

Enrichment & DEG Insights

Condition 1

Condition 2

Condition 3

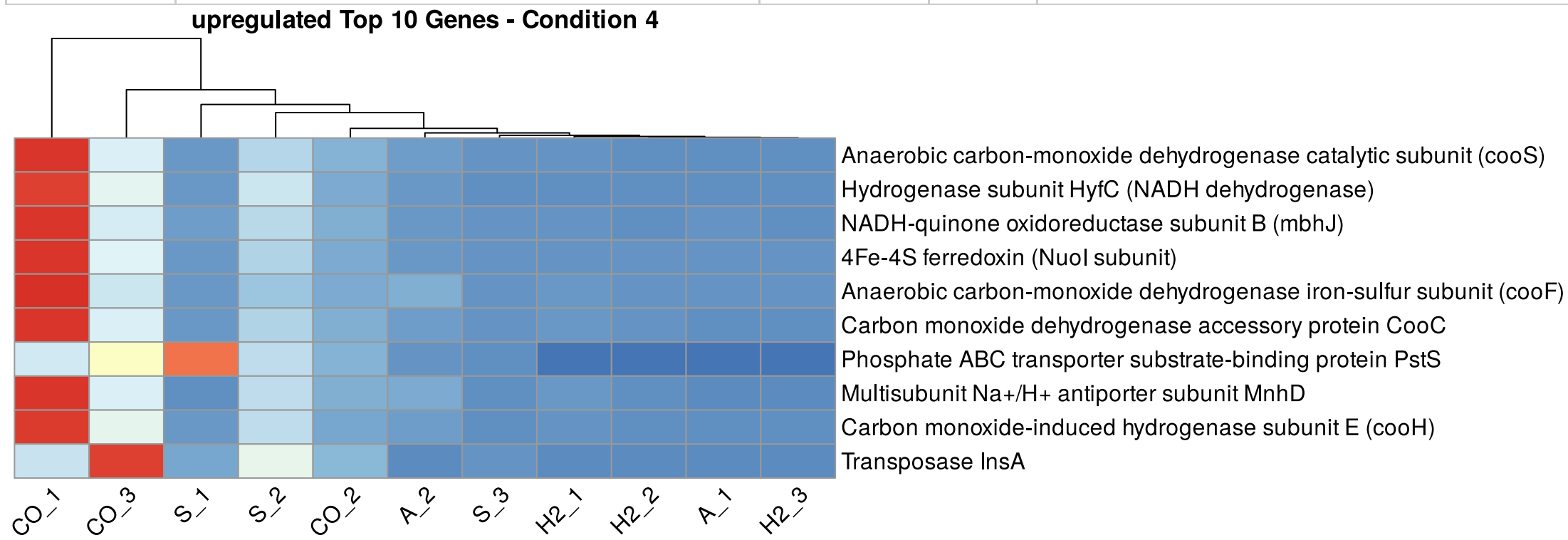
Condition 4

Experimental design:
control: H2
treated: CO

Upregulated: 438 | Downregulated: 377 | Total DEGs: 815

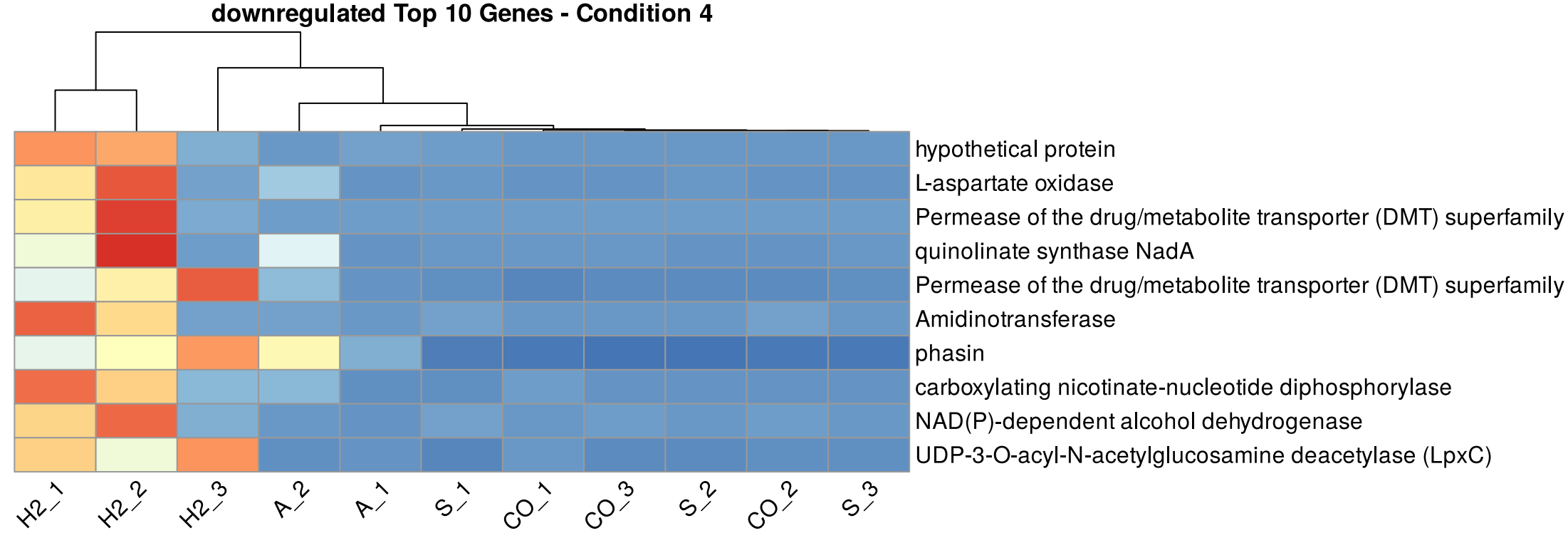
Top Upregulated DEGs

Locus_Tag	Protein Name	KO_IDs_list	log2FC	KEGG_Pathways_list	Tags_list	Subcategories	Confidence_Score	Notes
BFJEKD_15070	Anaerobic carbon-monoxide dehydrogenase catalytic subunit (cooS)	K00198	6.759119	Carbon fixation pathways in prokaryotes	carbon monoxide dehydrogenase, catalytic subunit, energy metabolism, CO oxidation	[Protein Folding, Quality Control & Stress Response]	High	Key catalytic subunit of anaerobic CO dehydrogenase complex, central to CO metabolism and energy conservation.
BFJEKD_15040	Hydrogenase subunit HyfC (NADH dehydrogenase)	K00337	6.440269	Oxidative phosphorylation, Carbon fixation pathways in prokaryotes	hydrogenase, NADH dehydrogenase, energy metabolism, oxidative phosphorylation	[Unknown & Hypothetical Proteins]	High	KO and EC consistent with NADH dehydrogenase function; extensive GO terms support role in energy metabolism and membrane localization.
BFJEKD_15045	NADH-quinone oxidoreductase subunit B (mbhJ)	K18023	6.228550	Oxidative phosphorylation	membrane-bound hydrogenase, NADH-quinone oxidoreductase, energy metabolism, oxidative phosphorylation	[Amino Acid Biosynthesis]	High	KO and EC confirm function as membrane-bound hydrogenase subunit; GO terms support electron transport and membrane localization.
BFJEKD_15050	4Fe-4S ferredoxin (Nuol subunit)		6.201388		ferredoxin, iron-sulfur protein, electron transfer, energy metabolism	[Amino Acid Biosynthesis]	Medium	Typical iron-sulfur cluster protein involved in electron transfer; lacks KO and EC but COG and PFAM support function.
BFJEKD_15065	Anaerobic carbon-monoxide dehydrogenase iron-sulfur subunit (cooF)	K00196, K05796	5.714208	Carbon fixation pathways in prokaryotes, Sulfur metabolism	iron-sulfur protein, electron transfer, CO dehydrogenase complex, energy metabolism	[Cell Wall & Envelope Biogenesis]	High	Iron-sulfur cluster protein subunit of anaerobic CO dehydrogenase complex, essential for electron transfer.
BFJEKD_15075	Carbon monoxide dehydrogenase accessory protein CooC	K07321	5.237672		CO dehydrogenase accessory protein, maturation factor, ATPase, protein assembly	[Toxin-Antitoxin & Phage Defense]	High	Accessory protein involved in maturation and assembly of CO dehydrogenase complex; important for enzyme functionality.
BFJEKD_10760	Phosphate ABC transporter substrate-binding protein PstS	K02040	4.743837	Phosphonate and phosphinate metabolism	phosphate transport, ABC transporter, substrate-binding protein, membrane transporter	[Toxin-Antitoxin & Phage Defense]	High	Well-annotated phosphate ABC transporter substrate-binding protein; key component of phosphate uptake system.
BFJEKD_15035	Multisubunit Na+/H+ antiporter subunit MnhD		4.698515		membrane transporter, Na+/H+ antiporter, ion transport	[Amino Acid Biosynthesis]	Medium	Likely part of Na+/H+ antiporter complex; no KO or EC assigned, but PFAM and COG support transporter function.
BFJEKD_15060	Carbon monoxide-induced hydrogenase subunit E (cooH)	K14090	4.681675	Sulfur metabolism	hydrogenase, energy metabolism, NiFe hydrogenase, electron transfer	[Cell Wall & Envelope Biogenesis]	High	Nickel-dependent hydrogenase subunit involved in CO metabolism and energy conservation.
BFJEKD_02545	Transposase InsA	K07488	4.625057	DNA transposase	transposase, mobile genetic element, DNA transposition	[Cell Wall & Envelope Biogenesis]	High	KO and COG consistent with transposase function; no EC or GO terms but strong evidence from KO and COG.



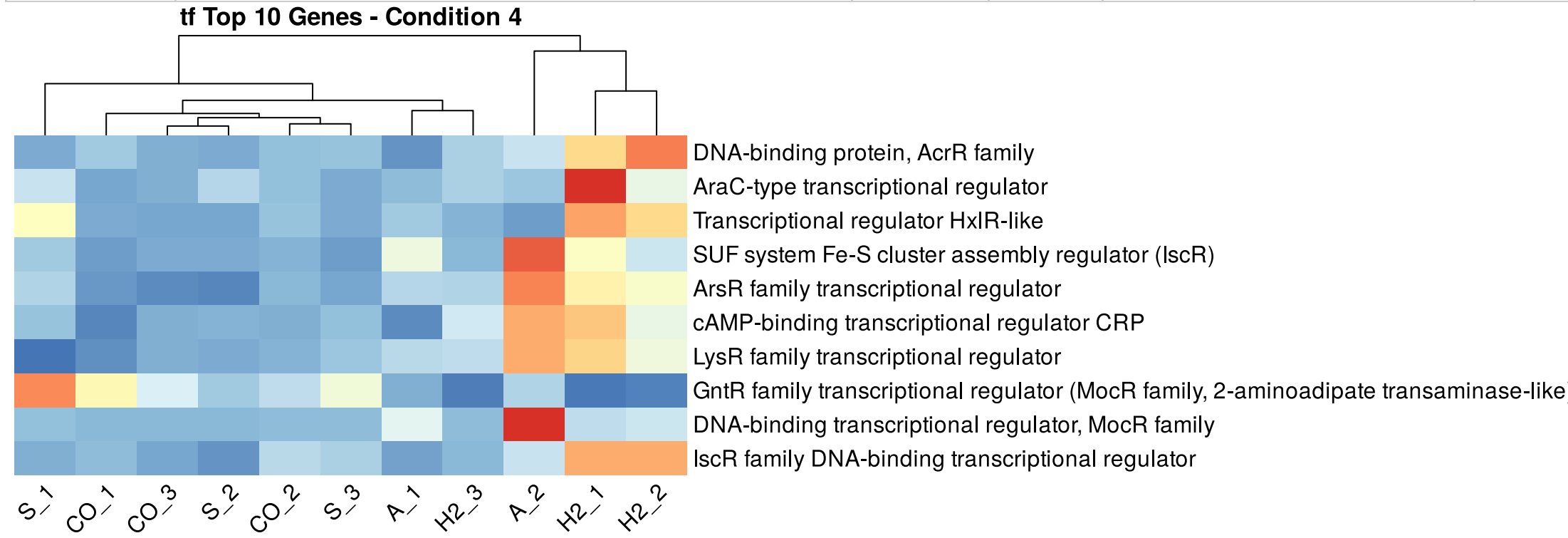
Top Downregulated DEGs

Locus_Tag	Protein Name	KO_IDs_list	log2FC	KEGG_Pathways_list	Tags_list	Subcategories	Confidence_Score	Notes
BFJEKD_05475	hypothetical protein		-6.933615		hypothetical protein, unknown function	[Secretion & Transport Systems]	Low	No functional annotation or domain detected; excluded from functional grouping and DE analysis.
BFJEKD_15100	L-aspartate oxidase	K00278	-6.105602	Nicotinate and nicotinamide metabolism	NAD biosynthesis, oxidoreductase, energy metabolism, L-aspartate oxidation	[Unknown & Hypothetical Proteins]	High	Well-annotated enzyme involved in NAD biosynthesis and energy metabolism.
BFJEKD_05480	Permease of the drug/metabolite transporter (DMT) superfamily		-5.750773		membrane transporter, DMT superfamily, permease, solute transport	[Secretion & Transport Systems]	Medium	Predicted transporter of drug/metabolite substrates; no KO or EC available; important for transport-related functional grouping.
BFJEKD_15105	quinolinate synthase NadA	K03517	-5.652842	Nicotinate and nicotinamide metabolism	NAD biosynthesis, coenzyme metabolism, ligase enzyme	[Secretion & Transport Systems]	High	Complete annotation with KO, EC, GO, and PFAM consistent; key enzyme in NAD biosynthesis pathway.
BFJEKD_03075	Permease of the drug/metabolite transporter (DMT) superfamily		-5.154984		membrane transporter, drug/metabolite transporter, DMT superfamily	[Glucosoneogenesis & Fructose Metabolism Enzyme]	Medium	Likely involved in transport of small molecules across membrane; no KO or EC assigned, but domain and COG support transporter function.
BFJEKD_05960	Amidino transferase		-4.825322		amidino transferase, amino acid metabolism, enzyme	[Protein Folding, Quality Control & Stress Response]	Medium	No KO or EC assigned; annotation based on PFAM and GO terms; likely involved in amino acid metabolism but function needs experimental confirmation.
BFJEKD_02630	phasin		-4.629074		PHA granule-associated protein, carbon storage	[DNA Recombination & Repair]	Low	No KO, EC, or GO terms; function inferred from PFAM and COG; likely involved in polyhydroxyalkanoate granule stabilization.
BFJEKD_15095	carboxylating nicotinate-nucleotide diphosphorylase	K00767	-4.379178	Nicotinate and nicotinamide metabolism	NAD biosynthesis, nicotinate metabolism, carboxylase, coenzyme metabolism	[Unknown & Hypothetical Proteins]	High	Complete and consistent annotation; involved in NAD biosynthesis pathway.
BFJEKD_08975	NAD(P)-dependent alcohol dehydrogenase	K05351	-4.235932	Pentose and glucuronate interconversions, Glycolysis / Gluconeogenesis	oxidoreductase, alcohol metabolism, NAD(P)-dependent enzyme	[Unknown & Hypothetical Proteins]	High	KO to EC mapping confirms EC number; involved in alcohol metabolism and energy production; relevant for metabolic pathway grouping.
BFJEKD_12580	UDP-3-O-acetyl-N-acetylglucosamine deacetylase (LpxC)	K02535	-4.124654	Lipopolysaccharide biosynthesis	lipid A biosynthesis, lipopolysaccharide biosynthesis, metalloenzyme	[Unknown & Hypothetical Proteins]	High	Key enzyme in lipid A biosynthesis, essential for outer membrane integrity; important for grouping in cell envelope and antibiotic target studies.



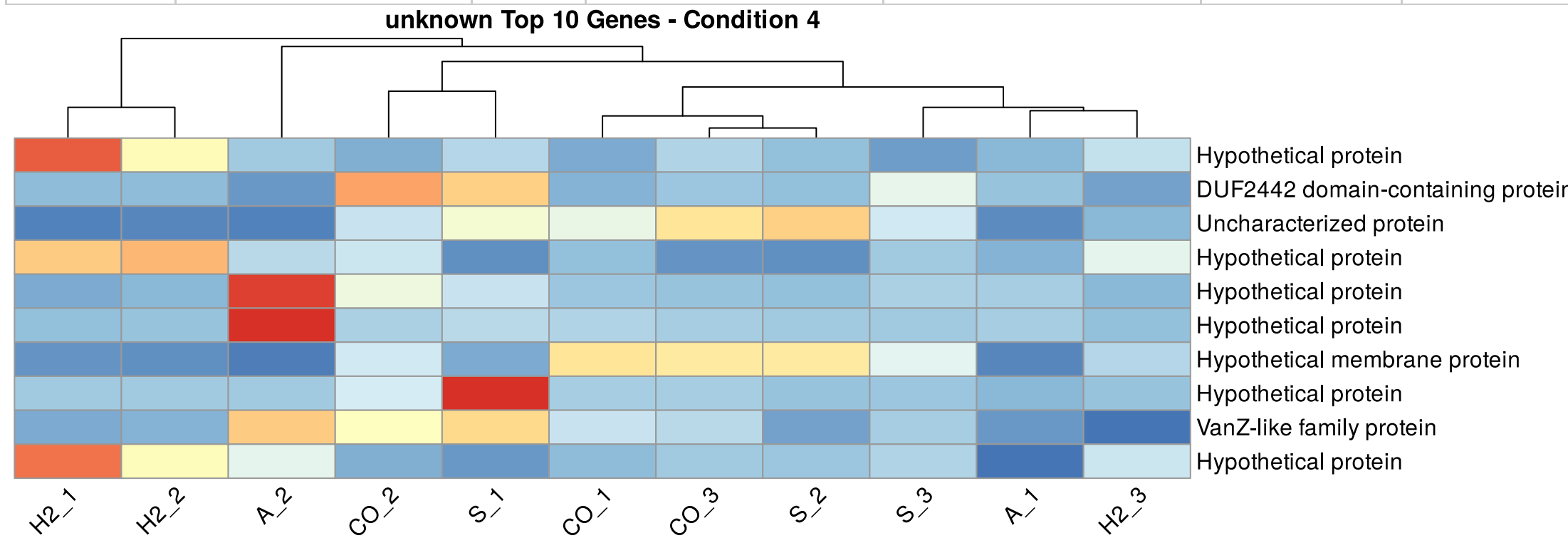
Transcription Factors

Locus_Tag	Protein Name	KO_IDs_list	log2FC	KEGG_Pathways_list	Tags_list	Subcategories	Confidence_Score	Notes
BFJEKD_00735	DNA-binding protein, AcrR family		-1.800119		transcriptional regulator, AcrR family, DNA binding, gene expression control	[Transcription Machinery & Regulators]	Medium	TetR family transcriptional regulator involved in gene expression regulation; no KO or EC assigned.
BFJEKD_00960	AraC-type transcriptional regulator		-2.845126		transcriptional regulator, DNA binding, AraC family	[Secretion & Transport Systems]	High	Well-annotated AraC-type transcriptional regulator with strong DNA-binding and transcription regulation evidence; useful for grouping under transcription factors.
BFJEKD_01130	Transcriptional regulator HxIR-like		-1.826920		transcriptional regulator, DNA-binding, helix-turn-helix	[Transcription Machinery & Regulators]	Medium	No KO or GO terms; annotation based on PFAM and COG; likely involved in transcriptional regulation.
BFJEKD_01390	SUF system Fe-S cluster assembly regulator (IscR)		-1.565803		transcriptional regulator, Fe-S cluster regulation, DNA-binding protein	[Mobile Genetic Elements & Plasmid]	High	IscR regulates expression of Fe-S cluster assembly genes, linking Fe-S cluster status to transcriptional control.
BFJEKD_01610	ArsR family transcriptional regulator	K22042	-1.183587	Two-component system	transcriptional regulator, arsenic resistance, two-component system	[Signal Transduction]	High	Well-annotated transcriptional regulator involved in virulence and metal resistance regulation; useful for regulatory network analysis.
BFJEKD_01715	cAMP-binding transcriptional regulator CRP	K21563	-1.218732	Two-component system	transcription regulator, cAMP-binding, signal transduction, CRP family	[Secretion & Transport Systems]	High	Duplicate of BFJEKD_01710 with identical annotations and strong evidence. Useful for transcriptional regulation and signal transduction grouping.
BFJEKD_03040	LysR family transcriptional regulator	K03566	-1.240738	Base excision repair	transcription regulator, LysR family, gene expression control	[Cell Wall & Envelope Biogenesis', 'Membrane Transporter]	High	Well-annotated transcriptional regulator; important for regulatory network analysis.
BFJEKD_03570	GntR family transcriptional regulator (MocR family, 2-aminoadipate transaminase-like)	K05825	2.337450	Valine, leucine and isoleucine degradation	transcriptional regulator, GntR family, aminotransferase-related, amino acid metabolism	[Polyhydroxyalkanoates & Storage Lipids]	High	KO and EC support aminotransferase-related regulatory function; relevant for amino acid metabolism and transcriptional regulation studies.
BFJEKD_03780	DNA-binding transcriptional regulator, MocR family		-1.800184		transcriptional regulator, MocR family, DNA-binding, aminotransferase domain, gene regulation	[Carbon Concentrating & Fixation]	Medium	No KO or EC assigned; GO terms and COG support transcriptional regulator function with aminotransferase domain. Useful for regulatory network analysis.
BFJEKD_05625	IscR family DNA-binding transcriptional regulator		-1.106181		transcriptional regulator, IscR family, DNA binding, iron-sulfur cluster regulation	[Toxin-Antitoxin & Phage Defense]	High	IscR is a well-known transcriptional regulator involved in iron-sulfur cluster biogenesis regulation; important for grouping under transcriptional regulators and metal cluster regulation.



Genes of Unknown Function

Locus_Tag	Protein Name	log2FC	Tags_list	Subcategories	Confidence_Score	Notes	upstream_Locus_Tag	upstream_tags	downstream_Locus_Tag	downstream_tags
BFJEKD_00225	Hypothetical protein	-1.178860	hypothetical protein, unknown function	[Transcription Machinery & Regulators]	Low	No functional annotation or domain detected; treat as unknown in downstream analyses.	BFJEKD_00220	[glycosyltransferase', 'carbohydrate metabolism', 'cell wall biosynthesis]	BFJEKD_00230	[hypothetical protein', 'unknown function']
BFJEKD_00595	DUF2442 domain-containing protein	1.226506	unknown function, DUF2442	[Amino Acid Biosynthesis]	Low	No functional annotation available; protein contains DUF2442 domain of unknown function. Not suitable for functional grouping or DE analysis without further experimental data.	BFJEKD_00590	[hypothetical protein', 'unknown function']	BFJEKD_00600	[membrane transporter', 'ABC transporter', 'amino acid transport', 'substrate-binding protein']
BFJEKD_00785	Uncharacterized protein	2.209795	hypothetical protein, unknown function	[Mobile Genetic Elements & Plasmid]	Low	No functional annotation available; sequence alone insufficient for confident functional prediction.	BFJEKD_00780	[anion transporter', 'Na+/H+ antiporter', 'membrane transporter', 'ion transport']	BFJEKD_00790	[hypothetical protein', 'unknown function']
BFJEKD_01210	Hypothetical protein	-1.258770	hypothetical protein, unknown function	[Unknown & Hypothetical Proteins]	Low	No functional annotation or domain information available; cannot assign function or group.	BFJEKD_01205	[hypothetical', 'unknown function']	BFJEKD_01215	[membrane transporter', 'MFS transporter', 'major facilitator superfamily']
BFJEKD_01420	Hypothetical protein	1.320369	unknown function	[Mobile Genetic Elements & Plasmid]	Low	No functional annotation or domain information available. Sequence does not match known domains or pathways.	BFJEKD_01415	[unknown function]	BFJEKD_01425	[unknown function]
BFJEKD_01425	Hypothetical protein	1.007605	unknown function	[Mobile Genetic Elements & Plasmid]	Low	No functional annotation or domain information available.	BFJEKD_01420	[unknown function]	BFJEKD_01430	[unknown function]
BFJEKD_02715	Hypothetical membrane protein	1.987352	membrane protein, hypothetical	[Aromatic Amino Acid Biosynthesis]	Low	No functional annotation available; predicted membrane localization based on hydrophobic sequence pattern; treat as unknown for grouping and DE analysis.	BFJEKD_02710	[flagellar motor', 'motility', 'membrane protein']	BFJEKD_02720	[two-component system', 'chemotaxis', 'phosphatase]
BFJEKD_04050	Hypothetical protein	1.156152	hypothetical protein, unknown function	[Carbon Concentrating & Fixation]	Low	No functional annotation or domain detected; cannot assign function or pathway.	BFJEKD_04045	[lipopolysaccharide biosynthesis', 'membrane protein', 'O-antigen polymerase]	BFJEKD_04055	[glycosyltransferase', 'carbohydrate metabolism', 'cell wall biosynthesis]
BFJEKD_04105	VanZ-like family protein	1.032192	unknown function, VanZ-like protein	[Cell Wall & Envelope Biogenesis]	Low	No functional annotation or domains detected; function remains unknown.	BFJEKD_04100	[glycosyltransferase', 'cell wall biosynthesis', 'carbohydrate metabolism]	BFJEKD_04110	[glycosyltransferase', 'cell wall biosynthesis', 'carbohydrate metabolism]
BFJEKD_04385	Hypothetical protein	-1.060610	hypothetical protein, unknown function	[Unknown & Hypothetical Proteins]	Low	No functional annotation or domain detected; consider experimental validation or further computational analysis.	BFJEKD_04380	[membrane transporter', 'EamA family', 'solute transport']	BFJEKD_04390	[amino acid biosynthesis', 'phenylalanine biosynthesis', 'enzyme', 'hydrolase]



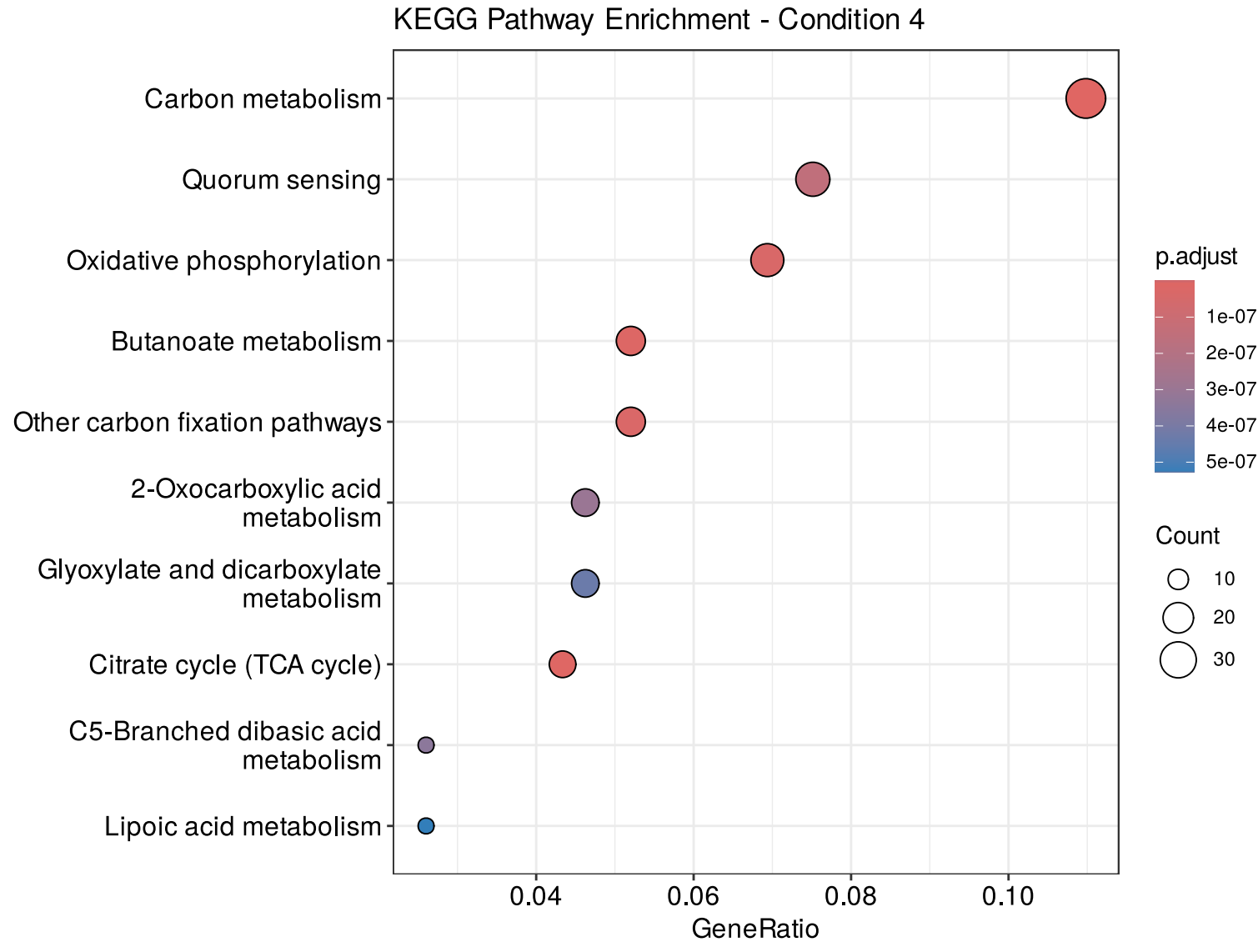
GO Enrichment

None found.

No GO plot available.

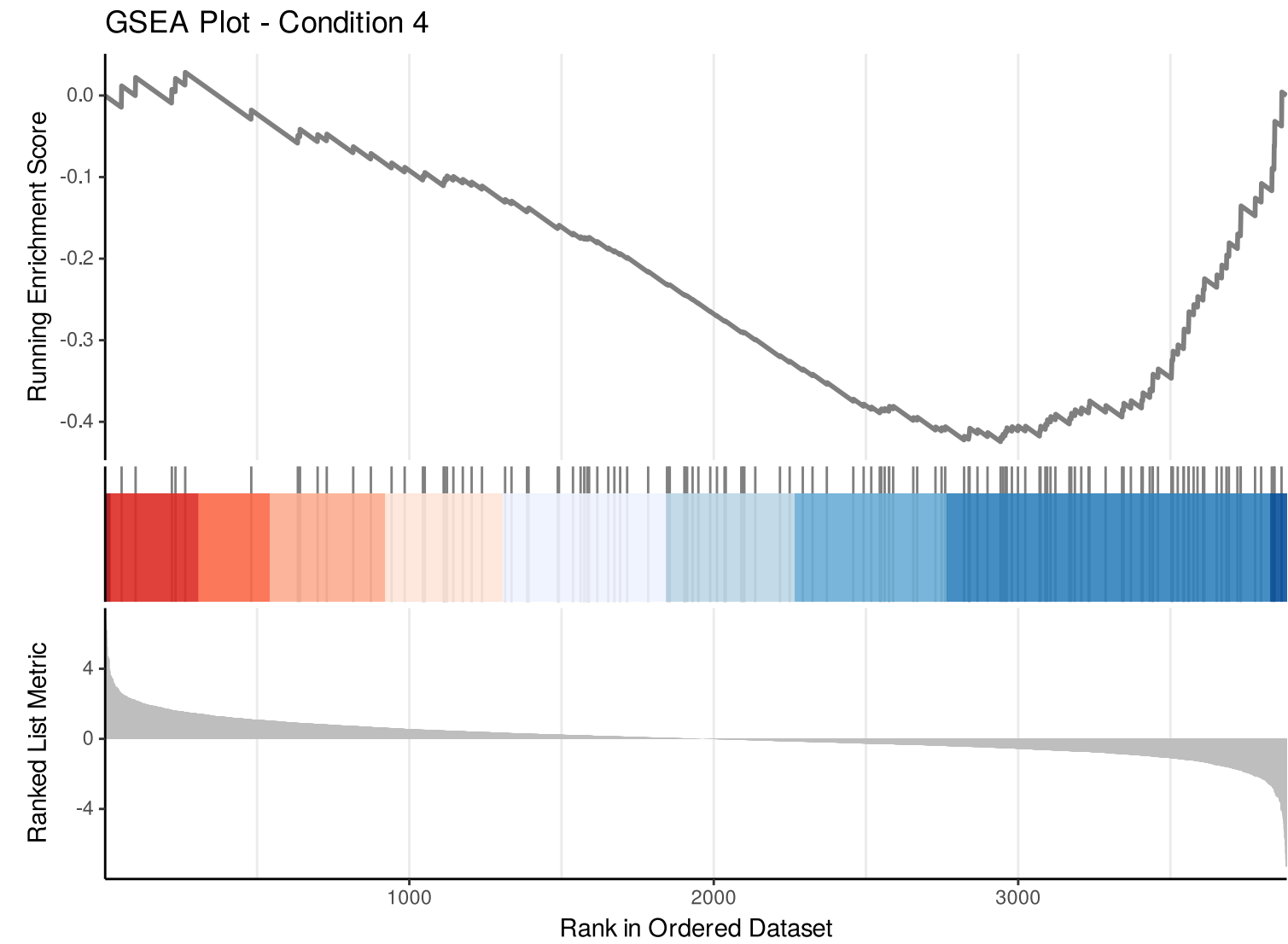
KEGG Pathway Enrichment

category	subcategory	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
Metabolism	Global and overview maps	ko1200	Carbon metabolism	38/346	377/14346	0	0e+00	0e+00	38
Metabolism	Carbohydrate metabolism	ko00020	Citrate cycle (TCA cycle)	15/346	70/14346	0	0e+00	0e+00	15
Metabolism	Carbohydrate metabolism	ko00650	Butanoate metabolism	18/346	114/14346	0	0e+00	0e+00	18
Metabolism	Energy metabolism	ko00720	Other carbon fixation pathways	18/346	121/14346	0	0e+00	0e+00	18
Metabolism	Energy metabolism	ko00190	Oxidative phosphorylation	24/346	224/14346	0	0e+00	0e+00	24
Cellular Processes	Cellular community - prokaryotes	ko2024	Quorum sensing	26/346	283/14346	0	1e-07	1e-07	26
Metabolism	Global and overview maps	ko1210	2-Oxocarboxylic acid metabolism	16/346	113/14346	0	3e-07	2e-07	16
Metabolism	Carbohydrate metabolism	ko00660	C5-Branched dibasic acid metabolism	9/346	29/14346	0	3e-07	2e-07	9
Metabolism	Carbohydrate metabolism	ko00630	Glyoxylate and dicarboxylate metabolism	16/346	118/14346	0	4e-07	3e-07	16
Metabolism	Metabolism of cofactors and vitamins	ko00785	Lipoic acid metabolism	9/346	31/14346	0	5e-07	4e-07	9



Gene Set Enrichment Analysis (GSEA)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalue	rank	leading_edge	name
GO:0003700	DNA-binding transcription factor activity	135	-0.4244043	-1.791971	0.0000613	0.0098110	0.0084555	941	tags=40%, list=24%, signal=31%	DNA-binding transcription factor activity
GO:0042802	identical protein binding	14	-0.7165486	-1.873934	0.0018356	0.0380662	0.0328070	447	tags=57%, list=12%, signal=51%	identical protein binding
GO:0004888	transmembrane signalling receptor activity	35	-0.5609304	-1.830798	0.0013722	0.0380662	0.0328070	535	tags=34%, list=14%, signal=30%	transmembrane signalling receptor activity
GO:0006099	tricarboxylic acid cycle	13	0.7315144	1.810447	0.0016347	0.0380662	0.0328070	445	tags=62%, list=11%, signal=55%	tricarboxylic acid cycle
GO:0071973	bacterial-type flagellum-dependent cell motility	17	0.6891804	1.800032	0.0019033	0.0380662	0.0328070	426	tags=53%, list=11%, signal=47%	bacterial-type flagellum-dependent cell motility
GO:0007165	signal transduction	114	-0.4071918	-1.670821	0.0011181	0.0380662	0.0328070	1040	tags=44%, list=27%, signal=33%	signal transduction
GO:0006355	regulation of DNA-templated transcription	212	-0.3500526	-1.568681	0.0007441	0.0380662	0.0328070	954	tags=36%, list=25%, signal=29%	regulation of DNA-templated transcription
GO:0005886	plasma membrane	317	0.3214784	1.426418	0.0016537	0.0380662	0.0328070	786	tags=29%, list=20%, signal=25%	plasma membrane



Condition 5

Condition 6