		-	normal with EC			= 72]	
	DD <sub>3</sub>	LL <sub>3</sub>	Diel <sub>3</sub>	DD <sub>6</sub>	LL <sub>6</sub>	Diel <sub>6</sub>	
K15509 hpsN; sulfopropanediol 3-dehydrogenase [EC:1.1.1.308]							SAR116_2138 histidinol dehydrogenase
K15509 hpsN; sulfopropanediol 3-dehydrogenase [EC:1.1.1.308]							SAR116_0046 histidinol dehydrogenase
K19265 gpr; L-glyceraldehyde 3-phosphate reductase [EC:1.1.1]							SAR116_2446 hypothetical protein
K21430 ylil; aldose sugar dehydrogenase [EC:1.1.5]							SAR116_1224 hypothetical protein
K23463 tgnC; (Z)-2-((N-methylformamido)methylene)-5-hydroxybutyrolactone dehydrogenase [EC:1.2.1]							SAR116_2117 aldehyde dehydrogenase family protein
K03518 coxS; aerobic carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3]							SAR116_1387 putative carbon monoxide dehydrogenase small chain
K03518 coxS; aerobic carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3]							SAR116_2163 (2Fe-2S)-binding protein
K03519 coxM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3]							SAR116_1386 molybdopterin dehydrogenase
K03519 coxM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3]							SAR116_2165 Carbon-monoxide dehydrogenase (acceptor)
K03520 coxL; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3]							SAR116_2164 Carbon-monoxide dehydrogenase
K03520 coxL; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3]							SAR116_0095 Carbon-monoxide dehydrogenase (acceptor)
K00311 ETFDH; electron-transferring-flavoprotein dehydrogenase [EC:1.5.5.1]							SAR116_1662 Dehydrogenase
K18208 RNLS; renalase [EC:1.6.3.5]							SAR116_2453 FAD dependent oxidoreductase
K07304 msrA; peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]							SAR116_0728 peptide methionine sulfoxide reductase
K07305 msrB; peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]							SAR116_0096 methionine-R-sulfoxide reductase
K11209 yghU; GSH-dependent disulfide-bond oxidoreductase [EC:1.8.4]							SAR116_0657 glutathione S-transferase-like protein
K07393 ECM4; glutathionyl-hydroquinone reductase [EC:1.8.5.7]						-	SAR116_2019 putative glutathione S-transferase protein
K07147 msrP; methionine sulfoxide reductase catalytic subunit [EC:1.8]							SAR116_2216 twin-arginine translocation pathway signal precursor
K17893 AOX1; ubiquinol oxidase [EC:1.10.3.11]							SAR116_0177 Alternative oxidase
K00428 E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5]							SAR116_0251 Di-heme cytochrome c peroxidase
K03564 BCP; thioredoxin-dependent peroxiredoxin [EC:1.11.1.24]							SAR116_1028 alkyl hydroperoxide reductase/Thiol specific antioxidant/Mal allergen
K24158 prx; thioredoxin-dependent peroxiredoxin [EC:1.11.1.24]							SAR116_0079 Peroxidase
K06911 PIR; quercetin 2,3-dioxygenase [EC:1.13.11.24]							SAR116_1544 pirin family protein
K21817 blh; beta-carotene 15,15'-dioxygenase [EC:1.13.11.63]						-	SAR116_2131 possible transmembrane protein
K00464 diox1; all-trans-8'-apo-beta-carotenal 15,15'-oxygenase [EC:1.13.11.75]							SAR116_2357 probable dioxygenase signal peptide protein
K07336 K07336; PKHD-type hydroxylase [EC:1.14.11]							SAR116_0954 2OG-Fe(II) oxygenase
K22342 dmmA; dimethylamine monooxygenase subunit A [EC:1.14.13.238]						-	SAR116_0238 hypothetical protein
K22343 dmmB; dimethylamine monooxygenase subunit B [EC:1.14.13.238]							SAR116_0237 oxidoreductase NAD-binding domain/2Fe-2S iron-sulfur cluster binding domain protein
K22344 dmmC; dimethylamine monooxygenase subunit C [EC:1.14.13.238]							SAR116_0236 hypothetical protein
K23464 tgnB; flavin-dependent trigonelline monooxygenase, oxygenase component [EC:1.14.14]							SAR116_2118 bacterial luciferase family protein
K00528 fpr; ferredoxin/flavodoxinNADP+ reductase [EC:1.18.1.2 1.19.1.1]							SAR116_0898 oxidoreductase FAD/NAD(P)–binding protein
K00537 arsC; arsenate reductase (glutaredoxin) [EC:1.20.4.1]							SAR116_1456 arsenate reductase
K03741 arsC; arsenate reductase (thioredoxin) [EC:1.20.4.4]							SAR116_1998 arsenate reductase
K00573 E2.1.1.77; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]							SAR116_0410 protein-L-isoaspartate O-methyltransferase
K00573 E2.1.1.77; protein=L=isoaspartate(D=aspartate) O=methyltransferase [EC:2.1.1.77]  K00573 E2.1.1.77; protein=L=isoaspartate(D=aspartate) O=methyltransferase [EC:2.1.1.77]							SAR116_0429 protein-L-isoaspartate(D-aspartate) O-methyltransferase
K00574 cfa; cyclopropane–fatty–acyl–phospholipid synthase [EC:2.1.1.79]							SAR116_0580 Cyclopropane-fatty-acyl-phospholipid synthase
K00574 cfa; cyclopropane–fatty–acyl–phospholipid synthase [EC:2.1.1.79]							SAR116_0655 Cyclopropane-fatty-acyl-phospholipid synthase
K00612 nodU; carbamoyltransferase [EC:2.1.3.–]							SAR116_0987 predicted carbamoyl transferase
K03820 Int; apolipoprotein N-acyltransferase [EC:2.3.1.269]							SAR116_1009 apolipoprotein N–acyltransferase
K03820 Int; apolipoprotein N-acyltransferase [EC:2.3.1.269]						-	SAR116_1586 Apolipoprotein N-acyltransferase
K03824 yhbS; putative acetyltransferase [EC:2.3.1.–]							SAR116_1273 hypothetical protein
K03824 yhbS; putative acetyltransferase [EC:2.3.1.–]							SAR116_0701 hypothetical protein
K03824 yhbS; putative acetyltransferase [EC:2.3.1]						-	SAR116_1519 hypothetical protein
K00684 aat; leucyl/phenylalanyl-tRNAprotein transferase [EC:2.3.2.6]							SAR116_1041 leucyl/phenylalanyl-tRNAprotein transferase
K21420 bpt; leucyl-tRNAprotein transferase [EC:2.3.2.29]							SAR116_0527 Putative arginyl–tRNA:protein arginylyltransferase
K17251 pglB; undecaprenyl-diphosphooligosaccharideprotein glycotransferase [EC:2.4.99.19]							SAR116_1659 oligosaccharide transferase
K13292 lgt; phosphatidylglycerolprolipoprotein diacylglyceryl transferase [EC:2.5.1.145]						-	SAR116_2197 prolipoprotein diacylglyceryl transferase
K09773 ppsR; [pyruvate, water dikinase]-phosphate phosphotransferase / [pyruvate, water dikinase] kinase [EC:2.7.4.28 2.7.11.33]						_	SAR116_1639 hypothetical protein
K00982 glnE; [glutamine synthetase] adenylyltransferase / [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase [EC:2.7.7.42 2.7.7.89]						-	SAR116_2480 (Glutamateammonia-ligase) adenylyltransferase
K08997 SELENOO; serine/tyrosine/threonine adenylyltransferase [EC:2.7.7]						-	SAR116_2540 protein of unknown function UPF0061
K07107 ybgC; acyl-CoA thioester hydrolase [EC:3.1.2]							SAR116_2295 4-hydroxybenzoyl-CoA thioesterase
K08296 sixA; phosphohistidine phosphatase [EC:3.1.3.–]							SAR116_0445 putative phosphohistidine phosphatase
K01133 betC; choline-sulfatase [EC:3.1.6.6]							SAR116_2122 Sulfatase
K03424 tatD; TatD DNase family protein [EC:3.1.21.–]							SAR116_0359 Mg-dependent DNase
K01185 E3.2.1.17; lysozyme [EC:3.2.1.17]							SAR116_2269 chain A
K01286 E3.4.16.4; D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]							SAR116_1050 D-alanyl-D-alanine carboxypeptidase
K01447 xlyAB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]							SAR116_2145 Negative regulator of beta-lactamase expression
K06015 E3.5.1.81; N-acyl-D-amino-acid deacylase [EC:3.5.1.81]							SAR116_2073 N-acyl-D-amino acid deacylase family protein
K01462 PDF; peptide deformylase [EC:3.5.1.88]							SAR116_1493 peptide deformylase protein
K11206 NIT1; deaminated glutathione amidase [EC:3.5.1.128]							SAR116_1917 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase
K01463 bshB1; N-acetylglucosamine malate deacetylase 1 [EC:3.5.1]							SAR116_2151 hypothetical protein
K23465 tgnD; (E)-2-((N-methylformamido)methylene)succinate hydrolase [EC:3.5.1]							SAR116_2119 3-oxoadipate enol-lactonase family protein
K18456 E3.5.4.32; 8-oxoguanine deaminase [EC:3.5.4.32]							SAR116_1373 hydroxydechloroatrazine ethylaminohydrolase
K20762 scnC; thiocyanate hydrolase subunit gamma [EC:3.5.5.8]							SAR116_1730 nitrile hydratase
K09022 ridA; 2-iminobutanoate/2-iminopropanoate deaminase [EC:3.5.99.10]							SAR116_0033 hypothetical protein
K07766 E3.6.1.52; diphosphoinositol-polyphosphate diphosphatase [EC:3.6.1.52]							SAR116_0476 NUDIX hydrolase
K23997 nnr; ADP-dependent NAD(P)H-hydrate dehydratase / NAD(P)H-hydrate epimerase [EC:4.2.1.136 5.1.99.6]							SAR116_0130 hypothetical protein
K01726 GAMMACA; gamma-carbonic anhydrase [EC:4.2.1]							SAR116_1423 hexapeptide transferase family protein
K01751 E4.3.1.15; diaminopropionate ammonia-lyase [EC:4.3.1.15]							SAR116_0768 diaminopropionate ammonia–lyase
K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]							SAR116_2176 peptidyl prolyl cis-trans isomerase (rotamase B)
K22131 otnl; 2-dehydrotetronate isomerase [EC:5.3.1.35]							SAR116_0899 hypothetical protein
K01949 gmaS; glutamatemethylamine ligase [EC:6.3.4.12]							SAR116_1707 glutamine synthetase III

Log<sub>2</sub> probe abundance

-20 -15 -10 -5