Experiment

DnarL_R1 vs.H37Rv_R1

DnarL_R2 vs.H37Rv_R2(DS)

DATASET S1

AEROBIC GROWTH (- Nitrate)

Gene	**Fold_DnarL_R1 vs.H37Rv_R1**	**d_DnarL_R2 vs.H37Rv_R2(**	**Geomean Fold _DnarL**	**SD**	**P-value**	Regulation	Description
PE20	**0.965**	**1.425**	**1.195**	**0.52**	**0.100**	**Up**	Rv1806, PE FAMILY PROTEIN
lat	**-0.801**	**-1.415**	**-1.108**	**0.14**	**0.131**	**Down**	Rv3290c, PROBABLE L-LYSINE-EPSILON AMINOTRANSFERASE
PPE39	**-1.444**	**-1.186**	**-1.315**	**0.05**	**0.057**	**Down**	Rv2353c, PPE FAMILY PROTEIN
Rv0188	**-1.146**	**-1.796**	**-1.471**	**0.12**	**0.139**	**Down**	Rv0188, PROBABLE CONSERVED TRANSMEMBRANE PROTEIN
Rv3289c	**-1.044**	**-1.401**	**-1.223**	**0.08**	**0.078**	**Down**	Rv3289c, POSSIBLE TRANSMEMBRANE PROTEIN

Experiment

DnarL_N_R1 vs.H37Rv_N_R1 **DATASET S2** **AEROBIC GROWTH (+NITRATE)**
DnarL_N_R2 vs.H37Rv_N_R2(DS)

Gene	Fold_DnarL_N_R1 vs.H37Rv_	Fold_DnarL_N_R2 vs.H37Rv_N_	Geomean Fold_DnarL_N	SD	P-value	Regulation	Description
PPE38	1.250	0.998	1.124	0.269	0.055	Up	Rv2352c, PPE FAMILY PROTEIN
rpmG1	1.157	0.942	1.049	0.219	0.047	Up	Rv2057c, Probable ribosomal protein L33
Rv0076c	1.136	1.077	1.107	0.062	0.013	Up	Rv0076c, PROBABLE MEMBRANE PROTEIN
Rv0268c	1.189	0.916	1.052	0.277	0.060	Up	Rv0268c, HYPOTHETICAL PROTEIN
Rv0965c	0.895	1.012	0.954	0.112	0.026	Up	Rv0965c, CONSERVED HYPOTHETICAL PROTEIN
Rv1765A	1.469	1.130	1.300	0.411	0.074	Up	Rv1765A, PUTATIVE TRANSPOSASE FRAGMENT
Rv2023A	1.052	0.953	1.003	0.098	0.022	Up	Rv2023A, HYPOTHETICAL PROTEIN
Rv2136c	1.195	1.036	1.116	0.169	0.035	Up	Rv2136c, Possible conserved transmembrane protein
Rv2142c	1.440	1.392	1.416	0.063	0.011	Up	Rv2142c, HYPOTHETICAL PROTEIN
Rv2452c	1.500	1.997	1.749	0.823	0.108	Up	Rv2452c, HYPOTHETICAL PROTEIN
Rv2562	1.006	0.889	0.948	0.111	0.026	Up	Rv2562, CONSERVED HYPOTHETICAL PROTEIN
Rv2961	1.549	0.955	1.252	0.699	0.128	Up	Rv2961, PROBABLE TRANSPOSASE
Rv3742c	1.027	0.886	0.957	0.135	0.031	Up	Rv3742c, POSSIBLE OXIDOREDUCTASE
Rv3745c	1.272	0.813	1.043	0.466	0.100	Up	Rv3745c, CONSERVED HYPOTHETICAL PROTEIN
whiB7	1.323	1.161	1.242	0.188	0.036	Up	Rv3197A, PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN WHIB-LIKE V
acg	-1.391	-1.419	-1.144	0.005	0.006	Down	Rv2032, Conserved hypothetical protein Acg
fdxA	-1.312	-1.744	-1.120	0.074	0.094	Down	Rv2007c, PROBABLE FERREDOXIN FDXA
gltA1	-1.812	-1.393	-1.350	0.068	0.091	Down	Rv1131, PROBABLE CITRATE SYNTHASE I GLTA1
lat	-1.371	-0.856	-1.123	0.117	0.111	Down	Rv3290c, PROBABLE L-LYSINE-EPSILON AMINOTRANSFERASE LAT L-LYSINE A
mmpL6	-0.888	-1.040	-0.951	0.038	0.034	Down	Rv1557, PROBABLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN M
narK2	-1.005	-0.821	-1.030	0.048	0.041	Down	Rv1737c, POSSIBLE NITRATENITRITE TRANSPORTER NARK2
narL	-6.067	-6.545	-2.064	0.003	0.104	Down	Rv0844c, POSSIBLE NITRATENITRITE RESPONSE TRANSCRIPTIONAL REGULAT
pdhC	-0.950	-1.013	-0.988	0.016	0.014	Down	Rv2495c, PROBABLE DIHYDROLIPOAMIDE S-ACETYLTRANSFERASE E2 COMP
Rv0079	-1.488	-1.383	-1.228	0.019	0.023	Down	Rv0079, HYPOTHETICAL PROTEIN
Rv0188	-0.936	-1.190	-0.987	0.060	0.056	Down	Rv0188, PROBABLE CONSERVED TRANSMEMBRANE PROTEIN
Rv0569	-0.961	-1.041	-1.033	0.020	0.018	Down	Rv0569, CONSERVED HYPOTHETICAL PROTEIN
Rv1130	-1.247	-1.271	-1.084	0.005	0.005	Down	Rv1130, CONSERVED HYPOTHETICAL PROTEIN
Rv1687c	-2.161	-2.058	-1.489	0.012	0.023	Down	Rv1687c, PROBABLE CONSERVED ATP-BINDING PROTEIN ABC TRANSPORTER
Rv1701	-0.914	-1.057	-0.962	0.035	0.031	Down	Rv1701, PROBABLE INTEGRASERECOMBINASE
Rv1733c	-1.116	-0.861	-1.055	0.063	0.056	Down	Rv1733c, PROBABLE CONSERVED TRANSMEMBRANE PROTEIN
Rv1734c	-1.485	-2.031	-1.213	0.080	0.118	Down	Rv1734c, CONSERVED HYPOTHETICAL PROTEIN
Rv1738	-1.696	-1.822	-1.298	0.018	0.028	Down	Rv1738, CONSERVED HYPOTHETICAL PROTEIN
Rv1856c	-1.162	-1.101	-1.067	0.013	0.013	Down	Rv1856c, POSSIBLE OXIDOREDUCTASE
Rv1996	-2.601	-2.466	-1.645	0.011	0.030	Down	Rv1996, CONSERVED HYPOTHETICAL PROTEIN
Rv2028c	-1.394	-1.140	-1.159	0.052	0.056	Down	Rv2028c, CONSERVED HYPOTHETICAL PROTEIN
Rv2087	-0.955	-1.716	-1.038	0.150	0.161	Down	Rv2087, CONSERVED HYPOTHETICAL PROTEIN
Rv2627c	-0.937	-1.061	-0.990	0.030	0.027	Down	Rv2627c, CONSERVED HYPOTHETICAL PROTEIN
Rv2650c	-1.068	-1.339	-1.046	0.058	0.059	Down	Rv2650c, POSSIBLE phiRv2 PROPHAGE PROTEIN
Rv2989	-0.997	-1.027	-1.042	0.007	0.007	Down	Rv2989, PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN
Rv3094c	-1.141	-1.152	-1.060	0.002	0.002	Down	Rv3094c, CONSERVED HYPOTHETICAL PROTEIN
Rv3127	-1.439	-1.751	-1.173	0.051	0.068	Down	Rv3127, CONSERVED HYPOTHETICAL PROTEIN
Rv3128c	-1.524	-1.451	-1.253	0.013	0.016	Down	Rv3128c, CONSERVED HYPOTHETICAL PROTEIN
Rv3130c	-1.951	-1.968	-1.430	0.002	0.004	Down	Rv3130c, CONSERVED HYPOTHETICAL PROTEIN
Rv3131	-4.092	-3.987	-1.798	0.003	0.023	Down	Rv3131, CONSERVED HYPOTHETICAL PROTEIN
Rv3134c	-1.094	-1.166	-1.052	0.016	0.016	Down	Rv3134c, CONSERVED HYPOTHETICAL PROTEIN

Experiment

DL48h hyp-rep1 JM11_Cy5 vs. Rv48h hyp-rep1 JM9_Cy3 DATASET S3 48 h HYPOXIA

DL48h hyp-rep2 JM12_Cy3 vs. Rv48h hyp-rep2 JM10_Cy5 (DS)

Gene	Fold_delta48h hyp_rep1	Fold_ delta48h hyp_rep2	Geomean Fold _delta48h	SD	Regulation	P-value	Description
accA2	**0.721**	**0.700**	**0.710**	**0.017**	**Up**	**0.005**	Rv0973c, PROBABLE ACETYL-PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN ALPHA SUBUNIT ACCA2: BIOTIN CARBOXYLASE + BIOTIN CARBOXYL CARRIER PROTEIN BCCP
icl	**0.626**	**0.609**	**0.618**	**0.012**	**Up**	**0.004**	Rv0467, ISOCITRATE LYASE ICL ISOCITRASE ISOCITRATASE
mmpL13b	**1.303**	**1.536**	**1.420**	**0.306**	**Up**	**0.051**	Rv1146, PROBABLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL13B
moaB1	**0.708**	**2.449**	**1.579**	**2.705**	**Up**	**0.315**	Rv3110, PROBABLE PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE MOAB1 PHS 4-ALPHA- HYDROXY-TETRAHYDROPTERIN DEHYDRATASE PTERIN-4-A-CARBINOLAMINE DEHYDRATASE
ppsC	**0.732**	**0.672**	**0.702**	**0.048**	**Up**	**0.013**	Rv2933, PHENOLPTHIOCEROL SYNTHESIS TYPE-I POLYKETIDE SYNTHASE PPSC
Rv0850	**0.891**	**1.798**	**1.345**	**1.148**	**Up**	**0.188**	Rv0850, PUTATIVE TRANSPOSASE FRAGMENT
Rv1118c	**0.620**	**0.928**	**0.774**	**0.259**	**Up**	**0.067**	Rv1118c, CONSERVED HYPOTHETICAL PROTEIN
Rv2265	**1.054**	**1.956**	**1.505**	**1.275**	**Up**	**0.187**	Rv2265, Possible conserved integral membrane protein
Rv2812	**0.611**	**2.682**	**1.647**	**3.457**	**Up**	**0.351**	Rv2812, PROBABLE TRANSPOSASE
Rv3333c	**0.604**	**4.723**	**2.663**	**17.604**	**Up**	**0.463**	Rv3333c, HYPOTHETICAL PROLINE RICH PROTEIN
Rv3448	**0.735**	**1.302**	**1.019**	**0.567**	**Up**	**0.122**	Rv3448, PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN
Rv3640c	**0.685**	**4.110**	**2.397**	**11.077**	**Up**	**0.441**	Rv3640c, PROBABLE TRANSPOSASE
Rv3839	**0.669**	**1.574**	**1.121**	**0.980**	**Up**	**0.188**	Rv3839, CONSERVED HYPOTHETICAL PROTEIN
tyrT	**2.735**	**0.927**	**1.831**	**3.363**	**Up**	**0.323**	MTB000005, tRNA-Tyr
ugpA	**0.750**	**2.219**	**1.485**	**2.102**	**Up**	**0.279**	Rv2835c, PROBABLE Sn-GLYCEROL-3-PHOSPHATE TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER UGPA
alaT	**-0.685**	**-1.183**	**-0.934**	**0.128**	**Down**	**0.108**	MTB000002, tRNA-Ala
alaU	**-1.229**	**-1.495**	**-1.362**	**0.051**	**Down**	**0.058**	MTB000041, tRNA-Ala
cysU	**-0.989**	**-0.643**	**-0.816**	**0.097**	**Down**	**0.076**	MTB000037, tRNA-Cys
gltA1	**-1.835**	**-1.103**	**-1.469**	**0.131**	**Down**	**0.155**	Rv1131, PROBABLE CITRATE SYNTHASE I GLTA1
Rv0188	**-1.088**	**-0.741**	**-0.914**	**0.091**	**Down**	**0.076**	Rv0188, PROBABLE CONSERVED TRANSMEMBRANE PROTEIN
Rv1130	**-1.013**	**-1.502**	**-1.258**	**0.101**	**Down**	**0.106**	Rv1130, CONSERVED HYPOTHETICAL PROTEIN
Rv2452c	**-0.762**	**-0.745**	**-0.753**	**0.005**	**Down**	**0.004**	Rv2452c, HYPOTHETICAL PROTEIN
Rv2699c	**-0.661**	**-0.759**	**-0.710**	**0.029**	**Down**	**0.022**	Rv2699c, CONSERVED HYPOTHETICAL PROTEIN
valT	**-0.745**	**-0.686**	**-0.716**	**0.018**	**Down**	**0.013**	MTB000035, tRNA-Val
valU	**-0.687**	**-1.308**	**-0.997**	**0.154**	**Down**	**0.133**	MTB000038, tRNA-Val
valV	**-1.074**	**-1.025**	**-1.050**	**0.012**	**Down**	**0.011**	MTB000027, tRNA-Val