Electronic Supplementary Material (ESI) for Molecular Omics.

Supplementary data

What transcriptomics and proteomics can tell us about a high borate perturbed boron tolerant Bacilli strain.

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Table S1. List of the upregulated DEGs (A) and proteins (B) involved in gycolysis / gluconeogenesis in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002489	*pfkA*	NZ_SJDS01000007.1:161683-162643	5.27605	6 phosphofructokinase 1
2.	XLOC_001757	*glpX*	NZ_SJDS01000004.1:205868-206825	2.33566	fructose-1,6-bisphosphatase II
3.	XLOC_002252	*gapA*	NZ_SJDS01000006.1:132064-133081	3.5671	glyceraldehyde 3-phosphate dehydrogenase
4.	XLOC_002505	*gapA*	NZ_SJDS01000007.1:182040-183063	4.12946	glyceraldehyde-3-phosphate dehydrogenase
5.	XLOC_002253	*pgk*	NZ_SJDS01000006.1:133618-134803	1.65317	phosphoglycerate kinase
6.	XLOC_002254	*gpmI*	NZ_SJDS01000006.1:134822-137118	2.95864	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
7.	XLOC_002255	*eno*	NZ_SJDS01000006.1:137120-138413	4.39093	enolase
8.	XLOC_002490	*pyk*	NZ_SJDS01000007.1:162669-164430	4.51764	pyruvate kinase
9.	XLOC_002588	*pckA*	NZ_SJDS01000007.1:33512-35099	2.97936	phosphoenolpyruvate carboxykinase (ATP)
10.	XLOC_002613	*yiaY*	NZ_SJDS01000007.1:127252-128458	1.88696	alcohol dehydrogenase

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	classII fructose-bisphosphate aldolase	K.AVIAGAEK.V	95.61 %
2.	classIIfructose-bisphosphatase	K.GTNGAMTVLAIADK.G	- 87.00 %

Table S2. List of the upregulated DEGs (A) and proteins (B) involved in citrate cycle (TCA cycle) in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002833	*lpdA*	NZ_SJDS01000008.1:234366-235794	3.34809	dihydrolipoamide dehydrogenase
2.	XLOC_002965	*lpdA*	NZ_SJDS01000009.1:128397-129813	6.42901	dihydrolipoamide dehydrogenase
3.	XLOC_000844	*acnA*	NZ_SJDS01000002.1:121407-124113	3.57017	aconitate hydratase
4.	XLOC_002493	*icd*	NZ_SJDS01000007.1:167416-168679	5.67032	isocitrate dehydrogenase
5.	XLOC_001143	*sucA*	NZ_SJDS01000002.1:361317-364143	5.4174	2-oxoglutarate dehydrogenase E1 component
6.	XLOC_001142	*sucB*	NZ_SJDS01000002.1:359964-361227	9.13204	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)
7.	XLOC_003299	*sucD*	NZ_SJDS01000011.1:139520-140423	4.97164	succinyl-CoA synthetase alpha subunit
8.	XLOC_003300	*sucC*	NZ_SJDS01000011.1:140440-141601	4.63142	succinyl-CoA synthetase beta subunit
9.	XLOC_002547	*sdhA*	NZ_SJDS01000007.1:237437-239192	5.73889	succinate dehydrogenase flavoprotein subunit
10.	XLOC_002548	*sdhB*	NZ_SJDS01000007.1:239197-239977	5.75301	succinate dehydrogenase iron-sulfur subunit
11.	XLOC_003336	EW028_RS19055	NZ_SJDS01000012.1:36345-37884	3.19149	fumarate hydratase
12.	XLOC_002494	*mdh*	NZ_SJDS01000007.1:168857-169796	3.94567	malate dehydrogenase
13.	XLOC_003050	*mqo*	NZ_SJDS01000010.1:77093-78575	2.5939	malate:quinone oxidoreductase
14.	XLOC_002588	*pckA*	NZ_SJDS01000007.1:33512-35099	2.97936	phosphoenolpyruvate carboxykinase (ATP)
15.	XLOC_002968	*pdhA*	NZ_SJDS01000009.1:132196-133312	5.82103	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha
16.	XLOC_002966	*pdhC*	NZ_SJDS01000009.1:129818-131168	6.67572	pyruvate dehydrogenase E2

					component (dihydrolipoamide acetyltransferase)
17.	XLOC_002967	EW028_RS16585	NZ_SJDS01000009.1:131215-132193	5.77895	alpha-ketoacid dehydrogenase subunit beta
18.	XLOC_002546	EW028_RS14545	NZ_SJDS01000007.1:236762-237371	5.18378	succinate dehydrogenase cytochrome b558 subunit
19.	XLOC_002831	EW028_RS15895	NZ_SJDS01000008.1:230765-232109	2.92901	2-oxo acid dehydrogenase subunit E2

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	ADP-forming succinate-CoA ligase subunit beta	K.VAKELGSNVTVVK.A	940.28 %
2.	malate:quinine oxidoreductase	R.MLIDHLKAK.D	170.55 %
3.	Pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha	K.LSDEELVELMTR.M	165.78 %
4.	NADP-dependent isocitrate dehydrogenase	K.GPLTTPIGGGIR.S	19.00 %
5.	Aspartate amino transferase family protein	K.EYYQRLRNICDR.N	- 95.00 %

Table S3. List of the upregulated DEGs (A) and proteins (B) involved in oxidative phosphorylation pathway in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_003583	*nuoL*	NZ_SJDS01000014.1:27533-30357	0.794793	NADH-quinone oxidoreductase subunit L
2.	XLOC_004030	*nuoL*	NZ_SJDS01000020.1:24750-29395	1.31154	NADH-quinone oxidoreductase subunit L
3.	XLOC_003864	*ndh*	NZ_SJDS01000017.1:68792-69977	2.73813	NADH:ubiquinone reductase (H+-translocating)
4.	XLOC_002547	*frdA*	NZ_SJDS01000007.1:237437-239192	5.73889	fumarate reductase flavoprotein subunit
5.	XLOC_002548	*frdB*	NZ_SJDS01000007.1:239197-239977	5.75301	fumarate reductase iron-sulfur subunit
6.	XLOC_001582	*qoxC*	NZ_SJDS01000003.1:56417-57301	1.1737	cytochrome o ubiquinol oxidase subunit III

7.	XLOC_001583	*qoxB*	NZ_SJDS01000003.1:57302-59246	0.866095	cytochrome o ubiquinol oxidase subunit I
8.	XLOC_001584	*qoxA*	NZ_SJDS01000003.1:59307-60213	1.22056	cytochrome o ubiquinol oxidase subunit II
9.	XLOC_001782	*atpA*	NZ_SJDS01000004.1:234028-235537	2.96375	F0F1 ATP synthase subunit alpha
10.	XLOC_001784	*atpD*	NZ_SJDS01000004.1:236493-237909	3.39475	F0F1 ATP synthase subunit beta
11.	XLOC_001783	*atpG*	NZ_SJDS01000004.1:235584-236442	4.0987	F0F1 ATP synthase subunit gamma
12.	XLOC_001785	*atpC*	NZ_SJDS01000004.1:237933-238341	3.97247	F0F1 ATP synthase subunit epsilon
13.	XLOC_001779	*atpB*	NZ_SJDS01000004.1:231774-232485	2.93575	F0F1 ATP synthase subunit A
14.	XLOC_001780	*atpE*	NZ_SJDS01000004.1:232548-232773	3.91516	F0F1 ATP synthase subunit C
15.	XLOC_001781	*atpF*	NZ_SJDS01000004.1:232945-234000	2.67862	F0F1 ATP synthase subunit delta
16.	XLOC_001778	EW028_RS10240	NZ_SJDS01000004.1:231366-231738	2.22624	ATP synthase subunit I
17.	XLOC_000167	EW028_RS01445	NZ_SJDS01000001.1:278337-278844	4.23521	ubiquinol-cytochrome c reductase iron-sulfur subunit
18.	XLOC_000169	EW028_RS01455	NZ_SJDS01000001.1:279579-280347	4.21647	menaquinol-cytochrome c reductase cytochrome b/c subunit
19.	XLOC_000168	EW028_RS01450	NZ_SJDS01000001.1:278863-279538	3.85052	cytochrome b6
20.	XLOC_002540	EW028_RS14510	NZ_SJDS01000007.1:228385-229159	2.644	electron transfer flavoprotein subunit beta/FixA family protein

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	F0F1 ATP synthase subunit beta	K.AISVPVGEVTLGR.V	48.10 %
2.	Cytochrome ubiquinol oxidase subunit I	R.GWQFIHSRWYR.W	72.00 %

Table S4. List of the upregulated DEGs involved in pentose phosphate pathway in *Lysinibacillus* sp. strain OL1 response to boron

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002888	*rpe*	NZ_SJDS01000009.1:4968-6287	1.65921	ribulose-phosphate 3-epimerase
2.	XLOC_000027	*tkt*	NZ_SJDS01000001.1:46336-48331	2.06365	transketolase
3.	XLOC_001772	*rpiB*	NZ_SJDS01000004.1:223989-224427	3.04358	ribose 5-phosphate isomerase B
4.	XLOC_001444	*deoC*	NZ_SJDS01000003.1:235745-236417	5.77882	deoxyribose-phosphate aldolase
5.	XLOC_000039	*deoB*	NZ_SJDS01000001.1:63233-64415	5.7354	phosphopentomutase
6.	XLOC_004077	*prsA*	NZ_SJDS01000022.1:4390-5350	3.01544	ribose-phosphate diphosphokinase
7.	XLOC_001672	EW028_RS09460	NZ_SJDS01000004.1:57049-58012	0.636923	D-glycerate dehydrogenase
8.	XLOC_001757	*glpX*	NZ_SJDS01000004.1:205868-206825	2.33566	fructose-1,6-bisphosphatase II
9.	XLOC_002489	*pfkA*	NZ_SJDS01000007.1:161683-162643	5.27605	6-phosphofructokinase

Table S5. List of the upregulated DEGs (A) and protein (B) involved in DNA replication in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Gene id	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002486	*dnaE*	NZ_SJDS01000007.1:155673-158757	1.01995	DNA polymerase III subunit alpha
2.	XLOC_003153	*dnaN*	NZ_SJDS01000010.1:7598-8735	1.12872	DNA polymerase III subunit beta
3.	XLOC_004125	*dnaX*	NZ_SJDS01000023.1:27826-29611	1.94314	DNA polymerase III subunit gamma/tau
4.	XLOC_001414	*holA*	NZ_SJDS01000003.1:194271-195282	3.32322	DNA polymerase III subunit delta
5.	XLOC_003025	*dnaB*	NZ_SJDS01000010.1:33184-34546	1.41322	replicative DNA helicase
6.	XLOC_001461	*dnaG*	NZ_SJDS01000003.1:259243-261076	1.77163	DNA primase
7.	XLOC_003020	*ssb*	NZ_SJDS01000010.1:26636-27203	5.68046	single-stranded DNA-binding protein
8.	XLOC_000131	EW028_RS01250	NZ_SJDS01000001.1:240518-241961	2.63917	ATP-dependent DNA helicase
9.	XLOC_003297	*topA*	NZ_SJDS01000011.1:136255-138334	3.56084	type I DNA topoisomerase

10.	XLOC_000866	*parC,parE*	NZ_SJDS01000002.1:166254-170666	3.05908	DNA topoisomerase IV subunit A
11.	XLOC_003150	*gyrB*	NZ_SJDS01000010.1:4113-6048	2.30925	DNA topoisomerase (ATP-hydrolyzing) subunit B
12.	XLOC_003149	*gyrA*	NZ_SJDS01000010.1:1622-4088	2.74872	DNA gyrase subunit A
13.	XLOC_002507	EW028_RS14290,dnaI	NZ_SJDS01000007.1:183743-186061	2.75487	DnaD domain protein
14.	XLOC_003302	EW028_RS18725	NZ_SJDS01000011.1:144008-144770	0.00555693	ribonuclease HII
15.	XLOC_003431	*ligA*	NZ_SJDS01000012.1:125776-127783	1.61301	NAD-dependent DNA ligase LigA
16.	XLOC_002502	*polA*	NZ_SJDS01000007.1:177714-180342	1.75678	DNA polymerase I

(B)

Sl. No.	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	TatD family hydrolase	K.INLPIIIHNR.D	1578.91 %
2.	PolC-type DNA polymerase III	K.ITLACMQEMEFMMLKTK.Y	136.46 %
3.	YbaB/EbfC family nucleoid-associated protein	M.RGMGNMQGMMKK.M	123.14 %
4.	DNA polymerase III subunit gamma/tau	R.AKNPNGYK.A	108.44 %
5.	DNA replication/repair protein RecF	K.ETLIIKYR.T	100.96 %
6.	typeI DNA topoisomerase	K.VVEEFYK.D	93.33 %
7.	DNA repair protein RadA	K.RMATGVDQNR.V	76.34 %
8.	DnaD domain protein	R.QKILEMLGK.S	48.89 %
9.	DNA ligase D	R.FLCEQKPGLYTIER.L	32.39 %
10.	DNA helicase RecQ	K.TLRELCDK.K	- 79.00 %
11.	ATP-dependent DNA helicase RecG	K.ERMQSMTETNDGFR.L	- 42.00 %
12.	DNA topoisomerase IV subunit B	R.DFGRGMPTGMHK.M	- 38.00 %
13.	DNA gyrase subunit A	R.RTEFDLRK.A	- 36.00 %

Table S6. List of the upregulated DEGs (A) and proteins (B) involved in transcription in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	**Geneid**	**GeneName**	**Locus**	**log2Fold change**	**Annotation**
1.	XLOC_003138	*rpoA*	NZ_SJDS01000010.1:193190-194135	3.96839	DNA-directed RNA polymerase subunit alpha

2.	XLOC_003102	*rpoB*	NZ_SJDS01000010.1:161414-164990	2.39045	DNA-directed RNA polymerase subunit beta
3.	XLOC_003103	*rpoC*	NZ_SJDS01000010.1:165192-168876	2.92211	DNA-directed RNA polymerase subunit beta'
4.	XLOC_002895	EW028_RS16035	NZ_SJDS01000009.1:17501-17729	3.86939	DNA-directed RNA polymerase subunit omega
5.	XLOC_001271	EW028_RS07140	NZ_SJDS01000002.1:535625-535913	3.61016	RNA polymerase alpha subunit C-terminal domain-containing protein
6.	XLOC_002865	EW028_RS16635	NZ_SJDS01000009.1:141754-141964	3.53278	DNA-dependent RNA polymerase auxiliary subunit epsilon family protein
7.	XLOC_000054	*sigX*	NZ_SJDS01000001.1:82235-84073	3.15894	RNA polymerase subunit sigma
8.	XLOC_001794	EW028_RS10325	NZ_SJDS01000004.1:245566-245857	2.45562	DNA-directed RNA polymerase subunit beta
9.	XLOC_000847	EW028_RS05025,EW028_RS05030	NZ_SJDS01000002.1:127107-128590	5.00376	sigma-70 family RNA polymerase sigma factor
10.	XLOC_002668	EW028_RS15260,EW028_RS15265	NZ_SJDS01000008.1:93240-94642	4.63963	RNA polymerase sigma factor
11.	XLOC_001686	EW028_RS09575	NZ_SJDS01000004.1:87262-87811	4.58187	RNA polymerase sigma factor
12.	XLOC_003266	EW028_RS18495	NZ_SJDS01000011.1:101161-101464	4.34795	RNA polymerase subunit sigma
13.	XLOC_002154	*sigW*	NZ_SJDS01000005.1:272049-272613	3.3297	RNA polymerase sigma factor SigW
14.	XLOC_001825	*ssrS*	NZ_SJDS01000004.1:5575-5768	6.46349	6S RNA
15.	XLOC_001371	*ssrS*	NZ_SJDS01000003.1:144490-144690	2.15311	6S RNA
16.	XLOC_001401	*greA*	NZ_SJDS01000003.1:180429-180918	3.78504	transcription elongation factor GreA
17.	XLOC_003255	*nusA*	NZ_SJDS01000011.1:84374-85514	3.14507	transcription termination factor NusA
18.	XLOC_003915	*nusB*	NZ_SJDS01000018.1:46359-46743	4.77045	transcription antitermination factor NusB
19.	XLOC_0030	*nusG*	NZ_SJDS01000010.1:157324-	2.91355	transcription

	96		157858		termination/antitermination protein NusG
20.	XLOC_000150	*mtrB*	NZ_SJDS01000001.1:260637-260856	5.02567	trp RNA-binding attenuation protein MtrB
21.	XLOC_000007	EW028_RS00050	NZ_SJDS01000001.1:11337-11715	3.18045	MerR family transcriptional regulator
22.	XLOC_001570	EW028_RS07275	NZ_SJDS01000003.1:20151-20502	4.21182	helix-turn-helix transcriptional regulator
23.	XLOC_001998	EW028_RS10845	NZ_SJDS01000005.1:44942-45248	3.31013	helix-turn-helix transcriptional regulator
24.	XLOC_001459	EW028_RS08455	NZ_SJDS01000003.1:257576-258209	2.83963	helix-turn-helix transcriptional regulator
25.	XLOC_002560	EW028_RS14640	NZ_SJDS01000007.1:251188-251437	2.78424	helix-turn-helix transcriptional regulator
26.	XLOC_001568	EW028_RS07250	NZ_SJDS01000003.1:15058-15280	2.45228	helix-turn-helix transcriptional regulator
27.	XLOC_002406	EW028_RS13465	NZ_SJDS01000006.1:273108-273330	2.43132	helix-turn-helix transcriptional regulator
28.	XLOC_002103	EW028_RS11635	NZ_SJDS01000005.1:197541-197925	2.14309	helix-turn-helix transcriptional regulator

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	RNA polymerase sigma factor	R.LHKALKIMR.K	286.39 %
2.	23S rRNA (uracil (1939)-C(5))-methyl transferase RlmD	K.GAIPGEEITAQVTKTQR.N	91.72 %
3.	3'-5' exoribonuclease YhaM	K.MYHAEAIVR.V	74.21 %
4.	helix-turn-helix domain-containing protein	K.KGQEMQQKEK.T	34.80 %
5.	MarR family transcriptional regulator	K.QLSSIHEQLHEKAR.N	22.00 %
6.	Transcription termination factor NusA	R.NFGRIAAQTAK.Q	- 65.00 %
7.	DNA-directed RNA polymerase subunit beta	K.LAHMVDDK.L	- 65.00 %

Table S7. List of the upregulated DEGs (A) and protein (B) involved in translation in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_000142	*rpsA*	NZ_SJDS01000001.1:252524-253661	4.32069	30S ribosomal protein S1
2.	XLOC_003264	*rpsB*	NZ_SJDS01000011.1:99697-100417	4.84677	30S ribosomal protein S2
3.	XLOC_003119	*rpsC*	NZ_SJDS01000010.1:183765-184419	4.77308	30S ribosomal protein S3
4.	XLOC_002614	*rpsD*	NZ_SJDS01000007.1:131368-131971	6.06394	30S ribosomal protein S4
5.	XLOC_003129	*rpsE*	NZ_SJDS01000010.1:188269-188773	5.47094	30S ribosomal protein S5
6.	XLOC_003019	EW028_RS17085	NZ_SJDS01000010.1:26305-26593	4.80106	30S ribosomal protein S6
7.	XLOC_003106	*rpsG*	NZ_SJDS01000010.1:169826-170297	5.54008	30S ribosomal protein S7
8.	XLOC_003126	*rpsH*	NZ_SJDS01000010.1:186887-187286	5.23142	30S ribosomal protein S8
9.	XLOC_003143	*rpsI*	NZ_SJDS01000010.1:198882-199275	4.07127	30S ribosomal protein S9
10.	XLOC_003113	*rpsJ*	NZ_SJDS01000010.1:180260-180569	3.94404	30S ribosomal protein S10
11.	XLOC_003137	*rpsK*	NZ_SJDS01000010.1:192661-193051	3.7367	30S ribosomal protein S11
12.	XLOC_003105	*rpsL*	NZ_SJDS01000010.1:169362-169782	6.24981	30S ribosomal protein S12
13.	XLOC_003136	*rpsM*	NZ_SJDS01000010.1:192270-192636	4.58397	30S ribosomal protein S13
14.	XLOC_003125	EW028_RS17880	NZ_SJDS01000010.1:186672-186858	5.8228	type Z 30S ribosomal protein S14
15.	XLOC_003249	*rpsO*	NZ_SJDS01000011.1:78229-78499	3.50382	30S ribosomal protein S15
16.	XLOC_003308	*rpsP*	NZ_SJDS01000011.1:148877-149150	3.84832	30S ribosomal protein S16
17.	XLOC_003121	*rpsQ*	NZ_SJDS01000010.1:185063-185327	4.54738	30S ribosomal protein S17
18.	XLOC_003021	EW028_RS17095	NZ_SJDS01000010.1:27243-27480	5.04253	30S ribosomal protein S18
19.	XLOC_003117	*rpsS*	NZ_SJDS01000010.1:183116-183395	4.98483	30S ribosomal protein S19
20.	XLOC_001600	EW028_RS08140	NZ_SJDS01000003.1:195377-195626	7.48132	30S ribosomal protein S20
21.	XLOC_001447	EW028_RS08375	NZ_SJDS01000003.1:240207-240381	6.31034	30S ribosomal protein S21
22.	XLOC_0030	*rplA*	NZ_SJDS01000010.1:158629-	3.70132	50S ribosomal protein

	98		159328		L1
23.	XLOC_003116	*rplB*	NZ_SJDS01000010.1:182225-183056	5.11824	50S ribosomal protein L2
24.	XLOC_003114	*rplC*	NZ_SJDS01000010.1:180614-181244	4.6563	50S ribosomal protein L3
25.	XLOC_003115	*rplD,rplW*	NZ_SJDS01000010.1:181270-182178	4.56518	50S ribosomal protein L4
26.	XLOC_003124	*rplE*	NZ_SJDS01000010.1:186111-186651	4.98689	50S ribosomal protein L5
27.	XLOC_003127	*rplF*	NZ_SJDS01000010.1:187316-187856	5.54072	50S ribosomal protein L6
28.	XLOC_003100	*rplL*	NZ_SJDS01000010.1:160133-160493	5.24505	50S ribosomal protein L7/L12
29.	XLOC_003024	*rplI*	NZ_SJDS01000010.1:30754-33171	2.17181	50S ribosomal protein L9
30.	XLOC_003099	*rplJ*	NZ_SJDS01000010.1:159559-160060	5.07325	50S ribosomal protein L10
31.	XLOC_003097	*rplK*	NZ_SJDS01000010.1:158087-158513	5.44508	50S ribosomal protein L11
32.	XLOC_003142	*rplM*	NZ_SJDS01000010.1:198419-198857	4.73344	50S ribosomal protein L13
33.	XLOC_003122	*rplN*	NZ_SJDS01000010.1:185370-185739	5.12136	50S ribosomal protein L14
34.	XLOC_003131	*rplO*	NZ_SJDS01000010.1:189003-190739	5.97924	50S ribosomal protein L15
35.	XLOC_003120	*rplP*	NZ_SJDS01000010.1:184420-185045	4.58469	50S ribosomal protein L16
36.	XLOC_003139	*rplQ*	NZ_SJDS01000010.1:194192-194573	1.71915	50S ribosomal protein L17
37.	XLOC_003128	*rplR*	NZ_SJDS01000010.1:187888-188248	5.7021	50S ribosomal protein L18
38.	XLOC_003305	*rplS*	NZ_SJDS01000011.1:146542-146887	4.69469	50S ribosomal protein L19
39.	XLOC_002511	*rplT*	NZ_SJDS01000007.1:189755-190115	5.60056	50S ribosomal protein L20
40.	XLOC_001342	*rplU*	NZ_SJDS01000003.1:100076-100385	6.47673	50S ribosomal protein L21
41.	XLOC_003118	*rplV*	NZ_SJDS01000010.1:183417-183762	5.43106	50S ribosomal protein L22
42.	XLOC_003123	*rplX*	NZ_SJDS01000010.1:185774-186083	5.26158	50S ribosomal protein L24
43.	XLOC_004078	EW028_RS23260	NZ_SJDS01000022.1:5603-6200	3.78667	50S ribosomal protein L25/general stress protein Ctc
44.	XLOC_001343	EW028_RS07665,*rpmA*	NZ_SJDS01000003.1:100401-101054	6.29661	50S ribosomal protein L27
45.	XLOC_002839	EW028_RS15970	NZ_SJDS01000009.1:4567-4756	6.15201	50S ribosomal protein L28
46.	XLOC_0031	*rpmD*	NZ_SJDS01000010.1:188786-	4.03494	50S ribosomal protein

	30		188969		L30
47.	XLOC_001764	*rpmE*	NZ_SJDS01000004.1:216487-216691	2.89376	50S ribosomal protein L31
48.	XLOC_002936	*rpmF*	NZ_SJDS01000009.1:83306-83480	4.40569	50S ribosomal protein L32
49.	XLOC_001501	*rpmG*	NZ_SJDS01000003.1:329941-330091	3.99243	50S ribosomal protein L33
50.	XLOC_003094	*rpmG*	NZ_SJDS01000010.1:156588-156735	3.49092	50S ribosomal protein L33
51.	XLOC_003006	*rpmH*	NZ_SJDS01000010.1:10845-10980	6.07984	50S ribosomal protein L34
52.	XLOC_002510	*rpmI*	NZ_SJDS01000007.1:189497-189698	5.41015	50S ribosomal protein L35
53.	XLOC_003135	*rpmJ*	NZ_SJDS01000010.1:192132-192246	2.19632	50S ribosomal protein L36
54.	XLOC_001343	EW028_RS07665,*rpmA*	NZ_SJDS01000003.1:100401-101054	6.29661	ribosomal-processing cysteine protease Prp
55.	XLOC_003104	EW028_RS17760	NZ_SJDS01000010.1:169014-169263	5.61832	ribosomal L7Ae/L30e/S12e/Gadd45 family protein
56.	XLOC_001439	*prmA*	NZ_SJDS01000003.1:228332-229274	3.1761	50S ribosomal protein L11 methyltransferase
57.	XLOC_003256	*rimP*	NZ_SJDS01000011.1:85538-86015	3.04942	ribosome maturation factor RimP
58.	XLOC_001320	EW028_RS07520	NZ_SJDS01000003.1:69706-70288	3.00083	ribosome biogenesis GTP-binding protein YihA/YsxC
59.	XLOC_003254	EW028_RS18420,EW028_RS18425	NZ_SJDS01000011.1:83654-84238	2.78924	YlxQ family RNA-binding protein
60.	XLOC_001454	*ybeY*	NZ_SJDS01000003.1:248471-248945	2.67532	rRNA maturation RNase YbeY
61.	XLOC_004088	EW028_RS23315	NZ_SJDS01000022.1:16918-17356	2.63325	RNA-binding protein S1
62.	XLOC_001476	EW028_RS08585	NZ_SJDS01000003.1:285443-286745	2.55647	DEAD/DEAH box helicase
63.	XLOC_000143	*der*	NZ_SJDS01000001.1:254065-255376	2.51547	ribosome biogenesis GTPase Der
64.	XLOC_001408	*yhbY*	NZ_SJDS01000003.1:187545-187848	2.49456	ribosome assembly RNA-binding protein YhbY
65.	XLOC_003252	*rbfA*	NZ_SJDS01000011.1:80660-81002	2.0692	30S ribosome-binding factor RbfA
66.	XLOC_003134	*infA*	NZ_SJDS01000010.1:191876-192095	4.56521	translation initiation factor IF-1
67.	XLOC_003253	*infB*	NZ_SJDS01000011.1:81079-83640	2.64761	translation initiation factor IF-2
68.	XLOC_0025	*infC*	NZ_SJDS01000007.1:188962-	4.8281	translation initiation

	09		189466		factor IF-3
69.	XLOC_003108	*tuf*	NZ_SJDS01000010.1:172554-173742	5.56812	elongation factor Tu
70.	XLOC_003263	EW028_RS18480	NZ_SJDS01000011.1:98708-99596	3.66022	translation elongation factor Ts
71.	XLOC_003107	*fusA*	NZ_SJDS01000010.1:170339-172418	5.14033	elongation factor G
72.	XLOC_000982	EW028_RS06835	NZ_SJDS01000002.1:486152-486806	4.23338	FusB/FusC family EF-G-binding protein
73.	XLOC_003901	*efp*	NZ_SJDS01000018.1:30827-31385	3.65141	elongation factor P
74.	XLOC_001418	*lepA*	NZ_SJDS01000003.1:201105-202932	1.76942	translation elongation factor 4
75.	XLOC_003549	*raiA*	NZ_SJDS01000013.1:112968-113520	3.26299	ribosome-associated translation inhibitor RaiA
76.	XLOC_003546	*prfB*	NZ_SJDS01000013.1:108218-109320	2.30343	peptide chain release factor 2
77.	XLOC_003296	*trmFO*	NZ_SJDS01000011.1:134922-136236	3.77297	FADH(2)-oxidizing methylenetetrahydrofolate--tRNA-(uracil(54)-C(5))-methyltransferase TrmFO
78.	XLOC_001354	*tgt*	NZ_SJDS01000003.1:110582-111728	3.73764	tRNA guanosine(34) transglycosylase Tgt
79.	XLOC_003090	EW028_RS17680	NZ_SJDS01000010.1:150912-152373	2.3401	glutamyl-tRNA synthetase
80.	XLOC_001392	*alaS*	NZ_SJDS01000003.1:170552-173213	1.63368	alanyl-tRNA synthetase
81.	XLOC_001370	*aspS*	NZ_SJDS01000003.1:142581-144351	0.765615	aspartyl-tRNA synthetase
82.	XLOC_000221	*asnS*	NZ_SJDS01000001.1:367168-368464	3.72235	asparaginyl-tRNA synthetase
83.	XLOC_001217	*thrS*	NZ_SJDS01000002.1:476367-478284	0.27775	threonyl-tRNA synthetase
84.	XLOC_004112	*serS*	NZ_SJDS01000023.1:8554-9835	0.434546	seryl-tRNA synthetase
85.	XLOC_003091	*cysS*	NZ_SJDS01000010.1:152702-155280	1.45431	cysteinyl-tRNA synthetase
86.	XLOC_004182	*metG*	NZ_SJDS01000026.1:5027-7004	0.740909	methionyl-tRNA synthetase
87.	XLOC_002892	*fmt*	NZ_SJDS01000009.1:9932-13374	2.24332	methionyl-tRNA formyltransferase
88.	XLOC_001331	*valS*	NZ_SJDS01000003.1:85963-88609	2.01623	valyl-tRNA synthetase
89.	XLOC_002432	EW028_RS13700	NZ_SJDS01000007.1:45982-48400	2.05203	leucyl-tRNA synthetase
90.	XLOC_004101	*lysS*	NZ_SJDS01000022.1:36379-37882	2.35834	lysyl-tRNA synthetase, class II

91.	XLOC_003258	*proS*	NZ_SJDS01000011.1:90950-92657	1.45306	prolyl-tRNA synthetase
92.	XLOC_001369	*hisS*	NZ_SJDS01000003.1:141247-142516	0.371897	histidyl-tRNA synthetase
93.	XLOC_002530	*pheS*	NZ_SJDS01000007.1:214518-215556	1.42741	phenylalanyl-tRNA synthetase alpha chain
94.	XLOC_002531	*pheT*	NZ_SJDS01000007.1:215568-217986	1.06347	phenylalanyl-tRNA synthetase beta chain
95.	XLOC_002468	*tyrS*	NZ_SJDS01000007.1:124993-126262	1.05275	tyrosyl-tRNA synthetase
96.	XLOC_002508	*thrS*	NZ_SJDS01000007.1:186615-188547	1.00035	threonine--tRNA synthetase
97.	XLOC_001612	EW028_RS08450	NZ_SJDS01000003.1:255763-257149	0.720011	glycine--tRNA synthetase

(B)

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	Ribosome small subunit-dependent GTPaseA	K.TGIISQSLGRGK.H	709.24 %
2.	Alanine-tRNA ligase	R.ITNAQK.S	676.61 %
3.	30S ribosomal protein S7	R.GEKTMEER.L	441.38 %
4.	30S ribosomal protein S5	R.AVLELAGITDILSK.S	434.34 %
5.	50S ribosomal protein L17	R.DLATDLIINER.I	161.03 %
6.	50S ribosomal protein L20	K.VAGIEVNR.K	73.21 %
7.	DEAD/DEAH box helicase	M.MTINANSPSPFSKTQQLRIDVAR.E	357.45 %
8.	Valine-tRNA ligase	K.QIVADLQEAGVLIR.I	297.06 %
9.	Proline-tRNA ligase	R.VTVGKKATEGIVEVK.F	244.13 %
10.	Histidine-tRNA ligase	K.TVELTSTFR.A	182.77 %
11.	Isoleucine-tRNA ligase	R.SIRNSQGMKVK.Q	133.41 %
12.	Aspartate-tRNA ligase	R.TDVSEDLRLKYR.Y	111.36 %
13.	FADH(2)-oxidizing methylene tetrahydrofolate--tRNA-(uracil(54)-C(5))-methyltransferase TrmFO	K.TGKRPYAVVQLR.Q	100.37 %
14.	Ribosome biogenesis GTPase YlqF	K.EKFDR.M	29.33 %
15.	Tyrosine-tRNA ligase	K.AKGRVALSDDMVK.Q	26.41 %
16.	30S ribosomal protein S17	K.IGDIVR.I	22.79 %
17.	Translation elongation factor Ts	R.DEVSAEEVER.E	21.25 %
18.	Ribosomere cycling factor	K.AGEITEDDLR.G	19.00 %
19.	Leucine-tRNA ligase	K.VEGIAKAIEWLEQK.G	- 40.00 %
20.	50S ribosomal protein L21	K.VLFVGGENVK.V	- 46.00 %
21.	Arginine-tRNA ligase	K.VVADAAKHRTPHR.I	- 86.00 %
22.	ABC-F type ribosomal protection protein	K.ITQAGNMSKREAHAKPNLTFMTK.S	- 65.00 %

Table S8. List of the upregulated DEGs (A) and proteins (B) involved in efflux in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl. No.	**Gene id**	**Gene name**	**Locus**	**log2 Fold change**	**Annotation**
	Major facilitator superfamily (MFS)				
1	XLOC_002437	EW028_RS13810	NZ_SJDS01000007.1:72213-73482	5.08666	OFA family MFS transporter
2	XLOC_000926	EW028_RS05820	NZ_SJDS01000002.1:290057-291272	3.35393	MFS transporter
3	XLOC_002698	EW028_RS14795	NZ_SJDS01000008.1:5975-7166	2.17468	MFS transporter
	ATP-binding cassette superfamily (ABC)				
4	XLOC_002738	EW028_RS15135	NZ_SJDS01000008.1:69605-70520	2.20415	zinc ABC transporter substrate-binding protein
5	XLOC_002012	EW028_RS10965	NZ_SJDS01000005.1:68967-69993	3.71279	siderophore ABC transporter substrate-binding protein
6	XLOC_000560	EW028_RS00645,EW028_RS00650	NZ_SJDS01000001.1:120503-122550	5.68941	proline/glycine betaine ABC transporter permease
7	XLOC_002651	*modA*	NZ_SJDS01000008.1:40605-41385	1.88354	molybdate ABC transporter substrate-binding protein
8	XLOC_002652	*modB*	NZ_SJDS01000008.1:41388-42045	1.21489	molybdate ABC transporter permease subunit
9	XLOC_001479	EW028_RS08605,EW028_RS08610	NZ_SJDS01000003.1:288857-290146	2.30452	metal ABC transporter permease
10	XLOC_002736	EW028_RS15120,EW028_RS15125	NZ_SJDS01000008.1:67117-68856	2.48144	metal ABC transporter permease
11	XLOC_002737	EW028_RS15130	NZ_SJDS01000008.1:68867-69596	2.36185	metal ABC transporter ATP-binding protein
12	XLOC_000354	EW028_RS02950,EW028_RS02955	NZ_SJDS01000001.1:593395-595397	2.41971	iron ABC transporter permease
13	XLOC_003455	EW028_RS19795	NZ_SJDS01000013.1:38610-39486	4.29538	glycine betaine ABC transporter substrate-binding protein
14	XLOC_000559	EW028_RS00640	NZ_SJDS01000001.1:119539-120424	5.9048	glycine betaine ABC transporter substrate-

					binding protein
15	XLOC_000867	EW028_RS05220	NZ_SJDS01000002.1:171037-172033	2.97211	ABC transporter substrate-binding protein
16	XLOC_003457	EW028_RS19815	NZ_SJDS01000013.1:44087-45584	2.04949	ABC transporter permease
17	XLOC_000363	EW028_RS03035	NZ_SJDS01000001.1:611441-612149	3.64831	ABC transporter ATP-binding protein
18	XLOC_000364	EW028_RS03040,EW028_RS03045	NZ_SJDS01000001.1:612236-614076	3.60892	ABC transporter ATP-binding protein
19	XLOC_001478	EW028_RS08600	NZ_SJDS01000003.1:288097-288844	2.01594	ABC transporter ATP-binding protein
20	XLOC_002013	EW028_RS10970,EW028_RS10975,EW028_RS10980	NZ_SJDS01000005.1:70056-72711	2.16437	ABC transporter ATP-binding protein
	Small multidrug resistance family (SMR)				
21	XLOC_003761	EW028_RS21530,EW028_RS21535	NZ_SJDS01000016.1:42032-42700	0.565816	QacE family quaternary ammonium compound efflux SMR transporter
	Resistance-nodulation-cell division superfamily (RND)				
22	XLOC_002868	EW028_RS16660	NZ_SJDS01000009.1:145693-148783	1.78553	efflux RND transporter permease subunit
	Multi antimicrobial extrusion protein family (MATE)				
23	XLOC_000957	EW028_RS06375	NZ_SJDS01000002.1:406602-407982	0.687126	MATE family efflux transporter
24	XLOC_000948	EW028_RS06185	NZ_SJDS01000002.1:370991-372338	0.141214	MATE family efflux transporter
	Other Transporters				
25	XLOC_000893	EW028_RS05440	NZ_SJDS01000002.1:213861-215292	4.02532	SulP family inorganic anion transporter
26	XLOC_004197	EW028_RS24000	NZ_SJDS01000027.1:4595-6032	5.41458	SulP family inorganic anion transporter
27	XLOC_001391	*corA*	NZ_SJDS01000003.1:169215-170181	1.9256	magnesium/cobalt transporter CorA
28	XLOC_003846	EW028_RS21940	NZ_SJDS01000017.1:38668-40063	4.26844	L-cystine transporter
29	XLOC_004010	EW028_RS22890	NZ_SJDS01000020.1:20727-21792	2.05399	inorganic phosphate transporter family protein
30	XLOC_002645	*crcB*	NZ_SJDS01000008.1:21578-22270	1.97933	fluoride efflux transporter CrcB
31	XLOC_000055	EW028_RS00460	NZ_SJDS01000001.1:84616-85204	2.5407	ECF transporter S component
32	XLOC_0006	EW028_R	NZ_SJDS01000001.1:460598-	1.86121	DMT family

	52	S02310	461498		transporter
33	XLOC_001123	EW028_RS05985	NZ_SJDS01000002.1:326521-327721	2.26477	AI-2E family transporter
34	XLOC_002621	EW028_RS14200	NZ_SJDS01000007.1:164632-165971	4.16284	AI-2E family transporter
Other genes					
35	XLOC_002538	EW028_RS14500	NZ_SJDS01000007.1:226901-227483	2.39925	TetR/AcrR family transcriptional regulator
36	XLOC_003760	EW028_RS21525	NZ_SJDS01000016.1:41379-41958	2.38197	TetR family transcriptional regulator
37	XLOC_002469	EW028_RS14035	NZ_SJDS01000007.1:129340-129805	2.35903	TetR/AcrR family transcriptional regulator
38	XLOC_001230	EW028_RS06855	NZ_SJDS01000002.1:488604-489501	2.26296	TetR/AcrR family transcriptional regulator
39	XLOC_002645	*crcB*	NZ_SJDS01000008.1:21578-22270	1.97933	fluoride efflux transporter CrcB

(B)

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	TetR/AcrR family transcriptional regulator	-.MARGRK.F	308.00 %
2.	magnesium/cobalt transporter CorA	-.MIKIHYFNHNSK.T	90.12 %
3.	dipeptide/oligopeptide/nickel ABC transporter ATP-binding protein	K.ELLREPLMAAHKSLTDR.E	59.93 %
4.	Efflux RND transporter permease subunit	K.RAEQPSVTTTR.A	55.69 %
5.	MFS transporter	K.HLTVSQASVVMGCGLLAR.A	43.78 %
6.	MATE family efflux transporter	R.KPAWLQWK.E	- 90.00 %
7.	Na/Pi cotransporter family protein	K.EEVLRMGEHALR.G	- 55.00 %
8.	ABC transporter permease/substrate-binding protein	K.SIEQAVK.A	- 43.00 %
9.	ABC transporter ATP-binding protein	R.LEINNITK.K	- 19.00%

Table S9. List of the upregulated DEGs (A) and protein (B) involved in stress response in *Lysinibacillus* sp. strain OL1 response to boron

(A)

SI No.	Geneid	GeneName	Locus	log2Fold change	Annotation
Oxidative stress related					
1.	XLOC_001491	EW028_RS08740	NZ_SJDS01000003.1:315989-316595	6.56062	superoxide dismutase
2.	XLOC_002981	EW028_RS16735	NZ_SJDS01000009.1:162388-162931	5.58177	peroxiredoxin
3.	XLOC_002480	*tpx*	NZ_SJDS01000007.1:147166-147670	5.51587	thiol peroxidase
4.	XLOC_003654	EW028_RS20745	NZ_SJDS01000014.1:107197-108703	4.48037	catalase
5.	XLOC_002250	EW028_RS12780	NZ_SJDS01000006.1:130091-130325	2.53904	glutaredoxin family protein
6.	XLOC_002980	EW028_RS16730	NZ_SJDS01000009.1:161789-162245	2.2172	redoxin domain-containing protein
7.	XLOC_002829	EW028_RS15875	NZ_SJDS01000008.1:225091-225532	4.44755	BrxA/BrxB family bacilliredoxin
8.	XLOC_001187	*msrA,msrB*	NZ_SJDS01000002.1:426922-427877	4.297	peptide-methionine (S)-S-oxide reductase MsrA
9.	XLOC_002671	EW028_RS15295	NZ_SJDS01000008.1:101287-101797	3.63577	ferritin
10.	XLOC_003359	*perR*	NZ_SJDS01000012.1:1757-2201	3.28511	peroxide-responsive transcriptional repressor PerR
11.	XLOC_000134	*ypdA*	NZ_SJDS01000001.1:243800-244766	2.26255	YpdA family putative bacillithiol disulfide reductase
12.	XLOC_001273	EW028_RS07155	NZ_SJDS01000002.1:538059-538530	2.0852	peptide-methionine (S)-S-oxide reductase
Other genes					
13.	XLOC_004196	EW028_RS23995	NZ_SJDS01000027.1:4163-4583	4.33543	universal stress protein
14.	XLOC_002618	EW028_RS14130	NZ_SJDS01000007.1:148750-149200	3.73637	universal stress protein
15.	XLOC_000894	EW028_RS05445	NZ_SJDS01000002.1:215304-215718	2.8572	universal stress protein
16.	XLOC_001315	EW028_RS07460	NZ_SJDS01000003.1:54835-55255	2.64186	universal stress protein
17.	XLOC_004017	*yugI*	NZ_SJDS01000020.1:40491-40869	3.87648	general stress protein 13
18.	XLOC_000273	EW028_RS02300	NZ_SJDS01000001.1:459554-459992	3.23836	general stress protein
19.	XLOC_002543	*trxA*	NZ_SJDS01000007.1:232086-232398	5.41304	thioredoxin

20.	XLOC_002400	EW028_RS13255	NZ_SJDS01000006.1:231750-232095	5.37095	thioredoxin family protein
21.	XLOC_001482	EW028_RS08645	NZ_SJDS01000003.1:296730-297210	2.80052	thioredoxin family protein
22.	XLOC_003426	EW028_RS19415	NZ_SJDS01000012.1:120359-120923	2.7999	thioredoxin family protein
23.	XLOC_001437	*dnaK*	NZ_SJDS01000003.1:225117-226959	5.86776	molecular chaperone DnaK
24.	XLOC_001135	EW028_RS06090	NZ_SJDS01000002.1:350601-350802	5.5439	cold-shock protein
25.	XLOC_000946	EW028_RS06120,EW028_RS06125	NZ_SJDS01000002.1:354596-356311	4.4946	5-bromo-4-chloroindolyl phosphate hydrolysis family protein
26.	XLOC_003914	EW028_RS22310	NZ_SJDS01000018.1:43272-43683	3.93748	Asp23/Gls24 family envelope stress response protein
27.	XLOC_003325	EW028_RS18860	NZ_SJDS01000011.1:171764-172124	3.69448	Asp23/Gls24 family envelope stress response protein
28.	XLOC_002672	EW028_RS15385	NZ_SJDS01000008.1:125251-125509	2.63458	GlsB/YeaQ/YmgE family stress response membrane protein
29.	XLOC_002153	EW028_RS12010	NZ_SJDS01000005.1:271409-272036	3.91811	anti-sigma factor
30.	XLOC_001853	*spx*	NZ_SJDS01000004.1:88387-88792	3.68073	transcriptional regulator Spx
31.	XLOC_003522	*spxA*	NZ_SJDS01000013.1:66272-66668	2.48251	transcriptional regulator SpxA
32.	XLOC_003367	EW028_RS18950	NZ_SJDS01000012.1:15282-15900	3.30736	TerD family protein

(B)

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	GTPase HflX	R.KIEDQIAK.I	148.00 %
2.	Molecular chaperone DnaK	R.TVGPVR.Q	125.95 %
3.	Protein arginine kinase	K.LQENYSYFAIK.D	36.84 %
4.	Chaperonin GroEL	K.VTLGPK.G	- 20.00%

Table S10. List of the upregulated DEGs (A) and proteins (B) involved in osmoregulation in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_000559	EW028_RS00640	NZ_SJDS01000001.1:119539-120424	5.9048	glycine betaine ABC transporter substrate-binding protein
2.	XLOC_000560	EW028_RS00645,EW028_RS00650	NZ_SJDS01000001.1:120503-122550	5.68941	proline/glycine betaine ABC transporter permease
3.	XLOC_002673	*mscL*	NZ_SJDS01000008.1:126446-126836	5.66912	large conductance mechanosensitive channel protein MscL
4.	XLOC_003455	EW028_RS19795	NZ_SJDS01000013.1:38610-39486	4.29538	glycine betaine ABC transporter substrate-binding protein

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	Mechanosensitive ion channel family protein	K.KLFLIRMR.S	- 66.00 %

Table S11. List of the upregulated DEGs (A) and protein (B) involved in pyruvate metabolism in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002966	*pdhC*	NZ_SJDS01000009.1:129818-131168	6.67572	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)
2.	XLOC_002833	*lpdA*	NZ_SJDS01000008.1:234366-235794	3.34809	dihydrolipoyl dehydrogenase
3.	XLOC_002965	*lpdA*	NZ_SJDS01000009.1:128397-129813	6.42901	dihydrolipoyl dehydrogenase
4.	XLOC_002613	EW028_RS14030	NZ_SJDS01000007.1:127252-128458	1.88696	alcohol dehydrogenase
5.	XLOC_002490	*pyk*	NZ_SJDS01000007.1:162669-164430	4.51764	pyruvate kinase

6.	XLOC_000913	EW028_RS05560,EW028_RS05565	NZ_SJDS01000002.1:236188-237986	2.34028	acetyl-CoA carboxylase carboxyl transferase subunit alpha
7.	XLOC_002488	EW028_RS14175,EW028_RS14180	NZ_SJDS01000007.1:159555-161362	6.17695	acetyl-CoA carboxylase carboxyl transferase subunit beta
8.	XLOC_003909	*accB*	NZ_SJDS01000018.1:35576-36083	2.25217	acetyl-CoA carboxylase biotin carboxyl carrier protein
9.	XLOC_003910	*accC*	NZ_SJDS01000018.1:36097-37465	1.56382	acetyl-CoA carboxylase, biotin carboxylase subunit
10.	XLOC_001505	EW028_RS08840	NZ_SJDS01000003.1:335432-336077	2.31481	hydroxyacylglutathione hydrolase
11.	XLOC_001672	EW028_RS09460	NZ_SJDS01000004.1:57049-58012	0.636923	glyoxylate/hydroxypyruvate/2-ketogluconate reductase
12.	XLOC_000259	EW028_RS02140	NZ_SJDS01000001.1:427011-428214	1.10788	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)
13.	XLOC_002494	*mdh*	NZ_SJDS01000007.1:168857-169796	3.94567	malate dehydrogenase
14.	XLOC_003050	EW028_RS17330	NZ_SJDS01000010.1:77093-78575	2.5939	malate dehydrogenase (quinone)
15.	XLOC_002547	*frdA*	NZ_SJDS01000007.1:237437-239192	5.73889	fumarate reductase flavoprotein subunit
16.	XLOC_002548	*frdB*	NZ_SJDS01000007.1:239197-239977	5.75301	fumarate reductase iron-sulfur subunit
17.	XLOC_002588	*pckA*	NZ_SJDS01000007.1:33512-35099	2.97936	phosphoenolpyruvate carboxykinase (ATP)

(B)

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	Dihydro lipoyl dehydrogenase	R.ALALNQSEGFVK.L	100.37 %

Table S12. List of the upregulated DEGs (A) and protein (B) involved in propanoate metabolism in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002833	*lpdA*	NZ_SJDS01000008.1:234366-235794	3.34809	dihydrolipoyl dehydrogenase
2.	XLOC_002965	*lpdA*	NZ_SJDS01000009.1:128397-129813	6.42901	dihydrolipoyl dehydrogenase
3.	XLOC_000590	EW028_RS00985	NZ_SJDS01000001.1:188805-189798	2.51278	acrylyl-CoA reductase (NADPH)
4.	XLOC_002539	EW028_RS14505	NZ_SJDS01000007.1:227497-228271	2.54531	enoyl-CoA hydratase
5.	XLOC_000913	EW028_RS05560,EW028_RS05565	NZ_SJDS01000002.1:236188-237986	2.34028	acetyl-CoA carboxylase carboxyl transferase subunit alpha
6.	XLOC_002488	EW028_RS14175,EW028_RS14180	NZ_SJDS01000007.1:159555-161362	6.17695	acetyl-CoA carboxylase carboxyl transferase subunit beta
7.	XLOC_003909	*accB*	NZ_SJDS01000018.1:35576-36083	2.25217	acetyl-CoA carboxylase biotin carboxyl carrier protein
8.	XLOC_003910	*accC*	NZ_SJDS01000018.1:36097-37465	1.56382	acetyl-CoA carboxylase, biotin carboxylase subunit
9.	XLOC_001903	EW028_RS10780	NZ_SJDS01000005.1:30399-31920	1.09677	propionyl-CoA:succinyl-CoA transferase
10.	XLOC_002714	EW028_RS14940	NZ_SJDS01000008.1:34518-36045	0.903639	propionyl-CoA:succinyl-CoA transferase
11.	XLOC_003300	*sucC*	NZ_SJDS01000011.1:140440-141601	4.63142	succinyl-CoA synthetase beta subunit
12.	XLOC_003299	*sucD*	NZ_SJDS01000011.1:139520-140423	4.97164	succinyl-CoA synthetase alpha subunit
13.	XLOC_002492	*citZ*	NZ_SJDS01000007.1:166221-167337	5.1086	2-methylcitrate synthase
14.	XLOC_000173	*mgsA*	NZ_SJDS01000001.1:284135-284540	2.71537	methylglyoxal synthase
15.	XLOC_004021	EW028_RS23020	NZ_SJDS01000020.1:47047-48211	4.31894	NADP-dependent alcohol dehydrogenase

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	Dihydro lipoyl dehydrogenase	R.ALALNQSEGFVK.L	100.37 %

Table S13. List of the upregulated DEGs (A) and protein (B) involved in carbon fixation in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002494	*mdh*	NZ_SJDS01000007.1:168857-169796	3.94567	malate dehydrogenase
2.	XLOC_002547	*frdA*	NZ_SJDS01000007.1:237437-239192	5.73889	fumarate reductase flavoprotein subunit
3.	XLOC_002548	*frdB*	NZ_SJDS01000007.1:239197-239977	5.75301	fumarate reductase iron-sulfur subunit
4.	XLOC_003299	*sucD*	NZ_SJDS01000011.1:139520-140423	4.97164	succinyl-CoA synthetase alpha subunit
5.	XLOC_003300	*sucC*	NZ_SJDS01000011.1:140440-141601	4.63142	succinyl-CoA synthetase beta subunit
6.	XLOC_002493	*icd*	NZ_SJDS01000007.1:167416-168679	5.67032	isocitrate dehydrogenase
7.	XLOC_000844	*acnA*	NZ_SJDS01000002.1:121407-124113	3.57017	aconitate hydratase
8.	XLOC_000913	*accA*	NZ_SJDS01000002.1:236188-237986	2.34028	acetyl-CoA carboxylase carboxyl transferase subunit alpha
9.	XLOC_002488	EW028_RS14175,EW028_RS14180	NZ_SJDS01000007.1:159555-161362	6.17695	acetyl-CoA carboxylase carboxyl transferase subunit beta
10.	XLOC_003909	*accB*	NZ_SJDS01000018.1:35576-36083	2.25217	acetyl-CoA carboxylase biotin carboxyl carrier protein
11.	XLOC_003910	*accC*	NZ_SJDS01000018.1:36097-37465	1.56382	acetyl-CoA carboxylase biotin carboxylase subunit
12.	XLOC_002654	*fdhF*	NZ_SJDS01000008.1:50074-53011	0.636515	formate dehydrogenase (hydrogenase)
13.	XLOC_0039	*folD*	NZ_SJDS01000018.1:46774-	3.26584	methylenetetrahydrof

	16		47629		olate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	NADP-dependent isocitrate dehydrogenase	K.GPLTTPIGGGIR.S	19.00 %

Table S14. List of the upregulated DEGs (A) and protein (B) involved in purine metabolism in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_000039	*deoB*	NZ_SJDS01000001.1:63233-64415	5.7354	phosphopentomutase
2.	XLOC_004077	EW028_RS23255	NZ_SJDS01000022.1:4390-5350	3.01544	ribose-phosphate pyrophosphokinase
3.	XLOC_001361	EW028_RS07805	NZ_SJDS01000003.1:129199-129712	4.64538	adenine phosphoribosyltransferase
4.	XLOC_000178	*ushA*	NZ_SJDS01000001.1:293111-295244	1.28547	5'-nucleotidase / UDP-sugar diphosphatase
5.	XLOC_002746	*yjjG*	NZ_SJDS01000008.1:83435-84140	2.31523	5'-nucleotidase
6.	XLOC_001185	*deoD*	NZ_SJDS01000002.1:423460-424168	5.39561	purine-nucleoside phosphorylase
7.	XLOC_004091	*hpt*	NZ_SJDS01000022.1:22427-22970	2.53181	hypoxanthine phosphoribosyltransferase
8.	XLOC_004107	*guaB*	NZ_SJDS01000023.1:343-1807	2.44196	IMP dehydrogenase
9.	XLOC_000154	*ndk*	NZ_SJDS01000001.1:263687-264104	5.48993	nucleoside-diphosphate kinase
10.	XLOC_002554	EW028_RS14585	NZ_SJDS01000007.1:243262-243856	2.24703	XTP/dITP diphosphohydrolase
11.	XLOC_003774	*guaA*	NZ_SJDS01000016.1:2955-4509	4.46904	GMP synthase (glutamine-hydrolysing)
12.	XLOC_002896	*gmk*	NZ_SJDS01000009.1:17733-18351	3.95467	guanylate kinase
13.	XLOC_002490	*pyk*	NZ_SJDS01000007.1:162669-164430	4.51764	pyruvate kinase

14.	XLOC_001081	EW028_RS05660,*nrdE*,*nrdF*,*nrdI*	NZ_SJDS01000002.1:251557-255184	2.35779	ribonucleoside-diphosphate reductase alpha chain
15.	XLOC_003026	EW028_RS17130	NZ_SJDS01000010.1:34790-36080	1.10223	adenylosuccinate synthase
16.	XLOC_003132	EW028_RS17920	NZ_SJDS01000010.1:190809-191463	4.54377	adenylate kinase
17.	XLOC_004011	*cysC*	NZ_SJDS01000020.1:21862-23592	2.94993	adenylyl-sulfate kinase
18.	XLOC_004084	*mazG*	NZ_SJDS01000022.1:13670-15131	0.89011	nucleoside triphosphate diphosphatase
19.	XLOC_001953	EW028_RS11840	NZ_SJDS01000005.1:233623-234835	0.00807875	allantoate deiminase
20.	XLOC_001202	*ureC*	NZ_SJDS01000002.1:451716-453797	3.06758	urease subunit beta
21.	XLOC_001203	*ureA*	NZ_SJDS01000002.1:453812-454115	2.04304	urease subunit gamma

(B)

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	Adenylosuccinate lyase	K.RNPIGSENMVGMSRLMR.G	181.69 %
2.	PucR family transcriptional regulator	R.SMKRAIAVSK.Q	124.89 %
3.	Adenylosuccinate synthase	K.IDGETYK.L	111.63 %
4.	IMP dehydrogenase	K.EDLITAPVGTTLEDAEK.I	87.29 %
5.	GTP pyrophospho kinase family protein	K.VKLKGMR.S	- 74.00 %

Table S15. List of the upregulated DEGs involved in pyrimidine metabolism in *Lysinibacillus* sp. strain OL1 response to boron

Sl No.	**Geneid**	**GeneName**	**Locus**	**log2Fold change**	**Annotation**
1.	XLOC_000154	*ndk*	NZ_SJDS01000001.1:263687-264104	5.48993	nucleoside-diphosphate kinase
2.	XLOC_000141	*cmk*	NZ_SJDS01000001.1:251747-252422	2.80782	CMP/dCMP kinase
3.	XLOC_000178	*ushA*	NZ_SJDS01000001.1:293111-295244	1.28547	5'-nucleotidase / UDP-sugar diphosphatase
4.	XLOC_002746	*yjjG*	NZ_SJDS01000008.1:83435-84140	2.31523	5'-nucleotidase
5.	XLOC_001776	*upp*	NZ_SJDS01000004.1:228921-229551	2.84632	uracil phosphoribosyltransferase
6.	XLOC_000653	*rutF*	NZ_SJDS01000001.1:465624-466110	0.439674	flavin reductase

7.	XLOC_002784	EW028_RS15490	NZ_SJDS01000008.1:143432-144188	0.66107	3-hydroxy acid dehydrogenase / malonic semialdehyde reductase
8.	XLOC_004084	*mazG*	NZ_SJDS01000022.1:13670-15131	0.89011	nucleoside triphosphate diphosphatase
9.	XLOC_001081	EW028_RS05660,*nrdE*,*nrdF*,*nrdI*	NZ_SJDS01000002.1:251557-255184	2.35779	ribonucleoside-diphosphate reductase alpha chain
10.	XLOC_001080	*dut*	NZ_SJDS01000002.1:251107-251545	2.82689	dUTP pyrophosphatase
11.	XLOC_001210	*thyA*	NZ_SJDS01000002.1:459402-460380	1.51534	thymidylate synthase
12.	XLOC_000040	*deoA*	NZ_SJDS01000001.1:64428-65679	4.84103	thymidine phosphorylase
13.	XLOC_001185	*deoD*	NZ_SJDS01000002.1:423460-424168	5.39561	purine-nucleoside phosphorylase
14.	XLOC_001765	*tdk*	NZ_SJDS01000004.1:216807-217380	0.371257	thymidine kinase
15.	XLOC_004188	*tmk*	NZ_SJDS01000026.1:13336-13966	0.205545	dTMP kinase
16.	XLOC_001363	*psuK*	NZ_SJDS01000003.1:131759-132851	1.70839	pseudouridine kinase
17.	XLOC_001364	*psuG*	NZ_SJDS01000003.1:132855-133770	1.32036	pseudouridylate synthase

Table S16. List of the upregulated DEGs (A) and protein (B) involved in amino acid metabolism in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_002439	*asnB*	NZ_SJDS01000007.1:76022-77873	3.06126	asparagine synthase
2.	XLOC_000220	EW028_RS01860	NZ_SJDS01000001.1:365946-367140	3.10113	alanine-synthesizing transaminase
3.	XLOC_001205	*aspA*	NZ_SJDS01000002.1:455987-457406	3.33372	aspartate ammonia-lyase
4.	XLOC_000008	*glnA*	NZ_SJDS01000001.1:11770-13105	2.77373	glutamine synthetase
5.	XLOC_002149	*glmS*	NZ_SJDS01000005.1:264748-266551	3.73363	glutamine---fructose-6-phosphate transaminase (isomerizing)
6.	XLOC_002254	*gpmI*	NZ_SJDS01000006.1:134822-137118	2.95864	2,3-bisphosphoglycerate-independent

					phosphoglycerate mutase
7.	XLOC_002833	*lpdA*	NZ_SJDS01000008.1:234366-235794	3.34809	dihydrolipoamide dehydrogenase
8.	XLOC_002965	*lpdA*	NZ_SJDS01000009.1:128397-129813	6.42901	dihydrolipoamide dehydrogenase
9.	XLOC_002312	*gcvH*	NZ_SJDS01000006.1:238588-238969	5.47919	glycine cleavage system H protein
10.	XLOC_003088	EW028_RS17670	NZ_SJDS01000010.1:149262-150204	2.19449	serine O-acetyltransferase
11.	XLOC_004096	*cysK*	NZ_SJDS01000022.1:29423-30353	3.57363	cysteine synthase
12.	XLOC_002426	*metK*	NZ_SJDS01000007.1:35865-37062	3.43924	S-adenosylmethionine synthetase
13.	XLOC_001403	*mtnN*	NZ_SJDS01000003.1:181781-182474	3.4746	Adenosylhomocysteine nucleosidase
14.	XLOC_002615	*msrC*	NZ_SJDS01000007.1:134412-134892	2.00237	L-methionine (R)-S-oxide reductase
15.	XLOC_000256	*sseA*	NZ_SJDS01000001.1:422769-423579	2.11936	thiosulfate/3-mercaptopyruvate sulfurtransferase
16.	XLOC_002494	*mdh*	NZ_SJDS01000007.1:168857-169796	3.94567	malate dehydrogenase
17.	XLOC_002539	EW028_RS14505	NZ_SJDS01000007.1:227497-228271	2.54531	enoyl-CoA hydratase
18.	XLOC_000220	*alaA*	NZ_SJDS01000001.1:365946-367140	3.10113	alanine-synthesizing transaminase
19.	XLOC_000172	EW028_RS01475,EW028_RS01480	NZ_SJDS01000001.1:282983-284116	2.04539	4-hydroxy-tetrahydrodipicolinate reductase
20.	XLOC_003498	EW028_RS19745	NZ_SJDS01000013.1:25865-27332	murE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
21.	XLOC_001142	*sucB*	NZ_SJDS01000002.1:359964-361227	9.13204	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)
22.	XLOC_001202	*ureC*	NZ_SJDS01000002.1:451716-453797	3.06758	urease subunit beta
23.	XLOC_001203	*ureA*	NZ_SJDS01000002.1:453812-454115	2.04304	urease subunit gamma
24.	XLOC_000220	*alaA*	NZ_SJDS01000001.1:365946-367140	3.10113	alanine-synthesizing transaminase
25.	XLOC_002859	*adiA*	NZ_SJDS01000009.1:121922-123392	2.20042	arginine decarboxylase
26.	XLOC_0025	*echA*	NZ_SJDS01000007.1:227497-	2.54531	enoyl-CoA hydratase

	39		228271		
27.	XLOC_001407	*aroE*	NZ_SJDS01000003.1:186709-187540	2.86797	quinate/shikimate dehydrogenase
28.	XLOC_002320	*sufD*	NZ_SJDS01000006.1:251627-254579	4.47168	cysteine desulfurase / selenocysteine lyase
29.	XLOC_002238	*trxB*	NZ_SJDS01000006.1:114099-115044	2.96608	thioredoxin-disulfide reductase
30.	XLOC_002493	*icd*	NZ_SJDS01000007.1:167416-168679	5.67032	isocitrate dehydrogenase

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	biosynthetic-type acetolactate synthase large subunit	K.ADLLLNIGAR.F	322.27 %
2.	acyl-CoA dehydrogenase family protein	R.LLVYRVGELKNK.G	199.01 %
3.	Asparagines synthase (glutamine-hydrolyzing)	R.VNDIDTK.Y	75.61 %
4.	PLP-dependent amino transferase family protein	K.HDQLTSILEK.Y	63.99 %
5.	NADP-dependent isocitrate dehydrogenase	K.GPLTTPIGGGIR.S	19.00 %
6.	methylmalonyl-CoA mutase family protein	R.EGEDPKR.Q	19.00 %
7.	ornithine--oxo-acid transaminase	K.EINNPVIK.E	- 94.00 %
8.	CoA-acylating methylmalonate-semialdehyde dehydrogenase	K.YIYETGSKYGK.R	- 82.00 %
9.	Aspartate kinase	K.VVNDPVEIK.E	- 67.00 %

Table S17. List of the upregulated DEGs (A) and proteins (B) involved in metabolism of cofactors and vitamins in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_001385	*iscS*	NZ_SJDS01000003.1:157197-158346	2.38501	cysteine desulfurase
2.	XLOC_003920	*dxs*	NZ_SJDS01000018.1:51441-54161	3.98045	1-deoxy-D-xylulose-5-phosphate synthase
3.	XLOC_002889	*rsgA*	NZ_SJDS01000009.1:6289-7174	2.10716	thiamine phosphate phosphatase
4.	XLOC_003132	*adk*	NZ_SJDS01000010.1:190809-191463	4.54377	adenylate kinase
5.	XLOC_000076	*ribD*	NZ_SJDS01000001.1:124357-126552	2.1011	diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-

					phosphoribosylamino) uracil reductase
6.	XLOC_000198	*ribB*	NZ_SJDS01000001.1:327829-328459	3.54495	3,4-dihydroxy 2-butanone 4-phosphate synthase
7.	XLOC_000199	*ribH*	NZ_SJDS01000001.1:328474-328957	3.59397	6,7-dimethyl-8-ribityllumazine synthase
8.	XLOC_000197	*ribE*	NZ_SJDS01000001.1:327166-327805	3.84052	riboflavin synthase
9.	XLOC_001185	*deoD*	NZ_SJDS01000002.1:423460-424168	5.39561	purine-nucleoside phosphorylase
10.	XLOC_002746	*yjjG*	NZ_SJDS01000008.1:83435-84140	2.31523	5'-nucleotidase
11.	XLOC_001409	*nadD*	NZ_SJDS01000003.1:187857-189330	3.06685	nicotinate-nucleotide adenylyltransferase
12.	XLOC_002482	*pntA*	NZ_SJDS01000007.1:149621-150737	2.04207	H+-translocating NAD(P) transhydrogenase subunit alpha
13.	XLOC_002504	*coaE*	NZ_SJDS01000007.1:181240-181834	2.54982	dephospho-CoA kinase
14.	XLOC_001795	*fabZ*	NZ_SJDS01000004.1:245913-246357	3.13951	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
15.	XLOC_003036	*queF*	NZ_SJDS01000010.1:53901-54402	2.17747	7-cyano-7-deazaguanine reductase
16.	XLOC_002653	*moaC*	NZ_SJDS01000008.1:45700-47257	2.07972	cyclic pyranopterin monophosphate synthase
17.	XLOC_002720	*moaD*	NZ_SJDS01000008.1:42082-44563	2.31348	molybdopterin molybdotransferase
18.	XLOC_003916	*folD*	NZ_SJDS01000018.1:46774-47629	3.26584	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase
19.	XLOC_002892	*fmt*	NZ_SJDS01000009.1:9932-13374	2.24332	methionyl-tRNA formyltransferase
20.	XLOC_001502	EW028_RS08815,EW028_RS08820	NZ_SJDS01000003.1:330203-330999	3.86895	5-formyltetrahydrofolate cyclo-ligase
21.	XLOC_003090	EW028_RS17680	NZ_SJDS01000010.1:150912-152373	2.3401	glutamyl-tRNA synthetase
22.	XLOC_001325	EW028_RS07545	NZ_SJDS01000003.1:77169-78534	3.42658	glutamyl-tRNA reductase
23.	XLOC_001328	*hemL*	NZ_SJDS01000003.1:82223-83516	3.00773	glutamate-1-semialdehyde 2,1-

					aminomutase
24.	XLOC_001327	EW028_RS07560,*hemB,hemC*	NZ_SJDS01000003.1:79562-82223	2.51727	porphobilinogen synthase
25.	XLOC_000152	EW028_RS01360	NZ_SJDS01000001.1:261902-262607	2.93929	demethylmenaquinone methyltransferase / 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase
26.	XLOC_002414	EW028_RS13530,*menD,menH*	NZ_SJDS01000007.1:9329-13229	2.38417	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase
27.	XLOC_002415	*menB*	NZ_SJDS01000007.1:13292-14111	3.71793	naphthoate synthase

(B)

Sl. No	Peptide	Sequence	Percentage Change (%)
1.	Riboflavin biosynthesis protein RibF	R.MLLGRPFEIK.G	206.07 %
2.	Riboflavin synthase	K.ESMKITVISSK.M	194.27 %
3.	Cysteine desulfurase	R.VPALTPGVTHER.G	175.14 %
4.	3,4-dihydroxy-2-butanone-4-phosphate synthase	K.MLGSQAKKTDFR.R	82.92 %
5.	glutamate-1-semialdehyde 2,1-amino mutase	K.IIGGGLPVGAYGGKR.E	21.67 %
6.	dephospho-CoA kinase	R.MHSQLPMSVKEK.G	- 33.00 %

Table S18. List of the upregulated DEGs (A) and proteins (B) involved in metabolism of terpenoids and polyketides in *Lysinibacillus* sp. strain OL1 response to boron

(A)

Sl No.	Geneid	GeneName	Locus	log2Fold change	Annotation
1.	XLOC_003920	EW028_RS22360,EW028_RS22365	NZ_SJDS01000018.1:51441-54161	3.98045	1-deoxy-D-xylulose-5-phosphate synthase
2.	XLOC_003260	EW028_RS18455	NZ_SJDS01000011.1:94098-95244	2.28925	1-deoxy-D-xylulose-5-phosphate reductoisomerase
3.	XLOC_003087	*ispD*	NZ_SJDS01000010.1:148264-148960	2.45524	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase

4.	XLOC_003089	EW028_RS17675	NZ_SJDS01000010.1:150345-150822	2.3687	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
5.	XLOC_001633	*ispG*	NZ_SJDS01000003.1:311318-312434	3.79228	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
6.	XLOC_001617	EW028_RS08545	NZ_SJDS01000003.1:274134-275103	5.77455	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase
7.	XLOC_003919	EW028_RS22355	NZ_SJDS01000018.1:50396-51278	3.0312	farnesyl diphosphate synthase
8.	XLOC_000153	*ispB*	NZ_SJDS01000001.1:262626-263601	3.12538	octaprenyl-diphosphate synthase
9.	XLOC_003198	*miaA*	NZ_SJDS01000011.1:884-2691	2.85351	tRNA dimethylallyltransferase
10.	XLOC_002539	EW028_RS14505	NZ_SJDS01000007.1:227497-228271	2.54531	enoyl-CoA hydratase
11.	XLOC_000027	*tkt*	NZ_SJDS01000001.1:46336-48331	2.06365	transketolase
12.	XLOC_000172	EW028_RS01475,EW028_RS01480	NZ_SJDS01000001.1:282983-284116	2.04539	4-hydroxy-tetrahydrodipicolinate reductase
13.	XLOC_003313	*acpP*	NZ_SJDS01000011.1:157251-157488	5.48634	acyl carrier protein

(B)

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**
1.	tRNA (adenosine(37)-N6)-dimethylallyl transferase MiaA	R.AKIAEIQARQK.L	- 91.00 %

Table S19. List of other proteins upregulated and downregulated in *Lysinibacillus* sp. strain OL1 response to boron

Sl. No	**Peptide**	**Sequence**	**Percentage Change (%)**	**Function**
1.	Mur ligase family protein	K.IIDENTIVLIKGDMYSEQVSK.L	339.23 %	biosynthesis of bacterial cell-wall peptidoglycan
2.	HAMP domain-containing histidine kinase	K.GLKTQLEEVFTK.S	251.30 %	sensor and chemotaxis proteins
3.	Ppx/GppA family	K.FVYALNVSK.R	232.12 %	bacterial

	phosphatase			survival and metabolism
4.	Bile acid:sodium symporter	K.HIGKRFK.L	242.89 %	bacterial survival and metabolism
5.	Ger(x)C family spore germination protein	K.NGFKGFIK.G	214.85 %	Sporulation
6.	Spore germination protein	R.GPIWSMKARPKDLNTQNR.W	50.82 %	Sporulation
7.	Sporulation protein YqfD	R.VLVKGIHQEK.V	35.71 %	Sporulation
8.	Sporulation protein	K.DYIRVEPTSLASHILDAIGQLGFR.L	- 45.00 %	Sporulation
9.	RNA polymerase sporulation sigma factor SigE	R.LEKKIIQDLR.E	- 24.00 %	Sporulation
10.	RNA polymerase sporulation sigma factor SigK	R.ALIKLYQLYKR.D	- 19.00 %	Sporulation
11.	Flagellar export chaperone FliS	K.QMLPLYEYMNHR.L	128.15 %	Motility
12.	Flagellin	K.NTEFNTQK.L	34.02 %	Motility
13.	Flagellin Hag	R.AGDDAAGLAISEK.M	- 46.00 %	Motility
14.	Mannonate oxidoreductase	K.MNVRAEVLQR.A	111.86 %	Carbohydrate metabolism
15.	GNAT family N-acetyltransferase	K.SEYIELNEEPR.L	75.37 %	aminoglycoside antibiotic resistance, transcription regulation, protein acetylation and stress reaction
16.	AAA family ATPase	K.EANELFK.K	74.07 %	essential to cell physiology
17.	toxic anion resistance protein	K.KGGFISKLFNK.G	57.68 %	
18.	Peptidylprolyl isomerase	K.GIYVVLSLLAIMFVLTGCGTAK.D	55.98 %	Protein folding
19.	Rod shape-determining protein	R.TPGSIVAIRPMK.D	50.78 %	Cell division
20.	UDP-N-acetylmuramate--L-alanine ligase	R.NVEKTTEGTK.F	49.44 %	Peptidoglycan biosynthesis
21.	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diamino pimelate ligase	K.NQKFPFSDQQCIK.D	38.71 %	Peptidoglycan biosynthesis
22.	penicillin-binding protein 1A	K.WSTGQTIVDERMTYTKSDK.V	31.34 %	Peptidoglycan biosynthesis
23.	LuxRC-terminal-related transcriptional regulator	R.TQVVASAFR.L	32.51 %	Quorum Sensing

24.	Histidine phosphatase family protein	K.GLGHGYEILGK.L	21.02 %	Metabolism
25.	polysaccharidede acetylase family protein	K.SILVRPPYGK.K	- 83.00 %	Cellular process
26.	SDR family oxidoreductase	K.VFAVNTTAVMR.S	- 82.00 %	
27.	assimilatory sulfite reductase(NADPH) flavoprotein subunit	K.KVYVQHK.L	- 82.00 %	
28.	Polysaccharide biosynthesis protein	K.IKFYIGDVR.D	- 81.00 %	
29.	Indole-3-glycerol phosphate synthase TrpC	K.QVAAMGASGVLVGEALMR.S	- 81.00 %	
30.	DNA translocase FtsK	R.AARIVDQMEQR.G	- 65.00 %	
31.	Poly ribonucleotide nucleotidyl transferase	K.IRPDGRK.L	- 31.00 %	mRNA catabolic process
32.	collagenase	R.SFHDKCLPALK.A	- 27.00 %	

Table S20. MCODE analysis of PPI network

Cluster	Node	Edge	Score
1	61	1721	57.367
2	8	19	5.429
3	5	10	5.000
4	4	5	3.333
5	6	8	3.200
6	3	3	3.000

Table S21. Cluster associated pathways

Cluster	Associated genes	Pathways
1	*rplB,rplC,rplX, rplV, rplP, efp,rplQ, rplN, rplO, rpsC, rpsD, rplT, rplU, rplR, rpsB, rplS, rpmI, rpmJ, fusA,rpsO, EFI67266.1, rpsP, rpmH, rpsM, nusG, rpsS, nusA, rpsQ, rpsG, tuf,rpsH,rpmE,rpsE, rpmF, rpsK,rpmD,rpsL, rpsI, rpsJ, aspS, pheT, infC, pheS, infA, infB, EFI69796.1, atpA, rpoC, rpoA, rpoB, lepA,rplI, rplF, rplL, prfB, rplM, rplJ, rplK, rplA, rplE,* EFI68417.1	tRNA binding, large ribosomal subunit rRNA binding, small ribosomal subunit, cellular nitrogen compound metabolic process, cellular biosynthetic process, organic substance biosynthetic process, gene expression, cellular amide metabolic process, organonitrogen compound biosynthetic process, peptide metabolic process, cellular protein, metabolic process, amide biosynthetic process, peptide biosynthetic process, translation, pyrophosphatase activity,carboxylic acid metabolic process, purine ribonucleoside binding, purine ribonucleotide binding, amino acid activation, RNA metabolic process, guanyl nucleotide binding, adenyl nucleotide binding, ATP binding, translation initiation factor activity, translational initiation, nucleoside-triphosphatase activity, adenyl ribonucleotide binding, guanyl ribonucleotide binding,RNA biosynthetic process, GTP binding, ncRNA metabolic process,GTPase activity, transcription, DNA-templated, tRNA aminoacylation, nucleic acid-templated transcription, tRNA metabolic process, tRNA aminoacylation for protein translation, regulation of macromolecule biosynthetic process, regulation of cellular biosynthetic process, regulation of cellular amide metabolic process.
2	*dnaK,atpD,pgk,atpG,valS, atpF, lysS,adk*	Nucleotide binding, ATP binding, purine nucleotide binding, adenyl nucleotide binding, ribonucleotide binding, purine ribonucleotide binding, adenyl ribonucleotide binding, purine ribonucleoside triphosphate binding, anion binding, nucleoside phosphate binding
3	*sdhA, sdhB, sucC, sucD,* EFI69962.1	Citrate cycle (TCA cycle), Oxidative Phosphorylation, Butanoate metabolism

4	*cysS, dnaX, guaA, eno*	Cation binding, metal ion binding, drug binding, organic cyclic compound metabolic process, nucleotide biosynthetic process, organophosphate metabolic process, purine ribonucleoside monophosphate metabolic process, purine ribonucleotide metabolic process, ribonucleotide biosynthetic process, purine nucleoside monophosphate biosynthetic process, phosphate-containing compound metabolic process, heterocycle biosynthetic process, aromatic compound biosynthetic process.
5	*alaS, gmk, greA*, EFI67782.1, *guaB,gyrA*	Nucleic acid binding, nucleic acid metabolic process, RNA metabolic process, cellular aromatic compound metabolic process, heterocycle metabolic process, organic cyclic compound metabolic process, nucleobase-containing compound metabolic process,drug binding,small molecule binding, small molecule metabolic process,carbohydrate derivative binding, anion binding, nucleoside phosphate binding, nucleotide binding, ribonucleotide binding, purine ribonucleoside triphosphate binding, purine nucleotide binding, purine ribonucleotide binding, adenyl nucleotide binding, ATP binding, adenyl ribonucleotide binding.
6	*acpP, atpC,polA*	Carbohydrate derivative metabolic process, small molecule metabolic process, phosphorus metabolic process, organophosphate metabolic process, phosphate-containing compound metabolic process, carbohydrate derivative biosynthetic process, organophosphate biosynthetic process

Supplementary Figures

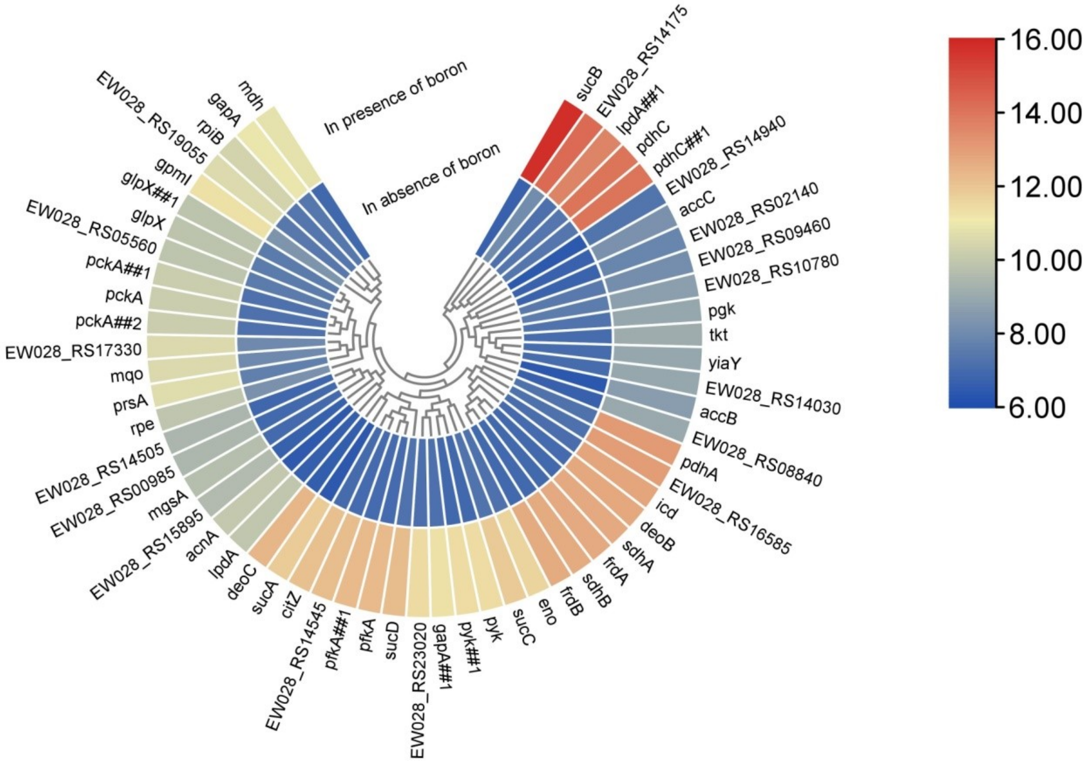

Figure S1. Significantly upregulated gene expression profile associated with carbohydrate metabolism in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

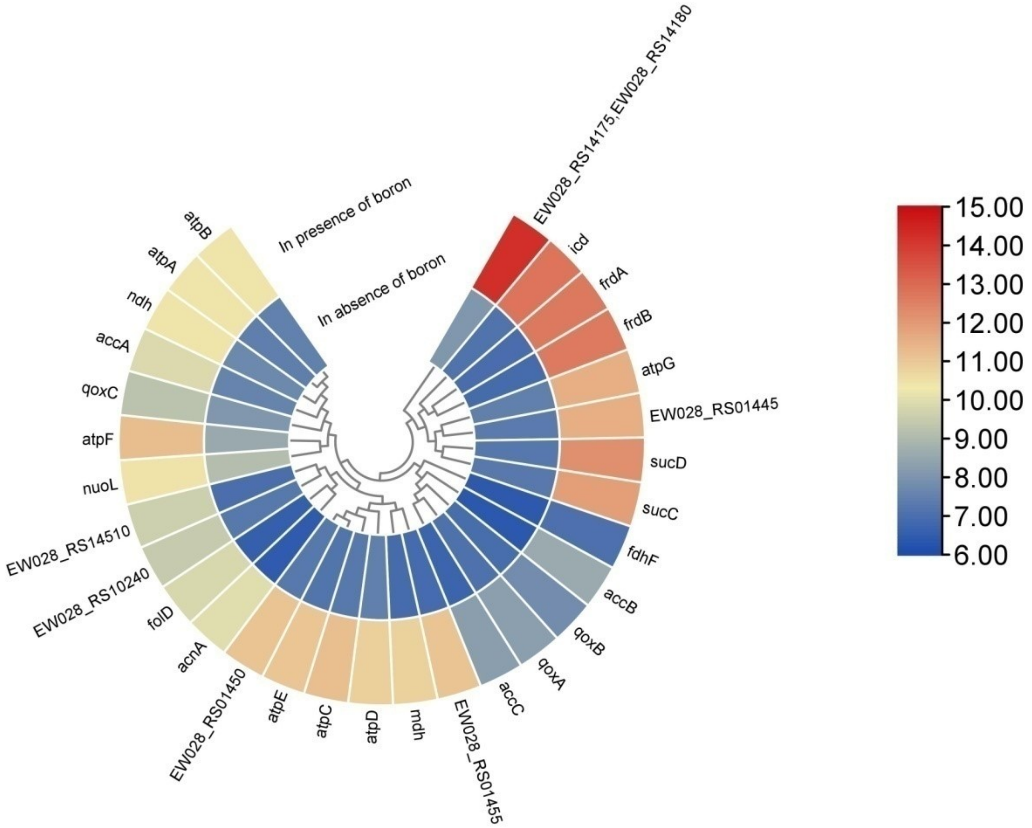

Figure S2. Significantly upregulated gene expression profile associated with energy metabolism in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

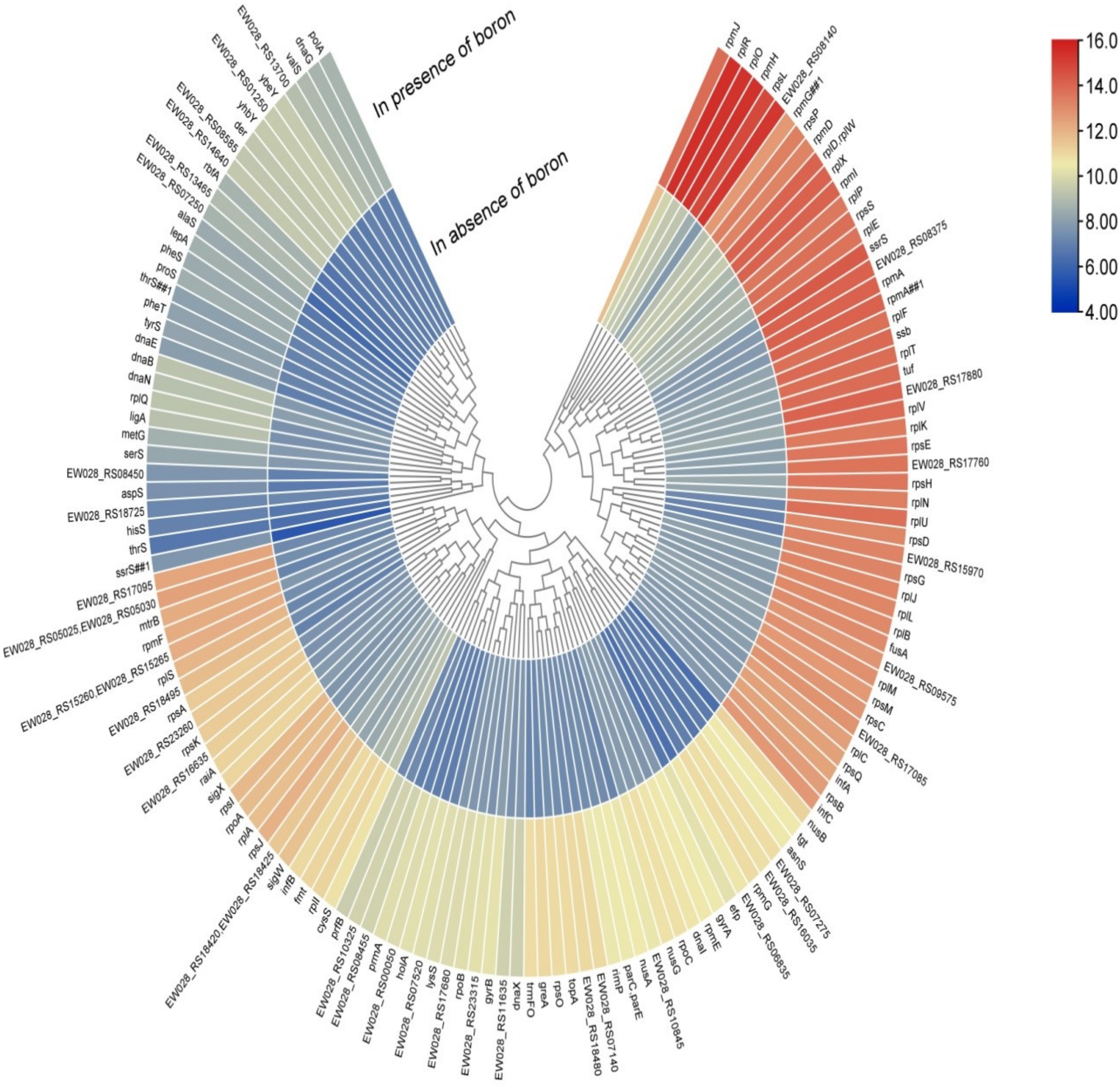

Figure S3. Significantly upregulated gene expression profile associated with genetic information processing in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

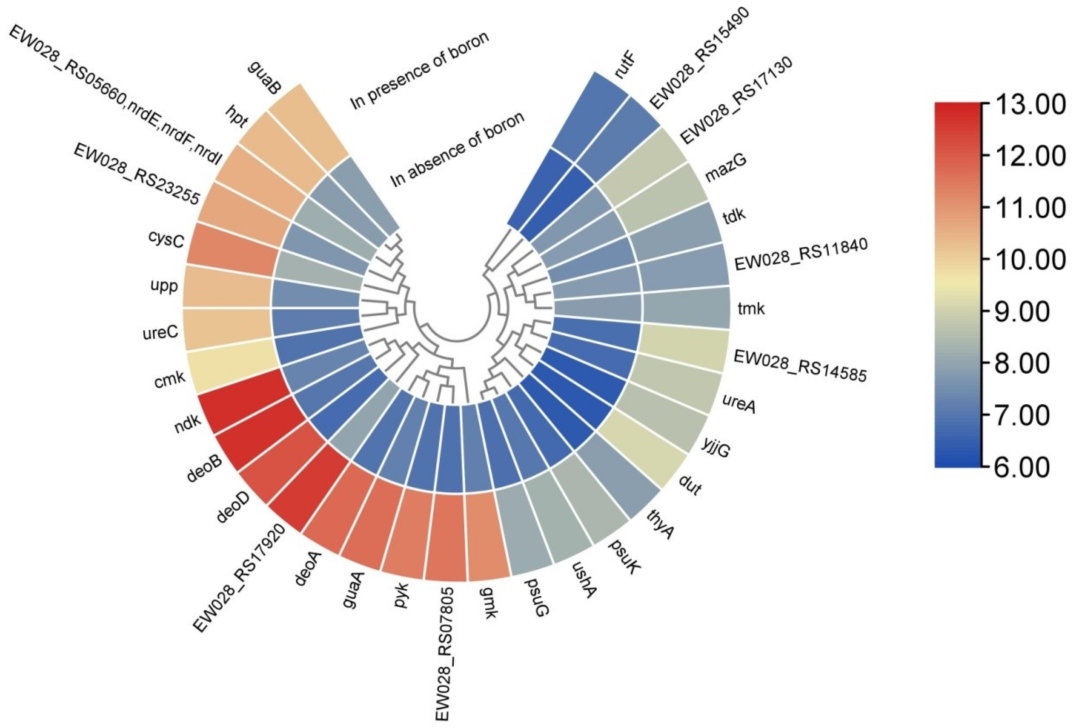

Figure S4. Significantly upregulated gene expression profile associated with nucleotide metabolism in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

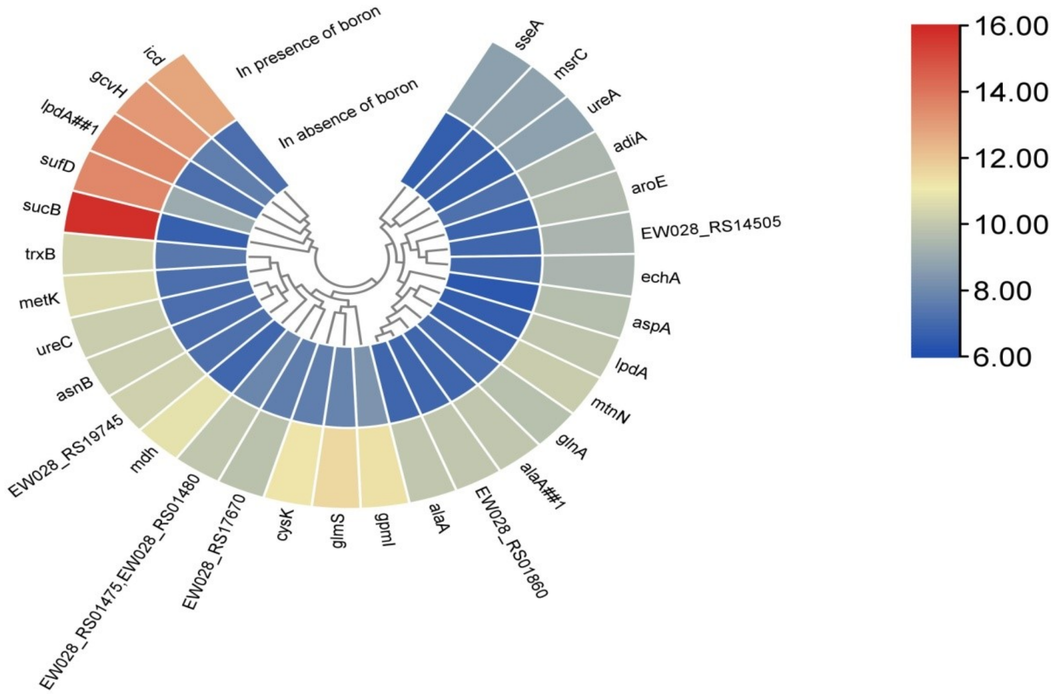

Figure S5. Significantly upregulated gene expression profile associated with amino acid metabolism in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

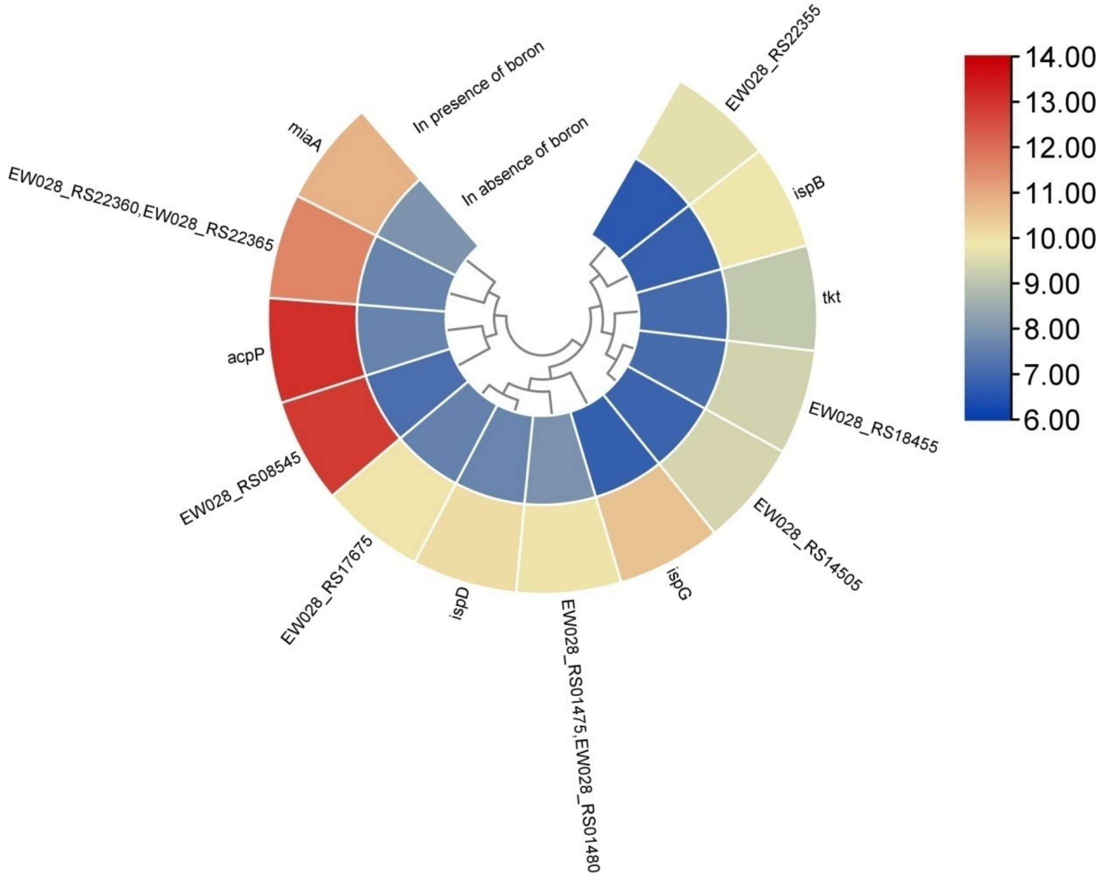

Figure S6. Significantly upregulated gene expression profile associated with metabolism of terpenoids and polyketides in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

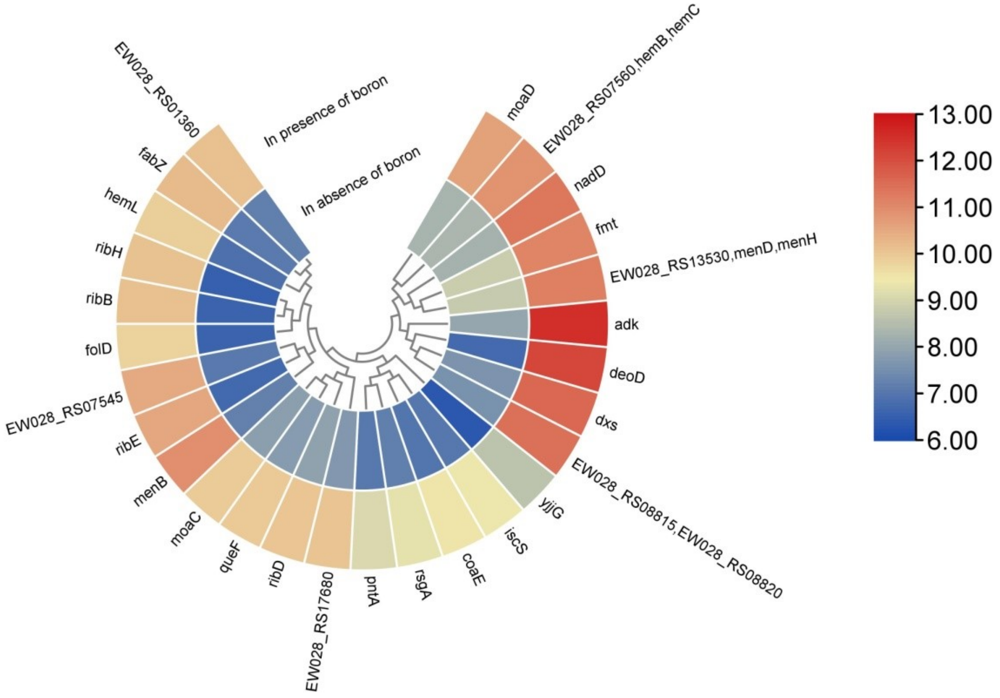

Figure S7. Significantly upregulated gene expression profile associated with Cofactor and vitamins metabolism in OL1 in presence of boron. Heat map was constructed using the FPKM value of both control and treated condition.

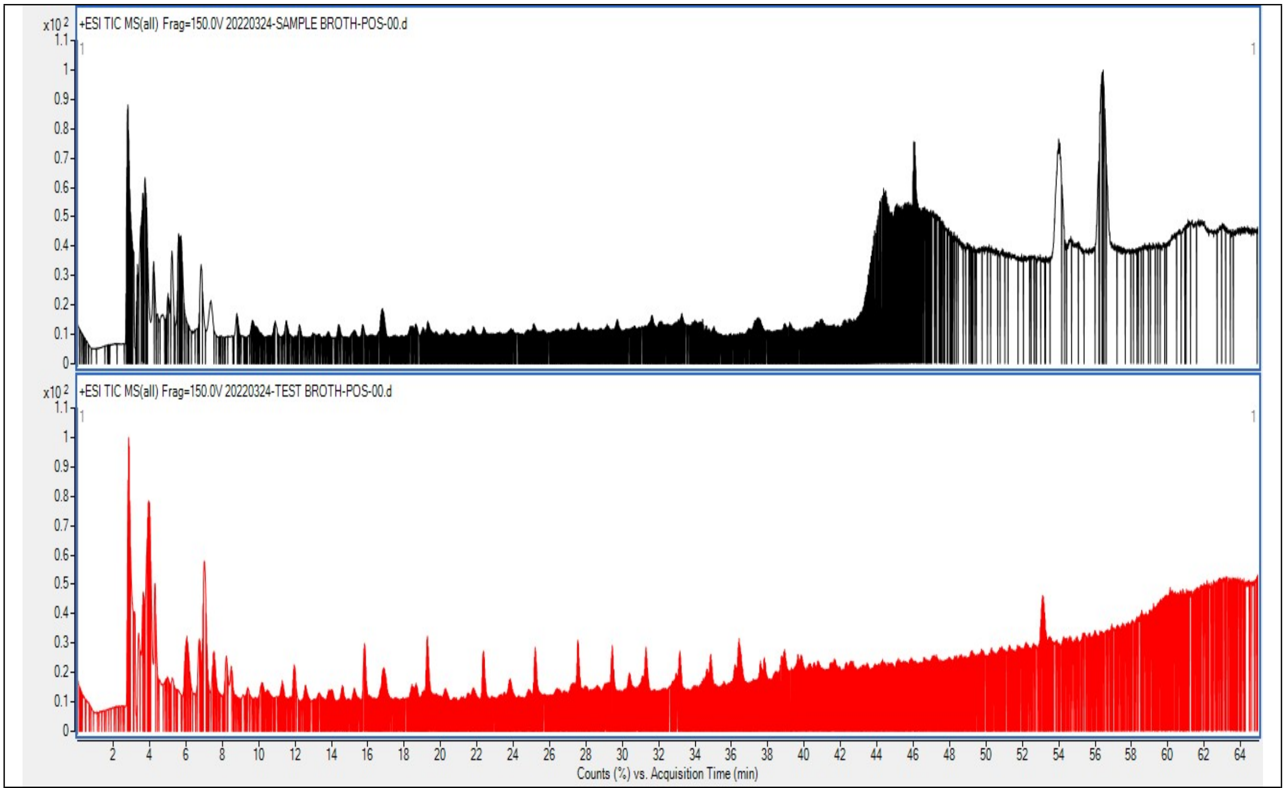

Figure S8. Mass spectroscopic analysis of proteins isolated from boron amended (red) and unamended (black) conditions.

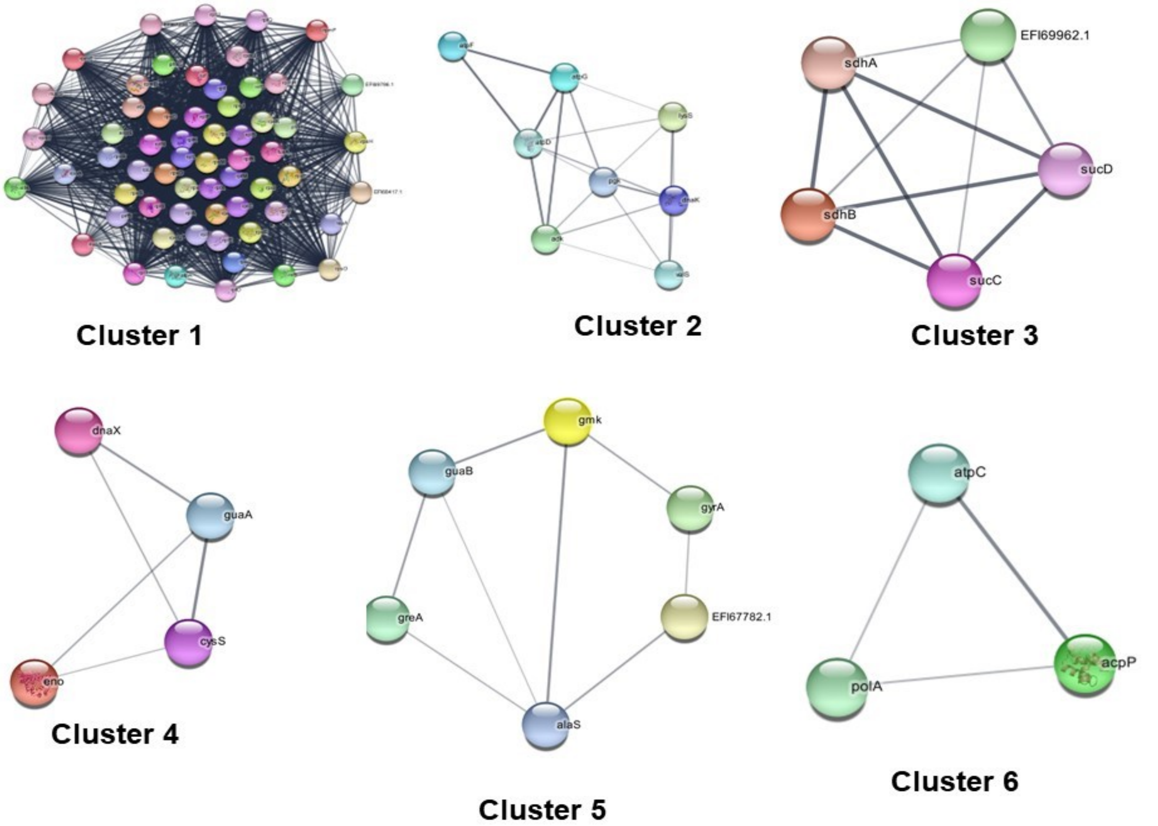

Figure S9. Cluster generation with all the upregulated DEGs using MCODE.

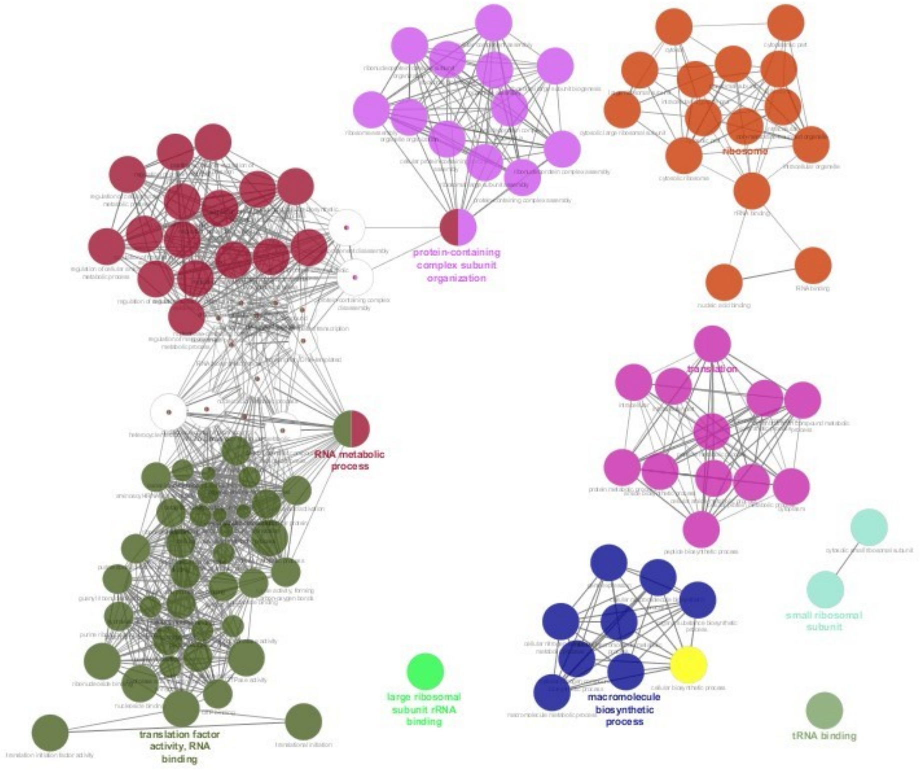

Figure S10. Constructed pathway network from cluster 1.

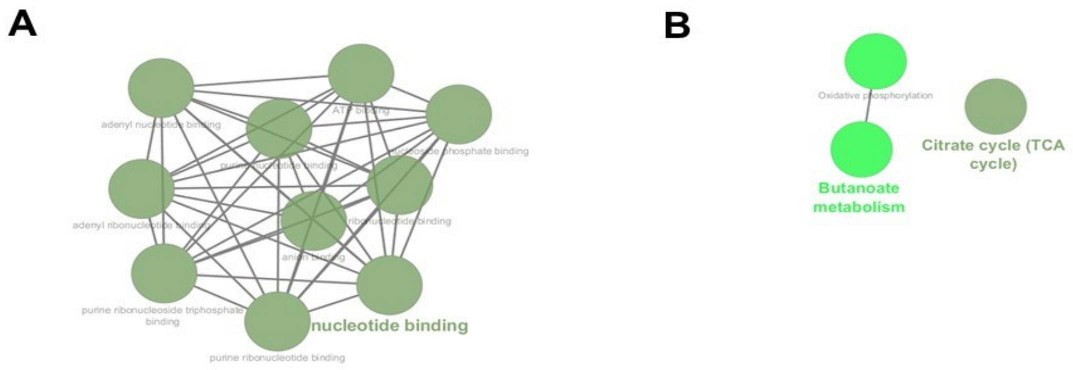

Figure S11. Constructed pathway network from cluster 2 (A) and cluster 3 (B).

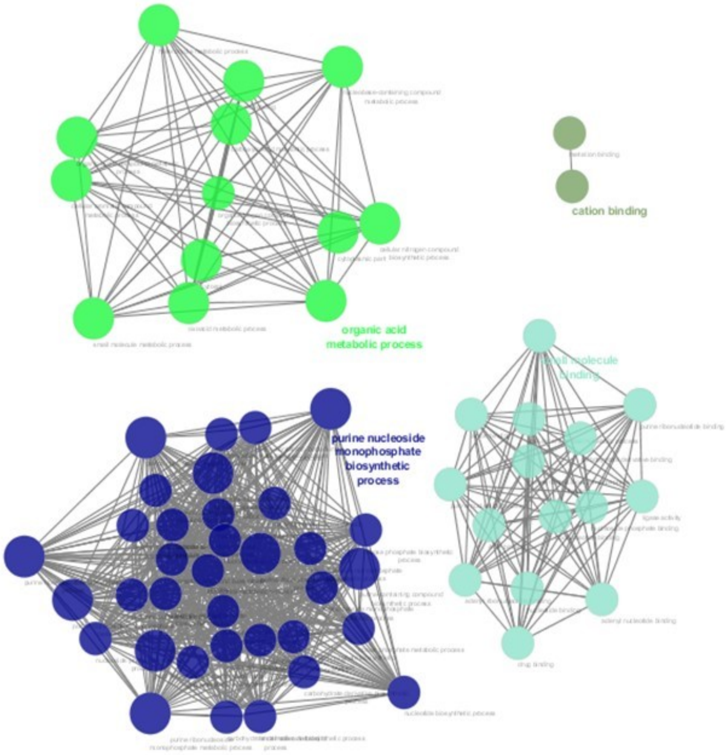

Figure S12. Constructed pathway network from cluster 4.

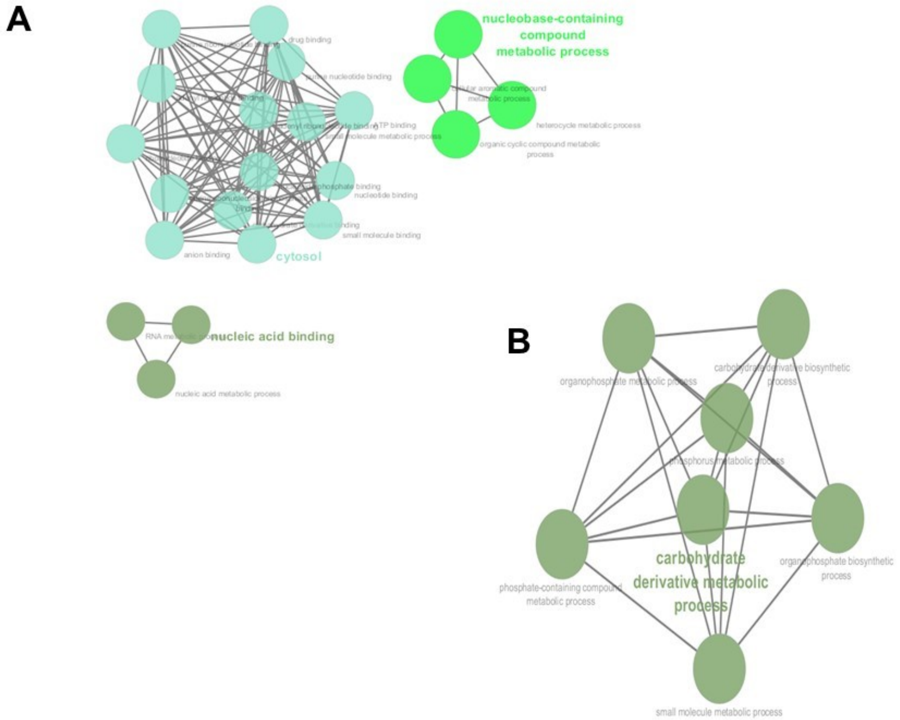

Figure S13. Constructed pathway network from cluster 5 (A) and cluster 6 (B).