

SUPPLEMENTAL FILE 1

Comparative Pathogenomics and In Silico Analysis of Energy Metabolism in *Acinetobacter baumannii* ST195 and Novel Turkish Isolates Encoding OXA-23, OXA-66, and OXA-852

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Table S1. The list of strain-specific (singleton) genes belong to *A. baumannii* strain T3

Cluster	Function	COG	COG categories
CLUSTER0372	HTH-type transcriptional repressor ComR	COG1048	C
CLUSTER0035	hypothetical protein	COG1048	C
CLUSTER0043	hypothetical protein	COG0667	C
CLUSTER0151	hypothetical protein	COG0667	C
CLUSTER5830	hypothetical protein	COG0667	C
CLUSTER5927	hypothetical protein	COG0667	C
CLUSTER6020	hypothetical protein	COG0667	C
CLUSTER6117	hypothetical protein	COG0667	C
CLUSTER6216	hypothetical protein	COG0667	C
CLUSTER6217	hypothetical protein	COG0282	C
CLUSTER6327	hypothetical protein	COG0667	C
CLUSTER0272	Putative toxin HigB2	COG0667	C
CLUSTER4142	sugar efflux transporter	COG1048	C
CLUSTER0268	hypothetical protein	COG2894	D
CLUSTER1617	hypothetical protein	COG1192	D
CLUSTER1740	hypothetical protein	COG1192	D
CLUSTER1867	hypothetical protein	COG1192	D
CLUSTER2094	hypothetical protein	COG1192	D
CLUSTER1488	Nucleoid occlusion protein	COG1192	D
CLUSTER1977	TelA-like protein	COG1192	D
CLUSTER0152	hypothetical protein	COG0079	E
CLUSTER0266	hypothetical protein	COG1063	E
CLUSTER0273	hypothetical protein	COG1063	E
CLUSTER0380	hypothetical protein	COG0079	E
CLUSTER0873	hypothetical protein	COG0512	E
CLUSTER1395	hypothetical protein	COG1063	E
CLUSTER2542	hypothetical protein	COG0512	E
CLUSTER2783	hypothetical protein	COG0512	E
CLUSTER3188	hypothetical protein	COG0512	E
CLUSTER4150	hypothetical protein	COG1063	E
CLUSTER4864	hypothetical protein	COG0512	E
CLUSTER5234	hypothetical protein	COG0512	E
CLUSTER5831	hypothetical protein	COG0079	E
CLUSTER6019	hypothetical protein	COG1063	E
CLUSTER4185	Replicative DNA helicase	COG0079	E
CLUSTER1397	Error-prone DNA polymerase	COG0209	F
CLUSTER4154	Error-prone DNA polymerase	COG0209	F
CLUSTER0846	hypothetical protein	COG0209	F
CLUSTER2531	hypothetical protein	COG0194	F
CLUSTER3181	hypothetical protein	COG0194	F
CLUSTER2306	hypothetical protein	COG1929	G
CLUSTER5833	Adhesin Ata autotransporter	COG0212	H

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CLUSTER0155	hypothetical protein	COG0212	H
CLUSTER0837	hypothetical protein	COG2918	H
CLUSTER0877	hypothetical protein	COG0212	H
CLUSTER2997	hypothetical protein	COG0294	H
CLUSTER4139	hypothetical protein	COG2918	H
CLUSTER4189	hypothetical protein	COG0212	H
CLUSTER5236	hypothetical protein	COG0212	H
CLUSTER0383	LexA repressor	COG0212	H
CLUSTER3332	ABC-F type ribosomal protection protein MsrE	COG1788	I
CLUSTER1383	hypothetical protein	COG1788	I
CLUSTER2977	hypothetical protein	COG1788	I
CLUSTER3179	hypothetical protein	COG1788	I
CLUSTER4839	hypothetical protein	COG1788	I
CLUSTER5208	hypothetical protein	COG1788	I
CLUSTER2525	IS66 family transposase IS1313	COG1788	I
CLUSTER2763	IS66 family transposase ISAb24	COG1788	I
CLUSTER0040	hypothetical protein	COG0162	J
CLUSTER0149	hypothetical protein	COG0162	J
CLUSTER0269	hypothetical protein	COG0162	J
CLUSTER0375	hypothetical protein	COG0162	J
CLUSTER0851	hypothetical protein	COG2026	J
CLUSTER5514	hypothetical protein	COG0162	J
CLUSTER5618	hypothetical protein	COG0162	J
CLUSTER5730	hypothetical protein	COG0162	J
CLUSTER5828	hypothetical protein	COG0162	J
CLUSTER5924	hypothetical protein	COG0162	J
CLUSTER6017	hypothetical protein	COG0162	J
CLUSTER6115	hypothetical protein	COG0162	J
CLUSTER6214	hypothetical protein	COG0162	J
CLUSTER6325	hypothetical protein	COG0162	J
CLUSTER0867	Competence protein ComM	COG1167	K
CLUSTER2086	Taurine import ATP-binding protein TauB	COG2188	K
CLUSTER0046	Adhesin Ata autotransporter	COG0582	L
CLUSTER5732	Adhesin Ata autotransporter	COG3385	L
CLUSTER6023	Adhesin Ata autotransporter	COG3385	L
CLUSTER0041	hypothetical protein	COG0389	L
CLUSTER0150	hypothetical protein	COG0389	L
CLUSTER0156	hypothetical protein	COG3385	L
CLUSTER0274	hypothetical protein	COG0582	L
CLUSTER0376	hypothetical protein	COG0389	L
CLUSTER0384	hypothetical protein	COG0582	L
CLUSTER0385	hypothetical protein	COG3385	L
CLUSTER0865	hypothetical protein	COG0389	L

Table S1. The list of strain-specific (singleton) genes belong to *A. baumannii* strain T3

CLUSTER0878	hypothetical protein	COG0582	L
CLUSTER1613	hypothetical protein	COG3039	L
CLUSTER1737	hypothetical protein	COG3039	L
CLUSTER1741	hypothetical protein	COG0178	L
CLUSTER2204	hypothetical protein	COG0389	L
CLUSTER2206	hypothetical protein	COG0305	L
CLUSTER2316	hypothetical protein	COG0389	L
CLUSTER2538	hypothetical protein	COG0389	L
CLUSTER2777	hypothetical protein	COG0389	L
CLUSTER2990	hypothetical protein	COG0389	L
CLUSTER3186	hypothetical protein	COG0389	L
CLUSTER3339	hypothetical protein	COG0305	L
CLUSTER4176	hypothetical protein	COG0389	L
CLUSTER4190	hypothetical protein	COG0582	L
CLUSTER4191	hypothetical protein	COG0305	L
CLUSTER4416	hypothetical protein	COG0389	L
CLUSTER4426	hypothetical protein	COG3385	L
CLUSTER4862	hypothetical protein	COG0389	L
CLUSTER4865	hypothetical protein	COG0305	L
CLUSTER5230	hypothetical protein	COG0389	L
CLUSTER5425	hypothetical protein	COG0389	L
CLUSTER5515	hypothetical protein	COG0389	L
CLUSTER5619	hypothetical protein	COG0389	L
CLUSTER5728	hypothetical protein	COG0847	L
CLUSTER5731	hypothetical protein	COG0389	L
CLUSTER5829	hypothetical protein	COG0389	L
CLUSTER5925	hypothetical protein	COG0389	L
CLUSTER5929	hypothetical protein	COG0582	L
CLUSTER5930	hypothetical protein	COG3385	L
CLUSTER6015	hypothetical protein	COG0847	L
CLUSTER6018	hypothetical protein	COG0389	L
CLUSTER6022	hypothetical protein	COG0582	L
CLUSTER6116	hypothetical protein	COG0389	L
CLUSTER6215	hypothetical protein	COG0389	L
CLUSTER6326	hypothetical protein	COG0389	L
CLUSTER6329	hypothetical protein	COG3385	L
CLUSTER2321	putative TonB-dependent receptor BfrD	COG0305	L
CLUSTER1864	putative type I restriction enzyme P M protein	COG3039	L
CLUSTER3336	Sporulation initiation inhibitor protein Soj	COG0389	L
CLUSTER0270	Trans-acting regulatory protein HvrA	COG0389	L
CLUSTER1485	Type-1 restriction enzyme R protein	COG3039	L
CLUSTER5231	Adhesin Ata autotransporter	COG0466	O
CLUSTER4178	Competence protein ComM	COG0606	O

Table S1. The list of strain-specific (singleton) genes belong to *A. baumannii* strain T3

CLUSTER0381	hypothetical protein	COG1764	O
CLUSTER0864	hypothetical protein	COG1651	O
CLUSTER1487	hypothetical protein	COG1651	O
CLUSTER1493	hypothetical protein	COG1764	O
CLUSTER1616	hypothetical protein	COG1651	O
CLUSTER1739	hypothetical protein	COG1651	O
CLUSTER1745	hypothetical protein	COG1764	O
CLUSTER1866	hypothetical protein	COG1651	O
CLUSTER1871	hypothetical protein	COG1764	O
CLUSTER1976	hypothetical protein	COG1651	O
CLUSTER2537	hypothetical protein	COG1651	O
CLUSTER2544	hypothetical protein	COG1764	O
CLUSTER2776	hypothetical protein	COG1651	O
CLUSTER2785	hypothetical protein	COG1764	O
CLUSTER2989	hypothetical protein	COG1651	O
CLUSTER2995	hypothetical protein	COG1764	O
CLUSTER3185	hypothetical protein	COG1651	O
CLUSTER3190	hypothetical protein	COG1764	O
CLUSTER3335	hypothetical protein	COG1651	O
CLUSTER3340	hypothetical protein	COG1764	O
CLUSTER4175	hypothetical protein	COG1651	O
CLUSTER4187	hypothetical protein	COG1764	O
CLUSTER4861	hypothetical protein	COG1651	O
CLUSTER5229	hypothetical protein	COG1651	O
CLUSTER5427	hypothetical protein	COG1764	O
CLUSTER5518	hypothetical protein	COG1764	O
CLUSTER5621	hypothetical protein	COG1764	O
CLUSTER5832	hypothetical protein	COG1764	O
CLUSTER5928	hypothetical protein	COG1764	O
CLUSTER6021	hypothetical protein	COG1764	O
CLUSTER6119	hypothetical protein	COG1764	O
CLUSTER4415	Protein TraC	COG1651	O
CLUSTER2093	Protein UmuC	COG1651	O
CLUSTER1980	putative TonB-dependent receptor	COG1764	O
CLUSTER1620	Secretory immunoglobulin A-binding protein EsiB	COG1764	O
CLUSTER0042	hypothetical protein	COG0659	P
CLUSTER0154	hypothetical protein	COG1629	P
CLUSTER2199	hypothetical protein	COG4525	P
CLUSTER2207	hypothetical protein	COG1629	P
CLUSTER2322	hypothetical protein	COG1629	P
CLUSTER5922	hypothetical protein	COG0659	P
CLUSTER2097	putative TonB-dependent receptor	COG1629	P

Table S1. The list of strain-specific (singleton) genes belong to *A. baumannii* strain T3

CLUSTER5418	putative TonB-dependent receptor BfrD	COG1629	P
CLUSTER6320	putative zinc-binding alcohol dehydrogenase	COG0038	P
CLUSTER6319	Chondramide synthase cmdD	COG1020	Q
CLUSTER0036	Dimodular nonribosomal peptide synthase	COG1020	Q
CLUSTER0034	hypothetical protein	COG1853	R
CLUSTER0039	hypothetical protein	COG2194	R
CLUSTER2082	hypothetical protein	COG2249	R
CLUSTER6315	hypothetical protein	COG1853	R
CLUSTER5926	putative zinc-binding alcohol dehydrogenase	COG2249	R
CLUSTER1743	ATP-dependent RecD-like DNA helicase	COG4683	S
CLUSTER1619	Coupling protein TraD	COG4683	S
CLUSTER0378	hypothetical protein	COG4683	S
CLUSTER0872	hypothetical protein	COG4683	S
CLUSTER1491	hypothetical protein	COG4683	S
CLUSTER1869	hypothetical protein	COG4683	S
CLUSTER1978	hypothetical protein	COG4683	S
CLUSTER2096	hypothetical protein	COG4683	S
CLUSTER2205	hypothetical protein	COG4683	S
CLUSTER2320	hypothetical protein	COG4683	S
CLUSTER2541	hypothetical protein	COG4683	S
CLUSTER2782	hypothetical protein	COG4683	S
CLUSTER2994	hypothetical protein	COG4683	S
CLUSTER3187	hypothetical protein	COG4683	S
CLUSTER3338	hypothetical protein	COG4683	S
CLUSTER4159	hypothetical protein	COG3647	S
CLUSTER4184	hypothetical protein	COG4683	S
CLUSTER4421	hypothetical protein	COG4683	S
CLUSTER4863	hypothetical protein	COG4683	S
CLUSTER5233	hypothetical protein	COG4683	S
CLUSTER5426	hypothetical protein	COG4683	S
CLUSTER5517	hypothetical protein	COG4683	S
CLUSTER6016	hypothetical protein	COG4681	S
CLUSTER6114	hypothetical protein	COG4681	S
CLUSTER0265	hypothetical protein	COG0589	T
CLUSTER1480	hypothetical protein	COG0745	T
CLUSTER1490	hypothetical protein	COG2199	T
CLUSTER1742	hypothetical protein	COG2199	T
CLUSTER2319	hypothetical protein	COG2199	T
CLUSTER2540	hypothetical protein	COG2199	T
CLUSTER2779	hypothetical protein	COG2199	T
CLUSTER5616	IS91 family transposase ISPPs1	COG2204	T
CLUSTER2201	hypothetical protein	COG0286	V
CLUSTER5834	Prophage integrase IntS	COG2602	V

Table S2. The list of strain-specific (singleton) genes belong to *A. baumannii* strain T14

Cluster	Function	COG	COG categories
CLUSTER6107	hypothetical protein	COG3039	L
CLUSTER2400	hypothetical protein	COG1047	O
CLUSTER0026	hypothetical protein	COG2199	T
CLUSTER0140	hypothetical protein	COG2199	T
CLUSTER0256	hypothetical protein	COG2199	T
CLUSTER1847	hypothetical protein	COG2199	T
CLUSTER1960	hypothetical protein	COG2199	T
CLUSTER2188	hypothetical protein	COG2199	T
CLUSTER5405	Elongation factor Tu	COG2199	T
CLUSTER6010	hypothetical protein	COG2199	T
CLUSTER6206	hypothetical protein	COG2199	T
CLUSTER0018	hypothetical protein	COG0841	V

Table S3. The list of strain-specific (singleton) genes belong to *A. baumannii* strain T24

Cluster	Function	COG	COG categories
CLUSTER1601	Succinylornithine transaminase	COG3138	E
CLUSTER5611	Succinylornithine transaminase	COG3138	E
CLUSTER0264	hypothetical protein	COG0050	J
CLUSTER0370	Succinylornithine transaminase	COG0050	J
CLUSTER0796	hypothetical protein	COG0050	J
CLUSTER4092	hypothetical protein	COG0050	J
CLUSTER6210	Hemolysin transporter protein ShlB	COG0050	J
CLUSTER5506	hypothetical protein	COG3039	L
CLUSTER6312	hypothetical protein	COG1047	O
CLUSTER5194	hypothetical protein	COG2199	T

Table S4. The summary of putative pathogenicity islands belong to *A.baumannii* T3, T14, and T24, which have reliable prediction scores

Genome	Putative Genomic Island	G+C Deviation	Codon Usage deviation	Virulence Factors	Hypothetical proteins	Gene Composition	Position	Prediction Score	Length (bp)
T3	Putative Pathogenicity Island 2	55%	55%	66%	44%	FIKEDNMC_01897- FIKEDNMC_01905	2010082..2019360	Normal	9278
T3	Putative Pathogenicity Island 1	50%	100%	50%	66%	FIKEDNMC_01540- FIKEDNMC_01545	1634927..1640030	Strong	5104
T14	Putative Pathogenicity Island 5	41%	16%	58%	41%	DHJAEFFA_03198- DHJAEFFA_03209	3412992..3424572	Normal	11581
T14	Putative Pathogenicity Island 3	45%	100%	36%	81%	DHJAEFFA_02455- DHJAEFFA_02465	2635866..2644769	Strong	8904
T24	Putative Pathogenicity Island 6	41%	16%	58%	41%	NPNKMEDG_03072- NPNKMEDG_03083	3301133..3312713	Normal	11581
T24	Putative Pathogenicity Island 7	28%	0%	57%	71%	NPNKMEDG_03642- NPNKMEDG_03648	3846521..3852955	Normal	6435
T24	Putative Pathogenicity Island 5	45%	100%	36%	81%	NPNKMEDG_02550- NPNKMEDG_02560	2753724..2762833	Strong	9110
KAB01	Putative Pathogenicity Island 1	36%	18%	45%	36%	FOBIIGCM_00086- FOBIIGCM_00093	87726..95339	Normal	7614
KAB01	Putative Pathogenicity Island 2	100%	100%	85%	28%	FOBIIGCM_01286- FOBIIGCM_01292	1324948..1333071	Strong	8124

Acinetobacter baumannii strain T3 chromosome, complete genome

GenBank: CP171394.1

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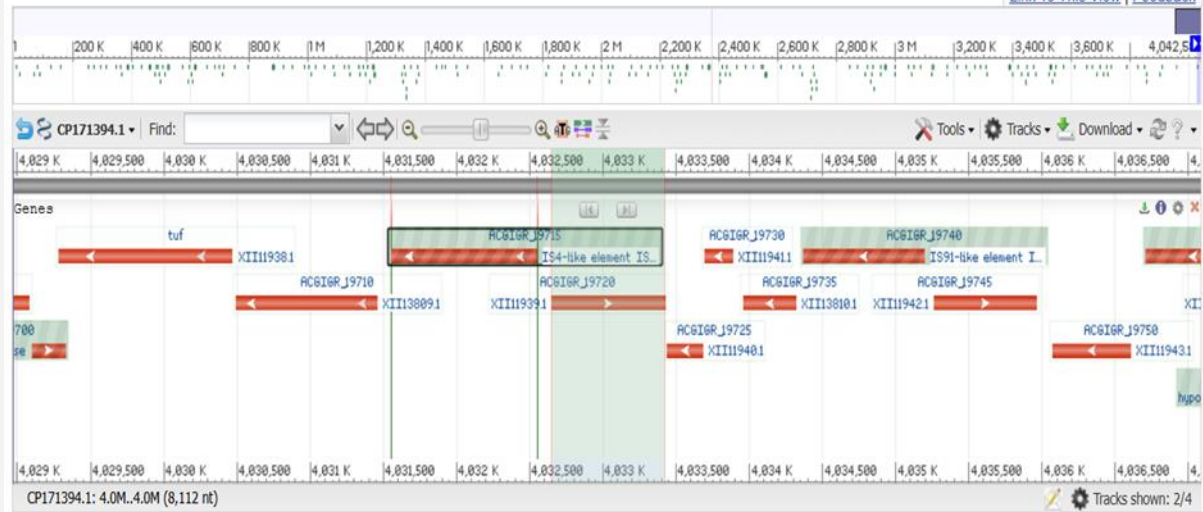


Fig S1. The GenBank graphics interface for the *A. baumannii* T3 genome demonstrates the presence of a transposon located upstream of the *APH(3')-Vla* gene. The vertical green zone indicates the *APH(3')-Vla* gene based on the FASTA sequence obtained from the CARD database. The *APH(3')-Vla* gene cannot be detected via NCBI. The horizontal green zone preceding the vertical zone indicates the IS4-like element ISAbal family transposase (ACGIGR_19715), which is also reported to be responsible for programmed frameshift.

Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*.

CLUSTAL W (1.83) multiple sequence alignment (*lpsB* gene)

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T14_lpsB      MKVMQLLPELNSGGVERGTLEIARALVAQGHQSLVVSNGGRLVSQLEAEG
T24_lpsB      MKVMQLLPELNSGGVERGTLEIARALVAQGHQSLVVSNGGRLVSQLEAEG
T3_lpsB        MKVMQLLPELNSGGVERGTLEIARALVAQGHQSLVVSNGGRLVSQLEAEG
*****:*****

T14_lpsB      STHLTLPIHKKSLSSLWQIRPLRQLIEEHQPDIVHVRSPVPAWLTHFALR
T24_lpsB      STHLTLPIHKKSLSSLWQIRPLRQLIEEHQPDIVHVRSPVPAWLTHFALR
T3_lpsB        STHLTLPIHKKSLSSLWQIRPLRQLIEEHQPDIVHVRSPVPAWLTHFALR
*****

T14_lpsB      KIPANKRPHLISTVHGFYSVNRYSAIMTQAEKVIAVSDSVVKYITEHYKN
T24_lpsB      KIPANKRPHLISTVHGFYSVNRYSAIMTQAEKVIAVSDSVVKYITEHYKN
T3_lpsB        KIPANKRPHLISTVHGFYSVNRYSAIMTQAEKVIAVSDSVVKYITDHYKN
*****:****

T14_lpsB      CPPQDIVRIYRGIDPAAFPHNYQPSAQWFNQVFNDFPELENKFLLCLPGR
T24_lpsB      CPPQDIVRIYRGIDPAAFPHNYQPSAQWFNQVFNDFPELENKFLLCLPGR
T3_lpsB        CPPQDIVRIYRGIDPAAFPHNYQPSAQWFNQVFNDFPELENKFLLCLPGR
*****

T14_lpsB      ITRLKGHESLIELMQQLHSQYPQLHAVVVGADVKKQAYLSELQNTIQSK
T24_lpsB      ITRLKGHESLIELMQQLHSQYPQLHAVVVGADVKKQAYLSELQNTIQSK
T3_lpsB        ITRLKGHESLIELMQLGEQYPQLHAVVVGADVKKQAYLSELQNTIQSK
*****:* .*****

T14_lpsB      GLADKITFVGHRSDIREWLAFSDIVLSLSNQAETFGRTALEALSVGTPVI
T24_lpsB      GLADKITFVGHRSDIREWLAFSDIVLSLSNQAETFGRTALEALSVGTPVI
T3_lpsB        GLADKITFVGHRSDIREWLAFSDIVLSLSNQAETFGRTALEALSVGTPVI
*****

T14_lpsB      GWNRGGVAEILSHVYPQGLVEAENEKALLEIVKHHIEQPQTVAPVTMFSL
T24_lpsB      GWNRGGVAEILSHVYPQGLVEAENEKALLEIVKHHIEQPQTVAPVTMFSL
T3_lpsB        GWNRGGVAEILSHVYPQGLVEAENEKALVETVKNHIEQPQTVAPVTMFSL
*****:* **:*

T14_lpsB      KDMCDQTLELYQSVLK
T24_lpsB      KDMCDQTLELYQSVLK
T3_lpsB        KDMCDQTLELYQSVLK
*****

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Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*

CLUSTAL W (1.83) multiple sequence alignment (*LpxA*)

```
gb|XII11168.1|_1-262 MSNHDLIHSTAIIDPSAVIASDVQIGPYCIIGPQVTIGAGTKLHSHVVVG
gb|XII14640.1|_1-262 MSNHDLIHSTAIIDPSAVIASDVQIGPYCIIGPQVTIGAGTKLHSHVVVG
gb|XII18261.1|_1-262 MSNHDLIHSTAIIDPSAVIASDVQIGPYCIIGPQVTIGAGTKLHSHVVVG
*****

gb|XII11168.1|_1-262 GFTRIGQNNEIFQFASVGEVCQDLKYKGEETWLEIGNNNLIREHCSLHRG
gb|XII14640.1|_1-262 GFTRIGQNNEIFQFASVGEVCQDLKYKGEETWLEIGNNNLIREHCSLHRG
gb|XII18261.1|_1-262 GFTRIGQNNEIFQFASVGEVCQDLKYKGEETWLEIGNNNLIREHCSLHRG
*****

gb|XII11168.1|_1-262 TVQDNALTKIGSHNLLMVNTHIAHDCIVGDHNI FANNVGVAGH V HIGDHV
gb|XII14640.1|_1-262 TVQDNALTKIGSHNLLMVNTHIAHDCIVGDHNI FANNVGVAGH V HIGDHV
gb|XII18261.1|_1-262 TVQDNALTKIGSHNLLMVNTHIAHDCIVGDHNI FANNVGVAGH V HIGDHV
*****

gb|XII11168.1|_1-262 IVGGNSGIHQFCKIDSYSMIGGASLILKDV PAYVMASGNPAHAFGINIEG
gb|XII14640.1|_1-262 IVGGNSGIHQFCKIDSYSMIGGASLILKDV PAYVMASGNPAHAFGINIEG
gb|XII18261.1|_1-262 IVGGNSGIHQFCKIDSYSMIGGASLILKDV PAYVMASGNPAHAFGINIEG
*****

gb|XII11168.1|_1-262 MRRKGWSKNTIQGLREAYKLIFKSGLT SVQAIDQIKSEILPSVPEAQLLI
gb|XII14640.1|_1-262 MRRKGWSKNTIQGLREAYKLIFKSGLT SVQAIDQIKSEILPSVPEAQLLI
gb|XII18261.1|_1-262 MRRKGWSKNTIQGLREAYKLIFKSGLT SVQAIDQIKSEILPSVPEAQLLI
*****

gb|XII11168.1|_1-262 DSLEQSERGIVR
gb|XII14640.1|_1-262 DSLEQSERGIVR
gb|XII18261.1|_1-262 DSLEQSERGIVR
*****
```

Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*

CLUSTAL W (1.83) multiple sequence alignment (*lpxB*)

```
T14_gb|XII15857.1|_1-391  MANRKLKIGIVVGEVSGDTLGVKLMRSFREQGIDAEFEGIGGPQMIAEGF
T24_gb|XII19489.1|_1-391  MANRKLKIGIVVGEVSGDTLGVKLMRSFREQGIDAEFEGIGGPQMIAEGF
T3_gb|XII13308.1|_1-391   MANRKLKIGIVVGEVSGDTLGVKLMRSFREQGIDAEFEGIGGPQMIAEGF
*****

T14_gb|XII15857.1|_1-391  NSYYPMETLSVMGIVEVLKDLKKLFAVRDGLINQWTQHPVDIFIGIDAPD
T24_gb|XII19489.1|_1-391  NSYYPMETLSVMGIVEVLKDLKKLFAVRDGLINQWTQHPVDIFIGIDAPD
T3_gb|XII13308.1|_1-391   NSYYPMETLSVMGIVEVLKDLKKLFAVRDGLINQWTQHPVDIFIGIDAPD
*****

T14_gb|XII15857.1|_1-391  FNLRLSKSIKEKNLPIKTVQYVSPSVAWRQGRVHGKQSIDLVLCCLFPF
T24_gb|XII19489.1|_1-391  FNLRLSKSIKEKNLPIKTVQYVSPSVAWRQGRVHGKQSIDLVLCCLFPF
T3_gb|XII13308.1|_1-391   FNLRLSKSIKEKNLPIKTVQYVSPSVAWRQGRVHGKQSIDLVLCCLFPF
*****

T14_gb|XII15857.1|_1-391  EKVFEQYEVPAAFVGHPLAKQLPLENPIQIAKQELGIDENQKHIALLPG
T24_gb|XII19489.1|_1-391  EKVFEQYEVPAAFVGHPLAKQLPLENPIQIAKQELGIDENQKHIALLPG
T3_gb|XII13308.1|_1-391   EKVFEQYEVPAAFVGHPLAKQLPLENPIQIAKQELGV DENQKHIALLPG
*****:*****

T14_gb|XII15857.1|_1-391  SRKGEVERLLPMLLGAANILHTKYPDIQFLIPAIN DARKQQIEQGV EQLA
T24_gb|XII19489.1|_1-391  SRKGEVERLLPMLLGAANILHTKYPDIQFLIPAIN DARKQQIEQGV EQLA
T3_gb|XII13308.1|_1-391   SRKGEVERLLPMLLGAANILHTKYPDIQFLIPAIN DARKQQIEQGV EQLA
*****

T14_gb|XII15857.1|_1-391  PQLKAKIHILENTDSESKIGRMVMNASDI IALASGTATLEAMLH RPMVT
T24_gb|XII19489.1|_1-391  PQLKAKIHILENTDSESKIGRMVMNASDI IALASGTATLEAMLH RPMVT
T3_gb|XII13308.1|_1-391   PQLKAKIHILENTDSESKIGRMVMNASDI IALASGTATLEAMLH RPMVT
*****

T14_gb|XII15857.1|_1-391  FYKLHWLTYLIAKFLVKIPYYSLPNIIAGKKVIEELIQADATPENLAAEI
T24_gb|XII19489.1|_1-391  FYKLHWLTYLIAKFLVKIPYYSLPNIIAGKKVIEELIQADATPENLAAEI
T3_gb|XII13308.1|_1-391   FYKLHWLTYLIAKFLVKIPYYSLPNIIAGKKVIEELIQADATPENLAAEI
*****

T14_gb|XII15857.1|_1-391  EKLMNVETAQIQVMQH LTMHKQLISGNTEDPVQA I LQCLNS
T24_gb|XII19489.1|_1-391  EKLMNVETAQIQVMQH LTMHKQLISGNTEDPVQA I LQCLNS
T3_gb|XII13308.1|_1-391   EKLMNVETAQIQVMQH LTMHKQLISGNTEDPVQA I LQCLNS
*****
```

Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*

CLUSTAL W (1.83) multiple sequence alignment (*lpxC*)

```
T14_gb|XII17155.1|_1-300  MVKQRTLNRVVKASGIGLHSGQKVMINFIPHTVDGGIVFRRIDLDPVVDI
T24_gb|XII20845.1|_1-300  MVKQRTLNRVVKASGIGLHSGQKVMINFIPHTVDGGIVFRRIDLDPVVDI
T3_gb|XII13653.1|_1-300   MVKQRTLNRVVKASGIGLHSGQKVMINFIPHTVDGGIVFRRIDLDPVVDI
*****

T14_gb|XII17155.1|_1-300  PANALLIQEAFMCSNLVTGDIKVGITIEHVMSAIALGLIDNLIVEVSASEV
T24_gb|XII20845.1|_1-300  PANALLIQEAFMCSNLVTGDIKVGITIEHVMSAIALGLIDNLIVEVSASEV
T3_gb|XII13653.1|_1-300   PANALLIQEAFMCSNLVTGDIKVGITIEHVMSAIALGLIDNLIVEVSASEV
*****

T14_gb|XII17155.1|_1-300  PIMDGSAGPFIYLLMQGGLREQDAPKKFIKILKPVEALIDDKKAIFSPHN
T24_gb|XII20845.1|_1-300  PIMDGSAGPFIYLLMQGGLREQDAPKKFIKILKPVEALIDDKKAIFSPHN
T3_gb|XII13653.1|_1-300   PIMDGSAGPFIYLLMQGGLREQDAPKKFIKILKPVEALIDDKKAIFSPHN
*****

T14_gb|XII17155.1|_1-300  GFQLNFTIDFDHPAFAKEYQSATIDFSTETFVYEVSEARTFGFMKDLDYL
T24_gb|XII20845.1|_1-300  GFQLNFTIDFDHPAFAKEYQSATIDFSTETFVYEVSEARTFGFMKDLDYL
T3_gb|XII13653.1|_1-300   GFQLNFTIDFDHPAFAKEYQSATIDFSTETFVYEVSEARTFGFMKDLDYL
*****

T14_gb|XII17155.1|_1-300  KANNLALGASLDNAIGVDDTGVVNEEGLRFADEFVRHKILDVAGDLYLLG
T24_gb|XII20845.1|_1-300  KANNLALGASLDNAIGVDDTGVVNEEGLRFADEFVRHKILDVAGDLYLLG
T3_gb|XII13653.1|_1-300   KANNLALGASLDNAIGVDDTGVVNEEGLRFADEFVRHKILDVAGDLYLLG
*****

T14_gb|XII17155.1|_1-300  HQIIAKFDGYKSGHALNNQLLRNVQSDPSNYEIVTFNDEKDCPIPYVSVT
T24_gb|XII20845.1|_1-300  HQIIAKFDGYKSGHALNNQLLRNVQSDPSNYEIVTFNDEKDCPIPYVSVT
T3_gb|XII13653.1|_1-300   HQIIAKFDGYKSGHALNNQLLRNVQSDPSNYEIVTFNDEKDCPIPYVSVT
*****;*****
```

Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*

CLUSTAL W (1.83) multiple sequence alignment (*lpxD*)

```

T14_gb|XII14638.1|_1-356  MKVQQYRLDELAHLVKGELIGESLQFSNLASLENAEVNHLTFVNGEKHL
T3_gb|XII11170.1|_1-356  MKVQQYRLDELAHLVKGELIGESLQFSNLASLENAEVNHLTFVNGEKHL
gb|XII18263.1|_1-356     MKVQQYRLDELAHLVKGELIGESLQFSNLASLENAEVNHLTFVNGEKHL
*****

T14_gb|XII14638.1|_1-356  DQAKVSRAGAYIVTAALKEHLPEKDNFIIVDNPYLAFAILTHVFDKKISS
T3_gb|XII11170.1|_1-356  DQAKVSRAGAYIVTAALKEHLPEKDNFIIVDNPYLAFAILTHVFDKKISS
gb|XII18263.1|_1-356     DQAKVSRAGAYIVTAALKEHLPEKDNFIIVDNPYLAFAILTHVFDKKISS
*****

T14_gb|XII14638.1|_1-356  TGIESTAQIHPSAVISETAYIGHYVVIENCVVGDNVTIQSHTKLDDNVE
T3_gb|XII11170.1|_1-356  TGIESTAQIHPSAVISETAYIGHYVVIENCVVGDNVTIQSHTKLDDNVE
gb|XII18263.1|_1-356     TGIESTAQIHPSAVISETAYIGHYVVIENCVVGDNVTIQSHTKLDDNVE
*****;*****

T14_gb|XII14638.1|_1-356  VGKDCFIDSHVTITGGSKLDRVRIHSSTVIGGEGFGFAPYQGKWHRIAQ
T3_gb|XII11170.1|_1-356  VGKDCFIDSHVTITGGSKLDRVRIHSSTVIGGEGFGFAPYQGKWHRIAQ
gb|XII18263.1|_1-356     VGKDCFIDSHVTITGGSKLDRVRIHSSTVIGGEGFGFAPYQGKWHRIAQ
*****

T14_gb|XII14638.1|_1-356  LGSVLIGNDVRIGSNCSIDRGALDNTILEDGVIIDNLVQIAHNVHIGSNT
T3_gb|XII11170.1|_1-356  LGSVLIGNDVRIGSNCSIDRGALDNTILEDGVIIDNLVQIAHNVHIGSNT
gb|XII18263.1|_1-356     LGSVLIGNDVRIGSNCSIDRGALDNTILEDGVIIDNLVQIAHNVHIGSNT
*****

T14_gb|XII14638.1|_1-356  AIAAKCGIAGSTKIGKNCILAGACGVAGHLSIADNVTLTGMSMVTKNISE
T3_gb|XII11170.1|_1-356  AIAAKCGIAGSTKIGKNCILAGACGVAGHLSIADNVTLTGMSMVTKNISE
gb|XII18263.1|_1-356     AIAAKCGIAGSTKIGKNCILAGACGVAGHLSIADNVTLTGMSMVTKNISE
*****

T14_gb|XII14638.1|_1-356  AGTYSSGTGLFENNHWKKTIVRLRQLADVPLTQITKRLDHIQAQIESLES
T3_gb|XII11170.1|_1-356  AGTYSSGTGLFENNHWKKTIVRLRQLADVPLTQITKRLDHIQAQIESLES
gb|XII18263.1|_1-356     AGTYSSGTGLFENNHWKKTIVRLRQLADVPLTQITKRLDHIQAQIESLES
*****

T14_gb|XII14638.1|_1-356  TFNLRK
T3_gb|XII11170.1|_1-356  TFNLRK
gb|XII18263.1|_1-356     TFNLRK
*****

```

Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*

CLUSTAL W (1.83) multiple sequence alignment (*lpxL*)

```

T14_lpxL      MSQKQPYTPGEFQWSFLLPKYWGVWIAITFLMLLAILPWAIQWRLAHGLA
T24_lpxL      MSQKQPYTPGEFQWSFLLPKYWGVWIAITFLMLLAILPWAIQWRLAHGLA
T3_lpxL       MSQKQPYTPGEFQWSFLLPKYWGVWIAITFLMLLAILPWAIQWRLAHGLA
               *****

T14_lpxL      NIAWKYLKSRRKTTIRNLEVCFPEWTPEKVQQQAKQVFVDMMLGVFETLN
T24_lpxL      NIAWKYLKSRRKTTIRNLEVCFPEWTPEKVQQQAKQVFVDMMLGVFETLN
T3_lpxL       NIAWKYLKSRRKTTIRNLEVCFPEWTPEKVQQQAKQVFVDMMLGVFETLN
               *:*****:*****

T14_lpxL      AWYKPYWFKNRVTIEGLEHITNAQAQGKGVLLLGTHSTLLDAGGYVCAQY
T24_lpxL      AWYKPYWFKNRVTIEGLEHITNAQAQGKGVLLLGTHSTLLDAGGYVCAQY
T3_lpxL       AWYKPYWFKNRVTIEGLEHITNAQAQGKGVLLLGTHSTLLDAGGYVCAQY
               *****

T14_lpxL      FEPDVVYRPQNNPLLDMLIYRCRGTIYKAQIDHDDMRGLIRHLKEGDAIW
T24_lpxL      FEPDVVYRPQNNPLLDMLIYRCRGTIYKAQIDHDDMRGLIRHLKEGDAIW
T3_lpxL       FEPDVVYRPQNNPLLDMLIYRCRGTIYKAQIDHDDMRGLIRHLKEGDAIW
               *****

T14_lpxL      YSPDQDFGLKQGVMAPFFGVPAATVTAHRRLLKISKAVAVPLYFYRHGDV
T24_lpxL      YSPDQDFGLKQGVMAPFFGVPAATVTAHRRLLKISKAVAVPLYFYRHGDV
T3_lpxL       YSPDQDFGLKQGVMAPFFGVPAATVTAHRRLLKISKAVAVPLYFYRHGDV
               *****:*****

T14_lpxL      QDPKYHILIEPAVDNLPSEDEVDDATRVNKIIENQLRIAPTQYMWFHRRF
T24_lpxL      QDPKYHILIEPAVDNLPSEDEVDDATRVNKIIENQLRIAPTQYMWFHRRF
T3_lpxL       QDPKYHILIEPAVDNLPSEDEVDDATRVNKIIENQLRIAPTQYMWFHRRF
               *****:*****

T14_lpxL      KTRPEGYEEIY
T24_lpxL      KTRPEGYEEIY
T3_lpxL       KTRPEGYEEIY
               *****

```

Fig S2. Alignment of amino acid sequences for LPS genes: *lpsB*, *lpxA*, *lpxB*, *lpxC*, *lpxD*, *lpxL*, and *lpxM*

CLUSTAL W (1.83) multiple sequence alignment (*lpxM*)

```

T14_lpxM      MNYQLLKTF SRQPIQFG RFLARLLAGLVNTLKITRTSKSIELNLRIALPY
T24_lpxM      MNYQLLKTF SRQPIQFG RFLARLLAGLVNTLKITRTSKSIELNLRIALPY
T3_lpxM       MNYQLLKTF SRQPIQFG RFLARLLAGLVNTLKITRTSKSIELNLRIALPY
*****

T14_lpxM      LTPQQRIAITEKAVRNELTSYFEFLSIWGSSNSKNISRIHRIEGEHFFHE
T24_lpxM      LTPQQRIAITEKAVRNELTSYFEFLSIWGSSNSKNISRIHRIEGEHFFHE
T3_lpxM       LTPQQRIAITEKAVRNELTSYFEFLSIWGSSNSKNISRIHRIEGEHFFHE
*****

T14_lpxM      ALAAKKGVVLIVPHFGTWEVMNAWCAQFTSMTILYKPVKNADADRFVREA
T24_lpxM      ALAAKKGVVLIVPHFGTWEVMNAWCAQFTSMTILYKPVKNADADRFVREA
T3_lpxM       ALAAKKGVVLIVPHFGTWEVMNAWCAQFTSMTILYKPVKNADADRFVREA
*****

T14_lpxM      RSREQANLVPTDESGVRQIFKALKQG ETTVILPDHTPNVGGDMVNYFGVP
T24_lpxM      RSREQANLVPTDESGVRQIFKALKQG ETTVILPDHTPNVGGDMVNYFGVP
T3_lpxM       RSREQANLVPTDESGVRQIFKALKQG ETTVILPDHTPNVGGDMVNYFGVP
*****

T14_lpxM      LASSNLSAKLIQKTAKALFLYAIRNENDGFTMHIEPMDEKIYEGTADDG
T24_lpxM      LASSNLSAKLIQKTAKALFLYAIRNENDGFTMHIEPMDEKIYEGTADDG
T3_lpxM       LASSNLSAKLIQKTAKALFLYAIRNENDGFTMHIEPMDEKIYEGTADDG
*****

T14_lpxM      TYVIHQAI EQLIYQYPEHYHWSYKR FKANPALDNIYNIDPTEALKIVDKL
T24_lpxM      TYVIHQAI EQLIYQYPEHYHWSYKR FKANPALDNIYNIDPTEALKIVDKL
T3_lpxM       TYVIHQAI EQLIYQYPEHYHWSYKR FKANPALDNIYNIDPTEALKIVDKL
*****

T14_lpxM      KAEALKTSTQPEPIQT SVM
T24_lpxM      KAEALKTSTQPEPIQT SVM
T3_lpxM       KAEALKTSTQPEPIQT SVM
*****

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