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

Log$_2$ fold change
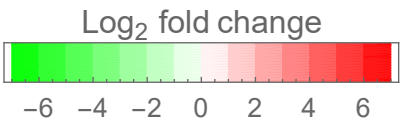
$\frac{LL_3}{DD_3}$	$\frac{Diel_3}{LL_3}$	$\frac{DD_3}{Diel_3}$	$\frac{LL_6}{DD_6}$	$\frac{Diel_6}{LL_6}$	$\frac{DD_6}{Diel_6}$

K11930 torT; periplasmic protein TorT — SAR116_1769 Putative ABC transporter

K02379 fdhD; FdhD protein — SAR116_0025 FdhD

K05524 fdxA; ferredoxin — SAR116_1071 4Fe–4S ferredoxin

K13795 citB; citrate/tricarballylate utilization protein — SAR116_1745 citrate utilization protein B

K13796 cobZ; tricarballylate dehydrogenase — SAR116_1744 hypothetical protein

K03521 fixA; electron transfer flavoprotein beta subunit — SAR116_1870 Electron transfer flavoprotein beta–subunit

K06997 yggS; PLP dependent protein — SAR116_1656 Protein of unknown function UPF0001

K21700 bauB; beta–alanine degradation protein BauB — SAR116_0437 hypothetical protein

K02234 cobW; cobalamin biosynthesis protein CobW — SAR116_0572 cobalamin biosynthesis protein CobW

K02498 hemY; HemY protein — SAR116_1472 HemY domain protein

K03688 ubiB; ubiquinone biosynthesis protein — SAR116_1564 Predicted unusual protein kinase

K03753 mobB; molybdopterin–guanine dinucleotide biosynthesis adapter protein — SAR116_2509 molybdopterin–guanine dinucleotide biosynthesis protein B

K18587 COQ9; ubiquinone biosynthesis protein COQ9 — SAR116_1337 rpsU–divergently transcribed protein

K18588 COQ10; coenzyme Q–binding protein COQ10 — SAR116_0210 Oligoketide cyclase/lipid transport protein

K19784 chrR; chromate reductase, NAD(P)H dehydrogenase (quinone) — SAR116_2242 hypothetical protein

K06999 K06999; phospholipase/carboxylesterase — SAR116_1152 Predicted esterase