Log$_2$ fold changes of probes
[Purine metabolism; n = 16]

	$\frac{LL_3}{DD_3}$	$\frac{LD_3}{LL_3}$	$\frac{DD_3}{LD_3}$	$\frac{LL_6}{DD_6}$	$\frac{LD_6}{LL_6}$	$\frac{DD_6}{LD_6}$	
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)
K04765 mazG; nucleoside triphosphate diphosphatase [EC:3.6.1.9]							SAR116_0223 mazg protein
K01524 ppx−gppA; exopolyphosphatase / guanosine−5′−triphosphate,3′−diphosphate pyrophosphatase [EC:3.6.1.11 3.6.1.40]							SAR116_1993 Ppx/GppA phosphatase
K00942 gmk; guanylate kinase [EC:2.7.4.8]							SAR116_0636 Guanylate kinase
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
K00769 gpt; xanthine phosphoribosyltransferase [EC:2.4.2.22]							SAR116_1505 Xgpt
							SAR116_1601 Adenosine kinase
K00761 upp; uracil phosphoribosyltransferase [EC:2.4.2.9]							SAR116_1611 uracil phosphoribosyltransferase
K00759 APRT; adenine phosphoribosyltransferase [EC:2.4.2.7]							SAR116_1668 Adenine phosphoribosyl transferase
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

Log$_2$ fold change

−6 −4 −2 0 2 4 6