

Supplemental Table 3: Gene changes at 120 minutes in adherent versus non-adherent samples

Affy_ID	Fold change	p-value	Realtime change	Annotation
SFV_4382_at	4.281338468	0.0008003	Increase_in_Adherent	NO_KEGG_DATA
b4060_s_at	3.34002235	0.019884584	Increase_in_Adherent	yjcB; hypothetical protein
V5655_s_at	3.106882837	0.003885457	Increase_in_Adherent	putative nucleotide di-P-sugar epimerase or dehydratase
A1454_s_at	3.094716282	0.003135214	Increase_in_Adherent	DNA-binding protein fis; K03557 Fis family transcriptional regulator, factor for inversion stimulation protein
V4066_s_at	3.083852319	0.004623869	Increase_in_Adherent	inositol monophosphatase ; K01092 myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]
ECP_0988_at	2.836800974	0.015013593	Increase_in_Adherent	putative cold-shock protein (fragment)
V2984_s_at	2.65886023	0.0149772	Increase_in_Adherent	lipid A biosynthesis palmitoleoyl acyltransferase ; K12974 palmitoleoyl transferase [EC:2.3.1.-]
V2042_x_at	2.656818213	0.001285575	Increase_in_Adherent	yqjG; putative transferase ; K07393 putative glutathione S-transferase
A3703_s_at	2.425885705	0.023131263	Increase_in_Adherent	cold shock protein CspG ; K03704 cold shock protein (beta-ribbon, CspA family)
EC869_5515_s_at	2.411558731	0.023813448	Increase_in_Adherent	yhdG; tRNA-dihydrouridine synthase B ; K05540 tRNA-dihydrouridine synthase B [EC:1.-.-.-]
A4345_s_at	2.377010978	0.037557797	Increase_in_Adherent	ydfK; conserved hypothetical protein; putative DNA-binding transcriptional regulator; Qin prophage
SS5_4206_s_at	2.360753464	0.028373914	Increase_in_Adherent	NO_KEGG_DATA
A1975_s_at	2.33331025	0.006707275	Increase_in_Adherent	hypothetical protein
O2R_70_s_at	2.325892147	0.032336955	Increase_in_Adherent	hypothetical protein
J0200_x_at	2.307657402	0.008657105	Increase_in_Adherent	rtcA; RNA 3'-terminal phosphate cyclase RtcA; K01974 RNA 3'-terminal phosphate cyclase [EC:6.5.1.4]
b4557_s_at	2.307163088	0.01576679	Increase_in_Adherent	hypothetical protein ; K08998 hypothetical protein
SD1_0959_s_at	2.254771973	0.002074655	Increase_in_Adherent	marA; DNA-binding transcriptional activator MarA
ECP_3905_s_at	2.133659552	0.019980177	Increase_in_Adherent	rpmA; ribonuclease P (EC:3.1.26.5); K03536 ribonuclease P protein component [EC:3.1.26.5]
ECP_3903_s_at	2.08293317	0.023840985	Increase_in_Adherent	dnaA; chromosomal replication initiation protein ; K02313 chromosomal replication initiator protein
ECP_3198_s_at	2.034610493	0.017096999	Increase_in_Adherent	NO_KEGG_DATA
pCoo002_at	1.998140063	0.038801161	Increase_in_Adherent	NO_KEGG_DATA
M4325_x_at	1.953664376	0.047218227	Increase_in_Adherent	transposase (IS4 family)
F2357_s_at	1.947895253	0.0467456	Increase_in_Adherent	hypothetical protein
EC869_2283_s_at	1.936063249	0.014002833	Increase_in_Adherent	metH; B12-dependent methionine synthase ; K00548 5-methyltetrahydrofolate--homocysteine methyltransferase [EC:2.1.1.13]
EC869_8015_x_at	1.906386087	0.008057988	Increase_in_Adherent	hcaA1; large terminal subunit of phenylpropionate dioxygenase ; K05708 large terminal subunit of phenylpropionate dioxygenase [EC:1.14.12.19]
M0299_x_at	1.855239406	0.044139114	Increase_in_Adherent	hypothetical protein ; K07090
ECP_3250_s_at	1.673332162	0.027457807	Increase_in_Adherent	deaD; ATP-dependent RNA helicase DeaD (EC:3.6.1.-); K05592 ATP-dependent RNA helicase DeaD
A4355_s_at	1.635988557	0.045519544	Increase_in_Adherent	csxB; cold shock-like protein CspB ; K03704 cold shock protein (beta-ribbon, CspA family)
U1189_C2981_s_at	1.627748393	0.001901677	Increase_in_Adherent	NO_KEGG_DATA
A1371_s_at	1.592477902	0.035245524	Increase_in_Adherent	yhbC; hypothetical protein ; K09748 hypothetical protein
S0305_s_at	1.545296461	0.017933593	Increase_in_Adherent	prfH; peptide chain release factor-like protein ; K02839 peptide chain release factor RF-H
F4344_s_at	1.529460198	0.005696783	Increase_in_Adherent	glnL; nitrogen regulation protein NR(II) ; K07708 two-component system, NtrC family, nitrogen regulation sensor histidine kinase GlnL [EC:2.7.13.3]
D1393_s_at	1.500022364	0.04974378	Increase_in_Adherent	repZ; replication initiation protein
A1254_s_at	1.49538928	0.024648497	Increase_in_Adherent	ribosomal protein S21 ; K02970 small subunit ribosomal protein S21
EC869_5327_s_at	1.487509441	0.03189865	Increase_in_Adherent	NO_KEGG_DATA
A2072_s_at	1.453360002	0.007835983	Increase_in_Adherent	NO_KEGG_DATA
A0552_s_at	1.438370195	0.003602548	Increase_in_Adherent	hscB; co-chaperone HscB ; K04082 molecular chaperone HscB
A2648_s_at	1.432491724	0.03446818	Increase_in_Adherent	NO_KEGG_DATA
c3926_s_at	1.418281213	0.036698109	Increase_in_Adherent	nusA; transcription elongation factor NusA ; K02600 N utilization substance protein A
V1799_s_at	1.41318667	0.022256415	Increase_in_Adherent	hscB; co-chaperone HscB ; K04082 molecular chaperone HscB
N1756_at	1.34816672	0.008914024	Increase_in_Adherent	NO_KEGG_DATA
A4072_x_at	1.343495624	0.01524488	Increase_in_Adherent	translation initiation factor SUI1 ; K03113 translation initiation factor SUI1
EC869_5325_x_at	1.336193259	0.019037522	Increase_in_Adherent	ATP-dependent RNA helicase DeaD ; K05592 ATP-dependent RNA helicase DeaD
V1929_s_at	1.310847498	0.029853489	Increase_in_Adherent	infB; translation initiation factor IF-2 ; K02519 translation initiation factor IF-2
A1908_s_at	1.288295674	0.007204921	Increase_in_Adherent	putative inner membrane protein translocase component YidC ; K03217 preprotein translocase subunit YidC
N4402_at	1.274470382	0.01638995	Increase_in_Adherent	NO_KEGG_DATA
S0022_s_at	1.260785397	0.003763512	Increase_in_Adherent	hypothetical protein
b0957_s_at	1.234910259	0.030328291	Increase_in_Adherent	NO_KEGG_DATA
D4792_s_at	1.218090262	0.012597833	Increase_in_Adherent	hypothetical protein
A3559_s_at	1.216475484	0.025305867	Increase_in_Adherent	infA; translation initiation factor IF-1 ; K02518 translation initiation factor IF-1
Z2553_s_at	1.211283961	0.008201771	Increase_in_Adherent	yciG; hypothetical protein; K06884
A2856_s_at	1.200826167	0.01964287	Increase_in_Adherent	mltD; membrane-bound lytic murein transglycosylase D ; K08307 membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]
EC869_8379_x_at	1.186421644	0.008559054	Increase_in_Adherent	asfE; succinylglutamate desuccinylase ; K05526 succinylglutamate desuccinylase [EC:3.5.1.96]
pWR501_p270_at	1.18383917	0.02755224	Increase_in_Adherent	transcriptional regulator MerD
ECs4791_s_at	1.183116634	0.014957484	Increase_in_Adherent	glnL; nitrogen regulation protein NR(II) (EC:2.7.13.3); K07708 two-component system, NtrC family, nitrogen regulation sensor histidine kinase GlnL [EC:2.7.13.3]
SDY_2842_s_at	1.181690701	0.030398508	Increase_in_Adherent	IS600 ORF2
b3350_s_at	1.157599308	0.015615069	Increase_in_Adherent	NO_KEGG_DATA
V1014_s_at	1.14591187	0.028708239	Increase_in_Adherent	mnmA; tRNA-specific 2-thiouridylase MnmA (EC:2.1.1.61); K00566 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [EC:2.1.1.61]
A1298_s_at	1.140294434	0.020531555	Increase_in_Adherent	NO_KEGG_DATA
V2302_x_at	1.134823562	0.025980187	Increase_in_Adherent	ribonucleotide-diphosphate reductase subunit alpha ; K00525 ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
V0550_s_at	1.110680567	0.043444694	Increase_in_Adherent	yegH; UPF0053 protein YegH
S3426_s_at	1.10796526	0.049834281	Increase_in_Adherent	infB; translation initiation factor IF-2 ; K02519 translation initiation factor IF-2
V1939_s_at	1.091340149	0.03435546	Increase_in_Adherent	NO_KEGG_DATA
F0478_s_at	1.056681543	0.01627106	Increase_in_Adherent	NO_KEGG_DATA
V0624_x_at	1.052312781	0.049038037	Increase_in_Adherent	hypothetical protein ; K05521 ADP-ribosylglycohydrolase [EC:3.2.-.-]

SBO_0242_s_at	1.034935706	0.022792143	Increase_in_Adherent	prfH; peptide chain release factor-like protein ; K02839 peptide chain release factor RF-H
V3388_s_at	-4.701720945	0.002718206	Decrease_in_adherent	ppsA; phosphoenolpyruvate synthase (EC:2.7.9.2); K01007 pyruvate, water dikinase [EC:2.7.9.2]
pCoo013_at	-4.580214693	0.004253352	Decrease_in_adherent	CS1 type fimbrial major subunit
V6213_s_at	-4.57914751	0.001068757	Decrease_in_adherent	OsmC family protein ; K04063 osmotically inducible protein OsmC
A3474_s_at	-4.563446644	0.018908558	Decrease_in_adherent	ybiI; hypothetical protein
EC869_3421_s_at	-4.493914525	0.000783394	Decrease_in_adherent	dadA; D-amino acid dehydrogenase small subunit (EC:1.4.99.1); K00285 D-amino-acid dehydrogenase [EC:1.4.99.1]
SB5_2457_s_at	-4.473359282	0.004951024	Decrease_in_adherent	cstA; carbon starvation protein A ; K06200 carbon starvation protein
V3384_s_at	-4.447056953	0.00369319	Decrease_in_adherent	phosphoenolpyruvate synthase ; K01007 pyruvate, water dikinase [EC:2.7.9.2]
A2032_s_at	-4.354893117	0.012397542	Decrease_in_adherent	metE; 5-methyltetrahydropteroyltryglutamate--homocysteine S-methyltransferase (EC:2.1.1.14); K00549 5-methyltetrahydropteroyltryglutamate--homocysteine metE
c1138_s_at	-4.31136521	0.023181908	Decrease_in_adherent	hypothetical protein
V4294_s_at	-4.236721133	0.00951363	Decrease_in_adherent	NO_KEGG_DATA
EC869_0579_s_at	-4.231889798	0.001248462	Decrease_in_adherent	slp; outer membrane protein induced after carbon starvation ; K07285 outer membrane lipoprotein
SD1_2370_s_at	-4.202660544	0.002988022	Decrease_in_adherent	NO_KEGG_DATA
A0363_at	-4.196611198	0.00636653	Decrease_in_adherent	NO_KEGG_DATA
A3234_s_at	-4.170853981	0.001584979	Decrease_in_adherent	ybdD; hypothetical protein
b4189_s_at	-4.058533598	0.032157335	Decrease_in_adherent	yjfO; hypothetical protein
V4370_s_at	-4.058225375	0.007049652	Decrease_in_adherent	grxB; glutaredoxin 2 ; K03675 glutaredoxin 2
H3672_s_at	-4.042458445	0.003503769	Decrease_in_adherent	kbl; 2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]
SD1_0481_s_at	-4.00234373	0.017971444	Decrease_in_adherent	glpD; glycerol-3-phosphate dehydrogenase (EC:1.1.5.3); K00111 glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]
A1237_s_at	-3.998681111	0.023081567	Decrease_in_adherent	glgS; glycogen synthesis protein GlgS
F4011_s_at	-3.968918566	0.003251886	Decrease_in_adherent	NO_KEGG_DATA
M2693_s_at	-3.924023554	0.013768202	Decrease_in_adherent	NO_KEGG_DATA
F3184_s_at	-3.893332454	0.002282172	Decrease_in_adherent	bgIA; 6-phospho-beta-glucosidase A, cryptic ; K01223 6-phospho-beta-glucosidase [EC:3.2.1.86]
SD1_0444_s_at	-3.870934172	0.026091508	Decrease_in_adherent	NO_KEGG_DATA
APECO1_1866_s_at	-3.862145319	0.01702479	Decrease_in_adherent	NO_KEGG_DATA
V5372_s_at	-3.821470942	0.006471064	Decrease_in_adherent	yhhA; hypothetical protein
SB5_4158_s_at	-3.792611294	0.022952944	Decrease_in_adherent	phoH; hypothetical protein ; K06217 phosphate starvation-inducible protein PhoH and related proteins
LH0106_s_at	-3.790584311	0.011122213	Decrease_in_adherent	colicin-Ib immunity protein
S3742_s_at	-3.784370434	0.010503741	Decrease_in_adherent	glpF; facilitated diffusion of glycerol ; K02440 glycerol uptake facilitator protein
A1055_at	-3.772273812	0.001608818	Decrease_in_adherent	ATPase
V2562_s_at	-3.752232274	0.000927498	Decrease_in_adherent	gst; glutathionine S-transferase ; K00799 glutathione S-transferase [EC:2.5.1.18]
V2522_s_at	-3.7515213	0.012191069	Decrease_in_adherent	fumA; fumarate hydratase (EC:4.2.1.2); K01676 fumarate hydratase, class I [EC:4.2.1.2]
SD1_0883_s_at	-3.744652436	0.000910817	Decrease_in_adherent	yncE; hypothetical protein
EC869_3291_s_at	-3.741026488	0.030010999	Decrease_in_adherent	NO_KEGG_DATA
EC869_3589_s_at	-3.733412064	0.007217955	Decrease_in_adherent	dps; DNA starvation/stationary phase protection protein Dps ; K04047 starvation-inducible DNA-binding protein
EC869_6087_s_at	-3.728797	0.000153903	Decrease_in_adherent	hypothetical protein ; K02782 PTS system, glucitol/sorbitol-specific IIB component [EC:2.7.1.69]; K02783 PTS system, glucitol/sorbitol-specific IIC component
N3879_s_at	-3.684081442	0.003509522	Decrease_in_adherent	qor; quinone oxidoreductase, NADPH-dependent ; K00344 NADPH2:quinone reductase [EC:1.6.5.5]
SS5_4357_s_at	-3.678645386	0.024059883	Decrease_in_adherent	yciR; RNase II stability modulator
S1555_s_at	-3.669256374	0.00469115	Decrease_in_adherent	hypothetical protein ; K07180 serine protein kinase
V5294_s_at	-3.643545171	0.015599898	Decrease_in_adherent	hypothetical protein ; K06149 universal stress protein A
b2597_s_at	-3.637237945	0.01512629	Decrease_in_adherent	hypothetical protein
V5800_at	-3.623983909	0.004194855	Decrease_in_adherent	yjE; hypothetical protein
EC869_5122_x_at	-3.605209206	0.028507213	Decrease_in_adherent	entF; enterobactin synthase subunit F ; K02364 enterobactin synthetase component F [EC:2.7.7.-]
b3236_s_at	-3.599104005	0.00435757	Decrease_in_adherent	mdh; malate dehydrogenase (EC:1.1.1.37); K00026 malate dehydrogenase [EC:1.1.1.37]
SS5_4345_s_at	-3.591552128	0.001282208	Decrease_in_adherent	aminobenzoyl-glutamate transport protein ; K12942 aminobenzoyl-glutamate transport protein
V0058_s_at	-3.579075765	0.01027263	Decrease_in_adherent	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01744 aspartate ammonia-lyase [EC:4.3.1.1]
F1479_s_at	-3.562625992	0.000167821	Decrease_in_adherent	NO_KEGG_DATA
M3390_at	-3.475562611	0.000773807	Decrease_in_adherent	NO_KEGG_DATA
A3230_s_at	-3.473230028	0.004245687	Decrease_in_adherent	entB; 2,3-dihydro-2,3-dihydroxybenzoate synthetase ; K01252 enterobactin isochorismatase [EC:3.3.2.1]
SDY_2364_s_at	-3.462252571	0.000977874	Decrease_in_adherent	hypothetical protein
A2345_s_at	-3.450251316	0.010466795	Decrease_in_adherent	yjD; hypothetical protein ; K06975
A1575_s_at	-3.448995139	0.002017461	Decrease_in_adherent	pckA; phosphoenolpyruvate carboxykinase (EC:4.1.1.49); K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]
V3798_x_at	-3.441278844	0.005625507	Decrease_in_adherent	yahO; hypothetical protein
b1603_s_at	-3.430487673	0.001341321	Decrease_in_adherent	pntA; NAD(P) transhydrogenase subunit alpha (EC:1.6.1.2); K00324 NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]
V1952_s_at	-3.429172707	0.006634199	Decrease_in_adherent	yhbS; hypothetical protein ; K03824 putative acetyltransferase [EC:2.3.1.-]
V3949_s_at	-3.427056034	0.018724818	Decrease_in_adherent	narL; transcriptional regulator NarL ; K07684 two-component system, NarL family, nitrate/nitrite response regulator NarL
EC869_4082_s_at	-3.425818367	0.003391417	Decrease_in_adherent	ompF; outer membrane protein F ; K09476 outer membrane pore protein F
SD1_0513_s_at	-3.421478313	0.000945869	Decrease_in_adherent	pckA; phosphoenolpyruvate carboxykinase (EC:4.1.1.49); K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]
H3052_s_at	-3.41578339	0.016544496	Decrease_in_adherent	NO_KEGG_DATA
A0215_s_at	-3.407051158	0.015815582	Decrease_in_adherent	yeiQ; putative dehydrogenase, NAD-dependent
ECP_2029_s_at	-3.375450374	0.004575448	Decrease_in_adherent	hypothetical protein
A3388_s_at	-3.371155783	0.011768587	Decrease_in_adherent	gpmA; phosphoglyceromutase 1 ; K01834 phosphoglycerate mutase [EC:5.4.2.1]
EC869_0354_s_at	-3.360958273	0.019110082	Decrease_in_adherent	NO_KEGG_DATA
SB5_1096_s_at	-3.356610758	0.032677729	Decrease_in_adherent	gabD; succinate-semialdehyde dehydrogenase I ; K00135 succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]
LH0125_s_at	-3.356287504	0.027225614	Decrease_in_adherent	NO_KEGG_DATA
A3718_s_at	-3.317253056	0.035017118	Decrease_in_adherent	yccJ; hypothetical protein

SD1_2813_s_at	-3.315304505	0.001395327	Decrease_in_adherent hchA; chaperone protein HchA ; K05523 molecular chaperone hchA (Hsp31)
V5011_s_at	-3.315054091	0.007310337	Decrease_in_adherent lldD; L-lactate dehydrogenase (EC:1.1.2.3); K00101 L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]
pCoo054_at	-3.309772569	0.005254768	Decrease_in_adherent EAL domain-containing protein
A3367_s_at	-3.306676764	0.000454788	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]
b0839_s_at	-3.302918496	0.008728671	Decrease_in_adherent dacC; D-alanyl-D-alanine carboxypeptidase fraction C (EC:3.4.16.4); K07258 D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6) [EC:3.4.16.4]
F4391_s_at	-3.301057408	0.012701424	Decrease_in_adherent yjiM; hypothetical protein
SD1_2994_s_at	-3.296129299	0.014945161	Decrease_in_adherent gmr; RNase II stability modulator
A2361_s_at	-3.282204117	0.001612682	Decrease_in_adherent groEL; chaperonin GroEL ; K04077 chaperonin GroEL
A4534_s_at	-3.281462864	0.01604509	Decrease_in_adherent hypothetical protein
pCoo074_at	-3.262661478	0.026771216	Decrease_in_adherent fimC; modulator of post-segregation killing protein
EC869_7817_x_at	-3.259838057	0.042987257	Decrease_in_adherent fhuF; ferric iron reductase involved in ferric hydroxamate transport
SD1_3595_s_at	-3.255931002	0.010592947	Decrease_in_adherent gpmA; phosphoglyceromutase 1 ; K01834 phosphoglycerate mutase [EC:5.4.2.1]
V0723_s_at	-3.254510361	0.017636831	Decrease_in_adherent cirA; colicin I receptor ; K02014 iron complex outer membrane receptor protein
EC869_5019_s_at	-3.251192809	0.002917043	Decrease_in_adherent gltA; type II citrate synthase (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
A4532_s_at	-3.242944201	0.00634244	Decrease_in_adherent pfkB; 6-phosphofructokinase 2 (EC:2.7.1.11); K00850 6-phosphofructokinase [EC:2.7.1.11]
A3285_s_at	-3.239988938	0.016855754	Decrease_in_adherent ybeL; hypothetical protein
APECO1_2795_at	-3.230709065	0.006314799	Decrease_in_adherent hypothetical protein
c1317_at	-3.214098268	0.010356198	Decrease_in_adherent NO_KEGG_DATA
D4048_at	-3.209978297	0.001619612	Decrease_in_adherent NO_KEGG_DATA
V5642_s_at	-3.204442904	0.016086341	Decrease_in_adherent bssR; biofilm formation regulatory protein BssR
V4298_s_at	-3.204150045	0.010807388	Decrease_in_adherent TrpR binding protein WrbA ; K03809 Trp repressor binding protein
b1136_s_at	-3.189372221	0.001992581	Decrease_in_adherent hypothetical protein
A1592_s_at	-3.187079372	0.02901082	Decrease_in_adherent transcriptional regulator MalT; K03556 LuxR family transcriptional regulator, maltose regulon positive regulatory protein
A3558_s_at	-3.182251081	0.005450524	Decrease_in_adherent ctpA; ATP-dependent Ctp protease ATP-binding subunit ; K03694 ATP-dependent Ctp protease ATP-binding subunit CtpA
A2210_s_at	-3.174869482	0.003254162	Decrease_in_adherent hupA; transcriptional regulator HU subunit alpha ; K05787 DNA-binding protein HU-alpha
EC869_5018_s_at	-3.170070731	0.002577603	Decrease_in_adherent gltA; type II citrate synthase (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
b3506_s_at	-3.158245167	0.013266712	Decrease_in_adherent slp; outer membrane lipoprotein ; K07285 outer membrane lipoprotein
V2453_s_at	-3.150948028	0.038451322	Decrease_in_adherent dhah; fused putative dihydroxyacetone-specific PTS enzymes: HPr component/EI component; K05881 PTS hybrid protein
A3862_at	-3.144557937	0.004134885	Decrease_in_adherent hypothetical protein
SDY_1914_s_at	-3.144333854	0.001103838	Decrease_in_adherent NO_KEGG_DATA
b3409_s_at	-3.142263072	0.018822926	Decrease_in_adherent feoB; ferrous iron transport protein B ; K04759 ferrous iron transport protein B
A3132_s_at	-3.140911771	0.008390153	Decrease_in_adherent hemH; ferrochelatase (EC:4.99.1.1); K01772 ferrochelatase [EC:4.99.1.1]
EC869_4095_s_at	-3.135298455	0.007205859	Decrease_in_adherent NO_KEGG_DATA
c2932_s_at	-3.134397752	0.00511918	Decrease_in_adherent nupC; nucleoside permease NupC ; K11535 nucleoside transport protein
b4232_s_at	-3.134098097	0.00467968	Decrease_in_adherent fbp; fructose-1,6-bisphosphatase (EC:3.1.3.11); K03841 fructose-1,6-bisphosphatase I [EC:3.1.3.11]
V7379_s_at	-3.127437577	0.003909375	Decrease_in_adherent putative 5-methylcytosine-specific restriction enzyme with GTPase activity (EC:3.1.21.-)
A1966_s_at	-3.119484701	0.01957593	Decrease_in_adherent yifE; hypothetical protein ; K09897 hypothetical protein
ECs5510_s_at	-3.117325396	0.005401674	Decrease_in_adherent hypothetical protein
EC869_4295_s_at	-3.115501234	0.008984389	Decrease_in_adherent glycine dehydrogenase ; K00282 glycine dehydrogenase subunit 1 [EC:1.4.4.2]; K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
b1508_s_at	-3.114277945	0.021875302	Decrease_in_adherent hipB; DNA-binding transcriptional regulator HipB
A4196_s_at	-3.113760196	0.005091909	Decrease_in_adherent ydcH; hypothetical protein; K09794 hypothetical protein
F3186_s_at	-3.112769957	0.00138684	Decrease_in_adherent gcvH; glycine cleavage system protein H ; K02437 glycine cleavage system H protein
SS5_4613_s_at	-3.104944662	0.003817665	Decrease_in_adherent D-ribose transporter subunit RbsB ; K10439 ribose transport system substrate-binding protein
EC869_8900_s_at	-3.099128231	0.015699272	Decrease_in_adherent hydrogenase 2 small subunit (EC:1.12.99.6); K06282 hydrogenase small subunit [EC:1.12.99.6]
F3644_x_at	-3.093997102	0.027477767	Decrease_in_adherent hypothetical protein ; K03747 Smg protein
V6408_s_at	-3.087848792	0.011313688	Decrease_in_adherent hypothetical protein ; K12941 aminobenzoyl-glutamate utilization protein B
V3875_s_at	-3.072376897	0.000115976	Decrease_in_adherent sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
SB5_0263_s_at	-3.06883365	0.031875638	Decrease_in_adherent yhiO; universal stress protein UspB ; K06144 universal stress protein B
UTI89_C2497_s_at	-3.044946403	0.009340129	Decrease_in_adherent NO_KEGG_DATA
ECs2487_s_at	-3.031691024	0.024681186	Decrease_in_adherent yeaA; methionine sulfoxide reductase B (EC:1.8.4.11); K07305 peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]
F0646_s_at	-3.031091752	0.028811117	Decrease_in_adherent NO_KEGG_DATA
SB5_2639_s_at	-3.030410019	0.019999325	Decrease_in_adherent hypothetical protein ; K07180 serine protein kinase
pCoo055_at	-3.016932017	0.020711381	Decrease_in_adherent ydeO; HTH-type transcriptional regulator YdeO
SD1_2076_s_at	-3.012512667	0.007386734	Decrease_in_adherent mntH; manganese transport protein MntH ; K03322 manganese transport protein
A1089_at	-3.011759942	0.014475753	Decrease_in_adherent hypothetical protein
b0865_s_at	-3.009321665	0.007512663	Decrease_in_adherent ybjP; putative lipoprotein
W4348_at	-3.008293995	0.011732632	Decrease_in_adherent putative cytoplasmic protein
SD1_3346_s_at	-3.000515667	0.022151023	Decrease_in_adherent ycbB; hypothetical protein
b3024_s_at	-2.994994173	0.026140462	Decrease_in_adherent ygiW; hypothetical protein
A1693_s_at	-2.983530831	0.018291974	Decrease_in_adherent hdeA; acid-resistance protein
SF0956_s_at	-2.983511375	0.010980582	Decrease_in_adherent ycbG; hypothetical protein ; K09911 hypothetical protein
SDY_3461_x_at	-2.982342955	0.027051632	Decrease_in_adherent hypothetical protein ; K03747 Smg protein
c4443_s_at	-2.973461469	0.000502327	Decrease_in_adherent tdh; L-threonine 3-dehydrogenase (EC:1.1.1.103); K00060 threonine 3-dehydrogenase [EC:1.1.1.103]
EC869_8327_s_at	-2.971398331	0.01960952	Decrease_in_adherent selenophosphate synthetase (EC:2.7.9.3); K01008 selenide, water dikinase [EC:2.7.9.3]
c4045_x_at	-2.96179608	0.021191116	Decrease_in_adherent smg; hypothetical protein; K03747 Smg protein
V5243_s_at	-2.959948112	0.006283166	Decrease_in_adherent putative ribonuclease ; K07058
D3045_s_at	-2.955793287	0.005588477	Decrease_in_adherent NO_KEGG_DATA

A2446_s_at	-2.952804419	0.01697969	Decrease_in_adherent NO_KEGG_DATA
SD1_2927_s_at	-2.952545792	0.021324303	Decrease_in_adherent ydaA; universal stress protein UspE
c3976_s_at	-2.948739645	0.022606095	Decrease_in_adherent NO_KEGG_DATA
A3364_s_at	-2.946555869	0.002238663	Decrease_in_adherent sucA; 2-oxoglutarate dehydrogenase E1 component (EC:1.2.4.2); K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
SD1_2417_s_at	-2.934775227	0.011465897	Decrease_in_adherent hydroxyglutarate oxidase
A1218_s_at	-2.934754464	0.013154761	Decrease_in_adherent hypothetical protein
A1938_s_at	-2.916309331	0.005174593	Decrease_in_adherent hypothetical protein
A3365_s_at	-2.913759808	0.00101552	Decrease_in_adherent sucB; dihydroliipoamide succinyltransferase (EC:2.3.1.61); K00658 2-oxoglutarate dehydrogenase E2 component (dihydroliipoamide succinyltransferase) [EC:2.3.1.61]
A3314_s_at	-2.910992612	0.002373405	Decrease_in_adherent nagE; N-acetyl glucosamine specific PTS system components IIAABC (EC:2.7.1.69); K02802 PTS system, N-acetylglucosamine-specific IIA component [EC:2.7.1.69]
A1262_s_at	-2.907707862	0.003725521	Decrease_in_adherent aer; aerotaxis sensor receptor, flavoprotein ; K03776 aerotaxis receptor
A2344_s_at	-2.905393023	0.017175137	Decrease_in_adherent yjdI; hypothetical protein
V4776_s_at	-2.90352993	7.09E-05	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]
SB5_0121_s_at	-2.903213785	0.024639378	Decrease_in_adherent dppA; dipeptide transporter ; periplasmic-binding component of ABC superfamily ; K12368 dipeptide transport system substrate-binding protein
pCoo049_x_at	-2.895160649	0.023218418	Decrease_in_adherent hypothetical protein
A4608_s_at	-2.893526457	0.020867144	Decrease_in_adherent yeaQ; hypothetical protein
A4642_s_at	-2.892447415	0.02347273	Decrease_in_adherent putative regulator
SD1_0411_s_at	-2.891247583	0.012096173	Decrease_in_adherent hypothetical protein
EC869_4486_s_at	-2.881305575	0.003238236	Decrease_in_adherent kbi; 2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]
A1694_s_at	-2.871593065	0.023601637	Decrease_in_adherent acid-resistance membrane protein
D4819_s_at	-2.866452744	0.025646191	Decrease_in_adherent putative transposase
A1692_s_at	-2.862825181	0.017369073	Decrease_in_adherent hdeB; acid-resistance protein
F2023_at	-2.860148277	0.006966263	Decrease_in_adherent hypothetical protein
SB5_2252_s_at	-2.858258296	0.011064319	Decrease_in_adherent NO_KEGG_DATA
EC869_3430_s_at	-2.857665705	0.023404186	Decrease_in_adherent NO_KEGG_DATA
A1125_s_at	-2.855553906	0.01806069	Decrease_in_adherent hypothetical protein
A2477_x_at	-2.847887717	0.003847295	Decrease_in_adherent yjgD; hypothetical protein ; K09893 hypothetical protein
SFV_1430_s_at	-2.837876612	0.00134001	Decrease_in_adherent hypothetical protein ; K07180 serine protein kinase
V0028_s_at	-2.830575204	0.017959462	Decrease_in_adherent frdA; fumarate reductase flavoprotein subunit (EC:1.3.99.1); K00244 fumarate reductase flavoprotein subunit [EC:1.3.99.1]
F1141_s_at	-2.829066368	0.003939648	Decrease_in_adherent hypothetical protein
A4533_s_at	-2.827071973	0.014419572	Decrease_in_adherent hypothetical protein
G4679_s_at	-2.824387383	0.006333726	Decrease_in_adherent entF; enterobactin synthase subunit F; K02364 enterobactin synthetase component F [EC:2.7.7.-]
A1093_s_at	-2.817025418	0.034196509	Decrease_in_adherent IS66 family transposase
c4499_s_at	-2.816023636	0.036536165	Decrease_in_adherent NO_KEGG_DATA
A2371_s_at	-2.813973795	0.044893676	Decrease_in_adherent blc; outer membrane lipoprotein Blc ; K03098 outer membrane lipoprotein Blc
F4980_s_at	-2.812295397	0.037667907	Decrease_in_adherent ferric iron reductase involved in ferric hydroximate transport
c1919_s_at	-2.812095128	0.049050331	Decrease_in_adherent hypothetical protein
A3916_s_at	-2.811474163	0.00321851	Decrease_in_adherent hypothetical protein
V5329_s_at	-2.810801434	0.017178216	Decrease_in_adherent hypothetical protein
A4482_s_at	-2.807628684	0.019715192	Decrease_in_adherent lpp; murein lipoprotein ; K06078 murein lipoprotein
A4412_s_at	-2.806427576	0.032286766	Decrease_in_adherent ydgA; hypothetical protein
A2205_s_at	-2.774964904	0.025555025	Decrease_in_adherent rsd; anti-RNA polymerase sigma 70 factor ; K07740 regulator of sigma D
V1199_s_at	-2.773349619	0.041022042	Decrease_in_adherent ycbB; hypothetical protein
H4310_x_at	-2.772854007	0.011619359	Decrease_in_adherent NO_KEGG_DATA
EC869_4317_s_at	-2.772845472	0.006570536	Decrease_in_adherent serA; D-3-phosphoglycerate dehydrogenase ; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]
ECs2493_s_at	-2.771756331	0.002545456	Decrease_in_adherent NO_KEGG_DATA
S1023_s_at	-2.770705544	0.010907863	Decrease_in_adherent NO_KEGG_DATA
V0004_s_at	-2.766905472	0.028023701	Decrease_in_adherent NO_KEGG_DATA
A3980_s_at	-2.765967321	0.010961457	Decrease_in_adherent adhE; bifunctional acetaldehyde-CoA/alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]; K04072 acetaldehyde dehydrogenase [EC:1.2.1.10]
A3097_s_at	-2.761160023	0.000747779	Decrease_in_adherent hupB; transcriptional regulator HU subunit beta ; K03530 DNA-binding protein HU-beta
SS5_4352_s_at	-2.756849946	0.000975064	Decrease_in_adherent NO_KEGG_DATA
pCoo005_at	-2.750168903	0.020837784	Decrease_in_adherent hypothetical protein
b0426_s_at	-2.746558058	0.009212485	Decrease_in_adherent putative nucleotide-binding protein ; K09767 hypothetical protein
V2584_s_at	-2.746024716	0.016671459	Decrease_in_adherent hypothetical protein
A3684_s_at	-2.743565438	0.008150627	Decrease_in_adherent NO_KEGG_DATA
ECs4252_x_at	-2.74197057	0.016578455	Decrease_in_adherent yhgG; hypothetical protein ; K07490 ferrous iron transport protein C
V2611_s_at	-2.739120286	0.014052551	Decrease_in_adherent sodB; superoxide dismutase ; K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
A4639_s_at	-2.731740605	0.016934318	Decrease_in_adherent cold shock-like protein CspC ; K03704 cold shock protein (beta-ribbon, CspA family)
D4749_s_at	-2.716897315	0.003548856	Decrease_in_adherent relaxosome component
EC869_4411_s_at	-2.716607688	0.014196254	Decrease_in_adherent NO_KEGG_DATA
A0371_s_at	-2.707159198	0.006386972	Decrease_in_adherent NO_KEGG_DATA
APECO1_3736_s_at	-2.701380823	0.007505041	Decrease_in_adherent ygdH; hypothetical protein ; K06966
SD1_2139_s_at	-2.698033448	0.00597171	Decrease_in_adherent NO_KEGG_DATA
EC869_4008_s_at	-2.697451947	0.044880738	Decrease_in_adherent pflB; formate acetyltransferase 1 ; K00656 formate C-acetyltransferase [EC:2.3.1.54]
A0053_s_at	-2.693841869	0.029023179	Decrease_in_adherent yefM; antitoxin YefM
A3820_s_at	-2.683638675	0.026299254	Decrease_in_adherent hinT; similar to histidine triad-like protein ycf of escherichia coli ; K12150 HIT-like protein HinT
SFV_4273_s_at	-2.682089379	0.005588011	Decrease_in_adherent cysQ; adenosine-3'(2'),5'-bisphosphate nucleotidase; K03677 CysQ protein
b3928_s_at	-2.681827923	0.025447431	Decrease_in_adherent yjU; hypothetical protein ; K09892 hypothetical protein

b2665_s_at	-2.6805374	0.001371559	Decrease_in_adherent ygaU; LysM domain/BON superfamily protein
SB5_3443_s_at	-2.67470379	0.007241326	Decrease_in_adherent yacA; hypothetical protein
V5691_s_at	-2.672355665	0.01076121	Decrease_in_adherent fii; catechol siderophore receptor Fii ; K02014 iron complex outermembrane receptor protein
A4591_s_at	-2.665988223	0.021831044	Decrease_in_adherent aldol/keto reductase family oxidoreductase (EC:1.1.1.218)
A4489_s_at	-2.663090094	0.007377095	Decrease_in_adherent sufA; iron-sulfur cluster assembly scaffold protein ; K05997 Fe-S cluster assembly protein SufA
K4295_at	-2.654837222	0.025020504	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
A4157_s_at	-2.651789036	0.011235065	Decrease_in_adherent NO_KEGG_DATA
V3693_s_at	-2.645272505	0.003917998	Decrease_in_adherent pepD; aminoacyl-histidine dipeptidase (peptidase D) (EC:3.4.13.3); K01270 aminoacylhistidine dipeptidase [EC:3.4.13.3]
c1093_s_at	-2.643178537	0.016008377	Decrease_in_adherent ompA; outer membrane protein A ; K03286 OmpA-OmpF porin, OOP family
V4643_s_at	-2.643016572	0.015802947	Decrease_in_adherent sfsA; sugar fermentation stimulation protein A ; K06206 sugar fermentation stimulation protein A
b0880_s_at	-2.641977512	0.006531667	Decrease_in_adherent cspD; stationary phase/starvation inducible regulatory protein CspD ; K03704 cold shock protein (beta-ribbon, CspA family)
EC536_1048_s_at	-2.639745773	0.011033175	Decrease_in_adherent putative glutamate dehydrogenase
EC536_4089_s_at	-2.638533018	0.011211886	Decrease_in_adherent pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
EC869_5027_s_at	-2.635544473	0.019525585	Decrease_in_adherent sdhA; succinate dehydrogenase flavoprotein subunit ; K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
V0354_s_at	-2.62997153	0.012004354	Decrease_in_adherent aceA; isocitrate lyase ; K01637 isocitrate lyase [EC:4.1.3.1]
A1663_s_at	-2.629798449	0.039840868	Decrease_in_adherent NO_KEGG_DATA
V1193_s_at	-2.628167817	0.010748133	Decrease_in_adherent aromatic amino acid aminotransferase ; K00813 aspartate aminotransferase [EC:2.6.1.1]
S95_1846_x_at	-2.627177264	0.005167132	Decrease_in_adherent sbcB; exonuclease I (EC:3.1.11.1); K01141 exodeoxyribonuclease I [EC:3.1.11.1]
c0999_s_at	-2.621288844	0.021957834	Decrease_in_adherent hypothetical protein
SD1_3168_s_at	-2.617172246	0.006810824	Decrease_in_adherent adhE; bifunctional acetaldehyde-CoA/alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]; K04072 acetaldehyde dehydrogenase [EC:1.2.1.10]
V7163_x_at	-2.613540624	0.034399092	Decrease_in_adherent sbcB; outer membrane receptor FepA ; K02014 iron complex outermembrane receptor protein
A0020_s_at	-2.613063774	0.009913623	Decrease_in_adherent hypothetical protein
A4742_s_at	-2.611180442	0.001923542	Decrease_in_adherent fliC; flagellin ; K02406 flagellin
A4772_s_at	-2.609306204	0.02346868	Decrease_in_adherent mannosyl-3-phosphoglycerate phosphatase (EC:3.1.3.70); K07026 mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]
V4383_s_at	-2.608338024	0.006261599	Decrease_in_adherent pflB; formate acetyltransferase 1 ; K00656 formate C-acetyltransferase [EC:2.3.1.54]
A3228_s_at	-2.605610441	0.042673644	Decrease_in_adherent entC; isochorismate hydroxymutase 2 ; K02361 isochorismate synthase [EC:5.4.4.2]
A3910_s_at	-2.604904704	0.040699625	Decrease_in_adherent minD; cell division inhibitor MinD ; K03609 septum site-determining protein MinD
EC869_4578_s_at	-2.598349706	0.038544953	Decrease_in_adherent gloB; hydroxyacylglutathione hydrolase (EC:3.1.2.6); K01069 hydroxyacylglutathione hydrolase [EC:3.1.2.6]
A3783_s_at	-2.589220532	0.011486417	Decrease_in_adherent rimJ; ribosomal-protein-S5-alanine N-acetyltransferase ; K03790 ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]
c4709_at	-2.587301362	0.001680186	Decrease_in_adherent hypothetical protein ; K00973 glucose-1-phosphate thymidyltransferase [EC:2.7.7.24]
A2329_s_at	-2.582720013	0.022911228	Decrease_in_adherent basR; DNA-binding transcriptional regulator BasR ; K07771 two-component system, OmpR family, response regulator BasR
V5388_s_at	-2.581894117	0.002366607	Decrease_in_adherent asd; aspartate-semialdehyde dehydrogenase (EC:1.2.1.11); K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]
V5387_s_at	-2.578590239	0.000832154	Decrease_in_adherent asd; aspartate-semialdehyde dehydrogenase (EC:1.2.1.11); K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]
b3339_s_at	-2.574864789	0.009014186	Decrease_in_adherent tufB; tuf, elongation factor Tu (EC:3.6.5.3); K02358 elongation factor EF-Tu [EC:3.6.5.3]
EC869_0326_s_at	-2.57363505	0.011664011	Decrease_in_adherent envZ; osmolarity sensor protein; K07638 two-component system, OmpR family, osmolarity sensor histidine kinase EnvZ [EC:2.7.13.3]
EC869_1970_s_at	-2.5655717	0.00339936	Decrease_in_adherent adhE; bifunctional acetaldehyde-CoA/alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]; K04072 acetaldehyde dehydrogenase [EC:1.2.1.10]
SB5_4743_s_at	-2.564280957	0.018781146	Decrease_in_adherent mobilization protein MobD
SB5_0350_s_at	-2.564223099	0.047564305	Decrease_in_adherent ppiA; peptidyl-prolyl cis-trans isomerase A (rotamase A) ; K03767 peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]
SB5_0122_s_at	-2.561792605	0.004616316	Decrease_in_adherent dppA; dipeptide transport protein ; K12368 dipeptide transport system substrate-binding protein
EC869_0977_s_at	-2.560191533	0.002507592	Decrease_in_adherent hypothetical protein ; K09161 hypothetical protein
N4689_at	-2.552549342	0.004433451	Decrease_in_adherent NO_KEGG_DATA
D3528_s_at	-2.55084499	0.028541349	Decrease_in_adherent predicted hydrolase
V6429_s_at	-2.547571478	0.003860241	Decrease_in_adherent tpx; thiol peroxidase ; K11065 thiol peroxidase, atypical 2-Cys peroxiredoxin [EC:1.11.1.15]
A0626_s_at	-2.546611478	0.005706567	Decrease_in_adherent NO_KEGG_DATA
A4547_s_at	-2.542630135	0.008385414	Decrease_in_adherent osmE; DNA-binding transcriptional activator OsmE ; K04064 osmotically inducible lipoprotein OsmE
V0312_s_at	-2.53808798	0.001049873	Decrease_in_adherent pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
A0064_s_at	-2.536213993	0.005884276	Decrease_in_adherent gnd; 6-phosphogluconate dehydrogenase (EC:1.1.1.44); K00033 6-phosphogluconate dehydrogenase [EC:1.1.1.44]
A3925_s_at	-2.535682871	0.015247961	Decrease_in_adherent ycgB; SpoVR family protein
pCoo091_at	-2.52792839	0.022698401	Decrease_in_adherent hypothetical protein
V4229_s_at	-2.526284358	0.009911082	Decrease_in_adherent clpB; protein disaggregation chaperone ; K03695 ATP-dependent Clp protease ATP-binding subunit ClpB
A2220_s_at	-2.524916145	0.041359898	Decrease_in_adherent NO_KEGG_DATA
V7181_s_at	-2.51707668	0.003402033	Decrease_in_adherent entF; enterobactin synthase subunit F ; K02364 enterobactin synthetase component F [EC:2.7.7.-]
A3541_s_at	-2.50328784	0.00919007	Decrease_in_adherent amid; N-acetylmuramoyl-L-alanine amidase AmiD (EC:3.5.1.28); K11066 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
V3982_s_at	-2.496524365	0.010400949	Decrease_in_adherent trpB; tryptophan synthase subunit beta (EC:4.2.1.20); K01696 tryptophan synthase beta chain [EC:4.2.1.20]
V0793_s_at	-2.495608777	0.000602467	Decrease_in_adherent pal; peptidoglycan-associated outer membrane lipoprotein ; K03640 peptidoglycan-associated lipoprotein
A0347_s_at	-2.494544255	0.002494474	Decrease_in_adherent hisJ; histidine ABC transporter, periplasmic histidine-binding protein ; K10014 histidine transport system substrate-binding protein
b1777_s_at	-2.491473391	0.003845569	Decrease_in_adherent yeaC; hypothetical protein ; K09916 hypothetical protein
SB5_3624_s_at	-2.491318139	0.014954134	Decrease_in_adherent NO_KEGG_DATA
A2199_s_at	-2.491262969	0.004801535	Decrease_in_adherent rpoC; DNA-directed RNA polymerase subunit beta' (EC:2.7.7.6); K03046 DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]
SFV_4079_at	-2.489588417	0.004750564	Decrease_in_adherent NO_KEGG_DATA
A4269_s_at	-2.488949465	0.018817646	Decrease_in_adherent hypothetical protein ; K13069 diguanylate cyclase [EC:2.7.7.65]
V6718_s_at	-2.48140861	0.044934886	Decrease_in_adherent fruR; DNA-binding transcriptional regulator FruR ; K03435 LacI family transcriptional regulator, fructose operon transcriptional repressor
V6990_s_at	-2.479996862	0.033010477	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II ; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor
D0009_s_at	-2.476558583	0.028329676	Decrease_in_adherent ydfG; 3-hydroxy acid dehydrogenase ; K00540 [EC:1.-.-.-]
V2352_s_at	-2.474889852	0.004228226	Decrease_in_adherent ppnK; inorganic polyphosphate/ATP-NAD kinase (EC:2.7.1.23); K00858 NAD+ kinase [EC:2.7.1.23]
A3372_s_at	-2.469317984	0.017227599	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.-]
ECP_4135_s_at	-2.466273515	0.030750217	Decrease_in_adherent glpK; glycerol kinase (EC:2.7.1.30); K00864 glycerol kinase [EC:2.7.1.30]

V3435_s_at	-2.459671461	0.023020073	Decrease_in_adherent ptsI; phosphoenolpyruvate-protein phosphotransferase (EC:2.7.3.9); K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]
W4306_s_at	-2.457435637	0.008866022	Decrease_in_adherent hypothetical protein
D4754_at	-2.456478367	0.003280304	Decrease_in_adherent eItA; heat-labile enterotoxin A ; K10928 cholera enterotoxin subunit A [EC:2.4.2.36]
F0588_s_at	-2.446319835	0.012425814	Decrease_in_adherent hypothetical protein
A3361_s_at	-2.445927626	0.027245132	Decrease_in_adherent sdhD; succinate dehydrogenase hydrophobic subunit ; K00242 succinate dehydrogenase hydrophobic membrane anchor protein [EC:1.3.99.1]
L1795_s_at	-2.444820567	0.007680009	Decrease_in_adherent hypothetical protein
V5399_s_at	-2.442876929	0.011747689	Decrease_in_adherent glgC; glucose-1-phosphate adenyltransferase (EC:2.7.7.27); K00975 glucose-1-phosphate adenyltransferase [EC:2.7.7.27]
A3909_s_at	-2.440168729	0.003903392	Decrease_in_adherent minE; cell division topological specificity factor MinE ; K03608 cell division topological specificity factor
A3411_x_at	-2.438417419	0.006636923	Decrease_in_adherent NO_KEGG_DATA
A4104_s_at	-2.428546828	0.00318349	Decrease_in_adherent pspE; thiosulfate:cyanide sulfurtransferase (EC:2.8.1.1); K03972 phage shock protein E
EC869_3090_s_at	-2.426222618	0.007426484	Decrease_in_adherent acetyl-coenzyme A synthetase (EC:6.2.1.1); K01895 acetyl-CoA synthetase [EC:6.2.1.1]
V5833_s_at	-2.423342504	0.026908463	Decrease_in_adherent hslV; ATP-dependent protease peptidase subunit ; K01419 ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.-]
A3349_s_at	-2.420093018	0.009040265	Decrease_in_adherent ybgL; LamB/YcsF family protein ; K07160
V7203_s_at	-2.416266214	0.000934969	Decrease_in_adherent entE; enterobactin synthase subunit E (EC:2.7.7.58); K02363 enterobactin 2,3-dihydroxybenzoate-AMP ligase / S-dihydroxybenzoyltransferase [EC:2.7.7.58 2.3.1.
A0254_s_at	-2.410302455	0.002113557	Decrease_in_adherent eco; ecotin ; K08276 ecotin
A0009_s_at	-2.408768255	0.00238599	Decrease_in_adherent amn; AMP nucleosidase ; K01241 AMP nucleosidase [EC:3.2.2.4]
A3221_at	-2.404409031	0.019361922	Decrease_in_adherent NO_KEGG_DATA
A0072_at	-2.390928447	0.028106796	Decrease_in_adherent glycosyl transferase group 2 family protein (EC:2.4.1.-)
J2890_s_at	-2.386950083	0.027712839	Decrease_in_adherent NO_KEGG_DATA
A4701_s_at	-2.378833997	0.005157093	Decrease_in_adherent cheY; chemotaxis regulatory protein CheY ; K03413 two-component system, chemotaxis family, response regulator CheY
V1095_s_at	-2.378478081	0.024162001	Decrease_in_adherent ybaS; glutaminase (EC:3.5.1.2); K01425 glutaminase [EC:3.5.1.2]
F4472_s_at	-2.370519759	0.010649199	Decrease_in_adherent rsd; anti-RNA polymerase sigma 70 factor ; K07740 regulator of sigma D
A0438_s_at	-2.369778669	0.02513402	Decrease_in_adherent crr; glucose-specific PTS system component (EC:2.7.1.-); K02777 PTS system, glucose-specific IIA component [EC:2.7.1.69]
G1746_s_at	-2.369425316	0.04784187	Decrease_in_adherent hypothetical protein
EC869_8291_s_at	-2.367006867	0.020390556	Decrease_in_adherent crr; glucose-specific PTS system component ; K02777 PTS system, glucose-specific IIA component [EC:2.7.1.69]
A3589_at	-2.363787387	0.029428263	Decrease_in_adherent hypothetical protein
b0145_s_at	-2.359316323	0.013926806	Decrease_in_adherent dksA; DnaK suppressor protein; K06204 DnaK suppressor protein
V5454_s_at	-2.3577512	0.006607624	Decrease_in_adherent NO_KEGG_DATA
A4340_s_at	-2.353263821	0.021380202	Decrease_in_adherent ydfG; 3-hydroxy acid dehydrogenase ; K00540 [EC:1.-.-.-]
A2739_s_at	-2.352023449	0.020400789	Decrease_in_adherent hypothetical protein
b3103_s_at	-2.349579281	0.006997073	Decrease_in_adherent putative inner membrane protein YhaH
EC869_5411_s_at	-2.347448909	0.016054353	Decrease_in_adherent yhbL; isoprenoid biosynthesis protein with amidotransferase-like domain
V3521_s_at	-2.346536798	0.026192474	Decrease_in_adherent transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]
EC869_5021_s_at	-2.346295523	0.008381563	Decrease_in_adherent sdhD; succinate dehydrogenase cytochrome b556 small membrane subunit (EC:1.3.5.1); K00242 succinate dehydrogenase hydrophobic membrane anchor protei
V2162_s_at	-2.343052275	0.025880873	Decrease_in_adherent tldD; protease TldD ; K03568 TldD protein
V6499_s_at	-2.340051172	0.023902145	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]
SFV_2948_s_at	-2.326297841	0.008240166	Decrease_in_adherent yqfB; hypothetical protein ; K09900 hypothetical protein
b3858_s_at	-2.325193818	0.000163682	Decrease_in_adherent hypothetical protein ; K09896 hypothetical protein
A3624_s_at	-2.318452738	0.003297858	Decrease_in_adherent aspC; aromatic amino acid aminotransferase (EC:2.6.1.57); K00813 aspartate aminotransferase [EC:2.6.1.1]
V6500_s_at	-2.313240703	0.004350088	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]
V4193_s_at	-2.310022529	0.011045905	Decrease_in_adherent DNA-binding transcriptional activator CaiF ; K08277 transcriptional activator CaiF
SS5_4205_s_at	-2.303886931	0.020972433	Decrease_in_adherent ycfP; hypothetical protein ; K07000
EC869_8306_s_at	-2.300926682	0.005202434	Decrease_in_adherent yfeH; putative cytochrome oxidase
SD1_3598_s_at	-2.296682855	0.028486123	Decrease_in_adherent galM; aldose 1-epimerase (EC:5.1.3.-); K01785 aldose 1-epimerase [EC:5.1.3.3]
A0334_s_at	-2.291249642	0.044900051	Decrease_in_adherent ackA; acetate kinase (EC:2.7.2.1); K00925 acetate kinase [EC:2.7.2.1]
M0375_s_at	-2.287931623	0.007771592	Decrease_in_adherent ptsI; phosphoenolpyruvate-protein phosphotransferase (EC:2.7.3.9); K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]
V0311_s_at	-2.286936029	0.032733258	Decrease_in_adherent pgj; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
LH0104_s_at	-2.286787096	0.021683112	Decrease_in_adherent hypothetical protein
A2459_s_at	-2.284632658	0.005567884	Decrease_in_adherent NO_KEGG_DATA
b4406_s_at	-2.281354558	0.006009685	Decrease_in_adherent yaeP; hypothetical protein
pMG8283_03_s_at	-2.274590037	0.02477919	Decrease_in_adherent mobilization protein MobA
SB5_4545_s_at	-2.273743561	0.013613811	Decrease_in_adherent ppnK; inorganic polyphosphate/ATP-NAD kinase (EC:2.7.1.23); K00858 NAD+ kinase [EC:2.7.1.23]
N0877_s_at	-2.271838513	0.03671766	Decrease_in_adherent sensory box-containing diguanylate cyclase
c5607_at	-2.269424363	0.002575037	Decrease_in_adherent NO_KEGG_DATA
A4380_s_at	-2.267596713	0.016451938	Decrease_in_adherent speG; spermidine N1-acetyltransferase (EC:2.3.1.57); K00657 diamine N-acetyltransferase [EC:2.3.1.57]
V0313_s_at	-2.267334806	0.023470799	Decrease_in_adherent pgj; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
G4653_s_at	-2.266462009	0.021574734	Decrease_in_adherent hypothetical protein
SDY_2498_s_at	-2.265546458	0.008292833	Decrease_in_adherent yfcF; hypothetical protein
EC869_2285_s_at	-2.265218082	0.021015204	Decrease_in_adherent NO_KEGG_DATA
F3693_s_at	-2.26277164	0.02611672	Decrease_in_adherent NO_KEGG_DATA
SB5_1469_s_at	-2.259943173	0.027598971	Decrease_in_adherent adhA, adhP; alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]
V6874_s_at	-2.257945183	0.009992837	Decrease_in_adherent gcvP; glycine dehydrogenase (EC:1.4.4.2); K00282 glycine dehydrogenase subunit 1 [EC:1.4.4.2]; K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
SD1_2134_s_at	-2.254157966	0.033703071	Decrease_in_adherent vacJ; lipoprotein precursor ; K04754 lipoprotein
A1330_s_at	-2.25389644	0.040600824	Decrease_in_adherent agaR; DNA-binding transcriptional regulator AgaR; K02081 DeoR family transcriptional regulator, aga operon transcriptional repressor
Z6074_s_at	-2.251892338	0.008326905	Decrease_in_adherent hypothetical protein
A0398_s_at	-2.250451005	0.044233674	Decrease_in_adherent evgA; DNA-binding transcriptional activator EvgA ; K07690 two-component system, NarL family, response regulator EvgA
A3843_s_at	-2.247842108	0.029454955	Decrease_in_adherent putative inner membrane protein

A4131_s_at	-2.241867905	0.009066445	Decrease_in_adherent ynaJ; hypothetical protein
V1509_s_at	-2.239056731	0.016351902	Decrease_in_adherent gapA; glyceraldehyde-3-phosphate dehydrogenase A ; K00134 glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
A3363_s_at	-2.235889557	0.009133328	Decrease_in_adherent sdhB; succinate dehydrogenase iron-sulfur subunit (EC:1.3.99.1); K00240 succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]
A0436_s_at	-2.234781565	0.009860457	Decrease_in_adherent ptsH; phosphocarrier protein HPr (EC:2.7.1.69 2.7.3.9); K02784 phosphocarrier protein HPr
UT189_C0886_at	-2.234543152	0.008899867	Decrease_in_adherent hypothetical protein
EC869_5211_s_at	-2.233038126	0.003537253	Decrease_in_adherent hypothetical protein
V1600_s_at	-2.226262407	0.008594725	Decrease_in_adherent mutS; DNA mismatch repair protein MutS ; K03555 DNA mismatch repair protein MutS
SD1_3403_s_at	-2.224146058	0.008851526	Decrease_in_adherent glutamate and aspartate transporter subunit ; K10001 glutamate/aspartate transport system substrate-binding protein
A2908_s_at	-2.223400092	0.006207485	Decrease_in_adherent cri; DNA-binding transcriptional regulator Cri ; K11926 sigma factor-binding protein Cri
ECs5520_s_at	-2.222127999	0.035007352	Decrease_in_adherent hypothetical protein
SD1_0613_s_at	-2.215606182	0.004300731	Decrease_in_adherent did; D-lactate dehydrogenase (EC:1.1.1.28); K03777 D-lactate dehydrogenase [EC:1.1.1.28]
A3442_s_at	-2.204028849	0.00899203	Decrease_in_adherent putative kinase inhibitor protein ; K06910
ECP_4493_x_at	-2.203462104	0.000730094	Decrease_in_adherent NO_KEGG_DATA
SD1_1682_s_at	-2.200710061	0.021896575	Decrease_in_adherent apbA; 2-dehydropantoate 2-reductase (EC:1.1.1.169); K00077 2-dehydropantoate 2-reductase [EC:1.1.1.169]
EC869_5178_s_at	-2.200189972	0.003773211	Decrease_in_adherent lpdA; dihydrolipoamide dehydrogenase (EC:1.8.1.4); K00382 dihydrolipoamide dehydrogenase [EC:1.8.1.4]
V0844_s_at	-2.197511231	0.014418334	Decrease_in_adherent hfq; RNA-binding protein Hfq ; K03666 host factor-I protein
A2897_s_at	-2.197476899	0.038024688	Decrease_in_adherent putative HicB
SD1_3096_s_at	-2.194090501	0.007614936	Decrease_in_adherent hypothetical protein
V1458_s_at	-2.191532336	0.03111944	Decrease_in_adherent sdaA; L-serine ammonia-lyase 1 (EC:4.3.1.17); K01752 L-serine dehydratase [EC:4.3.1.17]
A1013_s_at	-2.188901266	0.048096353	Decrease_in_adherent metK; S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]
b1519_s_at	-2.184148155	0.014415884	Decrease_in_adherent NO_KEGG_DATA
V0768_s_at	-2.183812471	0.030550836	Decrease_in_adherent fre; FMN reductase ; K05368 aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.29]
SB5_1470_x_at	-2.182081258	0.007190094	Decrease_in_adherent adhP, adhA; alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]
b1881_s_at	-2.181168843	0.001247363	Decrease_in_adherent cheZ; chemotaxis regulator CheZ ; K03414 chemotaxis protein CheZ
A4619_s_at	-2.177678848	0.000739541	Decrease_in_adherent fadD; long-chain-fatty-acid-CoA ligase (EC:6.2.1.3); K01897 long-chain acyl-CoA synthetase [EC:6.2.1.3]
A3777_s_at	-2.17294123	0.02749866	Decrease_in_adherent bssS, yoeP; biofilm formation regulatory protein BssS ; K12148 biofilm regulator BssS
SD1_0474_s_at	-2.171410714	0.028279303	Decrease_in_adherent glgC; glucose-1-phosphate adenylyltransferase (EC:2.7.7.27); K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]
A2643_s_at	-2.168298908	0.046726191	Decrease_in_adherent two-component response regulator ; K07773 two-component system, OmpR family, aerobic respiration control protein ArcA
A0621_s_at	-2.164511039	0.008150874	Decrease_in_adherent clpB; protein disaggregation chaperone ; K03695 ATP-dependent Clp protease ATP-binding subunit ClpB
A4519_s_at	-2.159511349	0.001083234	Decrease_in_adherent pheT; phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20); K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
A3557_s_at	-2.157681776	0.030871631	Decrease_in_adherent clpS; ATP-dependent Clp protease adaptor protein ClpS ; K06891 ATP-dependent Clp protease adaptor protein ClpS
A1527_s_at	-2.156753816	0.038572921	Decrease_in_adherent crp; cAMP-regulatory protein ; K10914 CRP/FNR family transcriptional regulator, cyclic AMP receptor protein
APECO1_2149_s_at	-2.154420003	0.026268183	Decrease_in_adherent yjgF; hypothetical protein ; K09022 UPF0076 protein YjgF
A4485_s_at	-2.152502355	0.018877548	Decrease_in_adherent sufS; bifunctional cysteine desulfurase/selenocysteine lyase (EC:2.8.1.7 4.4.1.16); K11717 cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]
b0605_s_at	-2.148900856	0.002335724	Decrease_in_adherent ahpC; alkyl hydroperoxide reductase subunit C (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
SD1_0562_s_at	-2.148375513	0.010518015	Decrease_in_adherent folE; GTP cyclohydrolase I (EC:3.5.4.16); K01495 GTP cyclohydrolase I [EC:3.5.4.16]
V2537_s_at	-2.146778094	0.043420129	Decrease_in_adherent hdhA; 7-alpha-hydroxysteroid dehydrogenase (EC:1.1.1.159); K00076 7-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.159]
SS5_4239_s_at	-2.135419109	0.014641823	Decrease_in_adherent putative aldehyde dehydrogenase ; K06447 succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]
V0732_s_at	-2.130136513	0.024025943	Decrease_in_adherent putative DNA-binding transcriptional regulator
A2631_s_at	-2.127005074	0.004055986	Decrease_in_adherent ybeJ; nicotinamide-nucleotide adenylyltransferase (EC:2.7.7.1); K00952 nicotinamide-nucleotide adenylyltransferase [EC:2.7.7.1]; K06210 ribosylnicotinamide kin
N4115_x_at	-2.126077651	0.002355293	Decrease_in_adherent yjgD; hypothetical protein ; K09893 hypothetical protein
A3915_s_at	-2.125434489	0.012466184	Decrease_in_adherent hypothetical protein ; K09902 hypothetical protein
A2373_s_at	-2.121718863	0.037076728	Decrease_in_adherent frdD; fumarate reductase subunit D ; K00247 fumarate reductase subunit D [EC:1.3.99.1]
V4574_s_at	-2.119956232	0.028121509	Decrease_in_adherent NO_KEGG_DATA
SD1_2489_s_at	-2.117920406	0.021658452	Decrease_in_adherent hypothetical protein
V0855_s_at	-2.1177966	0.040975778	Decrease_in_adherent purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]
A3486_s_at	-2.117521766	0.033101954	Decrease_in_adherent ompX; outer membrane protein X ; K11934 outer membrane protein X
A0582_s_at	-2.11748576	0.014601422	Decrease_in_adherent NO_KEGG_DATA
SB5_4039_s_at	-2.116739012	0.000555546	Decrease_in_adherent ybeJ; glutamate and aspartate transporter subunit ; K10001 glutamate/aspartate transport system substrate-binding protein
V3422_s_at	-2.114997556	0.027760539	Decrease_in_adherent kefG; glutathione-regulated potassium-efflux system ancillary protein KefG ; K11748 glutathione-regulated potassium-efflux system ancillary protein KefG
EC536_3670_s_at	-2.114407034	0.001757439	Decrease_in_adherent atpG; FOF1 ATP synthase subunit gamma (EC:3.6.3.14); K02115 F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]
V5396_s_at	-2.113888107	0.019752762	Decrease_in_adherent glgX; glycogen debranching enzyme ; K02438 glycogen operon protein GlgX [EC:3.2.1.-]
EC869_2844_s_at	-2.111588826	0.025517031	Decrease_in_adherent miaA; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase; K00791 tRNA delta(2)-isopentenylpyrophosphate transferase [EC:2.5.1.8]
EC869_2587_s_at	-2.111163264	0.018925867	Decrease_in_adherent cheY; chemotaxis response regulator ; K03413 two-component system, chemotaxis family, response regulator CheY
A3042_s_at	-2.10848894	0.0005506352	Decrease_in_adherent hypothetical protein ; K09913 hypothetical protein
A0057_s_at	-2.102705453	0.001485924	Decrease_in_adherent hisB; imidazoleglycerol-phosphate dehydratase/histidinol-phosphate phosphatase ; K01089 imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase [EC:
D3362_x_at	-2.101307798	0.035018986	Decrease_in_adherent tktA; transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]
V5769_s_at	-2.100656461	0.004093996	Decrease_in_adherent ppc; phosphoenolpyruvate carboxylase (EC:4.1.1.31); K01595 phosphoenolpyruvate carboxylase [EC:4.1.1.31]
V5918_s_at	-2.100535966	0.024679676	Decrease_in_adherent NO_KEGG_DATA
SD1_3571_s_at	-2.097598351	0.015859053	Decrease_in_adherent yaeO; Rho-binding antiterminator
SB0_3336_s_at	-2.095566583	0.008152529	Decrease_in_adherent yhfA; hypothetical protein ; K07397 putative redox protein
L4777_s_at	-2.089382105	0.047254149	Decrease_in_adherent parM; plasmid segregation protein ParM
A2905_s_at	-2.086039357	0.01999038	Decrease_in_adherent pepD; aminoacyl-histidine dipeptidase ; K01270 aminoacylhistidine dipeptidase [EC:3.4.13.3]
F1834_s_at	-2.085427571	0.012252619	Decrease_in_adherent transcriptional regulator SlyA ; K06075 MarR family transcriptional regulator, transcriptional regulator for hemolysin
V3698_x_at	-2.085322598	0.012027959	Decrease_in_adherent cri; DNA-binding transcriptional regulator Cri ; K11926 sigma factor-binding protein Cri
A2807_s_at	-2.084104236	0.015884955	Decrease_in_adherent pts; 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase (EC:3.2.2.9); K01243 S-adenosylhomocysteine/5'-methylthioadenosine nucleosidase [EC:3.2.2.9]
V4112_s_at	-2.083531506	0.016489829	Decrease_in_adherent glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]

V6875_s_at	-2.080086393	0.025048146	Decrease_in_adherent gcvP; glycine dehydrogenase (EC:1.4.4.2); K00282 glycine dehydrogenase subunit 1 [EC:1.4.4.2]; K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
A1361_s_at	-2.076412523	0.001795342	Decrease_in_adherent yhbW; hypothetical protein
V7054_s_at	-2.0732283	0.009607469	Decrease_in_adherent zwf; glucose-6-phosphate 1-dehydrogenase (EC:1.1.1.49); K00036 glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]
A1971_s_at	-2.067156749	0.007368372	Decrease_in_adherent iivD; dihydroxy-acid dehydratase (EC:4.2.1.9); K01687 dihydroxy-acid dehydratase [EC:4.2.1.9]
A2738_s_at	-2.054457751	0.033276903	Decrease_in_adherent ftsA; cell division protein FtsA; K03590 cell division protein FtsA
c3307_s_at	-2.054068104	0.017827443	Decrease_in_adherent RNA polymerase sigma factor RpoS; K03087 RNA polymerase nonessential primary-like sigma factor
EC869_3914_s_at	-2.053578425	0.002614654	Decrease_in_adherent elongation factor Tu; K02358 elongation factor EF-Tu [EC:3.6.5.3]
APECO1_3321_at	-2.050922449	0.027594094	Decrease_in_adherent NO_KEGG_DATA
SB5_3084_s_at	-2.049247516	0.022506242	Decrease_in_adherent cirA; colicin I receptor; K02014 iron complex outer membrane receptor protein
c0823_s_at	-2.046654628	0.006885553	Decrease_in_adherent hypothetical protein
F1227_s_at	-2.046077128	0.035747151	Decrease_in_adherent cupin family protein
EC869_8298_x_at	-2.043821894	0.008658103	Decrease_in_adherent cystK; cysteine synthase A; K01738 cysteine synthase A [EC:2.5.1.47]
F1880_s_at	-2.040513824	0.012112774	Decrease_in_adherent putative inner membrane protein
pCoo050_at	-2.038118169	0.04706861	Decrease_in_adherent NO_KEGG_DATA
SFV_3581_s_at	-2.029478971	0.002903448	Decrease_in_adherent cpxR; DNA-binding transcriptional regulator CpxR; K07662 two-component system, OmpR family, response regulator CpxR
V2361_s_at	-2.02686509	0.016094868	Decrease_in_adherent fliC; cystine transporter subunit; K02424 cystine transport system substrate-binding protein
UTI89_C0178_s_at	-2.024251714	0.001072527	Decrease_in_adherent yaeG; carbohydrate diacid transcriptional activator CdaR; K02647 carbohydrate diacid regulator
AFFX-r2-Bs-thr-3_s	-2.023501405	0.005603369	Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]
SD1_2453_s_at	-2.023411099	0.02496216	Decrease_in_adherent ppc; phosphoenolpyruvate carboxylase (EC:4.1.1.31); K01595 phosphoenolpyruvate carboxylase [EC:4.1.1.31]
b2908_s_at	-2.01680867	0.027832164	Decrease_in_adherent pepP; proline aminopeptidase P II; K01262 X-Pro aminopeptidase [EC:3.4.11.9]
EC869_3486_s_at	-2.016016146	0.008863375	Decrease_in_adherent artI; arginine 3rd transport system periplasmic binding protein; K09997 arginine transport system substrate-binding protein
V0404_s_at	-2.010865229	0.019344995	Decrease_in_adherent rpoB; DNA-directed RNA polymerase subunit beta (EC:2.7.7.6); K03043 DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
AFFX-ThrX-3_at	-2.009219041	0.007027587	Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]
V2140_s_at	-2.008483837	0.001763096	Decrease_in_adherent glnE; fused deadenylyltransferase/adenylyltransferase for glutamine synthetase (EC:2.7.7.42); K00982 glutamate-ammonia-ligase adenylyltransferase [EC:2.7.7.42]
AFFX-r2-Bs-phe-3_a	-2.008160906	0.00820383	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]
b1477_s_at	-2.007140663	0.005296862	Decrease_in_adherent yddM; hypothetical protein
V7305_s_at	-2.004695979	0.025465319	Decrease_in_adherent ycfQ; hypothetical protein
G3937_s_at	-2.00396883	0.038050665	Decrease_in_adherent putative PsiA
A2931_s_at	-2.003365243	0.044603669	Decrease_in_adherent yagU; hypothetical protein; K08996 putative membrane protein
EC869_7314_s_at	-2.003207387	0.030696837	Decrease_in_adherent tsx; nucleoside channel; K05517 nucleoside-specific channel-forming protein
A2260_s_at	-2.002025627	0.033528249	Decrease_in_adherent yjbJ; putative stress-response protein
EC869_2918_s_at	-2.000773441	0.005666664	Decrease_in_adherent dcuA; anaerobic C4-dicarboxylate transporter DcuA; K07791 anaerobic C4-dicarboxylate transporter DcuA
AFFX-ThrX-M_at	-2.000714496	0.005734643	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
F4536_s_at	-1.998122418	0.01269733	Decrease_in_adherent yjbK; zinc uptake transcriptional repressor; K09823 Fur family transcriptional regulator, zinc uptake regulator
A3911_s_at	-1.997816903	0.032272754	Decrease_in_adherent minC; septum formation inhibitor; K03610 septum site-determining protein MinC
J2220_s_at	-1.995636151	0.029384169	Decrease_in_adherent dinD; DNA-damage-inducible protein D
V4114_s_at	-1.995444807	0.006377349	Decrease_in_adherent glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
A3867_s_at	-1.994963252	0.041964511	Decrease_in_adherent hypothetical protein
b1094_s_at	-1.993514663	0.005515768	Decrease_in_adherent hypothetical protein
AFFX-r2-Bs-thr-5_s	-1.993476812	0.004707147	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
V0314_s_at	-1.986056871	0.035809829	Decrease_in_adherent pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
AFFX-r2-Bs-thr-M_s	-1.985497351	0.004804081	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
V3883_s_at	-1.983044318	0.007253868	Decrease_in_adherent succinate dehydrogenase, flavoprotein subunit
F3408_s_at	-1.979590679	0.01928341	Decrease_in_adherent glutathionylspermidine synthase family protein
V2981_s_at	-1.978962829	0.049597506	Decrease_in_adherent aminotransferase; K10907 aminotransferase [EC:2.6.1.-]
V3854_s_at	-1.975709885	0.004951059	Decrease_in_adherent ycfW; outer membrane-specific lipoprotein transporter subunit LolE; K09808 lipoprotein-releasing system permease protein
SDY_1801_s_at	-1.975358604	0.030990507	Decrease_in_adherent hypothetical protein
S3181_s_at	-1.974669358	0.020456359	Decrease_in_adherent reverse transcriptase-like protein
c0540_s_at	-1.974145892	0.023376158	Decrease_in_adherent NO_KEGG_DATA
A0849_s_at	-1.973915345	0.044099542	Decrease_in_adherent rimM; rRNA large subunit methyltransferase M; K06968
ECs2438_s_at	-1.97374199	0.010283155	Decrease_in_adherent katE; hydroperoxidase II (EC:1.11.1.6); K03781 catalase [EC:1.11.1.6]
b2741_s_at	-1.968725571	0.013531646	Decrease_in_adherent hypothetical protein
UTI89_C4861_x_at	-1.967326245	0.004012767	Decrease_in_adherent rraB; uncharacterized protein YjgD; K09893 hypothetical protein
A1609_s_at	-1.966417716	0.034467965	Decrease_in_adherent glgB; glycogen branching enzyme (EC:2.4.1.18); K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]
ECs0750_s_at	-1.965988599	0.002371473	Decrease_in_adherent hypothetical protein
EC869_8209_s_at	-1.962279566	0.025281673	Decrease_in_adherent transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]
A1064_s_at	-1.962118462	0.023812584	Decrease_in_adherent hypothetical protein
A3853_s_at	-1.961117545	0.005499159	Decrease_in_adherent hypothetical protein
b1886_s_at	-1.960310212	0.030261086	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor
D3529_at	-1.95721734	0.032684721	Decrease_in_adherent finO; fertility inhibition protein
M3861_s_at	-1.956957504	0.024568762	Decrease_in_adherent stable plasmid inheritance protein
AFFX-ThrX-5_at	-1.955063626	0.003616219	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
V2075_s_at	-1.954412642	0.008635036	Decrease_in_adherent ygiU; serine/threonine transporter SstT; K07862 serine/threonine transporter
S3180_s_at	-1.952672561	0.005011951	Decrease_in_adherent reverse transcriptase-like protein
AFFX-PheX-5_at	-1.952090152	0.006501378	Decrease_in_adherent pheB; hypothetical protein; K06209 chorismate mutase [EC:5.4.99.5]
A1530_s_at	-1.948974739	0.038852228	Decrease_in_adherent pabA; aminodeoxychorismate synthase subunit II
AFFX-r2-Bs-phe-M_i	-1.947618463	0.007986072	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]

SBO_0253_at	-1.946032462	0.009325759	Decrease_in_adherent IS629 ORF1
A2825_s_at	-1.944167967	0.023032809	Decrease_in_adherent hlpA; periplasmic chaperone ; K06142 outer membrane protein
V3607_s_at	-1.940916781	0.012333794	Decrease_in_adherent hypothetical protein
ECs1050_s_at	-1.940496891	0.019673632	Decrease_in_adherent hypothetical protein
V2862_s_at	-1.936157397	0.033392826	Decrease_in_adherent fba; fructose-bisphosphate aldolase (EC:4.1.2.13); K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13]
SD1_1536_s_at	-1.935560611	0.018489265	Decrease_in_adherent fecR; fec operon regulator FecR ; K07165 transmembrane sensor
AFFX-r2-Bs-phe-5_a	-1.934886673	0.005366732	Decrease_in_adherent pheB; hypothetical protein; K06209 chorismate mutase [EC:5.4.99.5]
V0767_s_at	-1.934366447	0.007425332	Decrease_in_adherent fre, ubiB, fadI; FMN reductase (EC:1.5.1.29); K05368 aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.29]
EC536_3561_s_at	-1.934028476	0.024471271	Decrease_in_adherent folE; GTP cyclohydrolase I (EC:3.5.4.16); K01495 GTP cyclohydrolase I [EC:3.5.4.16]
b3283_s_at	-1.933485461	0.046838407	Decrease_in_adherent yrdD; putative DNA topoisomerase ; K07479 putative DNA topoisomerase
EC869_5670_s_at	-1.932279004	0.01630529	Decrease_in_adherent luxS; S-ribosylhomocysteine lyase; K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21]
A1294_s_at	-1.929532104	0.030465862	Decrease_in_adherent yqjD; hypothetical protein
A0767_at	-1.926757739	0.019114662	Decrease_in_adherent mutS; DNA mismatch repair protein MutS ; K03555 DNA mismatch repair protein MutS
G1262_s_at	-1.923574603	0.027745324	Decrease_in_adherent trg; methyl-accepting chemotaxis protein III ; K05876 methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor
V5190_s_at	-1.923477159	0.048146951	Decrease_in_adherent bcsE; cellulose biosynthesis protein BcsE
EC869_3973_s_at	-1.921920632	0.005153532	Decrease_in_adherent transcriptional regulator, AsnC family
ECP_2590_s_at	-1.921179441	0.013835129	Decrease_in_adherent conserved hypothetical protein, putative transposase (fragment)
AFFX-PheX-3_at	-1.921006022	0.008835985	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]
EC536_6355_s_at	-1.920833806	0.038719093	Decrease_in_adherent trpS; tryptophanyl-tRNA synthetase (EC:6.1.1.2); K01867 tryptophanyl-tRNA synthetase [EC:6.1.1.2]
EC869_7926_s_at	-1.919979154	0.043453268	Decrease_in_adherent prolyl-tRNA synthetase ; K01881 prolyl-tRNA synthetase [EC:6.1.1.15]
AFFX-r2-Bs-dap-M_i	-1.916409249	0.004064818	Decrease_in_adherent mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3]
EC869_1963_s_at	-1.912649908	0.003898313	Decrease_in_adherent hns; global DNA-binding transcriptional dual regulator H-NS ; K03746 DNA-binding protein H-NS
A3035_s_at	-1.910556078	0.047475066	Decrease_in_adherent psiF; induced by phosphate starvation
A1054_at	-1.90952965	0.005244132	Decrease_in_adherent hypothetical protein
EC869_0563_s_at	-1.906889208	0.006339628	Decrease_in_adherent prfC; oligopeptidase A ; K01414 oligopeptidase A [EC:3.4.24.70]
EC869_2599_s_at	-1.906730833	0.012991255	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor
V7001_s_at	-1.906615575	0.000337173	Decrease_in_adherent tap; methyl-accepting protein IV ; K05877 methyl-accepting chemotaxis protein IV, peptide sensor receptor
AFFX-DapX-3_at	-1.905976116	0.005248425	Decrease_in_adherent ypjG; hypothetical protein
V3865_s_at	-1.903348577	0.016640244	Decrease_in_adherent hypothetical protein
V2288_x_at	-1.898394219	0.020598917	Decrease_in_adherent IS91, transposase, truncation
AFFX-r2-Bs-dap-3_a	-1.894845506	0.004674732	Decrease_in_adherent ypjG; hypothetical protein
V3201_s_at	-1.894570998	7.32E-05	Decrease_in_adherent pmrD; polymyxin resistance protein B
V6915_x_at	-1.89434072	0.001074144	Decrease_in_adherent modA; molybdate transport system periplasmic binding component ; K02020 molybdate transport system substrate-binding protein
EC869_6824_s_at	-1.893132282	0.001700048	Decrease_in_adherent aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
AFFX-PheX-M_at	-1.8889448	0.009279904	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]
V6747_s_at	-1.885387965	0.004245038	Decrease_in_adherent tas; putative aldo-keto reductase
V5725_s_at	-1.884777084	0.04435929	Decrease_in_adherent endonuclease/exonuclease/phosphatase family protein ; K06896
M1212_x_at	-1.884475594	0.039902027	Decrease_in_adherent IS629 transposase orfA
V7066_s_at	-1.884122275	0.004938791	Decrease_in_adherent hypothetical protein
EC869_7371_s_at	-1.88205164	0.014334183	Decrease_in_adherent NO_KEGG_DATA
A0419_s_at	-1.881366497	0.04811299	Decrease_in_adherent glk; glucokinase (EC:2.7.1.2); K00845 glucokinase [EC:2.7.1.2]
V0034_s_at	-1.880948452	0.042040542	Decrease_in_adherent frdC; fumarate reductase subunit C ; K00246 fumarate reductase subunit C [EC:1.3.99.1]
b0917_s_at	-1.878807908	0.026543778	Decrease_in_adherent ycaR; hypothetical protein ; K09791 hypothetical protein
EC869_6165_s_at	-1.874701041	0.00022407	Decrease_in_adherent NO_KEGG_DATA
AFFX-r2-Bs-dap-5_a	-1.871114953	0.003029346	Decrease_in_adherent dapB; dihydrodipicolinate reductase (EC:1.3.1.26); K00215 dihydrodipicolinate reductase [EC:1.3.1.26]
A1226_s_at	-1.86998463	0.037234246	Decrease_in_adherent hypothetical protein
c5600_s_at	-1.868724843	0.000529312	Decrease_in_adherent ybl4; hypothetical protein
V2868_s_at	-1.865570602	0.004964441	Decrease_in_adherent yggE; hypothetical protein ; K09807 hypothetical protein
AFFX-DapX-5_at	-1.864425304	0.003610178	Decrease_in_adherent dapB; dihydrodipicolinate reductase (EC:1.3.1.26); K00215 dihydrodipicolinate reductase [EC:1.3.1.26]
A3985_s_at	-1.863092007	0.003899668	Decrease_in_adherent oppD; oligopeptide transporter ATP-binding component ; K02031 peptide/nickel transport system ATP-binding protein
EC869_8425_s_at	-1.862924471	0.001861174	Decrease_in_adherent pheT; phenylalanyl-tRNA synthetase subunit beta ; K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
EC869_2220_s_at	-1.862000943	0.030496249	Decrease_in_adherent NO_KEGG_DATA
EC536_2379_s_at	-1.861259639	0.047334859	Decrease_in_adherent ygdE; putative RNA 2'-O-ribose methyltransferase ; K06968
SD1_2443_s_at	-1.859118459	0.021479999	Decrease_in_adherent udnA; soluble pyridine nucleotide transhydrogenase (EC:1.6.1.1); K00322 NAD(P) transhydrogenase [EC:1.6.1.1]
A0580_s_at	-1.855484567	0.043049043	Decrease_in_adherent glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
A1031_s_at	-1.853537903	0.013844257	Decrease_in_adherent yggL; hypothetical protein ; K09923 hypothetical protein
b3609_s_at	-1.853056209	0.021468093	Decrease_in_adherent secB; preprotein translocase subunit SecB ; K03071 preprotein translocase subunit SecB
SS5_3569_s_at	-1.850876248	0.041307425	Decrease_in_adherent putative enzyme ; K01061 carboxymethylenebutenolidase [EC:3.1.1.45]
AFFX-DapX-M_at	-1.844472501	0.004804447	Decrease_in_adherent mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3]
SD1_3424_s_at	-1.84427894	0.035437898	Decrease_in_adherent asnB; asparagine synthetase B ; K01953 asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]
A2395_s_at	-1.843147587	0.027634699	Decrease_in_adherent purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]
A2226_s_at	-1.842910616	0.01518046	Decrease_in_adherent iclR; transcriptional repressor IclR
EC869_2518_at	-1.840128492	0.0122147	Decrease_in_adherent NO_KEGG_DATA
V2049_s_at	-1.827139084	0.038372115	Decrease_in_adherent yqjE; hypothetical protein
ECs2281_at	-1.827025125	0.026988545	Decrease_in_adherent hypothetical protein
EC869_7445_s_at	-1.826544995	0.041850507	Decrease_in_adherent glnS; glutamyl-tRNA synthetase; K01886 glutamyl-tRNA synthetase [EC:6.1.1.18]
A4684_s_at	-1.824207458	0.002128906	Decrease_in_adherent NO_KEGG_DATA

G4205_s_at	-1.819847323	0.026188463	Decrease_in_adherent NO_KEGG_DATA
EC869_1162_s_at	-1.81571835	0.040334407	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]
V5405_s_at	-1.811281785	0.018525085	Decrease_in_adherent glgP; glycogen phosphorylase ; K00688 starch phosphorylase [EC:2.4.1.1]
EC869_0738_s_at	-1.81125737	0.00215314	Decrease_in_adherent bcsA; cellulose synthase catalytic subunit (EC:2.4.1.12); K00694 cellulose synthase (UDP-forming) [EC:2.4.1.12]
V7295_x_at	-1.810421818	0.009524873	Decrease_in_adherent hyaB; hydrogenase 1 large subunit ; K06281 hydrogenase large subunit [EC:1.12.99.6]
A3040_s_at	-1.810142892	0.033575408	Decrease_in_adherent yaiA; hypothetical protein
W4315_at	-1.807015153	0.030692096	Decrease_in_adherent yaaB; hypothetical protein
A0712_s_at	-1.806424244	0.049103064	Decrease_in_adherent ygaG; S-ribosylhomocysteinase ; K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21]
D4711_x_at	-1.805489896	0.026921279	Decrease_in_adherent IS629; transposase orfA
F3192_at	-1.805016278	0.021306605	Decrease_in_adherent NO_KEGG_DATA
A4654_s_at	-1.804976829	0.025209626	Decrease_in_adherent hypothetical protein
V3434_s_at	-1.803812562	0.003563716	Decrease_in_adherent cysK; cysteine synthase A (EC:2.5.1.47); K01738 cysteine synthase A [EC:2.5.1.47]
A0885_s_at	-1.802383812	0.018831784	Decrease_in_adherent ygdP; dinucleoside polyphosphate hydrolase ; K08311 putative (di) nucleoside polyphosphate hydrolase [EC:3.6.1.-]
A3917_s_at	-1.802063562	0.012016433	Decrease_in_adherent ycgN; hypothetical protein; K09160 hypothetical protein
EC869_8302_s_at	-1.801388498	0.015522759	Decrease_in_adherent NO_KEGG_DATA
A4152_s_at	-1.798579295	0.012178178	Decrease_in_adherent hypothetical protein
V3144_s_at	-1.797776998	0.04854934	Decrease_in_adherent yfB; hypothetical protein (EC:3.1.3.5); K08722 5'-nucleotidase [EC:3.1.3.5]
A0487_s_at	-1.796379094	0.016777433	Decrease_in_adherent hypothetical protein
D3534_s_at	-1.79211926	0.045324424	Decrease_in_adherent protein CopB
A2012_s_at	-1.790969744	0.029192864	Decrease_in_adherent dapF; diaminopimelate epimerase ; K01778 diaminopimelate epimerase [EC:5.1.1.7]
c0751_s_at	-1.787880859	0.040686136	Decrease_in_adherent NO_KEGG_DATA
V6719_s_at	-1.783306276	0.035815554	Decrease_in_adherent DNA-binding transcriptional regulator FruR ; K03435 LacI family transcriptional regulator, fructose operon transcriptional repressor
A0629_s_at	-1.778487385	0.021330073	Decrease_in_adherent NO_KEGG_DATA
EC869_3451_s_at	-1.777321343	0.030515286	Decrease_in_adherent minC; septum formation inhibitor ; K03610 septum site-determining protein MinC
V6217_s_at	-1.776384928	0.028122381	Decrease_in_adherent sfcA; malate dehydrogenase (EC:1.1.1.38); K00027 malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
11820_s_at	-1.776049438	0.031575169	Decrease_in_adherent NO_KEGG_DATA
A0342_s_at	-1.775622417	0.029735819	Decrease_in_adherent NAD-binding domain-containing protein ; K07071
B0435_s_at	-1.774923543	0.026125081	Decrease_in_adherent ynfA; transcriptional regulator BolA ; K05527 BolA protein
SD1_2556_s_at	-1.770991398	0.042510615	Decrease_in_adherent yihX; phosphatase ; K07025 putative hydrolase of the HAD superfamily
A1518_s_at	-1.769199269	0.021224967	Decrease_in_adherent slyD; FKBP-type peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K03775 FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]
EC869_5213_s_at	-1.767778454	0.007066164	Decrease_in_adherent hypothetical protein
SD1_2536_s_at	-1.764243871	0.00725255	Decrease_in_adherent fdoG; formate dehydrogenase-O, major subunit ; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]
A1296_s_at	-1.763173075	0.022698542	Decrease_in_adherent hypothetical protein
EC869_5452_s_at	-1.761209759	0.015949153	Decrease_in_adherent yhcK; transcriptional regulator NanR
A0011_s_at	-1.757627739	0.021957895	Decrease_in_adherent hypothetical protein
A2500_s_at	-1.757399372	0.007519942	Decrease_in_adherent hypothetical protein
SVF_3141_at	-1.755592343	0.027212768	Decrease_in_adherent yqjC; hypothetical protein
V1348_s_at	-1.754004865	0.01247763	Decrease_in_adherent NO_KEGG_DATA
F4327_s_at	-1.753646589	0.002909077	Decrease_in_adherent hypothetical protein
A0051_s_at	-1.752580027	0.036358863	Decrease_in_adherent NAD dependent epimerase/dehydratase family protein
V5882_s_at	-1.749726991	0.004410729	Decrease_in_adherent sodA; superoxide dismutase ; K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
EC869_0400_s_at	-1.745356751	0.002018133	Decrease_in_adherent glycogen branching enzyme ; K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]
SB5_4324_s_at	-1.743674778	0.007170009	Decrease_in_adherent NO_KEGG_DATA
A4644_s_at	-1.740459052	0.003741808	Decrease_in_adherent htpX; heat shock protein HtpX ; K03799 heat shock protein HtpX [EC:3.4.24.-]
A1555_s_at	-1.735672532	0.028189098	Decrease_in_adherent gph; phosphoglycolate phosphatase (EC:3.1.3.18); K01091 phosphoglycolate phosphatase [EC:3.1.3.18]
SS5_1387_s_at	-1.731948931	0.041351752	Decrease_in_adherent hypothetical protein
A4379_s_at	-1.729537441	0.008755657	Decrease_in_adherent hypothetical protein
AFFX-r2-Bs-lys-M_at	-1.72890531	0.011367728	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]
V3168_s_at	-1.728865479	0.005170488	Decrease_in_adherent nuoL; NADH:ubiquinone oxidoreductase, membrane subunit L; K00341 NADH dehydrogenase I subunit L [EC:1.6.5.3]
S2182_x_at	-1.727173953	0.042192395	Decrease_in_adherent IS629 orfB
A3063_s_at	-1.721533083	0.000732487	Decrease_in_adherent yajD; hypothetical protein
AFFX-LysX-3_at	-1.7111778318	0.010558958	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]
V0946_s_at	-1.709560305	0.003205729	Decrease_in_adherent NO_KEGG_DATA
F3897_s_at	-1.707736756	0.03715486	Decrease_in_adherent mdtE; multidrug efflux system protein MdtE
S1912_x_at	-1.70691936	0.016043577	Decrease_in_adherent hypothetical protein
A2552_at	-1.696923307	0.024622523	Decrease_in_adherent N4/N6-methyltransferase family protein
L3255_s_at	-1.694048344	0.038179726	Decrease_in_adherent cyoA; cytochrome o ubiquinol oxidase subunit II (EC:1.10.3.-); K02297 cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]
AFFX-r2-Bs-lys-3_at	-1.691426489	0.009424912	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]
SVF_1183_s_at	-1.69008526	0.005862908	Decrease_in_adherent ycgK; hypothetical protein
A3088_s_at	-1.689822119	0.011035324	Decrease_in_adherent cyoB; cytochrome o ubiquinol oxidase subunit I ; K02298 cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]
AFFX-LysX-5_at	-1.689378066	0.008258666	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]
A1678_s_at	-1.681854372	0.003206566	Decrease_in_adherent gor; glutathione reductase (EC:1.8.1.7); K00383 glutathione reductase (NADPH) [EC:1.8.1.7]
S1911_x_at	-1.680713213	0.021644239	Decrease_in_adherent IS629 orfB
SBO_4372_x_at	-1.678387877	0.000422226	Decrease_in_adherent IS629 ORF1
V4146_s_at	-1.673990246	0.003997995	Decrease_in_adherent pdxJ; pyridoxine 5'-phosphate synthase ; K03474 pyridoxine 5-phosphate synthase [EC:2.6.99.2]
F3053_s_at	-1.672192524	0.014695606	Decrease_in_adherent ycgF; hypothetical protein ; K10026 queuosine biosynthesis protein QueE
A0665_s_at	-1.671860603	0.006272882	Decrease_in_adherent IS21 family transposase

A2183_s_at	-1.671780393	0.003286916	Decrease_in_adherent yjyD; hypothetical protein
A0716_s_at	-1.669147069	0.014818365	Decrease_in_adherent csrA; carbon storage regulator; K03563 carbon storage regulator
SD1_0131_s_at	-1.668905075	0.041415656	Decrease_in_adherent secB; preprotein translocase subunit SecB ; K03071 preprotein translocase subunit SecB
V3318_s_at	-1.663818488	0.026762143	Decrease_in_adherent rtn; hypothetical protein
V5404_s_at	-1.663106627	0.015489683	Decrease_in_adherent glgA; glycogen synthase GlgA; K00703 starch synthase [EC:2.4.1.21]
SS5_4503_s_at	-1.652495485	0.015137522	Decrease_in_adherent nrdI; ribonucleotide reductase stimulatory protein ; K03647 protein involved in ribonucleotide reduction
B2276_s_at	-1.650745081	0.000742009	Decrease_in_adherent nuoN; NADH dehydrogenase subunit N (EC:1.6.5.3); K00343 NADH dehydrogenase I subunit N [EC:1.6.5.3]
b0623_s_at	-1.650085749	0.011734494	Decrease_in_adherent cspE; cold shock protein CspE ; K03704 cold shock protein (beta-ribon, CspA family)
A3821_s_at	-1.64722118	0.031131057	Decrease_in_adherent yfcl; hypothetical protein
V2860_s_at	-1.644521103	0.017708706	Decrease_in_adherent pgk; phosphoglycerate kinase ; K00927 phosphoglycerate kinase [EC:2.7.2.3]
b4142_s_at	-1.642615348	0.049270199	Decrease_in_adherent hypothetical protein
V6006_s_at	-1.642566491	0.003168539	Decrease_in_adherent tsx; nucleoside channel ; K05517 nucleoside-specific channel-forming protein
SSO_3593_x_at	-1.642051602	0.011951661	Decrease_in_adherent IS629 ORF2
A3713_s_at	-1.637359289	0.024281638	Decrease_in_adherent cbpM; chaperone-modulator protein CbpM
S3755_s_at	-1.636010699	0.028331386	Decrease_in_adherent cpxP; periplasmic repressor CpxP ; K06006 periplasmic protein CpxP
F4930_s_at	-1.635844125	0.04795441	Decrease_in_adherent NO_KEGG_DATA
b3279_s_at	-1.634261701	0.039582435	Decrease_in_adherent yrdA; putative transferase
M3859_s_at	-1.631640935	0.014049895	Decrease_in_adherent hypothetical protein
A3809_s_at	-1.630495445	0.021615386	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]
D2423_x_at	-1.63003887	0.015423027	Decrease_in_adherent NO_KEGG_DATA
A2812_s_at	-1.627842065	0.007932303	Decrease_in_adherent dapD; 2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase (EC:2.3.1.117); K00674 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [EC
EC869_4790_s_at	-1.627001268	0.036509177	Decrease_in_adherent frr; ribosome recycling factor ; K02838 ribosome recycling factor
D4055_s_at	-1.625698595	0.025149426	Decrease_in_adherent parM; plasmid segregation protein ParM
A2172_at	-1.624617885	0.014961245	Decrease_in_adherent NO_KEGG_DATA
D1898_s_at	-1.622879107	0.021897915	Decrease_in_adherent cyoA; cytochrome o ubiquinol oxidase subunit II ; K02297 cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]
EC869_0593_s_at	-1.62069482	0.004823418	Decrease_in_adherent putative Mg(2+) transport ATPase ; K07507 putative Mg2+ transporter-C (MgtC) family protein
EC869_3959_s_at	-1.612837418	0.042288841	Decrease_in_adherent putative phage repressor protein CI
V4772_s_at	-1.6095039	0.00148229	Decrease_in_adherent hypothetical protein
c2650_at	-1.605519833	0.030824947	Decrease_in_adherent NO_KEGG_DATA
A1221_s_at	-1.604409579	0.034247499	Decrease_in_adherent icc; cyclic 3',5'-adenosine monophosphate phosphodiesterase ; K03651 Icc protein
A2124_s_at	-1.603275684	0.030845343	Decrease_in_adherent cpxA; two-component sensor protein (EC:2.7.3.-); K07640 two-component system, OmpR family, sensor histidine kinase CpxA [EC:2.7.13.3]
ECs2477_x_at	-1.602957172	0.006930586	Decrease_in_adherent IS1203 transposase orfA
AFFX-LysX-M_at	-1.600251527	0.007870897	Decrease_in_adherent lysA; diaminoipimelate decarboxylase (EC:4.1.1.20); K01586 diaminoipimelate decarboxylase [EC:4.1.1.20]
V4620_s_at	-1.599831574	0.017179812	Decrease_in_adherent htrA; serine endoprotease ; K04771 serine protease Do [EC:3.4.21.107]
A3079_s_at	-1.598268628	0.003790576	Decrease_in_adherent cyoC; cytochrome o ubiquinol oxidase subunit III ; K02299 cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]
c5509_x_at	-1.596452062	0.019127286	Decrease_in_adherent NO_KEGG_DATA
G3623_s_at	-1.595710166	0.03830157	Decrease_in_adherent yjyA; hypothetical protein
b3916_s_at	-1.595589916	0.037598594	Decrease_in_adherent pfkA; 6-phosphofructokinase (EC:2.7.1.11); K00850 6-phosphofructokinase [EC:2.7.1.11]
V2374_s_at	-1.595472585	0.015026442	Decrease_in_adherent amyA; cytoplasmic alpha-amylase (EC:3.2.1.1); K01176 alpha-amylase [EC:3.2.1.1]
A4535_s_at	-1.587272373	0.018539036	Decrease_in_adherent hypothetical protein
b4039_s_at	-1.586825102	0.023319289	Decrease_in_adherent ubiC; chorismate pyruvate lyase ; K03181 chorismate--pyruvate lyase [EC:4.1.3.40]
SD1_3080_s_at	-1.583910758	0.016371148	Decrease_in_adherent proline dipeptidase ; K01271 X-Pro dipeptidase [EC:3.4.13.9]
V0560_s_at	-1.581877153	0.006400974	Decrease_in_adherent putative sensor protein
EC536_4700_s_at	-1.577695852	0.047825966	Decrease_in_adherent ycgB; SpoVR family protein
V2945_s_at	-1.575860096	0.030814174	Decrease_in_adherent ygdP; dinucleoside polyphosphate hydrolase ; K08311 putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]
SS5_2456_s_at	-1.573497944	0.019498691	Decrease_in_adherent smpA; hypothetical protein ; K06186 small protein A
AFFX-r2-Bs-lys-5_at	-1.56983111	0.004402931	Decrease_in_adherent lysA; diaminoipimelate decarboxylase (EC:4.1.1.20); K01586 diaminoipimelate decarboxylase [EC:4.1.1.20]
A2849_s_at	-1.563041882	0.036870172	Decrease_in_adherent yaeD; D,D-heptose 1,7-bisphosphate phosphatase ; K03273 D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.-]
SD1_1883_s_at	-1.561483799	0.035170717	Decrease_in_adherent lipA; lipoyl synthase ; K03644 lipoyl acid synthetase [EC:2.8.1.8]
A3866_s_at	-1.559213273	0.010528623	Decrease_in_adherent protein kinase domain-containing protein ; K08884 serine/threonine protein kinase, bacterial [EC:2.7.11.1]
H4060_s_at	-1.557133001	0.03538047	Decrease_in_adherent NO_KEGG_DATA
SDY_2662_s_at	-1.552360327	0.04404965	Decrease_in_adherent hypothetical protein
Z3923_x_at	-1.550990735	0.017957594	Decrease_in_adherent putative IS629 transposase OrfB
V3045_s_at	-1.55058202	0.032721669	Decrease_in_adherent vacJ; lipoprotein precursor ; K04754 lipoprotein
A3822_s_at	-1.550546856	0.033861273	Decrease_in_adherent ycfM; hypothetical protein ; K07337 hypothetical protein
V6706_s_at	-1.548788833	0.047645724	Decrease_in_adherent leuA; 2-isopropylmalate synthase (EC:2.3.3.13); K01649 2-isopropylmalate synthase [EC:2.3.3.13]
SSO_P039_x_at	-1.543142509	0.003814142	Decrease_in_adherent hypothetical protein
A4656_s_at	-1.540912781	0.01890088	Decrease_in_adherent yobA; hypothetical protein; K07156
A4075_s_at	-1.539788736	0.047395839	Decrease_in_adherent hypothetical protein
A3928_s_at	-1.538339869	0.046967125	Decrease_in_adherent hypothetical protein
M4990_s_at	-1.536805269	0.009281114	Decrease_in_adherent trxB; thioredoxin reductase ; K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
EC869_5683_s_at	-1.535392571	6.23E-05	Decrease_in_adherent hypothetical protein
D1931_s_at	-1.535370366	0.04336521	Decrease_in_adherent nlpD; lipoprotein NlpD ; K06194 lipoprotein NlpD
b4135_s_at	-1.53471194	0.02780162	Decrease_in_adherent yjyC; hypothetical protein
ECs2779_x_at	-1.531609238	0.031344227	Decrease_in_adherent amn; AMP nucleosidase; K01241 AMP nucleosidase [EC:3.2.2.4]
V7078_s_at	-1.530046411	0.003865161	Decrease_in_adherent yebZ; putative inner membrane protein; K07245 putative copper resistance protein D
A3296_s_at	-1.528419726	0.00048388	Decrease_in_adherent gtlL; glutamate/aspartate ABC transporter, ATP-binding protein ; K10004 glutamate/aspartate transport system ATP-binding protein [EC:3.6.3.-]

G3816_s_at	-1.524898223	0.007923156	Decrease_in_adherent cyoB; cytochrome o ubiquinol oxidase, subunit I [EC:1.10.3.-]; K02298 cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]
b1745_s_at	-1.51887948	0.001173345	Decrease_in_adherent astB; succinylarginine dihydrolase (EC:3.-.-.-); K01484 succinylarginine dihydrolase [EC:3.5.3.23]
F3246_s_at	-1.51077535	0.020590062	Decrease_in_adherent hypothetical protein
b2124_s_at	-1.510169956	0.043244412	Decrease_in_adherent yehS; hypothetical protein
SBO_1156_s_at	-1.508120279	0.018577398	Decrease_in_adherent yebG; DNA damage-inducible protein YebG; K09918 hypothetical protein
A2182_s_at	-1.505320548	0.018097182	Decrease_in_adherent yjC; DNA-binding transcriptional repressor FabR
V1254_s_at	-1.503088089	0.021134836	Decrease_in_adherent osmY; periplasmic protein; K04065 hyperosmotically inducible periplasmic protein
EC869_6281_s_at	-1.499579408	0.005490735	Decrease_in_adherent eno; phosphopyruvate hydratase; K01689 enolase [EC:4.2.1.11]
b4255_x_at	-1.493333797	0.025453378	Decrease_in_adherent yjgD; hypothetical protein; K09893 hypothetical protein
A4012_at	-1.489935894	0.035162438	Decrease_in_adherent putative phage repressor protein CI
A0435_s_at	-1.488907083	0.019114014	Decrease_in_adherent cysteine synthase A; K01738 cysteine synthase A [EC:2.5.1.47]
V2207_x_at	-1.484167971	0.02076926	Decrease_in_adherent IS629 ORF2
SS5_4135_s_at	-1.482965839	0.005782286	Decrease_in_adherent mhpR; DNA-binding transcriptional activator MhpR, 3HPP-binding; K05818 IclR family transcriptional regulator, mhp operon transcriptional activator
A1943_s_at	-1.479547487	0.006318519	Decrease_in_adherent FOF1 ATP synthase subunit C; K02110 F-type H+-transporting ATPase subunit c [EC:3.6.3.14]
ECs2526_s_at	-1.478533151	0.019726563	Decrease_in_adherent hypothetical protein
EC869_2692_s_at	-1.478438956	0.037097517	Decrease_in_adherent NO_KEGG_DATA
A1783_s_at	-1.467483857	0.000204945	Decrease_in_adherent putative glutathione S-transferase (EC:2.5.1.18)
SD1_3177_s_at	-1.467247431	0.042537604	Decrease_in_adherent purI; formyltetrahydrofolate deformylase (EC:3.5.1.10); K01433 formyltetrahydrofolate deformylase [EC:3.5.1.10]
b3054_s_at	-1.464503621	0.046412408	Decrease_in_adherent ygiF; predicted adenylate cyclase
A4727_s_at	-1.460278673	0.011209562	Decrease_in_adherent yecA; hypothetical protein; K07039
EC869_4608_x_at	-1.460045244	0.007153042	Decrease_in_adherent pgm; phosphoglucomutase (EC:5.4.2.2); K01835 phosphoglucomutase [EC:5.4.2.2]
D1412_s_at	-1.459728437	0.024064235	Decrease_in_adherent putative 60 kDa chaperonin
V1302_s_at	-1.455856196	0.032842094	Decrease_in_adherent putative ABC transporter ATP-binding protein
SB5_1478_x_at	-1.45360988	0.031472658	Decrease_in_adherent insertion sequence 2 OrfA protein
SD1_1429_s_at	-1.448451841	0.015899977	Decrease_in_adherent flagL; flagellar hook-associated protein flagL; K02397 flagellar hook-associated protein 3 flagL
SSO_2654_x_at	-1.446375653	0.000825622	Decrease_in_adherent IS629 ORF2; K07497 putative transposase
EC869_8104_s_at	-1.445291119	0.035164636	Decrease_in_adherent guaA; GMP synthase (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
A2067_s_at	-1.443693634	0.027210843	Decrease_in_adherent hemN; coproporphyrinogen III oxidase (EC:1.3.99.22); K02495 oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]
V0762_s_at	-1.443354052	0.047684145	Decrease_in_adherent pepQ; proline dipeptidase; K01271 X-Pro dipeptidase [EC:3.4.13.9]
F4838_s_at	-1.443097267	0.031106972	Decrease_in_adherent pyrI; aspartate carbamoyltransferase regulatory subunit; K00610 aspartate carbamoyltransferase regulatory subunit
c1749_s_at	-1.442104479	0.017447754	Decrease_in_adherent tetraatricopeptide repeat protein
V0008_x_at	-1.44040348	0.039544671	Decrease_in_adherent def; peptide deformylase (EC:3.5.1.88); K01462 [EC:3.5.1.88]
SB5_4103_s_at	-1.440200385	0.001953621	Decrease_in_adherent ybgF; tol-pal system protein YbgF
V2817_s_at	-1.431985941	0.021186907	Decrease_in_adherent speA; arginine decarboxylase; K01585 arginine decarboxylase [EC:4.1.1.19]
V2980_s_at	-1.42962984	0.030492988	Decrease_in_adherent aminotransferase; K10907 aminotransferase [EC:2.6.1.-]
c2115_s_at	-1.427099487	0.030386957	Decrease_in_adherent infC; translation initiation factor IF-3; K02520 translation initiation factor IF-3
b2573_s_at	-1.42199353	0.047787676	Decrease_in_adherent rpoE; RNA polymerase sigma factor RpoE; K03088 RNA polymerase sigma-70 factor, ECF subfamily
V0207_s_at	-1.420696556	0.030507528	Decrease_in_adherent NO_KEGG_DATA
EC869_7375_s_at	-1.420503017	0.005286061	Decrease_in_adherent ppiD; peptidyl-prolyl cis-trans isomerase D; K03770 peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]
SD1_1706_s_at	-1.419411358	0.000146755	Decrease_in_adherent secF; preprotein translocase subunit SecF; K03074 preprotein translocase subunit SecF
SD1_2252_s_at	-1.413057302	0.005303127	Decrease_in_adherent hisQ; histidine transport system permease protein; K10016 histidine transport system permease protein
c1536_x_at	-1.409936769	0.006078931	Decrease_in_adherent bet; recombination protein Bet
A2185_s_at	-1.408373129	0.028699925	Decrease_in_adherent btuB; vitamin B12/cobalamin outer membrane transporter; K02014 iron complex outermembrane receptor protein
c5177_x_at	-1.407755451	0.031076024	Decrease_in_adherent transposase ORF A, IS629
EC869_2361_s_at	-1.406852926	0.025453314	Decrease_in_adherent lexA; LexA repressor (EC:3.4.21.88); K01356 repressor LexA [EC:3.4.21.88]
V5187_s_at	-1.40383925	0.012234886	Decrease_in_adherent bcsE; cellulose biosynthesis protein BcsE
EC869_0979_s_at	-1.402132737	0.010363394	Decrease_in_adherent acetate kinase; K00925 acetate kinase [EC:2.7.2.1]
SB5_4770_x_at	-1.398153209	0.005889592	Decrease_in_adherent fimD; outer membrane usher protein FimD; K07347 outer membrane usher protein
SB5_4462_at	-1.39711313	0.020365859	Decrease_in_adherent NO_KEGG_DATA
V1769_s_at	-1.396006868	0.035974674	Decrease_in_adherent pepN; aminopeptidase N; K01256 aminopeptidase N [EC:3.4.11.2]
SBO_0235_x_at	-1.395243338	0.006898123	Decrease_in_adherent hypothetical protein
EC869_6334_s_at	-1.395106566	0.011556688	Decrease_in_adherent amyA; cytoplasmic alpha-amylase; K01176 alpha-amylase [EC:3.2.1.1]
K4902_x_at	-1.393813917	0.012353786	Decrease_in_adherent yhiH; putative ATP-binding component of a transport system, fragment 1; K01990 ABC-2 type transport system ATP-binding protein; K01992 ABC-2 type transport
F3392_s_at	-1.383364505	0.022367195	Decrease_in_adherent mdaB; modulator of drug activity B; K03923 modulator of drug activity B
A1670_s_at	-1.38293214	0.010058821	Decrease_in_adherent pyridine nucleotide-disulfide oxidoreductase family protein; K07007
EC869_2547_s_at	-1.381304105	0.011332617	Decrease_in_adherent ruvA; Holliday junction DNA helicase RuvA; K03550 holliday junction DNA helicase RuvA
A3085_s_at	-1.374164549	3.27E-05	Decrease_in_adherent cyoE; protoheme IX farnesyltransferase; K02301 protoheme IX farnesyltransferase [EC:2.5.1.-]
ECP_2591_s_at	-1.373481127	0.042478687	Decrease_in_adherent transposase
EC869_4505_s_at	-1.365924141	0.014528904	Decrease_in_adherent gpsA; NAD(P)H-dependent glycerol-3-phosphate dehydrogenase (EC:1.1.1.94); K00057 glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]
D1411_s_at	-1.365530701	0.037049931	Decrease_in_adherent ParA protein homolog; K03496 chromosome partitioning protein
A1230_s_at	-1.362502346	0.000589976	Decrease_in_adherent hypothetical protein
SB5_4783_x_at	-1.351889491	0.025194214	Decrease_in_adherent IS629 transposase orfB
c0884_s_at	-1.349696425	0.030553778	Decrease_in_adherent ybiB; uncharacterized protein YbiB
V5406_s_at	-1.346712963	0.022162399	Decrease_in_adherent glgP; glycogen phosphorylase; K00688 starch phosphorylase [EC:2.4.1.1]
A4299_at	-1.344074215	0.014885252	Decrease_in_adherent hypothetical protein
EC869_0211_s_at	-1.338164114	0.011917927	Decrease_in_adherent fkpA; FKBP-type peptidyl-prolyl cis-trans isomerase; K03772 FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]
V1568_s_at	-1.337356007	0.025929939	Decrease_in_adherent ispF; 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; K01770 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:4.6.1.12]

V3830_s_at	-1.331354481	0.002697012	Decrease_in_adherent cytosine deaminase ; K01485 cytosine deaminase [EC:3.5.4.1]
EC536_2323_s_at	-1.327955889	0.01129523	Decrease_in_adherent hypothetical protein
APECO1_956_s_at	-1.306794872	0.037883746	Decrease_in_adherent uvrY, sirA; response regulator ; K07689 two-component system, NarL family, invasion response regulator UvrY
A1640_s_at	-1.305986962	0.048358353	Decrease_in_adherent ftsX; cell division protein FtsX ; K09811 cell division transport system permease protein
A4682_s_at	-1.303716026	0.02022077	Decrease_in_adherent aspS; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
H3813_s_at	-1.302826563	0.002741457	Decrease_in_adherent rbsR; transcriptional repressor RbsR ; K02529 LacI family transcriptional regulator
SD1_0278_s_at	-1.291319554	0.024803611	Decrease_in_adherent pstS; phosphate ABC transporter periplasmic substrate-binding protein PstS ; K02040 phosphate transport system substrate-binding protein
ECP_0709_s_at	-1.289100384	0.023739923	Decrease_in_adherent pgm; phosphoglucomutase ; K01835 phosphoglucomutase [EC:5.4.2.2]
K3168_x_at	-1.285848038	0.015143245	Decrease_in_adherent hypothetical protein
EC869_6288_s_at	-1.285198838	0.005804796	Decrease_in_adherent relA; GDP/GTP pyrophosphokinase ; K00951 GTP pyrophosphokinase [EC:2.7.6.5]
F1250_s_at	-1.283655312	0.010275421	Decrease_in_adherent ycgJ; hypothetical protein
pC15-1a_040_x_at	-1.281670044	0.001491861	Decrease_in_adherent plasmid partition protein B ; K03497 chromosome partitioning protein, ParB family
A1805_s_at	-1.2816124	0.031989663	Decrease_in_adherent grxC; glutaredoxin 3 ; K03676 glutaredoxin 3
b3736_s_at	-1.279519423	0.017733336	Decrease_in_adherent atpF; F0F1 ATP synthase subunit B (EC:3.6.3.14); K02109 F-type H ⁺ -transporting ATPase subunit b [EC:3.6.3.14]
A1018_s_at	-1.275214581	0.039801007	Decrease_in_adherent gshB; glutathione synthetase (EC:6.3.2.3); K01920 glutathione synthase [EC:6.3.2.3]
EC869_0204_s_at	-1.272152741	0.010871969	Decrease_in_adherent fusA; elongation factor G ; K02355 elongation factor EF-G [EC:3.6.5.3]
A0224_s_at	-1.271766076	0.048698638	Decrease_in_adherent yejG; hypothetical protein
J5322_s_at	-1.267803012	0.008621137	Decrease_in_adherent cell wall-associated hydrolase
SBO_2370_x_at	-1.265733771	0.020597163	Decrease_in_adherent insertion sequence 2 OrfA protein
A4605_s_at	-1.265143875	0.001288875	Decrease_in_adherent yeaP; hypothetical protein ; K13069 diguanylate cyclase [EC:2.7.7.65]
c5616_s_at	-1.262898216	8.60E-05	Decrease_in_adherent cell wall-associated hydrolase
SD1_1970_s_at	-1.261872421	0.04518889	Decrease_in_adherent ylaB; hypothetical protein
A0227_at	-1.255426525	0.044483742	Decrease_in_adherent NO_KEGG_DATA
b0407_s_at	-1.254204859	0.008134519	Decrease_in_adherent yajC; preprotein translocase subunit YajC ; K03210 preprotein translocase subunit YajC
SD1_3091_s_at	-1.252650513	0.008273656	Decrease_in_adherent ubiB, aarF, yigQ, yigR; putative ubiquinone biosynthesis protein UbiB ; K03688 ubiquinone biosynthesis protein
A3567_s_at	-1.248966503	0.042724999	Decrease_in_adherent lraA; outer-membrane lipoprotein carrier protein ; K03634 outer membrane lipoproteins carrier protein
SDY_2200_s_at	-1.24504551	0.035837048	Decrease_in_adherent hypothetical protein
A0366_s_at	-1.240573469	0.034740961	Decrease_in_adherent putative transporting ATPase ; K09906 hypothetical protein
A0323_s_at	-1.240034106	0.043671698	Decrease_in_adherent nuoE; NADH dehydrogenase subunit E (EC:1.6.5.3); K00334 NADH dehydrogenase I subunit E [EC:1.6.5.3]
V0063_s_at	-1.239029462	0.024052252	Decrease_in_adherent putative transcriptional regulator
A0328_s_at	-1.237755806	0.035001069	Decrease_in_adherent aminotransferase AlaT ; K10907 aminotransferase [EC:2.6.1.-]
SD1_1241_s_at	-1.236605918	0.02866693	Decrease_in_adherent dapA; dihydrodipicolinate synthase (EC:4.2.1.52); K01714 dihydrodipicolinate synthase [EC:4.2.1.52]
SD1_3011_s_at	-1.231875665	0.003562658	Decrease_in_adherent valS; valyl-tRNA synthetase (EC:6.1.1.9); K01873 valyl-tRNA synthetase [EC:6.1.1.9]
A2456_s_at	-1.227519074	0.04963947	Decrease_in_adherent mpl; UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase; K02558 UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase; K02558
UTI89_C0218_s_at	-1.224819513	9.98E-05	Decrease_in_adherent NO_KEGG_DATA
SD1_1239_s_at	-1.222151597	0.028859947	Decrease_in_adherent nlpB; lipoprotein ; K07287 lipoprotein-34
V5408_s_at	-1.221018034	0.008726104	Decrease_in_adherent NO_KEGG_DATA
V7280_s_at	-1.217271704	0.020630781	Decrease_in_adherent yccZ; putative function in exopolysaccharide production ; K01991 polysaccharide export outer membrane protein
K3747_x_at	-1.214837915	0.035111903	Decrease_in_adherent putative plasmid SOS inhibition protein B
V6012_s_at	-1.209832758	0.036870415	Decrease_in_adherent secF; preprotein translocase subunit SecF ; K03074 preprotein translocase subunit SecF
SB5_4341_s_at	-1.20953701	0.024819739	Decrease_in_adherent ftsA; cell division protein FtsA ; K03590 cell division protein FtsA
V4018_s_at	-1.207743226	0.02868012	Decrease_in_adherent aceE; pyruvate dehydrogenase subunit E1 ; K00163 pyruvate dehydrogenase E1 component [EC:1.2.4.1]
A2189_s_at	-1.207063989	0.004475527	Decrease_in_adherent murB; UDP-N-acetylpyruvoylglucosamine reductase (EC:1.1.1.158); K00075 UDP-N-acetylmuramate dehydrogenase [EC:1.1.1.158]
A2633_s_at	-1.203961097	0.028082637	Decrease_in_adherent putative ABC transporter ATP-binding protein
A0532_s_at	-1.198236944	0.016347783	Decrease_in_adherent NO_KEGG_DATA
EC869_1180_s_at	-1.192527911	0.018172703	Decrease_in_adherent glucose-specific PTS system IIB components ; K02778 PTS system, glucose-specific IIB component [EC:2.7.1.69]; K02779 PTS system, glucose-specific IIC component
A2593_s_at	-1.188631918	0.045690092	Decrease_in_adherent yjiX; hypothetical protein
c2804_s_at	-1.18655182	0.020484762	Decrease_in_adherent menC; O-succinylbenzoate synthase (EC:4.2.1.-); K02549 O-succinylbenzoate synthase [EC:4.2.1.113]
A1888_s_at	-1.186285494	0.012209283	Decrease_in_adherent lbpA; heat shock protein lbpA ; K04080 molecular chaperone lbpA
M1538_s_at	-1.185192232	0.04889713	Decrease_in_adherent cysS; cysteinyl-tRNA synthetase ; K01883 cysteinyl-tRNA synthetase [EC:6.1.1.16]
EC536_6829_s_at	-1.184742037	0.019887824	Decrease_in_adherent nadD; nicotinic acid mononucleotide adenyltransferase (EC:2.7.7.18); K00969 nicotinate-nucleotide adenyltransferase [EC:2.7.7.18]
V4290_s_at	-1.184169728	0.025141091	Decrease_in_adherent cbpA; curved DNA-binding protein CbpA ; K05516 curved DNA-binding protein
A0687_at	-1.18395379	0.028117657	Decrease_in_adherent NO_KEGG_DATA
b1207_s_at	-1.180115945	0.032652105	Decrease_in_adherent prsA; ribose-phosphate pyrophosphokinase (EC:2.7.6.1); K00948 ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
SD1_2374_s_at	-1.176430564	0.040151797	Decrease_in_adherent recA; recombinase A ; K03553 recombination protein RecA
A2921_at	-1.176074691	0.012303902	Decrease_in_adherent hypothetical protein
V1059_s_at	-1.174475239	0.002871705	Decrease_in_adherent acrB; acridine efflux pump ; K03296 hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family
V2373_s_at	-1.171787672	0.011963839	Decrease_in_adherent NO_KEGG_DATA
V5920_s_at	-1.16969745	0.035728952	Decrease_in_adherent formate dehydrogenase-O subunit gamma ; K00127 formate dehydrogenase, gamma subunit [EC:1.2.1.2]
A2186_s_at	-1.158089431	0.043946563	Decrease_in_adherent murI; glutamate racemase (EC:5.1.1.3); K01776 glutamate racemase [EC:5.1.1.3]
A1495_s_at	-1.15335665	0.016358397	Decrease_in_adherent rpsQ; 30S ribosomal protein S17; K02961 small subunit ribosomal protein S17
c3026_s_at	-1.153052738	0.01645207	Decrease_in_adherent guaA; GMP synthase (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
A2102_s_at	-1.149508332	0.038268924	Decrease_in_adherent fdoH; formate dehydrogenase-O, iron-sulfur subunit ; K00124 formate dehydrogenase, beta subunit [EC:1.2.1.2]
SFV_1073_x_at	-1.147976067	0.028330322	Decrease_in_adherent IS629 ORF2
APECO1_3635_s_at	-1.144925847	0.008725271	Decrease_in_adherent recJ; ssDNA exonuclease RecJ; K07462 single-stranded-DNA-specific exonuclease [EC:3.1.-.-]
F4817_s_at	-1.144024036	0.01589836	Decrease_in_adherent ppa; inorganic pyrophosphatase (EC:3.6.1.1); K01507 inorganic pyrophosphatase [EC:3.6.1.1]
SFV_2993_s_at	-1.141652569	0.000515731	Decrease_in_adherent speA; arginine decarboxylase (EC:4.1.1.19); K01585 arginine decarboxylase [EC:4.1.1.19]

A1049_s_at	-1.133137348	0.008863798	Decrease_in_adherent putative PstII restriction-modification enzyme Res subunit
b2217_s_at	-1.127561738	0.031713943	Decrease_in_adherent transcriptional regulator RcsB ; K07687 two-component system, NarL family, capsular synthesis response regulator RcsB
A2745_s_at	-1.121474337	0.045076678	Decrease_in_adherent yacF; hypothetical protein
A4745_s_at	-1.121179264	0.027891035	Decrease_in_adherent flit; flagellar biosynthesis protein Flit; K02423 flagellar protein Flit
A2000_s_at	-1.11649128	0.041494362	Decrease_in_adherent hemY; putative protoheme IX biogenesis protein ; K02498 HemY protein
b0474_s_at	-1.110671965	0.041891827	Decrease_in_adherent NO_KEGG_DATA
SD1_3380_s_at	-1.107736838	0.009370998	Decrease_in_adherent rlpB; LPS-assembly lipoprotein RlpB ; K03643 LPS-assembly lipoprotein
b3204_s_at	-1.107175628	0.030873178	Decrease_in_adherent ptsN; PTS IIA-like nitrogen-regulatory protein PtsN ; K02806 PTS system, nitrogen regulatory IIA component [EC:2.7.1.69]
V2369_s_at	-1.105707978	0.001730677	Decrease_in_adherent flid; flagellar capping protein; K02407 flagellar hook-associated protein 2
SB5_0200_s_at	-1.103427943	0.001341871	Decrease_in_adherent NO_KEGG_DATA
A4513_s_at	-1.095875943	0.0291861	Decrease_in_adherent ydiV; hypothetical protein
A4558_s_at	-1.094820461	0.021268319	Decrease_in_adherent NO_KEGG_DATA
S1960_x_at	-1.093445519	0.044781995	Decrease_in_adherent IS629 ORF2
A3535_s_at	-1.084375197	0.019636655	Decrease_in_adherent artM; arginine transporter permease subunit ArtM ; K09998 arginine transport system permease protein
F3812_s_at	-1.081404065	0.005873056	Decrease_in_adherent rsmD; 16S rRNA m(2)G966-methyltransferase [EC:2.1.1.-]; K08316 ribosomal RNA small subunit methyltransferase D [EC:2.1.1.52]
SS5_4191_s_at	-1.078941298	0.011148841	Decrease_in_adherent putative oxidoreductase; K06969 putative SAM-dependent methyltransferase
SF1693_s_at	-1.068724835	0.040987659	Decrease_in_adherent IS-10 transposase
EC869_4438_s_at	-1.067995433	0.026498112	Decrease_in_adherent NO_KEGG_DATA
V1446_s_at	-1.064455253	0.032967974	Decrease_in_adherent threonyl-tRNA synthetase ; K01868 threonyl-tRNA synthetase [EC:6.1.1.3]
A1404_s_at	-1.055868088	0.048184904	Decrease_in_adherent hypothetical protein ; K06958
A3617_s_at	-1.054364814	0.042056488	Decrease_in_adherent smtA; putative metallothionein SmtA ; K06219 S-adenosylmethionine-dependent methyltransferase
M4031_at	-1.052528794	0.020328393	Decrease_in_adherent NO_KEGG_DATA
b1717_s_at	-1.050146756	0.028233906	Decrease_in_adherent hypothetical protein
F4711_s_at	-1.046763503	0.001206459	Decrease_in_adherent DNA methylase N-4/N-6 (EC:2.1.1.72)
A2730_s_at	-1.045712913	0.00799185	Decrease_in_adherent NO_KEGG_DATA
b1957_s_at	-1.043705261	0.033009947	Decrease_in_adherent hypothetical protein
J4318_at	-1.043694755	0.003041633	Decrease_in_adherent TrbC ; K12217 intracellular multiplication protein lcmO
V2818_s_at	-1.040292915	0.017654439	Decrease_in_adherent arginine decarboxylase ; K01585 arginine decarboxylase [EC:4.1.1.19]
EC869_1425_s_at	-1.038337703	0.007081748	Decrease_in_adherent ileS; isoleucyl-tRNA synthetase; K01870 isoleucyl-tRNA synthetase [EC:6.1.1.5]
A1378_s_at	-1.038217292	0.018014361	Decrease_in_adherent rrmJ; 23S rRNA methyltransferase J ; K02427 ribosomal RNA large subunit methyltransferase E [EC:2.1.1.-]
AFFX-18srRnab_at	-1.037314659	0.023731349	Decrease_in_adherent hypothetical protein
SD1_1796_s_at	-1.027815486	0.030634128	Decrease_in_adherent proB; gamma-glutamyl kinase (EC:2.7.2.11); K00931 glutamate 5-kinase [EC:2.7.2.11]
EC869_4727_s_at	-1.026555289	0.033687954	Decrease_in_adherent NO_KEGG_DATA
V1444_s_at	-1.024177615	0.003346884	Decrease_in_adherent thrS; threonyl-tRNA synthetase (EC:6.1.1.3); K01868 threonyl-tRNA synthetase [EC:6.1.1.3]
A2737_s_at	-1.016617571	0.036518349	Decrease_in_adherent ftsQ; cell division protein FtsQ ; K03589 cell division protein FtsQ
V0847_s_at	-1.009919138	0.026698339	Decrease_in_adherent hflK; FtsH protease regulator HflK ; K04088 membrane protease subunit HflK [EC:3.4.-.-]
A3297_s_at	-1.008955651	0.008239762	Decrease_in_adherent gltK; glutamate/aspartate ABC transporter, permease protein GltK ; K10002 glutamate/aspartate transport system permease protein
N1862_s_at	-1.007481339	0.026313682	Decrease_in_adherent hisM; histidine transport, membrane protein M ; K10015 histidine transport system permease protein
A3942_s_at	-1.007252688	0.046696482	Decrease_in_adherent ychF; GTP-dependent nucleic acid-binding protein EngD ; K06942
F1449_s_at	-1.003324469	0.036098502	Decrease_in_adherent pspC; DNA-binding transcriptional activator PspC ; K03973 phage shock protein C
ECs3554_s_at	-1.001498334	0.005213301	Decrease_in_adherent alanyl-tRNA synthetase (EC:6.1.1.7); K01872 alanyl-tRNA synthetase [EC:6.1.1.7]
F4312_s_at	-1.001389041	0.012877599	Decrease_in_adherent NO_KEGG_DATA