

**Ploidy-regulated variation in biofilm-related phenotypes in natural isolates of *Saccharomyces cerevisiae***

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**Table S1 *S. cerevisiae* strains included in this study**

NAME	GEOGRAPHICAL ORIGIN	ECOLOGICAL ORIGIN	MATING TYPE	DIPLOID INCLUDED
DBVPG6765	Unknown	Unknown	a	yes
SK1	USA	Soil	a	yes
DBVPG6044	West Africa	Bili wine, from <i>Osbeckia grandiflora</i>	a	yes
DBVPG1373	Netherland	Soil	a	yes
DBVPG1853	Ethiopia	White Teff	a	yes
Y55	France	Grape	a	yes
YPS128	Pennsylvania, USA	Soil beneath <i>Q. alba</i>	a	yes
DBVPG1106	Australia	Grapes	a	yes
DBVPG6040	Netherland	Fermenting fruit juice	a	yes
BC187	Napa Valley, USA	Barrel fermentation	a	yes
YPS606	Pennsylvania, USA	Bark of <i>Q. rubra</i>	a	yes
L-1374	Chile	Fermentation from must Pais	a	yes
L-1528	Chile	Fermentation from must Cabernet	a	yes
NCYC361	Ireland	Beer spoilage strain from wort	a	yes
K11	Japan	Shochu sake strain	a	yes
Y12	Africa - Ivory Coast	Palm wine strain	a	yes
YS2	Australia	Baker strain	a	no
YS4	Netherlands	Baker strain	a	no
YS9	Singapore	Baker strain	a	no
UWOPS83-787.3	Bahamas	Fruit, <i>Opuntia stricta</i>	a	yes
UWOPS87-2421	Hawaii	Cladode, <i>Opuntia megacantha</i>	a	yes
UWOPS05-217.3	Malaysia	Nectar, Bertram palm	a	yes
UWOPS05-227.2	Malaysia	<i>Trigona</i> spp (Stingless bee) collected near Bertram palm flower	a	yes
W303	Unknown	N/A	a	no
322134S	RVI, Newcastle, UK	Clinical isolate (throat sputum)	a	no
378604X	RVI, Newcastle, UK	Clinical isolate (sputum)	a	no
273614N	RVI, Newcastle, UK	Clinical isolate (fecal)	a	yes

YJM978	Bergamo, Italy	Clinical isolate (vaginitis)	a	yes
YJM981	Bergamo, Italy	Clinical isolate (vaginitis)	a	yes
YJM975	Bergamo, Italy	Clinical isolate (vaginitis)	a	yes
FY4	Laboratory strain	Laboratory strain	a	no

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**Table S2 Qualitative scoring metrics**

<b>ASSAY</b>	<b>SCORE</b>	<b>CRITERIA</b>
Complex colony morphology	0	simple colonies
	1	non-smooth colony surface
	2	signs of complex morphology
	3	moderate complex morphology (does not cover entire colony)
	4	strong complex morphology (covers entire colony)
	5	very strong complex morphology
Complex mat formation	0	simple mat
	1	very light sectoring and/or light ruffle on edge
	2	clear ruffle on edge or petals, can include sectoring
	3	obvious complexity at edges
	4	obvious complexity at edges and in center
	5	strong complexity across entirety of mat
Diploid filamentous growth	0	no filaments
	1	short filaments sparsely distributed around perimeter
	2	long filaments sparsely distributed around perimeter
	3	long filaments distributed around majority of perimeter moderate length filaments densely distributed around entire
	4	perimeter
	5	long filaments densely distributed around entire perimeter

**File S1**

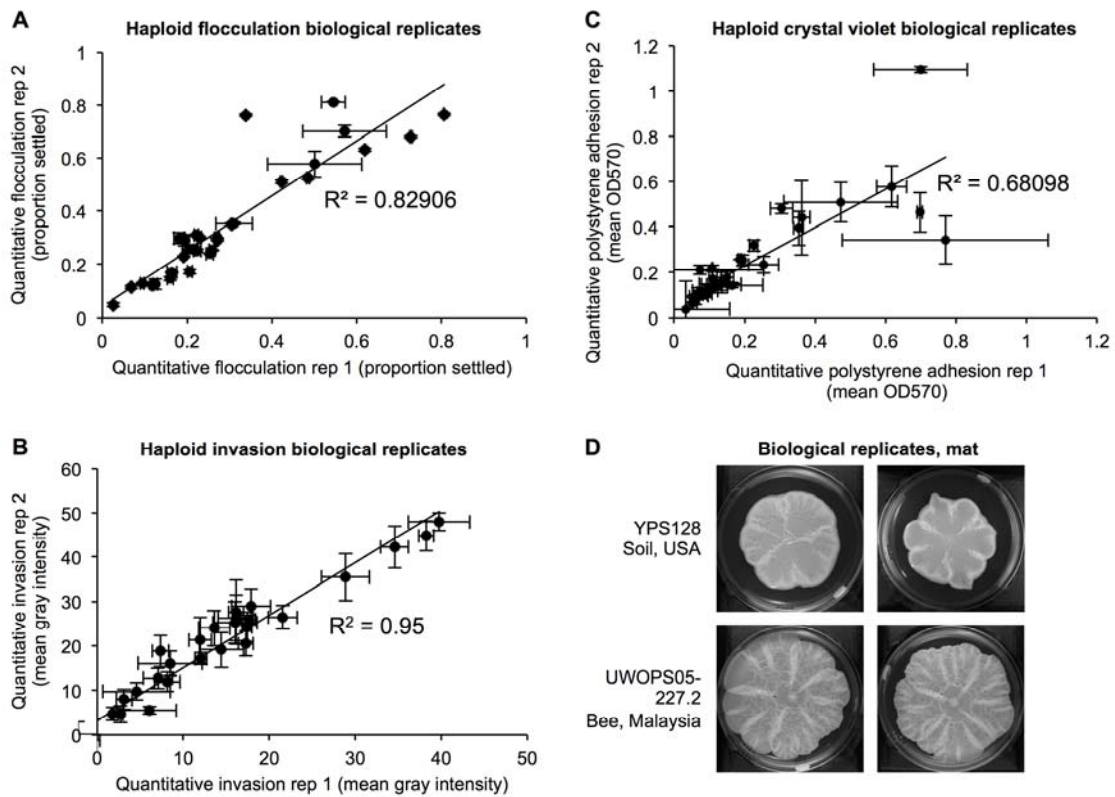
**Complete haploid phenotype dataset**

File S1 is available for download as a .pdf at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013250/-/DC1>

**Table S3 Qualitative score assignments**

<b>STRAIN</b>	<b>HAPLOID BIOREP1 COLONY</b>	<b>HAPLOID BIOREP2 COLONY</b>	<b>HAPLOID BIOREP1 MAT</b>	<b>DIPLOID COLONY</b>	<b>DIPLOID MAT</b>
DBVPG6765	0	0	0	0	1
SK1	4	4	4	4	4
DBVPG6044	2	2	2	1	4
DBVPG1373	0	0	0	0	3
DBVPG1853	1	2	0	1	3
Y55	1	0	2	2	0
YPS128	3	3	4	2	0
DBVPG1106	0	0	0	0	1
DBVPG6040	4	3	4	1	2
BC187	2	2	5	0	1
YPS606	3	3	5	0	0
L-1374	3	3	4	2	2
L-1528	4	5	5	3	3
NCYC361	0	0	0	0	3
K11	3	3	5	3	4
Y12	0	0	0	0	1
YS2	0	0	1		
YS4	1	1	3		
YS9	0	0	2		
UWOPS83- 787.3	1	1	0	0	0
UWOPS87- 2421	1	1	0	1	0
UWOPS05- 217.3	5	5	5	2	4
UWOPS05- 227.2	5	5	5	1	4
W303	0	0	2		
322134S	5		5		
378604X	1	1	2		
273614N	1	1	0	0	1
YJM978	3	2	5	0	3
YJM981	5	5	5	3	2
YJM975	0	0	1	2	2
FY4	2	2	3		

Strains are assigned qualitative scores based on the metric described in Table S2.



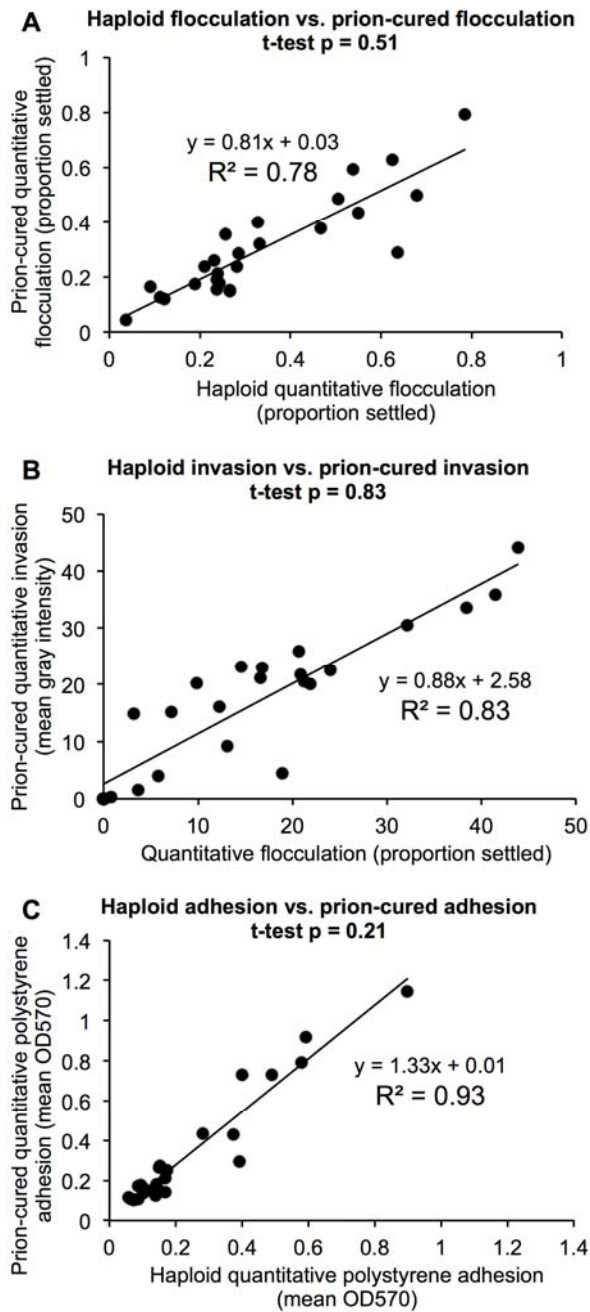
**Figure S1 Haploid biological replicates demonstrate consistency of quantitative assays** **a** Mean quantitative haploid flocculation data for one biological replicate (x-axis) is plotted against quantitative haploid flocculation data for a second biological replicate (y-axis) for correlation. Average taken and error bars calculated over three measurement replicates per strain. **b** Mean quantitative haploid invasion data for one biological replicate (x-axis) is plotted against quantitative haploid invasion data for a second biological replicate (y-axis) for correlation. Average taken and error bars calculated over three technical replicates per strain. **c** Mean quantitative haploid polystyrene adhesion data for one biological replicate (x-axis) is plotted against quantitative haploid polystyrene adhesion data for a second biological replicate (y-axis) for correlation. Average taken and error bars calculated over two technical replicates per strain. Outlier A shows the measurements from strain 322134S, and outlier B the measurements from strain SK1. Each of these strains was highly flocculent, and as a result the biofilm formed on polystyrene stained inconsistently across biological replicates and, in some cases, across technical replicates as well. If these outliers are eliminated from the analysis, the  $R^2$  value becomes 0.83. **d** Biological replicates of complex mat formation for two biological replicates of representative haploid strains. Photos taken at day 13 of growth.

**File S2**

**Complete prion-cured phenotype dataset**

File S2 is available for download as a .pdf at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013250/-/DC1>





**Figure S2 Prion-cured vs. haploid correlation plots show reproducibility** **a** Mean quantitative haploid flocculation data for all biological replicates (x-axis) is plotted against quantitative prion-cured flocculation data across all cured replicates (y-axis) for correlation. P-value is shown for two-tailed t-test assuming unequal variance. **b** Mean quantitative haploid invasion data for all biological replicates (x-axis) is plotted against quantitative prion-cured invasion data across all cured replicates (y-axis) for correlation **c** Mean quantitative haploid polystyrene adhesion data for all biological replicates (x-axis) is plotted against quantitative prion-cured polystyrene adhesion data across all cured replicates (y-axis) for correlation

**File S3**

**Table of quantitative assay results**

File S3 is available for download as a tab-delimited .txt file at  
<http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013250/-/DC1>

**Table S4 Quantitative changes in prion-cured strains vs. haploid strains**

	<b>FLOCCULATION<sup>a</sup></b>	<b>INVASION<sup>b</sup></b>	<b>ADHESION<sup>c</sup></b>
Significant decrease by FDR correction*	5	1	0
No change by FDR correction	20	20	23
Significant increase by FDR correction	1	2	2

The numbers of prion-cured strains that showed differences when compared to the original haploid strains across three quantitative metrics are shown. Quantitative values were compared using a two-tailed t-test assuming unequal variance across all technical replicates for each strain. *P*-values were evaluated for significance using the *q*-values package from Storey with the Benjamini-Hochberg method (Storey 2002).

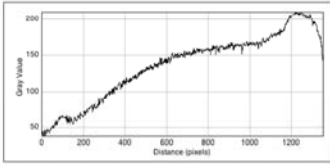
\* FDR = 0.05

<sup>a</sup> 26 strains

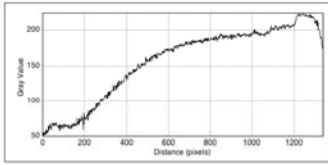
<sup>b</sup> 23 strains

<sup>c</sup> 25 strains

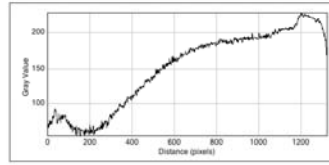
DBVPG6765 (YMD1152)



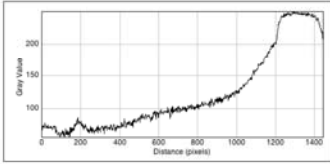
DBVPG1106 (YMD1166)



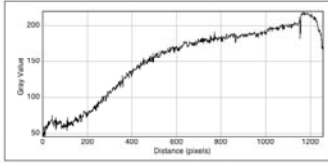
K11 (YMD1180)



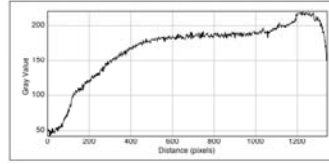
SK1 (YMD1154)



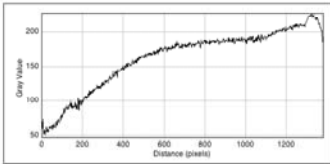
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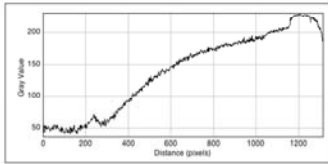
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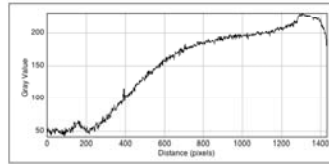
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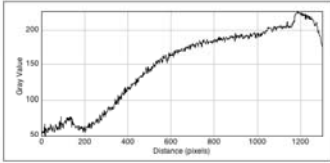
BC187 (YMD1170)



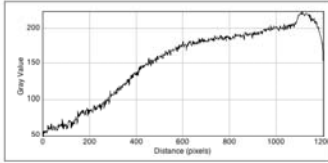
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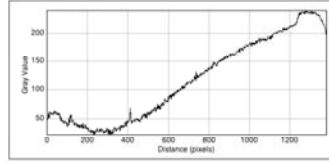
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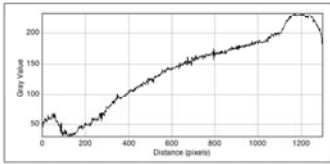
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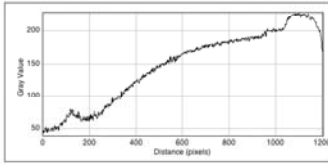
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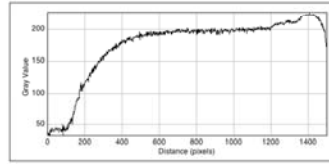
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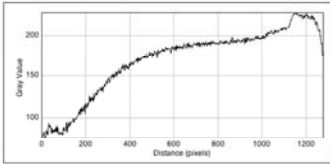
L-1374 (YMD1174)



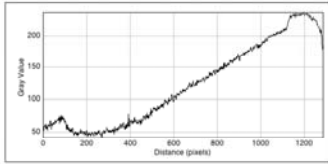
YS9 (YMD1188)



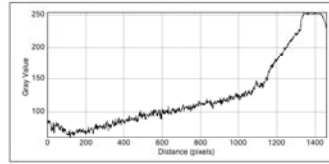
Y55 (YMD1162)



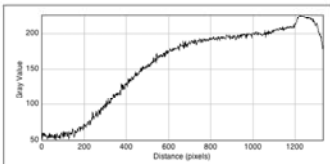
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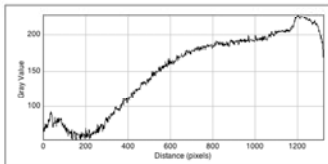
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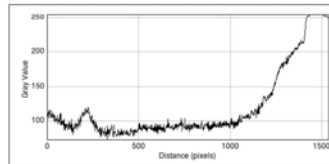
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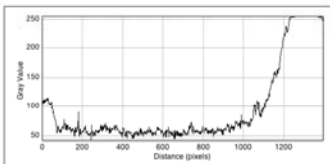
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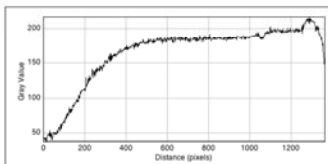
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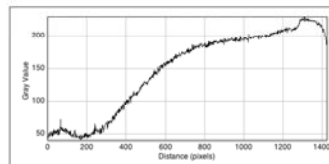
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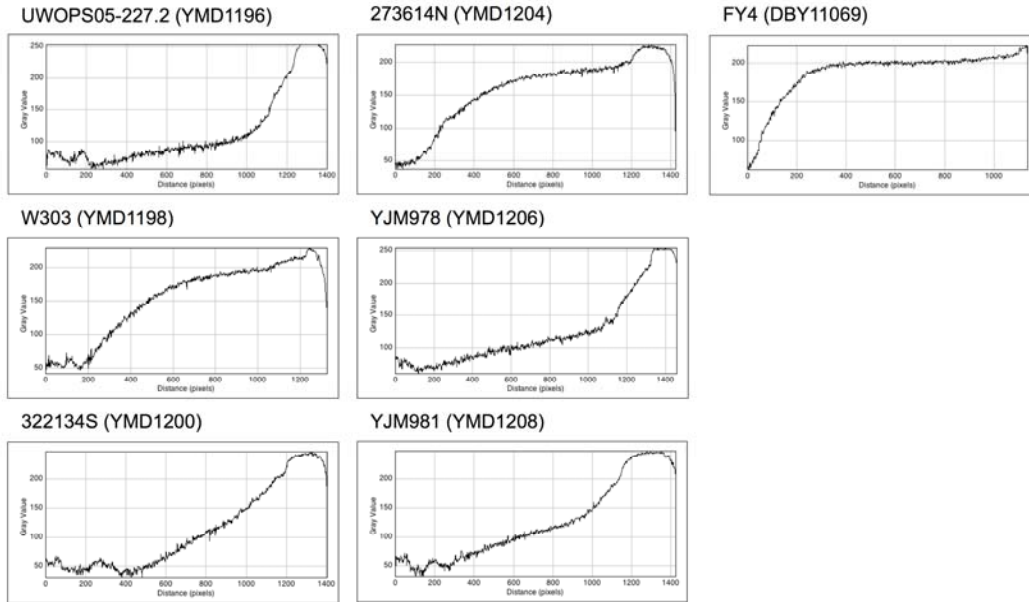


378604X (YMD1202)



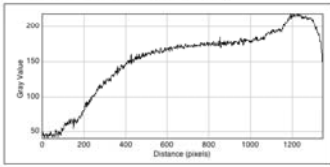
YJM975 (YMD1210)



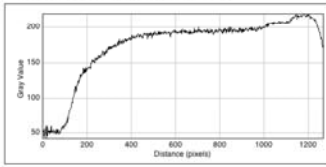


**Figure S3 Haploid settling plot profiles** A representative plot profile generated by ImageJ is shown for each strain in one biological replicate of the haploid quantitative flocculation assay. Plot profiles show mean gray value along a line drawn on the 60-minute time point settling image from the meniscus of the culture to the bottom of the tube with corresponding pixel distance values on the x-axis of the plot.

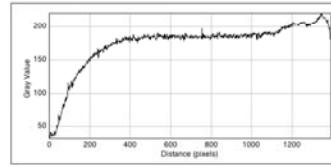
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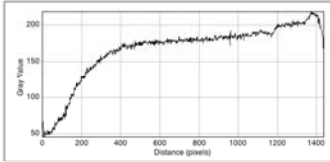
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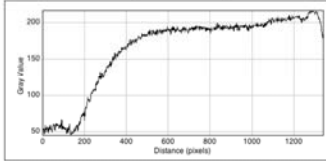
K11 (YMD2362)



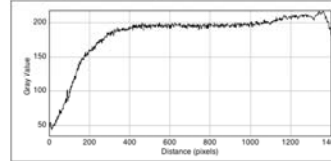
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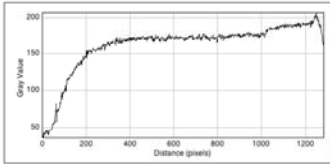
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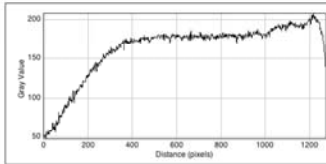
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DBVPG6044 (YMD2350)



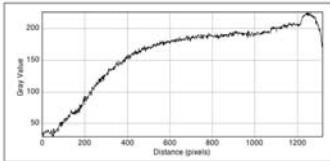
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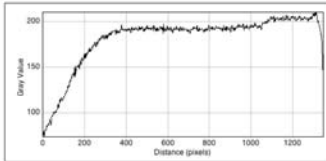
YS2 (YMD2364)

Diploid not tested

DBVPG1373 (YMD2351)



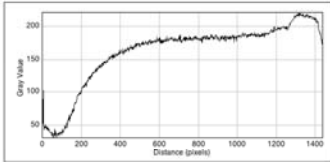
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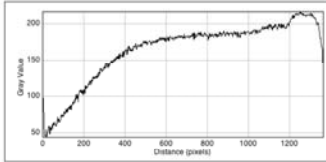
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Diploid not tested

DBVPG1853 (YMD2352)



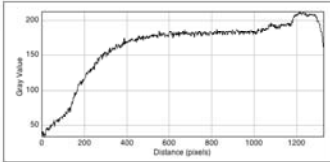
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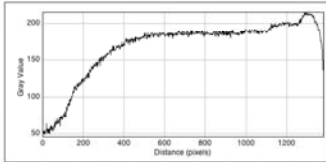
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Diploid not tested

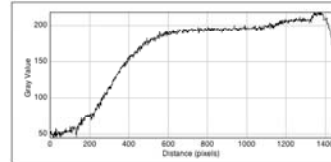
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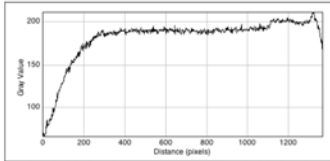
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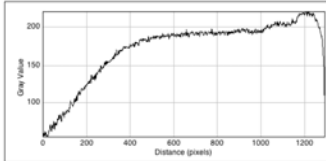
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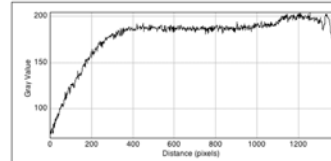
YPS128 (YMD2354)



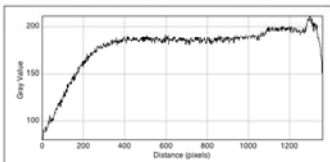
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UWOPS87-242.1 (YMD2368)



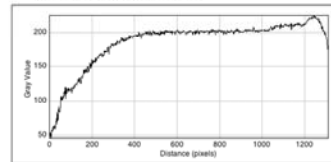
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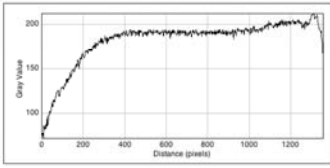
378604X (YMD2373)

Diploid not tested

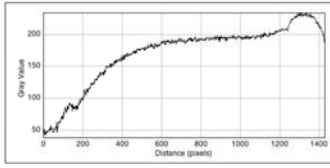
YJM975 (YMD2377)



UWOPS05-227.2 (YMD2370)



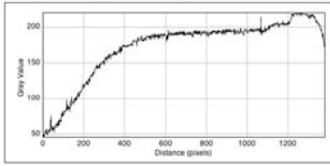
273614N (YMD2374)



W303 (YMD2371)

Diploid not tested

YJM978 (YMD2375)



322134S (YMD2372)

Diploid not tested

YJM981 (YMD2376)

Diploid not tested

**Figure S4 Diploid settling plot profiles** A representative plot profile generated by ImageJ is shown for each strain in the diploid quantitative flocculation assay. Plot profiles show mean gray value along a line drawn on the 60-minute time point settling image from the meniscus of the culture to the bottom of the tube with corresponding pixel distance values on the x-axis of the plot.

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