Lists

Terms:

SD	STD for a gene across all 6 timepoints × 6 strains
SD _{elm} , SD _{ref} , SD _{reg} ,	STD for a gene across all 6 timepoints for a certain strain
SD _{sak} , SD _{t210a} , SD _{tos}	
SDMax	Maximum(SD _{elm} , SD _{ref} , SD _{reg} , SD _{sak} , SD _{t210a} , SD _{tos})
SDMin	Minimum(SD _{elm} , SD _{ref} , SD _{reg} , SD _{sak} , SD _{t210a} , SD _{tos})
MIN _{elm} , MIN _{ref} ,	Minimum for a gene across all 6 timepoints for a certain strain
MIN _{reg} , MIN _{sak} ,	
MIN _{t210a} , MIN _{tos}	
MAX _{elm} , MAX _{ref} ,	Maximum for a gene across all 6 timepoints for a certain strain
MAX _{reg} , MAX _{sak} ,	
MAX _{t210a} , MAX _{tos}	
SPAN _x	MAX _x -MIN _x
MAXLOW	Minimum(MAX _{elm} , MAX _{ref} , MAX _{reg} , MAX _{sak} , MAX _{t210a} , MAX _{tos})
MINHIGH	Maximum(MIN _{elm} , MIN _{ref} , MIN _{reg} , MIN _{sak} , MIN _{t210a} , MIN _{tos})

List 1 – genes with very different expression levels between strains:

Genes with highest MINHIGH-MAXLOW, indicating a clear difference in expression level between strains. The genes marked with green are the deleted genes. A **clear distinction** can be seen between **Elm**, **Reg and Sak** on the one hand, and **Ref**, **T210A and Tos** on the other. Note also that there are **8 genes related to mating**.

Gene	GAP	High	Low	Comment
YDR028C	9.278963		Reg	Deleted in Reg
YCL066W	9.074428	Ref,T210A,Tos	Elm.Reg,Sak	HMLALPHA1 - Silenced copy of ALPHA1 at HML, encoding a transcriptional coactivator involved in the regulation of mating-type alpha-specific gene expression
YCR097W	8.788922	Elm,Reg,Sak	Ref,T210A,Tos	HMRA1 - Silenced copy of a1 at HMR; homeobox corepressor that interacts with Alpha2p to repress haploid-specific gene transcription in diploid cells
YNL145W	8.070672	Elm,Reg,Sak	Ref,T210A,Tos	MFA2 - Mating pheromone a- factor, made by a cells; interacts with alpha cells to induce cell cycle arrest and other responses leading to mating; biogenesis involves C- terminal modification, N-terminal proteolysis, and export; also encoded by MFA1 SD _{ref} , SD _{t210a} , SD _{tos} higher than the others.
YKL048C	7.903094		Sak,Tos	Deleted in Sak,Tos
YGL032C	7.261076	Elm,Reg,Sak	Ref,T210A	AGA2 - Adhesion subunit of a-

	1	1	1	-
				agglutinin of a-cells, C-terminal
				sequence acts as a ligand for
				alpha-agglutinin (Sag1p) during
				agglutination, modified with O-
				linked oligomannosyl chains,
				linked to anchorage subunit Aga1p
				via two disulfide bonds
				SD _{ref} , SD _{t210a} higher than the others.
				Tos intermediate in both
				expression and variation.
YGL179C	6.34959		Elm,Sak	Deleted in Elm,Sak
YER129W	6.29135		Elm,Tos	Deleted in Elm,Tos
YPL187W	6.02141	Ref,T210A,Tos	Elm,Reg,Sak	MF(ALPHA)1 - Mating pheromone
2207	0.021.11	1101/1220/1/100	Zimi,rtegjourt	alpha-factor, made by alpha cells;
				interacts with mating type a cells
				to induce cell cycle arrest and
				other responses leading to mating;
				also encoded by MF(ALPHA)2,
				although MF(ALPHA)1 produces
				most alpha-factor
YGL089C	5.218517	Ref,T210A,Tos	Elm,Reg,Sak	MF(ALPHA)2 - Mating pheromone
1020030	3.210317	1101,121071,103	Zim,reg,ouk	alpha-factor, made by alpha cells;
				interacts with mating type a cells
				to induce cell cycle arrest and
				other responses leading to mating;
				also encoded by MF(ALPHA)1,
				which is more highly expressed
				than MF(ALPHA)2
YIL015W	5.201769	Elm,Reg,Sak	Ref,T210A,Tos	BAR1 - Aspartyl protease
11202011	3.201703	Zimjitegjour	1101/1210/1/100	secreted into the periplasmic
				space of mating type a cells, helps
				cells find mating partners, cleaves
				and inactivates alpha factor
				allowing cells to recover from
				alpha-factor-induced cell cycle
				arrest
YKL178C	4.805807	Ref,T210A,Tos	Elm,Reg,Sak	STE3 - Receptor for a factor
2123		, ===,,.00	, 150,54	pheromone, transcribed in alpha
				cells and required for mating by
				alpha cells, couples to MAP kinase
				cascade to mediate pheromone
				response; ligand bound receptors
				are endocytosed and recycled to
				the plasma membrane; GPC
				SD _{elm} , SD _{reg} , SD _{sak} higher than the
				others.
YLR040C	4.525768	Elm,Reg	Ref,T210A,Tos	UNKNOWN - Putative protein of
TENU40C	4.323708	Lilli, Neg	NEI,1210A,108	unknown function; localizes to the
				cell wall; predicted to be a GPI-
				attached protein; upregulated by
				Mcm1p-Alpha1p transcription
				factor; partially overlaps the
				dubious ORF YLR041W;
				YLR040C is not essential
				Sak is intermediately expressed.
VII 170C	4.467727	Flm Dog Col	Dof TO104 To	
YJL170C	4.467737	Elm,Reg,Sak	Ref,T210A,Tos	ASG7 - Protein that regulates

		_	_	
				signaling from a G protein beta
				subunit Ste4p and its relocalization
				within the cell; specific to a-cells
				and induced by alpha-factor
YFL026W	4.447449	Elm,Reg,Sak	Ref,T210A,Tos	STE2 - Receptor for alpha-factor
				pheromone; seven
				transmembrane-domain GPCR
				that interacts with both pheromone
				and a heterotrimeric G protein to
				initiate the signaling response that
				leads to mating between haploid a
				and alpha cells
YNL146C-A	4.387727	Elm,Reg,Sak	Ref,T210A,Tos	UNKNOWN
YDR461W	4.100305	Elm,Reg,Sak	Ref,T210A,Tos	MFA1 - Mating pheromone a-
IDN401W	4.100303	Lilli,Neg,Jak	Nei,1210A,103	factor, made by a cells; interacts
				with alpha cells to induce cell cycle
				arrest and other responses leading
				to mating; biogenesis involves C-
				terminal modification, N-terminal
				proteolysis, and export; also
VIVI 2006	2.027045	Elm D. C. I	D-f T2404 T	encoded by MFA2 STE6 - Plasma membrane ATP-
YKL209C	2.927815	Elm,Reg,Sak	Ref,T210A,Tos	
				binding cassette (ABC) transporter
				required for the export of a-factor,
				catalyzes ATP hydrolysis coupled
				to a-factor transport; contains 12
				transmembrane domains and two
				ATP binding domains; expressed
VOD2046.4	2.005306		_	only in MATa cells
YOR394C-A	2.905386		Tos	UNKNOWN
YDR042C	2.593795	Sak,Tos,(T210A)	Elm,Ref,Reg	UNKONWN - Putative protein of
				unknown function; expression is
				increased in ssu72-ts69 mutant
YLR042C	2.13283	Sak,Tos		UNKNOWN - Protein of unknown
				function; localizes to the
				cytoplasm; YLL042C is not an
				essential gene
YLR377C	1.83239	Reg	T210A	FBP1 - Fructose-1,6-
				bisphosphatase, key regulatory
				enzyme in the gluconeogenesis
				pathway, required for glucose
				metabolism; undergoes either
				proteasome-mediated or
				autophagy-mediated degradation
				depending on growth conditions;
				interacts with Vid30p
YML058W-A	1.792083		Reg	HUG1 - Protein involved in the
				Mec1p-mediated checkpoint
				pathway that responds to DNA
				damage or replication arrest,
				transcription is induced by DNA
				damage
YLR157W-C	1.744076	Elm	T210A	UNKNOWN - Putative protein of
				unknown function identified by
				gene-trapping, microarray-based
				expression analysis, and genome- wide homology searching; partially

				overlaps a Ty1 element
YCL021W-A	1.571395	Sak,Tos		UNKNOWN
YBR069C	1.482656	Tos		TAT1 - Amino acid transport protein for valine, leucine, isoleucine, and tyrosine, lowaffinity tryptophan and histidine transporter; overexpression confers FK506 and FTY720 resistance
YLR156W	1.420307	Elm	T210A	UNKNOWN
YLL066W-B	1.27694	Tos		UNKNOWN

List 2 – genes that don't change in any strain:

1177 genes (NoChange.txt) are considered not changing. The cutoff was **highest expression value – lowest expression value < 1**.

List 3 – genes that change in all strains:

834 genes (AllChange.txt) are considered changing in all strains. The cutoff **highest expression value** – **lowest expression value** > **1** for all strains.

List 4 – genes that change markedly more in some strains:

The strain specific SDs (SD_{elm}, SD_{ref}, SD_{reg}, SD_{sak}, SD_{t210a}, SD_{tos}) were sorted in descending order, resulting in SD1 > SD2 > SD3 > SD4 > SD5 > SD6. MAXDIFF=Maximum(SD1-SD2, SD2-SD3, SD3-SD4, SD4-SD5, SD5-SD6) was used to find genes with different levels of change.

Some of these genes may be the result of an error in the microarray T210A, timepoint 4. These are marked in yellow.

Gene	MAXDIFF	High SD	Low SD	Comment
YBL112C	4.071889	T210A		
YBL111C	2.969122	T210A		
YPL056C	2.907423	T210A		
YNL106C	2.797661	T210A		
YDR223W	2.732876		T210A	Same shape – peak at timepoint 1, and then decreasing, but much lower peak in T210A.
YGL063W	2.588887	T210A		
YPL200W	2.408488		T210A	Same shape – peak at timepoint 1, and then decreasing, but much lower peak in T210A.
YKL198C	2.405416	T210A		

YMR273C	2.338032	T210A		
YDL156W	2.325745	T210A		
YCR010C	2.300415	TZIOA	T210A	Same shape – peak at timepoint 1, and then decreasing, but much lower peak in T210A.
YOR083W	2.294809	T210A		
YNL309W	2.279887	T210A		
YCL044C	2.236479	T210A		
YIL057C	2.223759		T210A	Same shape – peak at timepoint 1, and then decreasing, but much lower peak in T210A.
YJL083W	2.154625	T210A		
YAL043C	2.135954	T210A		
YGL089C	2.131873	Ref,T210A,Tos	Elm,Reg,Sak	
YOR140W	2.091263	T210A		
YIR014W	2.065149	T210A		
YKR045C	2.029395	T210A		
YOR181W	2.024643	T210A		
YDL197C	1.964739	T210A		
YPL015C	1.950557	T210A		
YCR068W	1.944126	T210A		
YHR126C	1.890216		T210A	Same shape – peak at timepoint 1, and then decreasing, but much lower peak in T210A. Sak and Tos also have peaks at timepoint 3.
YBR108W	1.879829	T210A		
YGR068C	1.81635	T210A		
YFR022W	1.798663	T210A		
YKL204W	1.778235	T210A		
YDR256C	1.767497		T210A	Same shape – peak at timepoint 1, and then decreasing, but much lower peak in T210A. Sak and Tos also have peaks at timepoint 3.
YBR301W	1.75149	Tos		Peak at timepoint 1 in Tos

YBR197C	1.746748	T210A		
YBR076W	1.746651	-	T210A	No peak at
				timepoint 1 in
				T210A.
YNL240C	1.7363	T210A		_
YGL073W	1.732318	T210A		
YOR388C	1.723708		T210A	Same shape –
				peak at timepoint
				1, and then
				decreasing, but
				much lower peak
				in T210A.
YNR015W	1.69919	T210A		
YLL010C	1.693445	T210A		
YAL013W	1.692205	T210A		
YOR237W	1.661461	Tos		Much higher peak
				at timepoint 1 in
YIRO06C	1.636678	T210A		Tos.
YJR153W	1.627156	Sak,Tos		
YPR194C	1.619884	3dK,105	T210A	Same shape – low
TPN194C	1.019004		1210A	at timepoint 1,
				and then
				increasing, but
				T210A is not as
				low as the others
				at timepoint 1.
YCR061W	1.600141	T210A		
YHR033W	1.589	T210A		
YDL220C	1.581359	T210A		
YLR438W	1.576216	T210A		
YOR373W	1.564632	T210A		
YLR139C	1.55961	T210A		
YEL076C-A	1.556729	T210A		
YDR534C	1.497931	T210A		
YOR072W-B	1.494768		Sak,Tos	Sak and Tos have
				high expression
				with little
YLR095C	1 40074	T2104		variation.
YLRU95C YIL101C	1.48874 1.485108	T210A T210A		
		Ref		Ref has low
YBR054W	1.482437	rei		expression at
				timepoint 3.
YLL012W	1.479197	T210A		сптеропте э.
YKR048C	1.473733	T210A		
YER089C	1.470704	T210A		
YER164W	1.467311	T210A		
YNL080C	1.463255	T210A		
YLR378C	1.439379	T210A		

YHR096C	1.435664	Elm,Ref		
YDR405W	1.432824	T210A		
YLR337C	1.425645	T210A		
YNL187W	1.421118	T210A		
YJL019W	1.409415	T210A		
YOR371C	1.398831	T210A		
YHR040W	1.390011	T210A		
YGR054W	1.387506	T210A		
YCL010C	1.384798	T210A		
YLR426W	1.384262	T210A		
YNL278W	1.377196	T210A		
YGL071W	1.374712	T210A		
YLR187W	1.329752	T210A		
YDL087C	1.323926	T210A		
YMR296C	1.309884	T210A		
YDR536W	1.305773	-	T210A	Low expression in
				T210A.
YBR214W	1.304593	T210A		
YFR034C	1.302609	T210A		
YBR233W	1.294955	T210A		
YHR034C	1.290455	T210A		
YCR088W	1.287518	T210A		
YGL181W	1.255564	T210A		
YBR241C	1.252029	T210A		
YLL056C	1.251892	T210A		
YCR084C	1.241283	T210A		
YGL216W	1.23512	T210A		
		Ref		Ref has low
				expression at
YER053C-A	1.232503			timepoint 3.
YLL038C	1.230078	T210A		
YIR003W	1.220913	T210A		
YHR042W	1.214939	T210A		
YNL317W	1.209633	T210A		
YKR102W	1.209526	T210A		
YBR112C	1.206558	T210A		
YPL190C	1.206192	T210A		
YOR156C	1.166681	T210A		
YMR206W	1.155073	Ref,Sak,Tos		
YNL241C	1.154642	T210A		
YLR116W	1.149961	T210A		
YER179W	1.148787	Ref		
YML109W	1.143687	T210A		
YPL201C	1.139683		T210A	
YPL055C	1.134026	T210A		
YPL187W	1.131083	Elm,Reg,Sak		