

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
WANO14FVH_at	0.9	7.6	4.3	3.7	SA1407	SA1203	SAR1384	SAS1311	SAV1371	MW1258	trpF	N-(Glyosphoribosyl)-anthranilate isomerase	Amino acid biosynthesis	Aromatic amino acid family	1.14	23.44	10.03	7.35	
WANO14FVL_at	1.9	2.2	44.4	19.0	13.9	SA1409	SA1205	SAR1386	SAS1313	SAV1373	MW1260	trpA	tryptophan synthase, alpha subunit	Amino acid biosynthesis	Aromatic amino acid family	-1.09	16.42	7.73	6.46
WANO14FVJ_at	1.4	1.3	22.8	10.7	8.9	SA1408	SA1204	SAR1385	SAS1312	SAV1372	MW1259	trpB	tryptophan synthase, beta subunit	Amino acid biosynthesis	Aromatic amino acid family	1.17	2.67	2.54	2.29
WANO14GCV_at	1.4	1.6	3.6	3.4	3.1	SA1428	SA0345	SAR0354	SAS0333	SAV0357	MW0333	metE2	homocysteine S-methyltransferase	Amino acid biosynthesis	Aspartate family	1.22	2.44	5.76	4.85
WANO14GCQ_at	1.3	2.0	3.9	9.3	3.7	SA1428	SA0325	SAR0326	SAS0333	SAV0393	MW1228	lysC	arginyl ester, monooxygenase class, putative	Amino acid biosynthesis	Aspartate family	1.36	2.92	2.10	3.73
WANO14GZ4_at	2.5	3.9	5.2	3.2	3.8	SA0345	SAR0353	SAR0352	SAS0322	SAV0293	MW0322	lysE	S- methylethanolamine-monooxygutamate-homocysteine methyltransferase	Amino acid biosynthesis	Aspartate family				
WANO14GRK_at	0.9	3.9	5.1	6.7	SA0964	SA0822	SAR0923	SAS0831	SAV0961	MW0843	argG	arginosuccinate synthase	Amino acid biosynthesis	Glutamate family					
WANO14GYD_at	3.0	1.6	28.18	236.8	105.6	SA0515	SA0431	SAR0472	SAS0430	SAV0473	MW0427	gltD	glutamate synthase, small subunit	Amino acid biosynthesis	Glutamate family	-1.85	93.27	78.39	34.96
WANO14GYA_at	2.3	1.7	116.1	114.9	56.2	SA0514	SA0430	SAR0473	SAS0429	SAV0472	MW0426	gltB	glutamate synthase, large subunit	Amino acid biosynthesis	Glutamate family	-1.39	49.52	49.00	23.97
WANO14GRH_at	1.1	1.1	7.7	13.0	SA0953	SA0822	SAR0922	SAS0830	SAV0960	MW0842	argH	arginyl ester lyase	Amino acid biosynthesis	Glutamate family	1.04	7.03	9.92	11.87	
WANO14GZ5_at	1.0	1.0	2.2	2.2	1.4	SA2701	SA2469	SAR2760	SAS2563	SAV2678	MW2597	hisC2	bistinol-phosphate aminotransferase, putative	Amino acid biosynthesis	Histidine family				
WANO14GD7_at	1.1	8.4	5.5	2.6	SA2700	SA2468	SAR2758	SAS2561	SAV2676	MW2595	hisB	imidazoglycerol-phosphate dehydratase	Amino acid biosynthesis	Histidine family					
WANO14GDS_at	7.0	7.0	5.0	2.5	SA2699	SA2467	SAR2757	SAS2560	SAV2675	MW2594	hisD	amidotransferase HisH	Amino acid biosynthesis	Histidine family					
WANO14I05_at	1.6	12.6	68.6	37.2	5.2	SA2696	SA2464	SAR2754	SAS2557	SAV2672	MW2591	hisF	phosphotribo-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase	Amino acid biosynthesis	Histidine family	-1.34	42.40	23.02	9.39
WANO14GZ6_at	1.5	18.0	13.4	1.5	1.5	SA2697	SA2465	SAR2755	SAS2558	SAV2674	MW2593	hisG	imidazoglycerol-phosphate, cyclase subunit	Amino acid biosynthesis	Histidine family	12.10	8.67	5.14	
WANO14GD5_at	1.0	0.8	7.7	5.1	2.3	SA2698	SA2466	SAR2756	SAS2559	SAV2674	MW2593	ATP phosphoribosyltransferase	Amino acid biosynthesis	Histidine family	-1.13	8.11	5.32	2.07	
WANO14GDF_at	1.3	4.1	2.7	1.6	SA2704	SA2472	SAR2762	SAS2565	SAV2680	MW2599	ATP	ATP phosphoribosyltransferase	Amino acid biosynthesis	Histidine family	3.28	2.14	1.25		
WANO14GDC_at	0.7	1.9	1.2	0.9	SA2703	SA2471	SAR2761	SAS2564	SAV2679	MW2598	ATP	ATP phosphoribosyltransferase	Amino acid biosynthesis	Histidine family	2.54	1.56	1.19		
WANO14G41_at	31.0	21.7	11.5	SA2042	SA1865	SAR1247	SAS1965	SAV2060	MW1984	leuD	3-isopropylmalate dehydratase, small subunit	Amino acid biosynthesis	Pyruvate family						
WANO14G44_at	1.3	0.9	33.5	37.2	18.1	SA1864	SA1860	SAR1248	SAS1963	SAV2059	MW1979	leuB	3-isopropylmalate dehydratase, large subunit	Amino acid biosynthesis	Pyruvate family	-1.52	40.09	32.19	17.94
WANO14G45_at	1.2	0.8	40.0	33.6	15.0	SA2043	SA1864	SAR1249	SAS1964	SAV2060	MW1983	leuC	isopropylmalate dehydratase, large subunit	Amino acid biosynthesis	Pyruvate family	34.76	32.11	18.53	
WANO14G46_at	1.6	54.1	50.0	28.9	SA2046	SA1862	SAR1244	SAS1962	SAV2057	MW1981	leuA	2-isopropylmalate synthase	Amino acid biosynthesis	Pyruvate family	33.46	26.37	16.76		
WANO14G4M_at	1.0	33.0	26.0	16.5	SA2050	SA1866	SAR1248	SAS1966	SAV2061	MW1985	leuB	threonine dehydratase, biosynthetic, putative	Amino acid biosynthesis	Pyruvate family	-1.29	31.68	27.71	16.14	
WANO14G40_at	2.7	21.1	86.8	75.9	4.4	SA2042	SA1859	SAR1241	SAS1959	SAV1978	MW1978	lelB	acetolactate synthase, large subunit, biosynthetic type	Amino acid biosynthesis	Pyruvate family	-1.44	26.34	25.70	14.23
WANO14G41_at	1.3	0.9	33.5	37.2	18.1	SA1861	SA1860	SAR1245	SAS1963	SAV1979	MW1979	leuB	acetolactate synthase, small subunit	Amino acid biosynthesis	Pyruvate family	-1.52	40.09	32.19	17.94
WANO14G43_at	1.5	3.5	37.2	36.7	1.6	SA2041	SA1860	SAR1245	SAS1963	SAV1979	MW1979	leuB	3-isopropylmalate dehydratase	Amino acid biosynthesis	Pyruvate family	34.76	32.11	18.53	
WANO14G31_at	3.9	14.4	72.7	65.5	39.9	SA2058	SA1859	SAR1240	SAS1968	SAV2053	MW1977	ldh	3-isopropylmalate dehydratase	Amino acid biosynthesis	Pyruvate family	-2.71	16.85	15.00	10.34
WANO14EY2_at	3.3	3.5	13.3	14.6	10.1	SA1772	SA1544	SAR1800	SAS1749	SAV1723	MW1665	serC	ammonium transcarbamoylase, class V	Amino acid biosynthesis	Seine family	1.07	4.02	4.42	3.07
WANO14EY5_at	5.2	7.1	19.3	19.3	1.7	SA1773	SA1545	SAR1801	SAS1650	SAV1724	MW1666	serA	D-3-phosphoglycerate dehydrogenase	Amino acid biosynthesis	Seine family	1.38	3.74	3.74	2.85
WANO14GXQ_at	1.2	14.0	3.8	2.2	3.2	SA2050	SA1862	SAR1849	SAS0419	SAV0460	MW0415	metB	trans-Sulfururase enzyme family protein	Amino acid biosynthesis	Seine family	12.15	3.34	8.89	2.13
WANO14G3D_at	1.8	3.4	4.7	4.3	3.7	SA1436	SA2046	SAR0355	SAS0334	SAV0358	MW0334	metB	trans-Sulfururase enzyme family protein	Amino acid biosynthesis	Seine family	1.37	2.66	2.46	2.10
WANO14GZ1_at	1.8	3.2	11.7	7.4	5.6	SA2082	SA1898	SAR1219	SAS1999	SAV2095	MW2020	sceB	panthenate kinase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Folate	3.00	2.30	2.93	
WANO14FZ2_at	2.9	9.5	132.6	24.5	2.2	SA2032	SA2329	SAR1200	SAS2059	SAV2055	MW2055	thiL	thiostreptose biosynthesis protein ThiL	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin	1.18	3.57	2.24	1.47
WANO14HR2_at	1.4	2.4	3.4	2.9	3.0	SA1950	SA1707	SAR1982	SAS1813	SAV1891	MW1832	cobQ	cobacyl acid synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin	1.77	2.46	2.09	2.18
WANO14GXA_at	2.0	1.1	4.6	3.4	4.3	SA0491	SA0450	SAR2704	SAS0450	SAV0450	MW0406	pepC	cobalamin synthesis protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Biosynthesis and degradation of murein saccus and peptidoglycan	-1.88	2.32	1.70	2.14
WANO14G83_at	0.8	0.9	1.6	1.4	1.3	SA2958	SA2668	SAR2560	SAS2459	SAV2562	MW2502	pepC	cobalamin synthesis protein, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Biosynthesis and degradation of murein saccus and peptidoglycan	1.13	2.09	1.85	1.72
WANO14GZ7_at	9.0	2.5	2.8	6.5	3.8	SA2771	SA0666	SAR0764	SAS0676	SAV1071	MW1073	pepB	4-pyruvyl tetrahydrodioxazine synthase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	2.29	2.63	2.08	2.78
WANO14GZ8_at	9.1	2.5	19.7	13.2	18.4	SA2561	SA2334	SAR2266	SAS2242	SAV2218	MW2210	pepC	6-pyruvyl tetrahydrodioxazine synthase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	1.84	4.23	3.16	3.25
WANO14G5C_at	8.4	10.7	38.3	31.2	28.4	SA2122	SA1932	SAR2218	SAS2120	SAV2120	MW2154	pepA	hydroxydipospho-glycerate-CoA synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	2.28	2.23	2.18	1.62
WANO14ZS5_at	1.8	1.4	11.7	7.4	5.4	SA2082	SA1998	SAR1979	SAS1969	SAV1975	MW1961	pepC	panthothenate kinase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	1.21	3.74	3.74	2.03
WANO14GZ6_at	3.8	4.9	12.0	9.3	9.1	SA1626	SA0598	SAR0602	SAS0608	SAV0642	MW0604	pbp4	peptidoglycan hydrolase	Biosynthesis of murein saccus and peptidoglycan	Biosynthesis and degradation of murein saccus and peptidoglycan	2.46	2.53	2.25	1.95
WANO14GZ7_at	3.4	4.4	8.5	8.6	6.5	SA1944	SA1154	SAR1157	SAS1151	SAV1181	MW1184	pbp1	penicillin binding protein 1	Biosynthesis of murein saccus and peptidoglycan	Biosynthesis and degradation of murein saccus and peptidoglycan	4.99	17.52	17.81	18.30
WANO14GZ7P_at	42.9	21.7	35.9	76.3	74.1	SA2584	SA2256	SAR2650	SAS2459	SAV2569	MW2490	isaA	immunodominant antigen A	Other	Other	2.75	5.97	5.75	5.47
WANO14LTL_at	1.9	5.2	11.3	10.3	10.3	SA2070	SA0684	SAR0783	SAS0783	SAV0729	MW0691	ldhB	integral membrane domain protein	Cell envelope	Cell envelope	1.77	5.61	4.43	4.41
WANO14HYM_at	8.0	14.0	44.6	35.2	35.2	SA2083	SA1979	SAR1979	SAS1994	SAV2090	MW2013	yidC	membrane protein, putative	Cell envelope	Cell envelope	3.25	2.97	2.87	3.01
WANO14FZP_at	1.1	3.6	3.7	3.7	3.7	SA2074	SA1978	SAR1978	SAS1978	SAV2074	MW2074	pepC	peptidoglycan hydrolase	Cell envelope	Cell envelope	9.04	4.11	3.63	3.67
WANO14FZT_at	28.8	26.0	105.9	87.1	10.3	SA0861	SA0747	SAR0848	SAS0747	SAV0716	MW0770	pepC	peptidoglycan hydrolase	Cell envelope	Cell envelope	1.03	10.87	14.13	11.24
WANO14GFX_at	63.5	65.1	69.6	87.3	74.3	SA2731	SA2494	SAR2709	SAS2567	SAV2704	MW2623	pepC	cold-shock protein CspB	Cellular processes	Cellular processes	-2.35	3.13	3.51	2.85
WANO14HER_at	35.6	15.1	111.2	124.0	101.3	SA2071	SA1861	SAR2073	SAS2497	SAV2612	MW2531	beta	low temperature requirement protein LtrA	Cellular processes	Cellular processes	4.45	2.79	3.26	2.62
WANO14GOM_at	3.5	3.4	9.7	11.3	9.1	SA2405	SA0341	SAR0350	SAS0329	SAV0353	MW0329	ldtA	similar to S	Cellular processes	Cellular processes	2.44	-1.06	-2.06	-2.06
WANO14GZ1_at	1.0	1.1	2.2	1.7	1.7	SA2405	SA2406	SAR2409	SAS2497	SAV2612	MW2531	ansC	aromatic resistance protein	Cellular processes	Cellular processes	-1.47	2.96	1.34	1.04
WANO14T2Z_at	6.3	22.8	23.6	21.0	2.2	SA1807	SA1808	SAR1247	SAS1241	SAV1577	MW1577	ldhD	detoxification	Cellular processes	Cellular processes	3.63	3.74	3.24	3.05
WANO14GFD_at	1.6	2.0	4.5	4.3	3.4	SA2713	SA2481	SAR2771	SAS2575	SAV2689	MW2609	ldh	detoxification	Cellular processes	Cellular processes	1.25	2.79	2.67	2.14
WANO14FZB_at	3.2	3.7	7.4	6.4</															

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	
WAN0141C4_at	16.3	29.7	61.1	48.1	48.9	SA1240	SA1069	SA1202	SA1160	SAV1226	MW1109	conserved hypothetical protein	Energy metabolism	Other	1.82	3.75	2.95	3.00		
WAN0141C4_at	4.9	5.3	10.4	7.3	9.0	SA0805	SA0697	SA0796	SA0707	SAV0742	MW0704	glycerate kinase family protein	Energy metabolism	Other	1.08	2.13	1.49	1.85		
WAN0141H4G_at	12.9	30.9	27.0	24.4	25.6	SA1571	SA1357	SA1604	SA1465	SAV1526	MW1479	acetyl-CoA carboxylase, biotin carboxylase	Fatty acid and phospholipid metabolism	Conserved	2.41	2.10	1.90	2.07		
WAN0141H4H_at	5.3	16.3	76.1	80.0	85.2	SA1136	SA0975	SA1100	SA1061	SAV1127	MW1009	conserved hypothetical protein	Hypothetical proteins	Conserved	3.06	14.70	15.05	16.03		
WAN0141H4I_at	29.4	60.0	253.3	247.0	322.0	SA1372	SA1372	SA1372	SA1372	SAV1372	MW1372	conserved hypothetical protein	Hypothetical proteins	Conserved	2.18	8.62	8.29	11.04		
WAN0141H4L_at	4.5	8.2	22.9	21.0	18.6	SA1380	SA1380	SA1355	SA1384	SAV1344	MW1331	conserved hypothetical protein	Hypothetical proteins	Conserved	1.86	5.71	4.04	4.11		
WAN0141H4T_at	4.1	5.5	22.9	24.1	17.3	SA0639	SA0550	SA0550	SA0552	SAV0593	MW0548	conserved hypothetical protein	Hypothetical proteins	Conserved	1.35	5.59	5.89	4.23		
WAN0142D2_at	1.3	6.7	7.5	5.9	SA2477	SA2256	SA2255	SA2393	SAV2468	MW2392	conserved hypothetical protein	Hypothetical proteins	Conserved	5.27	5.93	4.64				
WAN0142G2_at	1.8	8.6	8.7	7.2	SA2474	SA2257	SA2256	SA2360	SAV2469	MW2393	conserved hypothetical protein	Hypothetical proteins	Conserved	4.74	4.76	3.99				
WAN0142G7_at	2.5	7.0	10.5	9.8	8.8	SA2478	SA2258	SA2258	SA2361	SAV2470	MW2394	Membrane protein	Hypothetical proteins	Conserved	2.80	4.22	3.87	3.55		
WAN0142H1_at	1.8	7.5	5.8	6.2	SA2479	SA2259	SA2257	SA2361	SAV2471	MW2394	conserved hypothetical protein	Hypothetical proteins	Conserved	4.16	3.77	3.42				
WAN0142F4C_at	6.7	17.1	26.5	17.7	12.3	SA2371	SA2163	SA2462	SA2285	SAV2373	MW2295	conserved hypothetical protein	Hypothetical proteins	Conserved	2.53	3.93	2.62	1.82		
WAN0142GJN_at	3.5	8.9	13.4	11.5	12.0	SA0752	SA0746	SA0746	SA0658	SAV0893	MW0655	conserved hypothetical protein	Hypothetical proteins	Conserved	2.53	3.82	3.28	3.42		
WAN0142PH_at	4.7	5.8	15.4	12.2	11.7	SA1925	SA1984	SA1957	SA1789	SAV1867	MW1807	conserved hypothetical protein	Hypothetical proteins	Conserved	1.24	3.29	2.61	2.50		
WAN0142F6_at	3.1	5.1	8.0	7.1	8.8	SA1763	SA1536	SA1912	SA1641	SAV1714	MW1657	conserved hypothetical protein	Hypothetical proteins	Conserved	1.61	2.55	2.25	2.80		
WAN0142H4T_at	2.9	7.1	18.5	20.1	17.3	SA1764	SA1537	SA1912	SA1641	SAV1715	MW1658	conserved hypothetical protein	Hypothetical proteins	Conserved	1.26	2.41	2.68	1.73		
WAN0142D9_at	3.6	5.7	5.0	8.0	8.4	SA1501	SA1294	SA1472	SA1404	SAV1481	MW1351	conserved hypothetical protein	Hypothetical proteins	Conserved	1.23	2.22	1.76			
WAN0142B28_at	12.3	2.0	27.0	26.1	26.0	SA1526	SA1416	SA1425	SA1485	SAV1373	MW1373	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.54	2.19	2.11	2.11		
WAN0142FUX_at	4.0	14.1	8.2	8.8	8.8	SA2306	SA2106	SA2397	SA2213	SAV2263	MW2234	aberrate infection protein family	Hypothetical proteins	Conserved	3.56	2.08	2.22			
WAN0142WQ_at	1.6	2.5	3.3	2.2	2.6	SA2052	SA1867	SA2150	SA1967	SAV2062	MW1986	sprt protein, putative	Hypothetical proteins	Conserved	1.55	2.06	1.40	1.67		
WAN0142H4P_at	4.7	3.8	9.4	7.3	11.1	SA1286	SA1110	SA2143	SA2143	SAV2161	MW2167	SAV2165	conserved hypothetical protein	Hypothetical proteins	Conserved	-1.24	2.02	1.68	2.38	
WAN0142H4V_at	0.9	0.8	0.9	0.0	0.0	SA1761	SA1761	SA1761	SA1761	SAV1761	MW1761	hypothetical protein	Hypothetical proteins	Not Conserved	-1.63	7.14	9.24	11.00		
WAN0142H4G_at	11.0	28.4	62.3	53.7	48.2	SA1276	SA1455	SA1386	SA1443	SAV1443	MW1332	hypothetical protein	Hypothetical proteins	Not Conserved	2.39	5.64	5.31	4.46		
WAN0142GCY_at	1.3	6.5	6.5	6.1	2.5	SA2693	SA1482	SA1276	SA1455	SAV1455	MW1455	hypothetical protein	Hypothetical proteins	Not Conserved	4.90	4.61	1.88			
WAN0142BQGT_at	7.7	8.5	30.1	26.8	19.9	SA2152	SA2259	SA2069	SAV167	SAV2167	MW2094	sepA	hypothetical protein	hypothetical proteins	Not Conserved	1.10	3.90	3.70	2.58	
WAN0142GF_at	5.1	8.9	15.2	11.9	11.9	SA1761	SA1264	SA2122	SAV1288	SAV2128	MW1171	hypothetical protein	Hypothetical proteins	Not Conserved	1.75	2.98	3.10	2.33		
WAN0142B4P_at	1.9	0.9	3.5	3.8	3.8	SA1761	SA1264	SA2122	SAV1288	SAV2128	MW1171	hypothetical protein	Hypothetical proteins	Not Conserved	-1.45	2.85	2.60	2.39		
WAN0142BPD_at	17.6	1.7	47.5	47.5	63.3	SA2480	SA1440	SA1440	SA1440	SAV1440	MW1440	hypothetical protein	Hypothetical proteins	Not Conserved	-10.21	2.70	4.97	3.00		
WAN0142GNZ_at	3.4	3.9	8.0	7.1	6.6	SA0769	SA0664	SA0762	SA0764	SAV0709	MW0671	hypothetical protein	Hypothetical proteins	Not Conserved	1.16	2.35	2.08	1.94		
WAN0142TR_at	5.2	12.5	11.1	11.7	12.5	SA1376	SA1178	SA1353	SA1343	SAV1343	MW1230	hypothetical protein	Hypothetical proteins	Conserved	2.40	2.31	2.25	2.38		
WAN0142I1T_at	27.7	38.8	85.4	101.0	66.6	SA2134	SA1944	SA2230	SA2045	SAV2142	MW2066	hypothetical protein	Hypothetical proteins	Not Conserved	1.96	2.27	2.68	1.77		
WAN0142FTT_at	2.6	6.5	6.5	6.5	6.5	SA1374	SA1374	SA1374	SA1374	SAV1374	MW1374	hypothetical protein	Hypothetical proteins	Not Conserved	2.55	2.23	2.53	2.92		
WAN0142H4P_at	1.4	4.5	3.3	3.3	3.3	SA0948	SA0806	SA0907	SA0815	SAV0845	MW0827	hypothetical protein	Hypothetical proteins	Not Conserved	-1.17	2.10	2.26	2.46		
WAN0142GL_at	2.1	7.8	32.8	33.3	41.4	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	hypothetical protein	Hypothetical proteins	Role category not assigned	3.66	15.41	15.66	19.46		
WAN0142GLG_at	3.0	16	13.6	13.9	13.9	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	hypothetical protein	Hypothetical proteins	Role category not assigned	2.51	6.54	6.70	9.24		
WAN0142GOL_at	37.4	28.0	196.7	204.4	151.1	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	ATP-dependent protease, ATP-binding subunit CipX	Hypothetical proteins	Role category not assigned	-1.33	5.26	5.47	4.04		
WAN0142GLG_at	3.0	16	13.6	13.9	13.9	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	hypothetical protein	Hypothetical proteins	Role category not assigned	-1.91	4.59	4.48	5.70		
WAN0142GTH_at	2.3	2.7	8.0	8.8	12.3	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	hypothetical protein	Hypothetical proteins	Role category not assigned	1.19	3.49	3.77	5.39		
WAN0142ATH_at	1.5	0.9	5.6	5.3	2.6	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	hypothetical protein	Hypothetical proteins	Role category not assigned	-1.26	3.10	3.59	1.77		
WAN0142GPT_at	2.3	7.4	5.7	8.5	11.9	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	hypothetical protein	Hypothetical proteins	Role category not assigned	3.29	2.53	3.77	5.30		
WAN0142GKZ_at	7.5	19.0	16.6	17.2	19.6	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	truncated amidase-related protein	Mobile and extrachromosomal element functions	Propagule functions	-1.88	2.63	2.30	2.63		
WAN0142GP_at	3.5	14.6	16.7	16.7	16.7	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	transposase	Mobile and extrachromosomal element functions	Transposon functions	-2.50	2.53	2.03	1.61		
WAN0142H4D_at	10.4	28.6	29.0	27.0	27.0	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	No Data	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.74	2.21	1.80	1.56		
WAN0142H4V_at	8.7	11.4	22.7	19.7	16.2	SA1667	SA1264	SA2122	SAV1271	SAV2171	MW2074	peptidase, U32 family	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.40	3.01	2.35	2.57		
WAN0142H4W_at	4.0	3.7	9.9	7.0	6.7	SA1669	SA1441	SA1692	SA1549	SAV1613	MW1563	peptidase, U32 family	Protein fate	Degradation of proteins, peptides, and glycopeptides	-1.08	2.51	1.78	1.68		
WAN0142I3W_at	4.3	11.0	9.4	9.5	9.5	SA1281	SA1105	SA1238	SA1196	SAV1262	MW1145	membrane-associated zinc metalloprotease, putative	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.58	2.21	2.24	2.79		
WAN0142FTG_at	1.4	1.6	3.0	2.7	2.6	SA1373	SA1348	SA1278	SA1338	SAV1322	MW1326	SCP-like extracellular protein	Protein fate	Degradation of proteins, peptides, and glycopeptides	1.22	2.19	1.98	1.90		
WAN0142H4P_at	12.0	16.0	25.7	25.7	25.7	SA1761	SA1264	SA2122	SAV1271	SAV2171	MW2074	putative	Protein fate	Degradation of proteins, peptides, and glycopeptides	1.15	2.11	2.10	2.17		
WAN0142H4P_at	10.4	22.3	41.0	28.8	26.5	SA0968	SA0825	SA0926	SA0834	SAV0846	MW0846	pepA	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.10	3.93	2.70	2.54		
WAN0142H4L_at	18.6	41.3	60.0	51.6	51.6	SA1761	SA0968	SA0826	SA0837	SAV0847	MW0847	signal peptidase I	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.22	3.22	2.77	2.52		
WAN0142I5Z_at	6.8	11.2	12.9	8.8	8.8	SA1761	SA1755	SA1758	SA1679	SAV1722	MW1722	ribosomal protein L20	Protein fate	Degradation of proteins, peptides, and glycopeptides	1.73	3.13	3.14	4.15		
WAN0142I43L_at	17.2	34.5	244.6	216.6	267.4	SA1761	SA1264	SA1699	SA1699	SAV1690	MW1639	ribosomal protein L20	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.49	3.01	2.71	2.91		
WAN0142I7V_at	9.1	29.4	129.0	122.9	140.8	SA1761	SA1264	SA1761	SA1761	SAV1761	MW1761	ribosomal protein S4	Protein fate	Degradation of proteins, peptides, and glycopeptides	1.63	6.14	4.58	3.70		
WAN0142I20_at	4.8	9.6	10.7	10.3	10.3	SA1761	SA1264	SA1761	SA1761	SAV1761	MW1761	ribosomal protein L10	Protein fate	Degradation of proteins, peptides, and glycopeptides	2.99	2.45	2.47	1.01		
WAN0142I46_at	17.1	42.8	186.8	181.9	248.6	SA2238	SA2046	SA2344	SA2140	SAV2249	MW2168	rplD	Protein fate	Degradation of proteins, peptides, and glycopeptides	3.68	11.31	13.01	14.52		
WAN0142FRC_at	17.1	42.8	186.8	181.9	248.6	SA2238	SA2046	SA2344	SA2140	SAV2249	MW2168									

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
WAN014129_at	50.3	84.9	194.6	163.2	187.1	SA0583	SA0495	SA0542	SA0495	SA0537	MW0492	rplK	ribosomal protein L11	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN01415K_at	24.6	57.3	90.0	66.2	93.0	SA2212	SA2022	SA2308	SA2114	SAV2232	MW1242	rplQ	ribosomal protein L17	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN0141BQ_at	167.6	269.6	560.3	642.9	904.4	SA1700	SA1471	SA1725	SA1581	SAV1645	MW1595	rpmA	ribosomal protein L27	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN0141SQ_at	17.3	35.2	52.7	45.1	63.1	SA2215	SA2025	SA2310	SA2119	SAV2226	MW2145	rpmJ	ribosomal protein L36	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN0140E_at	69.4	145.7	210.4	173.3	288.1	SA2204	SA2024	SA2309	SA2120	SAV2223	MW2157	rplT	ribosomal protein S11	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN01415F_at	4.3	11.2	11.1	14.6	14.6	SA1642	SA1414	SA1683	SA1623	SAV1511	MW1537	rplT	ribosomal protein S10	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN01416M_at	3.9	8.8	10.5	11.1	13.2	SA1608	SA0467	SA1628	SA1489	SAV1551	MW1503	rplG	ribosomal protein L33	Protein synthesis	Ribosomal proteins: synthesis and modification
WAN0141GOM_at	1.6	4.6	9.3	6.6	5.8	SA0793	SA0782	SA0693	SA0703	MW0690		7-aminomethyl-7-carabaguine:NADP+ oxidoreductase	Protein synthesis	RNA and RNA modification	
WAN0141DE_at	5.6	6.9	77.4	71.0	79.0	SA1727	SA1504	SA1760	SA1609	SAV1680	MW1624	infC	translation initiation factor IF-3	Protein synthesis	Translation factors
WAN0141DQ_at	5.7	10.3	75.4	66.7	69.1	SA1116	SA1047	SA1104	SA1049	SAV1109	MW1109	tlyA	elongation factor, Tu family	Protein synthesis	Translation factors
WAN0141SV_at	18.2	34.4	41.3	63.9	50.8	SA1027	SA1223	SA1198	SA1209	SAV1247	MW1247	tsfA	translating ribosomal IF-1	Protein synthesis	Translation factors
WAN01412U_at	80.7	173.0	285.0	284.4	383.4	SA0593	SA0505	SA0505	SA0505	SAV0547	MW0502	fusA	translation elongation factor G	Protein synthesis	Translation factors
WAN0141ON_at	5.5	8.1	16.4	13.0	10.7	SA2110	SA1920	SA2206	SA2121	SAV2118	MW2042	prfA	peptide chain release factor 1	Protein synthesis	Translation factors
WAN01414B_at	38.1	85.8	28.5	61.2	72.6	SA1288	SA1245	SA1245	SA1245	SAV1269	MW1152	infC	translation initiation factor IF-2	Protein synthesis	Translation factors
WAN0141HAX_at	1.1	4.4	11.4	9.7	8.9	SA1868	SA1457	SA1711	SA1567	SAV1631	MW1581	hisS	histidyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN01418D_at	7.8	18.1	50.5	56.4	29.7	SA1808	SA1579	SA1579	SA1579	SAV1580	MW1580	valS	valyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN0141HJ_at	3.9	20.1	19.1	13.5	11.8	SA1808	SA1579	SA1579	SA1579	SAV1634	MW1760	WMT1	leucyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN0142BZL_at	10.5	58.5	42.8	36.2	37.8	SA1169	SA1127	SA1193	SA1193	SAV1106	MW1076	ileS	isoleucyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN0141ZU_s_at	7.7	40.0	24.4	21.1	24.6	SA1206	SA1036	SA1169	SA1169	SAV1193	MW1076	ileS	isoleucyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN01413Y_at	4.8	12.2	11.1	9.9	10.6	SA1284	SA1106	SA1239	SA1197	SAV1263	MW1146	proS	prolyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN01414C_at	1.6	3.9	3.7	3.3	3.3	SA1776	SA1550	SA1655	SA1655	SAV1729	MW1671	WMT1	aspartyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation
WAN01414R_at	7.7	10.1	10.8	69.8	69.8	SA1269	SA1049	SA1227	SA1185	SAV1251	MW1134	trmD	tRNA-Met	Protein synthesis	tRNA aminoacylation
WAN0141R4_at	52.5	64.6	585.5	617.8	479.4										
WAN0143CJ_at	18.4	26.2	19.1	19.1	17.9										
WAN0141R2_at	12.2	26.0	11.6	12.8	12.3										
WAN01412H2_at	5.0	4.3	45.9	33.8	51.0	SA0587	SA0546	SA0549	SA0549	SAV0541	MW0496				
WAN0141R6_at	35.0	103.4	245.7	279.7	229.5										
WAN0141P_at	1.8	1.7	8.8	8.3	8.3	SA1256	SA1049	SA1216	SA1174	SAV1240	MW1123	lmd	tRNA-Lys	Protein synthesis	RNA and RNA base modification
WAN0141L_x_at	60.9	80.3	383.4	409.7	443.7										
WAN0141H2O_at	1.9	2.6	11.1	7.9	8.0	SA1483	SA1277	SA1456	SA1387	SAV1444	MW1333	SA1206	putative RNA methylase family UPFO0200	Protein synthesis	RNA and RNA base modification
WAN0141CHD_x_at	57.2	78.0	33.2	36.1	45.6	SA1924	SA1924	SA1924	SA1924	SAV1924	MW1924	SA1924	putative RNA methylase family UPFO0200	Protein synthesis	RNA and RNA base modification
WAN0141R5_at	88.4	154.5	430.1	531.0	609.1										
WAN0141R6_at	13.2	15.6	56.0	60.3	60.3										
WAN0141GU_at	22.3	78.1	96.7	107.7	114.0										
WAN014134_at	8.1	19.8	31.2	30.5	37.3	SA1269	SA1094	SA1227	SA1185	SAV1251	MW1134	trmD	tRNA(M5U-54 methyltransferase	Protein synthesis	RNA and RNA base modification
WAN0141BF_at	7.8	8.7	29.4	27.9	29.0	SA1694	SA1655	SA1719	SA1575	SAV1639	MW1589	tgt	queuine tRNA-ribosyltransferase	Protein synthesis	RNA and RNA base modification
WAN0141GJD_at	144.6	97.1	513.9	546.9	451.8										
WAN0141BZL_at	5.7	13.2	18.2	13.3	13.3	SA1209	SA1040	SA1173	SA1131	SAV1197	MW1080	trmD	tRNA-Gln	Protein synthesis	RNA and RNA base modification
WAN0141BZL_at	60.6	63.6	20.0	20.0	18.6										
WAN0141GJ7_at	158.7	156.0	449.7	472.7	553.3										
WAN0141JFJ_at	10.3	91.5	29.1	27.0	26.4										
WAN0141GHJ_at	171.0	108.0	476.0	488.3	619.0										
WAN0141GJQ_at	3.7	3.8	3.8	3.8	3.8										
WAN0141BZL_at	3.5	2.3	7.2	7.9	9.8										
WAN0141H0_at	7.2	10.3	14.8	11.3	8.9	SA1793	SA1569	SA1833	SA1674	SAV1748	MW1691	trmD	tRNA(Gln-N(7)-methyltransferase	Protein synthesis	RNA and RNA base modification
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8	SA1699	SA1670	SA1724	SA1654	SAV1694	MW1694	cgtA	Gcg-binding protein, Oligo KsgA GTPase CgtA	Protein synthesis	RNA and RNA base modification
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1	SA1907	SA1688	SA1941	SA1771	SAV1850	MW1791	trmD	tRNA(Gln-N(7)-methyltransferase	Protein synthesis	RNA and RNA base modification
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13.8										
WAN0141G11_at	6.7	7.7	14.2	14.1	14.1										
WAN0141JZD_at	3.5	3.2	7.2	7.9	9.8										
WAN0141H9_at	7.0	12.3	10.4	11.3	8.9										
WAN0141GJK_at	86.9	55.9	178.9	167.6	192.0										
WAN0141BZL_at	14.9	17.2	15.2	13.8	13										

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				
														L6	30° in vivo	120° in vivo	360° in vivo			
WAN014G1X_at	2.4	3.9	5.6	6.5	5.8	SA2472	SAR2250	SAS2354	SAV2463	MW2387	opp-1F	peptide ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	1.64	2.37	2.46			
WAN014G29_at	4.5	3.7	9.9	9.3	8.7	SA2476	SAR2255	SAS2358	SAV2467	MW2391	opp-1A	peptide ABC transporter, peptide-binding protein	Transport and binding proteins	Amino acids, peptides and amines	-1.22	2.20	2.06	1.92		
WAN014G27_at	4.4	3.9	9.0	9.6	8.1	SA2475	SAR2254	SAR2553	SAS2357	SAV2466	MW2390	opp-1B	peptide ABC transporter, permease/protein, putative	Transport and binding proteins	Amino acids, peptides and amines	-1.11	2.06	2.19	1.85	
WAN014FX0_at	2.8	3.9	12.9	7.2	7.2	SA2386	SAR2176	SAR2476	SAS2278	SAV2388	MW2398	narK	nitrate transporter	Transport and binding proteins	Anions	1.39	4.67	2.62	2.60	
WAN014FBU_at	32.2	52.1	77.0	75.0	72.3	SA2472	SAR2250	SAR2354	SAS2356	SAV2468	MW2469	ptcG	phosphate transporter family protein	Transport and binding proteins	Anions	1.60	2.36	2.30	2.21	
WAN014FCH_at	1.3	1.4	4.5	12.8	12.8	SA2473	SAR2252	SAR2356	SAS2358	SAV2469	MW2469	PTC	PTC transporter-specific component	Transport and binding proteins	Cations	4.02	7.27	9.70	9.53	
WAN01BQN1_at	3.8	20.5	23.8	19.5	16.4	SA2401	SAR2191	SAR2318	SAS2294	SAV2403	MW2325	formate/infrate transporter	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	5.35	6.22	5.08	4.29		
WAN014FXX_at	15.6	61.3	57.5	43.3	49.1	SA2382	SAR2172	SAR2472	SAS2274	SAV2384	MW2304	gltT	sodium dicarboxylate symporter family	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	3.93	3.69	2.78	3.15	
WAN014H8A_at	12.2	23.7	28.2	34.4	52.6	SA0175	SA0183	SA0190	SA0164	SAV0189	MW0163	glcA	PTS system, glucose-specific component	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	1.95	2.31	2.82	4.31	
WAN014GDN_at	8.4	14.9	18.1	21.9	21.4	SA2245	SAR2148	SAR2149	SAS2175	SAV1709	MW2175	sugar transposon, putative	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	1.74	2.18	2.67	2.55		
WAN014G4D_at	2.1	3.5	12.2	12.3	14.3	SA0161	SA0161	SA0161	SA0166	SAV0458	MW0091	solute-transporter, putative	Transport and binding proteins	Cations	2.00	6.49	7.71	50.00		
WAN014H1P1_at	10.4	17.5	86.9	9.1	9.1	SA1026	SA0878	SA0981	SAV0980	SAV1022	MW0902	integral membrane protein TscC family	Transport and binding proteins	Cations	1.69	8.38	6.96	8.79		
WAN014FTC_at	5.2	7.6	22.3	17.2	17.4	SA2277	SAR2079	SAR2368	SAS2174	SAV2284	MW2202	iron compound ABC transporter, substrate-binding protein	Transport and binding proteins	Cations	1.46	4.26	3.28	3.33		
WAN014GTG_at	14.8	24.8	33.9	36.4	29.7	SA0086	SA0100	SA0110	SAS0081	SAV0104	MW0080	Na/Pi cotransporter, putative	Transport and binding proteins	Cations	1.68	2.29	2.46	2.00		
WAN014I31_at	2.7	4.0	21.9	19.8	23.7	SA2164	SAR1976	SAR2265	SAR2265	SAV2174	MW2100	transporter/gate domain protein	Transport and binding proteins	Cations and iron carrying compounds	1.48	8.04	9.48	8.68		
WAN014J7A_at	3.1	4.1	25.6	16.4	16.4	SA2474	SAR2242	SAR2242	SAR2238	SAR2144	MW2172	FeA domain protein	Transport and binding proteins	Cations and iron carrying compounds	1.16	7.18	4.78	2.02		
WAN014GBM_at	1.4	1.4	4.7	4.0	2.1	SA2565	SAR2338	SAR2338	SAR2347	SAR2351	MW2472	FeoA	FeA domain protein	Transport and binding proteins	1.00	2.59	2.31	1.47		
WAN014FRG_at	10.3	22.0	98.6	86.0	83.1	SA2242	SAR2050	SAR2238	SAR2144	SAR2144	MW2172	xanthine/uracil permease family protein	Transport and binding proteins	Nucleosides, purines and pyrimidines	2.13	9.56	8.33	8.05		
WAN014I04_at	1.0	7.6	7.6	3.9	2.2	SA1211	SA1042	SA1924	SAR1956	SAS1133	SAV1199	MW1082	pyrP	uracil permease	Transport and binding proteins	Nucleosides, purines and pyrimidines	7.50	3.80	2.19	
WAN014IPD_at	2.1	3.5	15.7	13.3	12.6	SA1924	SA1683	SA1683	SAV1788	SAS1788	SAV1866	MW1806	msbA	toxin/exporting ABC transporter, ATP-binding/permease protein	Transport and binding proteins	Other	1.62	7.35	6.23	5.89
WAN014IPD_HM_at	4.5	1.7	17.8	11.2	5.3	SA0086	SA0099	SA0109	SAS0080	SAV0103	MW0079	drug transporter, putative	Transport and binding proteins	Other	-2.61	3.99	2.54	1.19		
WAN014IPD_M_at	2.4	2.4	4.5	4.5	4.4	SA0087	SA0097	SA0109	SAR2020	SAR2350	MW2300	drug transporter, putative	Transport and binding proteins	Other	1.00	3.00	2.07	1.07		
WAN014FZG_at	1.3	1.9	3.7	3.3	2.6	SA1823	SA1592	SA1592	SA1592	SAV2266	MW2184	arsenical pump membrane protein	Transport and binding proteins	Other	1.61	2.86	2.57	2.01		
WAN014IH4_at	4.3	4.4	11.3	10.2	11.2	SA1809	SA1580	SA1580	SAR1844	SAS1685	SAV1761	MW1702	drug transporter, putative	Transport and binding proteins	Other	1.02	2.65	2.38	2.63	
WAN014HUO_at	2.1	1.4	4.9	4.3	4.6	SA2061	SAR2071	SAR2071	SAR2050	SAR2050	SAV0274	MW0250	drug transporter, putative	Transport and binding proteins	Other	-1.47	2.30	2.01	2.17	
WAN014FVY_at	2.5	9.9	16.9	14.9	16.6	SA1427	SAR1224	SAR1404	SAS1333	SAV1392	MW1260	ABC transporter, ATP-binding protein	Transport and binding proteins	Unknown substrate	3.89	6.63	5.86	6.51		
WAN014FVY_HM_at	2.4	1.9	15.9	13.7	13.5	SA1427	SAR1224	SAR1404	SAS1333	SAV1392	MW1260	ABC transporter, substrate-binding protein	Transport and binding proteins	Unknown substrate	-1.27	6.60	5.67	5.99		
WAN014HBT_at	2.3	3.5	12.4	10.1	10.1	SA1612	SA1584	SA1632	SAR1493	SAS1555	MW1507	znuB	ABC transporter family protein	Transport and binding proteins	Unknown substrate	1.61	5.43	4.41		
WAN014G9U_at	3.9	12.6	14.2	11.4	7.9	SA2375	SAR2166	SAR2465	SAS2298	SAR2376	MW2298	transporter	Transport and binding proteins	Unknown substrate	3.21	3.63	2.90	2.01		
WAN014H6V_at	1.3	1.3	3.9	3.3	2.8	SA1813	SAR1385	SAR1633	SAS1494	SAS1556	MW1508	znuC	ABC transporter, ATP-binding protein	Transport and binding proteins	Unknown substrate	1.02	3.04	2.82	2.20	
WAN014H7F_at	8.3	14.6	22.0	21.2	17.6	SA0695	SA0594	SA0648	SAR0648	SAS0604	SAV0638	MW0600	tagG	ABC-2 type transporter	Transport and binding proteins	Unknown substrate	1.77	2.66	2.57	2.14
WAN014GXV_at	0.9	3.7	2.5	2.4	2.0	SA0500	SAR0421	SAR0462	SAS0420	SAR0463	SAV0417	MW0417	ABC transporter, permease protein	Transport and binding proteins	Unknown substrate	3.85	2.65	2.51	2.07	
WAN014G9Y_at	6.0	9.0	17.4	18.1	18.1	SA2471	SAR2250	SAR2549	SAS2353	SAR2462	MW2386	transmembrane protein	Transport and binding proteins	Unknown substrate	1.54	2.59	2.74	2.54		
WAN014GY3_at	9.5	18.2	83.9	67.1	42.8	SAR2149	SAR2149	SAR2149	SAR2149	SAR2149	SAV0465	MW0465	autolysin (N-acetylmuramoyl-L-alanine amidase)	Unassigned	Role category not yet assigned	1.93	8.86	7.08	4.52	
WAN014HV1_at	0.6	0.5	3.6	4.6	4.9	SAR2149	SAR2149	SAR2149	SAR2149	SAR2149	SAV0465	MW0465	putative exported protein	Unassigned	Role category not yet assigned	-1.11	6.01	7.83	8.22	
WAN014G94_at	2.4	1.1	11.1	8.3	9.2	SA2620	SAR2397	SAR2682	SAS2489	SAV2604	MW2523	gabT	aminotransferase, class-III	Unknown function	Enzymes of unknown specificity	-2.28	4.58	3.42	3.79	
WAN014G7J_at	7.0	21.4	21.8	16.8	15.8	SA2582	SAR2354	SAR2649	SAS2453	SAV2567	MW2488	acetyltransferase	Unknown function	Enzymes of unknown specificity	3.07	3.13	2.39	2.26		
WAN014G28_at	2.0	3.1	16.6	6.4	6.4	SA2582	SAR2354	SAR2649	SAS2453	SAV2567	MW2488	exdA	Unknown function	Enzymes of unknown specificity	1.51	3.02	3.17	2.92		
WAN014G4T_at	5.2	4.5	13.9	11.6	8.2	SA2770	SAR2603	SAR2683	SAS2545	SAV0701	MW0672	radical activating enzyme family protein	Unknown function	Enzymes of unknown specificity	-1.48	2.68	2.23	1.59		
WAN014H1Y_at	2.5	4.8	6.3	4.9	5.6	SA1520	SA1311	SAR1498	SAS1420	SAR1420	MW1368	pyridine nucleotide-disulfide oxidoreductase	Unknown function	Enzymes of unknown specificity	1.94	2.55	1.99	2.25		
WAN014HF_A_at	0.6	0.7	1.5	1.5	1.2	SA1763	SA1538	SA1538	SA1538	SA1538	MW1538	aminotransferase, class V	Unknown function	Enzymes of unknown specificity	1.18	2.54	2.39	2.00		
WAN014H9Y_at	1.9	1.7	4.2	4.1	2.9	SA1669	SA1442	SAR1693	SAS1550	SAV1614	MW1564	O-methyltransferase family protein	Unknown function	Enzymes of unknown specificity	-1.07	2.27	2.19	1.55		
WAN014H9Y_HM_at	6.0	20.1	83.9	75.8	58.7	SA0600	SAR0497	SAR0497	SAS0497	SAR0497	MW0097	YjeF-related protein, C-terminal	Unknown function	General	3.34	13.97	12.61	9.68		
WAN014GC0_at	1.4	1.7	7.7	7.3	5.9	SAR0067	SAR0067	SAR0067	SAS0977	SAR0712	MW0772	exB	Unknown function	General	8.89	5.23	5.27	4.27		
WAN014HK1_at	4.0	4.1	15.9	12.4	8.2	SA2947	SAR0085	SAR0206	SAS0944	SAR0244	MW0826	yvuO	Unknown function	General	1.00	3.95	3.07	2.03		
WAN014HB1M_at	5.0	6.2	11.7	12.6	12.5	SA1698	SA1469	SAR1723	SAS1579	SAV1643	MW1593	pheB	ACT domain protein	General	1.25	2.37	2.54	2.53		
WAN014HWS_at	2.3	4.9	5.3	3.6	3.6	SA2053	SAR1668	SAR1668	SAR2151	SAS1968	SAV2063	MW1987	S1 binding domain protein	Unknown function	General	2.12	2.31	1.55	1.58	
WAN014I0J_at	4.8	6.9	10.2	8.1	6.1	SA2108	SA1918	SAR2204	SAS2019	SAV2116	MW2040	Sua5/YciD/YrdC/YwiC family protein	Unknown function	General	1.45	2.14	1.70	1.28		