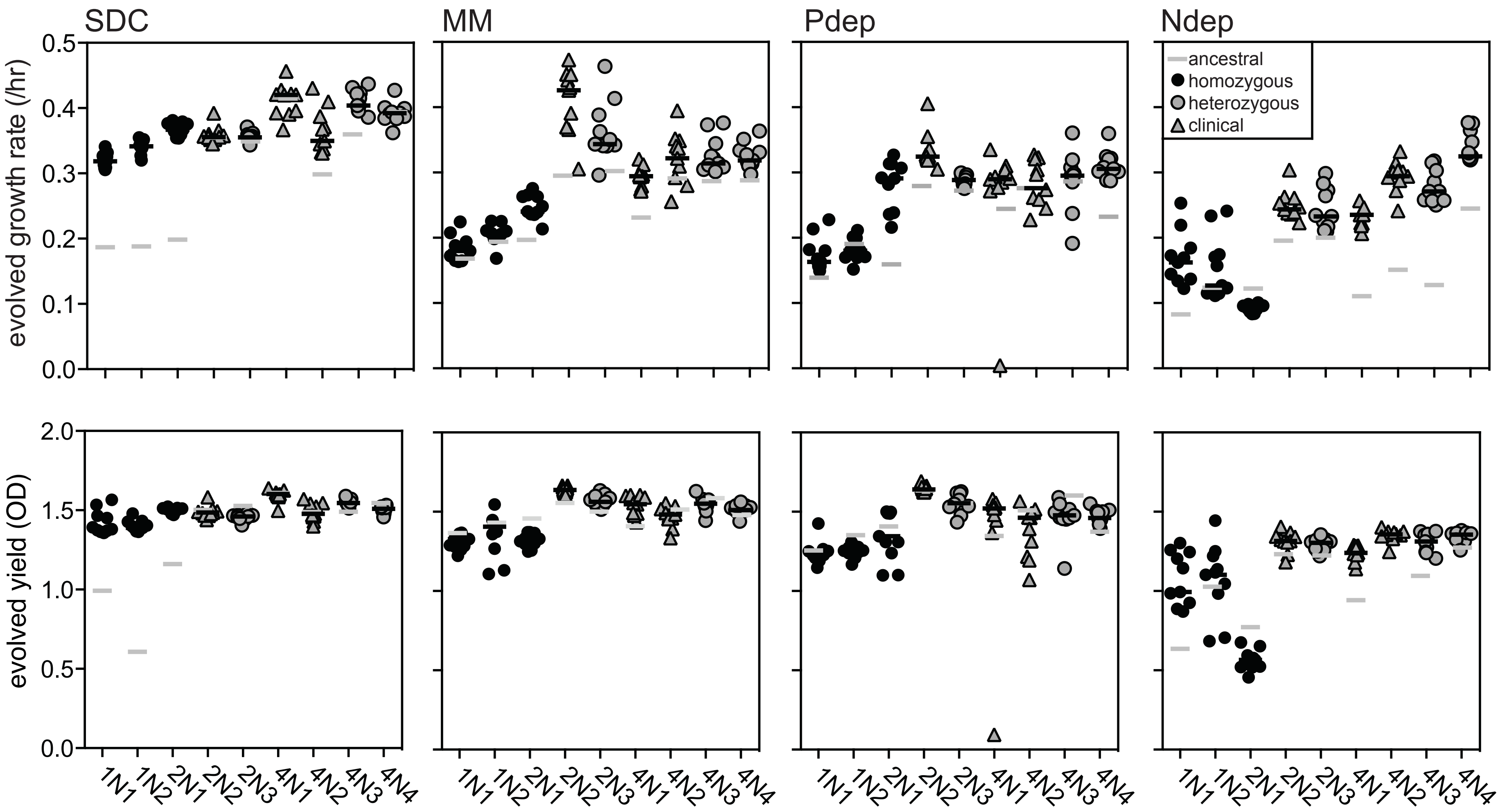

Figure S2. The majority of evolved lines increased in fitness. Each point is the evolved growth rate (top panel) and yield (bottom panel) of one of 10 replicate lines evolved for each ancestral strain. Black bars indicate the median of evolved growth rates and yield. Grey bars indicate the mean of ancestral growth rates and yield as presented in Figure 3.