

Fold change vs stationary phase

Systematic	Stat.	Log	30'	120'	360'	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function	TIGR Main Role	TIGR Sub Role	
WAN014HZE_at	1.9	1.8	0.9	1.0	1.4	SA0873	SA0756	SAR0860	SAS0799	SAV0829	MW0782	aroD	3-dehydroquinate dehydratase, type I	Amino acid biosynthesis	Aromatic amino acid family	
WAN014C39_at	13.9	1.9	2.4	2.0	1.6		SAR2109	SAS1926	SAV2006	MW1943	dapE	succinyl-diaminopimelate desuccinylase	Amino acid biosynthesis	Aspartate family		
WAN014GTL_at	26.4	14.7	10.4	9.1	10.3	SA1072	SA0915	SAR1037	SAS0999	SAV1063	MW0946	folD	methylene tetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	Biosynthesis of cofactors, prosthetic groups, and carriers	Folic acid	
WAN014GZ4_at	8.0	5.8	3.2	2.6	2.5	SA1461	SA1259	SAR1439	SAS1369	SAV1426	MW1316	folA	dihydrofolate reductase	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin	
WAN014GZ2_at	11.3	8.7	4.5	3.9	5.0	SA2028	SA1112	SAR2368	SAS2164	SAV2374	MW2102	cysA	serine synthetase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Methylotolylate	
WAN014GZ1_at	12.7	7.4	5.1	5.0	3.6	SA2029	SA1230	SAR2369	SAS2163	SAV2273	MW2191	moeA	methyldopoterin biosynthesis MoeA protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Methyldopoterin	
WAN014FSO_at	6.1	8.1	2.9	2.6	3.2	SA2266	SA2068	SAR2357	SAS2163	SAV2273	MW2191	moeA	methyldopoterin biosynthesis MoeA protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Methyldopoterin	
WAN014FSB_at	7.3	5.7	3.7	2.9	3.3	SA2265	SA2064	SAR2353	SAS2159	SAV2269	MW2187	mobA	methyldopoterin-guanine dinucleotide biosynthesis protein A, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Methyldopoterin	
WAN014G7D_at	36.5	0.9	3.6	1.6	2.4	SA2570	SA2351	SAR2645	SAS2450	SAV2564	MW2485	crtP	phytoene dehydrogenase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Other	
WAN014G7E_at	15.4	3.7	5.1	3.0	3.3	SA0181	SA0181	SAR0157	SAS1030	SAV1055	MW1030	entB	isocitrate lyase (2,3 dihydro-2,3 dihydroxybenzoate synthase)	Biosynthesis of cofactors, prosthetic groups, and carriers	Other	
WAN014HTS_at	4.4	6.5	1.6	1.4	2.4	SA1975	SA1975	SAR2006	SAS1837	SAV1913	MW1854	nrdB	nicotinamide riboside transferase	Biosynthesis of cofactors, prosthetic groups, and carriers	Pyridine nucleotides	
WAN014HTL_at	4.0	5.4	1.6	1.2	1.5	SA1974	SA1728	SAR2005	SAS1836	SAV1912	MW1853	nrdB	NAD(P)H-dependent NAD+ synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	Pyridine nucleotides	
WAN014H1C_at	19.1	7.5	3.3	7.1	11.8	SA0564	SA0477	SAR0522	SAS0476	SAV0519	MW0474	pdxB	pyridoxine biosynthesis protein	Biosynthesis of cofactors, prosthetic groups, and carriers	Pyridoxine	
WAN014HYO_at	1.3	1.7	0.6	0.7	1.0	SA2085	SA1984	SAR1909	SAS1995	SAV2091	MW2014	thiE	thiamine-phosphate pyrophosphorylase	Biosynthesis of cofactors, prosthetic groups, and carriers	Thiamine	
WAN014G6B_at	32.8	8.7	0.9	0.3	1.1	SA1017	SA0185	SAR0192	SAS0166	SAV0191	MW0165	murQ	N-acetyl muramic acid 6-phosphate esterase IEC4.2--1. Glucokinase regulator-related	Biosynthesis and degradation of murein saccus and peptidoglycan	Cell envelope	
WAN014G6C_at	22.4	8.7	3.5	2.0	2.0	SA1018	SA0186	SAR0193	SAS0167	SAV0192	MW0166	capH	capH	Biosynthesis and degradation of murein saccus and peptidoglycan	Cell envelope	
WAN014G6D_at	15.1	2.0	1.3	1.1	1.4	SA1328	SA0146	SAR0153	SAS1621	SAV1501	MW1026	capN	N-acetylglucosamine 2-epimerase Cap5G	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G6E_at	6.2	1.0	0.7	1.1	1.1	SA1424	SA0150	SAR0157	SAS1030	SAV1055	MW1030	cap5G	UDP-N-acetylglucosamine 2-epimerase Cap5G	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G7B_at	14.8	2.3	1.2	2.2	2.2	SA2570	SA2265	SAR2645	SAS2469	SAV2563	MW2484	ctrQ	glycosyl transferase family protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G2T_at	19.8	1.6	3.3	2.2	3.3	SA0134	SA0144	SAR0151	SAS124	SAV1049	MW1024	cap5A	cap5A protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G5T_at	6.3	1.1	1.0	0.9	0.9	SA1411	SA0149	SAR0149	SAS124	SAV1054	MW1025	cap5F	cap5F protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G4R_at	4.1	1.1	0.8	0.8	0.9	SA0159	SA0159	SAR0159	SAS124	SAV1053	MW1023	cap5G	cap5G protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014F9V_at	7.3	1.5	0.9	1.1	1.50	SA150	SA1058	SAR1065	SAS1038	SAV1063	MW1038	cap5O	cap5O protein/UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014F4U_at	6.1	1.3	1.2	0.8	1.1	SA147	SA0155	SAR1062	SAS1063	SAV1060	MW1035	cap5U	cap5U protein/glycosyltransferase, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014HAQ_at	31.5	6.4	6.6	3.3	4.8	SA7604	SA0659	SAR0757	SAS0669	SAV0704	MW0686	gctM	glycosyl transferase family protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014HMQ_at	2.1	0.5					SA0131	SA0131	SA0131	SA0131	SA0131	MW0131	capH	capsular oligopeptide biosynthesis protein Cps4B, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope
WAN014H22_at	67.1	52.2	20.5	16.6	21.6	SA1522	SA1312	SAR1048	SAS1044	SAV1511	MW1033	murQ	glutamate racemase	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G4T_at	3.9	1.0	0.6	0.4	1.1	SA0148	SA0156	SAR0163	SAS0136	SAV0161	MW0136	ebpA	elastinolytic protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014HMS_at	3.5	0.9	1.0	1.5	1.5	SA0148	SA0156	SAR0163	SAS0133	SAV0160	MW0133	cap1	capsular polysaccharide biosynthesis galactosyltransferase Cap5M	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014FVP_at	2.4	0.7				SA0149	SA0157	SAR0164	SAS0137	SAV0162	MW0137	wecM	maltofuranose transferase, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014I06_at	28.5	15.0	8.0	6.9	7.8	SA2105	SA1913	SAR2199	SAS2114	SAV2111	MW2035	wecB	UDP-N-acetylglucosamine 2-epimerase	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014F0X_at	6.2	1.9	1.8	1.2	1.2	SA1501	SA0159	SAR0164	SAS0139	SAV0164	MW0139	cap5P	UDP-N-acetylglucosamine 2-epimerase Cap5P	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014H4T_at	4.1	1.1	0.9	0.9	0.9	SA1408	SA0148	SAR0159	SAS0159	SAV0159	MW0132	cap5T	capsular oligopeptide biosynthesis protein Cps4B, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014HMT_at	2.0	0.8	0.6	0.6	0.7	SA1611	SA0161	SAR1611	SAS134	SAV153	MW1034	cap5U	cap5U protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G3P_at	4.5	3.8	1.5	1.6	1.8	SA2500	SA2288	SAR2579	SAS2386	SAV2500	MW2419	galU	UTP-glucose 1-phosphate uridylyltransferase	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014E3E_at	#NA	#NA	#NA	#NA	#NA	SA0137	SA0145	SAR0165	SAS1123	SAV1068	MW1031	capH	cap5B oligopeptide biosynthesis protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014H9X_at	13.7	1.6	5.0	4.4	3.3	SA1611	SA0161	SAR0167	SAS1123	SAV1068	MW1031	murQ	glutamate racemase	Biosynthesis and degradation of murein saccus and peptidoglycan	Cell envelope	
WAN014G9D_at	3.3	3.5	1.5	1.5	1.4	SA0161	SA0161	SAR0163	SAS0166	SAV0161	MW0136	tagY	tagY protein	Biosynthesis and degradation of murein saccus and peptidoglycan	Cell envelope	
WAN014H71_at	2.5	1.5	2.0	1.5	1.5	SA0166	SA0166	SAR0169	SAS0169	SAV0160	MW0133	tagY	tagY protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014H60_at	12.2	6.1	5.9	5.7	5.6	SA1609	SA1381	SAR1629	SAS1490	SAV1552	MW1504	pbp3	penicillin-binding protein 3	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G6F_at	62.1	1.0	4.2	2.2	3.1	SA2197	SA2006	SAR2295	SAS2104	SAV2205	MW2130	map protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope		
WAN014HXM_at	8.2	2.0	0.7	2.2	2.4	SA1616	SA1004	SAR1092	SAS1159	SAV1159	MW1041	fb	fibrinogen-binding protein precursor-related protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014I01_at	86.5	2.9	2.1	1.2	1.2	SA1616	SA1004	SAR2780	SAS2170	SAV2170	MW2019	membrane protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope		
WAN014H4M_at	11.8	2.9	3.0	2.8	2.8	SA1616	SA1004	SAR2780	SAS2170	SAV2170	MW2019	membrane protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope		
WAN014E4Y_at	10.1	1.7	2.8	2.5	2.6	SA0411	SA0329	SAR0338	SAS0317	SAV0341	MW0317	murQ	29-kDa cell surface protein, staphylococcal cell wall anchored protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014GUU_at	2.3	3.8	0.7	0.8	0.9	SA1130	SA1064	SAR1064	SAS1130	SAV1130	MW1102	sa1	stfR protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014IVL_x_at	25.6	19.4	8.2	8.3	6.9	SA2019	SA1839	SAR2032	SAS2032	SAV1956	MW1956	sdhT	sdhT protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014GJ7_at	6.3	2.4	2.4	2.5	2.4	SA0632	SA0543	SAR0591	SAS0544	SAV0586	MW0541	membrane protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope		
WAN014GJ7V_at	24.0	18.1	8.4	6.4	7.4	SA0632	SA0543	SAR0591	SAS0544	SAV0586	MW0541	membrane protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope		
WAN014H4M_at	1.3	0.9	0.7	0.7	0.7	SA1411	SA0178	SAR1104	SAS1055	SAV1131	MW1103	isdC	ISD(C) cell wall surface anchor protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014H4M5_at	11.0	41.2	8.1	4.5	5.6	SA0985	SA0841	SAR0844	SAS0844	SAV0881	MW0863	mapB	map protein, putative	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014F9Y_at	47.4	37.7	6.6	6.5	7.7	SA1753	SA1523	SAR1874	SAS1633	SAV1706	MW1649	universal stress protein family	Biosynthesis and degradation of universal stress protein family	Cell envelope		
WAN014FVE_at	62.0	3.0	11.8	6.8	6.5	SA2321	SA2119	SAR2213	SAS2221	SAV2238	MW2249	ydaD	general stress protein 39	Biosynthesis and degradation of general stress protein 39	Cell envelope	
WAN014FVE_at	11.8	14.7	3.8	3.8	3.8	SA1863	SA0114	SAR0114	SAS1735	SAV1812	MW1754	spf	general stress protein 39	Biosynthesis and degradation of general stress protein 39	Cell envelope	
WAN014H3H_at	42.3	10.5	13.8	7.45	9.68	SA2173	SA1584	SAR2273	SAS2182	SAV2182	MW2180	aspP23	alkaline shock protein 23	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014B3Z_at	29.1	37.1	11.5	11.5	11.8	SA1689	SA1460	SAR1714	SAS1570	SAV1570	MW1584	relA	GTP pyrophosphokinase	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014B3C_at	6.5	4.2	3.2	3.0	3.1	SA1771	SA1543	SAR1799	SAS1648	SAV1722	MW1684	rela	heat shock protein GrpE	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014B3G_at	25.8	20.0	9.3	10.2	12.6	SA2026	SA1844	SAR2126	SAS1944	SAV2039	MW1963	sodA	sodA	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014B3G_at	5.18	27.9	11.4	8.6	9.5	SA1645	SA1645	SAR1647	SAS1666	SAV1589	MW1580	comEB	comEB operon protein 2	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014G3C_at	7.4	5.7	2.4	2.2	3.3	SA2016	SA1838	SAR2118	SAS2111	SAV2120	MW2105	abpC	abortive infection protein	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014P2_at	7.4	5.1	1.9	1.4	1.8	SA2042	SA2042	SAR2042	SAS2042	SAV2043	MW2040	spf	serine protease Spf	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014P2_at	9.4	6.1	2.9	3.4	3.7	SA2025	SA2043	SAR2025	SAS2043	SAV2038	MW2036	spf	serine protease Spf	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014P2_at	10.4	7.3	3.7	4.7	3.3	SA0270	SA0270	SAR0278	SAS0257	SAV0281	MW0257	ssaa	ssaa homologous antigen precursor SsaA	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014HQD_at	17.6	9.7	8.7	8.3	11.7	SA1743	SA1170a	SAR150	SAS107a	SAV1740	MW1056	beta-lactamase	beta-lactamase	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Cell envelope	
WAN014HY9_at	256.5	170.5	3.7	7.4	26.4	SA1186	SA1187	SAR1741	SAS1170a	SAV1740	MW1056	psbM	antibacterial protein	Toxin production and resistance	Cell envelope	
WAN014HYB_at	32.0															

Fold change vs stationary phase

Systematic	Stat.	Loc	30°	120°	360°	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function		TIGR Main Role	TIGR Sub Role	LB	30° in vivo			
													luKS	synergoheminotropic toxin luKS	epidemiin immunity protein F	Toxin production and resistance	Toxin production and resistance	-2.45	-3.29	-2.82	-1.19
WAN014HML_at	2.9	3.3	1.4	1.0	1.2	2.8	SA1861	SA1638	SAS1749	SAV1820	MW1768	mapV_2	truncated cell surface protein map-w	epidemiin immunity protein F	Toxin production and resistance	Toxin production and resistance	-3.52	-3.08	-6.79	-4.12	
WAN014IP8_X_at	3.3	3.3	0.9	1.1	0.5	0.8	SA1871	SA1634	SAS1739	SAS1739	MW1758	epiG	N-acetyltransferase	N-acetyltransferase	Toxin production and resistance	Toxin production and resistance	-1.41	-2.77	-1.95	-1.68	
WAN014HLQ_at	3.3	1.7	1.2	0.6	0.9	1.0	SA1888	SA2317	SAR2017	SAS1849	SAS1825	MW1866	acyl-coenzyme A-5-aminopentanoic acid acyl-transferase	acyl-coenzyme A-phosphoglucomamine mutase	Toxin production and resistance	Toxin production and resistance	1.23	-2.63	-2.72	-4.02	
WAN014GZ2_at	6.5	8.1	2.5	2.4	1.6	2.8	SA1888	SA2317	SAR2017	SAS1849	SAS1825	MW1866	acyl-coenzyme A-5-aminopentanoic acid acyl-transferase	acyl-coenzyme A-phosphoglucomamine mutase	Toxin production and resistance	Toxin production and resistance	1.14	-2.54	-3.02	-3.08	
WAN014GZ1_at	13.3	18.6	4.0	4.4	3.4	4.3	SA1891	SA1631	SAR2252	SAS2093	SAS2094	MW0519	femB	glycosyl transferase, group 1	glycosyl transferase, group 1	Toxin production and resistance	Toxin production and resistance	-1.40	-2.53	-2.72	-2.67
WAN014GIV_at	18.2	13.0	7.2	6.7	6.8	6.8	SA0612	SA0523	SAR0569	SAS0523	SAS0565	MW0520	leukocidin precursor, F subunit, putative	leukocidin precursor, F subunit, putative	Toxin production and resistance	Toxin production and resistance	1.16	-2.50	-2.65	-2.65	
WAN014H3O_at	2.4	2.8	1.0	0.9	SA0611	SAS0522	SAR0568	SAS0522	SAS0564	SAS0564	MW0519	leukocidin precursor, F subunit, putative	leukocidin precursor, F subunit, putative	Toxin production and resistance	Toxin production and resistance	-1.05	-2.33	-2.44	-1.47		
WAN014AAB2-seo2	12.6	12.0	5.4	5.2	8.6	8.6	SA0164	SA0173	SAR0180	SAS1504	SAS1719	MW0153	gramicidin S synthetase 2	gramicidin S synthetase 2	Toxin production and resistance	Toxin production and resistance	-1.63	-2.18	-3.37	-3.01	
WAN014GCBT_at	8.7	9.5	4.3	2.9	SA2292	SAR2278	SAS2253	SAS2244	SAS2259	SAS2259	MW2588	gtfB	coiled-coil hypothetical protein	coiled-coil hypothetical protein	Toxin production and resistance	Toxin production and resistance	1.03	-2.19	-2.58	-2.68	
WAN014GZ4_at	3.4	3.6	1.6	1.3	1.3	1.3	SA1916	SA1916	SAR1147	SAS1106	SAS1106	MW1054	exofactor, tRNA	exofactor, tRNA	Toxin production and resistance	Toxin production and resistance	-1.11	-2.13	-2.44	1.02	
WAN014IUC_at	1.6	1.4	0.7	0.6	1.6	1.6	SA2004	SA1912	SAR1745	SAS1745	SAS1745	MW1054	lukF	leukocidin precursor, F subunit, putative	leukocidin precursor, F subunit, putative	Toxin production and resistance	Toxin production and resistance	1.23	-2.14	-1.91	-1.56
WAN014I2A_at	30.7	15.9	4.1	3.6	5.0	SA2145	SAR2242	SAS2055	SAS2154	SAS2154	MW2080	glcNAc	glucosamine-fructose-6-phosphate aminotransferase (isomerizing)	glucosamine-6-phosphate isomerase, putative	Central intermediary metabolism	Central intermediary metabolism	-1.93	-7.57	-8.58	-6.12	
WAN014IHF_at	57.4	6.8	14.6	10.2	10.1	10.1	SA1912	SA1761	SAR1945	SAS1777	SAS1784	MW1795	crtN	D-isomer specific 2-hydroxyacid dehydrogenase family protein	D-isomer specific 2-hydroxyacid dehydrogenase family protein	Central intermediary metabolism	Central intermediary metabolism	-8.48	-3.93	-5.64	-5.69
WAN014GB1_at	19.1	14.0	1.8	1.7	2.3	2.3	SA2292	SA2289	SAS2196	SAS2196	SAS2196	MW2224	dehydrogenase, putative	dehydrogenase, putative	Central intermediary metabolism	Central intermediary metabolism	-1.37	-10.34	-9.81	-8.34	
WAN014GZ5_at	22.1	1.6	3.1	3.1	3.1	3.1	SA0624	SA2122	SAR2210	SAS2025	SAS2122	MW2046	dehydrogenase, putative	dehydrogenase, putative	Central intermediary metabolism	Central intermediary metabolism	-13.99	-7.06	-10.45	-9.98	
WAN014GZ7_at	7.3	7.3	1.3	1.0	2.3	2.3	SA2577	SA2549	SAR2210	SAS2210	SAS2210	MW2246	dehydrogenase, putative	dehydrogenase, putative	Central intermediary metabolism	Central intermediary metabolism	-1.69	-4.26	-8.37	-8.37	
WAN014GW0_at	150.0	9.0	35.2	17.9	17.9	17.9	SA2114	SA2104	SAR2210	SAS2025	SAS2122	MW2046	dehydrogenase, putative	dehydrogenase, putative	Central intermediary metabolism	Central intermediary metabolism	1.13	-3.02	-3.17	-3.09	
WAN014JLJ_at	12.8	14.4	4.2	4.0	4.1	4.1	SA0932	SA0791	SAR0892	SAS0800	SAS0800	MW0812	dehydrogenase, putative	dehydrogenase, putative	Central intermediary metabolism	Central intermediary metabolism	-1.91	-2.95	-3.46	-3.46	
WAN014GZ2_at	10.3	5.4	3.5	2.7	3.0	3.0	SA2574	SA2546	SAR2640	SAS2445	SAS2559	MW2480	menC	D-isomer specific 2-hydroxyacid dehydrogenase family protein	D-isomer specific 2-hydroxyacid dehydrogenase family protein	Central intermediary metabolism	Central intermediary metabolism	-1.49	-2.29	-2.46	-3.09
WAN014IHC_at	6.5	5.5	3.3	3.3	3.3	3.3	SA2007	SA2007	SAR2007	SAS2033	SAS2033	MW0849	suftide reductase (NADPH) flavoprotein alpha-component	suftide reductase (NADPH) flavoprotein alpha-component	Central intermediary metabolism	Central intermediary metabolism	1.11	-2.06	-2.24	-2.64	
WAN014GAO_at	3.8	4.6	1.2	1.2	1.6	1.6	SA2639	SA2413	SAR2688	SAS2560	SAS2560	MW1054	cysJ	sulfite reductase (NADPH) flavoprotein alpha-component	sulfite reductase (NADPH) flavoprotein alpha-component	Central intermediary metabolism	Central intermediary metabolism	1.21	-3.04	-3.29	-2.41
WAN014HM1_at	45.4	36.9	21.2	23.8	29.5	29.5	SA1842	SA1842	SAR1473	SAS1473	SAS1473	MW1362	hup	DNA-binding protein Hup	DNA-binding protein Hup	Chromosome-associated proteins	Chromosome-associated proteins	-1.23	-2.14	-1.91	-1.56
WAN014HEP_at	39.9	4.7	1.3	1.7	2.5	2.5	SA0866	SA0746	SAR0847	SAS0756	SAS0756	MW0769	thermonuclease precursor	thermonuclease precursor	DNA metabolism	DNA metabolism	-8.55	-31.38	-23.11	-16.06	
WAN014KPT_at	31.9	5.7	6.0	6.3	6.3	6.3	SA1711	SA1741	SAR1744	SAS1693	SAS1693	MW1620	tag	DNA invertase Pin homolog	DNA invertase Pin homolog	DNA replication, recombination, and repair	DNA replication, recombination, and repair	-5.59	-5.34	-5.07	-4.05
WAN014HJ1_at	35.1	6.0	4.2	4.2	4.2	4.2	SA0621	SA0621	SAR0613	SAS0719	SAS0719	MW0721	uvrA	DNA methyladenine glycosylase I	DNA methyladenine glycosylase I	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.10	-4.46	-3.46	-3.98
WAN014CUP_at	17.1	1.4	1.4	1.4	4.6	4.6	SA0004	SA0004	SAR0004	SAS0004	SAS0004	MW0788	uvrA	DNA methyladenine glycosylase I	DNA methyladenine glycosylase I	DNA replication, recombination, and repair	DNA replication, recombination, and repair	-3.69	-4.10	-3.72	-2.18
WAN014HDY_at	8.0	8.1	2.7	2.3	2.6	2.6	SA2173	SA2153	SAR1769	SAS1691	SAS1691	MW1633	pofA	DNA polymerase I	DNA polymerase I	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.02	-2.95	-3.50	-3.10
WAN014HOJ_at	38.7	25.7	13.2	10.0	14.4	14.4	SA0005	SA0005	SAR0005	SAS0005	SAS0005	MW0005	gyrB	DNA gyrase B subunit	DNA gyrase B subunit	DNA replication, recombination, and repair	DNA replication, recombination, and repair	-1.51	-2.93	-3.68	-2.68
WAN014HNU_at	4.9	6.0	1.9	1.8	1.6	1.6	SA1906	SA1862	SAR1935	SAS1765	SAS1765	MW1785	gyrA	DNA gyrase A subunit	DNA gyrase A subunit	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.23	-2.53	-2.71	-3.00
WAN014HPL_at	9.2	13.1	3.9	3.4	3.6	3.6	SA0971	SA0971	SAR0971	SAS0967	SAS0967	MW0849	recA	exonuclease III family protein	exonuclease III family protein	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.35	-2.52	-2.82	-2.68
WAN014HPR_at	7.1	5.1	30.3	30.3	30.3	30.3	SA0968	SA0968	SAR0968	SAS0968	SAS0968	MW0949	recA	exonuclease III family protein	exonuclease III family protein	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.34	-3.21	-3.17	-1.67
WAN014GZ2_at	2.9	3.5	1.4	1.2	1.5	1.5	SA0266	SA0266	SAR0485	SAS0485	SAS0484	MW0439	holB	DNA polymerase III, delta prime subunit	DNA polymerase III, delta prime subunit	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.20	-2.15	-2.38	-1.90
WAN014H42_at	4.7	3.7	2.2	2.0	2.6	2.6	SA1359	SA1597	SAS1458	SAS1519	SAS1519	MW1472	recN	DNA polymerase IV	DNA polymerase IV	DNA replication, repair RecN	DNA replication, repair RecN	-1.27	-2.13	-2.40	-1.84
WAN014HD1_at	52.1	26.4	25.9	21.7	31.4	31.4	SA0824	SA0714	SAR0813	SAS0719	SAS0719	MW0721	uvrA	exonuclease ABC, A subunit	exonuclease ABC, A subunit	DNA replication, recombination, and repair	DNA replication, recombination, and repair	-1.98	-2.01	-2.41	-1.66
WAN014FB7_at	9.4	1.7	3.7	2.4	2.4	2.4	SA0880	SA0768	SAR0867	SAS0776	SAS0785	MW0788	topA	Topoisomerase	Topoisomerase	DNA replication, recombination, and repair	DNA replication, recombination, and repair	-5.52	-2.58	-3.89	-2.75
WAN014LH1_at	4.0	4.4	1.6	1.6	1.7	1.7	SA1862	SA1626	SAR1899	SAS1732	SAS1732	MW1731	hsdR	type I restriction-modification enzyme, M subunit	type I restriction-modification enzyme, M subunit	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.21	-3.21	-2.61	-2.18
WAN014HLQ_at	2.6	2.7	1.3	1.1	1.4	1.4	SA1861	SA1861	SAR1733	SAS1733	SAS1733	MW1750	hsdS	type I restriction-modification enzyme, S subunit, EcoA family	type I restriction-modification enzyme, S subunit, EcoA family	DNA replication, recombination, and repair	DNA replication, recombination, and repair	1.01	-2.58	-2.55	-2.31
WAN014GZ3_at	14.3	17.7	4.7	4.5	3.2	3.2	SA2000	SA2149	SAR2208	SAS2208	SAS1936	MW1878	ascC	amino transferase, putative	amino transferase, putative	Amino acid transport and metabolism	Amino acid transport and metabolism	-1.51	-2.93	-3.68	-2.68
WAN014GGS_at	15.6	51.9	4.7	4.9	5.9	5.9	SA1569	SA2341	SAR2341	SAS2440	SAS2440	MW0840	gluA	glutamate dehydrogenase	glutamate dehydrogenase	Amino acid transport and metabolism	Amino acid transport and metabolism	-3.00	-32.95	-15.67	-8.07
WAN014GZ5_at	14.3	13.1	4.4	3.3	3.1	3.1	SA1800	SA1801	SAR1835	SAS1676	SAS1676	MW1693	rocA	ropeptide amidinotransferase	ropeptide amidinotransferase	Amino acid transport and metabolism	Amino acid transport and metabolism	-3.91	-11.37	-8.47	-5.95
WAN014GZ6_at	14.3	13.1	4.4	3.3	3.1	3.1	SA1801	SA1801	SAR1835	SAS1676	SAS1676	MW1693	rocB	ropeptide amidinotransferase	ropeptide amidinotransferase	Amino acid transport and metabolism	Amino acid transport and metabolism	-4.06	-10.84	-10.86	-8.46
WAN014GZ7_at	2.4	2.5	1.8	1.8	2.9	2.9	SA0008	SA0008	SAR0008	SAS0008	SAS0008	MW0008	dltA	D-amino acid amidinotransferase	D-amino acid amidinotransferase	Amino acid transport and metabolism	Amino acid transport and metabolism	-2.37	-7.83	-7.39	-4.52
WAN014H9B_at	14.4	13.1	4.3	3.3	4.1	4.1	SA0453	SA0453	SAR0474	SAS0442	SAS0475	MW0429	amyA	alpha amylase family protein	alpha amylase family protein	Amino acid transport and metabolism	Amino acid transport and metabolism	-4.19	-7.16	-6.02	-3.92
WAN014GY1_at	2.8	6.7	1.3	1.6	2.4	2.4	SA0517	SA0517	SAR0474	SAS0474	SAS0475	MW0429	qoxA	NAD(P)H-flavin oxidoreductase	NAD(P)H-flavin oxidoreductase	Energy metabolism	Energy metabolism	-1.34	-3.51	-2.65	-2.05
WAN014GTJ_at	13.7	17.3	3.7	4.0	3.7	3.7	SA1079	SA1093	SAR0134	SAS0996	SAS0996	MW0944	qoxA	quinol oxidase, subunit II	quinol oxidase, subunit II	Energy metabolism	Energy metabolism	-1.34	-3.55	-3.04	-2.86
WAN014HF4_at	54.1	10.2	17.2	17.2	19.1	19.1	SA0881	SA0823	SAR0832	SAS0736	SAS0736	MW0789	thioredoxin, putative	thioredoxin, putative	Energy metabolism	Energy metabolism	-5.37	-3.17	-3.86	-2.86	
WAN014GZ8_at	62.4	52.5	26.0	26.0	26.0	26.0	SA1069	SA1069	SAR1069	SAS1069	SAS1069	MW1051	thioredoxin, putative	thioredoxin, putative	Energy metabolism	Energy metabolism	-1.00	-3.17	-3.10	-2.46	
WAN014GTH_at	56.9	73.0	20.7	20.7	31.0	31.0	SA1069	SA1069	SAR1069	SAS0943	SAS0943	MW0943	qoxB	quinol oxidase, subunit I	quinol oxidase, subunit I	Energy metabolism	Energy metabolism	-1.24	-2.93	-2.93	

Fold change vs stationary phase

Systematic	Stat.	Log	30°	120°	360°	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function	TIGR Main Role	TIGR Sub Role	Fold change vs stationary phase			
														LB	30° in vivo	120° in vivo	360° in vivo		
WAN014H96_at	5.2	6.3	1.0	0.9	1.4	SA0708	SA0060	SA0661	SA0616	SA0651	MW0613	dhal	dihydroxyacetone kinase, L. subunit	Other	1.20	-5.39	-5.58	-3.65	
WAN014H84_at	6.4	8.4	1.2	1.4	2.2	SA0707	SA0065	SA0660	SA0615	SA0650	MW0612	dhal	dihydroxyacetone kinase family protein	Other	1.30	-5.21	-4.69	-2.89	
WAN014G98_at	77.8	34.6	16.1	11.9	13.3	SA2624	SA2402	SA2687	SA2494	SA2699	MW2528	acs	acetyl-CoA synthetase, putative	Energy metabolism	-2.25	-4.82	-6.52	-5.84	
WAN014IUF_at	61.4	57.9	14.2	10.6	15.1	SA0123	SA0133	SA0123	SA0123	SA0123	MW0159	deoC	deoxyribose-phosphate aldolase	Energy metabolism	-1.06	-4.31	-5.81	-4.07	
WAN014FJL_at	44.1	33.2	16.7	13.7	16.1	SA0120	SA0120	SA0120	SA0120	SA0120	MW0159	fumarylacetoacetate hydrolase family protein	Energy metabolism	-1.33	-2.65	-3.34	-2.69		
WAN014H82_at	8.7	1.1	0.9	0.4	2.6	SA0330	SA0114	SA0114	SA0114	SA0114	MW1183	gpkI	glycerokinase, putative	Energy metabolism	1.06	-2.22	-2.66	-1.16	
WAN014EV0_at	6.9	13.7	3.0	2.8	2.3	SA2329	SA2127	SA2422	SA2223	SA2336	MW2256	rpIA	ribose-5-phosphate isomerase	Pentose phosphate pathway	1.99	-2.30	-2.46	-3.03	
WAN014FXL_at	56.7	58.2	28.3	29.3	25.7	SA1549	SA1336	SA1582	SA1445	SA1505	MW1459	zwf	glucose-6-phosphate 1-dehydrogenase	Energy metabolism	1.03	-2.01	-1.94	-2.12	
WAN014I33_at	5.7	9.3	1.1	1.3	1.4	SA0598	SA0510	SA0557	SA0510	SA0552	MW0507	araB	L-ribulokinase	Energy metabolism	1.60	-5.06	-4.42	-4.18	
WAN014FJF_at	4.2	1.1	0.1	0.7	1.7	SA1405	SA0223	SA0223	SA0223	SA0223	MW1050	ribulose-5-phosphate 5'-dehydrogenase	Sugars	1.32	-3.92	-5.88	-2.56		
WAN014IS5_at	25.5	8.6	5.8	4.9	6.5	SA0529	SA0529	SA0574	SA0528	SA0528	MW0525	hxa	heulic acid synthase, putative	Energy metabolism	-2.97	-3.72	-5.18	-3.89	
WAN014GC5_at	5.9	12.2	2.0	2.0	1.9	SA2501	SA2279	SA2576	SA2378	SA2491	MW2411	phosphoglucomutase/phosphomannomutase family protein	Energy metabolism	2.08	-2.95	-2.98	-3.18		
WAN014HV_P_at	6.4	6.6	2.3	2.3	2.6	SA2028	SA1945	SA2127	SA1945	SA2040	MW1984	frk	fructose kinase, putative	Energy metabolism	1.04	-2.79	-2.81	-2.49	
WAN014GY5_at	10.5	6.2	2.0	0.8	5.6	SA1446	SA1244	SA1425	SA1355	SA1514	MW1302	2-oxoglutarate dehydrogenase, E1 component	Energy metabolism	-1.91	-12.25	-12.79	-9.25		
WAN014GY9_at	10.5	6.2	2.0	0.8	5.6	SA1444	SA1444	SA1425	SA1356	SA1513	MW1303	sucA	2-oxoglutarate dehydrogenase, E1 component, dihydrolipoamide succinyltransferase	Energy metabolism	-1.70	-10.76	-12.65	-6.87	
WAN014FJ1_at	27.1	1.6	2.0	3.0	2.0	SA1388	SA1184	SA1362	SA1289	SA1350	MW1237	2-oxoglutarate dehydrogenase, E1 component	Energy metabolism	-1.51	-9.46	-10.47	-7.00		
WAN014HV1_at	33.9	18.7	1.1	1.1	6.8	SA1158	SA0594	SA1120	SA1081	SA1147	MW1030	sdhC	succinate dehydrogenase, cytochrome b558 subunit	TCA cycle	1.65	-7.46	-4.96	-5.35	
WAN014HWT_at	120.3	63.4	17.1	27.3	33.0	SA1509	SA0995	SA1121	SA1082	SA1148	MW1031	sdhB	succinate dehydrogenase, flavoprotein subunit	TCA cycle	1.87	-7.04	-4.42	-3.64	
WAN014FWY_at	62.3	31.2	10.8	10.3	17.8	SA2362	SA1255	SA2454	SA2365	SA2366	MW2298	mdoB	malate quinone oxidoreductase	Energy metabolism	2.00	-5.79	-6.06	-3.49	
WAN014HW_V_at	92.5	50.4	18.6	21.6	25.5	SA1614	SA0996	SA1122	SA1083	SA1149	MW1032	sucB	succinate dehydrogenase, iron-sulfur protein	TCA cycle	-1.83	-4.97	-4.28	-3.25	
WAN014GY7_at	7.1	5.1	1.6	1.3	2.0	SA2455	SA1245	SA1425	SA1355	SA1513	MW1213	2-oxoglutarate dehydrogenase, E1 component	Energy metabolism	-1.52	-4.75	-4.93	-3.55		
WAN014HE7_at	67.6	70.1	16.0	15.4	30.1	SA1262	SA1262	SA1262	SA1262	SA1262	MW1210	fadE	2-oxoglutarate dehydrogenase, E1 component	TCA cycle	1.03	-4.15	-4.46	-3.12	
WAN014HE5_at	52.1	18.2	14.6	19.5	40.0	SA1741	SA1517	SA1733	SA1623	SA1694	MW1639	gltA	citrate synthase, beta subunit	TCA cycle	-2.28	-3.90	-2.83	-1.58	
WAN014FUH_at	68.6	51.3	19.5	24.9	30.4	SA1388	SA1184	SA1362	SA1289	SA1350	MW1237	isocitrate dehydrogenase, NADP-dependent	TCA cycle	-2.87	-3.56	-2.67	-1.30		
WAN014FJU_at	14.2	114.4	60.0	60.0	62.1	SA1263	SA1089	SA1222	SA1180	SA1246	MW1129	sucD	aconitate hydratase	TCA cycle	-1.34	-3.51	-2.76	-1.27	
WAN014FV1_at	28.0	15.3	14.0	12.0	10.8	SA1263	SA2023	SA2023	SA2021	SA2021	MW2027	atpD	acetyl-CoA synthetase, alpha subunit	TCA cycle	-1.25	-2.38	-2.30	-1.21	
WAN014HTL_at	7.8	7.1	3.1	2.9	3.5	SA1628	SA1268	SA1646	SA1519	SA1519	MW1521	atpA	acetyl-CoA synthetase, class II	Biosynthesis	-8.12	-9.05	-8.64	-4.45	
WAN014GZP_at	4.3	1.4	2.0	1.5	1.5	SA2482	SA2260	SA2472	SA2472	SA2472	MW2443	3-oxacyl-(acyl carrier protein) reductase, authentic point mutation	Fatty acid and phospholipid metabolism	-1.11	-2.53	-2.71	-3.24		
WAN014GCV_at	128.3	18.0	2.1	2.3	4.5	SA2694	SA2673	SA2556	SA2671	SA2671	MW2590	lip	3-oxacyl-(acyl carrier protein) reductase, authentic point mutation	Degradation	-3.00	-2.20	-2.79	-2.78	
WAN014HEU_at	9.9	0.4	0.3	0.2	0.2	SA2123	SA2025	SA2025	SA2023	SA2023	MW2049	fadD	acetyl-CoA dehydrogenase family protein	Fatty acid and phospholipid metabolism	-7.13	-61.82	-56.48	-28.36	
WAN014HE9_at	6.2	0.8	0.2	0.2	0.2	SA2123	SA2244	SA2022	SA2022	SA2022	MW2048	3-hydroxyacyl-CoA dehydrogenase family protein	Fatty acid and phospholipid metabolism	-23.28	-33.01	-5.00	-5.00		
WAN014HJF_at	4.0	0.9	0.7	0.7	1.5	SA2043	SA2043	SA2043	SA2043	SA2043	MW2047	fadE	long-chain acyl-CoA ligase, putative	Degradation	-8.00	-2.40	-2.40	-2.40	
WAN014GSV_at	29.5	24.0	8.4	7.3	9.9	SA2549	SA2223	SA2315	SA2342	SA2345	MW2456	estE	esterase, putative	Fatty acid and phospholipid metabolism	-1.22	-3.50	-4.01	-2.97	
WAN014HSU_at	2.1	14.4	0.7	0.7	0.9	SA0708	SA0091	SA2015	SA2015	SA0708	MW0070	plc	1-phosphatidylinositol phosphodiesterase precursor	Fatty acid and phospholipid metabolism	-1.45	-3.10	-3.05	-2.29	
WAN014FV2_at	42.4	19.0	4.2	4.9	3.9	SA2346	SA2140	SA2435	SA2140	SA2350	MW2271	estE	esterase, putative	Fatty acid and phospholipid metabolism	-1.54	-2.93	-2.54	-3.14	
WAN014HR1_at	65.7	47.7	21.1	23.3	32.3	SA1054	SA0898	SA1019	SA0984	SA1045	MW0929	menB	enoyl-CoA hydratase/isomerase family protein	Fatty acid and phospholipid metabolism	-1.38	-2.42	-2.68	-2.03	
WAN014HJF_at	28.0	29.5	14.0	14.0	14.0	SA0704	SA0704	SA0704	SA0704	SA0704	MW2508	fadB	3-hydroxyacyl-CoA dehydrogenase family protein	Fatty acid and phospholipid metabolism	-1.46	-3.44	-4.14	-3.28	
WAN014FWY_at	9.0	2.0	2.2	2.2	2.7	SA1439	SA1236	SA1416	SA1416	SA1416	MW1292	acpY	acyl-CoA dehydrogenase family protein	Fatty acid and phospholipid metabolism	-1.46	-2.77	-2.71	-2.34	
WAN014H41_at	2.1	1.4	0.9	1.1	1.0	SA0621	SA0533	SA0580	SA0573	SA0575	MW0530	vraA	substrate-CoA ligase, putative	Other	-1.46	-2.77	-2.71	-2.03	
WAN014G5N_at	18.4	4.4	0.6	0.4	1.3	SA176	SA176	SA1901	SA1901	SA1901	MW1904	conserved	conserved hypothetical protein	Other	-4.23	-33.30	-48.05	-13.90	
WAN014G64_at	45.4	14.4	1.8	5.2	6.3	SA1625	SA0704	SA2264	SA2074	SA2074	MW2099	hypothetical proteins	conserved hypothetical protein	-3.16	-24.88	-8.81	-7.24		
WAN014GNV_at	27.0	1.1	1.3	2.0	2.7	SA0708	SA0708	SA0708	SA0708	SA0708	MW0670	hypothetical proteins	conserved hypothetical protein	-5.50	-20.43	-10.59	-4.74		
WAN014HJF_at	46.0	3.5	0.5	0.5	1.3	SA0622	SA0622	SA0622	SA0622	SA0622	MW0622	hypothetical proteins	conserved hypothetical protein	-4.02	-4.47	-4.07	-4.08		
WAN014H35_at	31.5	24.4	3.2	4.2	6.2	SA0599	SA0591	SA0591	SA0593	SA0593	MW0508	wcaG	conserved hypothetical protein	conserved hypothetical protein	-1.29	-9.84	-7.52	-5.08	
WAN014G02_at	25.7	16.1	3.1	3.6	5.6	SA1845	SA1617	SA1937	SA2223	SA2038	MW2135	hypothetical protein	conserved hypothetical protein	-1.59	-8.17	-7.16	-4.58		
WAN014I11_at	91.3	75.3	11.5	10.5	13.1	SA1217	SA1937	SA1937	SA1937	SA1937	MW2059	hypothetical protein	conserved hypothetical protein	-1.21	-7.93	-8.67	-6.98		
WAN014G8L_at	12.6	1.1	1.6	1.3	1.4	SA2605	SA2474	SA2474	SA2474	SA2474	MW2508	hypothetical protein	conserved hypothetical protein	-1.09	-7.84	-9.74	-8.94		
WAN014G7L_at	5.2	1.4	2.5	2.3	2.3	SA1121	SA1121	SA1041	SA1041	SA1041	MW0989	hypothetical protein	conserved hypothetical protein	-3.90	-8.60	-3.67	-3.20		
WAN014GIV_at	58.0	21.1	13.2	10.5	18.1	SA1631	SA1403	SA1651	SA1512	SA1512	MW1526	hypothetical protein	conserved hypothetical protein	-2.05	-3.39	-5.78	-4.92		
WAN014H7X_at	10.1	0.9	0.5	0.5	0.5	SA0517	SA0517	SA0517	SA0517	SA0517	MW0515	hypothetical protein	conserved hypothetical protein	-1.37	-4.78	-5.04	-4.19		
WAN014H7D_at	12.9	4.7	1.1	5.7	6.9	SA6565	SA0478	SA0478	SA0478	SA0478	MW2075	ybbM	hypothetical protein	conserved hypothetical protein	-2.75	-4.39	-5.53	-3.20	
WAN014HIM_at	29.6	7.6	7.1	5.7	4.8	SA9292	SA9781	SA8083	SA8083	SA8083	MW0803	hypothetical protein	conserved hypothetical protein	-2.17	-4.20	-4.11	-1.86		
WAN014GE3_at	136.6	6.9	3.2	19.7	31.9	SA2723	SA2491	SA2491	SA2491	SA2491	MW2169	hypothetical protein	conserved hypothetical protein	-3.88	-4.18	-5.22	-6.15		
WAN014IE5_at	78.4	28.2	18.3	11.0	12.2	SA1754	SA1529	SA1529	SA1529	SA1529	MW1650	hypothetical protein	conserved hypothetical protein	-2.05	-4.11	-6.93	-4.28		
WAN014H7V_at	89.0	31.1	20.2	16.0	30.2	SA1402	SA1650	SA1513	SA1513	SA1513	MW1525	hypothetical protein	conserved hypothetical protein	-2.47	-4.04	-5.70	-2.94		
WAN014BQD_at	29.0	1.9	7.6	5.0	6.3	SA0210	SA2329	SA2200	SA2208	SA2208	MW2228	hypothetical protein	conserved hypothetical protein	-3.03	-3.91	-5.99	-4.75		
WAN014GSA_at	2.0	2.0	0.5	0.5	0.5	SA0648	SA0648	SA0559	SA0559	SA0559	MW0555	hypothetical protein	conserved hypothetical protein	-1.01	-3.74	-3.50	-3.87		
WAN014H56_at	6.6																		

Fold change vs stationary phase

Systematic	Stat.	Log	30°	120°	360°	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function	TIGR Main Role	TIGR Sub Role	Fold change vs stationary phase			
																LB	30° in vivo	120° in vivo	360° in vivo
WAN0141GE_at	136.3	20.0	56.8	34.9	33.2	SA1789	SA1560	SA1817	SA1665	SAV1739	MW1682	conserved hypothetical protein	Hypothetical proteins	Conserved	-6.83	-2.40	-3.91	-4.11	
WAN0142F_at	2.1	2.1	0.9	0.7	0.8	SA2152	SA1966	SA2253	SA2064	SAV162	MW2089	conserved hypothetical protein	Hypothetical proteins	Conserved	-6.03	-2.37	-2.80	-2.47	
WAN014GMU_at	3.6	2.6	1.5	1.7	1.4		SAS041	SA1333	SA1263	SAV1323	MW1210	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.40	-2.33	-2.17	-2.56	
WAN014GNB_at	203.2	145.7	88.7	75.0	115.6	SA0271	SA2271	SA0279	SA0258	SAV0282	MW0258	esxA	Hypothetical proteins	Conserved	-1.39	-2.29	-2.71	-1.76	
WAN014HJL_at	5.2	1.6	2.3	1.8	2.0	SA2682	SA2452	SA2740	SA2545	SAV2659	MW2579	conserved hypothetical protein	Hypothetical proteins	Conserved	-3.29	-2.27	-2.95	-3.80	
WAN014KMX_at	4.9	2.9	1.6	1.8	2.0	SA2153	SA1967	SA2092	SA0360	SAV0374	MW0349	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.77	-2.26	-2.07	-1.65	
WAN014GVF_at	125.4	10.0	56.4	42.1	75.5	SA0446	SA0360	SA0392	SA0351	SAV0374	MW0349	conserved hypothetical protein	Hypothetical proteins	Conserved	-12.54	-2.23	-2.98	-1.64	
WAN014GHW_at	2498.3	157.0	113.6	132.6	136.5		SAS050	SA1709	SA1565	SAV1629	MW1579	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.59	-2.20	-1.88	-1.83	
WAN014FWI_at	5.4	3.1	2.4	1.9	1.7	SA1440	SA1237	SA1417	SA1346	SAV1405	MW1293	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.72	-2.20	-2.88	-3.11	
WAN014HNF_at	15.0	21.3	7.1	6.1	6.4	SA1440	SA1237	SA1417	SA1346	SAV1405	MW1293	conserved hypothetical protein	Hypothetical proteins	Conserved	1.37	-2.19	-2.59	-2.45	
WAN014HJF_at	5.2	3.3	2.2	2.2	2.2	SA2404	SA2166	SA2087	SA0367	SAV0368	MW0383	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.32	-2.17	-2.57	-2.33	
WAN014EVX_at	4.6	6.1	2.1	1.8	2.3	SA2334	SA2131	SA2426	SA2238	SAV2340	MW2260	naB	Hypothetical proteins	Conserved	1.32	-2.17	-2.59	-2.03	
WAN014GZ2_at	2.3	2.9	1.1	1.2	1.4	SA1947	SA1705	SA1980	SA1811	SAV1889	MW1829	ygaE	Hypothetical proteins	Conserved	1.25	-2.16	-1.88	-1.69	
WAN014HO1_at	9.4	14.6	4.4	4.3	4.1	SA1011	SA0865	SA0974	SA0876	SAV1007	MW0888	ppmK	Hypothetical proteins	Conserved	1.55	-2.14	-1.97	-2.30	
WAN014HWF_at	2.0	1.3	0.9	1.1	1.0		SA1913						conserved hypothetical protein	Hypothetical proteins	Conserved	-1.48	-2.14	-1.77	-2.06
WAN014HJL_at	3.1	1.6	1.1	1.1	1.0	SA1796	SA1987	SA1908	SA1987	SAV1987	MW1925	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.52	-2.14	-2.02	-1.73	
WAN014GYS_at	51.3	51.9	24.0	18.4	22.7	SA0521	SA0437	SA0478	SA0438	SAV0479	MW0434	conserved hypothetical protein TIGR0103	Hypothetical proteins	Conserved	1.61	-2.14	-2.78	-2.85	
WAN014LW_x_at	1.2	0.6	0.8	1.0	0.8	SA2866							conserved hypothetical protein	Hypothetical proteins	Conserved	-2.05	-2.13	-1.57	-1.24
WAN014G53_at	3.2	1.3	1.5	1.4	1.7	SA2529	SA2306						conserved hypothetical protein	Hypothetical proteins	Conserved	-2.48	-2.11	-2.31	-1.88
WAN014HN_at	3.7	5.2	1.8	1.6	1.4	SA1009	SA0863	SA0972	SA0874	SAV1005	MW0886	conserved hypothetical protein	Hypothetical proteins	Conserved	1.39	-2.09	-2.34	-2.68	
WAN014HJF_at	1.9	2.1	0.9	0.7	0.9	SA106	SA0118	SA0125	SA0096	SAV1028	MW0095	conserved hypothetical protein	Hypothetical proteins	Conserved	1.12	-2.06	-2.37	-2.43	
WAN014JWU_at	1.6	1.0	0.6	0.5	0.9	SA0930	SA0789	SA0790	SA0798	SAV0292	MW0810	conserved hypothetical protein	Hypothetical proteins	Conserved	1.06	-2.07	-1.80	-1.23	
WAN014HDJ_at	1.5	1.6	0.7	0.8	1.2	SA0930	SA0789	SA0790	SA0798	SAV0292	MW0370	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.28	-2.07	-2.60	-2.00	
WAN014GED_at	4.7	2.2	2.3	1.5	2.5	SA2598	SA2366	SA2600	SA2466	SAV2580	MW2500	conserved hypothetical protein	Hypothetical proteins	Conserved	-2.12	-2.06	-3.18	-1.84	
WAN014G5X_at	22.1	35.4	10.7	9.2	7.8	SA2550	SA2324	SA2616	SA2422	SAV2536	MW2457	conserved hypothetical protein	Hypothetical proteins	Conserved	1.60	-2.06	-2.41	-2.85	
WAN014GZ_x_at	1.1	0.9	0.5	0.3	0.2	SA0296	SA0229						conserved hypothetical protein	Hypothetical proteins	Conserved	-1.15	-2.00	-3.02	-3.52
WAN014Y2_x_at	1.2	1.5	1.6	1.6	1.6		SAS2374						conserved hypothetical protein	Hypothetical proteins	Conserved	1.05	-2.03	-2.03	-2.03
WAN014GGD_at	2.5	2.0	1.2	1.3	1.5	SA0467	SA0381	SA0421	SA0342	SAV1027	MW0381	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.27	-2.02	-1.91	-1.72	
WAN014GSD_at	6.2	7.0	3.1	2.4	2.7	SA1006	SA0860	SA0869	SA0871	SAV1001	MW0883	conserved hypothetical protein	Hypothetical proteins	Conserved	1.12	-2.00	-2.20	-2.28	
WAN014GZH_at	7.8	8.9	3.1	3.0	3.0	SA1467	SA1264	SA1444	SA1374	SAV1431		conserved hypothetical protein	Hypothetical proteins	Conserved	1.15	-1.98	-2.48	-2.60	
WAN014GQ4_at	16.5	10.8	1.9	2.5	2.4	SA1816	SA1748	SA2021	SA1853	SAV1929	MW1870	conserved domain protein	Hypothetical proteins	Domain	-1.53	-8.95	-7.68	-6.76	
WAN014JWU_at	19.3	12.1	4.5	4.5	4.5	SA2592	SA2032	SA0637	SA0647	SAV0682	MW0644	conserved domain protein	Hypothetical proteins	Domain	-0.93	-4.33	-7.78	-7.23	
WAN014GUJ_at	27.6	2.6	1.2	1.2	1.2	SA1870		SAS2178				hypothetical protein	Hypothetical proteins	Not Conserved	-10.73	-2.85	-23.80	-2.80	
WAN014GGG_at	58.6	34	2.8	3.6	7.0	SA0480	SA0395	SA0407	SA0398	SAV0396	MW0396	hypothetical protein	Hypothetical proteins	Not Conserved	-17.22	-20.71	-16.40	-8.34	
WAN01BQVN_at	8.9	2.2	0.5	0.7	1.3	SA2363		SAS0371				hypothetical protein	Hypothetical proteins	Not Conserved	-4.01	-17.44	-12.83	-6.79	
WAN014FTL_at	16.0	10.6	1.9	1.6	1.6	SA0467	SA0372					hypothetical protein	Hypothetical proteins	Not Conserved	-1.52	-8.64	-9.05	-5.67	
WAN014HJF_at	297.0	28.7	34.0	27.6	37.0	SA0467	SA0372					hypothetical protein	Hypothetical proteins	Not Conserved	-3.86	-7.48	-6.95	-6.92	
WAN014HPL_at	9.2	8.0	2.0	1.6	2.6	SA1033	SA0883	SA0906	SA0995	SAV1027	MW0097	hypothetical protein	Hypothetical proteins	Not Conserved	-4.67	-7.38	-5.63	-3.51	
WAN014GP1_at	5.3	8.7	0.8	0.9	1.2	SA0851	SA0739	SA0839	SA0749	SAV0808	MW0761	hypothetical protein	Hypothetical proteins	Not Conserved	1.62	-6.94	-5.75	-4.49	
WAN014GSO_at	57.6	7.6	8.4	6.7	9.6	SA1046	SA1202	SA1092	SA1074	SAV1028	MW0922	hypothetical protein	Hypothetical proteins	Not Conserved	-7.61	-6.88	-8.57	-5.97	
WAN014GZ2_at	41.1	32.1	6.7	4.9	4.3	SA1992	SA1743	SA2021	SA1853	SAV1929	MW1870	hypothetical protein	Hypothetical proteins	Not Conserved	-1.28	-6.16	-8.31	-9.52	
WAN014FX4_at	63.1	28.1	10.7	5.7	5.9	SA2365	SA2062	SA09105	SA0112	SAV0108	MW0082	hypothetical protein	Hypothetical proteins	Not Conserved	-3.38	-9.34	-11.71	-10.84	
WAN014HJF_at	9.0	1.3	1.1	1.1	1.2	SA2362	SA2062	SA09105	SA0112	SAV0108	MW0082	hypothetical protein	Hypothetical proteins	Not Conserved	-3.03	-9.34	-11.71	-10.84	
WAN014GJL_at	109.7	44.3	20.2	75.4	11.7	SA2765	SA2616	SA0850	SA0537	SAV0573	MW0534	hypothetical protein	Hypothetical proteins	Not Conserved	-2.48	-5.42	-1.45	1.07	
WAN01BQPR_at	19.7	7.5	3.7	3.9	7.5	SA0490	SA0449	SA0449	SA0449	SAV0449	MW0405	hypothetical protein	Hypothetical proteins	Not Conserved	-2.63	-5.27	-5.03	-2.61	
WAN014GCC_at	11.6	5.4	2.3	2.0	2.2	SA2456	SA0371	SA0404	SA0362	SAV0386	MW0362	hypothetical protein	Hypothetical proteins	Not Conserved	2.16	-5.01	-5.75	-5.32	
WAN014HJF_at	60.8	13.3	12.8	6.6	7.8	SA2174	SA1985	SA2274	SA2084	SAV1833	MW2109	hypothetical protein	Hypothetical proteins	Not Conserved	-4.81	-4.75	-9.17	-7.82	
WAN014GZ2_at	14.1	1.8	3.0	2.0	2.5	SA0242	SA0242	SA0242	SA0242	SAV0242	MW0242	hypothetical protein	Hypothetical proteins	Not Conserved	-7.74	-4.69	-7.22	-5.71	
WAN014HJF_at	2.8	0.6				SA0166	SA0164					hypothetical protein	Hypothetical proteins	Not Conserved	-4.46				
WAN014GBV_at	24.2	8.6	5.6	6.6	5.8	SA1978		SAS2374				hypothetical protein	Hypothetical proteins	Not Conserved	-2.81	-4.28	-3.69	-4.14	
WAN014GPH_at	9.2	16.9	2.2	1.9	2.1	SA1850						hypothetical protein	Hypothetical proteins	Not Conserved	1.84	-4.23	-4.78	-4.35	
WAN014GSL_at	7.4	78.0	1.8	1.9	2.3	SA2136	SA1948	SA2234	SA2049	SAV2146	MW2070	hypothetical protein	Hypothetical proteins	Not Conserved	10.52	-4.16	-3.95	-3.21	
WAN014HTT_at	69.9	34.9	16.8	12.6	18.8	SA1629	SA1401	SA1649	SA1510	SAV1572	MW1524	hypothetical protein	Hypothetical proteins	Not Conserved	-1.88	-4.42	-4.26	-4.39	
WAN014HJF_at	29.1	123.3	56.1	45.1	47.4	SA2488		SAS0176				hypothetical protein	Hypothetical proteins	Not Conserved	-1.14	-3.97	-3.53	-4.01	
WAN014HMN_at	5.6	1.4	1.4	1.6	1.4	SA1100	SA1211					hypothetical protein	Hypothetical proteins	Not Conserved	-1.25	-3.85	-3.73	-3.73	
WAN014V1_at	3.2	0.2	0.8	0.8	0.6	SA2740	SA2488					hypothetical protein	Hypothetical proteins	Not Conserved	-1.61	-3.77	-1.60	-1.17	
WAN014G30_at	16.3	13.0	4.4	4.4	4.4	SA2027		SAS2343	SA2426	SAV2556	MW2477	hypothetical protein	Hypothetical proteins	Not Conserved	-4.21	-3.60	-3.60	-2.02	
WAN014PFR_at	7.2	1.2	2.4	2.2	2.2	SA2049	SA2241	SA2049	SA2337	SAV2143	MW2252	hypothetical protein	Hypothetical proteins	Not Conserved	1.05	-3.54	-2.77	-2.31	
WAN014HEW_at	51.3	23.2	14.6	19.8	19.8	SA2157	SA1759	SA2470	SA2273	SAV2383	MW2303	hypothetical protein	Hypothetical proteins	Not Conserved	-2.21	-2.59	-2.59	-1.81	
WAN014BLB_at	2.8	3.8	0.8	1.0	1.2	SA2433	SA2171	SA2171	SA2172	SAV2172	MW217								

Fold change vs stationary phase

Systematic	Stat.	Log	30'	120'	360'	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function	TIGR Main Role	TIGR Sub Role	Fold change vs stationary phase			
																LB	30' in vivo	120' in vivo	360' in vivo
WAN014HZZ_at	13.5	12.8	6.4	7.3	8.7	SA2087						MW2018	hypothetical protein	Hypothetical proteins	Not Conserved	-1.06	-2.10	-1.86	-1.55
WAN014LH_at	6.9	2.1	3.3	2.4	2.7	SA2489	SA2267	SAR2568	SAS2371	SAV2479	MW2404		hypothetical protein	Hypothetical proteins	Not Conserved	-3.24	-2.09	-2.89	-2.59
WAN014GP_at	7.3	9.9	3.5	2.8	4.4	SA0300	SA0292	SAR0301	SAS0281	SAV304	MW2021		hypothetical protein	Hypothetical proteins	Not Conserved	1.35	-2.07	-2.58	-1.66
WAN014GNV_at	2.5	3.4	1.2	1.0	0.9	SA0280	SA0280	SAS0267	SAS0292	MW2027			hypothetical protein	Hypothetical proteins	Not Conserved	1.36	-2.05	-2.45	
WAN014GJ_at	1.7	1.8	0.8	0.7	0.9	SA1654	SA1431	SAS1539	SAS1539	SAS1603	MW1553		hypothetical protein	Hypothetical proteins	Not Conserved	1.05	-2.04	-2.04	
WAN014GK_at	1.4	1.6	0.2	0.2	0.2	SA2400							hypothetical protein	Hypothetical proteins	Not Conserved	1.26	-2.01	-2.92	-1.88
WAN014QJM_at	2.1	2.1	1.1	0.9	1.2	#N/A							hypothetical protein	Hypothetical proteins	Not Conserved	1.26	-2.01	-2.92	-1.88
WAN014H36_at	3.5	4.4	1.7	1.2	1.9	SA1544	SA1332	SAR1577	SAS1501	SAS1501	MW0265	esxB	hypothetical protein	Hypothetical proteins	Not Conserved	1.26	-2.01	-2.92	-1.88
WAN014GNP_at	1.1	2.2	0.6	0.2	0.2	SA0278	SA0278	SAS0265	SAS0290	MW0265			hypothetical protein	Hypothetical proteins	Not Conserved	2.02	-2.00	-6.89	
WAN01BQ50_at	4.2	2.8	2.1	2.6	2.2	SA1755							hypothetical protein	Hypothetical proteins	Not Conserved	-1.53	-2.00	-1.60	-1.89
WAN014GK_at	69.0	33.9	50.3	33.3	34.7	SA0669	SA0570	SAR0622	SAS0581	SAS0581	SAS0577		hypothetical protein	Hypothetical proteins	Not Conserved	2.95	-1.99	-2.95	-2.88
WAN014GK_at	2.3	2.3	1.1	0.9	1.2	#N/A							antibiotic efflux pump	Antibiotic efflux pumps	Not Conserved	1.04	-2.12	-2.66	-1.92
WAN014GLL_at	1.3	0.8	0.3			SAS1885							uncharacterized phage protein (possible DNA packaging)	Mobile and extrachromosomal element functions	Propagule functions	1.54	-3.84		
WAN014GMH_at	6.0	3.0	2.0	1.5	2.1	#N/A							hypothetical phage protein-related protein	Mobile and extrachromosomal element functions	Propagule functions	2.01	-3.06	-3.88	-2.85
WAN01B2Z3A_at	3.7	1.4	0.9	0.7	0.9	SAS2573							hypothetical protein	No Data	No Data	2.70	-4.16	-5.02	-4.13
WAN014FTJ_at	1.8	1.0	0.6	0.7	0.7	SAR2237	SAR2051	SAR2051	SAR2072	SAR2072	MW0375		hypothetical protein	No Data	No Data	-1.82	-3.15	-2.80	-2.65
WAN014FJL_at	51.8	24.9	23.3	27.6	30.7	SAR2237	SAR2051	SAR2051	SAR2072	SAR2072	MW0375		hypothetical protein	No Data	No Data	-2.02	-2.47	-1.86	-1.98
WAN014XK_at	37.1	21.4	11.2	12.7	10.4	SA2058	SA1973	SAR2158	SAS2083	SAS2083	MW1995	pepX	pepX	pepX	-1.28	-2.61	-2.92	-3.59	
WAN014HN_at	21.1	23.1	9.2	7.1	7.7	SA1898	SA1660	SAR1933	SAS1842	SAS1783	cbf1	cbf1	cbf1	cbf1	1.10	-2.30	-2.96	-2.74	
WAN014GRZ_at	1.4	1.0	0.7	0.6	1.0	SA0360							bacteriophage L54a, hypothetical protein	Other categories	Propagule functions	-1.39	-2.16	-2.25	-1.46
WAN014HMG_at	5.1	5.1	1.8	2.4	1.8	SAS1746							IS1181, transposase	Other categories	Transposon functions	1.01	-2.75	-2.82	-2.09
WAN014GST_at	91.4	11.3	7.1	7.1	4.6	SA1055	SA0899	SAR1020	SAS0982	SAS0982	MW0390	sspc	Staphylococcal SspB	Staphylococcal SspB	Degradation of proteins, peptides, and glycoproteins	-8.03	-12.72	-18.88	-19.61
WAN014GK_at	24.0	14.4	2.2	2.1	2.1	SAR2007	SAR1022	SAS0988	SAS0948	SAS0948	MW0392	sspc (v8)	Staphylococcal SspB precursor	Staphylococcal SspB	Degradation of proteins, peptides, and glycoproteins	5.41	-1.10	-2.02	-1.41
WAN014GSW_at	5.8	1.7	0.9	1.1	1.0	SA1056	SA0900	SAR1021	SAS0947	SAS0947	MW1047	sspc	Staphopain	Staphopain	Degradation of proteins, peptides, and glycoproteins	-3.31	-6.11	-5.42	-5.51
WAN014G37_s_at	13.9	2.5	2.4	1.5	1.6	SA2075	SA1814						peptidase, M20/M25/M40 family, authentic frameshift	Protein fate	Degradation of proteins, peptides, and glycoproteins	-9.16	-5.84	-9.58	-8.86
WAN014HN_at	22.1	34.4	4.4	4.6	4.7	SA1005	SAS0968	SAS0870	SAS0870	SAS0870	SAS0882	pepF	oligoendopeptidase F	Protein fate	1.96	-5.08	-4.83	-4.75	
WAN014GDA_at	11.4	4.3	2.7	2.1	2.1	SAR1751	SAR1694	SAR2628	SAS2458	SAS2458	MW2409	cipC	ATP-dependent Cip protease, ATP-binding subunit CipC	Protein fate	2.63	-4.27	-9.08	-6.57	
WAN014FJL_at	4.3	5.3	1.3	1.8	1.3	SA1750	SAR2050	SAR2051	SAR2051	SAR2051	MW0384	ampA	proline dipeptidase	Protein fate	1.09	-3.72	-3.17	-3.74	
WAN014GK_at	6.8	2.3	1.4	0.4	1.8	SA1940	SA1637	SAR2001	SAS1832	SAS1832	MW1895	sspB	Staphylococcal SspB	Staphylococcal SspB	Degradation of proteins, peptides, and glycoproteins	-2.48	-3.50	-1.74	1.18
WAN014HL_at	12.5	5.1	3.6	7.2	14.8	SA2079	SA0835	SAR0938	SAS0975	SAS0975	MW0387	ccpB	ATP-dependent Cip protease, ATP-binding subunit CipB	Protein fate	1.49	-3.48	-3.69	-3.35	
WAN014H3L_at	7.4	5.0	2.1	2.8	2.2	SA1555	SA1423	SAR1590	SAS1515	SAS1515	MW1465	pepT	peptidase T	Protein fate	-1.14	-3.36	-3.08	-1.96	
WAN014H1L_at	29.7	26.0	8.8	9.8	5.2	SA2070	SAR0528	SAR0528	SAS0525	SAS0525	MW0480	cipC	ATP-dependent Cip protease, ATP-binding subunit CipC, authentic frameshift	Protein fate	1.09	-3.02	-3.08	-4.05	
WAN014FPU_at	15.7	17.1	5.2	5.1	3.9	SA1419	SAR1216	SAR1309	SAS1325	SAS1325	MW1272	pepF	oligoendopeptidase F	Protein fate	1.03	-2.74	-2.46	-2.16	
WAN014FJL_at	17.6	22.6	6.1	6.1	6.1	SAR1751	SAR1694	SAR2051	SAS2051	SAS2051	MW1704	htrA	htrA	htrA	-1.13	-2.66	-2.96	-2.31	
WAN014GJL_at	9.0	8.0	3.4	3.0	3.9	SA2463	SAR2244	SAS2345	SAS2345	SAS2345	MW2379	peptidase	M24 family	Protein fate	1.75	-2.64	-3.61	-3.13	
WAN014HGR_at	10.1	5.7	3.8	2.8	3.2	SA1793	SAS1566	SAR1823	SAS1671	SAS1671	MW1688	peptidase	M24 family	Protein fate	1.75	-2.64	-3.61	-3.13	
WAN014H9D_at	33.9	35.9	13.5	11.8	10.2	SA1801	SAR1836	SAS1677	SAS1751	SAS1751	MW1694	peptidase	M20/M25/M40 family	Protein fate	1.06	-2.51	-2.87	-3.32	
WAN014HKH_at	12.5	12.5	5.1	4.7	4.9	SA0941	SA0893	SAR0904	SAS0812	SAS0812	MW0384	ampA	peptidase	M20/M25/M40 family	Protein fate	1.23	-2.42	-2.68	-2.52
WAN014GK_at	5.4	12.9	2.3	2.3	3.4	SA1054	SA0957	SAR0554	SAS0549	SAS0549	MW0384	ampA	peptidase	M20/M25/M40 family	Protein fate	2.40	-2.36	-2.40	-1.56
WAN014HDL_at	3.2	4.1	1.1	1.1	1.1	SAR1752	SAR1752	SAR1752	SAR1752	SAR1752	MW1895	secA	SecA	SecA	-1.51	-2.16	-2.43	-1.52	
WAN014GZG_at	4.3	5.5	1.1	1.9	2.9	SAR1897	SAS1659	SAR1932	SAS1763	SAS1763	MW1841	prnsA	protease maturation protein	Protein fate	1.04	-2.06	-2.33	-1.47	
WAN014GCD_at	9.0	6.0	2.4	2.1	3.1	SA2671	SAR2288	SAR2288	SAS2649	SAS2649	MW2570	secA2	SecA	Protein fate	-1.48	-3.69	-4.32	-2.92	
WAN014GAB0-seq1	11.4	30.1	3.6	4.0	3.9	SA2676	SAR2734	SAR2734	SAS2540	SAS2540	MW2575	sasA	LXP1G-to-motif cell wall anchor domain protein	Protein fate	2.65	-3.12	-2.80	-2.88	
WAN014GAB0-seq2	14.3	31.0	5.3	5.4	5.0	SA2502	SAR2695	SAR2695	SAS2695	SAS2695	MW2575	sasA	LXP1G-to-motif cell wall anchor domain protein	Protein fate	2.13	-2.75	-2.96	-2.92	
WAN014GK_at	1.5	0.5	0.5	0.5	0.5	SAR2674	SAR2674	SAR2674	SAS2651	SAS2651	MW2572	aspA2	accessory secretory protein AspA2	Protein fate	1.52	-2.43	-2.01	-2.01	
WAN014HVE_at	15.2	11.6	3.1	2.7	3.0	SA2016	SAR1836	SAS1923	SAS1188	SAS1188	MW1107	rmpA	ribosomal-protein-synthesis acetyltransferase	Protein synthesis	-1.31	-4.92	-5.64	-5.02	
WAN014H99_at	52.2	31.1	14.8	17.6	24.1	SA1637	SAR1637	SAR1637	SAS1518	SAS1518	MW1532	dnaK	chaperone	Protein synthesis	-1.68	-3.53	-2.96	-2.17	
WAN014HVL_at	5.7	5.7	1.7	1.7	2.6	SA2063	SAR1837	SAR1837	SAS1937	SAS1937	MW1954	groES	chaperone	Protein synthesis	-1.15	-3.42	-3.15	-2.18	
WAN014H99_at	16.7	20.5	8.7	7.3	7.3	SAR1752	SAR1752	SAR1752	SAS1752	SAS1752	MW1954	groEL	chaperone	Protein synthesis	1.16	-2.31	-2.31	-1.93	
WAN014H99_at	49.0	5.7	7.1	19.0	17.8	SA1946	SAR1946	SAR1946	SAS1978	SAS1978	MW1828	map	mannosidase amidopeptidase, type I	Protein modification and repair	-1.07	-2.32	-2.57	-2.75	
WAN014HD7_at	17.0	20.3	7.4	5.7	5.7	SA2826	SAR0716	SAR0815	SAS2076	SAS2076	MW1723	lgt	protoprotein dicycloleucyl transferase	Protein modification and repair	1.20	-2.28	-2.99	-2.35	
WAN014H5L_at	11.7	8.7	5.3	4.9	3.9	SA1591	SAR1610	SAR1610	SAS1741	SAS1741	MW1485	lipoteichoic acid ligase	Protein modification and repair	Protein modification and repair	-1.35	-2.23	-2.41	-3.02	
WAN014GW_at	8.7	7.2	4.4	2.5	2.5	SA2031	SAR0881	SAR0897	SAS2079	SAS2079	MW0364	xpeA	peptide methionine sulfoxide reductase	Protein modification and repair	1.19	-2.20	-2.17	-1.91	
WAN014GK_at	32.5	18.9	7.9	9.1	14.8	SA0815	SAR0707	SAR0806	SAS2077	SAS2077	MW0271	W0247	ribosomal-protein synthetase	Protein synthesis	-1.72	-4.13	-3.59	-2.19	
WAN014HDL_at	62.1	40.3	14.6	15.0	12.7	SAR1729	SAR1606	SAR1606	SAS1611	SAS1611	MW1626	thrs	threonine/thRNA synthetase	Protein synthesis	-1.54	-4.26	-4.14	-4.90	
WAN014GXT_at	32.5	27.5	25.5	23.2	22.7	SAR1213	SAR1394	SAR1642	SAS1563	SAS1563	MW1517	glyS	glycyl-tRNA synthetase	Protein synthesis	-2.42	-2.61	-2.87	-2.93	
WAN014H4F_at	5.5	1.1	1.7	1.5	1.5	SAR1294	SAR1294	SAR1294	SAS1520	SAS1520	MW1514	trnU	tRNA pseudouridine 55 synthase	Protein synthesis	-5.18	-3.19	-3.58	-2.87	
WAN014H4F_at	20.0	1.6	1.7	1.7	1.7	SAR1290	SAR1297	SAR1297	SAS1947	SAS1947	MW1966	scr1	tRNA pseudouridine 55 synthase	Protein					

Fold change vs stationary phase

Systematic	Stat.	Log	30'	120'	360'	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function	TIGR Main Role	TIGR Sub Role	L8	30' in vivo	120' in vivo	360' in vivo
WAN014GK4_at	8.5	5.0	2.4	3.1	3.2	SA1740	SA1516	SA1772	SA1621	SAV1932	MW1637	phoP	DNA-binding response regulator	Signal transduction	Two-component systems	-1.72	-3.51	-2.61	-2.61
WAN014GK5_at	10.8	19.7	3.5	4.1	3.5	SA0245	SA0250	SA0257	SA0237	SAV2026	MW0236	lysT	sensor histidine kinase	Signal transduction	Two-component systems	<b>1.82</b>	-3.07	-2.64	-3.05
WAN014GKV_s_at	8.8	8.1	3.3	3.4	3.5	SA0019	SA0017	SA0018	SA0018	SAV0018	MW0018	lysC	DNA-binding response regulator	Signal transduction	Two-component systems	-1.09	-2.72	-2.64	-2.52
WAN014HOS_at	6.9	5.5	3.0	2.9	2.8	SA1906	SA1667	SA1964	SA1770	SAV1849	MW1790	sensor histidine kinase, putative	Signal transduction	Two-component systems	-1.26	-2.26	-2.42	-2.48	
WAN014IAT	2.3	2.7	1.0	1.0	1.2	SA2358	SA2347	SA2350	SA2350	SAV2238	MW2238	sensor histidine kinase	Signal transduction	Two-component systems	1.20	-2.19	-2.01	-1.97	
WAN014ING_at	18.9	25.4	8.7	6.8	6.0	SA0018	SA0018	SA0018	SA0018	SAV019	MW0190	lysC	sensor histidine kinase YycG	Signal transduction	Two-component systems	1.24	-2.18	-2.79	-3.17
WAN014IMX_at	7.2	7.5	3.4	2.7	1.9	SA0717	SA0618	SA0625	SA0625	SAV060	MW0622	lysT	sensor histidine kinase	Signal transduction	Two-component systems	1.03	-2.16	-2.68	-3.81
WAN014GAT_at	2.4	2.0	1.1	1.1	1.2	SA2071	SA1983	SA2167	SA1984	SAV2079	MW2003	kdpE	DNA-binding response regulator	Signal transduction	Two-component systems	-1.16	-2.13	-2.20	-1.92
WAN014GZV_at	146.1	17.8	66.2	36.2	30.8	SA0540	SA0455	SA0498	SA0454	SAV0497	MW0452	ribonuclease L-PSP, putative	endoribonuclease BN, putative	Degradation of RNA	-8.22	-2.21	-4.04	-4.75	
WAN014GIY_at	7.5	30.5	1.5	1.5	1.5	SA1941	SA1941	SA1941	SA1941	SAV1933	MW1923	lysT	sensor histidine kinase	Signal transduction	Two-component systems	-3.63	-2.17	-3.77	-3.46
WAN014GJF_at	11.3	19.9	1.8	1.8	1.8	SA2227	SA2228	SA2229	SA2229	SAV2230	MW2230	amino acid permease	Transport and binding proteins	Amino acids, peptides and amines	1.76	-3.75	-3.33	-3.96	
WAN014GZP_at	29.5	5.5	4.0	3.1	3.7	SA1476	SA1270	SA1449	SA1380	SAV1437	MW1326	amino acid ABC transporter, permease protein	Transport and binding proteins	Amino acids, peptides and amines	-3.96	-7.44	-9.65	-8.00	
WAN014GOK_at	12.1	36.2	3.3	2.2	1.8	SA2450	SA2234	SA2535	SA2237	SAV2445	MW2389	opuCD	amino acid ABC transporter, permease protein	Transport and binding proteins	Amino acids, peptides and amines	<b>3.00</b>	-3.64	-5.55	-6.64
WAN014HDG_at	12.8	1.7	3.9	3.1	3.9	SA1725	SA1761	SA1610	SA1610	SAV1681	MW1625	lysP	amino acid permease	Transport and binding proteins	Amino acids, peptides and amines	-7.62	-3.33	-4.15	-3.32
WAN014GON_at	3.5	12.0	1.1	0.7	1.3	SA2451	SA2235	SA2536	SA2234	SAV2446	MW2370	opuCC	amino acid transporter, putative	Transport and binding proteins	Amino acids, peptides and amines	3.42	-3.17	-4.72	-2.71
WAN014GPO_at	2.2	8.9	1.0	0.9	0.9	SA2150	SA2150	SA2150	SA2150	SAV2233	MW2233	opuCA	amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	-4.00	-3.00	-2.67	-2.76
WAN014GZC_at	54.4	2.0	25.1	26.1	23.5	SA1963	SA1718	SA1994	SA1923	SAV1922	MW1943	lysT	sensor histidine kinase	Signal transduction	Two-component systems	-2.69	-2.12	-2.01	-3.11
WAN014HA1_at	9.0	7.4	3.3	2.6	2.6	SA0750	SA0645	SA0743	SA0655	SAV0690	MW0652	anion transporter family protein	Transport and binding proteins	Anions	-1.22	-2.72	-3.50	-3.47	
WAN014BXAT_at	6.4	6.5	1.1	1.1	1.1	SA0516	SA0402	SA0407	SA0434	SAV074	MW0428	trep	PTS system component	Carbohydrates, organic alcohols, and acids	99.4	-5.73	-5.80	-3.98	
WAN014GZG_at	9.5	85.1	1.8	1.8	1.9	SA1962	SA2246	SA1989	SA2158	SAV2084	MW1844	mtBA	PTS system component	Carbohydrates, organic alcohols, and acids	<b>8.83</b>	-5.31	-5.21	-5.15	
WAN014HDF_at	8.5	1.1	1.4	1.4	2.0	SA1448	SA2231	SA2231	SA2231	SAV2231	MW1921	lysH	PTS system-specific IICB component	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	-2.42	-4.05	-5.59	-3.27
WAN014GZL_at	6.5	5.7	2.0	2.4	2.4	SA2514	SA2293	SA2582	SA2390	SAV2505	MW2423	GntF family permease	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	-1.16	-3.83	-3.34	-2.75	
WAN014ID3_at	90.4	37.1	33.1	28.4	27.1	SA0095	SA0106	SA0108	SA0108	SAV110	MW0093	lctP	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	-2.44	-2.73	-3.19	-3.33	
WAN014FVB_at	7.8	8.4	2.9	1.9	2.6	SA2316	SA2114	SA2408	SA2216	SAV2323	MW2244	glcV	PTS system component	Carbohydrates, organic alcohols, and acids	1.07	-2.70	-4.05	-3.00	
WAN014GFT_at	2.5	1.9	1.0	1.2	1.2	SA1904	SA2028	SA0103	SA0103	SAV0215	MW0191	malF	maltose ABC transporter, permease protein	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	-1.30	-2.56	-2.07	-2.00
WAN014GZL_at	6.5	23.1	2.7	3.7	3.7	SA0511	SA0491	SA0491	SA0491	SAV0491	MW0485	sgtA	SGt, sigma factor	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	<b>3.78</b>	-2.07	-3.40	-1.47
WAN014ISG_at	306.7	4.4	138.3	93.3	9.1	SA1901	SA0409	SA1056	SA1018	SAV1084	MW0985	psbH	phosphotransferase system enzyme II, glucose-specific, factor IIIB	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	-1.45	-2.23	-3.51	-3.42
WAN014GFQ_at	6.7	31.3	3.2	5.0	7.6	SA2663	SA2434	SA2720	SA2577	SAV2841	MW2562	lysH	PTS system, fructose-specific IICB component	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	<b>4.64</b>	-2.08	-3.44	<b>1.13</b>
WAN014GFL_at	0.8	0.6	0.4	0.4	0.8	SA1909	SA0208	SA0192	SA0192	SAV0216	MW1912	malG	maltose ABC transporter, permease protein	Transport and binding proteins	Cations	-1.42	-2.06	<b>1.08</b>	-1.08
WAN014TD1_at	4.3	14.9	2.6	2.1	2.1	SA1978	SA1732	SA2009	SA1840	SAV1916	MW1857	sodium-dependent transporter	Transport and binding proteins	Cations	-3.07	-7.34	-6.32	-5.57	
WAN014FYS2_at	6.2	2.8	1.4	1.3	2.0	SA1056	SA1063	SA1070	SA1043	SAV1688	MW1643	cation efflux family protein	Transport and binding proteins	Cations	-2.17	-4.27	-4.85	-3.06	
WAN014GK3_at	16.5	3.5	2.0	2.0	2.0	SA2404	SA2404	SA2404	SA2404	SAV1921	MW1921	ureH	ureH	Transport and binding proteins	Cations	-4.01	-4.77	-5.16	-5.16
WAN014T74_at	38.4	4.0	10.8	5.6	8.8	SA0685	SA0883	SA0883	SA0883	SAV0837	MW0837	NaV14+ antiporter component	Transport and binding proteins	Cations	9.59	-3.54	-6.91	-4.37	
WAN014MV_at	15.0	2.5	4.4	3.3	4.4	SA0680	SA0579	SA0631	SA0590	SAV0623	MW0586	NaV14+ antiporter component	Transport and binding proteins	Cations	-5.95	-3.41	-4.52	-3.04	
WAN014I1L_at	3.6	3.8	1.1	2.0	2.0	SA0311	SA0303	SA0311	SA0311	SAV0314	MW0291	sodium solute symporter family protein	Transport and binding proteins	Cations	<b>10.79</b>	-3.34	-1.80	<b>1.06</b>	
WAN014J76_at	27.2	2.8	8.2	4.2	6.3	SA0584	SA0584	SA0584	SA0584	SAV056	MW0584	NaV14+ antiporter component	Transport and binding proteins	Cations	-9.73	-3.32	-6.42	-4.29	
WAN014GZD_at	26.1	6.5	8.1	6.1	6.1	SA0511	SA0511	SA0511	SA0511	SAV0588	MW0588	MnHc	MnHc component	Transport and binding proteins	Cations	-3.07	-4.05	-4.04	-4.04
WAN014GZ2_at	13.3	1.9	2.1	2.8	4.9	SA0682	SA0881	SA0881	SA0882	SAV0529	MW0588	NaV14+ antiporter component	Transport and binding proteins	Cations	6.86	-3.22	-4.77	-2.72	
WAN014J72_at	5.7	1.2	1.9	1.2	2.2	SA0694	SA0692	SA0692	SA0693	SAV0626	MW0589	NaV14+ antiporter component	Transport and binding proteins	Cations	-4.75	-3.03	-4.78	-2.65	
WAN014MV_at	5.4	0.9	1.5	1.5	2.8	SA0681	SA0680	SA0680	SA0682	SAV0631	MW0587	NaV14+ antiporter component	Transport and binding proteins	Cations	-5.72	-2.82	-3.68	-1.95	
WAN014T79_at	51.3	28.5	19.1	15.4	25.4	SA0687	SA0687	SA0687	SA0687	SAV0629	MW0592	NaV14+ antiporter	Transport and binding proteins	Cations	-1.80	-2.69	-3.33	-2.21	
WAN014GZT_at	7.7	1.6	1.1	3.1	3.1	SA2292	SA2292	SA2292	SA2292	SAV2301	MW2219	molybdenum-binding protein	Transport and binding proteins	Cations	<b>1.48</b>	-2.50	-2.47	-2.51	
WAN014M1I_at	14.8	5.5	6.1	6.5	6.5	SA0516	SA0516	SA0516	SA0516	SAV0516	MW0516	NaV14+ antiporter	Transport and binding proteins	Cations	-2.46	-2.29	-2.49	-1.89	
WAN014M1L_at	3.2	3.3	1.4	1.4	1.6	SA2272	SA2272	SA2274	SA2274	SAV0274	MW0274	modA	modA	Transport and binding proteins	Cations	<b>1.66</b>	-2.32	-2.87	-1.99
WAN014GRB_at	52.0	72.7	23.6	26.9	29.4	SA0955	SA0914	SA0822	SA0822	SAV0824	MW0834	mmhA	glycine uptake nucleotide protein	Transport and binding proteins	Cations	1.40	-2.20	-1.93	<b>1.77</b>
WAN014GRB_at	8.2	10.0	3.8	3.8	3.8	SA1011	SA0593	SA0811	SA0820	SAV0850	MW0832	MnHc	MnHc component	Transport and binding proteins	Cations	1.21	-2.18	-2.27	-2.67
WAN014GTM_at	2.3	3.2	1.1	1.2	1.6	SA1084	SA0927	SA1049	SA1049	SAV1017	MW0985	cobalt transport protein	Transport and binding proteins	Cations	1.38	-2.16	-1.84	<b>1.40</b>	
WAN014GZL_at	10.1	4.1	1.8	1.8	1.8	SA0516	SA0516	SA0516	SA0516	SAV1394	MW1325	lentin family protein	Transport and binding proteins	Cations	-2.36	-6.07	-5.86	-5.86	
WAN014GZC_at	41.8	50.9	11.8	18.5	18.5	SA1952	SA1709	SA1984	SA1984	SAV1831	MW1834	lentin family protein	Transport and binding proteins	Cations	-1.49	-3.54	-2.27	-2.26	
WAN014GD2_at	2.3	2.6	0.8	0.8	0.8	SA0666	SA0567	SA0619	SA0578	SAV0510	MW0574	fecCD	iron compound ABC transporter, permease protein	Transport and binding proteins	Cations	1.15	-2.93	-2.83	-2.70
WAN014H6A_at	4.5	9.1	2.0	2.4	2.4	SA0666	SA0616	SA0616	SA0577	SAV0609	MW0573	iron compound ABC transporter, substrate-binding protein, putative	Transport and binding proteins	Cations	<b>2.01</b>	-2.28	-1.85	-1.82	
WAN014HCL_at	2.3	3.8	1.1	1.0	1.3	SA2020	SA0217	SA0217	SA0217	SAV0225	MW0220	afuA	iron compound ABC transporter, substrate-binding protein, putative	Transport and binding proteins	Cations	1.69	-2.06	-2.36	-1.79
WAN014GZG_at	99.4	18.0	18.0	18.0	18.0	SA0504	SA0504	SA0504	SA0504	SAV0509	MW0515	xanthine permease	Transport and binding proteins	Cations	-1.24	-5.51	-4.26	-2.51	
WAN014GZM_at	8.0	3.5	1.7	1.8	2.8	SA1475	SA1269	SA1448	SA1448	SAV1436	MW1432	glcP	glucitol uptake nucleotide protein	Transport and binding proteins	Cations	-2.36	-4.82	-4.56	-2.91
WAN014GZL_at	3.8	2.7	0.9	1.2	1.8	SA0303	SA0305	SA0304	SA0304	SAV0307	MW0284	acid phosphatase-nucleotide, lipoprotein e(P4) family	Transport and binding proteins	Other	<b>6.18</b>	-4.12	-3.24	-2.14	
WAN014H51_at	2.8	3.0	1.2	1.2	1.2	SA0407	SA0255	SA0255	SA0255	SAV0289	MW0281	transporter, ATP-binding/protease	Transport and binding proteins	Other	<b>3.82</b>	-3.81	-2.05	-1.42	
WAN014H45_at	24.8	12.4	9.0	6.5	9.5	SA0745	SA0605	SA0605	SA0605	SAV0643	MW0605	abcA	ABC transporter, ATP-binding/protease	Transport and binding proteins	Other	-2.00	-2.75	-3.79	-4.17
WAN014H45_at																			

Fold change vs stationary phase

Systematic	Stat.	Log	30'	120'	360'	COL	N315	MRSA	MSSA	Mu50	MW2	GENE NAME	Protein Function		TIGR Main Role	TIGR Sub Role	Fold change vs stationary phase			
													30' in vivo	120' in vivo	360' in vivo	L8	30' in vivo	120' in vivo	360' in vivo	
WAN014HN1_at	81.4	15.3	16.9	17.4	35.3	SA0111	SA0122	SAR0129	SAS0101	SAV0126	MW1900	butA	oxidoreductase, short-chain dehydrogenase/reductase family	Unknown function	Enzymes of unknown specificity	General	-5.33	-4.82	-4.67	-2.31
WAN014G30_at	16.8	8.3	3.9	4.3	4.0	SA2021	SA1841	SAR2121	SAS1940	SAV2034	MW1988	carbon-nitrogen hydrolase family protein	Unknown function	Enzymes of unknown specificity	General	-2.02	-4.28	-3.92	-4.25	
WAN014H3A_at	7.2	11.3	1.9	1.7	2.3	SA0602	SA0513	SAR0560	SAS0513	SAV0555	MW0510	gph	hydrolase, haloacid dehalogenase-like family	Unknown function	Enzymes of unknown specificity	General	1.56	-3.71	-4.32	-3.21
WAN014H1U_at	5.2	4.8	1.5	1.5	2.4	SA0569	SA0582	SAR0527	SAS0485	SAV0524	MW0479	ATP:guano disphosphotransferase family protein	Unknown function	Enzymes of unknown specificity	General	-1.09	-3.50	-3.38	-2.19	
WAN014GLU_at	6.5	1.2	1.9	1.3	1.8	SA0396	SA0395	SAR0325	SAS0395	SAV0305	MW0305	oxidoreductase, putative	Unknown function	Enzymes of unknown specificity	General	-5.42	-3.46	-5.05	-3.62	
WAN014H1C_at	2.7	2.3	0.4	0.9	0.9	SA0687	SA0688	SAR0687	SAS0578	SAV0611	MW0573	hydrolase, ester	Unknown function	Enzymes of unknown specificity	General	1.03	-3.45	-2.90	-2.00	
WAN014HQJ_at	2.2	2.1	0.7	0.6	0.6	SA1048	SA0983	SAR1014	SAS0978	SAV0104	MW1040	acetyltransferase, GNAT family	Unknown function	Enzymes of unknown specificity	General	-1.07	-3.29	-3.86	-2.07	
WAN014H50_at	6.0	6.8	2.0	1.9	1.6	SA0655	SA0557	SAR0608	SAS0568	SAV0600	MW0563	oxidoreductase, aldo/keto reductase 2 family	Unknown function	Enzymes of unknown specificity	General	1.14	-3.01	-3.05	-3.70	
WAN014H3E_at	4.5	5.0	1.5	1.5	1.5	SA0606	SA0517	SAR0564	SAS0517	SAV0559	MW0514	hydrolase, haloacid dehalogenase-like family	Unknown function	Enzymes of unknown specificity	General	1.10	-2.97	-2.95	-3.05	
WAN014H9O_at	3.5	0.8	1.2	1.0	1.0	SA0735	SA0534	SAR0642	SAS0642	SAV0679	MW0511	acetyltransferase, GNAT family	Unknown function	Enzymes of unknown specificity	General	-4.39	-2.95	-3.72	-3.49	
WAN014H4F_at	14.0	3.5	3.5	3.1	4.1	SA0643	SA0643	SAR0235	SAS0242	SAV2230	MW0230	NAD(P)H:quinone oxidoreductase dehydrogenase family protein	Unknown function	Enzymes of unknown specificity	General	-3.00	-2.94	-3.44	-3.44	
WAN014H6I_at	2.5	2.7	0.9	0.8	0.9	SA0668	SA0569	SAR0621	SAS0580	SAV0812	MW0576	hydrolase, alpha/beta fold family	Unknown function	Enzymes of unknown specificity	General	1.05	-2.78	-3.11	-2.76	
WAN014G75_at	6.9	2.9	2.5	1.7	2.4	SA2575	SA2247	SAR2641	SAS2446	SAV2260	MW2481	amino transferase, class I	Unknown function	Enzymes of unknown specificity	General	-2.37	-2.78	-4.03	-2.92	
WAN014H38_at	4.2	5.5	1.5	1.3	1.9	SA1545	SA1333	SAR1578	SAS1442	SAV1502	MW1456	oxidoreductase, short-chain dehydrogenase/reductase family	Unknown function	Enzymes of unknown specificity	General	1.30	-2.75	-3.20	-2.26	
WAN014GV_G_at	13.3	3.7	4.9	4.8	4.3	SA1186	SA1019	SAR1152	SAS1110	SAV1176	MW1059	acetyltransferase, GNAT family	Unknown function	Enzymes of unknown specificity	General	-3.57	-2.74	-2.76	-3.12	
WAN014H39_at	1.9	1.4	0.4	0.4	0.4	SA1187	SA1020	SAR1153	SAS1111	SAV1175	MW1058	oxidoreductase, short-chain dehydrogenase/reductase family	Unknown function	Enzymes of unknown specificity	General	-1.20	-2.62	-2.62	-2.00	
WAN014GCO_at	30.1	10.1	11.8	6.0	7.4	SA2532	SA2309	SAR2601	SAS2406	SAV2521	MW2441	acetyltransferase, GNAT family	Unknown function	Enzymes of unknown specificity	General	-1.65	-2.55	-2.62	-4.08	
WAN014G6L_at	6.6	7.4	2.7	3.0	2.4	SA2245	SA2052	SAR2340	SAS2146	SAV2255	MW2174	acetyltransferase, GNAT family	Unknown function	Enzymes of unknown specificity	General	1.11	-2.47	-2.18	-2.70	
WAN014H9D_at	11.2	10.5	4.7	3.9	3.7	SA0827	SA0717	SAR0816	SAS0727	SAV0762	MW0724	acetyltransferase, putative	Unknown function	Enzymes of unknown specificity	General	-1.07	-2.40	-2.86	-3.05	
WAN014BQMM_at	23.8	6.0	10.1	6.6	7.0	SA2368	SA2460	SAR2460	SAS2460	SAV2395	MW2231	acetyltransferase, GNAT family	Unknown function	Enzymes of unknown specificity	General	-3.94	-2.35	-3.60	-3.38	
WAN014H3U_at	2.8	1.8	1.3	1.1	1.3	SA2104	SA2104	SAR1645	SAS1506	SAV1568	MW1520	cdd	inositol monophosphate family protein	Unknown function	Enzymes of unknown specificity	General	-1.65	-2.27	-2.65	-2.27
WAN014GZ2_at	8.0	6.5	3.0	3.0	3.0	SA2368	SA2368	SAR2368	SAS2368	SAV2368	MW2368	cystidine and deoxyuridine deaminase family protein	Unknown function	Enzymes of unknown specificity	General	-1.24	-2.40	-2.70	-2.27	
WAN014H7L_at	19.2	18.1	9.2	7.2	8.1	SA1625	SA1397	SAR1645	SAS1506	SAV1568	MW1726	oxidoreductase, aldo/keto reductase family	Unknown function	Enzymes of unknown specificity	General	-1.06	-2.09	-2.69	-2.38	
WAN014H4UT_at	6.7	6.0	3.3	2.4	2.3	SA1833	SA1606	SAR1868	SAS1709	SAV1788	MW1726	hydrolase, alpha/beta fold family	Unknown function	Enzymes of unknown specificity	General	-1.13	-2.05	-2.84	-2.92	
WAN014H6P_at	8.1	4.0	2.6	4.1	SA0671	SA0572	SAR0624	SAS0583	SAV0615	MW0579	hemolysin, putative	Unknown function	Enzymes of unknown specificity	General	-2.02	-3.14	-1.98	-1.98		
WAN014HYD_at	3.2	2.3	1.6	1.3	1.9	SA1186	SA1019	SAR1151	SAS1109	SAV1175	MW1058	hydrolase, haloacid dehalogenase-like family	Unknown function	Enzymes of unknown specificity	General	-1.37	-1.99	-2.46	-1.65	
WAN014H3D_at	40.1	13.5	4.2	3.7	3.5	SA2243	SA2140	SAR2258	SAS2258	SAV2358	MW2358	immunodominant antigen B	Unknown function	Enzymes of unknown specificity	General	-3.00	-9.55	-10.00	-7.70	
WAN014C26_at	16.3	1.5	2.0	2.0	3.0	SA2494	SA2482	SAR2561	SAS2395	SAV2474	MW2498	aliphatic/aromatic AhpD family	Unknown function	Enzymes of unknown specificity	General	-2.07	-5.93	-8.22	-5.45	
WAN014GP2_at	3.4	6.0	0.6	0.5	1.2	SA0313	SA0305	SAR0213	SAS0293	SAV3016	MW0293	R0X family protein	Unknown function	Enzymes of unknown specificity	General	1.77	-5.27	-6.32	-2.90	
WAN014HQ2_at	10.8	14.3	21.9	14.5	16.1	SA1933	SA1692	SAR1965	SAS1797	SAV1875	MW1815	ThiU/Ppi family protein	Unknown function	Enzymes of unknown specificity	General	-7.73	-5.06	-7.64	-6.88	
WAN014V3_at	6.1	1.8	1.5	1.4	1.4	SA0410	SA0328	SAR0316	SAS0340	SAV0340	MW0316	FMN reductase-related protein	Unknown function	Enzymes of unknown specificity	General	-3.42	-4.10	-4.34	-4.24	
WAN014GU_G_at	3.5	1.0	1.0	1.0	1.3	SA0406	SA0326	SAR0334	SAS0314	SAV0338	MW0314	glyoxalase family protein	Unknown function	Enzymes of unknown specificity	General	-3.65	-3.65	-3.41	-2.77	
WAN014H3Q_at	103.0	40.0	26.0	20.0	30.0	SA0648	SA0648	SAR0575	SAS0529	SAV0571	MW0526	SIS3 domain protein	Unknown function	Enzymes of unknown specificity	General	2.48	-3.50	-3.50	-3.52	
WAN014GB5_at	4.7	4.4	1.4	1.1	1.5	SA2602	SA2372	SAR2602	SAS2372	SAV2372	MW2372	chromosome assembly protein homolog, putative	Unknown function	Enzymes of unknown specificity	General	-1.06	-3.33	-4.29	-3.06	
WAN014H1G_at	4.1	1.3	1.4	0.9	1.2	SA0921	SA0780	SAR0882	SAS0790	SAV0019	MW0802	hemolysin, putative	Unknown function	Enzymes of unknown specificity	General	-3.13	-2.93	-4.64	-3.44	
WAN014JH1_at	3.0	4.3	1.1	1.2	1.1	SA0931	SA0790	SAR0891	SAS0799	SAV0929	MW0811	p-nitrophenyl phosphatase	Unknown function	Enzymes of unknown specificity	General	1.42	-2.63	-2.47	-2.76	
WAN014H7S_at	6.7	4.1	2.7	2.3	2.6	SA1628	SA1400	SAR1648	SAS1509	SAV1571	MW1523	phoH family protein	Unknown function	Enzymes of unknown specificity	General	-1.63	-2.46	-2.91	-2.54	
WAN014H3K_at	53.0	45.5	22.5	17.8	19.7	SA1628	SA1400	SAR1648	SAS1509	SAV1571	MW1523	N-acetylmuramyl-L-alanine amidase domain protein	Unknown function	Enzymes of unknown specificity	General	-1.20	-2.37	-3.00	-2.69	
WAN014GOU_at	2.2	1.6	1.1	1.1	1.3	SA1894	SA1656	SAR1629	SAS1789	SAV1838	MW1778	HIT family protein	Unknown function	Enzymes of unknown specificity	General	-1.22	-2.38	-2.04	-1.62	
WAN014HSS_at	2.2	3.7	0.9	1.0	1.1	SA0657	SA0559	SAR0610	SAS0570	SAV0602	MW0565	protease synthase and sporulation negative regulatory protein paf 1, putative	Unknown function	Enzymes of unknown specificity	General	1.66	-2.36	-2.14	-1.95	
WAN014H6J_at	2.0	1.6	0.9	0.8	0.8	SA1607	SA1380	SAR1627	SAS1488	SAV1550	MW1502	5-formyltetrahydrofolate cyclo-ligase family protein	Unknown function	Enzymes of unknown specificity	General	-1.27	-2.29	-2.43	-2.63	
WAN014GZ2_at	11.6	10.5	5.1	3.9	4.3	SA1467	SA1258	SAR1438	SAS1368	SAV1425	MW1315	degV family protein	Unknown function	Enzymes of unknown specificity	General	-1.11	-2.28	-2.96	-2.69	
WAN014H5WV_at	9.1	15.0	4.2	3.3	3.6	SA0406	SA0395	SAR0406	SAS0393	SAV0403	MW1303	HD domain protein	Unknown function	Enzymes of unknown specificity	General	1.59	-2.25	-2.77	-2.45	
WAN014H4C_at	12.2	10.0	3.0	3.7	4.8	SA0222	SA0202	SAR0201	SAS0201	SAV0201	MW0201	ydcD	Unknown function	Enzymes of unknown specificity	General	1.09	-2.19	-3.33	-2.55	
WAN014GZ2_at	106.8	15.8	51.1	25.2	23.0	SA0541	SA0456	SAR0499	SAS0455	SAV0498	MW0453	spvG	stage V population protein G	Unknown function	General	-6.75	-2.09	-4.23	-4.65	
WAN014HLJ_at	116.7	113.4	57.9	50.8	48.7	SA0977	SA0833	SAR0935	SAS0842	SAV0972	MW0854	mrp protein homolog	Unknown function	Enzymes of unknown specificity	General	-1.03	-2.02	-2.30	-2.40	