Log₂ fold changes of probes [Valine, leucine and isoleucine degradation; n = 37]

	,	Dial	DD		Dial	, DD	
	DD ₃	LL ₃	DD ₃ Diel ₃	DD ₆	LL ₆	Diel ₆	
K00826 E2.6.1.42; branched-chain amino acid aminotransferase [EC:2.6.1.42]							SAR116_2206 branched-chain amino acid aminotransferase
K00826 E2.6.1.42; branched-chain amino acid aminotransferase [EC:2.6.1.42]							SAR116_0958 putative branched-chain amino acid aminotransferase
K00382 DLD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]							SAR116_1836 dihydrolipoamide dehydrogenase
K00382 DLD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]							SAR116_0208 Pyruvate/2–oxoglutarate dehydrogenase complex
K00249 ACADM; acyl-CoA dehydrogenase [EC:1.3.8.7]							- SAR116_0877 acyl-CoA dehydrogenase
K00249 ACADM; acyl-CoA dehydrogenase [EC:1.3.8.7]							- SAR116_0922 acyl-CoA dehydrogenase domain protein
K01782 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]							SAR116_0556 putative fatty acid oxidation complex alpha subunit
K05606 MCEE; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]							SAR116_0158 methylmalonyl–CoA epimerase
K01847 MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]							- SAR116_1400 methylmalonyl–CoA mutase
K01847 MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]							- SAR116_1401 Methylmalonyl–CoA mutase
K00020 HIBADH; 3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]							SAR116_1436 3-hydroxyisobutyrate dehydrogenase family protein
K00020 HIBADH; 3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]							SAR116_1425 6-phosphogluconate dehydrogenase NAD-binding protein
K00140 mmsA; malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]							SAR116_1384 malonic semialdehyde oxidative decarboxylase
K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]							SAR116_0754 aldehyde dehydrogenase family protein
K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]							- SAR116_1715 Betaine-aldehyde dehydrogenase
K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]							- SAR116_2169 Betaine-aldehyde dehydrogenase
K00822 E2.6.1.18; beta-alaninepyruvate transaminase [EC:2.6.1.18] Log ₂ fold change							- SAR116_2023 aminotransferase class-III
K01907 AACS; acetoacetyl-CoA synthetase [EC:6.2.1.16]							- SAR116_0685 acetyl-coenzyme A synthetase
K00626 ACAT; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]							- SAR116_0063 beta-ketothiolase
K01754 E4.3.1.19; threonine dehydratase [EC:4.3.1.19]							SAR116_2430 Pyridoxal–5'–phosphate–dependent enzyme
K01754 E4.3.1.19; threonine dehydratase [EC:4.3.1.19]							- SAR116_0526 putative Threonine ammonia-lyase
K01754 E4.3.1.19; threonine dehydratase [EC:4.3.1.19]							SAR116_0543 Pyridoxal-5'-phosphate-dependent enzyme
K01703 leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]							SAR116_1821 3–isopropylmalate dehydratase large subunit region
K01704 leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]							SAR116_1822 3–isopropylmalate dehydratase small subunit
K00052 leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]							SAR116_1823 Isocitrate/isopropylmalate dehydrogenase
K01652 E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]							SAR116_2120 sulfoacetaldehyde acetyltransferase
K01652 E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]							- SAR116_0072 benzaldehyde lyase
K01652 E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]							- SAR116_0713 Acetolactate synthase
K01652 E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]							SAR116_0777 acetolactate synthase II large subunit
K01652 E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]							- SAR116_0997 predicted thiamine pyrophosphate enzyme
K01653 E2.2.1.6S; acetolactate synthase I/III small subunit [EC:2.2.1.6]							- SAR116_0712 acetolactate synthase
K00053 ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]							- SAR116_0711 ketol–acid reductoisomerase
K01687 ilvD; dihydroxy-acid dehydratase [EC:4.2.1.9]							SAR116_0426 dihydroxy–acid dehydratase
K00826 E2.6.1.42; branched-chain amino acid aminotransferase [EC:2.6.1.42]							- SAR116_2206 branched-chain amino acid aminotransferase
K00826 E2.6.1.42; branched-chain amino acid aminotransferase [EC:2.6.1.42]							- SAR116_0958 putative branched-chain amino acid aminotransferase
K01649 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]							SAR116_1223 2-isopropylmalate synthase
K01649 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]							SAR116_0677 2-isopropylmalate synthase/homocitrate synthase

-6 -4 -2 0 2