Table S1. Significant differentially expressed genes ($p < 0.05$; FC* > 1.5): R88 vs R115 (Δ*ypeIR* Δ*ypsIR* Δ*luxS::Kan*) cells, 37°C.

ID	*p* value	*q* value	FC	qRT-PCR	Gene	Gene function	Process	COG	COG function categories
YPO3300	8.43E-06	0.014634	15.78247		*luxS*	Autoinducer-2 production protein	AI-2	COG1854	T
YPO4080	0.003415	0.119003	8.030124		*malS*	Alpha-amylase protein	Maltose operon	COG0366	G
YPO3711	0.001863	0.09505	7.907408	12.52	*lamB, malB*	Maltoporin	Maltose operon		
YPO0832	0.00465	0.136149	6.506489	5.87	*agaZ*	Putative tagatose 6-phosphate kinase	Degradation of carbon compounds		
YPO3788	8.67E-06	0.014634	5.295196	19.64	*metE*	5-methyltetrahydropteroyltriglutamate--homc	Aspartate family biosynthesis	COG0620	E
YPO3681	0.000167	0.041071	5.182046			Putative insecticial toxin	Pathogenicity	COG1196	D
YPO0324	0.004904	0.139505	5.05309		*uvrA, dinE, b458*	Excinuclease ABC subunit A	DNA replication, restriction/modification, recombination and r	COG0178	L
malF	0.009932	0.172851	4.550331		*malF*	Maltose transport system permease protein M	Maltose operon		
YPO3714	0.027757	0.236717	4.393824		*malE*	Maltose-binding periplasmic protein precursc	Maltose operon	COG2182	G
YPO0845	0.000151	0.041071	4.381101			ThiJ,PfpI-family thiamine biogenesis protein	Thiamine Biosynthesis	COG0693	R
YPO0325	9.64E-05	0.041071	4.312423		*ssb, exrB, lexC*	Single-strand binding protein	DNA replication, restriction/modification, recombination and r	COG0629	L
YPO3200	0.000228	0.043857	4.061693		*malZ*	Putative maltodextrin glucosidase	Maltose operon	COG0366	G
YPO0844	0.000234	0.043857	4.059663		*agaY, kba*	Putative aldolase	Degradation of carbon compounds	COG0191	G
malK	0.008457	0.163608	4.003624		*malK*	Maltose,maltodextrin transport ATP-binding	Maltose operon		
YPO3716	0.003894	0.12735	3.819044		*malG*	Maltose transport system permease protein M	Maltose operon	COG0395	G
YPO0286	0.021274	0.208418	3.783691			Putative coproporphyrinogen III oxidase	Heme and porphyrin Biosynthesis	COG0635	H
YPO0931	0.000107	0.041071	3.581566		*metK*	S-adenosylmethionine synthetase	Central intermediary metabolism	COG0192	H
YPO3710	0.006463	0.15096	3.568695		*malM, molA*	Maltose operon periplasmic protein	Maltose operon		
YPO3715	0.006972	0.153829	3.496981		*malF*	Maltose transport system permease protein M	Maltose operon	COG1175	G
YPO0285	0.015452	0.192194	3.472935			Conserved hypothetical protein	Unknown		
YPO0821	0.037416	0.258303	3.427051			Hypothetical protein	Unknown	COG0086	K
YPO0284	0.010056	0.172851	3.271341			Conserved hypothetical protein	Unknown	COG0702	MG
YPO3712	0.016969	0.193113	3.269706		*malK*	Maltose,maltodextrin transport ATP-binding	Maltose operon	COG1130	G
agaY	0.001364	0.090259	3.212341		*agaY, kba*	Putative aldolase	Degradation of carbon compounds		
YPO0822	0.045111	0.286789	3.095037			Putative exported protein	Membranes, lipoproteins and porins		
malG	0.007692	0.156319	3.068227		*malG*	Maltose transport system permease protein M	Maltose operon		
YPO0626	0.002127	0.101111	3.059648			Conserved hypothetical protein	Unknown	COG2964	S
YPO0627	0.002363	0.106347	3.052314			Putative translational inhibitor protein	Unknown	COG0251	J
YPO0833	0.04228	0.277144	3.044388			Putative phosphosugar isomerase	Degradation of carbon compounds	COG2222	M
YPO3713	0.011278	0.172851	3.037394			Hypothetical protein	Unknown		
YPO3631	0.001315	0.090259	2.787653			Putative exported protein	Membranes, lipoproteins and porins		
YPO0319	0.001137	0.089242	2.390972		*qor, hcz, b451*	Quinone oxidoreductase	Degradation of small molecule	COG0604	CR
YPO0415	0.027009	0.236717	2.321701		*lsrK*	Kinase phosphorylates carbon-5 of the open f	AI-2	COG1070	G
YPO3738	0.003902	0.12735	2.191311			Hypothetical protein	Unknown		
YPO0842	0.01728	0.193113	2.155451			Putative sulfatase	Sulphur metabolism	COG3119	P
YPO1241	0.00033	0.053827	2.150069			Putative bacteriophage protein	Phage-related functions and prophage	COG0234	O
YPO1108	0.000787	0.083063	2.118482		*gltA, gluT, icdB*	Citrate synthase GltA	Tricarboxylic acid cycle	COG0372	C
YPO3682	0.00071	0.077266	2.096984			Putative lysR-family transcriptional regulator	Broad regulatory functions	COG0583	K
YPO0628	0.007204	0.15491	2.080275			Putative translational inhibitor protein	Unknown	COG0251	J
YPO2975	0.005024	0.139505	2.044596			Putative aminotransferase	Unknown	COG0436	E
YPO0839	0.001355	0.090259	2.032975		*kduD2*	2-deoxy-D-gluconate 3-dehydrogenase	Degradation of carbon compounds	COG1028	IQR
YPO3050	0.044882	0.285875	1.987743			Putative exported protein	Membranes, lipoproteins and porins	COG1840	P
YPO0316	0.0278	0.236717	1.969934			Conserved hypothetical protein	Unknown	COG0042	J

YPO0401	0.029592	0.244243	1.951308		Putative transcriptional regulator	Broad regulatory functions	COG2207	K
YPO3070	0.015151	0.191354	1.938084	*yfgD*	Putative arsenate reductase	Drug/analogue sensitivity	COG1393	P
YPO1242	0.000654	0.076151	1.903321		Putative bacteriophage tail sheath protein	Phage-related functions and prophage		
YPO2623	0.00348	0.119349	1.899328	*asnB*	Asparagine synthetase B	Aspartate family biosynthesis	COG0367	E
YPO1240	0.003183	0.11824	1.889477		Putative ATP-binding protein	Unknown		
YPO3566	0.021059	0.207866	1.852804	*degQ, hhoA*	Protease	Degradation of Proteins, peptides and glycopeptides	COG0265	O
YPO0841	0.013741	0.184497	1.832718		Putative regulatory protein	Broad regulatory functions	COG0641	R
YPO0948	0.036307	0.253758	1.79535		Conserved hypothetical protein (pseudogene)	Unknown		
YPO3789	0.035857	0.25256	1.778731	*metR*	LysR-family transcriptional regulatory protei	Broad regulatory functions	COG0583	K
YPO3658	0.045842	0.28872	1.774289	*accC, fabG*	Biotin carboxylase	Fatty acid biosynthesis	COG0439	I
YPO3741	0.001034	0.085175	1.739504	*thiF*	Thiamine biosynthesis protein ThiF	Thiamine Biosynthesis	COG0476	H
YPO2907	0.011434	0.172851	1.735855	*glyA*	Serine hydroxymethyltransferase	Central intermediary metabolism	COG0112	E
YPO1072	0.016064	0.192194	1.722196		ABC transporter permease protein	Transport/binding proteins	COG2011	P
YPO3991	0.010986	0.172851	1.721335		Putative insulinase family protease	Degradation of Proteins, peptides and glycopeptides	COG0612	R
YPO0569a	0.002185	0.10244	1.696895		Conserved hypothetical protein	Unknown		
YPO1683	0.033296	0.247878	1.661798		Probable N-acetylmuramoyl-L-alanine amida	Degradation of Proteins, peptides and glycopeptides	COG3023	V
YPO2974	0.027644	0.236717	1.656323		Putative B-type cytochrome	Electron transport	COG3038	C
YPO3740	0.008972	0.167713	1.645592	*thiE*	Thiamine-phosphate pyrophosphorylase	Thiamine Biosynthesis	COG0352	H
YPO1548	0.012259	0.175355	1.643618	*hisD*	Histidinol dehydrogenase	Histidine biosynthesis	COG0141	E
YPO3727	0.019177	0.200985	1.632806	*metA*	Homoserine O-succinyltransferase	Aspartate family biosynthesis	COG1897	E
YPO1501	0.012251	0.175355	1.624662		Putative esterase	Unknown	COG0627	R
YPO1654	0.007724	0.156319	1.622389	*lacZ*	Beta-galactosidase	Lactose operon	COG3250	G
YPO3049	0.001267	0.090259	1.615913		Putative binding protein-dependent transport	Transport/binding proteins	COG1178	P
YPO2162	0.037573	0.258855	1.613329	*sppA*	Protease IV	Degradation of Proteins, peptides and glycopeptides	COG0616	OU
YPO3237	0.000225	0.043857	1.608658	*nqrD, nqr4*	Na+-translocating NADH-quinone reductase	Electron transport	COG1347	C
YPO1244	0.010556	0.172851	1.606086		Hypothetical protein	Unknown		
YPO1383	0.016335	0.19281	1.590741	*pflB, pfl*	Formate acetyltransferase 1	Anaerobic respiration	COG1882	C
YPO1547	0.002986	0.115868	1.586611	*hisC*	Histidinol-phosphate aminotransferase	Histidine biosynthesis	COG0079	E
YPO0318	0.033351	0.247878	1.584549	*pspG*	Putative exported protein	Membranes, lipoproteins and porins	COG1175	G
YPO3069	0.005989	0.148668	1.581858		Putative exported protein	Membranes, lipoproteins and porins	COG0501	O
YPO0091	0.011141	0.172851	1.571138	*glpF*	Glycerol uptake facilitator protein	Membranes, lipoproteins and porins	COG0580	G
YPO3235	0.001759	0.09505	1.567371	*nqrF, nqr6*	NADH-uniquinone oxidoreductase subunit F	Electron transport	COG2871	C
YPO0287	0.045541	0.287764	1.562364		Putative methylenetetrahydrofolate reductase	Aspartate family biosynthesis	COG0685	E
YPMT1.7	0.031171	0.247878	1.559554				COG1502	I
YPO2815	0.025345	0.228164	1.538334		Putative acyltransferase	Unknown	COG0204	I
YPO0525	0.005609	0.145179	1.536643		Hypothetical protein	Unknown		
YPO0397	0.02322	0.217447	1.536643		Hypothetical protein	Unknown		
YPO1641	0.010866	0.172851	1.53526	*icdA, icd, icdE*	Isocitrate dehydrogenase [NADP]	Tricarboxylic acid cycle	COG0538	C
YPO1098	0.034706	0.249875	1.525009		Putative prophage integrase		COG0582	L
YPO1570	0.012677	0.1781	1.524094	*argG*	Argininosuccinate synthase	Glutamate family biosynthesis	COG0137	E
YPO2270	0.033483	0.247878	1.500652		Putative membrane protein	Membranes, lipoproteins and porins	COG0038	P
YPO1866	0.027686	0.236717	-1.50441	*uvrC*	Excinuclease ABC subunit C	DNA replication, restriction/modification, recombination and r	COG0322	L
YPO0727	0.001243	0.090259	-1.50471	*flgF*	Putative flagellar basal-body rod protein (pse	Chemotaxis and mobility		
YPO0881	0.023712	0.218705	-1.5124		Conserved hypothetical protein	Unknown	COG2944	K
caf1M	0.008	0.159797	-1.5174	*caf1M*	Putative F1 chaperone protein, caf1M			
YPO3365	0.049898	0.29892	-1.51771	*cysN*	Sulfate adenylyltransferase subunit 1	Sulphur metabolism	COG2895	P
YPO2904	0.021362	0.208418	-1.52288	*hcaT*	Putative transport permease protein	Transport/binding Carbohydrates,organic acids and alcohols	COG0477	GEPR

YPO3864	0.010814	0.172851	-1.52592		*rffE, wecB, nfrC*	UDP-N-acetylglucosamine 2-epimerase	Surface polysaccharides, lipopolysaccharides and antigens	COG0381	M
yscI	0.002543	0.108361	-1.52806		*yscI, lcrO*				
YPO1121	0.033334	0.247878	-1.53634		*tolQ*	TolQ colicin import protein	Colicin-related functions	COG0811	U
YPO0882	0.034979	0.25071	-1.54141			Conserved hypothetical protein	Unknown		
YPO1092	0.040614	0.271993	-1.55053			Putative DNA-binding prophage protein	Phage-related functions and prophage	COG0582	L
YPO2574	0.000209	0.043857	-1.55255			Putative membrane protein	Membranes, lipoproteins and porins	COG3477	S
YPO3366	0.022486	0.214259	-1.55255		*cysD*	Sulfate adenylyltransferase subunit 2	Sulphur metabolism	COG0175	EH
YPCD1.18	0.042411	0.277255	-1.55488						
sycN	0.044007	0.281364	-1.55846		*sycN*	Putative type III secretion protein	T3SS		
YPO1176	0.004128	0.12946	-1.5608		*pbpG*	Penicillin-binding protein 7 precursor	Murein sacculus and peptidoglycan	COG1686	M
YPO1706	0.005333	0.142328	-1.56111		*htpX*	Putative heat shock protein	Adaptions and atypical conditions	COG0501	O
YPO3817	0.001561	0.09505	-1.56236			Putative membrane protein	Membranes, lipoproteins and porins		
YPO0332	0.021611	0.209044	-1.56643		*rhaS, rhaC2, b395*	L-rhamnose operon regulatory protein	Broad regulatory functions	COG2207	K
YPO2674	0.021611	0.209044	-1.57318			Putative exported protein	Membranes, lipoproteins and porins		
rffE	0.014095	0.184652	-1.57507		*rffE, wecB, nfrC*	UDP-N-acetylglucosamine 2-epimerase	Surface polysaccharides, lipopolysaccharides and antigens		
nusG	0.041153	0.273471	-1.57586		*nusG*	Transcription antitermination protein	RNA synthesis, RNA modification and DNA transcription		
YPO3661	0.010149	0.172851	-1.58202			Putative membrane protein	Membranes, lipoproteins and porins	COG2717	S
feoA	0.035229	0.251721	-1.58502		*feoA*	Hypothetical ferrous iron transport protein A	Unknown		
YPO2897	0.006256	0.14978	-1.58645		*yfhP*	Conserved hypothetical protein	Unknown	COG1959	K
YPO3203	0.006947	0.153829	-1.59472		*pstS*	Phosphate binding protein	Transport/binding Anions	COG0226	P
YPO1373	0.041002	0.27301	-1.59871		*cydD, htrD*	Transport ATP-binding protein	Transport/binding proteins	COG1132	V
YPO3359	0.006679	0.15211	-1.60015			Conserved hypothetical protein	Unknown	COG0585	S
YPO0404	0.012181	0.175355	-1.6093			PTS system, IIC component	Transport/binding Carbohydrates,organic acids and alcohols	COG1299	G
YPO3865	0.001574	0.09505	-1.61268		*wzzE, wzz, b3785*	Putative lipopolysaccharide biosynthesis prot	Surface polysaccharides, lipopolysaccharides and antigens		
YPO3361	0.009099	0.167848	-1.62743		*ispD, b2747*	4-diphosphocytidyl-2C-methyl-D-erythritol s	Central intermediary metabolism	COG1211	I
YPO2394	0.032455	0.247878	-1.63673		*lpp, mlpA*	Major outer membrane lipoprotein	Membranes, lipoproteins and porins	COG0840	NT
YPO3360	0.002958	0.115868	-1.64856		*ispF, mecS, b2746*	2C-methyl-D-erythritol 2,4-cyclodiphosphate	Central intermediary metabolism	COG0245	I
YPO1513	0.034617	0.249875	-1.64955		*yohK*	Putative membrane protein	Membranes, lipoproteins and porins	COG1346	M
yscJ	1.9E-05	0.016001	-1.65616		*yscJ, ylpB*				
YPO2671	0.018226	0.194763	-1.66646		*ureD*	Urease accessory protein (pseudogene)	Pathogenicity		
yscK	0.009874	0.172851	-1.6713		*yscK*				
YPO3428	0.003217	0.11824	-1.68371		*guaC*	GMP reductase	Purine ribonucleotide biosynthesis	COG0516	F
yscS	0.021686	0.209163	-1.68523		*yscS*				
yscT	0.024122	0.220678	-1.68742		*yscT*				
yscL	0.013843	0.184497	-1.69114		*yscL*				
YPO2895	0.017734	0.193113	-1.69791		*nifU,iscU/yfhN*	NifU family protein	Unknown	COG0822	C
mtlA	0.002548	0.108361	-1.69825		*mtlA*	PTS system, mannitol-specific IIABC compo	Transport/binding Carbohydrates,organic acids and alcohols		
pim	0.039241	0.265341	-1.69825		*pim*				
YPO2894	0.007045	0.154422	-1.70404		*iscA/yfhF*	Conserved hypothetical protein	Unknown	COG0316	S
yscX	0.01144	0.172851	-1.70557		*yscX*				
YPO3986	0.016639	0.193113	-1.71292		*cdh*	CDP-diacylglycerol pyrophosphatase	Fatty acid biosynthesis	COG2134	I
YPO2703	0.019593	0.201649	-1.71292		*pcp*	Putative pyrrolidone-carboxylate peptidase	Degradation of Proteins, peptides and glycopeptides	COG2039	O
YPCD1.73	0.049837	0.29892	-1.71463						
YPO3363	0.016761	0.193113	-1.72823		*ygbE*	Putative membrane protein	Membranes, lipoproteins and porins	COG0477	GEPR
YPO2893	0.009042	0.167713	-1.73169			Chaperone protein HscB		COG1076	O
lcrF	0.014179	0.184652	-1.73343	-1.53	*lcrF, virF*				
YPO2896	0.007676	0.156319	-1.7395		*iscS, nifS, yfhO*	Putative aminotransferase	Unknown	COG1104	E

YPO2267	0.015248	0.191354	-1.75786			LysR-family transcriptional regulatory protei	Broad regulatory functions		
yopE	0.015787	0.192194	-1.76315		*yopE*	Putative outer membrane virulence protein	YOP		
YPO1435	0.049042	0.298303	-1.7923		*ompA, tolG, tut, con*	Putative outer membrane porin A protein	Cell envelop	COG2885	M
yscY	0.011478	0.172851	-1.79876		*yscY*				
YPO0326	0.019353	0.200985	-1.80381			Conserved hypothetical protein	Unknown	COG3254	S
YPO2390	0.000345	0.053827	-1.80832		*cfa, cdfA*	Cyclopropane-fatty-acyl-phospholipid syntha	Fatty acid biosynthesis	COG2230	M
YPO1302	0.016561	0.193113	-1.81176		*psaF*	putative membrane protein	Membranes, lipoproteins and porins		
yscM	0.011316	0.172851	-1.81811		*yscM, lcrQ*				
YPO3388	0.001855	0.09505	-1.82851		*yadQ*	Putative chloride channel protein	Transport/binding Anions	COG0038	P
YPO4113	0.003289	0.11824	-1.8504		*phoU, nmpA*	Putative phosphate transport system protein	Central intermediary metabolism	COG0704	P
yscQ	0.013859	0.184497	-1.87367		*yscQ*				
YPO4116	0.007196	0.15491	-1.87573		*pstC, phoW*	Putative phosphate transport system permeas	Transport/binding proteins	COG0573	P
YPO4085	0.027838	0.236717	-1.9058		*ibpA, hslT, htpN*	Heat shock protein	Adaptions and atypical conditions	COG0071	O
YPO4115	0.002792	0.115144	-1.90961		*pstA, phoT*	Putative phosphate transport system permeas	Transport/binding proteins	COG0581	P
lcrD	0.027298	0.236717	-1.92418		*lcrD, yscV*				
YPO3369	0.017367	0.193113	-1.92765			Conserved hypothetical protein	Unknown	COG1598	S
yopT	0.00017	0.041071	-1.9288	-2.81	*yopT*	Putative cytotoxic effector protein			
YPO1222	0.009336	0.169436	-1.94741		*ompC, meoA, par*	Outer membrane protein C, porin	Cell envelop	COG3203	M
YPO3137	0.015617	0.192194	-1.95972			Conserved hypothetical protein	Unknown		
caf1A	0.000364	0.053827	-1.96148		*caf1A*	Putative F1 capsule anchoring protein, caf1A			
yscO	0.025004	0.225942	-1.96737		*yscO*				
YPO1855	0.028234	0.23769	-2.00471			Putative exported protein	Membranes, lipoproteins and porins	COG2822	P
YPO1856	0.035986	0.25256	-2.00993			Conserved hypothetical protein	Unknown	COG2837	P
ompC	0.014223	0.184652	-2.01456		*ompC, meoA, par*	Outer membrane protein C, porin	Cell envelop		
YPO4114	0.003315	0.11824	-2.02466		*pstB, phoT*	Putative phosphate transport ATP-binding prc	Transport/binding proteins	COG1117	P
yscR	0.034433	0.249875	-2.04031		*yscR*				
bfr	0.007399	0.156319	-2.04971		*bfr*	Bacterioferritin	Iron uptake		
pstB	0.012715	0.1781	-2.05053		*pstb*	Putative phosphate transport ATP-binding prc	Transport/binding proteins		
YPO3367	0.000534	0.072102	-2.06618		*cysG*	Siroheme synthase	Heme and porphyrin Biosynthesis	COG0007	H
yscP	0.011984	0.175131	-2.06721		*yscP*				
YPO3387	0.001084	0.087108	-2.08882			Conserved hypothetical protein	Unknown	COG0316	S
YPO1608	2.62E-05	0.017707	-2.11573		*ptsG, glcA, umG*	PTS system, glucose-specific IIBC componen	Transport/binding Carbohydrates,organic acids and alcohols	COG1263	G
YPO3013	0.00491	0.139505	-2.1533		*cysW*	Sulfate transport system permease protein Cy	Transport/binding Anions	COG0555	O
yscN	0.024068	0.220678	-2.24431		*yscN*				
YPO3138	0.004112	0.12946	-2.26778		*ymoA*	Modulating protein YmoA (histone-like prote	Broad regulatory functions	COG0326	O
YPO1305	0.019409	0.200985	-2.26959		*psaC*	Outer membrane usher protein PsaC precurso	Surface structures	COG3188	NU
YPO0445	0.006345	0.150831	-2.29011			Conserved hypothetical protein	Unknown	COG3177	S
YPO1854	0.007095	0.154523	-2.35396			Putative membrane protein	Membranes, lipoproteins and porins	COG0672	P
YPO1847	0.017714	0.193113	-2.42759		*yecS*	Putative amino-acid ABC transporter (permea	Transport/binding Amino acids and amines	COG0765	E
YPO3321	0.001779	0.09505	-2.48035		*cybB*	Probable cytochrome B561	Electron transport	COG3038	C
YPO1754	0.001748	0.09505	-2.49378		*yebN*	Putative membrane protein	Membranes, lipoproteins and porins	COG1971	S
ypkA	0.003194	0.11824	-2.51582		*ypkA*				
YPO1848	0.04297	0.277312	-2.52616		*yecC*	Putative amino-acid ABC transporter (ATP-bi	Transport/binding Amino acids and amines	COG1126	E
YPO1992	0.008309	0.162789	-2.52717			Conserved hypothetical protein	Unknown	COG0500	QR
yopP	0.001417	0.090259	-2.65276		*yopP, yopJ*	Putative targeted effector protein	YOP		
YPO1301	0.006181	0.149538	-2.71014	-3.8	*psaE*	Putative regulatory protein	Broad regulatory functions	COG0745	TK
YPO3320	0.000108	0.041071	-2.71991		*cybC*	Putative cytochrome B562	Electron transport		

YPO4064	0.00064	0.076151	-3.045		Hypothetical protein	Unknown		
yscB	0.010442	0.172851	-3.2117	*yscB*	A			
sycE	0.000972	0.084194	-3.2792	*sycE*	Putative yopE chaperone			
YPO1995	0.030055	0.245148	-3.38008		Hypothetical protein	Unknown		
yscC	0.007625	0.156319	-3.45838	*yscC*				
YPO1994	0.018029	0.193833	-3.60853		Hypothetical protein	Unknown		
YPO1649	0.000876	0.083832	-3.64881		Conserved hypothetical protein	Unknown	COG1566	V
YPO4110	0.029733	0.244815	-4.17202	*gltJ*	ABC transporter permease	Transport/binding proteins	COG0765	E
YPO4109	0.029303	0.24245	-4.20175		Putative amino acid transport system permeas	Transport/binding Amino acids and amines	COG0765	E
YPO1993	0.000111	0.041071	-7.47153		Putative dehydrogenase	Unknown	COG1028	IQR

* FC = Fold Change