Log$_2$ fold changes of probes

[Purine metabolism; n = 16]

LL$_3$	LD$_3$	DD$_3$	LL$_6$	LD$_6$	DD$_6$
DD$_3$	LL$_3$	LD$_3$	DD$_6$	LL$_6$	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