Log$_2$ fold changes of probes
[Translational Machinery; n = 18]

	$\frac{LL_3}{DD_3}$	$\frac{LD_3}{LL_3}$	$\frac{DD_3}{LD_3}$	$\frac{LL_6}{DD_6}$	$\frac{LD_6}{LL_6}$	$\frac{DD_6}{LD_6}$	
K02357 tsf; elongation factor Ts							SAR116_0518 translation elongation factor Ts
							SAR116_1222 GTP−binding protein LepA
K02519 infB; translation initiation factor IF−2							SAR116_1580 Translation initiation factor 2
K02355 fusA; elongation factor G							SAR116_2388 translation elongation factor G
K02358 tuf; elongation factor Tu							SAR116_2389 Translation elongation factor Tu
K03595 era; GTPase							SAR116_0530 GTP−binding protein Era
K03665 hflX; GTPase							SAR116_0793 GTP−binding protein HflX
K03979 obgE; GTPase [EC:3.6.5.−]							SAR116_1854 GTPase ObgE
K06942 ychF; ribosome−binding ATPase							SAR116_2191 redox−regulated ATPase YchF
K03977 engA; GTPase							SAR116_2501 ribosome biogenesis GTPase Der
06925 tsaE; tRNA threonylcarbamoyladenosine biosynthesis protein TsaE							SAR116_1263 tRNA (adenosine(37)−N6)−threonylcarbamoyltransferase complex ATPase subunit type 1 Tsa
K03650 mnmE; tRNA modification GTPase [EC:3.6.−.−]							SAR116_1645 tRNA modification GTPase TrmE
K06020 ettA; energy−dependent translational throttle protein EttA							SAR116_2318 energy−dependent translational throttle protein EttA
K03072 secD; preprotein translocase subunit SecD							SAR116_0406 protein translocase subunit SecD [Candidatus Puniceispirillum marinum]
							SAR116_1978 diguanylate cyclase/phosphodiesterase, GAF domain−containing protein
K06207 typA; GTP−binding protein							SAR116_2002 TypA
K19265 gpr; L−glyceraldehyde 3−phosphate reductase [EC:1.1.1.−]							SAR116_2446 GPR/YghZ/AKR14A1
							SAR116_2458 diguanylate cyclase (GGDEF domain) with PAS/PAC sensor

Log$_2$ fold change

−6 −4 −2 0 2 4 6