

Supplementary Table 1: Differentially expressed transcripts, lung surfactant over lactate-alone.

Transcript ID	survanta Bi-weight Avg Signal (log2)	lactate Bi-weight Avg Signal (log2)	Fold Change (linear) (Survanta/lactate)	ANOVA p-value	Gene Title	Locus Tag	Target Description
CP000647-002024_at	10.02	5.76	19.16	0.013213	<i>dhCA</i>	KPN_02053	putative acetyl-CoA:acetoacetyl-CoA transferase alpha subunit
CP000647-004291_at	11.67	8.06	12.25	0.003561	<i>fadB</i>	KPN_04340	4-enzyme protein: 3-hydroxyacyl-CoA dehydrogenase
CP000647-000228_at	12.29	8.7	12.06	0.003477	<i>fadE</i>	KPN_00235	acyl-CoA dehydrogenase
CP000647-002025_at	9.51	5.97	11.69	0.009721	<i>dhCB</i>	KPN_02054	putative acetyl-CoA:acetoacetyl-CoA transferase beta subunit
CP000647-002029_at	8.04	4.92	8.68	0.001302	<i>KPN_02058</i>	KPN_02058	putative transcriptional regulator (LysR family)
CP000647-002026_at	7.88	4.81	8.41	0.005143	<i>atoB</i>	KPN_02055	beta-ketothiolase
CP000647-001963_at	7.96	5.07	7.41	0.005082	<i>nemaA</i>	KPN_01989	N-ethylmaleimide reductase
CP000647-003219_at	9.34	6.6	6.67	0.029047	<i>mrkC</i>	KPN_03278	putative bacterial pili assembly chaperone
CP000647-002466_at	7.46	4.83	6.16	0.006439	<i>Kp52D</i>	KPN_02505	Possible glycosyltransferase
CP000647-004290_at	11.02	8.44	5.96	0.006467	<i>fadA</i>	KPN_04339	acetyl-CoA acetyltransferase
CP000647-002028_at	7.86	5.29	5.94	0.005519	<i>KPN_02057</i>	KPN_02057	short chain dehydrogenase
CP000647-001609_at	9.14	6.66	5.58	0.015562	<i>ynel</i>	KPN_01635	putative aldehyde dehydrogenase
CP000647-001133_at	9.46	7.02	5.4	0.012926	<i>KPN_01159</i>	KPN_01159	hypothetical protein
CP000647-000398_at	8.85	6.43	5.36	0.007495	<i>queC</i>	KPN_00406	putative (aluminum) resistance protein
CP000647-002027_at	7.72	5.39	5.04	0.013195	<i>bdhB</i>	KPN_02056	3-hydroxybutyryl-CoA dehydrogenase
CP000647-002684_at	10.34	8.04	4.93	0.000741	<i>fadI</i>	KPN_02724	acetyl-CoA acetyltransferase
CP000647-001539_at	11.05	8.82	4.68	0.006105	<i>mdtJ</i>	KPN_01565	multidrug transport protein (SMR superfamily)
CP000647-003218_at	8.79	6.64	4.44	0.022995	<i>mrkB</i>	KPN_03277	putative fimbrial usher protein
CP000647-001290_at	11.27	9.13	4.41	0.01338	<i>KPN_01316</i>	KPN_01316	hypothetical protein
CP000647-002957_at	5.37	3.37	4	0.008294	<i>proV</i>	KPN_03008	ATP-binding component of transport system for glycine
CP000647-002683_at	9.82	7.82	3.99	0.009272	<i>fadJ</i>	KPN_02723	bifunctional fatty acid oxidation complex protein
CP000650-000047_at	9.13	7.17	3.88	0.013586	<i>PN_pKPN5p0820</i>	KPN_pKPN5p08207	hypothetical protein
CP000647-003485_at	8.95	7.02	3.82	0.028091	<i>fadH</i>	KPN_03510	2,4-dienoyl-CoA reductase
CP000647-001701_at	7.55	5.68	3.65	0.000961	<i>KPN_01727</i>	KPN_01727	hypothetical protein
CP000647-001650_at	8.55	6.75	3.49	0.003375	<i>KPN_01676</i>	KPN_01676	hypothetical protein
CP000647-003455_at	7.78	5.98	3.47	0.022547	<i>evgA</i>	KPN_03480	putative bacterial regulatory protein
CP000647-004074_at	11.02	9.24	3.44	0.029644	<i>KPN_04108</i>	KPN_04108	putative inner membrane protein
CP000647-004398_at	8.85	7.1	3.37	0.033145	<i>yjcB</i>	KPN_04460	hypothetical protein
CP000647-002775_at	6.36	4.61	3.36	0.035152	<i>KPN_02822</i>	KPN_02822	putative glycoside hydrolase
CP000647-002522_at	8.04	6.3	3.34	0.000233	<i>yehS</i>	KPN_02561	hypothetical protein
CP000647-003220_at	12.01	10.28	3.32	0.04074	<i>mrkD</i>	KPN_03279	putative fimbrial-like protein
CP000648-000028_at	5.31	3.62	3.22	0.028084	<i>PN_pKPN3p0588</i>	KPN_pKPN3p05887	transposase
CP000647-004349_at	7.66	5.98	3.19	0.037534	<i>yfeH</i>	KPN_04411	putative cytochrome oxidase
CP000647-003813_at	7.29	5.64	3.14	0.01725	<i>arnA</i>	KPN_03845	hypothetical protein
CP000647-000367_at	7.63	5.98	3.14	0.042949	<i>thiL</i>	KPN_00375	thiamine biosynthesis protein ThiL
CP000650-000032_at	6.33	4.7	3.11	0.001789	<i>glnp-like</i>	KPN_pKPN5p08192	hypothetical protein
CP000647-002147_at	7.95	6.32	3.09	0.001374	<i>pheS</i>	KPN_02176	phenylalanyl-tRNA synthetase alpha subunit
CP000647-004348_at	6.95	5.34	3.07	0.011945	<i>yjbD</i>	KPN_04410	hypothetical protein
CP000647-003046_at	7.86	6.24	3.06	0.020144	<i>KPN_03102</i>	KPN_03102	putative cytoplasmic protein
CP000647-003392_at	7.86	6.26	3.03	0.029265	<i>zupT</i>	KPN_03453	zinc transporter ZupT
CP000647-000079_at	8.79	7.24	2.92	0.015548	<i>leuB</i>	KPN_00079	3-isopropylmalate dehydrogenase
CP000647-001367_at	5.56	4.02	2.91	0.003218	<i>KPN_01393</i>	KPN_01393	hypothetical protein
CP000647-004363_at	9.81	8.27	2.91	0.031979	<i>lamB</i>	KPN_04425	maltoporin precursor
CP000647-000117_at	9.49	7.95	2.9	0.047796	<i>pdhR</i>	KPN_00117	transcriptional regulator of pyruvate dehydrogenase complex
CP000647-000856_at	11.33	9.8	2.89	0.02951	<i>ybjM</i>	KPN_00879	hypothetical protein
CP000647-001344_at	7.52	6	2.85	0.00818	<i>KPN_01370</i>	KPN_01370	hypothetical protein

CP000647-004111_at	8.39	6.89	2.83	0.024055	<i>gidB</i>	KPN_04145	glucose-inhibited division protein B
CP000647-002444_at	8.67	7.17	2.83	0.030008	<i>KPN_02483</i>	KPN_02483	Possible glycosylhydrolase
CP000647-001962_at	7.62	6.14	2.79	0.020701	<i>nemR</i>	KPN_01988	hypothetical transcriptional regulator
CP000647-002176_at	9.04	7.57	2.78	0.027301	<i>ychJ</i>	KPN_02205	hypothetical protein
CP000647-000405_at	7.54	6.08	2.74	0.034841	<i>glnK</i>	KPN_00413	nitrogen regulatory protein P-II 2
CP000647-001134_at	6.74	5.29	2.74	0.037908	<i>KPN_01160</i>	KPN_01160	hypothetical protein
CP000647-002403_at	6.62	5.17	2.73	0.011601	<i>KPN_02440</i>	KPN_02440	putative bacterial regulatory protein
CP000647-001540_at	7.27	5.82	2.73	0.023785	<i>mdtI</i>	KPN_01566	multidrug transport protein (SMR superfamily)
CP000647-001528_at	6.6	5.15	2.72	0.005243	<i>mgo</i>	KPN_01554	malate:quinone oxidoreductase
CP000648-000015_at	7.55	6.11	2.71	0.025646	<i>PN_pKPN3p0587</i>	KPN_pKPN3p05873	putative alginate lyase
CP000647-000736_s_at	8.92	7.49	2.7	0.006465	<i>KPN_00759</i>	KPN_00759	putative IS1 transposase
CP000647-000861_at	10.47	9.05	2.68	0.002334	<i>ybjN</i>	KPN_00884	putative sensory transduction regulator
CP000650-000020_at	10.78	9.36	2.67	0.010714	<i>strB</i>	KPN_pKPN5p08180	streptomycin resistance protein B
CP000647-004497_at	6.52	5.11	2.66	0.037031	<i>KPN_04560</i>	KPN_04560	putative arginine-binding periplasmic protein
CP000647-003528_at	7.59	6.18	2.65	0.013587	<i>fic</i>	KPN_03553	hypothetical protein
CP000647-003598_at	8.87	7.46	2.64	0.000487	<i>gltD</i>	KPN_03625	glutamate synthase
CP000647-001852_at	7.32	5.94	2.61	0.014432	<i>KPN_01878</i>	KPN_01878	putative transcriptional regulator
CP000647-001703_at	7.73	6.34	2.61	0.029647	<i>KPN_01729</i>	KPN_01729	carbohydrate kinase
CP000647-000515_at	7.04	5.66	2.61	0.04942	<i>KPN_00524</i>	KPN_00524	putative bacterial extracellular solute-binding protein
CP000647-002800_at	8.58	7.2	2.6	0.007315	<i>yfgB</i>	KPN_02847	putative pyruvate formate lyase activating enzyme 2
CP000647-000255_at	7.27	5.9	2.59	0.008787	<i>stbE</i>	KPN_00262	putative fimbriae
CP000647-002034_at	7.72	6.34	2.59	0.034923	<i>KPN_02063</i>	KPN_02063	putative acetyl transferase
CP000650-000033_at	9.82	8.45	2.59	0.036231	<i>PN_pKPN5p0819</i>	KPN_pKPN5p08193	hypothetical protein
CP000647-003903_at	6.73	5.36	2.58	0.003115	<i>avtA</i>	KPN_03936	valine-pyruvate transaminase
CP000647-003489_at	7.46	6.09	2.57	0.016169	<i>ygjP</i>	KPN_03514	hypothetical protein
CP000647-002454_at	9.14	7.78	2.57	0.025707	<i>ugd</i>	KPN_02493	UDP-glucose dehydrogenase
CP000647-001848_at	8.61	7.26	2.56	0.018339	<i>catC</i>	KPN_01874	putative muconolactone delta-isomerase
CP000647-003217_at	6.72	5.37	2.55	0.00088	<i>mrkA</i>	KPN_03276	putative fimbrial-like protein
CP000647-000101_at	9.02	7.66	2.55	0.015677	<i>secM</i>	KPN_00101	SecA regulator SecM
CP000647-002954_at	10.03	8.69	2.54	0.042808	<i>nrpI</i>	KPN_03005	hypothetical protein
CP000647-000165_at	8.19	6.85	2.53	0.004475	<i>fhuA</i>	KPN_00165	outer membrane pore protein
CP000647-000102_at	9.24	7.9	2.53	0.039615	<i>secA</i>	KPN_00102	translocase
CP000647-000213_at	7.19	5.86	2.52	0.04867	<i>KPN_00213</i>	KPN_00213	D- and L-methionine transport protein (ABC superfamily)
CP000647-000460_at	6.52	5.19	2.51	0.016441	<i>ybbL</i>	KPN_00468	putative ATP-binding component of a transport system
CP000647-000769_at	6.77	8.37	-3.04	0.009176	<i>hutI</i>	KPN_00792	Imidazolonepropionase
CP000647-000773_at	5.18	6.85	-3.17	0.002584	<i>hutH</i>	KPN_00796	histidine ammonia lyase
CP000647-001453_at	6.9	8.73	-3.55	0.006045	<i>paaK</i>	KPN_01479	phenylacetate-CoA ligase
CP000647-001448_at	6.57	8.91	-5.06	0.036461	<i>paaF</i>	KPN_01474	probable enoyl-CoA hydratase
CP000647-000772_at	5.1	7.45	-5.08	0.013334	<i>hutU</i>	KPN_00795	putative urocanase
CP000647-001445_at	5.74	8.12	-5.23	0.016451	<i>paaC</i>	KPN_01471	phenylacetic acid degradation protein
CP000647-001451_at	6.82	9.24	-5.35	0.031845	<i>paal</i>	KPN_01477	phenylacetic acid degradation protein
CP000647-001447_at	6.32	8.87	-5.86	0.046877	<i>paaE</i>	KPN_01473	probable phenylacetic acid degradation NADH oxidoreductase
CP000647-001446_at	6.01	8.75	-6.65	0.020266	<i>paaD</i>	KPN_01472	phenylacetic acid degradation protein

Transcript Class	No. of transcripts
general metabolism	20
phospholipid/fatty acid metabolism	12
hypothetical	16

<b>nitrogen metabolism</b>	9
<b>oxidative stress</b>	3
<b>membrane stress</b>	2
<b>virulence</b>	4
<b>gene regulation</b>	6
<b>cytosolic stress</b>	5
<b>biofilm</b>	6
<b>antibiotic resistance</b>	3
<b>cation transport</b>	3

Supplementary Table 2: Primers used in this study

Primer Name	Sequence	Function
Kppri_leuABCD_KO_F1_PvuI	aatcgatcgAGACGCACAGATGGAACACG	<i>leuABCD</i> gene deletion construct
Kppri_leuABCD_KO_SOE_R1	gccacgcatcaacggctCTACTGGCTCATGGTTGGATCCTT	<i>leuABCD</i> gene deletion construct
Kppri_leuABCD_KO_SOE_F2	taggaccgttgatgctggcGCAAGCTGCCGGCGTTTATG	<i>leuABCD</i> gene deletion construct
Kppri_leuABCD_KO_R2_PvuI	taacgatcgTCCTGGCAGAGCTCAAGAATAC	<i>leuABCD</i> gene deletion construct
Kppri_proV_R2_KpnI	aataggtaccAAGGCGAGTGAAGCCCC	<i>proV</i> gene deletion construct
Kppri_proV_KO_SOE_F2	gTGActgTAGGTGTGAGTcAGCGAGGGGTGAATCATGGCTGA	<i>proV</i> gene deletion construct
Kppri_proV_SOE_R1	tGACTCACACCTAcagTCAcGCCATGCAATAGAGAAGTTCTCG	<i>proV</i> gene deletion construct
Kppri_proV_KO_F1_SphI	atagcatgcTTCGCGTCTTTACCGGATTGA	<i>proV</i> gene deletion construct
Kppri_mrk_KO_F1_bamHI	atagatccGATGGCGTGTATGGGATTGA	<i>mrkABC</i> gene deletion construct
Kppri_mrk_KO_SOE_R1	gctctagcgtcacactcacgtCATTGCCATTTCTTGTCAGAG	<i>mrkABC</i> gene deletion construct
Kppri_mrk_KO_SOE_F2	acgtgagtgtagcctagagcTAAGTGACGTTAAAGGCCGGG	<i>mrkABC</i> gene deletion construct
Kppri_mrk_KO_R2_kpnI	taaggtaccGGTTCATAGCCACCGCATCCA	<i>mrkABC</i> gene deletion construct
Kppri_mdtJI_KO_F1_xmaI	taTcccGGATGGCGCCCATACCTTCTAC	<i>mdtJI</i> gene deletion construct
Kppri_mdtJI_KO-SOER1	gctgcgagTCAtcgTTAactCATGATCCCTTCTCTGCTTGAGA	<i>mdtJI</i> gene deletion construct
kppri_mdtJI_KO-SOEF2	agtTAAcgaTGActgagcagcTGACGTCTCCGCCGCTGCAAAG	<i>mdtJI</i> gene deletion construct
Kppri_mdtJI_KO_R2_xmaI	AAATcccgggAGCACAAGCAGAACACTGGT	<i>mdtJI</i> gene deletion construct
Kppri_leu_KO_scrn_F	CCGCTGGATTACTTCAATGTC	PCR screen for gene deletion
Kppri_leu_KO_scrn_R	CGATATCCGTTGCCAGACCAA	PCR screen for gene deletion
kppri_proV_KO_scrnR	TCAATCGAGACAATCCCGACA	PCR screen for gene deletion
Kppri_proV_KO_scrnF	CAGGCGAAGCATCAACGCA	PCR screen for gene deletion
Kppri_mrkC_KO_scrnF	GTAGGCGGGTCCGATAACAG	PCR screen for gene deletion
Kppri_mrkC_KO_scrnR	CGCTTCTTACCAGACCT	PCR screen for gene deletion
Kppri_mdtJI_KO_scrnR	CCAGGGACAGAATGCCGTA	PCR screen for gene deletion
Kppri_mdtJI_KO_scrn_F	CTATGCGTTGTGGGAAGGG	PCR screen for gene deletion
Kpn_mdtJ_qRT_R	TTTTTCTGGGTGCCGACTT	qRT-PCR
Kpn_leuB_qRT_F	ACCAGCCAGTATGACGTTGG	qRT-PCR
Kpn_leuB_qRT_R	AGCCCTGATACAGTTTGGC	qRT-PCR
Kpn_04184_qRT_F	CGC TGG TTG AGG CAT TTA TT	qRT-PCR
Kpn_04184_qRT_R	GCT GAA CAT GGC TAA CTG AC	qRT-PCR
Kpn_proV_qRT_F	CAT GGT TCG CCT TCT CAA TC	qRT-PCR
Kpn_proV_qRT_R	AAG GAC TGA AAA ACC ATC GC	qRT-PCR
Kpn_02789_qRT_F	CCA TCC GTT TGC TGT TAC TG	qRT-PCR
Kpn_02789_qRT_R	CCG TTT TTG ACG AAG ATG CT	qRT-PCR
Kpn_mrkB_qRT_F	TAA AGA GAC GCT GTG GTG GC	qRT-PCR
Kpn_mrkB_qRT_R	TTG ATG GCG AGA CTA CTG CC	qRT-PCR
Kpn_fadB_qRT_F	AAG ATG TCG AGA CGC CGA AG	qRT-PCR
Kpn_fadB_qRT_R	GGT TTC CGC TAG TAC GGC TT	qRT-PCR
Kpn_02053_qRT_F	CCATTTGTTACGGGTCAGC	qRT-PCR
Kpn_02053_qRT_R	CGGCCGACACTACATCCTT	qRT-PCR
Kpn_03845_qRT_R	ATG CTC AAC GTC CTG GTA GC	qRT-PCR
Kpn_03845_qRT_F	CTG CGA CGG GCA GAT CAT TA	qRT-PCR