Table S1: Oligonucleotide sequences used in this study.

Primer Name	Oligonucleotide sequences (5’ to 3’)
5’P2 m	CACCAAATTAAT*CCCCAC*AATTATGTTATTCGTGC*CCACTC*TTCATAGTTGGTTATTC
3’ P2m	TAAATTATTAAAAAATAACATTAATTTAGG
5’P3m	AATTTTTCATTTTT*CCCAAA*AAAATTTTGAAAAAT*CCACTC*AAATAGTAGAAGAAGT
3’P3m	TTTATAATTTTTTTAATTTAGTAATTCTCAGTGC
5’P1m	TAAACACTTTTTTG*CCCCAA*CTCATTTTTAATTAGT*CCACTC*TAACTAAATAATAGAG
3’P1m	TAAAACAAATTATTCATTAGACACAGTGATTG
5’ teg49 deletion	TTGTTTACTTCTCATTTTTAATTAGTTAT
3’ teg49 deletion	TTAACTCTTCCAAGTTAACTTCTTCTACTA
5’teg48 deletion	TATATTATCGGGCAAATGTATCGAGCAA
3’ teg48 deletion	TATATTTAATGCTCTATTATTTAGTTAA
Teg49 F	GAATATCGAAACATTTAATTGCGCTA
Teg49R	AAACAAATTATTCATTAG ACACAGT
SaoUHSC_2167F	ACTTGCGGGAACTTTAGCAATCGT
SaoUHSC_2167R	AGTGCTTCGTCAATTTCGTTATAA
SaoUHSC_2160F	AGTGAAATTCCCAGTAACAATAAATA
SaoUHSC_2160R	AGAATTTAAGTTCAATATCTACCTT
SaoUHSC_0401F	AGGTTTTAGTAGCTACGGCAAT
SaoUHSC_0401R	ACGTGTTCATATTTTGAAACATCA
SaoUHSC_2841F	AAGTATGCACCGTACGGTAAACA
SaoUHSC_2841R	ACCTGTACATGTTAGTGCTCCA
SaoUHSC_0715F	TGACCCACTTACTGATCGTG
SaoUHSC_0715R	CGTAACCATTAACTTCTGGCATC
SaoUHSC_2235F	GTACAATCACCCGACCAAGATAG
SaoUHSC_2235R	GGGAGGTGTGAGTTGAGAAAA
SaoUHSC_1575F	AACAAACTCACACCTCCCC
SaoUHSC_1575R	AAACGTTCTCCTACACCAGC
SaoUHSC_0383F	GGGTAAACACTATTTAGAAGTCACAG
SaoUHSC_0383R	CACATCTATATTTGAGTTTTCTCCGTC
SaoUHSC_1114F	TCGAATATGGTGCACGTCC
SaoUHSC_1114R	ACTGCCTTTTGTGCTTTTCTG
SaoUHSC_0121F	GGTGTTCCTGCAAAAGTGATTAAG
SaoUHSC_0121R	AAATCCTTTTAGTTTGTCAGGCG
SaoUHSC_2708F	CAACATTGTCACACGAAAGAGG
SaoUHSC_2708R	GGCTAAACGATGTCTTGTCAC
SaoUHSC_2241F	ACGAAATGGAAATTTATGGGCG
SaoUHSC_2251R	GAAACCATGGCGATTCCAATC
SaoUHSC_0241F	ATGAGCATTGTTGCATTACTTATC
SaoUHSC_0241R	ATGACCAATGCCTGGCCAATT
SaoUHSC_1147F	CAAACACGCTAGCAACACAG

SaoUHSC_1147R	ACCGATTTCCCTTGACTATTACC
SaoUHSC_1925F	ATGGATAGATTAAAATATTCACTT
SaoUHSC_1925R	TCATTTCTTTAAAATTCCTAAAAATAT
SaoUHSC_0158F	GGTGGCGTATTTAGTGGATTTATC
SaoUHSC_0158R	GTGTTGCGTTTACATCTTACCC
SaoUHSC_1053F	AGTCGCTGTTGGTTACATGG
SaoUHSC_1053R	AGTCCATACCTGTTGCTATTCC
SaoUHSC_1942F	GAGTAAAGGTAAAGGCGGAGG
SaoUHSC_1942R	CTTTCACTTTTGCTCCGTCTG

Table S2: Upregulated gene expression in teg49 mutant versus the wild type.

Gene designation	Gene name or description	Wild type SH1000 expression value	ALC7907, teg49 mutant expression value	Fold change
Metabolism	**and enzyme families**			
SAOUHSC_00716	thiosulfate dehydrogenase	152	27833	183.11
SAOUHSC_01322,*thrB*	homoserine kinase	49	3957	80.75
SAOUHSC_01320,*metL*	homoserine dehydrogenase	65	4851	74.63
SAOUHSC_01321,*thrC*	threonine synthase	74	5296	71.57
SAOUHSC_-1319,*thrA*	aspartate kinase	13	818	62.92
SAOUHSC_03021	adenosyl-fluoride synthase	9	297	33.00
SAOUHSC_02283	acetolactate synthase I regulatory subunit	7	211	30.14
SAOUHSC_01833,*serA*	D-3-phosphoglycerate dehydrogenase	34	945	27.79
SAOUHSC_01832	aminotransferase class V	46	1206	26.21
SAOUHSC_02284,*ilvC*	ketol-acid reductoisomerase	13	311	23.92
SAOUHSC_02285,*leuA*	2-isopropylmalate synthase	12	276	23.00
SAOUHSC_02282,*ilvB*	acetolactate synthase large subunit	14	307	21.93
SAOUHSC-02287,*leuC*	isopropylmalate isomerase large subunit	10	212	21.20
SAOUHSC_02288,*leuD*	3-isopropylmalate dehydratase small subunit	10	197	19.7
SAOUHSC_03017	acetyltransferase (GNAT) family	6	106	17.66
SAOUHSC_02289,ilvA	threonine dehydratase	8	138	17.25
SAOUHSC_02286,*leuB*	3-isopropylmalate dehydrogenase	14	240	17.14
SAOUHSC_02924	4-aminobutyrate aminotransferase	39	557	14.28
SAOUHSC_02281,*ilvD*	dihydroxy-acid dehydrtase	17	229	13.47
SAOUHSC_01323	haloacid dehalogenase-like hydrolase	313	3967	12.67
SAOUHSC_00989	aminotransferase	68	710	10.44
SAOUHSC_00733,*hisC*	Histidinol-phosphate aminotransferase	27	251	9.29
SAOUHSC_01397,*dapB*	4-hydroxyl-tetrahydrodipicolinate reductase	101	849	8.40
SAOUHSC_00174	peptidase domain containing protein	13	109	8.38
SAOUHSC_01398,*dapD*	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	81	651	8.03
SAOUHSC_00013	homoserine O-acetyltransferase	30	232	7.73
SAOUHSC_01396,*dapA*	4-hydroxy-tetrahydrodipicolinate synthase	115	889	7.73
SAOUHSC_2605	peptidase family protein	32	234	7.31
SAOUHSC_0086,*butA*	acetoin reductase	837	5900	7.05
SAOUHSC_01395,*asd*	Aspartate semialdehyde dehydrigenase	127	778	6.12
SAOUHSC_02271	Sulfur transferase, TusA	51	302	5.91
SAOUHSC_00338,metE	5-methyltetrahydropteroyl triglutamate homocysteine S-transferase	12	69	5.75
SAOUHSC_01835	Hydrolase haloaciddehydrolase	78	440	5.64
SAOUHSC_00734	5' nucleotidase	95	472	4.96
SAOUHSC_02374	Aminobenoyl-glutamate protein B	50	245	4.9
SAOUHSC_01400,*alr2*	Alanine racemase	60	286	4.76
SAOUHSC_00722,p*abA*	Para-aminobenzoate synthase	16	77	4.81
SAOUHSC_02941,*nrdG*	Anaerobic ribonucleoside triphosphate reductase	1607	7696	4.78
SAOUHSC_01852	Bifunctional 3-deoxy-7-phosphoheptulonate synthase	267	1232	4.61
SAOUHSC_00171,*ggt*	Gamma-glutamyltranspeptidase	18	82	4.55
SAOUHSC_02139	Pyrazinamidase/nicotinamidase	344	1539	4.47
SAOUHSC_00536,*ilvE*	Branched-chain amino acid	579	2546	4.39

	aminotransferase			
SAOUHSC_02373	Peptidase family, ATP –grasp domain	59	245	4.15
SAOUHSC_00724,*pabC*	Chorismate binding protein	41	170	4.14
SAOUHSC_00723,*pabB*		34	141	4.14
SAOUHSC_02942,*nrdD*	Anaerobic ribonucleoside triphosphate reductase	1284	5133	4.0
SAOUHSC_00538	Haloacid dehalogenase-like hydrolase	141	552	4.98
Cell wall and	**Transportation systems**			
SAOUHSC_00717	Electron transfer domain protein	63	35464	562.92
SAOUHSC_01053	Manganese transport protein, MntH	50	11688	233.76
SAOUHSC_00424	ABC transporter permease	27	1098	40.66
SAOUHSC_02888	PTS phosphortransferase system	19	758	39.89
SAOUHSC_00426	ABC transporter substrate binding protein	72	2775	38.54
SAOUHSC_00423	D-methionine transport system ATP binding protein	37	1383	37.37
SAOUHSC_03020	Energy transporter	15	417	27.8
SAOUHSC_03019	ABC transporter ATP binding protein	13	325	25
SAOUHSC_03018	Energy-coupling factor transport system permease	8	165	20.62
SAOUHSC_02389	Cation efflux family protein	35	645	18.42
SAOUHSC_00927	Oligopeptide ABC transporter substrate binding protein	100	1543	15.43
SAOUHSC_00925,*oppD*	Oligopeptide ABC transporter protein D	81	1220	15.06
SAOUHSC_00012	Branched-chain amino acid transport protein, AzlD	20	295	14.75
SAOUHSC_00324	50S ribosomal protein L7 serine acetyltransferase	28	370	13.21
SAOUHSC_01323	Branched-chain amino acid transport protein, AzlC	18	216	12
SAOUHSC_00170,*rpl*	RGD-containing lipoprotein	8	96	12
SAOUHSC_02923	Basic amino acid antiporter, APA family	120	1434	11.95
SAOUHSC_00136	NitT/TauT family transport system ATP-binding protein	35	397	11.34
SAOUHSC_00169	peptide ABC transporter permease	7	81	11.57
SAOUHSC_00924,*oppC*	Oligopeptide ABC transporter protein C	65	687	10.57
SAOUHSC_00137	NitT/TauT family transport system substrate -binding protein	34	344	10.11
SAOUHSC_00209	PTS system glucose-specific transporter subunit IIBC	36	384	10.56
SAOUHSC_00843	D-methionine transport system permease protein	43	398	9.25
SAOUHSC_00923,*oppB*	Oligopeptide ABC transporter protein B	53	465	8.77
SAOUHSC_00138	NitT/TauT family transport system permease protein	36	310	8.61
SAOUHSC_00949	Alanine cation symporter	14	111	7.93
SAOUHSC_02595	Bile acid: na+ symporter, BASS family	13	100	7.69
SAOUHSC_00168	peptide/nickel transport system permease protein	8	56	7.00
SAOUHSC_02272	Sulfur transport protein	23	150	6.52

SAOUHSC_02704	Cation efflux protein	49	302	6.16
SAOUHSC_02108	ferritin	3111	17396	5.59
SAOUHSC_02596	Transporter –like protein	11	60	5.45
SAOUHSC_02773	transporter	131	561	4.28
Cellular process	**and regulatory systems**			
SAOUHSC_01575	helix-turn-helix domain-containing protein	0	166	166
SAOUHSC_02053	transcriptional activator rinB-like protein	0	143	143
SAOUHSC_00715	Response regulator, SaeR	298	31113	104.40
SAOUHSC_02077	Mga helix-turn-helix domain protein	0	72	72
SAOUHSC_02235	repressor	0	55	55
SAOUHSC_00714	Sensor histidine kinase SaeS	425	22405	52.72
SAOUHSC_00230,*lytS*	Two-component sensor histidine kinase	102	384	3.76
Virulence	**factors**			
SAOUHSC_02167	Staphylococcal complement inhibitor	10	32147	3214.7
SAOUHSC_02160	Map domain protein	27	20766	769.11
SAOUHSC_02161,*map*	MHC class II analog protein	30	20205	673.5
SAOUHSC_00401	staphylococcal complement inhibitor SCIN	77	36003	467.57
SAOUHSC_01115	Staphylococcal complement inhibitor	26	7600	292.30
SAOUHSC_01114	Fibrinogen-binding protein	26	7399	284.57
SAOUHSC_02166	Putative holing-like protein	0	254	254
SAOUHSC_02706	Immunoglobulin G-binding Sbi	19	3767	198.26
SAOUHSC_02170	Peptidoglycan hydrolase	0	193	193
SAOUHSC_02708,*hlgA*	gamma-hemolysin h-gamma-II subunit	12	1902	158.5
SAOUHSC_01110	fibrinogen-binding protein-like protein	21	3142	149.61
SAOUHSC_01112	formyl peptide receptor-like 1 inhibitory protein	34	4726	139
SAOUHSC_00354	Staphylococcal/Streptococcal toxin, beta-grasp domain	11	1119	101.72
SAOUHSC_02710,*hlgB*	leukocidin F subunit	37	3416	92.32
SAOUHSC_02243	leukotoxin LukS	84	5299	63.08
SAOUHSC_02171	staphylokinase	0	55	55
SAOUHSC_02023	Bifunctional autolysin	0	42	42
SAOUHSC_02019	autolysin	0	34	34
SAOUHSC_01576	exonuclease family protein	0	27	27
SAOUHSC_02241	leukotoxin LukF	130	3494	26.87
SAOUHSC_00393	superantigen-like protein 8	4	91	22.75
SAOUHSC-00816,*ssp*	extracellular matrix and plasma binding protein	20	407	20.35
SAOUHSC_00394	superantigen-like protein 9	4	74	18.5
SAOUHSC_00382	superantigen-like protein 1	27	464	17.18
SAOUHSC_00191	staphylococcal complement inhibitor	5	68	13.6
SAOUHSC_00395	superantigen-like protein 10	11	132	12
SAOUHSC_01127	superantigen-like protein	10	100	10
SAOUHSC_01125	superantigen-like protein	8	79	9.87
SAOUHSC_00392	superantigen-like protein 7	8	72	9
SAOUHSC_00192	Staphylocoagulase, Coa	7	46	6.57
SAOUHSC_01124	superantigen-like protein	11	68	6.18
SAOUHSC_03045	Cold shock protein B	7372	30223	4.09
SAOUHSC_00232	Murein hydrolase regulator, LrgA	141	602	4.26

Unknown	**functional proteins**			
SAOUHSC_02176	Unknown function protein	0	492	492
SA)UHSC_02164	Unknown function protein	0	374	374
SAOUHSC_01111	Small ORF of 30 amino acids	16	1562	97.62
SAOUHSC_01569	Small ORF of 53 amino acids	0	74	74
SAOUHSC_00561	VraX, unknown function	646	13460	20.83
SAOUHSC_02388,*czrA*	hypothetical protein	24	447	18.6
SAOUHSC_00208	hypothetical protein	29	332	11.44
SAOUHSC_00135	hypothetical protein	207	1926	9.3
SAOUHSC_02857	hypothetical protein	22	200	9.09
SAOUHSC_02858	hypothetical protein	17	150	8.82
SAOUHSC_00962	IDEAL domain unknown protein	1848	13906	7.52
SAOUHSC_00290,*pfoR*	hypothetical protein	76	523	6.88
SAOUHSC_00863	hypothetical protein	33	210	6.36

TABLE S3: RNA-seq analysis, downregulated genes ALC7907, teg49 mutant versa the wild type SH1000.

Gene name or designation	Gene description	Wild type SH1000 expression value	ALC7907 Teg49 mutant expression value	Fold change
Metabolism and	**enzyme families**			
SAOHSC_01198,*fabD*	malonyl CoA-acyl carrier protein transacylase	1810	37	48.92
SAOUHSC_00128,*capO*	Cap5O protein/UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	414	20	20.7
SAUOHSC_00120,*capG*	UDP-N-acetylglucosamine 2-epimerase	529	26	20.34
SAOUHSC_00125,*capL*	Cap5L protein/glycosyltransferase	376	19	19.78
SAOUHSC_00124,*capK*	capsular polysaccharide biosynthesis protein Cap5K	135	7	19.28
SAOUHSC_00121,*capH*	capsular polysaccharide biosynthesis protein O-acetyl transferase Cap5H	423	22	19.22
SAOUHSC_00126,*capM*	capsular polysaccharide biosynthesis protein Cap5M	408	22	18.54
SAOUHSC_00122,*capI*	capsular polysaccharide biosynthesis protein Cap5I	369	20	18.45
SAOUHSC_00438,*treC*	alpha amylase family protein	867	48	18.06
SAOUHSC_00920,*fabH*	3-oxoacyl-ACP synthase III	1432	81	17.67
SAOUHSC_00123,*capJ*	capsular polysaccharide biosynthesis protein Cap5J	223	13	17.15
SAOUHSC_00119,*capF*	capsular polysaccharide biosynthesis protein Cap5F	525	31	16.93
SAOUHSC_00127,*capN*	cap5N protein/UDP-glucose 4-epimerase	419	25	16.76
SAOUHSC_00155,*glcA*	PTS system glucose specific protein	1020	68	15.00
SAOUHSC_00118,*capE*	capsular polysaccharide biosynthesis protein Cap5E	494	36	13.72

SAOUHSC_00439,*treR*	trehalose operon transcription repressor	695	53	13.11
SAOUHSC_01197,*plsX*	glycerol-3-phosphate acyltransferase PlsX	1459	120	12.15
SAOUHSC_01199,*fabG*	3-oxoacyl-(acyl-carrier-protein) reductase	2117	176	12.01
SAOUHSC_00117,*capD*	capsular polysaccharide biosynthesis protein Cap5D	488	44	11.09
SAOUHSC_02806,*gntP*	gluconate permease	405	38	10.65
SAOUHSC_02399,*glmS*	glucosamine--fructose-6-phosphate aminotransferase	1010	103	9.80
SAOUHSC_01256	peptidase M16/insulinase	159	17	9.35
SAOUHSC_01910,*pckA*	phosphoenolpyruvate carboxykinase	637	70	9.1
SAOUHSC_01257	3-oxoacyl reductase	170	20	8.50
SAOUHSC_01601,*malA*	alpha-D-1,4-glucosidase	141	17	8.29
SAOUHSC_00437,*treP*	PTS threhalose-specific component II	2656	328	8.09
SAOUHSC_00921,*fab*	3-oxoacyl- synthase	2321	276	8.40
SAOUHSC_01255	peptidase M16 inactive domain protein	74	9	8.22
SAOUHSC_00153,*ipdC*	indolepyruvate decarboxylase	113	14	8.07
SAOUHSC_00239,*rbsK*	ribokinase	301	38	7.92
SAOUHSC_00241,*rbsU*	Putative ribose uptake protein	235	30	7.83
SAOUHSC_00116,*capC*	capsular polysaccharide biosynthesis protein Cap8C	682	87	7.83
SAOUHSC_02808,*gntK*	gluconate kinase	238	31	7.67
SAOUHSC_02647,*mqo*	malate:quinone oxidoreductase	299	39	7.66
SAOUHSC_00798,*pgm*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	7601	1012	7.51
SAOUHSC_00336	acetyl-CoA acyltransferase	336	45	7.46
SAOUHSC_00240,*rbsD*	D-ribose pyranase	327	45	7.26
SAOUHSC_00312	PTS ascorbate specific component II A	58	8	7.25
SAOUHSC_01146,*mra*Y	phospho-N-acetylmuramoyl-pentapeptide- transferase	343	48	7.14
SAOUHSC_01147,*murD*	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	544	77	7.06
SAOUHSC_O1216,*sucC*	succinyl-CoA synthetase subunit beta	1539	226	6.81
SAOUHSC_01218,*sucD*	succinyl-CoA synthetase subunit alpha	2142	316	6.77
SAOUHSC_00579,*mvaK2*	phosphomevalonate kinase	288	43	6.69
SAOUHSC_00656	dihydroxyacetone kinase	174	26	6.69
SAOUHSC_00129,*capP*	UDP-N-acetylglucosamine 2-epimerase	350	53	6.60
SAOUHSC_02403,*mtlD*	mannitol-1-phosphate 5-dehydrogenase	515	80	6.40
SAOUHSC_00797,*tpi*	triosephosphate isomerase	7834	1219	6.42
SAOUHSC_00115,*capB*	capsular polysaccharide biosynthesis protein Cap5B	552	89	6.20
SAOUHSC_01918	Excalibur Ca 2+ binding protein	1507	250	6.02
SAOUHSC_00796,*pgk*	phosphoglycerate kinase	5085	848	5.99
SAOUHSC_01611,*bmfBB*	2-oxoisovalerate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	526	89	5.91
SAOUHSC_00311	PTS ascorbate specific component IIB	71	12	5.91

SAOUHSC_00577,*mvaK1*	mevalonate kinase	164	28	5.85
SAOUHSC_02401	manitol operon transcription antiterminator	197	34	5.79
SAOUHSC_00146	putative membrance protein	4608	814	5.66
SAOUHSC_01857	DNA segregation ATPase FtsK/SpoIII family	485	86	5.63
SAOUHSC_01612,*bfmBAB*	2-oxoisovalerate dehydrogenase, E1 component subunit beta	506	91	5.56
SAOUHSC_00578,*mvaD*	mevalonate diphosphate decarboxylase	244	44	5.54
SAOUHSC_02885	acyltransferase family	501	92	5.44
SAOUHSC_02869,*rocA*	1-pyrroline-5-carboxylate dehydrogenase	409	76	5.38
SAOUHSC_00309	short chain dehydrogenase	545	102	5.34
SAOUHSC_01845,*fhs*	formate--tetrahydrofolate ligase	1203	226	5.32
SAOUHSC_01614,*lpdA*	dihydrolipoamide dehydrogenase	403	76	5.30
SAOUHSC_01613,*bfmBAA*	2-oxoisovalerate dehydrogenase, E1 component subunit alpha	503	95	5.29
SAOUHSC_02377,*pdp*	pyrimidine-nucleoside phosphorylase	724	138	5.34
SAOUHSC_00799, *eno*	phosphopyruvate hydratase	9964	1905	5.23
SAOUHSC_02926	fructose-1,6-bisphosphate aldolase	3339	647	5.16
SAOUHSC_00710,*nagA*	N-acetylglucosamine-6-phosphate deacetylase	198	39	5.07
SAOUHSC_01418,*kgd*	2-oxoglutarate dehydrogenase E1 component	1045	208	5.02
SAOUHSC_02793	phosphoglucomutase	105	21	5.00
SAOUHSC_00655	dihydroxyacetone kinase subunit DhaK	134	27	4.96
Cell wall and	**transporter systems**			
SAOUHSC_00634	ABC transport substrate binding protein	2646	191	13.85
SAOUHSC_00636	iron (chelated) ABC transporter permease	1839	152	12.09
SAOUHSC_02848,*ptsG*	PTS system glucose-specific transporter subunit IIABC	920	85	10.82
SAOUHSC_00637	Mn 2+/Zn2+ transport system ATP binding protein	2242	220	10.19
SAOUHSC_02661,*scrA*	PTS system sucrose-specific transporter subunit IIBC	1821	229	7.95
SAOUHSC_02986	accessory Sec system protein Asp3	74	11	6.72
SAOUHSC_00658	PTS system mannnose-specific family transporter subunit IIA	165	25	6.60
SAOUHSC_01456	PepSY associated transmembrane protein	120	20	6.00
SAOUHSC_02753	ABC transport system permease	278	47	5.91
SAOUHSC_02402,*mtlA*	PTS system mannitol-specific transporter subunit IIA	435	74	5.87
SAOUHSC_02987	accessory Sec system protein Asp2	69	12	5.75
SAOUHSC_02662,*ptsIIB*	PTS system sucrose-specific	1181	204	5.78

	transporter subunit IIBC			
SAOUHSC_00625,*mnhA*	monovalent cation/H+ antiporter subunit A	102	19	5.36
Cellular process,	**transcriptional regulators, and**	**virulence**	**factors**	
SAOUHSC_01196	fatty acid biosynthesis transcriptional regulator	1075	115	9.34
SAOUHSC_01204, *smc*	SMC domain-containing protein	209	35	5.97
SAOUHSC_01206	DNA-binding protein	259	47	5.51
Unknown	**function proteins**			
SAOUHSC_00154	hypothetical small peptide of 33 amino acids	263	23	11.43
SAOUHSC_01200	hypothetical small peptide of 32 amino acids	1585	163	9.72
SAOUHSC_00280	hypothetical protein	328	34	9.64
SAOUHSC_02905	unknown domain protein	55	7	7.85
SAOUHSC_02378	hypothetical small peptide of 42 amino acids	247	39	6.33
SAOUHSC_01919	unknown domain protein	1405	222	6.32
SAOUHSC_00838	unknown domain protein	214	34	6.29
SAOUHSC_02701	hypothetical protein	259	41	6.31
SAOUHSC_00279	unknown domain protein	106	17	6.23
SAOUHSC_02663	unknown domain protein	226	39	5.79
SAOUHSC_01859	unknown domain protein	158	31	5.09