Log$_2$ fold changes of probes
[Nucleotide metabolism; n = 26]

	$\frac{LL_3}{DD_3}$	$\frac{LD_3}{LL_3}$	$\frac{DD_3}{LD_3}$	$\frac{LL_6}{DD_6}$	$\frac{LD_6}{LL_6}$	$\frac{DD_6}{LD_6}$	

SAR116_0091 DNA recombination−mediator protein A (TIGR00730 family Rossman fold protein)

K03978 engB; GTP−binding protein — SAR116_1501 Ribosome biogenesis GTP−binding protein YihA/YsxC

K03574 mutT; 8−oxo−dGTP diphosphatase [EC:3.6.1.55] — SAR116_1921 NUDIX hydrolase

SAR116_2183 probable MutT/nudix family protein

K02316 dnaG; DNA primase [EC:2.7.7.101] — SAR116_2232 DNA primase

K01139 spoT; GTP diphosphokinase / guanosine−3',5'−bis(diphosphate) 3'−diphosphatase [EC:2.7.6.5 3.1.7.2] — SAR116_0536 SpoT/RelA, (p)ppGpp synthetase I (GTP pyrophosphokinase)

K00942 gmk; guanylate kinase [EC:2.7.4.8] — SAR116_0636 Guanylate kinase

SAR116_1601 Adenosine kinase

K00759 APRT; adenine phosphoribosyltransferase [EC:2.4.2.7] — SAR116_1668 Adenine phosphoribosyl transferase

K00764 purF; amidophosphoribosyltransferase [EC:2.4.2.14] — SAR116_0651 purF; Glutamine phosphoribosylpyrophosphate amidotransferase

K01756 purB; adenylosuccinate lyase [EC:4.3.2.2] — SAR116_0667 Adenylosuccinate lyase

K01923 purC; phosphoribosylaminoimidazole−succinocarboxamide synthase [EC:6.3.2.6] — SAR116_0668 Phosphoribosylaminoimidazole−succinocarboxamide synthase

K00945 cmk; CMP/dCMP kinase [EC:2.7.4.25] — SAR116_1251 Cytidylate kinase

K00760 hprT; hypoxanthine phosphoribosyltransferase [EC:2.4.2.8] — SAR116_1426 HGPRT

K00769 gpt; xanthine phosphoribosyltransferase [EC:2.4.2.22] — SAR116_1505 Xanthine−guanine phosphoribosyltransferase

K00761 upp; uracil phosphoribosyltransferase [EC:2.4.2.9] — SAR116_1611 Uracil phosphoribosyltransferase

K01524 ppx−gppA; exopolyphosphatase / guanosine−5'−triphosphate,3'−diphosphate pyrophosphatase [EC:3.6.1.11 3.6.1.40] — SAR116_1993 Ppx/GppA phosphatase

K01939 purA; adenylosuccinate synthase [EC:6.3.4.4] — SAR116_2308 Adenylosuccinate synthase

K00088 IMPDH; IMP dehydrogenase [EC:1.1.1.205] — SAR116_2483 Inosine−5'−monophosphate dehydrogenase

K06204 dksA; DnaK suppressor protein — SAR116_0086 dksA

K03060 rpoZ; DNA−directed RNA polymerase subunit omega [EC:2.7.7.6] — SAR116_0537 RpoZ/omega

K03086 rpoD; RNA polymerase primary sigma factor — SAR116_2233 RpoD/sigma 70

K03043 rpoB; DNA−directed RNA polymerase subunit beta [EC:2.7.7.6] — SAR116_2384 RpoB

K03046 rpoC; DNA−directed RNA polymerase subunit beta' [EC:2.7.7.6] — SAR116_2385 RpoC

K03040 rpoA; DNA−directed RNA polymerase subunit alpha [EC:2.7.7.6] — SAR116_2415 RpoA

K08311 nudH; putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.−] — SAR116_1846 RNA pyrophosphohydrolase

Log$_2$ fold change

−6 −4 −2 0 2 4 6