

		LOGFC		LOGFC							
	ID	FAAERvsAER	FAANAvsANA	F	P.Value	adj.P.Val	COMMON NAME	ALIAS	CHROMOSOME	DESCRIPTION	
2171	YDR380W	3,691699526	5,448953054	686,2142	2,41E-11	2,63388E-07	ARO10		chromosome 4	Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway	
8081	YLR155C	0,237613669	-3,062852394	518,025	9,58E-11	4,82E-07	ASP3-1	ASP3	chromosome 12	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C	
6040	YHR137W	1,969873805	4,535503522	275,9719	2,08E-09	4,54072E-06	ARO9		chromosome 8	Aromatic aminotransferase II, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism	
3176	YAL062W	1,982577323	-2,021585801	200,1853	9,85E-09	9,78645E-06	GDH3	FUN51	chromosome 1	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh1p; expression regulated by nitrogen and carbon sources	
4020	YFR017C	0,861060799	-1,42998535	167,6529	2,32E-08	1,40595E-05			chromosome 6	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and is induced in response to the DNA-damaging agent MMS; YFR017C is not an essential gene	
4608	YMR175W	0,563315997	-2,374722639	170,4855	2,14E-08	1,40595E-05	SIP18		chromosome 13	Protein of unknown function whose expression is induced by osmotic stress	
3020	YIL057C	0,434795359	-4,208965106	153,6247	3,52E-08	1,49279E-05			chromosome 9	Putative protein of unknown function; expression induced under carbon limitation and repressed under high glucose	
3610	YOL151W	0,691289473	2,142860999	128,7509	8,2E-08	1,82848E-05	GRE2		chromosome 15	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway	
5609	YLR157W-C	0,991408408	-2,618706548	121,9559	1,06E-07	2,07609E-05					
4936	YOL052C-A	0,258962408	-1,387854354	102,1059	2,46E-07	3,32361E-05	DDR2	YOL053C-A DDRA2	chromosome 15	Multistress response protein, expression is activated by a variety of xenobiotic agents and environmental or physiological stresses	
644	YDL085W	0,742303863	-1,531377468	101,023	2,59E-07	3,34708E-05	NDE2	NDH2	chromosome 4	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic NADH to the mitochondrial respiratory chain	
9295	YFL051C	0,334265652	1,202781879	95,62288	3,36E-07	3,66768E-05			chromosome 6	Putative protein of unknown function; YFL051C is not an essential gene	
9197	YNR002C	0,295128933	-2,270554253	94,03457	3,63E-07	3,85281E-05	ATO2	FUN34	chromosome 14	Putative transmembrane protein involved in export of ammonia, a starvation signal that promotes cell death in aging colonies; phosphorylated in mitochondria; member of the TC 9.B.33 YaaH family; homolog of Ady2p and Y. lipolytica Gpr1p	
3313	YJL163C	0,472507699	-1,1725994	90,41345	4,37E-07	4,1499E-05			chromosome 10	Putative protein of unknown function	
8873	YLR136C	0,792793982	1,802084962	88,78019	4,76E-07	4,22639E-05	TIS11	CTH2	chromosome 12	mRNA-binding protein expressed during iron starvation; binds to a sequence element in the 3'-untranslated regions of specific mRNAs to mediate their degradation; involved in iron homeostasis	
5835	YPL230W	0,51245363	-1,371643745	88,27924	4,88E-07	4,27056E-05	USV1		chromosome 16	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in protein folding, ATP binding, and cell wall biosynthesis	

5306	YBR241C	0,991470524	-1,051856273	87,75309	5,02E-07	4,35026E-05			chromosome 2	Putative transporter, member of the sugar porter family; green fluorescent protein (GFP)-fusion protein localizes to the vacuolar membrane; YBR241C is not an essential gene
150	YJL185C	0,626878539	-1,075800531	85,6314	5,63E-07	4,60943E-05			chromosome 10	Putative protein of unknown function; mRNA is weakly cell cycle regulated, peaking in G2 phase; YJL185C is a non-essential gene
7359	YCL026C-B	-0,635951281	1,067686362	81,46436	7,11E-07	5,47388E-05	HBN1	YCL027C-A	chromosome 3	Putative protein of unknown function; similar to bacterial nitroreductases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus
2546	YNL160W	0,441562251	1,345045298	76,04413	9,8E-07	6,45261E-05	YGP1		chromosome 14	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved in adaptation prior to stationary phase entry; has similarity to Sps100p
6704	YMR206W	1,19108045	-2,476292294	74,87942	1,05E-06	6,63464E-05			chromosome 13	Putative protein of unknown function; YMR206W is not an essential gene
8375	YCR046C	-0,127534031	-1,001400408	73,75401	1,13E-06	6,89689E-05	IMG1		chromosome 3	Mitochondrial ribosomal protein of the large subunit, required for respiration and for maintenance of the mitochondrial genome
34	YIL160C	1,221672926	-1,510417521	73,43749	1,15E-06	6,95811E-05	POT1	POX3 FOX3	chromosome 9	3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids
3938	YBR037C	-0,675432791	-1,204215042	72,63683	1,21E-06	7,16258E-05	SCO1	PET161	chromosome 2	Copper-binding protein of the mitochondrial inner membrane, required for cytochrome c oxidase activity and respiration; may function to deliver copper to cytochrome c oxidase; has similarity to thioredoxins
2996	YLR108C	-0,256710445	1,365846585	70,54477	1,39E-06	7,6164E-05			chromosome 12	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YLR108C is not an essential gene
7959	YMR174C	0,578824956	-1,500515542	70,48739	1,39E-06	7,6164E-05	PAI3		chromosome 13	Cytoplasmic proteinase A (Pep4p) inhibitor, dependent on Pbs2p and Hog1p protein kinases for osmotic induction; intrinsically unstructured, N-terminal half becomes ordered in the active site of proteinase A upon contact
6556	YLR156W	0,424516657	-3,569347115	68,72508	1,57E-06	8,11099E-05			chromosome 12	Putative protein of unknown function; exhibits a two-hybrid interaction with Jsn1p in a large-scale analysis
4822	YMR006C	-0,543453968	-1,754282398	68,02251	1,64E-06	8,23548E-05	PLB2		chromosome 13	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; displays transacylase activity in vitro; overproduction confers resistance to lysophosphatidylcholine
5191	YNL200C	0,74675745	-1,071309276	66,54574	1,82E-06	8,67312E-05			chromosome 14	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
8358	YGL248W	1,048186996	1,03560511	65,02978	2,02E-06	9,0964E-05	PDE1		chromosome 7	Low-affinity cyclic AMP phosphodiesterase, controls glucose and intracellular acidification-induced cAMP signaling, target of the cAMP-protein kinase A (PKA) pathway; glucose induces transcription and inhibits translation
5388	YHR091C	0,043513693	-1,222795653	63,44653	2,26E-06	9,66138E-05	MSR1		chromosome 8	Mitochondrial arginyl-tRNA synthetase
1450	YLR237W	-0,952169169	-1,062528234	62,88637	2,36E-06	9,68457E-05	THI7	THI10	chromosome 12	Plasma membrane transporter responsible for the uptake of thiamine, member of the major facilitator superfamily of transporters; mutation of human ortholog causes thiamine-responsive megaloblastic anemia

10131	YBR056W-A	1,977021072	1,238193457	62,46365	2,43E-06	9,80463E-05			chromosome 2	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the dubious ORF YBR056C-B
8076	YGR243W	0,66343632	-1,420382773	61,74148	2,56E-06	0,000101175			chromosome 7	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
9312	YIL072W	-0,962688696	1,10603186	61,77215	2,56E-06	0,000101175	HOP1		chromosome 9	Meiosis-specific DNA binding protein that displays Red1p dependent localization to the unsynapsed axial-lateral elements of the synaptonemal complex; required for homologous chromosome synapsis and chiasma formation
5124	YIL113W	-0,388606869	-1,797618667	60,58305	2,8E-06	0,000104758	SDP1		chromosome 9	Stress-inducible dual-specificity MAP kinase phosphatase, negatively regulates Slt2p MAP kinase by direct dephosphorylation, diffuse localization under normal conditions shifts to punctate localization after heat shock
309	YJL047C-A	-0,480398434	-1,052971589	58,16713	3,37E-06	0,000117946			chromosome 10	Putative protein of unknown function
7259	YOR226C	-0,256224656	1,294505653	56,31139	3,9E-06	0,0001297	ISU2	NUA2	chromosome 15	Conserved protein of the mitochondrial matrix, required for synthesis of mitochondrial and cytosolic iron-sulfur proteins, performs a scaffolding function in mitochondria during Fe/S cluster assembly; isu1 isu2 double mutant is inviable
10540	YGR260W	0,144332067	-1,016908731	55,97259	4,01E-06	0,000131462	TNA1		chromosome 7	High affinity nicotinic acid plasma membrane permease, responsible for uptake of low levels of nicotinic acid; expression of the gene increases in the absence of extracellular nicotinic acid or para-aminobenzoate (PABA)
10334	YLR121C	1,700836194	1,287091851	55,37763	4,21E-06	0,000136232	YPS3	YPS4	chromosome 12	Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor
2568	YLR204W	-0,619522369	-1,142267928	55,37648	4,21E-06	0,000136232	QRI5	COX24	chromosome 12	Mitochondrial inner membrane protein, required for accumulation of spliced COX1 mRNA; may have an additional role in translation of COX1 mRNA
800	YOR178C	1,299123279	-1,397295311	54,9755	4,36E-06	0,000138349	GAC1		chromosome 15	Regulatory subunit for Glc7p type-1 protein phosphatase (PP1), tethers Glc7p to Gsy2p glycogen synthase, binds Hsf1p heat shock transcription factor, required for induction of some HSF-regulated genes under heat shock
1673	YJL063C	-0,618428633	-1,275850457	53,2597	5,03E-06	0,000150351	MRPL8	HRD238	chromosome 10	Mitochondrial ribosomal protein of the large subunit
1290	YPL134C	-0,894879907	-1,442333289	52,61851	5,31E-06	0,000155106	ODC1		chromosome 16	Mitochondrial inner membrane transporter, exports 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol for lysine and glutamate biosynthesis and lysine catabolism; suppresses, in multicopy, an fmc1 null mutation
1704	YDL222C	0,999977536	-1,157806175	51,65126	5,78E-06	0,00016513	FMP45		chromosome 4	Integral membrane protein localized to mitochondria (untagged protein) and eisosomes, immobile patches at the cortex associated with endocytosis; sporulation and sphingolipid content are altered in mutants; has homologs SUR7 and YNL194C
10553	YLR162W-A	-0,684589265	-2,524525327	51,40162	5,9E-06	0,000166732			chromosome 12	Putative protein of unknown function identified by fungal homology comparisons and RT-PCR
8198	YIL101C	0,266147181	-1,291140017	48,91882	7,38E-06	0,000192585	XBP1		chromosome 9	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, and late in meiosis; member of the Swi4p/Mbp1p family; potential Cdc28p substrate

10101	YDR033W	0,857403403	1,994951887	47,87161	8,13E-06	0,00019577	MRH1	chromosome 4	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; the authentic, non-tagged protein is detected in mitochondria in a phosphorylated state; has similarity to Hsp30p and Yro2p
10140	YDR115W	-0,948040079	-1,155569779	48,11422	7,95E-06	0,00019577		chromosome 4	Putative mitochondrial ribosomal protein of the large subunit, has similarity to E. coli L34 ribosomal protein; required for respiratory growth, as are most mitochondrial ribosomal proteins
7311	YMR081C	0,148726091	-1,779377717	47,72831	8,24E-06	0,00019672	ISF1	MBR3	Serine-rich, hydrophilic protein with similarity to Mbr1p; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; expression is under glucose control; cotranscribed with NAM7 in a cyp1 mutant
9830	YER018C	-0,176785218	-1,002376908	47,62762	8,32E-06	0,000198127	SPC25		Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint activity and kinetochore clustering
494	YOL071W	-0,123434201	-1,069197648	47,52634	8,4E-06	0,000199592	EMI5		Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation
5105	YNR019W	0,000797378	1,436377265	47,46635	8,45E-06	0,000200194	ARE2	SAT1	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the presence of oxygen
7469	YGR289C	0,545899246	-1,754695349	46,97888	8,85E-06	0,000206193	MAL11	MALT AGT1	Maltose permease, inducible high-affinity maltose transporter (alpha-glucoside transporter); encoded in the MAL1 complex locus; member of the 12 transmembrane domain superfamily of sugar transporters
2411	YNR037C	-0,191322446	-1,024889598	46,71883	9,07E-06	0,000208273	RSM19		Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S19 ribosomal protein
6110	YKL137W	-0,772481827	-1,115141093	46,1889	9,55E-06	0,000214227			Putative protein of unknown function; mutation results in growth defect on a non-fermentable (respiratory) carbon source
6687	YGL208W	-0,030809618	-1,228156281	44,82489	1,09E-05	0,000232491	SIP2	SPM2	One of three beta subunits of the Snf1 serine/threonine protein kinase complex involved in the response to glucose starvation; null mutants exhibit accelerated aging; N-mristoylprotein localized to the cytoplasm and the plasma membrane
683	YLR346C	2,563230679	-1,611802633	44,74877	1,1E-05	0,000233349			Putative protein of unknown function found in mitochondria; expression is regulated by transcription factors involved in pleiotropic drug resistance, Pdr1p and Yrr1p; YLR346C is not an essential gene
1541	YKL187C	0,284030256	-1,102935029	43,43426	1,26E-05	0,000253244			Putative protein of unknown function; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies
6824	YJL077W-B	0,234769188	-1,247060342	43,11579	1,3E-05	0,000258697			Putative protein of unknown function; identified by gene-trapping, microarray-based expression analysis, and genome-wide homology searching
5809	YOR150W	-0,668736173	-1,023951945	41,84954	1,48E-05	0,000282184	MRPL23		Mitochondrial ribosomal protein of the large subunit
9158	YHR096C	0,668319063	-1,446647844	40,93909	1,63E-05	0,000298239	HXT5		Hexose transporter with moderate affinity for glucose, induced in the presence of non-fermentable carbon sources, induced by a decrease in growth rate, contains an extended N-terminal domain relative to other HXTs
5832	YDR462W	-0,462764686	-1,06236729	40,56862	1,7E-05	0,000302591	MRPL28		Mitochondrial ribosomal protein of the large subunit
5064	YJL066C	0,425787866	-1,108353493	40,30457	1,75E-05	0,000308184	MPM1		Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches
5880	YDL045W-A	-0,902648753	-1,025077847	39,74283	1,86E-05	0,000319593	MRP10		Mitochondrial ribosomal protein of the small subunit

4036	YML129C	-0,401022462	-1,201818838	39,41606	1,93E-05	0,000328026	COX14	chromosome 13	Mitochondrial membrane protein, involved in translational regulation of Cox1p and assembly of cytochrome c oxidase (complex IV); associates with complex IV assembly intermediates and complex III/complex IV supercomplexes
6717	YKL218C	-0,57220883	1,684099916	39,32853	1,95E-05	0,000329955	SRY1	chromosome 11	3-hydroxyaspartate dehydratase, deaminates L-threo-3-hydroxyaspartate to form oxaloacetate and ammonia; required for survival in the presence of hydroxyaspartate
4149	YMR107W	0,503919356	-1,33212074	39,20789	1,97E-05	0,000331916	SPG4	chromosome 13	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources
41	YOR072W-B	-0,975766744	-2,046968283	38,76725	2,07E-05	0,000342487		chromosome 15	Putative protein of unknown function; identified by expression profiling and mass spectrometry
10037	YDR070C	0,424031438	-1,049324131	38,62257	2,11E-05	0,000343369		chromosome 4	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
7964	YIR014W	-0,836759216	-1,354319038	38,6124	2,11E-05	0,000343369		chromosome 9	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; expression directly regulated by the metabolic and meiotic transcriptional regulator Ume6p; YIR014W is a non-essential gene
3403	YBR262C	-0,662724807	-1,283220658	38,06574	2,25E-05	0,000358059	FMP51	chromosome 2	Protein of unknown function; non-tagged protein is detected in purified mitochondria in high-throughput studies; null mutant displays decreased frequency of mitochondrial genome loss and reduced growth rate in minimal glycerol media
3292	YPR166C	-0,971570973	-1,121675871	37,80299	2,32E-05	0,000365537	MRP2	chromosome 16	Mitochondrial ribosomal protein of the small subunit
8448	YGR138C	1,492150583	2,511727451	37,14198	2,5E-05	0,000384662	TPO2	chromosome 7	Polyamine transport protein specific for spermine; localizes to the plasma membrane; transcription of TPO2 is regulated by Haa1p; member of the major facilitator superfamily
7292	YKL107W	1,336720098	-1,044993617	37,04461	2,53E-05	0,000387463		chromosome 11	Putative protein of unknown function
8222	YPL265W	3,156170538	-1,10029184	36,64164	2,66E-05	0,000400239	DIP5	chromosome 16	Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate and L-aspartate; also a transporter for Gln, Asn, Ser, Ala, and Gly
9204	YDR041W	-0,844564884	-1,242928772	36,21302	2,8E-05	0,000413876	RSM10	chromosome 4	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S10 ribosomal protein; essential for viability, unlike most other mitoribosomal proteins
10275	YOR255W	0,301967639	-1,239936626	35,97024	2,88E-05	0,000422171	OSW1	chromosome 15	Protein involved in sporulation; required for the construction of the outer spore wall layers; required for proper localization of Spo14p
2852	YDR178W	0,022569365	-1,343412676	35,75763	2,95E-05	0,000428028	SDH4	chromosome 4	Membrane anchor subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone
1053	YBR108W	0,948149872	1,138028966	35,72593	2,96E-05	0,000428545		chromosome 2	Protein interacting with Rsv167p; null mutant displays decreased frequency of mitochondrial genome loss (petite formation) and severe growth defect in minimal glycerol media
3747	YPL054W	0,295411155	-1,247986538	35,37188	3,1E-05	0,00044108	LEE1	chromosome 16	Zinc-finger protein of unknown function
1717	YER093C-A	-0,78844114	-1,075163328	35,31485	3,12E-05	0,000443026		chromosome 5	Putative protein of unknown function; YER093C-A contains an intron; null mutant displays increased frequency of mitochondrial genome loss (petite formation)

10052	YDR059C	0,383975937	-1,046798716	35,18918	3,17E-05	0,000446451	UBC5	chromosome 4	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins, central component of the cellular stress response; expression is heat inducible
5282	YKR080W	-0,755675452	1,054934058	34,61646	3,4E-05	0,000470862	MTD1	chromosome 11	NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase, plays a catalytic role in oxidation of cytoplasmic one-carbon units; expression is regulated by Bas1p and Bas2p, repressed by adenine, and may be induced by inositol and choline
4029	YER182W	-0,642826982	-1,499878965	34,57353	3,42E-05	0,0004728		chromosome 5	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
8632	YMR157C	-0,684940401	-1,052915216	33,80707	3,77E-05	0,000503713	FMP39	chromosome 13	Protein of unknown function; non-tagged protein is detected in purified mitochondria in high-throughput studies; null mutant displays increased frequency of mitochondrial genome loss and reduced growth rate in minimal glycerol media
4589	YDL245C	-0,129733279	-2,605647179	33,38695	3,97E-05	0,000521424	HXT15	chromosome 4	Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose
9986	YMR316W	2,234465229	1,418335416	33,1878	4,08E-05	0,000529323	DIA1	chromosome 13	Protein of unknown function, involved in invasive and pseudohyphal growth; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
531	YHL032C	0,582879803	-1,063563918	32,43339	4,5E-05	0,000564246	GUT1	chromosome 8	Glycerol kinase, converts glycerol to glycerol-3-phosphate; glucose repression of expression is mediated by Adr1p and Ino2p-Ino4p; derepression of expression on non-fermentable carbon sources is mediated by Opi1p and Rsf1p
10391	YER053C-A	0,767829679	1,756784271	32,15568	4,67E-05	0,000580139		chromosome 5	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum
1742	YJR150C	0,044285157	-5,301331726	31,51821	5,09E-05	0,000613962	DAN1	chromosome 10	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic growth
1205	YJL100W	-0,171686643	1,334670757	31,02679	5,44E-05	0,000640354	LSB6	chromosome 10	Phosphatidylinositol 4-kinase that binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization
2825	YKR071C	0,655252545	1,174317462	30,57973	5,79E-05	0,000669002	DRE2	chromosome 11	Protein of unknown function; mutation displays synthetic lethal interaction with the pol3-13 allele of CDC2
1155	YMR280C	0,71852095	-1,604813072	30,5399	5,82E-05	0,000672016	CAT8	chromosome 13	Zinc cluster transcriptional activator necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements
4358	YDL194W	0,377199463	-1,016693127	30,10173	6,19E-05	0,000702037	SNF3	chromosome 4	Plasma membrane glucose sensor that regulates glucose transport; has 12 predicted transmembrane segments; long cytoplasmic C-terminal tail is required for low glucose induction of hexose transporter genes HXT2 and HXT4
7450	YBL059C-A	-0,697829553	-1,241449302	29,89443	6,38E-05	0,000711177		chromosome 2	Putative protein of unknown function; contains twin Cx9C motifs that can form coiled coil-helix-coiled-coil helix fold; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus
27	YKL138C	-0,54709679	-1,273527803	29,88701	6,38E-05	0,000711177	MRPL31	chromosome 11	Mitochondrial ribosomal protein of the large subunit

2378	YNL270C	0,705802905	-1,870004397	29,60351	6,65E-05	0,000729163	ALP1	APL1	chromosome 14	Arginine transporter; expression is normally very low and it is unclear what conditions would induce significant expression
6589	YMR070W	-0,353791933	1,154311571	29,49447	6,75E-05	0,000734978	MOT3	ROX7	chromosome 13	Nuclear transcription factor with two Cys2-His2 zinc fingers; involved in repression of a subset of hypoxic genes by Rox1p, repression of several DAN/TIR genes during aerobic growth, and repression of ergosterol biosynthetic genes
10382	YHL044W	-0,969358782	-1,363235747	29,34504	6,9E-05	0,000745032			chromosome 8	Putative integral membrane protein, member of DUP240 gene family; green fluorescent protein (GFP)-fusion protein localizes to the plasma membrane in a punctate pattern
7299	YDL039C	2,140691692	2,096266523	28,51534	7,79E-05	0,000816842	PRM7		chromosome 4	Pheromone-regulated protein, predicted to have one transmembrane segment; promoter contains Gcn4p binding elements
5473	YCR071C	-0,533342908	-1,000733464	28,09063	8,3E-05	0,000856982	IMG2		chromosome 3	Mitochondrial ribosomal protein of the small subunit
3774	YJL079C	-0,20902113	-1,061304492	27,99771	8,41E-05	0,00086049	PRY1		chromosome 10	Protein of unknown function, has similarity to Pry2p and Pry3p and to the plant PR-1 class of pathogen related proteins
1533	YDR381C-A	-0,955418163	-1,337873633	27,87519	8,57E-05	0,000872826			chromosome 4	Protein of unknown function, localized to the mitochondrial outer membrane
4038	YPL183W-A	-0,653386727	-1,01368538	27,09863	9,65E-05	0,000951981		GON5	chromosome 16	Homolog of the prokaryotic ribosomal protein L36, likely to be a mitochondrial ribosomal protein coded in the nuclear genome
5640	YPL201C	0,735767866	-1,927819251	27,03631	9,74E-05	0,000959116	YIG1		chromosome 16	Protein that interacts with glycerol 3-phosphatase and plays a role in anaerobic glycerol production; localizes to the nucleus and cytosol

