Log$_2$ fold changes of probes

[Glycerophospholipid metabolism; n = 13]

Log$_2$ fold change

-6 -4 -2 0 2 4 6

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

K00057 gpsA; glycerol−3−phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94] — SAR116_1477 glycerol−3−phosphate dehydrogenase

K00111 glpA; glycerol−3−phosphate dehydrogenase [EC:1.1.5.3] — SAR116_0892 aerobic glycerol−3−phosphate dehydrogenase

K08591 plsY; acyl phosphate:glycerol−3−phosphate acyltransferase [EC:2.3.1.275] — SAR116_0615 hypothetical protein

K00655 plsC; 1−acyl−sn−glycerol−3−phosphate acyltransferase [EC:2.3.1.51] — SAR116_2351 phospholipid/glycerol acyltransferase

K01048 pldB; lysophospholipase [EC:3.1.1.5] — SAR116_0022 lysophospholipase

K01126 E3.1.4.46; glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46] — SAR116_2029 Glycerophosphoryl diester phosphodiesterase

K00981 E2.7.7.41; phosphatidate cytidylyltransferase [EC:2.7.7.41] — SAR116_0514 phosphatidate cytidylyltransferase

K17103 CHO1; CDP−diacylglycerol−−serine O−phosphatidyltransferase [EC:2.7.8.8] — SAR116_1156 CDP−diacylglycerol−−serine O−phosphatidyltransferase

K01613 psd; phosphatidylserine decarboxylase [EC:4.1.1.65] — SAR116_0093 phosphatidylserine decarboxylase related protein

K01613 psd; phosphatidylserine decarboxylase [EC:4.1.1.65] — SAR116_1157 Phosphatidylserine decarboxylase−related:Phosphatidylserine decarboxylase−related protein

K01095 pgpA; phosphatidylglycerophosphatase A [EC:3.1.3.27] — SAR116_0212 phosphatidylglycerophosphatase A

K08744 CRLS; cardiolipin synthase (CMP−forming) [EC:2.7.8.41] — SAR116_2208 CDP−diacylglycerol−−glycerol−3−phosphate 3−phosphatidyltransferase

K07406 melA; alpha−galactosidase [EC:3.2.1.22] — SAR116_1196 glycoside hydrolase family 4