Table S3 Genes showing strong differential expression between the two parental strains. (A) Genes overexpressed in 59A. (B) Genes overexpressed in S288c.

A

Name	logFC	Ratio	Adj PVal	Function
PAU5	3.256	9.555	8.56E-16	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions
PAU4	3.242	9.458	9.26E-15	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions
PAU12	2.83	7.112	1.97E-15	Hypothetical protein
PAU20	2.827	7.094	3.61E-15	Hypothetical protein
PAU6	2.483	5.592	1.43E-13	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions
PAU1	2.412	5.322	1.78E-14	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions
PAU13	2.324	5.007	8.02E-13	Putative protein of unknown function
INO1	2.287	4.88	1.05E-12	Inositol 1-phosphate synthase
PAU10	2.281	4.861	7.24E-14	Hypothetical protein
PAU14	2.239	4.721	7.27E-14	Hypothetical protein
PAU11	2.214	4.64	7.88E-13	Putative protein of unknown function
PAU8	2.133	4.385	7.85E-12	Hypothetical protein
PAU7	2.038	4.107	3.78E-14	Part of 23-member seripauperin multigene family
PAU18	1.973	3.926	1.96E-12	Hypothetical protein
HXK1	1.877	3.674	2.70E-10	Hexokinase isoenzyme 1
PAU19	1.85	3.606	3.87E-13	Hypothetical protein
HUG1	1.752	3.368	1.51E-11	Protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication arrest
TRK2	1.642	3.122	2.47E-11	Component of the Trk1p-Trk2p potassium transport system
YGR126W	1.641	3.119	3.61E-11	Putative protein of unknown function
YNL324W	1.638	3.112	2.74E-12	Dubious ORF unlikely to encode a functional protein
YDR102C	1.589	3.008	4.15E-12	Dubious open reading frame
YPR126C	1.558	2.945	2.35E-14	Dubious open reading frame unlikely to encode a functional protein
DAN3	1.549	2.925	5.89E-10	Cell wall mannoprotein with similarity to Tir1p
DDR48	1.544	2.917	1.37E-07	DNA damage-responsive protein
DAN2	1.513	2.855	1.23E-12	Cell wall mannoprotein with similarity to Tir1p
GPH1	1.437	2.707	1.05E-12	Non-essential glycogen phosphorylase required for the mobilization of glycogen
MFA2	1.413	2.664	4.15E-09	Mating pheromone a-factor
YDL085C-A	1.402	2.643	8.24E-09	Putative protein of unknown function
YPR050C	1.373	2.59	1.28E-12	Dubious open reading frame unlikely to encode a protein
YDR355C	1.334	2.521	9.76E-12	Dubious: Dubious open reading frame unlikely to encode a protein
YIL067C	1.326	2.507	5.74E-12	Uncharacterized protein of unknown function
YCL020W	1.302	2.466	2.57E-09	Retrotransposon TYA Gag gene co-transcribed with TYB Pol
SOL2	1.301	2.464	9.67E-11	Protein with a possible role in tRNA export
JSN1	1.272	2.415	9.71E-14	Member of the Puf family of RNA-binding proteins
GPM1	1.271	2.412	7.16E-10	Tetrameric phosphoglycerate mutase
MSG5	1.256	2.389	4.09E-10	Dual-specificity protein phosphatase required for maintenance of a low level of signaling through the cell integrity pathway
DBP5	1.248	2.375	3.52E-10	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus
YBR099C	1.246	2.372	4.78E-11	Dubious open reading frame unlikely to encode a protein
SDS24	1.223	2.334	1.77E-10	One of two S
HRT1	1.221	2.33	1.20E-11	RING finger containing subunit of Skp1-Cullin-F-box ubiquitin protein ligases (SCF)
PAU17	1.218	2.326	2.77E-09	Putative protein of unknown function
PEX11	1.207	2.309	8.92E-11	Peroxisomal membrane protein required for peroxisome proliferation and medium-chain fatty acid oxidation

MSH6	1.206	2.307	4.89E-09	Protein required for mismatch repair in mitosis and meiosis
FLO5	1.205	2.306	1.71E-13	Lectin-like cell wall protein (flocculin) involved in flocculation
YFL052W	1.205	2.306	1.93E-13	Putative zinc cluster protein that contains a DNA binding domain
YKR045C	1.202	2.3	2.57E-10	Putative protein of unknown function
YJL127W-A	1.201	2.298	1.22E-08	Dubious open reading frame unlikely to encode a protein
DAN1	1.2	2.297	3.92E-10	Cell wall mannoprotein with similarity to Tir1p
ENP1	1.189	2.28	2.20E-08	Protein associated with U3 and U14 snoRNAs
YHR049C-A	1.188	2.279	7.03E-11	Dubious open reading frame unlikely to encode a functional protein

B

Name	logFC	Ratio	Adj PVal	Function
PLC1	4.693	25.864	4.07E-19	Phospholipase C
YNL284C-A*	4.252	19.047	1.89E-19	Retrotransposon TYA Gag gene co-transcribed with TYB Pol
AI2*	4.235	18.833	3.92E-18	Reverse transcriptase required for splicing of the COX1 pre-mRNA
RTC4	3.439	10.844	3.68E-18	Putative protein of unknown function
CDC5	2.857	7.246	2.82E-17	Polo-like kinase with similarity to Xenopus Plx1 and S
ARH1	2.77	6.823	1.55E-17	Oxidoreductase of the mitochondrial inner membrane
YGR051C	2.53	5.776	2.24E-17	Dubious open reading frame unlikely to encode a protein
YER084W	2.49	5.617	4.91E-16	Dubious open reading frame unlikely to encode a protein
YNL285W	2.459	5.498	1.12E-17	Dubious open reading frame unlikely to encode a functional protein
ELG1	2.437	5.413	1.57E-14	Protein required for S phase progression and telomere homeostasis
ATE1	2.41	5.316	1.89E-19	Arginyl-tRNA-protein transferase
YER138W-A	2.379	5.201	5.74E-12	Putative protein of unknown function
SCH9	2.365	5.152	3.30E-16	Protein kinase involved in transcriptional activation of osmostress-responsive genes
YBL107W-A	2.234	4.705	6.28E-14	Dubious open reading frame unlikely to encode a protein
RSA1	2.204	4.609	5.55E-18	Protein involved in the assembly of 60S ribosomal subunits
THI80	2.157	4.459	1.55E-16	Thiamine pyrophosphokinase
HSP30	2.121	4.349	3.76E-08	Hydrophobic plasma membrane localized
YBL111C	2.068	4.192	9.79E-18	Helicase-like protein encoded within the telomeric Y element
YHR218W	2.018	4.051	2.21E-16	Helicase-like protein encoded within the telomeric Y element
YIR014W	1.93	3.809	2.68E-15	Putative protein of unknown function
GIN4	1.894	3.717	1.51E-17	Protein kinase involved in bud growth and assembly of the septin ring
HSP12	1.885	3.695	2.94E-14	Plasma membrane localized protein that protects membranes from desiccation
PBP1	1.857	3.623	1.05E-14	Protein interacting with poly(A)-binding protein Pab1p
YHL005C	1.842	3.584	6.15E-17	Dubious open reading frame unlikely to encode a protein
AUA1	1.801	3.485	8.96E-09	Protein required for the negative regulation by ammonia of Gap1p
TPO3	1.8	3.481	9.65E-14	Polyamine transport protein specific for spermine
RPL2B	1.767	3.402	2.51E-14	Protein component of the large (60S) ribosomal subunit
YER053C-A	1.745	3.352	1.89E-06	Putative protein of unknown function
MCM22	1.737	3.334	6.76E-15	Protein involved in minichromosome maintenance
ASP3-1	1.734	3.326	9.66E-15	Cell-wall L-asparaginase II
SPS100	1.712	3.276	1.94E-11	Protein required for spore wall maturation
ASP3-3	1.704	3.257	4.88E-14	Cell-wall L-asparaginase II
NPY1	1.669	3.18	5.89E-15	NADH diphosphatase (pyrophosphatase)
HST1	1.665	3.172	3.56E-15	NAD(+)-dependent histone deacetylase
YLR281C	1.665	3.17	1.01E-16	Putative protein of unknown function
SPR3	1.644	3.125	3.61E-15	Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes
ASP3-2	1.628	3.09	1.70E-15	Cell-wall L-asparaginase II
YNL260C	1.614	3.06	1.72E-15	Putative protein of unknown function with similarity to a human protein overexpressed in oral cancers
KAR9	1.581	2.991	8.55E-10	Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules
VIP1	1.577	2.984	8.36E-14	Inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) kinase

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DOT1	1.572	2.973	1.32E-13	Nucleosomal histone H3-Lys79 methylase
AI3	1.557	2.942	1.99E-13	Endonuclease I-SceIII
MRPL13	1.54	2.909	6.20E-13	Mitochondrial ribosomal protein of the large subunit
YLR280C	1.54	2.909	5.89E-15	Dubious open reading frame unlikely to encode a functional protein
ASP3-4	1.536	2.899	2.40E-15	Cell-wall L-asparaginase II
ITC1	1.519	2.865	6.51E-14	Component of the ATP-dependent Isw2p-Itc1p chromatin remodeling complex
YIL089W	1.511	2.851	6.00E-13	Putative protein of unknown function
RPA49	1.498	2.824	7.21E-06	RNA polymerase I subunit A49
HXT5	-1.477	2.783	3.80 E-15	Hexose transporter
THI72	-1,477	2.783	1.71 E-11	Transporter of thiamine or related compound

For each gene the $\log_2$ of fold change, the ratio of expression, the adjusted p-value and the function are indicated.
These are Ty1 genes, only one member of each was considered since they cross hybridize.