Table S2 Genes identified as differentially expressed in *MAT*a and *MAT*α-playing-a cells using RNA sequencing

Gene	Log$_2$ Fold Change: Unstimulated *MAT*α-playing-**a** ÷ Unstimulated *MAT***a**	Log$_2$ Fold Change: Stimulated *MAT*α-playing-**a** ÷ Stimulated *MAT***a**
MATα1	**7.56***	**7.86***
YCR097W-A	**3.97***	**6.96***
YDR008C	**4.30***	**5.70***
SAG1	**3.63***	**5.49***
YCL065W	**2.91***	**5.33***
TRP1	**4.35***	**5.31***
MATα2	**1.28***	**3.08***
YLR040C	**3.41***	**2.38***
YLR041W	**3.21***	**2.03***
YML131W	0.66*	0.69*
TPO2	-0.74*	0.53*
YPR158C-D	-0.61*	-0.48*
ADE17	-0.75*	-0.48*
BAP2	-0.94*	-0.54*
FSF1	-0.64*	-0.58*
ILV3	-0.75*	-0.58*
GDH1	-0.87*	-0.60*
FIT3	-0.84*	-0.63*
ALD5	**-1.03***	-0.88*
BAT1	**-1.70***	**-1.20***
OAC1	**-2.27***	**-1.57***
LEU1	**-2.47***	**-1.82***
ADE2	**-1.38***	**-1.93***
GYP8	**-1.02***	**-2.05***
STE2	**-2.67***	**-2.18***
MFA1	**-1.23***	**-2.80***
YNL146C-A	**-2.57***	**-4.00***
MFA2	**-5.51***	**-6.85***
ASG7	**-2.68***	**-9.11***
AGA2	**-7.29***	**-9.28***
Genes whose expression changed significantly only in pheromone-stimulated cells		
YHR145C	-0.61	**3.63***

YCR041W	**2.14**	**3.53***
PCL1	-0.12	**1.85***
SNL1	0.05	**1.75***
YLR346C	**1.20**	**1.70***
TOS6	-0.03	**1.30***
INO1	0.16	**1.30***
PST1	-0.06	**1.16***
OYE3	-0.22	**1.05***
TOS4	-0.04	**1.03***
YOX1	-0.12	0.97*
IMD2	0.02	0.95*
PIR3	0.47	0.95*
LEU2	0.21	0.91*
SPO11	0.05	0.88*
MCD1	0.07	0.87*
HES1	0.29	0.85*
GRE2	0.13	0.80*
AAD16	0.00	0.80*
YJL218W	0.41	0.79*
YGL230C	0.05	0.78*
AAD6	0.03	0.77*
EGT2	0.12	0.76*
YJR154W	0.19	0.74*
MCH2	0.35	0.73*
HTA2	-0.17	0.73*
YDR134C	0.06	0.69*
PIR1	-0.11	0.69*
KDX1	0.52	0.68*
HSP31	0.22	0.68*
YGR035C	0.17	0.66*
APL1	0.07	0.66*
YNR064C	0.02	0.64*
YBR071W	-0.04	0.63*
HAL1	0.48	0.62*
YOL159C	0.04	0.62*
CRG1	0.22	0.62*
YNL134C	-0.04	0.60*
AAD10	-0.15	0.60*
SVS1	-0.09	0.59*

SPI1	0.44	0.58*
YDR034W-B	-0.51	0.57*
RNR1	0.07	0.56*
SRL3	0.08	0.56*
YNL058C	0.21	0.55*
YKE4	-0.02	0.54*
ACA1	0.28	0.52*
SSA4	-0.10	0.50*
HHF1	-0.09	0.50*
DSE4	0.29	0.48*
OAZ1	0.13	0.47*
SEO1	0.24	0.47*
NIS1	-0.11	0.47*
YEH1	0.01	0.46*
HXT1	-0.08	-0.47*
PHO12	-0.24	-0.50*
YOL103W-B	-0.31	-0.50*
SIT1	-0.46	-0.51*
PHO11	-0.24	-0.52*
ENA1	0.00	-0.52*
LEU9	-0.22	-0.52*
HIS4	-0.50	-0.52*
YPL257W-B	-0.31	-0.53*
ALT2	-0.20	-0.54*
PDH1	0.08	-0.56*
PRY2	-0.29	-0.57*
HXK1	-0.03	-0.57*
TAT1	-0.35	-0.57*
YJR003C	-0.15	-0.66*
THI22	-0.26	-0.81*
FET3	-0.32	-0.83*
AXL1	-0.52	-0.93*
Genes whose expression changed significantly only in unstimulated cells		
RDN5-2	**2.90***	**1.33**
RDN5-5	**2.75***	0.73
RDN5-4	**2.66***	**1.02**
RDN5-3	**2.51***	0.93
RDN5-1	**2.34***	0.99
RDN5-6	**2.34***	0.99

YLR042C	0.66*	0.31
HER1	0.64*	0.15
HAP4	0.55*	0.23
YJL171C	-0.59*	-0.20
DRE2	-0.59*	-0.19
HMX1	-0.64*	-0.32
GAP1	-0.64*	-0.25
ARN2	-0.65*	-0.41
FUS1	-0.65*	-0.06
MAE1	-0.70*	-0.15
AGA1	-0.85*	-0.15
FIT2	-0.89*	-0.40
ISU2	-0.92*	-0.28
YGP1	**-1.04***	-0.10
DIC1	**-1.26***	-0.28

* Indicates statistical significance determined by the default settings in Cufflinks ($p<0.001$) (Trapnell *et al.* 2010). Numbers in bold indicate that there is a greater than two-fold change between the expression of the gene in *MAT*α-playing-**a** and *MAT***a** cells.

LITERATURE CITED

Trapnell, C., B. A. Williams, G. Pertea, A. Mortazavi, G. Kwan *et al*, 2010 Transcript assembly and quantification by RNA-seq reveals unannotated transcripts and isoform switching during cell differentiation. Nat. Biotechnol. **28:** 511-515.