Log$_2$ fold changes of probes
[Purine metabolism; n = 45]

$\frac{LL_3}{DD_3}$ $\frac{Diel_3}{LL_3}$ $\frac{DD_3}{Diel_3}$ $\frac{LL_6}{DD_6}$ $\frac{Diel_6}{LL_6}$ $\frac{DD_6}{Diel_6}$

Log$_2$ fold change
−6 −4 −2 0 2 4 6

K00948 PRPS; ribose−phosphate pyrophosphokinase [EC:2.7.6.1]	SAR116_2194 ribose−phosphate pyrophosphokinase
K00764 purF; amidophosphoribosyltransferase [EC:2.4.2.14]	SAR116_0651 Glutamine phosphoribosylpyrophosphate amidotransferase
K01945 purD; phosphoribosylamine−−−glycine ligase [EC:6.3.4.13]	SAR116_1137 phosphoribosylamine−−glycine ligase
K11175 purN; phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]	SAR116_0627 phosphoribosylglycinamide formyltransferase putative
K23269 purL; phosphoribosylformylglycinamidine synthase subunit PurL [EC:6.3.5.3]	SAR116_0671 phosphoribosylformylglycinamidine synthase II
K23264 purS; phosphoribosylformylglycinamidine synthase subunit PurS [EC:6.3.5.3]	SAR116_0669 phosphoribosylformylglycinamidine synthase
K23265 purQ; phosphoribosylformylglycinamidine synthase subunit PurQ / glutaminase [EC:6.3.5.3 3.5.1.2]	SAR116_0670 phosphoribosylformylglycinamidine synthase I
K01933 purM; phosphoribosylformylglycinamidine cyclo−ligase [EC:6.3.3.1]	SAR116_0626 phosphoribosylaminoimidazole synthetase
K01589 purK; 5−(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	SAR116_1335 Phosphoribosylaminoimidazole carboxylase
K01588 purE; 5−(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]	SAR116_1334 phosphoribosylaminoimidazole carboxylase
K01923 purC; phosphoribosylaminoimidazole−succinocarboxamide synthase [EC:6.3.2.6]	SAR116_0668 phosphoribosylaminoimidazole−succinocarboxamide synthase
K01756 purB; adenylosuccinate lyase [EC:4.3.2.2]	SAR116_0667 adenylosuccinate lyase
K00602 purH; phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]	SAR116_1095 phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
K00759 APRT; adenine phosphoribosyltransferase [EC:2.4.2.7]	SAR116_1668 Adenine phosphoribosyl transferase
K03787 surE; 5'/3'−nucleotidase [EC:3.1.3.5 3.1.3.6]	SAR116_0411 Survival protein SurE
K05810 LACC1; purine−nucleoside/S−methyl−5'−thioadenosine phosphorylase / adenosine deaminase [EC:2.4.2.1 2.4.2.28 3.5.4.4]	SAR116_2195 protein of unknown function DUF152
K00760 hprT; hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]	SAR116_1426 hypoxanthine−guanine phosphoribosyltransferase
K00088 IMPDH; IMP dehydrogenase [EC:1.1.1.205]	SAR116_2483 inosine−5'−monophosphate dehydrogenase
K00940 ndk; nucleoside−diphosphate kinase [EC:2.7.4.6]	SAR116_0628 nucleoside diphosphate kinase
K01519 rdgB; XTP/dITP diphosphohydrolase [EC:3.6.1.66]	SAR116_1621 HAM1−like protein
K00769 gpt; xanthine phosphoribosyltransferase [EC:2.4.2.22]	SAR116_1505 Xanthine−guanine phosphoribosyltransferase
K13481 xdhA; xanthine dehydrogenase small subunit [EC:1.17.1.4]	SAR116_1380 xanthine dehydrogenase
K13482 xdhB; xanthine dehydrogenase large subunit [EC:1.17.1.4]	SAR116_1379 xanthine dehydrogenase
K01951 guaA; GMP synthase (glutamine−hydrolysing) [EC:6.3.5.2]	SAR116_2485 GMP synthase – glutamine amidotransferase protein
K00942 gmk; guanylate kinase [EC:2.7.4.8]	SAR116_0636 Guanylate kinase
K00525 E1.17.4.1A; ribonucleoside−diphosphate reductase alpha chain [EC:1.17.4.1]	SAR116_0387 putative ribonucleoside−diphosphate reductase
K00525 E1.17.4.1A; ribonucleoside−diphosphate reductase alpha chain [EC:1.17.4.1]	SAR116_1045 ribonucleoside−diphosphate reductase
K01129 dgt; dGTPase [EC:3.1.5.1]	SAR116_0422 putative deoxyguanosinetriphosphate triphosphohydrolase
K06952 yfdR; 5'−nucleotidase [EC:3.1.3.89]	SAR116_0660 hypothetical protein
K01139 spoT; GTP diphosphokinase / guanosine−3',5'−bis(diphosphate) 3'−diphosphatase [EC:2.7.6.5 3.1.7.2]	SAR116_0536 (p)ppGpp synthetase I (GTP pyrophosphokinase)
K01524 ppx−gppA; exopolyphosphatase / guanosine−5'−triphosphate,3'−diphosphate pyrophosphatase [EC:3.6.1.11 3.6.1.40]	SAR116_1993 Ppx/GppA phosphatase
K01768 E4.6.1.1; adenylate cyclase [EC:4.6.1.1]	SAR116_1431 putative adenylate/guanylate cyclase
K01768 E4.6.1.1; adenylate cyclase [EC:4.6.1.1]	SAR116_0475 adenylate/guanylate cyclase
K01939 purA; adenylosuccinate synthase [EC:6.3.4.4]	SAR116_2308 Adenylosuccinate synthase
K09769 ymdB; 2',3'−cyclic−nucleotide 2'−phosphodiesterase [EC:3.1.4.16]	SAR116_2290 metallophosphoesterase
K00939 adk; adenylate kinase [EC:2.7.4.3]	SAR116_2412 adenylate kinase
K04765 mazG; nucleoside triphosphate diphosphatase [EC:3.6.1.9]	SAR116_0223 mazg protein
K19710 E2.7.7.53; ATP adenylyltransferase [EC:2.7.7.53]	SAR116_1362 Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolase
K00955 cysNC; bifunctional enzyme CysN/CysC [EC:2.7.7.4 2.7.1.25]	SAR116_1532 binfunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein
K00957 cysD; sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]	SAR116_1531 sulfate adenylyltransferase
K07127 uraH; 5−hydroxyisourate hydrolase [EC:3.5.2.17]	SAR116_1381 Transthyretin
K07127 uraH; 5−hydroxyisourate hydrolase [EC:3.5.2.17]	SAR116_0073 hypothetical protein
K13485 PRHOXNB; 2−oxo−4−hydroxy−4−carboxy−5−ureidoimidazoline decarboxylase [EC:4.1.1.97]	SAR116_1382 hypothetical protein
K01477 alc; allantoicase [EC:3.5.3.4]	SAR116_1375 allantoicase
K01483 allA; ureidoglycolate lyase [EC:4.3.2.3]	SAR116_1374 ureidoglycolate hydrolase