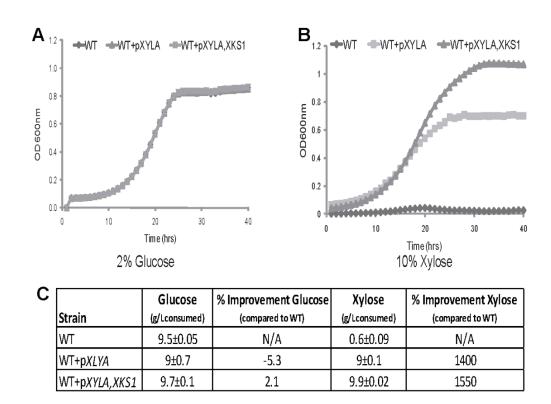


**Figure S1 (A)** Schematic map *pXYLA*. The pYES2 plasmid containing the exogenous XI gene *XYLA* from *Piromyces SpE2*. **(B)** Schematic map of *pXYLA,XKS1*. The pYES2 plasmid containing the XI gene *XYLA* and an additional copy of the endogenous XK gene *XKS1* from *S. cerevisiae*.



**Figure S2** The addition of pXYLA or pXYLA,XKS1 increases the xylose utilization of *S. cerevisiae*. Growth analysis of wild-type (WT, Y7092), to transformed strains, WT + pXYLA (YKB2179) and WT + pXYLA,XKS1 (YKB2178) in liquid media containing 2% glucose (**A**) or 10% xylose (**B**). Growth analysis was performed in triplicate on Multiskan Ascent plate reader (Thermo Electron Corporation), with OD<sub>600</sub> taken every 30 min over a 20-hour period at 30°. The error bars represent 1 standard deviation and are smaller than the data marker. (**C**) Sugar consumption table of wild-type (WT, Y7092), or wild-type transformed with pXYLA (YKB2179), or pXYLA,XKS1 (YKB2178) starting in either 13% glucose or xylose media. Fermentations were pitched with 1.5x10<sup>7</sup> cells/ml and carried out at 30°. The calculation for g/L consumed of sugars corresponds to the concentrations of sugars observed at the end of the batches compared to the starting amount.

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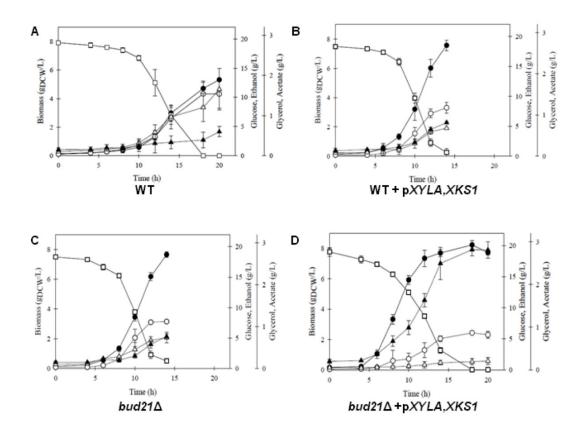


Figure S3 Fermentation profile of the *S. cerevisiae* CEN.PK 113-13D derivative strains during aerobic batch cultivation in glucose (20g/L). (A) CEN.PK 113-13D wild-type (WT, YKB2684), (B) WT transformed with *pXYLA,XKS1* (YKB2680), (C) *bud21*Δ (YKB2666) and (D) *bud21*Δ transformed with *pXYLA,XKS1* (YKB2667). Biomass (*closed circles*), glucose (*open squares*), ethanol (*open circles*), glycerol (*open triangles*), and acetate (*closed triangles*). The batches were terminated when no further changes in OD was observed. Each data point represents the mean±SD from duplicated experiments.

## Table S1 Excel sheet containing the confirmed genetic interactions.

Table S1 is available for download at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.111.000695/-/DC1/TableS1.xls.

## Spreadsheets:

DMA-xylose = screen of the DMA on 2% xylose

XYLA - xylose = pXYLA SGA screen on 2% xylose

XYLA,XKS1 - xylose = pXYLA,XKS1 SGA screen on 2% xylose

XYLA - glucose = pXYLA SGA screen on 2% glucose

XYLA,XKS1 - glcuose = pXYLA,XKS1 SGA screen on 2% glucose

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Table S2 Double mutants do not display additive improvement in xylose utilization.

Strain	Glucose (g/L	Improvement Glucose	Xylose (g/L	Improvement Xylose
	consumed)	(compared to WT)	consumed)	(compared to WT)
WT	8±0.05	N/A	0.5±0.04	N/A
alp1∆ isc1∆	7.1±0.015	-11.25	6.5±0.05	1200
alp1 $\Delta$ rpl20b $\Delta$	7.2±0.02	-10	6.7±0.08	1240
isc1∆ rpl20b∆	7±0.06	-12.5	6.6±0.074	1216
bud $21\Delta$ alp $1\Delta$	8.1±0.09	1.25	6.2±0.06	1140
bud21∆ isc1∆	8.4±0.08	5	7.15±0.15	1330
bud21Δ rpl20bΔ	8.3±0.1	3.75	6.5±0.06	1200

Strain	Glucose (g/L consumed)	Improvement Glucose (compared to WT +pXYLA,XKS1)	Xylose (g/L consumed)	Improvement Xylose
				(compared to WT +pXYLA,XKS1)
alp1∆ isc1∆				
+pXYLA,XKS1	8.6±0.08	6.2	7.2±0.02	24.1
alp1∆ rpl20b∆				
+pXYLA,XKS1	8.2±0.074	1.23	7±0.03	20.7
isc1∆ rpl20b∆				
+pXYLA,XKS1	8.3±0.08	2.5	6.2±0.02	6.9
bud21 $\Delta$ alp1 $\Delta$				
+pXYLA,XKS1	8.0±0.08	-1.23	7.2±0.03	24.16
bud21∆ isc1∆				
+pXYLA,XKS1	8.4±0.09	3.7	7.4±0.04	27.6
bud21∆ rpl20b∆				
+pXYLA,XKS1	8.2±0.1	1.23	6.8±0.1	17.26

Analysis of the consumption of glucose and xylose of the double mutants of the suppressors. Strains tested were Wild-type (YKB731),  $alp1\Delta$   $isc1\Delta$  (YKB2534),  $alp1\Delta$   $rpl20b\Delta$  (YKB2535),  $isc1\Delta$   $rpl20b\Delta$  (YKB2536),  $bud21\Delta$   $alp1\Delta$  (YKB2537),  $bud21\Delta$   $isc1\Delta$  (YKB2538),  $bud21\Delta$   $rpl20b\Delta$  (YKB2539) without (top table) and with pXYLA,XKS1 (bottom table). Growth cultures were started in either 13% glucose or xylsoe media, pitched with 1.5 x  $10^7$  cells/ml and carried out at 30° with for 168 hours. The calculation for g/L consumed of sugars corresponds to the concentrations of sugars observed at the end of the batches compared to the starting amount.