

Supplemental Table 1: Gene changes at 30 minutes in adherent versus non-adherent samples					
Affy_ID	Fold change	p-value	Realtime_change	Annotation	Derivation of annotation
AFFX-25srRnad_at	4.470920958	0.017607843	Increase_in_Adherent	hypothetical protein	ppp:PHYPADRAFT_103626
V0624_x_at	4.325939656	0.004215304	Increase_in_Adherent	hypothetical protein ; K05521 ADP-ribosylglycohydrolase [EC:3.2.-.]	sdv:SDY_2272
V0231_s_at	3.911784536	0.02822872	Increase_in_Adherent	ssb; single-stranded DNA-binding protein ; K03111 single-strand DNA-binding protein	sdv:SDY_4508
SD1_1765_at	3.456357913	0.010221594	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
AFFX-18srRnaa_at	3.375808388	0.020720921	Increase_in_Adherent	hypothetical protein LOC769550	gga:769550
ECP_3198_s_at	3.152545933	0.004126118	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
V2042_x_at	2.970183536	0.048314839	Increase_in_Adherent	yqjG; putative transferase ; K07393 putative glutathione S-transferase	sdv:SDY_3291
SB5_0762_s_at	2.649128398	0.042215803	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SS5_3223_s_at	2.389038504	0.003368608	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
AFFX-18srRnad_at	2.316797628	0.044815725	Increase_in_Adherent	hypothetical protein	cre:CHLREDRAFT_155068
b0957_s_at	2.294675608	0.004411227	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SD1_0959_s_at	2.254413702	0.001920777	Increase_in_Adherent	marA; DNA-binding transcriptional activator MarA	sdv:SDY_1596
EC869_4610_x_at	2.064036433	0.008647714	Increase_in_Adherent	phosphoglucomutase ; K01835 phosphoglucomutase [EC:5.4.2.2]	cck:CKO_02471
EC869_2545_s_at	2.03112288	0.03857958	Increase_in_Adherent	ruvB; Holliday junction DNA helicase RuvB (EC:3.1.22.4); K03551 holliday junction DNA helicase RuvB	sdv:SDY_1147
A0552_s_at	1.896042476	0.000440449	Increase_in_Adherent	hscB; co-chaperone HscB ; K04082 molecular chaperone HscB	sdv:SDY_2723
EC869_2283_s_at	1.872276581	0.007504228	Increase_in_Adherent	metH; B12-dependent methionine synthase ; K00548 5-methyltetrahydrofolate--homocysteine methyltransferase [EC:2.1.1.13]	cck:CKO_03902
N4402_at	1.866897448	0.002845441	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
ECP_0062_s_at	1.862963467	0.01829172	Increase_in_Adherent	araD; L-ribulose-5-phosphate 4-epimerase (EC:5.1.3.4); K01786 L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]	kpe:KPK_4682
V0550_s_at	1.752660578	0.033176747	Increase_in_Adherent	yegH; UPF0053 protein YegH	ctu:ctu_27600
A3829_s_at	1.728097527	0.009607232	Increase_in_Adherent	ycfR; hypothetical protein ; K12151 multiple stress resistance protein BhsA	sdv:SDY_2038
F0704_at	1.694801028	0.015316544	Increase_in_Adherent	rihA; ribonucleoside hydrolase 1; K01250 pyrimidine-specific ribonucleoside hydrolase [EC:3.2.-.]	asa:ASA_2899
EC536_4654_x_at	1.621475824	0.036949765	Increase_in_Adherent	ybjU; L-threonine aldolase ; K01620 threonine aldolase [EC:4.1.2.5]	sdv:SDY_2393
b4060_s_at	1.568394879	0.022484572	Increase_in_Adherent	yjcB; hypothetical protein	sdv:SDY_4507
b3772_s_at	1.245901861	0.024266896	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
APECO1_538_at	1.21722829	0.049137631	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
A0549_s_at	1.136101811	0.033053849	Increase_in_Adherent	yfhJ; hypothetical protein	sdv:SDY_2720
ECs1782_x_at	1.120720706	0.027837234	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SD1_0481_s_at	-7.223991574	0.022917096	Decrease_in_adherent	glpD; glycerol-3-phosphate dehydrogenase (EC:1.1.5.3); K00111 glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	sbv:SBBS512_E3808
V2454_s_at	-6.332994897	0.048405801	Decrease_in_adherent	dhaL; dihydroxyacetone kinase ADP-binding subunit (EC:2.7.1.-); K05879 dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]	sbv:SBBS512_E1358
ECP_4135_s_at	-5.885074041	0.022606293	Decrease_in_adherent	glpK; glycerol kinase (EC:2.7.1.30); K00864 glycerol kinase [EC:2.7.1.30]	sdv:SDY_3818
A1237_s_at	-5.432857895	0.011475071	Decrease_in_adherent	glgS; glycogen synthesis protein GlgS	sdv:SDY_3228
b4189_s_at	-5.307529193	0.003453076	Decrease_in_adherent	yjFO; hypothetical protein	sdv:SDY_4358
D4048_at	-5.138879246	0.036237835	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC869_4008_s_at	-4.759298317	0.023899362	Decrease_in_adherent	pfkB; formate acetyltransferase 1 ; K00656 formate C-acetyltransferase [EC:2.3.1.54]	sdv:SDY_2358
A2373_s_at	-4.664693451	0.035059433	Decrease_in_adherent	frdD; fumarate reductase subunit D ; K00247 fumarate reductase subunit D [EC:1.3.99.1]	sdv:SDY_4395
A3460_s_at	-4.631782184	0.018128331	Decrease_in_adherent	ybhQ; hypothetical protein	sdv:SDY_0812
A1575_s_at	-4.415890215	0.03172692	Decrease_in_adherent	pckA; phosphoenolpyruvate carboxykinase (EC:4.1.1.49); K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	eci:UTI89_C3903
p166897_140_s_at	-4.386728208	0.038029993	Decrease_in_adherent	mok; modulator of post-segregation killing protein	ecv:APECO1_O1CoBM20
SD1_0513_s_at	-4.373967506	0.033309929	Decrease_in_adherent	pckA; phosphoenolpyruvate carboxykinase (EC:4.1.1.49); K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	sdv:SDY_3673
V2453_s_at	-4.330542027	0.04250194	Decrease_in_adherent	dhaH; fused putative dihydroxyacetone-specific PTS enzymes: HPr component/EI component; K05881 PTS hybrid protein	eoh:ECO103_1300
EC869_0354_s_at	-4.218228956	0.009430225	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
S2143_x_at	-4.175134165	0.027093037	Decrease_in_adherent	putative cell killing protein of prophage	sfz:S2143
pCoo074_at	-4.140504998	0.020261097	Decrease_in_adherent	flmC; modulator of post-segregation killing protein	ecp:PECS88_0057
b1376_s_at	-4.096458464	0.042866434	Decrease_in_adherent	ynaF; stress-induced protein, ATP-binding protein	ebr:ECB_01347
V0034_s_at	-4.049579703	0.011568516	Decrease_in_adherent	frdC; fumarate reductase subunit C ; K00246 fumarate reductase subunit C [EC:1.3.99.1]	sbv:SBBS512_E4684
F2023_at	-4.022872514	0.013751706	Decrease_in_adherent	hypothetical protein	sdv:SDY_1970
M3390_at	-4.01348977	0.004038399	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
V4759_s_at	-3.919556048	0.008285338	Decrease_in_adherent	rbsD; D-ribose pyranase ; K06726 D-ribose pyranase [EC:5.-.-.]	sbv:SBBS512_E4172
A2504_s_at	-3.847347788	0.005788862	Decrease_in_adherent	virK; regulator of VirG protein ; K09824 hypothetical protein	ecq:ECED1_5142
A3486_s_at	-3.801684766	0.014359919	Decrease_in_adherent	ompX; outer membrane protein X ; K11934 outer membrane protein X	sdv:SDY_0781
A4639_s_at	-3.715093427	0.018412821	Decrease_in_adherent	cold shock-like protein CspC ; K03704 cold shock protein (beta-ribon, CspA family)	cck:CKO_01152
V0028_s_at	-3.588551543	0.012823351	Decrease_in_adherent	frdA; fumarate reductase flavoprotein subunit (EC:1.3.99.1); K00244 fumarate reductase flavoprotein subunit [EC:1.3.99.1]	sdv:SDY_4398
SD1_0444_s_at	-3.568812714	0.008546842	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A3388_s_at	-3.545975813	0.044092556	Decrease_in_adherent	gpmA; phosphoglyceromutase 1 ; K01834 phosphoglycerate mutase [EC:5.4.2.1]	sdv:SDY_0702
APECO1_1866_s_at	-3.541356073	0.016097667	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
ECs0987_s_at	-3.528561093	0.030543274	Decrease_in_adherent	focA; formate transporter ; K06212 formate transporter	sdv:SDY_2357
SB5_0930_x_at	-3.524850355	0.041498854	Decrease_in_adherent	relF; polypeptide destructive to membrane potential	sdv:SDY_1432
EC869_3973_s_at	-3.492847032	0.011403082	Decrease_in_adherent	transcriptional regulator, AsnC family	etr:ETA_E2200
V4449_s_at	-3.489894981	0.016197632	Decrease_in_adherent	dmsA; anaerobic dimethyl sulfoxide reductase subunit A ; K07306 anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.99.-]	sbo:SBO_0827
F0555_s_at	-3.471876393	0.042310262	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
W4348_at	-3.404942754	0.008225376	Decrease_in_adherent	putative cytoplasmic protein	stm:STM4002
EC869_3430_s_at	-3.400923688	0.040124383	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A2345_s_at	-3.392649924	0.021081437	Decrease_in_adherent	yjdJ; hypothetical protein ; K06975	sdv:SDY_4240
A1592_s_at	-3.365985888	0.027425645	Decrease_in_adherent	transcriptional regulator MalT; K03556 LuxR family transcriptional regulator, maltose regulon positive regulatory protein	eci:EcolC_0295
V4294_s_at	-3.336375417	0.042559551	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
b2597_s_at	-3.323309199	0.04442532	Decrease_in_adherent	hypothetical protein	eci:UTI89_C2930
UT189_C2497_s_at	-3.320190255	0.016752562	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A4608_s_at	-3.311394611	0.042141297	Decrease_in_adherent	yeaQ; hypothetical protein	sdv:SDY_1695
A2210_s_at	-3.299638245	0.035258695	Decrease_in_adherent	hupA; transcriptional regulator HU subunit alpha ; K05787 DNA-binding protein HU-alpha	sdv:SDY_3726
A0068_at	-3.259733347	0.017566618	Decrease_in_adherent	vipB; Vi polysaccharide biosynthesis protein VipB/TviC	ecw:EcE24377A_2324
S1023_s_at	-3.252535784	0.013598245	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA

A0302_s_at	-3.220450258	0.044592052	Decrease_in_adherent galG; maltose transporter permease ; K10110 maltose/maltodextrin transport system permease protein	ssn:SSON_4210
V5399_s_at	-3.196176977	0.034902666	Decrease_in_adherent glcK; glucose-1-phosphate adenylyltransferase (EC:2.7.7.27); K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]	sdj:SDY_3576
A4742_s_at	-3.189399709	0.020412123	Decrease_in_adherent fltC; flagellin ; K02406 flagellin	ecw:E0243774_2158
A1301_s_at	-3.183249419	0.002607063	Decrease_in_adherent putative inner membrane protein	sbc:SBB5512_E3254
b3339_s_at	-3.163257277	0.002135027	Decrease_in_adherent tuFb, tuf, elongation factor Tu [EC:3.6.5.3]; K02358 elongation factor EF-Tu [EC:3.6.5.3]	sdj:SDY_3748
SB5_1096_s_at	-3.15504836	0.02955258	Decrease_in_adherent gabD; succinate-semialdehyde dehydrogenase 1; K00135 succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]	cko:CKO_04008
A1966_s_at	-3.14381204	0.0119913	Decrease_in_adherent yIfE; hypothetical protein ; K09897 hypothetical protein	sdj:SDY_3984
c1093_s_at	-3.137432379	0.010580129	Decrease_in_adherent ompA; outer membrane protein A ; K03286 OmpA-OmpF porin, OOP family	efe:EFER_1094
EC536_0181_s_at	-3.11566593	0.021704303	Decrease_in_adherent dsdA; D-serine dehydratase (EC:4.3.1.18); K01753 D-serine dehydratase [EC:4.3.1.18]	eum:ECUMN_2695
A2446_s_at	-3.11216834	0.015516565	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A4412_s_at	-3.090699703	0.019054073	Decrease_in_adherent ydgA; hypothetical protein	ssn:SSON_1546
A2825_s_at	-3.081820804	0.001257776	Decrease_in_adherent hlpA; periplasmic chaperone ; K06142 outer membrane protein	sdj:SDY_0194
A2260_s_at	-3.066645	0.025841585	Decrease_in_adherent yjbJ; putative stress-response protein	sdj:SDY_4529
APECO1_3321_at	-3.055990403	0.038872056	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2344_s_at	-3.055869296	0.030996683	Decrease_in_adherent yjdI; hypothetical protein	sbo:SBO_4330
V0059_s_at	-3.03297055	0.012649494	Decrease_in_adherent hypothetical protein	cko:CKO_03698
pCoo013_at	-3.008891096	0.024089807	Decrease_in_adherent CS1 type fibrillar major subunit	spe:Spro_0216
N4689_at	-3.003200769	0.022818542	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SB5_3099_s_at	-2.997607797	0.022047248	Decrease_in_adherent fruB; bifunctional fructose-specific PTS IIA/HPr protein (EC:2.7.1.-); K02768 PTS system, fructose-specific IIA component [EC:2.7.1.-]; K02777 PTS system, glucose-specific IIA component [EC:2.7.1.-]	sbc:SBB5512_E0794
V5372_s_at	-2.994996594	0.020437474	Decrease_in_adherent yhhA; hypothetical protein	sdj:SDY_3596
V0004_s_at	-2.9880727	0.030424799	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0438_s_at	-2.960997374	0.018983387	Decrease_in_adherent crr; glucose-specific PTS system component [EC:2.7.1.-]; K02777 PTS system, glucose-specific IIA component [EC:2.7.1.-]	kpe:KPK_1374
F1837_s_at	-2.957538417	0.011063329	Decrease_in_adherent hypothetical protein	ssn:SSON_1509
EC5510_s_at	-2.954846897	0.003548481	Decrease_in_adherent hypothetical protein	ecp:ECF_2774
A1218_s_at	-2.944140608	0.01737733	Decrease_in_adherent hypothetical protein	eci:UTI89_C3456
b3024_s_at	-2.944117078	0.041558572	Decrease_in_adherent ygiW; hypothetical protein	sdj:SDY_3215
EC869_3357_s_at	-2.936271242	0.031500452	Decrease_in_adherent dsdA; D-serine dehydratase (EC:4.3.1.18); K01753 D-serine dehydratase [EC:4.3.1.18]	eum:ECUMN_2695
V2584_s_at	-2.931373689	0.032353635	Decrease_in_adherent hypothetical protein	sdj:SDY_1871
EC869_4082_s_at	-2.930883571	0.017996515	Decrease_in_adherent ompF; outer membrane protein F ; K09476 outer membrane pore protein F	sdj:SDY_2328
APECO1_2795_at	-2.924268172	0.022449992	Decrease_in_adherent hypothetical protein	cko:CKO_05114
V5396_s_at	-2.912570201	0.047041568	Decrease_in_adherent glgX; glycogen debranching enzyme ; K02438 glycogen operon protein GlgX [EC:3.2.1.-]	sdj:SDY_3577
A4482_s_at	-2.903366448	0.011386964	Decrease_in_adherent lpp; murein lipoprotein ; K06078 murein lipoprotein	sdj:SDY_1908
SFV_4079_at	-2.894859807	0.004999097	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A4701_s_at	-2.893924137	0.049528634	Decrease_in_adherent cheY; chemotaxis regulatory protein CheY ; K03411 two-component system, chemotaxis family, response regulator CheY	sbc:SBB5512_E2175
Z4365_s_at	-2.885163993	0.023961402	Decrease_in_adherent dkgA; 2,5-diketo-D-glulonate reductase A ; K02621 2,5-diketo-D-glulonate reductase A [EC:1.1.1.274]	etw:SCP_3988
M1848_s_at	-2.869503811	0.041769494	Decrease_in_adherent hypothetical protein	sbc:SBB5512_A0294
V3949_s_at	-2.835942057	0.028593841	Decrease_in_adherent narL; transcriptional regulator NarL ; K07684 two-component system, NarL family, nitrate/nitrite response regulator NarL	sdj:SDY_1275
SDY_3461_x_at	-2.822584234	0.016017765	Decrease_in_adherent hypothetical protein ; K03747 Smg protein	cko:CKO_04697
A1294_s_at	-2.807377788	0.047303588	Decrease_in_adherent yqjD; hypothetical protein	sdj:SDY_3285
SB5_0121_s_at	-2.800662344	0.032865982	Decrease_in_adherent dppA; dipeptide transporter ; periplasmic-binding component of ABC superfamily ; K12368 dipeptide transport system substrate	efe:EFER_3541
SD1_0194_s_at	-2.788062966	0.030437167	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
F3644_x_at	-2.786231337	0.022993544	Decrease_in_adherent hypothetical protein ; K03747 Smg protein	cko:CKO_04697
H2868_s_at	-2.778621031	0.017943481	Decrease_in_adherent ygeA; putative resistance proteins	sfv:SfV_2918
V2072_s_at	-2.77694744	0.038712243	Decrease_in_adherent ygiU; serine/threonine transporter SstT ; K07862 serine/threonine transporter	sdj:SDY_3274

A4340_s_at	-2.645755969	0.023369281	Decrease_in_adherent ydfG; 3-hydroxy acid dehydrogenase ; K00540 [EC:1.-.-.-]	sdv:SDY_1586
ECs5340_s_at	-2.645066666	0.011255873	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_8209_s_at	-2.640220346	0.016305397	Decrease_in_adherent transketolase [EC:2.2.1.1]; K00615 transketolase [EC:2.2.1.1]	ecs:ECs3327
V0789_s_at	-2.634646315	0.019454405	Decrease_in_adherent putative enzyme ; K01061 carboxymethylenebutenolide	sdv:SDY_3913
G3937_s_at	-2.631098282	0.001941474	Decrease_in_adherent putative PstA	eqj:EC026_p2-29
V1419_s_at	-2.630118868	0.044062828	Decrease_in_adherent N,N'-diacetylchitobiose-specific PTS system transporter subunit IIB ; K02760 PTS system, cellobiose-specific IIB component [EC:1.1.1.45]	cko:CKO_01763
H4105_s_at	-2.617324386	0.025738669	Decrease_in_adherent aphA; acid phosphatase/phosphotransferase [EC:3.1.3.2]; K03788 acid phosphatase (class B) [EC:3.1.3.2]	ecr:ECIAI_4287
A3867_s_at	-2.615482989	0.002995882	Decrease_in_adherent hypothetical protein	ecw:ECe24377A_1438
A2648_s_at	-2.613411304	0.009999934	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2205_s_at	-2.608904001	0.045187252	Decrease_in_adherent rsd; anti-RNA polymerase sigma 70 factor ; K07740 regulator of sigma D	sbv:SBBS512_E4886
V0844_s_at	-2.607383169	0.012990425	Decrease_in_adherent hfq; RNA-binding protein Hfq ; K03666 host factor-I protein	sbo:SBO_4284
A3777_s_at	-2.600396377	0.039538609	Decrease_in_adherent bssS, yceP; biofilm formation regulatory protein BssS ; K12148 biofilm regulator BssS	sdv:SDY_2095
V2049_s_at	-2.594410577	0.049454699	Decrease_in_adherent yqjE; hypothetical protein	sdv:SDY_3286
A1840_s_at	-2.58297481	0.004088921	Decrease_in_adherent dinD; DNA-damage-inducible protein D	sdv:SDY_4076
SD1_2578_s_at	-2.579316174	0.009446506	Decrease_in_adherent polA; DNA polymerase I [EC:2.7.7.7]; K02335 DNA polymerase I [EC:2.7.7.7]	sbv:SBBS512_E4337
J2220_s_at	-2.573166152	0.04710654	Decrease_in_adherent dinD; DNA-damage-inducible protein D	ssn:SSON_3761
V4643_s_at	-2.56497662	0.018327755	Decrease_in_adherent sfsA; sugar fermentation stimulation protein A ; K06206 sugar fermentation stimulation protein A	sdv:SDY_0162
G1262_s_at	-2.563248604	0.033873451	Decrease_in_adherent trg; methyl-accepting chemotaxis protein III ; K05876 methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor	ssn:SSON_1721
V3435_s_at	-2.55985515	0.005750668	Decrease_in_adherent ptsI; phosphoenolpyruvate-protein phosphotransferase [EC:2.7.3.9]; K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]	sdv:SDY_2613
SS5_4352_s_at	-2.557107256	0.022249681	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
c5607_at	-2.555362864	0.005749752	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0712_s_at	-2.54743645	0.031840461	Decrease_in_adherent ygaG; S-ribosylhomocysteinase ; K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21]	sdv:SDY_2884
A1428_s_at	-2.543718687	0.034375237	Decrease_in_adherent putative periplasmic serine protease Do, heat shock protein HtrA; K04772 serine protease DegQ [EC:3.4.21.-]	sfl:SF3274
A0044_s_at	-2.540933283	0.030937391	Decrease_in_adherent sbmC; DNA gyrase inhibitor ; K07470 DNA gyrase inhibitor	ecq:ECED1_2360
SB5_0122_s_at	-2.536100637	0.045469389	Decrease_in_adherent dppA; dipeptide transport protein ; K12368 dipeptide transport system substrate-binding protein	sdv:SDY_4567
SD1_0474_s_at	-2.521889747	0.022629155	Decrease_in_adherent glgC; glucose-1-phosphate adenyllyltransferase [EC:2.7.7.27]; K00975 glucose-1-phosphate adenyllyltransferase [EC:2.7.7.27]	sdv:SDY_3576
A0073_at	-2.516827841	0.014400991	Decrease_in_adherent rfbC; dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]; K01790 dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]	ecw:ECe24377A_2329
F4391_s_at	-2.515045651	0.018330596	Decrease_in_adherent yjiM; hypothetical protein	eum:ECUMN_4439
ECP_3137_s_at	-2.511576515	0.010186434	Decrease_in_adherent hypothetical protein ; K09806 hypothetical protein	sdv:SDY_3227
A4480_s_at	-2.51130002	0.049080249	Decrease_in_adherent hypothetical protein	sdv:SDY_1904
A3372_s_at	-2.501747941	0.02994567	Decrease_in_adherent cydA; cytochrome d ubiquinol oxidase, subunit I [EC:1.10.3.-]; K00425 cytochrome bd-I oxidase subunit I [EC:1.10.3.-]	sbv:SBBS512_E0654
ECs5520_s_at	-2.498665343	0.027017823	Decrease_in_adherent hypothetical protein	ecy:ECSE_3407
A2739_s_at	-2.497188784	0.017034863	Decrease_in_adherent hypothetical protein	sbo:SBO_0084
V5876_x_at	-2.491602166	0.000691199	Decrease_in_adherent hypothetical protein	sbv:SBBS512_E4390
EC869_3060_s_at	-2.491349534	0.045715968	Decrease_in_adherent fdhF; formate dehydrogenase-H, selenopolypeptide subunit; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]	etw:ECSP_5176
A1722_s_at	-2.488842736	0.033201788	Decrease_in_adherent bcsF; cellulose biosynthesis protein BcsF	sbv:SBBS512_E3999
A0071_at	-2.486981526	0.001374033	Decrease_in_adherent glycosyl transferase, group 2 family protein ; K07011	ecw:ECe24377A_2327
EC869_3914_s_at	-2.486591119	0.016349671	Decrease_in_adherent elongation factor Tu ; K02358 elongation factor EF-Tu [EC:3.6.5.3]	cko:CKO_03011
A4157_s_at	-2.484840545	0.019301254	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V0313_s_at	-2.451398277	0.047103134	Decrease_in_adherent pgi; glucose-6-phosphate isomerase [EC:5.3.1.9]; K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
EC869_2599_s_at	-2.433029359	0.005494966	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	etw:ECSP_2460
V2498_s_at	-2.42629146	0.048165868	Decrease_in_adherent mic; putative NAGC-like transcriptional regulator	sdv:SDY_1562
A1408_s_at	-2.421525238	0.004001419	Decrease_in_adherent yhbL; isoprenoid biosynthesis protein with amidotransferase-like domain	sdv:SDY_3390
b2989_s_at	-2.42138774	0.027131027	Decrease_in_adherent putative glutathione S-transferase YghU [EC:2.5.1.18]; K11209 GST-like protein	sbv:SBBS512_E3416
SD1_0131_s_at	-2.419447896	0.027446526	Decrease_in_adherent secB; preprotein translocase subunit SecB ; K03071 preprotein translocase subunit SecB	sdv:SDY_4042
V2075_s_at	-2.417216482	0.028220053	Decrease_in_adherent ygiJ; serine/threonine transporter SstT ; K07862 serine/threonine transporter	sdv:SDY_3274
A2755_s_at	-2.411917607	0.012157235	Decrease_in_adherent ampE; regulatory protein AmpE ; K03807 AmpE protein	sdv:SDY_0141
A1805_s_at	-2.403184093	0.017394329	Decrease_in_adherent grxC; glutaredoxin 3 ; K03676 glutaredoxin 3	sdv:SDY_4043
b1743_s_at	-2.390814801	0.001593017	Decrease_in_adherent hypothetical protein	eci:UT189_C1937
V2685_s_at	-2.389030097	0.042562137	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
AFFX-r2-Bs-phe-3_a	-2.38716443	0.004116256	Decrease_in_adherent pheA; prephenate dehydratase [EC:4.2.1.51]; K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
V5406_s_at	-2.384962203	0.01725071	Decrease_in_adherent glgP; glycogen phosphorylase ; K00688 starch phosphorylase [EC:2.4.1.1]	sdv:SDY_3574
A1055_at	-2.38490084	0.011128219	Decrease_in_adherent ATPase	ecw:ECe24377A_3331
ECP_2591_s_at	-2.377796862	0.017290098	Decrease_in_adherent transposase	sbv:SBBS512_E1228
AFFX-r2-Bs-lys-3_at	-2.376561699	0.007213925	Decrease_in_adherent lysA; diaminopimelate decarboxylase [EC:4.1.1.20]; K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
EC536_1048_s_at	-2.375879892	0.043725965	Decrease_in_adherent putative glutamate dehydrogenase	eci:UT189_C0015
SB5_1469_s_at	-2.375453492	0.025308564	Decrease_in_adherent adhA, adhP; alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]	ecs:ECs2082
A3910_s_at	-2.374609661	0.00901464	Decrease_in_adherent minD; cell division inhibitor MinD ; K03609 septum site-determining protein MinD	sdv:SDY_1206
EC869_2220_s_at	-2.370704667	0.045751591	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b0222_s_at	-2.368920871	0.017761698	Decrease_in_adherent gmhA; phosphoheptose isomerase [EC:5.3.1.-]; K03271 phosphoheptose isomerase [EC:5.-.-.-]	sbv:SBBS512_E0218
V3521_s_at	-2.367053651	0.036126585	Decrease_in_adherent transketolase [EC:2.2.1.1]; K00615 transketolase [EC:2.2.1.1]	ent:Ent638_2960
D4444_s_at	-2.360019882	0.023516275	Decrease_in_adherent rpsD; 30S ribosomal protein S4 ; K02986 small subunit ribosomal protein S4	cko:CKO_04709
EC869_2796_s_at	-2.343464571	0.007699655	Decrease_in_adherent uiaR; transcriptional repressor UiaR ; K03477 DeoR family transcriptional regulator, ulaG and ulaABCDEF operon transcription factor	sbv:SBBS512_E4720
AFFX-PheX-3_at	-2.343391841	0.005485637	Decrease_in_adherent pheA; prephenate dehydratase [EC:4.2.1.51]; K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
V4568_s_at	-2.340640261	0.002572386	Decrease_in_adherent anaerobic ribonucleoside triphosphate reductase [EC:1.17.4.2]; K00527 ribonucleoside-triphosphate reductase [EC:1.17.4.2]	ppr:PBPRB0442
V1970_s_at	-2.338771837	0.009283254	Decrease_in_adherent yraM; putative glycosylase ; K07121	sdv:SDY_3326
SD1_0493_s_at	-2.336860367	0.01376915	Decrease_in_adherent malP; maltodextrin phosphorylase ; K00688 starch phosphorylase [EC:2.4.1.1]	ssn:SSON_3549
A1822_s_at	-2.333153564	0.02220915	Decrease_in_adherent waaO, rfaI; UDP-glucose:(glucosyl) LPS alpha1,3-glucosyltransferase WaaO ; K03275 UDP-glucose:(glucosyl)LPS alpha-1,3-glucosyltransferase	ebr:ECB_03486
A2459_s_at	-2.329186443	0.004089684	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1492_s_at	-2.326157965	0.007033527	Decrease_in_adherent rplE; 50S ribosomal protein L5 ; K02931 large subunit ribosomal protein L5	kpu:KP1_5029
EC869_8291_s_at	-2.326042959	0.040618829	Decrease_in_adherent crr; glucose-specific PTS system component ; K02777 PTS system, glucose-specific IIA component [EC:2.7.1.69]	sdv:SDY_2614
SD1_0613_s_at	-2.322676759	0.015832694	Decrease_in_adherent did; D-lactate dehydrogenase [EC:1.1.1.28]; K03777 D-lactate dehydrogenase [EC:1.1.1.28]	sdv:SDY_2155
A2740_s_at	-2.322507748	0.027456889	Decrease_in_adherent lpxC; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase ; K02535 UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	sdv:SDY_0126
A0254_s_at	-2.320069734	0.036340872	Decrease_in_adherent eco; ecotin ; K08276 ecotin	sbv:SBBS512_E0731

b3303_s_at	-2.319463182	0.021252692	Decrease_in_adherent hypothetical protein	ecc:c4064
A2738_s_at	-2.3142691	0.038842493	Decrease_in_adherent ftsA; cell division protein FtsA	cko:CKO_03281
A1494_s_at	-2.313597582	0.035493527	Decrease_in_adherent hypothetical protein	eci:UT189_C3759
A1858_s_at	-2.311657531	0.024391627	Decrease_in_adherent nlpA; cytoplasmic membrane lipoprotein-28 ; K02073 D-methionine transport system substrate-binding protein	sdv:SDY_4499
SDY_1018_s_at	-2.304814789	0.032796545	Decrease_in_adherent insertion element IS2 transposase InsD	sdv:SDY_P215
APECO1_3736_s_at	-2.302799351	0.00584675	Decrease_in_adherent ygdH; hypothetical protein ; K06966	sbo:SBO_2676
A0334_s_at	-2.302543245	0.049344224	Decrease_in_adherent ackA; acetate kinase (EC:2.7.2.1); K00925 acetate kinase [EC:2.7.2.1]	sbc:SbBS512_E2672
V4816_s_at	-2.301784074	0.040296977	Decrease_in_adherent yieE; hypothetical protein	sdv:SDY_4201
A1959_s_at	-2.301623107	0.034883057	Decrease_in_adherent rbsB; D-ribose transporter subunit RbsB ; K10439 ribose transport system substrate-binding protein	efe:EFER_4050
EC869_5211_s_at	-2.29680588	0.021415208	Decrease_in_adherent hypothetical protein	sbo:SBO_0084
W0610_s_at	-2.290848742	0.009740668	Decrease_in_adherent ybeM; putative amidase	sdv:SDY_0548
b1717_s_at	-2.290481666	0.036201147	Decrease_in_adherent hypothetical protein	cko:CKO_01743
b4473_s_at	-2.289253131	0.01095831	Decrease_in_adherent smf; hypothetical protein ; K04096 DNA processing protein	ebr:ECB_03136
A1196_s_at	-2.288751991	0.044600742	Decrease_in_adherent yghA; oxidoreductase ; K00540 [EC:1.-.-.-]	ssn:SSON_3147
pCoo091_at	-2.284771224	0.028747107	Decrease_in_adherent hypothetical protein	sdv:SDY_0400
D0009_s_at	-2.284695774	0.029258063	Decrease_in_adherent ydfG; 3-hydroxy acid dehydrogenase ; K00540 [EC:1.-.-.-]	sdv:SDY_1586
b4232_s_at	-2.28318029	0.018146441	Decrease_in_adherent fbp; fructose-1,6-bisphosphatase (EC:3.1.3.11); K03841 fructose-1,6-bisphosphatase I [EC:3.1.3.11]	sdv:SDY_4250
A2460_s_at	-2.283150472	0.002324012	Decrease_in_adherent nrdG; anaerobic ribonucleotide reductase activating protein ; K04068 anaerobic ribonucleoside-triphosphate reductase activating protein	kpu:KP1_0523
I1228_s_at	-2.267423375	0.011812626	Decrease_in_adherent hypothetical protein	sbc:SbBS512_E3471
SFV_3194_s_at	-2.260283233	0.006020478	Decrease_in_adherent pnp; polynucleotide phosphorylase/polyadenylase (EC:2.7.7.8); K00962 polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	sbc:SbBS512_E3607
A1819_s_at	-2.255318124	0.009253675	Decrease_in_adherent waaV; lipopolysaccharide 1,2-galactosyltransferase ; K12985 (galactosyl)LPS 1,2-glucosyltransferase [EC:2.4.1.-]	sbc:SbBS512_E4051
EC869_0982_s_at	-2.251102572	0.039755182	Decrease_in_adherent hypothetical protein	eci:UT189_C2580
A0842_s_at	-2.247085453	0.030881675	Decrease_in_adherent fucO; L-1,2-propanediol oxidoreductase; K00048 lactaldehyde reductase [EC:1.1.1.77]	sfx:S3008
b3698_x_at	-2.246977884	0.019885424	Decrease_in_adherent yidB; hypothetical protein	sdv:SDY_4180
F0627_s_at	-2.234157265	0.01123948	Decrease_in_adherent ybdF; hypothetical protein	eum:ECUMN_0669
A2931_s_at	-2.230990929	0.011163993	Decrease_in_adherent yagU; hypothetical protein; K08996 putative membrane protein	eoj:ECO26_0322
A1485_s_at	-2.230513218	0.035843522	Decrease_in_adherent secY; preprotein translocase subunit SecY ; K03076 preprotein translocase subunit SecY	sbc:SbBS512_E3685
F3184_s_at	-2.228185981	0.040515722	Decrease_in_adherent bgIA; 6-phospho-beta-glucosidase A, cryptic ; K01223 6-phospho-beta-glucosidase [EC:3.2.1.86]	ssn:SSON_3054
AFFX-LysX-3_at	-2.225862186	0.005398828	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
V0706_s_at	-2.223254918	0.023130564	Decrease_in_adherent putative resistance protein ; K07245 putative copper resistance protein D	sdv:SDY_1126
M1380_x_at	-2.222259587	0.029759989	Decrease_in_adherent phnO; aminoalkylphosphonic acid N-acetyltransferase ; K09994 PhnO protein [EC:2.3.1.-]	sdv:SDY_4123
A2552_at	-2.21953293	0.030454585	Decrease_in_adherent N4/N6-methyltransferase family protein	ecw:EcE24377A_4904
F0793_s_at	-2.211824983	0.001030624	Decrease_in_adherent pal; peptidoglycan-associated outer membrane lipoprotein ; K03640 peptidoglycan-associated lipoprotein	sbc:SbBS512_E0663
SD1_3096_s_at	-2.211120824	0.024518611	Decrease_in_adherent hypothetical protein	ecc:c4772
A2764_s_at	-2.209395066	0.007162866	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V3520_s_at	-2.203778585	0.035516328	Decrease_in_adherent talI; transaldolase A (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]	sbc:SbBS512_E2830
V1288_x_at	-2.203019624	0.039198371	Decrease_in_adherent lplA; lipote-protein ligase A (EC:6.3.2.-); K03800 lipote-protein ligase A [EC:2.7.7.63]	sbc:SbBS512_E4933
N4246_s_at	-2.198986294	0.005396183	Decrease_in_adherent gpmB; phosphoglycerate mutase (EC:5.4.2.1); K01834 phosphoglycerate mutase [EC:5.4.2.1]	ssn:SSON_4545
A3909_s_at	-2.197376954	0.030681172	Decrease_in_adherent minE; cell division topological specificity factor MinE ; K03608 cell division topological specificity factor	sdv:SDY_1205
EC869_8327_s_at	-2.191345367	0.026305176	Decrease_in_adherent selenophosphate synthetase (EC:2.7.9.3); K01008 selenide, water dikinase [EC:2.7.9.3]	ent:Ent638_1683
V3795_s_at	-2.187688526	0.046912402	Decrease_in_adherent yahK; putative oxidoreductase	ssn:SSON_0308
A1493_s_at	-2.177021385	0.048525524	Decrease_in_adherent ribosomal protein L24 ; K02895 large subunit ribosomal protein L24	dda:Dd703_0416
EC869_2217_s_at	-2.174450912	0.001652157	Decrease_in_adherent did; D-lactate dehydrogenase (EC:1.1.1.28); K03777 D-lactate dehydrogenase [EC:1.1.1.28]	sdv:SDY_2155
AFFX-PheX-5_at	-2.172467819	0.001747308	Decrease_in_adherent pheB; hypothetical protein; K06209 chorismate mutase [EC:5.4.9.5]	bsu:BSU27910
A4724_s_at	-2.170001952	0.039049755	Decrease_in_adherent fnn; ferritin ; K02217 ferritin 1	sdv:SDY_1113
EC869_8985_s_at	-2.162370904	0.018571085	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A4591_s_at	-2.161735676	0.033150948	Decrease_in_adherent aldo/keto reductase family oxidoreductase (EC:1.1.1.218)	ecw:EcE24377A_2005
AFFX-r2-Bs-phe-5_a	-2.158569893	0.001063355	Decrease_in_adherent pheB; hypothetical protein; K06209 chorismate mutase [EC:5.4.9.5]	bsu:BSU27910
V0787_s_at	-2.158465056	0.015271829	Decrease_in_adherent hypothetical protein	ecc:c4772
A3152_s_at	-2.15727236	0.042641015	Decrease_in_adherent ybbA; putative ABC transporter ATP-binding protein YbbA ; K02003	sdv:SDY_0405
AFFX-r2-Bs-thr-3_s_	-2.153867711	0.001756705	Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]	bsu:BSU32240
AFFX-r2-Bs-phe-M_i	-2.149877515	0.006229183	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
b3983_s_at	-2.149829777	0.002371106	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_4522
ECP_2592_s_at	-2.149377028	0.015782012	Decrease_in_adherent transposase	sbc:SbBS512_E1228
pCoo004_s_at	-2.146695787	0.037953922	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_D0044
SB5_4126_s_at	-2.139255818	0.045370818	Decrease_in_adherent grxB; glutaredoxin 2 ; K03675 glutaredoxin 2	sdv:SDY_2089
V1952_s_at	-2.138432746	0.049856312	Decrease_in_adherent yhbS; hypothetical protein ; K03824 putative acetyltransferase [EC:2.3.1.-]	sdv:SDY_3335
V5408_s_at	-2.134835022	0.029333794	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
AFFX-ThrX-3_at	-2.129036274	0.002251387	Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]	bsu:BSU32240
V3429_s_at	-2.125456601	0.004922501	Decrease_in_adherent phosphoribulokinase/uridine kinase family protein ; K00855 phosphoribulokinase [EC:2.7.1.19]	sbc:SbBS512_E3730
A2659_s_at	-2.123173609	0.010267959	Decrease_in_adherent nhaA; pH-dependent sodium/proton antiporter ; K03313 Na ⁺ /H ⁺ antiporter, NhaA family	sbc:SbBS512_E0019
SS5_4205_s_at	-2.122111685	0.033353371	Decrease_in_adherent ycfP; hypothetical protein ; K07000	sdv:SDY_2042
SP0956_s_at	-2.119486961	0.046768138	Decrease_in_adherent ycfG; hypothetical protein ; K09911 hypothetical protein	sdv:SDY_0929
F4536_s_at	-2.11914787	0.026868314	Decrease_in_adherent yjbK; zinc uptake transcriptional repressor ; K09823 Fur family transcriptional regulator, zinc uptake regulator	sdv:SDY_4528
b1846_s_at	-2.118396055	0.003323013	Decrease_in_adherent hypothetical protein	ecx:EcHS_A1937
F3193_s_at	-2.117770503	0.03809498	Decrease_in_adherent ygfB; hypothetical protein ; K09895 hypothetical protein	sdv:SDY_3172
A4104_s_at	-2.117531905	0.034525662	Decrease_in_adherent pspE; thiosulfate:cyanide sulfurtransferase (EC:2.8.1.1); K03972 phage shock protein E	sbc:SbBS512_E1544
F3183_s_at	-2.115022281	0.004876805	Decrease_in_adherent bgIA; 6-phospho-beta-glucosidase BglA (EC:3.2.1.86); K01223 6-phospho-beta-glucosidase [EC:3.2.1.86]	sbc:SbBS512_E3322
V1930_s_at	-2.112712912	0.01874942	Decrease_in_adherent pnp; polynucleotide phosphorylase/polyadenylase ; K00962 polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	sdv:SDY_3343
A1818_s_at	-2.111867299	0.013793087	Decrease_in_adherent glycosyl transferase, group 2 family protein (EC:2.4.1.-); K12983 UDP-glucose:(glucosyl)LPS beta-1,3-glucosyltransferase [EC:2.4.1.10]	sbc:SbBS512_E4050
A1480_s_at	-2.11099992	0.009708878	Decrease_in_adherent DNA-directed RNA polymerase subunit alpha ; K03040 DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]	cko:CKO_04708
A1064_s_at	-2.109780721	0.038223591	Decrease_in_adherent hypothetical protein	ecz:ECSS8_2090
F1250_s_at	-2.109037107	0.024779055	Decrease_in_adherent ycgJ; hypothetical protein	ect:ECIA39_1896
A1821_s_at	-2.101803114	0.040027522	Decrease_in_adherent rfaJ2; lipopolysaccharide 1,2-glucosyltransferase (EC:2.4.1.58); K03276 UDP-glucose/galactose:(glucosyl)LPS alpha-1,2-glucosyltransferase	sbc:SbBS512_E4053

EC869_5719_s_at	-2.101617292	0.00906198	Decrease_in_adherent pntB; pyridine nucleotide transhydrogenase (EC:1.6.1.2); K00325 NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]	sdv:SDY_1551
AFFX-PheX-M_at	-2.095485519	0.004930538	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
AFFX-r2-Bs-lys-5_at	-2.088818571	0.021856054	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
A4154_s_at	-2.088284308	0.012433318	Decrease_in_adherent idhA; D-lactate dehydrogenase (EC:1.1.1.28); K03778 D-lactate dehydrogenase [EC:1.1.1.28]	sbc:SbBS512_E1618
W4306_s_at	-2.087918415	0.017759449	Decrease_in_adherent hypothetical protein	sec:SC2696
C4709_at	-2.086919106	0.04689935	Decrease_in_adherent hypothetical protein ; K00973 glucose-1-phosphate thymidyllyltransferase [EC:2.7.7.24]	cko:CKO_00130
AFFX-ThrX-M_at	-2.085286265	0.001434537	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	bsu:BSU32250
EC869_2195_s_at	-2.083500792	0.007145303	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
S3180_s_at	-2.083321946	0.042537645	Decrease_in_adherent reverse transcriptase-like protein	sfx:S3180
AFFX-r2-Bs-lys-M_at	-2.082929224	0.005693102	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
SD1_3346_s_at	-2.081025705	0.049898422	Decrease_in_adherent ycbB; hypothetical protein	sdv:SDY_2332
S3181_s_at	-2.080898861	0.047600728	Decrease_in_adherent reverse transcriptase-like protein	sfx:S3181
b3320_s_at	-2.078180658	0.038911559	Decrease_in_adherent hypothetical protein	eci:UT189_C3774
V5404_s_at	-2.077067582	0.027273022	Decrease_in_adherent glgA; glycogen synthase GlgA; K00703 starch synthase [EC:2.4.1.21]	eqj:ECO26_4519
A1609_s_at	-2.070038125	0.016354262	Decrease_in_adherent glgB; glycogen branching enzyme (EC:2.4.1.18); K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	ssn:SSON_3672
b2908_s_at	-2.066420735	0.027908476	Decrease_in_adherent pepP; proline aminopeptidase P II ; K01262 X-Pro aminopeptidase [EC:3.4.11.9]	sdv:SDY_3173
AFFX-r2-Bs-thr-5_s_	-2.065092433	0.001665177	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	bsu:BSU32250
A4665_s_at	-2.054811165	0.01026574	Decrease_in_adherent eda; keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase (EC:4.1.2.14 4.1.3.16); K01625 2-dehydro-3-deoxy	sbc:SbBS512_E2125
AFFX-r2-Bs-thr-M_s_	-2.039901151	0.001516586	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	bsu:BSU32250
A1638_s_at	-2.038213288	0.005649696	Decrease_in_adherent livJ; high-affinity amino acid transport system periplasmic binding protein ; K01999 branched-chain amino acid transport system	sdv:SDY_3611
A3367_s_at	-2.03079881	0.01315913	Decrease_in_adherent sucD; succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]	sbc:SbBS512_E0648
A2811_s_at	-2.026198946	0.035513277	Decrease_in_adherent yaeH; hypothetical protein	sdv:SDY_0181
A3040_s_at	-2.021317376	0.049964509	Decrease_in_adherent yaiA; hypothetical protein	sdv:SDY_0354
SB5_0712_s_at	-2.017689748	0.019876349	Decrease_in_adherent qor; quinone oxidoreductase, NADPH-dependent (EC:1.6.5.5); K00344 NADPH2:quinone reductase [EC:1.6.5.5]	ect:ECIAI39_4471
A1504_s_at	-2.004329824	0.025131372	Decrease_in_adherent rpsJ, nusE; 30S ribosomal protein S10 ; K02946 small subunit ribosomal protein S10	sdv:SDY_3497
A1486_s_at	-2.003263161	0.016585239	Decrease_in_adherent rplO; 50S ribosomal protein L15 ; K02876 large subunit ribosomal protein L15	cko:CKO_04713
SB5_0774_s_at	-2.00204317	0.00050454	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_4522
EC869_3782_s_at	-2.001825232	0.042411313	Decrease_in_adherent rplD; 50S ribosomal protein L4 ; K02926 large subunit ribosomal protein L4	cko:CKO_04737
W4315_at	-2.001335341	0.024744644	Decrease_in_adherent hypothetical protein	eca:ECAI014
EC869_1736_s_at	-1.999804098	0.036677212	Decrease_in_adherent galR; DNA-binding transcriptional repressor; K02529 LacI family transcriptional regulator	etw:ECSPP_3790
b3305_s_at	-1.99978708	0.044941647	Decrease_in_adherent rplF; 50S ribosomal protein L6 ; K02933 large subunit ribosomal protein L6	sdv:SDY_3481
V1849_s_at	-1.998455608	0.013940074	Decrease_in_adherent yhdA; regulatory protein CsrD	sdv:SDY_3427
AFFX-ThrX-5_at	-1.989622177	0.001320752	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	bsu:BSU32250
AFFX-LysX-5_at	-1.987499541	0.008525596	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
V5991_s_at	-1.981398568	0.002710742	Decrease_in_adherent dxs; 1-deoxy-D-xylulose-5-phosphate synthase (EC:2.2.1.7); K01662 1-deoxy-D-xylulose-5-phosphate synthase [EC:2.2.1.7]	sdv:SDY_0310
b3186_s_at	-1.962582482	0.029905836	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_3672
AFFX-LysX-M_at	-1.961351486	0.01024491	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
A4073_s_at	-1.961243891	0.034576236	Decrease_in_adherent lipoprotein ; K04062 osmotically inducible lipoprotein OsmB	cko:CKO_01367
A1290_s_at	-1.959752266	0.001562048	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_0737_s_at	-1.959548949	0.03878028	Decrease_in_adherent bcsA; cellulose synthase catalytic subunit (EC:2.4.1.12); K00694 cellulose synthase (UDP-forming) [EC:2.4.1.12]	sbo:SBO_3532
A2616_s_at	-1.959540298	0.044543568	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A4835_at	-1.958862316	0.047733073	Decrease_in_adherent hypothetical protein	ecy:ECSE_2244
A3916_s_at	-1.958424242	0.035372692	Decrease_in_adherent hypothetical protein	sbc:SbBS512_E1335
SD1_2876_s_at	-1.957885969	0.031084002	Decrease_in_adherent ycfJ; hypothetical protein	sdv:SDY_2040
b3928_s_at	-1.956974622	0.013351026	Decrease_in_adherent ytiU; hypothetical protein ; K09892 hypothetical protein	sdv:SDY_3816
A1483_s_at	-1.956543049	0.02709938	Decrease_in_adherent rpsM; 30S ribosomal protein S13 ; K02952 small subunit ribosomal protein S13	sdv:SDY_3474
b2572_s_at	-1.953384576	0.042197022	Decrease_in_adherent rseA; anti-RNA polymerase sigma factor SigE ; K03597 sigma-E factor negative regulatory protein RseA	sdv:SDY_2813
pC15-1a_039_s_at	-1.95328342	0.0383316	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0074_x_at	-1.950410382	0.006986047	Decrease_in_adherent rfbA1; glucose-1-phosphate thymidyllyltransferase (EC:2.7.7.24); K00973 glucose-1-phosphate thymidyllyltransferase [EC:2.7.7.24]	ecw:EcE24377A_2330
A3985_s_at	-1.945071579	0.038407916	Decrease_in_adherent oppD; oligopeptide transporter ATP-binding component ; K02031 peptide/nickel transport system ATP-binding protein	sbc:SbBS512_E1415
SD1_3577_s_at	-1.945009524	0.005099854	Decrease_in_adherent ldcC; lysine decarboxylase 2, constitutive ; K01582 lysine decarboxylase [EC:4.1.1.18]	ssn:SSON_0199
SD1_2776_s_at	-1.943081484	0.019750013	Decrease_in_adherent nadE; NH(3)-dependent Nad(+) synthetase	elf:LF82_1436
SB5_1833_x_at	-1.942206505	0.000928844	Decrease_in_adherent eutC; ethanolamine ammonia-lyase small subunit (EC:4.3.1.7); K03736 ethanolamine ammonia-lyase small subunit [EC:4.3.1.7]	sdv:SDY_2638
A2860_s_at	-1.941989364	0.019844909	Decrease_in_adherent dnaG; DNA polymerase III subunit epsilon ; K02342 DNA polymerase III subunit epsilon [EC:2.7.7.7]	sdv:SDY_0234
A4769_s_at	-1.941700395	0.018665534	Decrease_in_adherent hypothetical protein	ecv:APEC01_991
V5405_s_at	-1.938852511	0.047723301	Decrease_in_adherent glgP; glycogen phosphorylase ; K00688 starch phosphorylase [EC:2.4.1.1]	sdv:SDY_3574
A2197_s_at	-1.928430605	0.015723321	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_4526
V3363_s_at	-1.922644218	0.037848197	Decrease_in_adherent aroD; 3-dehydroquinate dehydratase (EC:4.2.1.10); K03785 3-dehydroquinate dehydratase I [EC:4.2.1.10]	sdv:SDY_1474
ECs1050_s_at	-1.920661973	0.044121655	Decrease_in_adherent hypothetical protein	eci:UT189_C1032
F1202_s_at	-1.914938031	0.00829116	Decrease_in_adherent ycfM; hypothetical protein ; K07337 hypothetical protein	sdv:SDY_2045
b1251_s_at	-1.90502387	0.029600862	Decrease_in_adherent yciI; YciI-like protein ; K09780 hypothetical protein	sbo:SBO_1814
V6992_s_at	-1.903768831	0.021349642	Decrease_in_adherent hypothetical protein ; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	cko:CKO_01066
F4930_s_at	-1.901635338	0.021270656	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V3344_s_at	-1.899897302	0.006200037	Decrease_in_adherent ydiJ; putative oxidase ; K06911	sdv:SDY_1675
EC869_6490_x_at	-1.899142057	0.022442821	Decrease_in_adherent yqiG; putative transferase ; K07393 putative glutathione S-transferase	sdv:SDY_3291
A3589_at	-1.894479093	0.031101254	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_0989
A0767_at	-1.891153971	0.031908931	Decrease_in_adherent mutS; DNA mismatch repair protein MutS ; K03555 DNA mismatch repair protein MutS	ecw:EcE24377A_3030
EC869_2285_s_at	-1.88949112	0.039860102	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3801_s_at	-1.889349174	0.033191241	Decrease_in_adherent me; RNase E: endoribonuclease for rRNA processing and mRNA degradation ; K08300 ribonuclease E [EC:3.1.26.12]	hde:HDEF_0352
A0061_x_at	-1.8864453	0.031365034	Decrease_in_adherent hisI; bifunctional phosphoribosyl-AMP cyclodiolase/phosphoribosyl-ATP pyrophosphatase protein (EC:3.6.1.31 3.5.4.19); K11	ssn:SSON_2097
AFFX-DapX-3_at	-1.885327176	0.003104355	Decrease_in_adherent ypgJ; hypothetical protein	bsu:BSU22470
A1745_s_at	-1.883348479	0.036354598	Decrease_in_adherent yiaG; putative transcriptional regulator ; K07726 putative transcriptional regulator	sdv:SDY_4348
J5322_s_at	-1.882021731	0.006882226	Decrease_in_adherent cell wall-associated hydrolase	bmj:BMULJ_05090
EC536_5493_s_at	-1.876708758	0.032497804	Decrease_in_adherent hypothetical protein	eci:UT189_C0464

V6990_s_at	-1.874672248	0.001898303	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II ; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	ssn:SSON_1231
V2732_s_at	-1.874413695	0.019240863	Decrease_in_adherent glcB; malate synthase G; K01638 malate synthase [EC:2.3.3.9]	ecj:ECC026_4076
c5012_s_at	-1.871654681	0.03018548	Decrease_in_adherent hypothetical protein	ecj:c5012
SD1_2556_s_at	-1.869494711	0.026160304	Decrease_in_adherent yihX; phosphatase ; K07025 putative hydrolase of the HAD superfamily	sdj:SDY_3858
V7336_s_at	-1.868257236	0.008956466	Decrease_in_adherent hypothetical protein	ecj:UT189_C3749
A3783_s_at	-1.868157371	0.01528032	Decrease_in_adherent rimJ; ribosomal-protein-S5-alanine N-acetyltransferase ; K03790 ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]	sdj:SDY_2086
V1600_s_at	-1.867141509	0.013010743	Decrease_in_adherent mutS; DNA mismatch repair protein MutS ; K03555 DNA mismatch repair protein MutS	sdj:SDY_2933
A2000_s_at	-1.864848597	0.021521355	Decrease_in_adherent hemY; putative prothrome IX biogenesis protein ; K02498 HemY protein	sbcb:SbBS512_E4261
SD1_2274_s_at	-1.860400737	0.021917446	Decrease_in_adherent aas; bifunctional acyl-[acyl carrier protein] synthetase-2-acylglycerophosphoethanolamine acyltransferase (EC:2.3.1.40 6.2.1.20)	sbcb:SbBS512_E3026
F3408_s_at	-1.859902936	0.037634922	Decrease_in_adherent glutathionylspermidine synthase family protein	sbcb:SbBS512_E3470
EC869_0195_s_at	-1.857594867	0.027736482	Decrease_in_adherent strA; aminoglycoside-3"-phosphotransferase	cur:cur_1538
AFXF-r2-Bs-dap-3_a	-1.855090849	0.001911642	Decrease_in_adherent ypjG; hypothetical protein	bsu:BSU22470
AFXF-DapX-5_at	-1.851933922	0.00258375	Decrease_in_adherent dapB; dihydroadipiculate reductase (EC:1.3.1.26); K00215 dihydroadipiculate reductase [EC:1.3.1.26]	bsu:BSU22490
V4776_s_at	-1.850770659	0.008717744	Decrease_in_adherent atpD; F0F1 ATP synthase subunit beta [EC:3.6.3.14]; K02112 F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]	sdj:SDY_4016
EC536_2379_s_at	-1.849646214	0.030708441	Decrease_in_adherent ygdE; putative RNA 2'-O-ribose methyltransferase ; K06968	sdj:SDY_3024
EC869_5814_x_at	-1.849482877	0.046628629	Decrease_in_adherent N-ethylmaleimide reductase ; K10680 N-ethylmaleimide reductase [EC:1.-.-.-]	esa:ESA_02010
b3984_s_at	-1.845899093	0.008520268	Decrease_in_adherent rplA; 50S ribosomal protein L1 ; K02863 large subunit ribosomal protein L1	sdj:SDY_3744
AFXF-r2-Bs-dap-5_a	-1.842096634	0.003271585	Decrease_in_adherent dapB; dihydroadipiculate reductase (EC:1.3.1.26); K00215 dihydroadipiculate reductase [EC:1.3.1.26]	bsu:BSU22490
A2049_s_at	-1.839529393	0.013451336	Decrease_in_adherent pepQ; prolidine dipeptidase ; K01271 X-Pro dipeptidase [EC:3.4.13.9]	sdj:SDY_3898
A0182_s_at	-1.831187625	0.009913178	Decrease_in_adherent cdd; cytidine deaminase (EC:3.5.4.5); K01489 cytidine deaminase [EC:3.5.4.5]	sbcb:SbBS512_E0828
ECP_2590_s_at	-1.829625217	0.009267053	Decrease_in_adherent conserved hypothetical protein, putative transposase (fragment)	ecj:ECCED1_3022
b1341_s_at	-1.829472882	0.027904989	Decrease_in_adherent hypothetical protein	sdj:SDY_1420
EC869_0563_s_at	-1.82713166	0.013237837	Decrease_in_adherent prfC; oligopeptidase A ; K01414 oligopeptidase A [EC:3.4.24.70]	sdj:SDY_3564
V6996_s_at	-1.822425276	0.041140436	Decrease_in_adherent tap; methyl-accepting protein IV ; K05877 methyl-accepting chemotaxis protein IV, peptide sensor receptor	sbcb:SbBS512_E2178
V1014_s_at	-1.821679744	0.012911915	Decrease_in_adherent cvpA; colicin V production protein ; K03558 membrane protein required for colicin V production	sdj:SDY_2512
V5329_s_at	-1.815715847	0.037814953	Decrease_in_adherent hypothetical protein	cko:CKO_0490
SBO_3336_s_at	-1.814369327	0.023898688	Decrease_in_adherent ynfA; hypothetical protein ; K07397 putative redox protein	sdj:SDY_3518
V7066_s_at	-1.814234516	0.001734494	Decrease_in_adherent hypothetical protein	ecj:EchHS_A1937
AFXF-DapX-M_at	-1.81204451	0.002894394	Decrease_in_adherent mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3]	bsu:BSU22480
V6896_s_at	-1.810557229	0.020588378	Decrease_in_adherent pncC; required for NMN transport ; K03811 nicotianamine mononucleotide transporter	sdj:SDY_0695
AFXF-r2-Bs-dap-M_i	-1.808025418	0.003404193	Decrease_in_adherent mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3]	bsu:BSU22480
V0414_s_at	-1.807496071	0.008939783	Decrease_in_adherent fusA; elongation factor G ; K02355 elongation factor EF-G [EC:3.6.5.3]	sdj:SDY_3501
A1482_s_at	-1.804630723	0.01211266	Decrease_in_adherent rpsK; 30S ribosomal protein S11 ; K02948 small subunit ribosomal protein S11	sdj:SDY_3473
A2067_s_at	-1.804516569	0.047510923	Decrease_in_adherent hemN; coproporphyrinogen III oxidase (EC:1.3.99.22); K02495 oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]	sbcb:SbBS512_E4342
EC869_2844_s_at	-1.800985107	0.013261066	Decrease_in_adherent miaA; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase ; K07971 tRNA delta(2)-isopentenylpyrophosphate transferase [EC:2.7.7.1]	ecj:ECCSP_5271
A1499_s_at	-1.79568207	0.026339725	Decrease_in_adherent hypothetical protein	scj:SC3369
EC869_5206_s_at	-1.793446273	0.019382775	Decrease_in_adherent secA; azi, div; preprotein translocase subunit SecA ; K03070 preprotein translocase subunit SecA	sdj:SDY_0128
SS5_3503_s_at	-1.792077217	0.01710286	Decrease_in_adherent yieP; hypothetical protein	ssn:SSON_3925
A1230_s_at	-1.780213953	0.004403403	Decrease_in_adherent hypothetical protein	sbcb:SbBS512_E3475
EC869_4279_s_at	-1.780076409	0.003838237	Decrease_in_adherent channel protein, hemolysin III family ; K11068 hemolysin III	sbcb:SbBS512_E3320
F3660_s_at	-1.776385315	0.013937713	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
F3192_at	-1.772483841	0.029238428	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V1601_s_at	-1.771326849	0.009517249	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
D0357_x_at	-1.763122082	0.008842884	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3838_s_at	-1.761382614	0.039099851	Decrease_in_adherent cobB; NAD-dependent deacetylase ; K12410 NAD-dependent deacetylase [EC:3.5.1.-]	sdj:SDY_2030
A2040_s_at	-1.759690921	0.024818477	Decrease_in_adherent tatA; twin arginine translocase protein A ; K03116 sec-independent protein translocase protein TatA	sdj:SDY_3907
EC869_4308_x_at	-1.754265077	0.04822162	Decrease_in_adherent pepP; prolidine aminopeptidase P.II (EC:3.4.11.9); K01262 X-Pro aminopeptidase [EC:3.4.11.9]	sbcb:SbBS512_E3329
EC536_2815_s_at	-1.753342847	0.047573619	Decrease_in_adherent ampE; predicted inner membrane protein; K03807 AmpE protein	ecj:ECCSP_0112
A0436_s_at	-1.748525156	0.044913603	Decrease_in_adherent ptsH; phosphocarrier protein HPr (EC:2.7.1.69 2.7.3.9); K02784 phosphocarrier protein HPr	ctu:ctu_30130
pWRMS01_p125_at	-1.744982805	0.000470059	Decrease_in_adherent hypothetical protein	ecj:ECPC88_0004
V2056_s_at	-1.744697117	0.005593048	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_1228_s_at	-1.742528457	0.0434917	Decrease_in_adherent cobB; Sir2 family NAD-dependent protein deacetylase; K12410 NAD-dependent deacetylase [EC:3.5.1.-]	asa:ASA_1963
V5190_s_at	-1.738258552	0.003832738	Decrease_in_adherent bcsE; cellulose biosynthesis protein BcsE	sbcb:SbBS512_E4000
V3848_s_at	-1.737672071	0.021621828	Decrease_in_adherent tolC; outer membrane channel protein ; K12340 outer membrane channel protein TolC	sdj:SDY_3205
SD1_2612_s_at	-1.737599173	0.014131708	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V5388_s_at	-1.735907469	0.032968013	Decrease_in_adherent aas; aspartate-semialdehyde dehydrogenase (EC:1.2.1.11); K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	sbcb:SbBS512_E3891
A4294_at	-1.721553713	0.002569809	Decrease_in_adherent hypothetical protein	ecw:ECE24377A_1703
SSO_2654_x_at	-1.71663299	0.006589989	Decrease_in_adherent IS629 ORF2 ; K07497 putative transposase	ssn:SSON_2654
A2283_s_at	-1.707365898	0.000342475	Decrease_in_adherent yjcE; hypothetical protein ; K03316 monovalent cation:H+ antiporter, CPA1 family	sdj:SDY_4502
A0009_s_at	-1.704488819	0.036433344	Decrease_in_adherent amn; AMP nucleosidase ; K01241 AMP nucleosidase [EC:3.2.2.4]	etfLF_D28_0084
A3304_s_at	-1.700543238	0.020511375	Decrease_in_adherent putative metalloprotease ; K07042	sbcb:SbBS512_E0588
A3365_s_at	-1.700513162	0.024235765	Decrease_in_adherent sucB; dihydrolipoamide succinyltransferase (EC:2.3.1.61); K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamoyl)	sdj:SDY_0665
EC869_7371_s_at	-1.696183395	0.023573993	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SBO_2958_x_at	-1.695796638	0.031240562	Decrease_in_adherent insD; IS2 element protein	ecj:JW5933
A2354_s_at	-1.695741445	0.014658753	Decrease_in_adherent cutA; divalent-cation tolerance protein CutA ; K03926 periplasmic divalent cation tolerance protein	sdj:SDY_4442
A2625_s_at	-1.691663534	0.049000851	Decrease_in_adherent deoD; purine nucleoside phosphorylase (EC:2.4.2.1); K03784 purine-nucleoside phosphorylase [EC:2.4.2.1]	sdj:SDY_4644
EC869_3772_s_at	-1.691085919	0.022497576	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2185_s_at	-1.68922901	0.041928947	Decrease_in_adherent btuB; vitamin B12/cobalamin outer membrane transporter ; K02014 iron complex outer membrane receptor protein	ssn:SSON_4139
SB5_4569_s_at	-1.688360246	0.044862864	Decrease_in_adherent putative transposase	kpu:KP1_3603
A0847_s_at	-1.687359978	0.040452733	Decrease_in_adherent fucI; protein of fucose operon ; K02431 L-fucose mutarotase [EC:5.1.3.-]	sdj:SDY_3022
N4419_at	-1.685879877	0.040427603	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1747_s_at	-1.685498331	0.002202968	Decrease_in_adherent glyS; glycyl-tRNA synthetase subunit beta (EC:6.1.1.14); K01879 glycyl-tRNA synthetase beta chain [EC:6.1.1.14]	sbcb:SbBS512_E3966
V3472_s_at	-1.684429623	0.037197143	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2272_s_at	-1.683813405	0.003338814	Decrease_in_adherent hypothetical protein	cko:CKO_03844

A1330_s_at	-1.683648255	0.005975563	Decrease_in_adherent agaR; DNA-binding transcriptional regulator AgaR; K02081 DeoR family transcriptional regulator, aga operon transcriptional repressor	sf: S3381
A1221_s_at	-1.683276456	0.027735947	Decrease_in_adherent icc; cyclic 3',5'-adenosine monophosphate phosphodiesterase; K03651 Icc protein	sd: SDY_3208
V1285_s_at	-1.682223022	0.00487318	Decrease_in_adherent deoB; phosphopentomutase (EC:5.4.2.7); K01839 phosphopentomutase [EC:5.4.2.7]	sd: SDY_4643
A3853_s_at	-1.67875985	0.005600448	Decrease_in_adherent hypothetical protein	ec: ECH74115_2279
ECP_3173_s_at	-1.675657819	0.021857139	Decrease_in_adherent hypothetical protein	ec: ECP_3173
b2217_s_at	-1.670862433	0.035219713	Decrease_in_adherent transcriptional regulator RcsB; K07687 two-component system, NarL family, capsular synthesis response regulator RcsB	cko: CKO_00553
L1644_s_at	-1.665387639	0.049757078	Decrease_in_adherent mvpT; putative post-segregational killing toxin	ec: E2C026_3521
b3283_s_at	-1.661590032	0.049007997	Decrease_in_adherent yrdD; putative DNA topoisomerase; K07479 putative DNA topoisomerase	sd: SDY_3460
SDM_4116_x_at	-1.659165282	0.003377262	Decrease_in_adherent transposase	spi: MGAS10750_Spy0657
A1678_s_at	-1.65896197	0.044613432	Decrease_in_adherent gor; glutathione reductase (EC:1.8.1.7); K00383 glutathione reductase (NADPH) [EC:1.8.1.7]	sd: SDY_3562
EC869_0750_s_at	-1.658643949	0.033681143	Decrease_in_adherent yhjL; putative oxidoreductase subunit	sbo: SBO_3529
SS5_4621_s_at	-1.657842655	0.024608571	Decrease_in_adherent yihF; hypothetical protein	ec: ECO103_4309
V5395_s_at	-1.651176359	0.046731677	Decrease_in_adherent glgX; glycogen debranching enzyme; K02438 glycogen operon protein GlgX [EC:3.2.1.-]	sd: SDY_3577
V2429_s_at	-1.64964153	0.001009995	Decrease_in_adherent fadR; fatty acid metabolism regulator; K03603 GntR family transcriptional regulator, negative regulator for fad regulon and positive regulator for fad regulon	sd: SDY_1224
A2816_s_at	-1.642063212	0.003835267	Decrease_in_adherent hypothetical protein	ec: APEC01_1817
A0532_s_at	-1.638950026	0.019058861	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SFV_3732_s_at	-1.632619741	0.029358285	Decrease_in_adherent ilvE; branched-chain amino acid aminotransferase (EC:2.6.1.42); K00826 branched-chain amino acid aminotransferase [EC:2.6.1.42]	sf: SFV_3732
V2162_s_at	-1.626758992	0.021585055	Decrease_in_adherent tldD; protease TldD; K03568 TldD protein	ssn: SS0N_3386
SD1_1427_x_at	-1.62639457	0.011049472	Decrease_in_adherent rne; fused ribonucleaseE: endoribonuclease/RNA-binding protein/RNA degradosome binding protein; K08300 ribonuclease E [EC:3.1.27.1]	ec: BWG_0932
V6077_s_at	-1.626274701	0.036788534	Decrease_in_adherent ddi; D-alanyl-alanine synthetase A (EC:6.3.2.4); K01921 D-alanine-D-alanine ligase [EC:6.3.2.4]	sb: SbBS512_E0298
V0117_s_at	-1.621627085	0.025485811	Decrease_in_adherent yjcZ; hypothetical protein	ec: E2C026_5222
A1527_s_at	-1.604954134	0.019911665	Decrease_in_adherent crp; cAMP-regulatory protein; K10914 CRP/FNR family transcriptional regulator, cyclic AMP receptor protein	ec: EcE24377A_3827
A4774_s_at	-1.604673562	0.039638059	Decrease_in_adherent hypothetical protein	ec: ECUMN_2248
S1910_x_at	-1.602758746	0.036894431	Decrease_in_adherent IS629 orfB	sf: S1910
A1830_s_at	-1.600239712	0.032820124	Decrease_in_adherent rpmB; 50S ribosomal protein L28; K02902 large subunit ribosomal protein L28	kpu: KP1_5329
A1226_s_at	-1.584526716	0.011936434	Decrease_in_adherent hypothetical protein	sb: SbBS512_E3469
EC869_5213_s_at	-1.579036658	0.033041796	Decrease_in_adherent hypothetical protein	sbo: SBO_0084
EC536_0056_s_at	-1.575346743	0.017518671	Decrease_in_adherent galK; galactokinase (EC:2.7.1.6); K00849 galactokinase [EC:2.7.1.6]	sd: SDY_0704
EC869_2729_s_at	-1.571062196	0.046551007	Decrease_in_adherent ushA; bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic precursor (EC:3.1.3.5 3.6.1.45); K11751 5'-nucleotidase / UDP-glucose 5-phosphatase	sd: SDY_0438
SSO_3593_x_at	-1.568250578	0.0233295	Decrease_in_adherent IS629 ORF2	sd: SDY_P062
V1458_s_at	-1.560700395	0.030793693	Decrease_in_adherent sdaA; L-serine ammonia-lyase 1 (EC:4.3.1.17); K01752 L-serine dehydratase [EC:4.3.1.17]	sb: SbBS512_E2075
F4327_s_at	-1.558594934	0.005874529	Decrease_in_adherent hypothetical protein	bmj: BMULJ_05092
c3926_s_at	-1.558269939	0.004797683	Decrease_in_adherent nusA; transcription elongation factor NusA; K02600 N utilization substance protein A	ssn: SS0N_3315
V2858_s_at	-1.55578134	0.042782613	Decrease_in_adherent epd; erythrose 4-phosphate dehydrogenase; K03472 D-erythrose 4-phosphate dehydrogenase [EC:1.2.1.72]	sd: SDY_3155
V6233_s_at	-1.555117376	0.011399756	Decrease_in_adherent fdnG; formate dehydrogenase N, nitrate-inducible, alpha subunit; K08348 formate dehydrogenase-N, alpha subunit [EC:1.2.1.2]	sbo: SBO_1583
A1479_s_at	-1.553258699	0.005318093	Decrease_in_adherent rplQ; 50S ribosomal protein L17; K02879 large subunit ribosomal protein L17	sd: SDY_3470
A0762_s_at	-1.552545488	0.033614957	Decrease_in_adherent IS3 ORF1	sf: SFV_2924
F3693_s_at	-1.552448076	0.044195674	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V4454_s_at	-1.551263287	0.040786766	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SD1_1429_s_at	-1.545814815	0.017190173	Decrease_in_adherent figL; flagellar hook-associated protein FigL; K02397 flagellar hook-associated protein 3 FigL	sd: SDY_2068
b3207_s_at	-1.544619153	0.035134191	Decrease_in_adherent yrbL; hypothetical protein	ssn: SS0N_3355
A0078_s_at	-1.540399612	0.027401744	Decrease_in_adherent galF; UTP--glucose-1-phosphate uridylyltransferase subunit GalF; K00963 UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.1.60]	sd: SDY_2203
EC869_1179_s_at	-1.536666035	0.034721666	Decrease_in_adherent ptsG; glucose-specific PTS system IIBC components; K02778 PTS system, glucose-specific IIB component [EC:2.7.1.69]; K02779 PTS system, glucose-specific IIB component	sd: SDY_2049
SB5_1478_x_at	-1.53616951	0.008111675	Decrease_in_adherent insertion sequence 2 OrfA protein	sd: SDY_2774
c3662_s_at	-1.528786538	0.010871909	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2092_s_at	-1.528192741	0.038500621	Decrease_in_adherent hypothetical protein	ec: E2C026_4700
SB5_0532_x_at	-1.527343078	0.025686622	Decrease_in_adherent IS1 orfA	sf: S4666
c3612_x_at	-1.522878137	0.04029976	Decrease_in_adherent insC; IS2 insertion element repressor InsA; KpLE2 phage-like element	ec: ECUMN_3359
EC536_6355_s_at	-1.518395157	0.010478881	Decrease_in_adherent trpS; tryptophanyl-tRNA synthetase (EC:6.1.1.2); K01867 tryptophanyl-tRNA synthetase [EC:6.1.1.2]	sd: SDY_3695
SF1779_s_at	-1.516019914	0.034415803	Decrease_in_adherent hypothetical protein	sf: S1495
K2638_s_at	-1.504680573	0.004560684	Decrease_in_adherent flgK; flagellar hook-associated protein FlgK; K02396 flagellar hook-associated protein 1 FlgK	cko: CKO_01977
SS5_0656_x_at	-1.497202741	0.014762491	Decrease_in_adherent insC; insertion sequence 2 OrfA protein	ec: p1ECUMN_0004
A3809_s_at	-1.494008419	0.023982112	Decrease_in_adherent fabG; 3-ketoacyl-(acyl-carrier-protein) reductase (EC:1.1.1.100); K00059 3-oxoacyl-(acyl-carrier protein) reductase [EC:1.1.1.100]	sb: SbBS512_E2231
APEC01_2262_x_at	-1.491420619	0.002237151	Decrease_in_adherent insA; IS1 repressor protein InsA	ec: ECS88_4717
SB5_4770_x_at	-1.488896614	0.027814789	Decrease_in_adherent fimD; outer membrane usher protein FimD; K07347 outer membrane usher protein	ec: ECO111_5171
S1960_x_at	-1.480929803	0.035830695	Decrease_in_adherent IS629 ORF2	sf: SFV_3863
A3397_s_at	-1.476855794	0.000387101	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0665_s_at	-1.476127421	0.002668371	Decrease_in_adherent IS21 family transposase	ec: EcE24377A_E0036
A2894_s_at	-1.473933435	0.008928402	Decrease_in_adherent hypothetical protein	ec: EcE24377A_0258
V1968_s_at	-1.473493808	0.044075849	Decrease_in_adherent yraO; DnaA initiator-associating protein DiaA; K12961 DnaA initiator-associating protein	sd: SDY_3328
SSO_P077_s_at	-1.471674687	0.000866555	Decrease_in_adherent putative transposase	sd: SDY_P156
LH0104_s_at	-1.468751739	0.039990871	Decrease_in_adherent hypothetical protein	ssn: SS0N_2657
A3018_s_at	-1.467434202	0.043883532	Decrease_in_adherent hmbB; delta-aminolevulinic acid dehydratase (EC:4.2.1.24); K01698 porphobilinogen synthase [EC:4.2.1.24]	sd: SDY_0501
A3567_s_at	-1.464936793	0.049065666	Decrease_in_adherent lolA; outer-membrane lipoprotein carrier protein; K03634 outer membrane lipoproteins carrier protein	sd: SDY_2370
SBO_0426_x_at	-1.463580351	0.043296895	Decrease_in_adherent insertion sequence 2 OrfA protein	sd: SDY_P216
b3231_s_at	-1.46099813	0.023128866	Decrease_in_adherent rplM; 50S ribosomal protein L13; K02871 large subunit ribosomal protein L13	sf: SFV_3258
EC869_1162_s_at	-1.456975187	0.03050516	Decrease_in_adherent fabG; 3-ketoacyl-(acyl-carrier-protein) reductase (EC:1.1.1.100); K00059 3-oxoacyl-(acyl-carrier protein) reductase [EC:1.1.1.100]	sd: SDY_2057
SDY_2663_s_at	-1.455037411	0.035323272	Decrease_in_adherent hypothetical protein; K07054	sd: SDY_2663
SD1_1891_s_at	-1.452352606	0.002077395	Decrease_in_adherent ybaO; putative LRP-like transcriptional regulator; K05800 Lrp/AsnC family transcriptional regulator	sd: SDY_0384
A2206_s_at	-1.447465334	0.037085448	Decrease_in_adherent nudC; NADH pyrophosphatase (EC:3.6.1.22); K03426 NAD+ diphosphatase [EC:3.6.1.22]	sb: SbBS512_E4487
S1911_x_at	-1.445719746	0.009563749	Decrease_in_adherent IS629 orfB	sf: S1911
b1886_s_at	-1.444509564	0.005603204	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	ssn: SS0N_1231
c5509_x_at	-1.438135039	0.028318503	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
S0120_s_at	-1.434519209	0.032260379	Decrease_in_adherent speE; spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]	sd: SDY_0028

V6499_s_at	-1.432319882	0.031540026	Decrease_in_adherent fabI; enoyl-(acyl carrier protein) reductase (EC:1.3.1.10); K00208 enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9]	sdv:SDY_1368
EC869_5327_s_at	-1.429192817	0.005419602	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V7153_s_at	-1.421811203	0.015710049	Decrease_in_adherent rnfB; dihydropteridine reductase (EC:1.5.1.34); K10679 nitroreductase / dihydropteridine reductase [EC:1.5.1.34]	efe:EFER_2531
ECP_3250_s_at	-1.419817615	0.026619956	Decrease_in_adherent dead; ATP-dependent RNA helicase Dead (EC:3.6.1.-); K05592 ATP-dependent RNA helicase Dead	sbcb:SbBS512_E3609
SD1_3080_s_at	-1.415504644	0.045384944	Decrease_in_adherent proline dipeptidase; K01271 X-Pro dipeptidase [EC:3.4.13.9]	cko:CKO_00190
F4312_s_at	-1.41264553	0.048691814	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V5769_s_at	-1.4111405305	0.043055029	Decrease_in_adherent ppc; phosphoenolpyruvate carboxylase (EC:4.1.1.31); K01595 phosphoenolpyruvate carboxylase [EC:4.1.1.31]	sdv:SDY_3791
SBO_4349_x_at	-1.4101114975	0.006122424	Decrease_in_adherent insertion element IS2 transposase InsD	sdv:SDY_P215
b1577_s_at	-1.409661949	0.027052892	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0582_s_at	-1.407965839	0.048362303	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
F0132_s_at	-1.406057968	0.010762135	Decrease_in_adherent speE; spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]	sdv:SDY_0028
pCoo050_at	-1.402997709	0.046907334	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b0097_s_at	-1.402497434	0.04154231	Decrease_in_adherent yacA; SecA regulator SecM	ssn:SSON_0105
SD1_1426_s_at	-1.399860136	0.027441821	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3822_s_at	-1.39863414	0.022221006	Decrease_in_adherent ycfM; hypothetical protein ; K07337 hypothetical protein	sdv:SDY_2045
V0946_s_at	-1.396775583	0.00268964	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SBS_4491_x_at	-1.394371139	0.01071121	Decrease_in_adherent insertion element protein	kpn:KPN_02839
A3624_s_at	-1.394320022	0.015288639	Decrease_in_adherent aspC; aromatic amino acid aminotransferase (EC:2.6.1.57); K00813 aspartate aminotransferase [EC:2.6.1.1]	sdv:SDY_2329
EC869_8104_s_at	-1.392464533	0.044905182	Decrease_in_adherent guaA; GMP synthase (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]	sbo:SBO_2531
A3448_s_at	-1.384949605	0.009663793	Decrease_in_adherent uvrB; excinuclease ABC subunit B ; K03702 excinuclease ABC subunit B	sdv:SDY_0827
A1640_s_at	-1.363355164	0.024452233	Decrease_in_adherent ftsX; cell division protein FtsX ; K09811 cell division transport system permease protein	sdv:SDY_3613
EC869_7544_s_at	-1.361771763	0.020987803	Decrease_in_adherent lipA; lipoyl synthase ; K03644 lipoyl synthetase [EC:2.8.1.8]	sdv:SDY_0550
V4620_s_at	-1.357735618	0.02412651	Decrease_in_adherent htrA; serine endoprotease ; K04771 serine protease Do [EC:3.4.21.107]	sdv:SDY_0178
L2312_s_at	-1.355876558	0.026819826	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b0917_s_at	-1.348228501	0.04892529	Decrease_in_adherent ycaR; hypothetical protein ; K09791 hypothetical protein	sdv:SDY_2341
V3441_x_at	-1.345224058	0.002192194	Decrease_in_adherent yfeK; hypothetical protein	sbo:SBO_2445
A0889_s_at	-1.341274108	0.013047312	Decrease_in_adherent tas; putative aldo-keto reductase	sdv:SDY_3051
b2293_s_at	-1.340796805	0.012024691	Decrease_in_adherent yfbT; putative phosphatase	sdv:SDY_2489
V0855_s_at	-1.339560495	0.028196655	Decrease_in_adherent purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]	sdv:SDY_4412
EC869_0399_s_at	-1.337286192	0.034559368	Decrease_in_adherent glgB; glycogen branching enzyme (EC:2.4.1.18); K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	sdv:SDY_3578
V6412_s_at	-1.333073368	0.033670147	Decrease_in_adherent fumarate/nitrate reduction transcriptional regulator ; K01420 CRP/FNR family transcriptional regulator, anaerobic regulatory protein	cko:CKO_01409
A1103_at	-1.329903768	0.039656872	Decrease_in_adherent rafR; HTH-type transcriptional regulator RafR ; K02529 LacI family transcriptional regulator	ecw:EcE24377A_3379
pWR501_p053_x_at	-1.329178424	0.003089726	Decrease_in_adherent insA; IS1 ORF1	ctf:CP0049
A3267_s_at	-1.329071299	0.008173239	Decrease_in_adherent lipoyl synthase ; K03644 lipoyl synthetase [EC:2.8.1.8]	cko:CKO_02530
ECP_0709_s_at	-1.329068299	0.037429633	Decrease_in_adherent pgm; phosphoglucomutase ; K01835 phosphoglucomutase [EC:5.4.2.2]	eff:LF82_1632
A2172_at	-1.32891141	0.049728114	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A4461_s_at	-1.327612825	0.042021335	Decrease_in_adherent purR; DNA-binding transcriptional repressor PurR ; K03604 LacI family transcriptional regulator, purine nucleotide synthesis repressor	sbcb:SbBS512_E1857
EC869_8432_s_at	-1.32549676	0.006455924	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3821_s_at	-1.323531787	0.017301821	Decrease_in_adherent ycfL; hypothetical protein	ssn:SSON_1124
A2002_s_at	-1.321683224	0.03704478	Decrease_in_adherent hemD; uroporphyrinogen III synthase HemD; K01719 uroporphyrinogen-III synthase [EC:4.2.1.75]	eoj:ECO26_4785
ECs3179_s_at	-1.318234708	0.04208142	Decrease_in_adherent hypothetical protein ; K09899 hypothetical protein	sdv:SDY_2491
EC869_8932_s_at	-1.31676988	0.002353625	Decrease_in_adherent yihA; GTP-binding protein; K03978 GTP-binding protein	etw:ECSP_4917
A1472_s_at	-1.315739554	0.04725499	Decrease_in_adherent def; peptide deformylase (EC:3.5.1.88); K01462 [EC:3.5.1.88]	sdv:SDY_3463
EC869_4317_s_at	-1.309076623	0.008713328	Decrease_in_adherent serA; D-3-phosphoglycerate dehydrogenase ; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	sdv:SDY_3169
EC869_3950_s_at	-1.306045176	0.028486761	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V1193_s_at	-1.305997908	0.01543759	Decrease_in_adherent aromatic amino acid aminotransferase ; K00813 aspartate aminotransferase [EC:2.6.1.1]	cko:CKO_02139
b3375_s_at	-1.303345587	0.019486203	Decrease_in_adherent friR; DNA-binding transcriptional regulator FriR ; K10711 GntR family transcriptional regulator, friABCD operon transcriptional repressor	sbcb:SbBS512_E3752
A2027_at	-1.302844963	0.0050975	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SFV_2319_s_at	-1.302061844	0.039596556	Decrease_in_adherent competence damage-inducible protein A ; K03742 competence/damage-inducible protein ClnA	ssn:SSON_2310
V4150_s_at	-1.296487937	0.030570637	Decrease_in_adherent recO; DNA repair protein RecO ; K03584 DNA repair protein RecO (recombination protein O)	sdv:SDY_2806
A1497_s_at	-1.294588957	0.01556704	Decrease_in_adherent hypothetical protein	eci:UT189_C3763
SDM_3114_x_at	-1.293424472	0.012604231	Decrease_in_adherent insA; IS1 ORF1	sdv:SDY_3303
V3565_s_at	-1.291393625	0.047829285	Decrease_in_adherent lipoprotein ; K07287 lipoprotein-34	cko:CKO_00310
A1555_s_at	-1.281383769	0.007217384	Decrease_in_adherent gph; phosphoglycolate phosphatase (EC:3.1.3.18); K01091 phosphoglycolate phosphatase [EC:3.1.3.18]	ecw:EcE24377A_3854
SBS_0656_s_at	-1.281077913	0.049821738	Decrease_in_adherent phnA; hypothetical protein ; K06193 phosphonoacetate hydrolase [EC:3.11.1.2]	sdv:SDY_4109
D4795_s_at	-1.279597405	0.035209711	Decrease_in_adherent ybl207; hypothetical protein	ebi:B21_03841
SD1_2025_s_at	-1.277569285	0.045699387	Decrease_in_adherent yafK; hypothetical protein	efe:EFER_0250
A1139_x_at	-1.277050367	0.044148455	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_3416
EC869_4608_x_at	-1.27609242	0.033190442	Decrease_in_adherent pgm; phosphoglucomutase (EC:5.4.2.2); K01835 phosphoglucomutase [EC:5.4.2.2]	sdv:SDY_0628
V1937_s_at	-1.275577024	0.007829111	Decrease_in_adherent ATP-dependent RNA helicase Dead ; K05592 ATP-dependent RNA helicase Dead	cko:CKO_04559
EC869_4323_s_at	-1.274360887	0.037598331	Decrease_in_adherent iclA; chromosome replication initiation inhibitor protein ; K05596 LysR family transcriptional regulator, chromosome initiation inhibitor	sdv:SDY_3165
A1392_s_at	-1.272927762	0.021250145	Decrease_in_adherent Moe family protein ; K02067 putative ABC transport system substrate-binding protein	sbcb:SbBS512_E3577
b0219_s_at	-1.259937826	0.048733265	Decrease_in_adherent yafV; hypothetical protein; K01506 [EC:3.5.-.-]	sfk:S0290
EC869_1548_s_at	-1.256998996	0.01204497	Decrease_in_adherent nudF; ADP-ribose pyrophosphatase NudF (EC:3.6.1.13); K01515 ADP-ribose pyrophosphatase [EC:3.6.1.13]	sdv:SDY_3206
S0607_x_at	-1.256882001	0.034816699	Decrease_in_adherent IS1 orfA	sfk:S0607
A1510_s_at	-1.25398898	0.048128607	Decrease_in_adherent rpsG; 30S ribosomal protein S7; K02992 small subunit ribosomal protein S7	ctu:CTu_38550
V4364_s_at	-1.253176535	0.015155379	Decrease_in_adherent dinI; DNA damage-inducible protein I ; K12149 DNA-damage-inducible protein I	ssn:SSON_1081
V6747_s_at	-1.252364413	0.044411664	Decrease_in_adherent tas; putative aldo-keto reductase	sdv:SDY_3051
c5166_x_at	-1.250429942	0.035622453	Decrease_in_adherent partial transposase	ecc:c5166
EC869_8287_x_at	-1.248528128	0.034301641	Decrease_in_adherent yfeK; hypothetical protein	sbo:SBO_2445
V2361_s_at	-1.241351143	0.013460532	Decrease_in_adherent flilY; cystine transporter subunit ; K02424 cystine transport system substrate-binding protein	sbcb:SbBS512_E1048
EC869_8539_s_at	-1.238691065	0.033689828	Decrease_in_adherent purB; adenylosuccinate lyase (EC:4.3.2.2); K01756 adenylosuccinate lyase [EC:4.3.2.2]	sbcb:SbBS512_E1309
A2736_s_at	-1.237905996	0.016035431	Decrease_in_adherent ddi; D-alanine-D-alanine ligase (EC:6.3.2.4); K01921 D-alanine-D-alanine ligase [EC:6.3.2.4]	ecw:EcE24377A_0094
A2277_s_at	-1.236068368	0.007366908	Decrease_in_adherent soxS; DNA-binding transcriptional regulator SoxS	sbcb:SbBS512_E4580

EC869_4779_s_at	-1.23337565	0.004821461	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
L0896_x_at	-1.224407781	0.013767351	Decrease_in_adherent insA; IS1 repressor protein InsA; KpLE2 phage-like element	eum:ECUMN_4863
D4749_s_at	-1.22358806	0.03995356	Decrease_in_adherent relaxosome component	seh:SeHA_A0073
A3799_s_at	-1.221967216	0.041660457	Decrease_in_adherent flgK; flagellar hook-associated protein FlgK ; K02396 flagellar hook-associated protein 1 FlgK	sbcs:SbBS512_E2243
K3789_x_at	-1.214367085	0.022861184	Decrease_in_adherent IS1 orfA	sfx:S4666
SD1_2374_s_at	-1.203872042	0.011095895	Decrease_in_adherent recA; recombinase A ; K03553 recombination protein RecA	sdys:SDY_2895
SBO_0253_at	-1.203337891	0.028635786	Decrease_in_adherent IS629 ORF1	sbo:SBO_0253
A4465_s_at	-1.200869872	0.043657135	Decrease_in_adherent ribE; riboflavin synthase subunit alpha (EC:2.5.1.9); K00793 riboflavin synthase alpha chain [EC:2.5.1.9]	sdys:SDY_1888
V7090_s_at	-1.195816594	0.013066062	Decrease_in_adherent yebT; hypothetical protein	eoj:ECO26_2604
b4392_s_at	-1.194458882	0.013133345	Decrease_in_adherent slt; lytic murein transglycosylase ; K08309 soluble lytic murein transglycosylase [EC:3.2.1.-]	sdys:SDY_4653
SB5_0182_x_at	-1.189726122	0.00036108	Decrease_in_adherent insA; hypothetical protein	sdys:SDY_PA02
V0344_x_at	-1.180326435	0.023975449	Decrease_in_adherent methH; B12-dependent methionine synthase (EC:2.1.1.13); K00548 5-methyltetrahydrofolate--homocysteine methyltransferase [sbo:SBO_4040
V2369_s_at	-1.169264095	0.014852187	Decrease_in_adherent flhD; flagellar capping protein; K02407 flagellar hook-associated protein 2	eum:ECUMN_2216
A4817_s_at	-1.163580523	0.019530294	Decrease_in_adherent IS21 family transposition helper protein	ecw:Ece24377A_E0035
A2124_s_at	-1.158075181	0.009214396	Decrease_in_adherent cpxA; two-component sensor protein (EC:2.7.3.-); K07640 two-component system, OmpR family, sensor histidine kinase CpxA [sbcs:SbBS512_E4391
b3771_s_at	-1.149661215	0.011712624	Decrease_in_adherent dihydroxy-acid dehydratase (EC:4.2.1.9); K01687 dihydroxy-acid dehydratase [EC:4.2.1.9]	ppr:PBPA3595
S0328_x_at	-1.148882939	0.016678603	Decrease_in_adherent IS629, orfA	sfx:S0328
EC869_7445_s_at	-1.143759666	0.043894134	Decrease_in_adherent glnS; glutamyl-tRNA synthetase; K01886 glutamyl-tRNA synthetase [EC:6.1.1.18]	etw:ECSF_0727
A4644_s_at	-1.142757794	0.026640689	Decrease_in_adherent htpX; heat shock protein HtpX ; K03799 heat shock protein HtpX [EC:3.4.24.-]	sdys:SDY_1977
SB5_4819_x_at	-1.140889607	0.000137195	Decrease_in_adherent insertion element protein	eci:EcolC_3185
SB5_1543_x_at	-1.137608949	0.002731049	Decrease_in_adherent IS1 transposase orfA	sbcs:SbBS512_E3449
V5131_x_at	-1.134028764	0.028154581	Decrease_in_adherent glyS; glycyl-tRNA synthetase subunit beta (EC:6.1.1.14); K01879 glycyl-tRNA synthetase beta chain [EC:6.1.1.14]	sbcs:SbBS512_E3966
V2336_x_at	-1.129018627	0.031194561	Decrease_in_adherent IS1 ORF	ssn:SSON_0977
V5164_s_at	-1.117250049	0.031653576	Decrease_in_adherent phosphoethanolamine transferase (EC:3.1.6.-); K12975 phosphoethanolamine transferase	sbcs:SbBS512_E3983
V0008_x_at	-1.117120822	0.034561338	Decrease_in_adherent def; peptide deformylase (EC:3.5.1.88); K01462 [EC:3.5.1.88]	sdys:SDY_3463
V4159_s_at	-1.116399864	0.04110553	Decrease_in_adherent GTP-binding protein LepA ; K03596 GTP-binding protein LepA	nmu:Nmul_A1751
A3266_s_at	-1.114396497	0.019362425	Decrease_in_adherent tatE; twin arginine translocase protein E ; K03425 sec-independent protein translocase protein TatE	sdys:SDY_0549
J0063_at	-1.112552261	0.005044151	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2297_s_at	-1.108261238	0.004501139	Decrease_in_adherent yjcO; hypothetical protein ; K07126	ssn:SSON_4259
SDY_2387_x_at	-1.104287838	0.00553387	Decrease_in_adherent IS1 ORF1	sdys:SDY_4618
A1427_s_at	-1.097574829	0.020849895	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3788_s_at	-1.096484451	0.008249961	Decrease_in_adherent flgM; anti-sigma28 factor FlgM ; K02398 negative regulator of flagellin synthesis FlgM	sdys:SDY_2081
O2CoIV182_x_at	-1.089795521	0.003963483	Decrease_in_adherent IS1A; transposase IS1 orfA	sez:Sez_0733
c5616_s_at	-1.086935161	0.039856391	Decrease_in_adherent cell wall-associated hydrolase	bmj:BMULJ_05090
EC869_1515_s_at	-1.085461442	0.015506799	Decrease_in_adherent sufI; repressor protein for FtsI ; K04753 suppressor of ftsI	sdys:SDY_3220
p166897_075_x_at	-1.084632454	0.004954624	Decrease_in_adherent transposase, ORF A, insertion element IS1	efe:PEFER_0012
SDM_0733_x_at	-1.077078154	0.005687383	Decrease_in_adherent insA; IS1 ORF1	ssn:SSON_4466
V2525_s_at	-1.072473036	0.039231204	Decrease_in_adherent manA; mannose-6-phosphate isomerase ; K01809 mannose-6-phosphate isomerase [EC:5.3.1.8]	elf:LF82_1270
H2119_x_at	-1.058399766	0.002549268	Decrease_in_adherent IS1 orfA	sfx:S4666
EC869_0326_s_at	-1.058276506	0.03647233	Decrease_in_adherent envZ; osmolarity sensor protein; K07638 two-component system, OmpR family, osmolarity sensor histidine kinase EnvZ [EC:2.7	etr:ETA_E_3278
SB5_3171_x_at	-1.056325518	0.00107728	Decrease_in_adherent insertion element protein	kpn:KPN_02839
V2220_x_at	-1.047525191	0.024983652	Decrease_in_adherent IS1A; transposase IS1 orfA	sez:Sez_0733
V3428_s_at	-1.032353616	0.033850763	Decrease_in_adherent phosphoribulokinase/uridine kinase family protein ; K00855 phosphoribulokinase [EC:2.7.1.19]	sbcs:SbBS512_E3730
A4248_s_at	-1.030664943	0.039752138	Decrease_in_adherent fdnH; formate dehydrogenase-N, nitrate-inducible, iron-sulfur beta subunit ; K08349 formate dehydrogenase-N, beta subunit [E	sdys:SDY_1605
V0280_s_at	-1.029928856	0.002725882	Decrease_in_adherent plsB; glycerol-3-phosphate acyltransferase (EC:2.3.1.15); K00631 glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]	sdys:SDY_4533
SD1_3523_s_at	-1.025401079	0.032813294	Decrease_in_adherent rplJ; 50S ribosomal protein L10 ; K02864 large subunit ribosomal protein L10	kco:CKO_03004
SD1_0419_s_at	-1.019256688	0.010445091	Decrease_in_adherent ftsE; cell division protein FtsE ; K09812 cell division transport system ATP-binding protein	sdys:SDY_3614
V0964_s_at	-1.018585769	0.01925716	Decrease_in_adherent hypothetical protein	sbcs:SbBS512_E3562
S0495_x_at	-1.015150052	0.005219949	Decrease_in_adherent putative lipoprotein	sbcs:SbBS512_E0474
V1934_s_at	-1.000079059	0.022139127	Decrease_in_adherent hypothetical protein	ecw:Ece24377A_3648