

SI Table 1. List of representative *M. tuberculosis* genes involved in central and lipid metabolism.

Pathways	Gene	Rv #	Product
Glycolysis	<i>ppgK</i>	<i>Rv2702</i>	glucokinase
	<i>pfkA</i>	<i>Rv3010c</i>	phosphofructokinase
	<i>pfkB</i>	<i>Rv2029c</i>	phosphofructokinase
	<i>gap</i>	<i>Rv1436</i>	glyceraldehyde 3-P dehydrogenase
	<i>pykA</i>	<i>Rv1617</i>	pyruvate kinase
	<i>lpdC</i>	<i>Rv0462</i>	E3 subunit of pyruvate dehydrogenase
	<i>dlaT</i>	<i>Rv2215</i>	E2 subunit of pyruvate dehydrogenase
PPP	<i>devB</i>	<i>Rv1445c</i>	6-phosphogluconolactonase
	<i>zwf1</i>	<i>Rv1121</i>	glucose 6-P 1-dehydrogenase
	<i>zwf2</i>	<i>Rv1447c</i>	glucose 6-P 1-dehydrogenase
	<i>tkt</i>	<i>Rv1449c</i>	transketolase
Fatty acid β-oxidation	<i>fadE5</i>	<i>Rv0244c</i>	acyl-CoA dehydrogenase
	<i>fadE23</i>	<i>Rv3140</i>	acyl-CoA dehydrogenase
	<i>fadA4</i>	<i>Rv1323</i>	acyl-CoA acetyltransferase
	<i>fadB</i>	<i>Rv0860</i>	fatty acid oxidation protein
TCA cycle	<i>citA</i>	<i>Rv0889c</i>	citrate synthase II
	<i>gltA2</i>	<i>Rv0896</i>	citrate synthase I
	<i>acn</i>	<i>Rv1475c</i>	aconitase
	<i>icd1</i>	<i>Rv3339c</i>	isocitrate dehydrogenase
	<i>icd2</i>	<i>Rv0066c</i>	isocitrate dehydrogenase
	<i>kgd</i>	<i>Rv1248c</i>	α -ketoglutarate decarboxylase
	<i>sdhA</i>	<i>Rv3318</i>	flavoprotein of succinate dehydrogenase
	<i>sdhC</i>	<i>Rv3316</i>	cytochrome B-556 of succinate dehydrogenase
	<i>mdh</i>	<i>Rv1240</i>	malate dehydrogenase
Glyoxylate shunt and methylcitrate cycle	<i>icl</i>	<i>Rv0467</i>	isocitrate lyase
	<i>glcB</i>	<i>Rv1837c</i>	malate synthase
	<i>prpC</i>	<i>Rv1131</i>	methylcitrate synthase
Gluconeogenesis	<i>mez</i>	<i>Rv2332</i>	malic enzyme
	<i>pckA</i>	<i>Rv0211</i>	phosphoenolpyruvate carboxykinase
	<i>glpX</i>	<i>Rv1099c</i>	fructose 1,6-bisphosphatase
Glutamate synthesis	<i>gltB</i>	<i>Rv3859c</i>	glutamate synthase (large subunit)
	<i>glnA1</i>	<i>Rv2220</i>	glutamine synthetase
	<i>gdh</i>	<i>Rv2476c</i>	glutamate dehydrogenase

SI Table 1 (continued)

Pathways	Gene	Rv #	Product
TAG synthesis	<i>plsB2</i>	<i>Rv2482c</i>	glycerol 3-P acyltransferase
	<i>Rv2182c</i>	<i>Rv2182c</i>	1-acylglycerol 3-P O-acyltransferase
	<i>tgs1</i>	<i>Rv3130c</i>	triacylglycerol synthase
	<i>Rv3734c</i>	<i>Rv3734c</i>	triacylglycerol synthase
	<i>Rv3371</i>	<i>Rv3371</i>	triacylglycerol synthase
Mycolic acid synthesis	<i>fas</i>	<i>Rv2524c</i>	fatty acid synthase
	<i>fabH</i>	<i>Rv0533c</i>	β -ketoacyl-AcpM synthase III
	<i>kasA</i>	<i>Rv2245</i>	β -ketoacyl-AcpM synthase
	<i>fabG1</i>	<i>Rv1483</i>	β -ketoacyl-AcpM reductase
Multimethyl-branched lipid synthesis	<i>accD5</i>	<i>Rv3280</i>	propionyl-CoA carboxylase β chain 5
	<i>mas</i>	<i>Rv2940c</i>	mycocerosic acid synthase
	<i>fadD26</i>	<i>Rv2930</i>	fatty-acid-CoA ligase
	<i>fadD28</i>	<i>Rv2941</i>	fatty-acid-CoA synthetase
	<i>papA5</i>	<i>Rv2939</i>	conserved polyketide synthase
	<i>pks2</i>	<i>Rv3825c</i>	polyketide synthase

SI Table 2. Normalized copy number of *M. tuberculosis* transcripts encoding enzymes involved in central metabolism and lipid metabolism in infected mouse lungs.

Pathways	Days of infection						
	12	15	18	21	30	50	100
Glycolysis							
<i>ppgK (rv2702)</i>	9.05384E-06	7.68374E-06	7.42879E-06	7.68859E-06	3.25553E-06	2.92922E-06	2.18645E-06
	2.26932E-06	1.46707E-06	1.80539E-06	1.2114E-06	1.20631E-06	2.36274E-06	7.44899E-07
<i>pfkA (rv3010c)</i>	4.10322E-05	2.62999E-05	2.24073E-05	1.44781E-05	1.5874E-05	6.44185E-06	8.25625E-06
	5.73168E-06	8.43619E-06	3.63535E-06	5.49592E-06	3.29631E-06	7.08969E-07	1.30734E-06
<i>pfkB (rv2029c)</i>	1.13033E-06	6.36083E-06	7.30358E-05	4.29272E-05	6.71498E-05	2.37429E-05	3.64158E-05
	8.29191E-07	7.03403E-07	3.64377E-05	2.28433E-05	1.63369E-05	1.74753E-05	2.65626E-05
<i>gap (rv1436)</i>	1.53579E-05	1.2745E-05	9.98871E-06	6.15353E-06	1.06437E-06	1.85227E-06	2.02134E-06
	4.3241E-06	1.90284E-06	2.24729E-06	6.33624E-06	8.51671E-07	8.36269E-07	1.63998E-06
<i>pykA (rv1617)</i>	1.3645E-05	7.63762E-06	9.34367E-06	6.48558E-06	2.24008E-06	3.25764E-06	3.67734E-06
	2.91594E-06	5.60469E-07	1.28319E-06	4.41465E-07	2.48742E-07	8.7649E-07	1.71364E-06
<i>lpdc* (rv0462)</i>	0.000105529	9.5216E-05	8.79322E-05	5.37133E-05	1.55274E-05	2.77536E-05	2.8081E-05
	2.72573E-05	3.88432E-05	2.84694E-05	1.58991E-05	6.14296E-06	9.65306E-06	7.55299E-06
<i>dlaT* (rv2215)</i>	3.3864E-05	1.81924E-05	2.14792E-05	1.73273E-05	2.87566E-06	5.85063E-06	4.97514E-06
	4.31275E-06	6.25983E-06	7.28475E-06	2.39674E-06	1.03079E-06	1.35554E-06	2.1691E-06
PPP							
<i>devB (rv1445c)</i>	1.54938E-05	1.00575E-05	7.46582E-06	4.74119E-06	1.81074E-06	3.532E-06	2.09861E-06
	6.79032E-06	2.38579E-06	3.34738E-06	2.40889E-06	6.29289E-07	1.35435E-06	7.41624E-07
<i>zwf1 (rv1121)</i>	6.57115E-06	4.81127E-06	4.99134E-06	4.03128E-06	1.35366E-06	2.1167E-06	1.36972E-06
	1.80406E-06	3.67408E-07	7.04186E-07	1.60134E-06	6.60915E-07	7.363E-07	8.05535E-07
<i>zwf2 (rv1447c)</i>	4.83537E-06	1.83956E-06	2.51945E-06	1.958E-06	7.63559E-07	5.84472E-07	1.08132E-06
	2.95568E-06	1.03998E-06	1.41608E-06	5.29556E-07	5.33406E-07	2.55908E-07	6.73376E-07
<i>tkt (rv1449c)</i>	5.83932E-05	6.69893E-05	6.09075E-05	5.06701E-05	2.49529E-05	1.79211E-05	1.70746E-05
	2.72771E-05	1.17199E-05	2.02566E-05	2.14949E-05	2.23502E-06	4.03043E-06	2.6166E-06
Fatty acid β oxidation							
<i>fadE5 (rv0244c)</i>	8.88563E-05	7.92886E-05	0.000183644	0.000306994	0.000361944	5.9063E-05	9.44083E-05
	2.95431E-05	1.06897E-05	9.3261E-05	0.00012582	7.61092E-05	1.85054E-05	3.9911E-05
<i>fadE23 (rv3140)</i>	3.20743E-05	5.10961E-05	5.83045E-05	4.30324E-05	3.39034E-05	2.37681E-05	1.94371E-05
	7.49899E-06	3.20622E-06	1.16467E-05	5.14216E-06	1.66469E-06	6.27577E-06	7.01548E-06
<i>fadA4 (rv1323)</i>	0.000119368	9.53595E-05	0.000338431	0.000239769	0.000206366	4.43596E-05	6.8403E-05
	4.08235E-05	2.6636E-05	0.00010769	4.57886E-05	1.55752E-05	2.87485E-05	3.20873E-05
<i>fadB (rv0860)</i>	0.000171995	8.62992E-05	6.32905E-05	2.27704E-05	1.26664E-05	2.74319E-05	1.69535E-05
	9.36046E-05	3.79351E-05	2.15606E-05	9.69193E-06	2.49828E-06	1.73491E-05	7.2273E-06
TCA cycle							
<i>citA (rv0889c)</i>	2.83919E-05	3.11835E-05	2.14401E-05	2.19603E-05	1.04944E-05	1.22858E-05	1.52042E-05
	1.22683E-05	9.82193E-06	1.10943E-06	5.68013E-06	1.89574E-06	2.36832E-06	6.50493E-06
<i>gltA2 (rv0896)</i>	9.30454E-05	9.61549E-05	6.28276E-05	8.3946E-05	1.77085E-05	2.46586E-05	2.32581E-05
	3.23128E-05	5.24517E-05	1.04805E-05	2.27917E-05	3.8604E-06	1.64372E-05	1.65083E-05
<i>acn (rv1475c)</i>	3.06431E-05	1.58613E-05	1.14699E-05	7.18235E-06	1.18189E-06	2.04679E-06	2.15373E-06
	1.14591E-05	2.32049E-06	2.63145E-06	3.67761E-06	3.89121E-07	1.08814E-06	5.22882E-07
<i>icd1 (rv3339c)</i>	2.60235E-05	1.05568E-05	7.74481E-06	3.682E-06	3.62162E-06	ND	5.28688E-07
	1.17208E-05	2.67525E-06	2.99631E-06	1.13029E-06	3.86139E-06	ND	8.3123E-08
<i>icd2 (rv0066c)</i>	1.79135E-05	1.34039E-05	1.32357E-05	1.18325E-05	3.40407E-06	3.62006E-06	4.69232E-06
	4.74252E-06	1.15026E-06	4.35992E-06	4.30255E-06	1.36261E-06	1.52816E-07	9.01917E-07
<i>kgd (rv1248c)</i>	7.23633E-05	3.84323E-05	4.17792E-05	3.06932E-05	9.55461E-06	1.3433E-05	1.05619E-05
	2.03883E-05	4.83759E-06	7.51826E-06	3.57843E-06	1.83611E-06	3.06357E-07	3.96982E-06
<i>sdhA (rv3318)</i>	1.53932E-05	1.29993E-05	1.11335E-05	9.78081E-06	2.34983E-06	4.32151E-06	3.32021E-06
	3.91703E-06	4.22348E-06	3.77118E-06	4.47151E-06	7.04495E-07	6.78269E-07	1.39097E-06
<i>sdhC (rv3316)</i>	3.85867E-05	3.19684E-05	2.03404E-05	2.31849E-05	5.27252E-06	7.76189E-06	3.93389E-06
	1.531E-05	5.19525E-06	1.80206E-06	4.53961E-06	5.04856E-07	4.05706E-06	1.98844E-06
<i>mdh (rv1240)</i>	7.26377E-05	5.87525E-05	3.28667E-05	1.7638E-05	5.21855E-06	1.21265E-05	9.43317E-06
	2.47131E-05	2.24937E-05	1.37145E-05	2.07786E-06	2.99317E-06	8.22615E-06	4.77338E-06

SI Table 2 (continued)

Pathways	Days of infection						
	12	15	18	21	30	50	100
Glyoxylate shunt and methylcitrate cycle							
<i>icl</i> (rv0467)	0.000183312	0.000380105	0.000608721	0.000442637	0.000272511	0.000218837	0.000161962
	4.1447E-05	0.000159613	9.78344E-05	0.00011384	3.4484E-05	7.18729E-05	8.23911E-05
<i>glcB</i> (rv1837c)	0.000210304	0.000143608	0.000117905	6.11685E-05	2.12806E-05	3.09695E-05	3.12091E-05
	4.02926E-05	1.85188E-05	4.90975E-05	2.54491E-05	2.56937E-06	8.58333E-06	1.2008E-05
<i>ppcC</i> (rv1131)	1.29133E-05	7.11741E-05	0.00012553	0.000182437	4.50653E-05	9.9562E-05	6.63613E-05
	1.63523E-05	3.64068E-05	4.35858E-05	7.24282E-05	9.57736E-06	2.0383E-05	1.67576E-05
Gluconeogenesis							
<i>mez</i> (rv2332)	8.30555E-06	2.93574E-06	2.43633E-06	2.74783E-06	1.18532E-06	1.22544E-06	1.55868E-06
	2.03475E-06	7.75784E-07	2.93043E-07	2.07179E-07	1.12364E-07	5.25031E-07	8.27661E-07
<i>pckA</i> (rv0211)	0.000146958	0.000226716	0.000319643	0.000449064	0.000452811	0.000257331	0.000174815
	1.77632E-05	7.40275E-05	9.91622E-05	6.47696E-05	3.69551E-05	5.78635E-05	4.72547E-05
<i>glpX</i> (rv1099c)	3.5883E-05	2.70453E-05	1.7973E-05	1.69866E-05	2.91287E-06	9.74604E-06	5.21855E-06
	8.26645E-06	4.97042E-06	1.52846E-06	5.79479E-06	6.25005E-07	6.33363E-06	1.3669E-06
Glutamate synthesis							
<i>gltB</i> (rv3859c)	1.70454E-05	1.83996E-05	5.46115E-05	5.05452E-05	2.70532E-05	1.09362E-05	1.30658E-05
	4.59967E-06	8.27673E-06	1.62473E-05	5.9093E-06	4.10586E-06	6.40877E-06	6.60425E-06
<i>gdh</i> (rv2476c)	2.66211E-05	2.16055E-05	1.64666E-05	1.75057E-05	5.35476E-06	3.0984E-06	6.87099E-06
	6.47667E-06	5.38079E-06	6.05535E-06	4.96901E-06	1.42229E-06	1.85104E-06	1.72445E-06
<i>glnA1</i> (rv2220)	0.000117699	0.000132625	0.0001478	0.000124347	1.96032E-05	2.35287E-05	2.87047E-05
	1.17925E-05	2.77527E-05	1.0933E-05	4.47855E-05	7.17851E-06	9.34435E-06	1.04633E-05
TAG synthesis							
<i>plsB2-C</i> (rv2482-3c)	7.53945E-06	1.07415E-05	1.09454E-05	1.2094E-05	8.47531E-06	1.00793E-05	1.26733E-05
	1.92981E-06	1.28702E-06	9.10889E-07	2.40074E-06	3.62646E-07	2.1031E-06	5.24879E-06
<i>rv2182c</i>	3.92681E-06	4.35022E-06	4.73787E-06	4.40532E-06	2.31389E-06	2.0624E-06	1.75097E-06
	1.38023E-06	4.43094E-07	1.03806E-06	1.29888E-06	5.01721E-07	5.26841E-07	7.6991E-07
<i>tgs1</i> (rv3130c)	8.62465E-06	0.000109393	0.000245128	0.000452601	0.000500924	0.00030534	0.000204164
	2.07228E-06	4.5884E-05	2.82764E-05	2.0568E-05	8.39744E-05	3.65596E-05	7.86104E-05
<i>rv3734c</i>	0.00023576	0.000201308	0.000206792	0.000232691	9.21536E-05	8.13409E-05	5.0957E-05
	6.6799E-05	5.33295E-05	2.89146E-05	3.4961E-05	1.35174E-05	3.49697E-05	2.16843E-05
<i>rv3371</i>	5.00312E-05	0.000105706	0.000107265	0.000155857	0.000121688	5.91089E-05	9.55668E-05
	2.40771E-05	2.71038E-05	6.88854E-06	3.91415E-05	2.37021E-05	6.42744E-06	4.7773E-05
Mycolic acid synthesis							
<i>fas</i> (rv2524c)	6.86102E-06	6.46905E-05	6.67184E-05	4.85915E-05	1.16518E-05	1.09658E-06	1.4202E-05
	5.69784E-07	2.09047E-05	2.89832E-05	9.20021E-06	3.26434E-06	9.43539E-07	7.2318E-06
<i>fabH</i> (rv0533c)	3.95558E-05	2.27834E-05	2.2286E-05	7.05329E-06	1.58681E-06	3.21403E-06	5.65212E-06
	1.40535E-05	2.33592E-06	5.76509E-06	2.46356E-06	1.20521E-06	1.53734E-06	2.56198E-06
<i>kasA</i> (rv2245)	0.000113406	0.000195104	0.000240841	0.000224133	8.7212E-05	5.30101E-05	3.31323E-05
	3.90453E-05	2.57451E-05	1.95218E-05	5.27117E-05	1.22946E-05	1.31813E-05	6.36276E-06
<i>fabG1</i> (rv1483)	0.000206536	0.00018898	0.00018588	8.74864E-05	2.34988E-05	4.64985E-05	4.31319E-05
	2.17541E-05	3.06123E-05	4.01673E-05	2.41496E-05	5.15526E-06	1.12084E-05	1.59558E-05
Multimethyl-branched lipid synthesis							
<i>accD5</i> (rv3280)	0.000258119	0.000252825	0.000258071	0.000203479	6.19734E-05	6.60769E-05	5.03022E-05
	1.5557E-05	4.3454E-05	2.33638E-05	5.22226E-05	6.94686E-06	1.86095E-05	2.01831E-05
<i>mas</i> (rv2940c)	1.32215E-05	1.15131E-05	1.46385E-05	1.11693E-05	1.6929E-06	2.77187E-06	2.83188E-06
	5.0463E-06	2.3509E-06	5.65669E-06	5.68567E-06	1.5019E-06	2.07135E-06	1.23924E-06
<i>fadD26</i> (rv2930)	0.00011409	7.77331E-05	6.59766E-05	4.85455E-05	1.28845E-05	3.52723E-05	2.18025E-05
	7.49297E-06	2.66096E-05	1.99035E-05	1.32026E-05	3.47165E-06	9.95042E-06	6.24483E-06
<i>fadD28</i> (rv2941)	0.000177139	0.000222965	0.00017139	0.000141095	5.33261E-05	9.66528E-05	5.57203E-05
	3.48763E-05	7.92935E-05	2.3209E-05	1.81103E-05	7.3511E-06	5.56695E-05	1.56861E-05
<i>papA5</i> (rv2939)	8.16829E-05	4.38857E-05	3.17539E-05	2.0583E-05	9.8595E-06	1.64851E-05	1.15743E-05
	4.25053E-05	2.1761E-05	2.17165E-06	7.94932E-06	1.49314E-06	2.11632E-06	5.87264E-06
<i>pks2</i> (rv3825c)	2.34105E-05	3.52122E-05	3.76658E-05	5.95741E-05	3.1867E-05	3.59042E-05	2.21725E-05
	4.64722E-06	1.40896E-05	9.59033E-06	2.24762E-05	5.67847E-06	1.09653E-05	5.81364E-06

Enumeration of bacterial transcripts by qPCR and normalization to 16S rRNA were as previously described (Shi et al., 2003). Normalized copy numbers of *M. tuberculosis* mRNA copy numbers against 16S rRNA were expressed as mean + SD of data obtained from lungs of 3 or 4 mice per time point. * indicates that *dlaT* and *lpdC* encode E2 and E3 subunits of pyruvate dehydrogenase, respectively (Tian et al., 2005). ND indicates under detection limit.

SI Table 3. Biomass composition of *M. tuberculosis* at different growth states.

Cell states	Biomass composition
Growing	0.214 protein + 0.036 RNA + 0.022 DNA + 0.050 small molecules + 0.009 phosphatidylethanolamine + 0.016 triglyceride + 0.073 Phosphatidylinositol mannoside + 0.006 lipoarabinomannan + 0.188 mycolic acid–arabinogalactan-peptidoglycan complex + 0.041 poly-L-glutamate/glutamine + 0.012 cardiolipin + 0.053 lipomannan + 0.012 trehalosedimycolate + 0.006 trehalosemonomycolate + 0.004 polyacyctrehalose + 0.002 diacyctrehalose + 0.0001 mannosyl-β-1-phosphodolichol + 0.002 dimycocerosate + 0.031 phenolglycolipid antigen (PLG-Tb 1) + 0.026 sulfolipid-1 + 0.1 glucan + 47 ATP = 1 BIOMASS + 47 ADP + 47 PI
Nongrowing	0.016 triglyceride + 0.041 poly-L-glutamate/glutamine + 0.012 trehalose dimycolate + 47 ATP = 1 BIOMASS + 47 ADP + 47 PI

SI Table 5A. Changes of *M. tuberculosis* transcripts encoding enzymes involved in intermediary metabolism and lipid metabolism in Wayne model.

Pathways	No. hours of Wayne cultures									
	0	78	102	126	168	240	288	342	460	578
Glycolysis										
<i>ppgK (rv2072)</i>	1.00	0.91	0.60	0.36	0.77	1.15	0.80	0.53	0.01	0.00
<i>pfkA (rv3010c)</i>	1.00	0.86	0.75	1.14	1.20	1.85	1.42	1.49	0.41	0.19
<i>pfkB (rv2029c)</i>	1.00	34.28	19.67	24.33	79.27	133.05	37.03	46.67	0.82	0.70
<i>gap (rv1436)</i>	1.00	0.90	0.77	0.66	0.82	1.06	0.51	0.54	0.02	0.00
<i>pykA (rv1617)</i>	1.00	0.66	0.69	0.62	0.89	1.19	0.83	0.72	0.10	0.04
<i>*lpdC (rv0462)</i>	1.00	0.90	1.01	1.10	1.83	2.44	1.11	1.20	0.02	0.01
<i>*dlaT (rv2215)</i>	1.00	2.72	2.02	3.42	2.54	3.59	2.20	2.06	0.09	0.03
PPP										
<i>devB (rv1445c)</i>	1.00	0.49	0.44	0.32	0.53	1.05	0.24	0.33	0.00	0.00
<i>zwf1 (rv1221)</i>	1.00	0.27	0.26	0.29	0.42	1.21	0.47	0.34	0.00	0.00
<i>zwf2 (rv1447c)</i>	1.00	0.44	0.42	0.44	0.21	0.91	0.29	0.43	0.00	0.00
<i>tkt (rv1449c)</i>	1.00	0.77	0.56	0.75	0.93	1.40	0.76	0.87	0.04	0.02
Fatty acid β oxidation										
<i>fadE23 (rv3140)</i>	1.00	2.17	1.82	1.13	1.37	1.15	1.35	1.31	0.03	0.01
<i>fadB (rv0860)</i>	1.00	1.83	2.08	2.37	0.97	1.54	1.01	1.74	0.07	0.02
<i>fadA4 (rv1323)</i>	1.00	1.04	1.17	1.24	1.04	0.94	0.74	0.74	0.08	0.05
<i>fadE5 (rv0244c)</i>	1.00	0.44	0.37	1.10	0.85	0.99	1.24	1.70	0.64	0.38
TCA cycle										
<i>citA (rv0889c)</i>	1.00	0.45	0.41	0.42	0.78	1.35	0.88	0.76	0.14	0.05
<i>gltA2 (rv0896)</i>	1.00	1.07	0.98	0.96	0.82	1.19	0.92	0.86	0.06	0.01
<i>acn (rv1475c)</i>	1.00	1.07	0.98	0.96	0.82	1.18	0.92	0.86	0.06	0.01
<i>icd1 (rv3339c)</i>	1.00	0.38	0.40	0.32	0.80	1.81	0.88	0.96	0.06	0.02
<i>icd2 (rv0066c)</i>	1.00	0.91	0.60	0.97	0.68	1.07	1.11	0.89	0.02	0.01
<i>kgd (rv1248c)</i>	1.00	0.75	0.79	0.68	0.75	1.11	0.77	0.78	0.04	0.02
<i>sdhA (rv3318)</i>	1.00	0.73	0.85	0.45	0.53	0.26	0.22	0.28	0.01	0.01
<i>sdhC (rv3316)</i>	1.00	1.24	0.67	0.53	0.39	0.39	0.48	0.39	0.02	0.00
<i>mdh (rv1240)</i>	1.00	0.72	1.15	0.94	1.31	0.82	0.66	0.53	0.02	0.01
Glyoxylate shunt and methylcitrate cycle										
<i>icl (rv0467)</i>	1.00	3.15	3.80	1.86	1.01	0.77	0.28	0.54	0.06	0.02
<i>glcB (rv1837c)</i>	1.00	0.78	0.89	0.99	1.04	1.17	0.91	0.71	0.01	0.01
<i>prpC (rv1131)</i>	1.00	1.17	5.97	0.99	1.10	0.57	0.38	0.53	0.06	0.01
Gluconeogenesis										
<i>mez (rv2332)</i>	1.00	0.81	1.12	0.93	1.28	1.74	0.57	0.83	0.04	0.03
<i>pckA (rv0211)</i>	1.00	1.08	1.37	2.59	1.68	1.87	0.87	1.11	0.37	0.09
<i>pca (rv2967c)</i>	1.00	0.45	0.39	0.31	0.48	0.52	0.23	0.23	0.02	0.03
<i>glpX (rv1099c)</i>	1.00	1.05	0.87	0.77	1.05	1.13	0.44	0.39	0.00	0.00
Glutamate metabolism										
<i>gltB (rv3859c)</i>	1.00	0.61	0.48	0.42	0.79	1.12	0.54	0.62	0.01	0.01
<i>gdh (rv2476c)</i>	1.00	0.24	0.21	0.21	0.50	0.62	0.33	0.32	0.02	0.01
<i>glnA1 (rv2220)</i>	1.00	1.27	1.35	0.78	0.92	0.81	0.34	0.36	0.02	0.01
TAG synthesis										
<i>plsB2-C (rv2482-3c)</i>	1.00	0.50	0.72	0.54	0.56	1.06	1.25	1.23	0.08	0.05
<i>rv2182c</i>	1.00	0.69	0.60	0.69	0.94	2.03	1.14	1.49	0.06	0.02
<i>tgs1 (rv3130c)</i>	1.00	1305.38	379.93	1119.12	888.32	1705.66	1310.55	1253.38	92.91	15.59
<i>rv3734c</i>	1.00	1.37	1.64	1.11	0.74	0.65	0.37	0.38	0.05	0.02
<i>rv3371</i>	1.00	0.57	0.97	0.41	0.82	1.13	0.76	1.50	0.06	0.03
Mycolic acid synthesis										
<i>fas (rv2524c)</i>	1.00	1.88	5.25	1.66	1.27	1.19	0.42	0.85	0.01	0.01
<i>fabH (rv0533c)</i>	1.00	0.70	0.58	0.33	0.56	0.59	0.25	0.29	0.01	0.00
<i>kasA (rv2245)</i>	1.00	1.97	4.88	2.07	1.67	0.70	0.17	0.70	0.02	0.00
<i>fabG1 (rv1483)</i>	1.00	0.68	0.96	1.08	2.45	2.57	1.21	1.15	0.02	0.01
Multimethyl-branched lipid synthesis										
<i>accD5 (rv3280)</i>	1.00	1.26	1.63	1.08	1.6	1.27	0.7	0.7	0.01	0.01
<i>mas (rv2940c)</i>	1.00	0.69	2.19	0.94	1.72	1.43	0.79	1.05	0.01	0.00
<i>fadD26 (rv2930)</i>	1.00	0.58	2.11	1.09	1.74	1.25	0.35	0.53	0.01	0.01
<i>fadD28 (rv2941)</i>	1.00	1.14	1.60	1.20	1.13	1.22	0.89	1.04	0.04	0.01
<i>papA5 (rv2939)</i>	1.00	0.74	1.55	0.94	1.37	1.14	0.7	0.89	0.06	0.02
<i>pks2 (rv3825c)</i>	1.00	0.79	3.26	1.23	0.62	0.52	0.13	0.2	0.01	0.01

SI Table 5B. Changes of *M. tuberculosis* transcripts encoding enzymes involved in intermediary metabolism and lipid metabolism after treatment with NO.

Pathways	NO concentration (µM)					
	0	25	50	100	250	500
Glycolysis						
<i>ppgK</i> (rv2072)	1.00	1.02	0.93	0.99	0.41	0.27
<i>pfkA</i> (rv3010c)	1.00	0.93	0.79	0.74	0.54	0.61
<i>pfkB</i> (rv2029c)	1.00	92.25	177.38	157.03	20.14	14.59
<i>gap</i> (rv1436)	1.00	0.93	1.00	0.72	0.37	0.27
<i>pykA</i> (rv1617)	1.00	0.94	0.92	0.72	0.23	0.16
* <i>lpdC</i> (rv0462)	1.00	1.18	1.09	0.68	0.32	0.24
* <i>dlaT</i> (rv2215)	1.00	0.89	0.78	0.60	0.55	0.53

PPP

<i>devB</i> (rv1445c)	1.00	0.79	0.53	0.36	0.05	0.07
<i>zwf1</i> (rv1121)	1.00	1.01	0.67	0.42	0.16	0.25
<i>zwf2</i> (rv1447c)	1.00	0.90	0.70	0.54	0.19	0.13
<i>tkt</i> (rv1449c)	1.00	1.17	0.91	0.71	0.76	0.96

Fatty acid β oxidation

<i>fadE23</i> (rv3140)	1.00	1.87	1.69	4.18	7.20	5.89
<i>fadB</i> (rv0860)	1.00	1.05	0.78	0.50	2.92	4.34
<i>fadA4</i> (rv1323)	1.00	1.07	1.13	0.95	0.73	0.76
<i>fadE5</i> (rv0244c)	1.00	1.02	1.32	1.60	2.57	3.71

TCA cycle

<i>citA</i> (rv0889c)	1.00	0.93	0.92	0.85	0.32	0.32
<i>gltA2</i> (rv0896)	1.00	0.99	0.79	0.77	0.76	0.59
<i>acn</i> (rv1475c)	1.00	0.99	0.79	0.78	0.76	0.60
<i>icd1</i> (rv3339c)	1.00	0.82	0.75	0.51	0.13	0.11
<i>icd2</i> (rv0066c)	1.00	1.03	0.87	0.80	1.19	1.60
<i>kgd</i> (rv1248c)	1.00	0.99	0.78	0.43	0.47	0.68
<i>sdhA</i> (rv3318)	1.00	1.72	0.87	0.61	0.19	0.11
<i>sdhC</i> (rv3316)	1.00	2.07	1.30	1.12	0.68	0.43
<i>mdh</i> (rv1240)	1.00	1.03	0.89	0.48	0.17	0.06

Glyoxylate shunt and methylcitrate cycle

<i>icl</i> (rv0467)	1.00	1.00	1.20	3.61	0.67	0.87
<i>glcB</i> (rv1837c)	1.00	0.84	0.73	0.67	0.25	0.35
<i>prpC</i> (rv1131)	1.00	0.92	1.02	0.70	0.27	0.28

Gluconeogenesis

<i>mez</i> (rv2332)	1.00	0.97	0.70	0.39	0.22	0.16
<i>pckA</i> (rv0211)	1.00	0.84	1.18	2.16	2.17	2.41
<i>pca</i> (rv2967c)	1.00	0.73	0.67	0.57	0.13	0.26
<i>glpX</i> (rv1099c)	1.00	1.05	1.00	0.67	0.13	0.05

Glutamate metabolism

<i>gltB</i> (rv3859c)	1.00	0.94	0.86	0.58	0.20	0.25
<i>gdh</i> (rv2476c)	1.00	0.98	0.83	0.51	0.22	0.46
<i>glnA1</i> (rv2220)	1.00	1.02	0.94	0.57	0.20	0.11

TAG synthesis

<i>plsB2-C</i> (rv2482-3c)	1.00	1.02	0.61	0.26	0.19	0.27
<i>rv2182c</i>	1.00	1.23	0.76	0.73	1.19	1.05
<i>tgs1</i> (rv3130c)	1.00	285.68	734.40	851.58	2080.99	2062.32
<i>rv3734c</i>	1.00	1.56	0.94	0.68	1.38	1.39
<i>rv3371</i>	1.00	0.88	0.90	0.63	0.36	0.32

Mycolic acid synthesis

<i>fas</i> (rv2524c)	1.00	1.52	0.85	2.22	1.14	0.40
<i>fabH</i> (rv0533c)	1.00	0.92	0.69	0.46	0.08	0.10
<i>kasA</i> (rv2245)	1.00	1.58	1.47	2.96	0.92	0.31
<i>fabG1</i> (rv1483)	1.00	0.95	1.10	0.45	0.17	0.05

Multimethyl-branched lipid synthesis

<i>accD5</i> (rv3280)	1.00	1.52	0.92	0.59	0.19	0.06
<i>mas</i> (rv2940c)	1.00	1.29	0.98	0.54	0.16	0.13
<i>fadD26</i> (rv2930)	1.00	1.72	1.32	0.88	0.21	0.08
<i>fadD28</i> (rv2941)	1.00	1.57	1.08	0.81	0.54	0.57
<i>papA5</i> (rv2939)	1.00	1.77	0.99	0.53	0.18	0.14
<i>pks2</i> (rv3825c)	1.00	1.40	1.00	0.75	0.65	0.42

SI Table 5C. Normalized copy number of *M. tuberculosis* transcripts encoding enzymes involved in central metabolism and lipid metabolism in cultures after treatment with DETA/NO

Pathways	NO concentration (μM)					
	Mid-log	25	50	100	250	500
Glycolysis						
<i>ppgK (rv2702)</i>	6.41129E-06	6.54413E-06	5.9641E-06	6.36131E-06	2.6058E-06	1.7536E-06
	9.75777E-07	2.1956E-06	3.07119E-06	8.98826E-07	3.3709E-07	7.01213E-07
<i>pfkA (rv3010c)</i>	1.34428E-05	1.25469E-05	1.05821E-05	1.00135E-05	7.2679E-06	8.15135E-06
	4.51153E-07	2.25848E-06	2.72717E-06	2.7028E-06	2.5696E-06	2.36057E-06
<i>pfkB (rv2029c)</i>	1.9298E-07	1.78015E-05	3.42307E-05	3.03039E-05	3.8859E-06	2.81655E-06
	8.99532E-08	2.3269E-06	1.14736E-05	8.11208E-06	2.0689E-06	8.57418E-07
<i>gap (rv1436)</i>	6.55363E-05	6.06639E-05	6.52423E-05	4.72468E-05	2.4282E-05	1.79785E-05
	6.30539E-06	1.80304E-05	1.89366E-05	1.52454E-05	3.8749E-06	4.13419E-06
<i>pykA (rv1617)</i>	2.44476E-05	2.29904E-05	2.25971E-05	1.7626E-05	5.6649E-06	3.81512E-06
	4.08974E-06	4.72539E-06	6.98992E-06	5.84003E-06	1.2841E-06	4.36365E-07
<i>lpdc* (rv0462)</i>	4.4903E-05	5.29277E-05	4.90298E-05	3.05519E-05	1.4556E-05	1.0669E-05
	7.16242E-06	1.29726E-05	1.57069E-05	7.68346E-06	9.8515E-07	5.47945E-07
<i>dlaT* (rv2215)</i>	6.23065E-05	5.52171E-05	4.88252E-05	3.74347E-05	3.4497E-05	3.29796E-05
	1.2205E-05	1.15475E-05	1.40708E-05	1.41545E-05	6.2084E-06	3.61446E-06
PPP						
<i>devB (rv1445c)</i>	8.01413E-05	6.30507E-05	4.26063E-05	2.84594E-05	4.3785E-06	5.5402E-06
	2.78444E-05	1.55003E-05	1.23563E-05	9.31361E-06	1.7382E-06	1.73557E-06
<i>zwf1 (rv1121)</i>	1.57791E-05	1.59921E-05	1.05361E-05	6.55043E-06	2.4982E-06	3.90085E-06
	5.42932E-06	5.46036E-06	1.51321E-06	1.22806E-06	7.3567E-07	6.08579E-07
<i>zwf2 (rv1447c)</i>	1.45823E-05	1.30669E-05	1.02131E-05	7.81352E-06	2.7221E-06	1.82487E-06
	6.30785E-06	2.43534E-06	8.5749E-07	3.32547E-06	7.4314E-07	6.25016E-07
<i>tkt (rv1449c)</i>	0.000350979	0.00041113	0.000319724	0.000249715	0.00026735	0.000336712
	5.65143E-05	7.96078E-05	7.37463E-05	5.23233E-05	8.3653E-05	4.37531E-05
Fatty acid β oxidation						
<i>fadE5 (rv0244c)</i>	6.46545E-06	6.59746E-06	8.51014E-06	1.03616E-05	1.6613E-05	2.40066E-05
	1.11471E-06	1.06163E-06	1.96577E-06	3.70814E-06	1.7599E-06	7.30527E-06
<i>fadE23 (rv3140)</i>	1.98401E-05	3.7161E-05	3.34396E-05	8.30049E-05	0.0001429	0.000116759
	6.05266E-06	5.11408E-06	8.35039E-06	1.67116E-05	4.3958E-05	3.26731E-05
<i>fadA4 (rv1323)</i>	8.62039E-05	9.24344E-05	9.70917E-05	8.1535E-05	6.2561E-05	6.51919E-05
	1.45663E-05	2.02757E-05	3.09946E-05	2.28247E-05	8.682E-06	7.23384E-06
<i>fadB (rv0860)</i>	3.32564E-06	3.49005E-06	2.59511E-06	1.65988E-06	9.7007E-06	1.44247E-05
	1.41459E-06	7.98127E-07	5.96722E-07	6.70186E-07	1.1999E-06	3.50226E-06
TCA cycle						
<i>citA (rv0889c)</i>	1.25753E-05	1.17124E-05	1.15517E-05	1.06489E-05	4.0082E-06	4.06181E-06
	1.5201E-06	1.38274E-06	2.98305E-06	3.45666E-06	6.5194E-07	7.04345E-07
<i>glfA2 (rv0896)</i>	4.17983E-05	4.14736E-05	3.28892E-05	3.23829E-05	3.1696E-05	2.48405E-05
	1.10614E-05	1.15027E-05	9.59838E-06	8.65827E-06	9.4108E-07	5.10601E-06
<i>acn (rv1475c)</i>	3.05073E-05	3.02009E-05	2.40199E-05	2.36443E-05	2.3088E-05	1.81642E-05
	8.0353E-06	8.35333E-06	7.00323E-06	6.30913E-06	6.5085E-07	3.7091E-06
<i>icd1 (rv3339c)</i>	2.13128E-06	1.73887E-06	1.59921E-06	1.09589E-06	2.721E-07	2.38431E-07
	4.19267E-07	4.58467E-07	5.35577E-07	3.71453E-07	6.7226E-08	6.24251E-08
<i>icd2 (rv0066c)</i>	1.13033E-05	1.16914E-05	9.85107E-06	8.99199E-06	1.3471E-05	1.81038E-05
	2.50331E-06	2.57336E-06	1.67135E-06	3.27511E-06	1.881E-06	3.01396E-06
<i>kgd (rv1248c)</i>	3.55388E-05	3.50483E-05	2.7786E-05	1.51628E-05	1.6755E-05	2.40749E-05
	8.60016E-06	7.96486E-06	5.46463E-06	3.97673E-06	2.9404E-06	3.39307E-06
<i>sdhA (rv3318)</i>	2.84393E-06	4.88904E-06	2.46302E-06	1.74534E-06	5.2614E-07	3.02237E-07
	5.73408E-07	6.27363E-07	4.26105E-07	2.05725E-07	1.5175E-07	2.8119E-08
<i>sdhC (rv3316)</i>	2.63895E-06	5.45583E-06	3.43553E-06	2.94738E-06	1.7901E-06	1.14784E-06
	4.03829E-07	1.02108E-06	8.4061E-07	5.26875E-07	9.366E-08	5.81201E-07
<i>mdh (rv1240)</i>	0.000218589	0.000224541	0.000193879	0.0001051	3.7003E-05	1.3985E-05
	5.37614E-05	5.37037E-05	6.93912E-05	2.31412E-05	5.4058E-06	2.32699E-06

Pathways	NO concentration (μM)					
	12	15	18	21	30	50
Glyoxylate shunt and methylcitrate cycle						
<i>icl</i> (rv0467)	6.99063E-06	7.0715E-06	8.45594E-06	2.60662E-05	4.7016E-06	6.09446E-06
	1.39946E-06	1.11615E-06	1.69899E-06	7.90421E-06	4.9337E-07	6.50023E-07
<i>glcB</i> (rv1837c)	0.000292385	0.000247044	0.000212092	0.000197356	7.4104E-05	0.000101782
	5.47967E-05	9.70429E-05	6.48172E-05	6.53571E-05	2.5474E-05	9.11626E-06
<i>pprC</i> (rv1131)	1.18579E-06	1.09518E-06	1.2072E-06	8.30144E-07	3.2063E-07	3.29167E-07
	3.29637E-07	3.189E-07	3.29085E-07	6.84203E-08	1.6496E-07	1.70798E-07
Gluconeogenesis						
<i>mez</i> (rv2332)	8.67285E-06	8.43383E-06	6.10206E-06	3.34809E-06	1.9255E-06	1.395E-06
	2.04803E-06	2.10379E-06	6.4372E-07	9.11256E-07	3.3467E-07	4.06739E-07
<i>pckA</i> (rv0211)	0.000146958	0.000226716	0.000319643	0.000449064	0.00045281	0.000257331
	1.77632E-05	7.40275E-05	9.91622E-05	6.47696E-05	3.6955E-05	5.78635E-05
<i>pca</i> (rv2967c)	5.59837E-06	4.08981E-06	3.74656E-06	4.02317E-06	7.1416E-07	1.47689E-06
	1.68216E-06	1.13379E-06	7.67879E-07	6.46531E-07	9.4113E-08	5.55835E-07
<i>glpX</i> (rv1099c)	6.87927E-05	7.21687E-05	6.89724E-05	4.63258E-05	8.6165E-06	3.32607E-06
	7.5643E-06	2.25725E-05	2.2089E-05	1.69871E-05	8.3358E-07	3.65944E-07
Glutamate synthesis						
<i>gltB</i> (rv3859c)	2.76587E-05	2.60949E-05	2.37659E-05	1.60808E-05	5.5599E-06	6.93609E-06
	3.26889E-06	5.61951E-06	6.7952E-06	6.08998E-06	1.304E-06	9.88743E-07
<i>gdh</i> (rv2476c)	0.00023002	0.000224283	0.000190848	0.00011828	5.1424E-05	0.000106703
	5.14536E-05	5.6196E-05	7.27483E-05	3.58407E-05	8.2257E-06	1.89709E-05
<i>glnA1</i> (rv2220)	4.44458E-05	4.53437E-05	4.18374E-05	2.55344E-05	8.7069E-06	4.854E-06
	1.52422E-06	6.47203E-06	1.08183E-05	1.22333E-05	9.7577E-07	7.05804E-07
TAG synthesis						
<i>plsB2-C</i> (rv2482-3c)	4.75128E-06	4.83424E-06	2.90459E-06	1.2352E-06	9.1534E-07	1.29667E-06
	2.12769E-06	1.1228E-06	3.02207E-07	4.24701E-09	2.0723E-07	6.10353E-07
<i>rv2182c</i>	1.4077E-06	1.73047E-06	1.0664E-06	1.02582E-06	1.6739E-06	1.4829E-06
	4.42913E-07	4.64219E-07	2.23699E-07	4.08058E-07	3.9836E-07	4.06917E-07
<i>tgs1</i> (rv3130c)	8.26473E-08	2.36105E-05	6.06964E-05	7.03808E-05	0.00017199	0.000170445
	3.71999E-08	1.68055E-06	1.52791E-05	3.38651E-05	2.447E-05	4.68265E-05
<i>rv3734c</i>	2.83036E-06	4.4071E-06	2.65261E-06	1.91451E-06	3.9113E-06	3.92816E-06
	4.37686E-07	1.01928E-06	1.80029E-07	3.12662E-07	9.1121E-07	1.36688E-06
<i>rv3371</i>	9.62158E-07	8.43253E-07	8.62733E-07	6.05532E-07	3.4675E-07	3.12213E-07
	1.895E-07	9.95179E-08	1.57513E-07	1.881E-07	1.2606E-07	7.18908E-08
Mycolic acid synthesis						
<i>fas</i> (rv2524c)	1.43495E-05	2.18317E-05	1.22221E-05	3.1829E-05	1.6359E-05	5.71956E-06
	3.34775E-06	7.79826E-06	9.03918E-07	6.60515E-06	5.5389E-06	1.21321E-06
<i>fabH</i> (rv0533c)	5.79071E-06	5.30049E-06	4.02181E-06	2.64904E-06	4.5045E-07	5.66621E-07
	1.71731E-06	1.04624E-06	1.66028E-07	9.70144E-07	2.3652E-07	1.55921E-07
<i>kasA</i> (rv2245)	1.18343E-05	1.87243E-05	1.74023E-05	3.50464E-05	1.0837E-05	3.65225E-06
	9.48304E-07	6.14968E-06	5.20345E-06	9.73305E-06	2.8841E-06	1.00461E-06
<i>fabG1</i> (rv1483)	5.00449E-06	4.76074E-06	5.49446E-06	2.25801E-06	8.411E-07	2.59343E-07
	2.93571E-06	1.05352E-06	5.00779E-07	7.83753E-07	1.0049E-07	6.69065E-08
Multimethyl-branched lipid synthesis						
<i>accD5</i> (rv3280)	7.57568E-06	1.14987E-05	6.94349E-06	4.4541E-06	1.455E-06	4.42681E-07
	7.02198E-07	3.55368E-06	7.52877E-07	1.16659E-06	2.9054E-07	2.4358E-07
<i>mas</i> (rv2940c)	2.61265E-06	3.35776E-06	2.57332E-06	1.4107E-06	4.1087E-07	3.28828E-07
	7.59262E-07	2.09251E-06	7.02174E-07	2.00641E-07	1.0378E-07	1.36348E-07
<i>fadD26</i> (rv2930)	2.1222E-06	3.65793E-06	2.80162E-06	1.86927E-06	4.4213E-07	1.63985E-07
	2.20071E-07	1.18452E-06	8.81952E-07	3.06926E-07	1.3362E-07	3.17296E-08
<i>fadD28</i> (rv2941)	9.53487E-06	1.49334E-05	1.02913E-05	7.73019E-06	5.1767E-06	5.42484E-06
	1.81059E-06	4.68906E-06	9.64616E-07	1.93036E-06	8.0959E-07	2.18237E-06
<i>papA5</i> (rv2939)	3.23856E-06	5.73833E-06	3.1949E-06	1.712E-06	5.7212E-07	4.4266E-07
	4.15311E-07	1.692E-06	6.17677E-07	1.38023E-07	1.5453E-07	2.7496E-07
<i>pks2</i> (rv3825c)	2.96369E-06	4.14784E-06	2.96511E-06	2.22267E-06	1.9296E-06	1.23327E-06
	6.55902E-07	1.17119E-06	2.17857E-07	3.35034E-07	3.4458E-07	5.65964E-07

M. tuberculosis mid-log cultures were exposed to gradual oxygen depletion or treated with increasing concentrations of the NO donor DETA/NO for 30 min, as described in Experimental procedure. RNA extraction, reverse transcription and real-time PCR with molecular beacons were described in Shi et al (Shi et al., 2003). Levels of transcripts per cell were obtained by dividing mRNA copy number by the corresponding 16S rRNA copy number. Shown are ratios between normalized mRNA copy numbers at various time points during hypoxia or 30 min after NO treatment and the data from mid-log-phase culture. The hypoxia data are from one of two independent repeats, which gave very similar results (SI Table 5A). The NO treatment data were obtained from triplicate samples (SI Table 5B); shown in SI Table 5C are means and SD of normalized mRNA copy number from triplicate cultures. *indicates that *dlaT* and *lpdC* encode E2 and E3 subunits of pyruvate dehydrogenase, respectively (Tian et al., 2005).

SI Table 6. Composition of simplified Middlebrook 7H9 and LIM minimal media.

6A. Modified Middlebrook 7H9 Medium

Components	Quantity (mg per 1000ml)
Ammonium Sulfate	500
L-Glutamic Acid	500
Sodium Citrate	100
Pyridoxine	1
Biotin	0.5
Disodium Phosphate	2,500
Monopotassium Phosphate	1,000
Ferric Ammonium Citrate	40
Magnesium Sulfate	50
Calcium Chloride	0.5
Zinc Sulfate	1
Copper Sulfate	1
Sodium Chloride	850
Glucose	2,000
Tyloxapol	500

6B. LIM minimal medium

Components	Quantity (mg per 1000ml)
Disodium Phosphate Anhydrous	2,200
Potassium Dihydrogen Phosphate	1,000
Ferric Chloride Hexahydrate	0.5
Magnesium Sulfate Heptahydrate	20
Calcium Chloride	0.5
Ammonium Chloride	200
Glucose	10,000
Tyloxapol	500

SI Table 7. Activity of key metabolic enzymes during hypoxia

Enzyme	Activity	Time	Mid-log culture	Hr 70	Hr 115	Hr 150	Hr 220
Isocitrate lyase	1.9 +/- 0.0	6.3 +/- 1.0	7.3 +/- 1.2	4.3 +/- 0.3	0.5 +/- 0.0		
PEP carboxykinase	22.5 +/- 2.5	34.7 +/- 3.3	50.5 +/- 1.6	NM	132.3 +/- 16.4		
Methylcitrate synthase	4.1 +/- 0.6	1.1 +/- 0.2	2.3 +/- 0.4	0.6 +/- 0.1	3.2 +/- 0.5		
Malate dehydrogenase	1,210.5 +/- 21.1	NM	NM	892.1 +/- 65.9	530.1 +/- 149.8		
Glutamine synthase	4.2 +/- 1.5	NM	NM	0.5 +/- 0.4	0.4 +/- 0.1		
Glutamate synthase	4.1 +/- 0.7	NM	NM	< 0.1	< 0.1		
Citrate synthase	220.7 +/- 31.2	76.7 +/- 5.3	186.3 +/- 40.4	NM	117.4 +/- 51.5		
Phosphofructokinase	26.0 +/- 3.1	29.1 +/- 6.0	NM	33.4 +/- 1.8	18.9 +/- 3.3		

Enzyme activity measurement was described in Experimental procedure. Activity is expressed in nmol/min/mg protein except for glutamine synthase for which the activity is expressed as relative units per mg protein. NM indicates not measured.

SI Table 8. Nucleotide sequences of primers and probes used for *M. tuberculosis* mRNA measurement by real-time RT-PCR.

Gene	RT primers	PCR primers	Molecular beacons
<i>ppgK</i> (<i>rv2702</i>)	GCGGCATCAGCGTCGTTGA	GACCTATCCCGGCGTCTCACTC CGCGTGCGTTGGTCCCTATCC	TGGGGCTCCGGACCGCGGCTAACGCCCA
<i>pfkA</i> (<i>rv3010c</i>)	TGCGGCACCAGTTTGAGTT	CGGGGACTCGCATTTCATC CTGCGCCGCTACACCTGT	ACCGGCGGGGACGATCATGCTGCGCGAGGCCGGT
<i>pfkB</i> (<i>rv2029c</i>)	ACGATCGGGTGCCAAACGTA	CGAGCGTGCGGGAAct CTGAGATCCAAGCGAGACCA	ACGCGCCAActGGCCGCGCACACGAAGCGCGT
<i>gap</i> (<i>rv1436</i>)	TGGCCGCATTGGTGAACAG	GCGCATCTGCTCAAATTCGACT CGCGAGCGCCTTGATTTT	ACCGCGACACCATCGTCGTCGGCCGCGCGCGGT
<i>pykA</i> (<i>rv1617</i>)	GAGGCTACCCGGACCCGCTCAT A	CGCGGGAAAATCGTCTGCACTCT AGTTCATTGGGCGACGTCCATT	ACCGCGTCAGAGCGCTGGTCGAGGCCGCGGT
<i>lpdC</i> (<i>rv0462</i>)	CAACACCTTTTCCGCCTTAAGC	CACTGTGGCCAACGTAGTCAC CACCAGCTCCGGCAATAATGA	CGTGCGAACAGATCCTGTCCCGAGAGCGCAGC
<i>dlaT</i> (<i>rv2215</i>)	TCGGTGTCGACAGCGAATCCTA	ACCTGACCTTCCTGCCGTTCTTC GTGCTCGGCGTCGTAGTAGGTG	CCCAGGCGAACATCAACGCTAGCTACAACGAGCCTGGG
<i>devB</i> (<i>rv1445c</i>)	TGCGGGAACAGCGAGTTA ATG	AGACGATGACGAGCGCAATCT CGGCCAGCACCTGTTCGTAG	TGCGCGATTCCATCGAACCAGGTGCACCCCGCGCA
<i>zwf1</i> (<i>rv1121</i>)	GCCACGTCTGCTCGATGCTG	CCCAACCAGATTGTGCTGCGTAT GAGGTCCACCGCGAACGA	CGCGCTGATCCGGGTATGCGACTGCAGAGCGCG
<i>zwf2</i> (<i>rv1447c</i>)	GGCCGAGAGCACCTTGATCTT	CTTCCGCATCGACCACTACCT GGCCATGGTGATCTGTACGTG	AGGCCCAGAACATCCTGGCGCTGCGGGGCCCT
<i>tkt</i> (<i>rv1449c</i>)	GTGTCCTCACACAGCGCGATGTT	GAAGAAGGGGTGACCTCGGA GATCTGGTTGCGGTCGTAGAACA	AGGCGGCCGCGGTCCAGCAACTCCGCCT

SI Table 8 (continued)

Gene	RT primers	PCR primers	Molecular beacons
<i>citA</i> (rv0889c)	CCCAGTTGAGGCGATCACACG	TCCGCACGGGGCATCTA CGACACCCAGTAGGCGTCAAT	ACGGGCGAGCCAGACCCCAGACACATCGAGGCCCGT
<i>gltA2</i> (rv0896)	CCACGCTCAGTGAGTTATCTGG	GTTGTCCAGCGTGGTCAATGC CGTACGCGGCATGGTG	ACCGCGTGCTCTGGACCCCATGGACAACGGACGCGGT
<i>acn</i> (rv1475c)	CGTTGTCGTTAACCGCTTTTGA	TCCAACCCCGAAGTAATGCT AGGCCGGATCTGTCTAGTAGT	ACCGGGTGGACTGACCTCGAAGCCGTGGGACCCGGT
<i>icd1</i> (rv3339c)	CAGTCGCGGCACATTAGAAAT	CTCGACATCCGCTTGGACTATT GTGATCGTCGCGCACTTTA	CCGGGTGAGCACCGCGACGCCACCGACGACACCCGG
<i>icd2</i> (rv0066c)	GAGTTTGGCCCGCTCGTTAC	GCGACTACCTCACCGACCTGT CCGCCCCCGTCTCGTAC	AGGCGCTGTCCGTCGTTCCGCTGATGCGCCT
<i>kgd</i> (rv1248c)	GCGGCCAGCTCGTAATACAG	TTCACGCCCAAGTCGATGTT CCGATGCCGTCCTCATAGGT	AGCGCGCTTCACCGAGATCAAGTTCCGCCGCGCT
<i>sdhA</i> (rv3318)	AGGTCGGTGTTGAAGCGTTTCC	GTTATGCGCAGGGTCACGACTTT CGGCGTTGTTGTCCATCGACT	CCGGGGGGGTCAGCGACATCCTGTCCGAACCCCGG
<i>sdhC</i> (rv3316)	CCACGCCTGCCGGAACCATC	CGGTGCTGGCGACCTACAAGAC CAAGATGACCCGAATCCCGTTCA	ACGGGCCCTAGTCGCCGCGGTCCTTTTGCCCGT
<i>mdh</i> (rv1240)	CCAGGCTCACACCATCGAAG	TAGTCCTCTCAAGGTCGCCGTTA GCAGTCGTCGAGTTCATCA	CGGGTCCCCTGACCGTCCGATCGAGCTGGACCCG
<i>icl</i> (rv0467)	GGCCCTCTTCGGTGGAAC	GGCCCTCTTCGGTGGAAC CCAGAACCAGATGAGCGCGTAT	ACGCCCGGGGCTACACCGCGACCAAGGGCGT
<i>glcB</i> (rv1837c)	GATGCACGCCTTGAGGTTGAC	TGGCGTTTACCTGCGAACTGT GATGCACGCCTTGAGGTTGAC	CGCGCGATGAAGATCGGCATCATGGACGAGCGCGG
<i>prpC</i> (rv1131)	CGTCCTCGTCCGGGTCC	ATTCGTTGACCTACCGGGGATA CAG CAT CGA GCG GTC CAC	TGCGCGGTTTCGAGCAGGTCGCCTTCCTCGCGCA

SI Table 8 (continued)

Gene	RT primers	PCR primers	Molecular beacons
<i>mez</i> (rv2332)	CCGGGCACCAGCGACAAT	AGATCGCATCGCCCACTATCCT AGCGGAAAGATCATCGGGTGT	TGCGCGAAAGAGGTGGTTCGAGGCGATGACGCGCGCA
<i>pckA</i> (rv0211)	CATGCAACCCCGGTACAGGTCT	AGCGGCTCTGCGATCAGCTAGT CGCCGAGCAGATGTACGTCC	CGCTGCC CCG AGAAGCACAA GAACTCCTAC CT GGCAGCG
<i>pca</i> (rv2967c)	GAAGAACTGGTTGGCCGACAAT	GTTGGGCAGGCTGGTTAAGGTC CCGCAGAAATCCGAGTACCGA	CCGCCGACGAATTCGCCTCCGATCCAGCCGGCGG
<i>glpX</i> (rv1099c)	GGTGAAGTCGATCGCGGAGTATT	TCTGGTGTCCGGGAAAACGTCT TGCAGCCGCCGGGTAGTAAC	CCGACC CTTC TGCGCCACTG GGGTCACCG GGTCGG
<i>fadE5</i> (rv0244c)	GGAGCCCACACCCTTGACTACC	TGCGTGCCTCTACCTCTACAC GTTGACCTTGACGGCCAACTT	CGGGCTCTGTCCCGAGGTGGTGCAAGCCCG
<i>fadE23</i> (rv3140)	TTTCCGGGTTCCCAAGTAGGTT	GCCGATAGCCCGCAAGTACGAC GGCTCCGGCAAAGTTGAACGAT	ACGCGCCCGGTGCAACTCGACACCCTGATCGCGCG
<i>fadA4</i> (rv1323)	CTCTGGCCCGAATGAGTTGA	GCTGGCGCGCGTACA CCTGGCCCATGATCACGTAC	ACCGGGTGGCAAGTTGATGGGCTCCCTGAAGACCCGGT
<i>fadB</i> (rv0860)	ATGGCCAAGGTGTAGTCGAACA	GCTACTTCGCGTCGTTGGTCAC GCACCCAGCACACCGATCC	AGCGCCGACCTGCAGGCCATCAATGCCGGGCGCT
<i>glfB</i> (rv3859c)	CGGTGCAGTTGGTCAGGTAATG	GCTGGCCATCGCAATGAA GGGCGGAGGCTACCTGCTTAAT	ACGGGGCGAGGACGTCAAGCGATTTGACCCCGT
<i>gdh</i> (rv2476c)	GACTCGGCCTTGATGTAAGTGC	GGTGTACAGCCGCGAACAGA GCAGAATCGCCGAATAAGGTT	ACCGGTCCCTCGGCATCGACGGCTCAGTTGACCGGT
<i>glnA1</i> (rv2220)	GTTGACCGGCTCGATCTCGTTTT	TGGCAGGCCTGGACGGTATC CGGCGGCAGCTCGTAGAGA	CGCGCTAAGATCGAGCCGCAGGCGCCAGCGCG

SI Table 8 (continued)

Gene	RT primers	PCR primers	Molecular beacons
<i>fas</i> (rv2524c)	AGCAACTCACCGACGGGTTTCAT	GACACTCAGGGCACCGACCAAT TGCGCTGTTGTCGATCTCGTG	TGCGCGTCCAGCCGCAGTCAGCTCGGTGCCCGCGCA
<i>fabH</i> (rv0533c)	CGGTTCGTCAGTAATTCGGCCATC	CATACGGCAGGACATCGACTGGA GAA CGC TGC CCA ACG GAA GA	AGGCGCTCAAAATCCCAGCGGCCACGCCAGCGCCT
<i>kasA</i> (rv2245)	GCCCCGATTCATCAGGTCGTAG	CAAGTTGCTGGGCGGACAG TCCTCTCGGCTCCACCTAGACC	ACCCGCGTCGATCCAGACCGTTTCGCCGTTGCGGGT
<i>fabG1</i> (rv1483)	CCACATTCGCGGTCACGTT	CCGTCACCCACCGTGGAT AGCACCTCGACCGGACCCT	ACCCCGCCGTCGATCGCGCCTTCACGGGGT
<i>accD5</i> (rv3280)	TGATCAACGAGATTTGCGGGATG	TGGCGAGGTGTACGGCGAGAA GGCCAGGATGTTGTTGCGAAAGA	AGCGCGAAGACCGGCCGTCCGCTCATCCGCGCT
<i>mas</i> (rv2940c)	GTCCCGGTTCCCATGCGTAG	GCGCCTGGTGTGTCGTAACCTT CAGCAGAGCGGTGATGTCGTA	CGCGCTGCCGAAGATGACTGCCCGCCGAGCGCG
<i>fadD26</i> (rv2930)	TGGTCTCCGGGTTGACGAT	GGGCCTGATTCTCGGAATTT GCACGGCCAGCTCGAAG	CGCGACATTTTTGCGCCGTCCGGCCCGTCGCG
<i>fadD28</i> (rv2941)	CCCAGTCTAGCCATCGCGTCCT	CGACGAGAGTGAGCGCACGTT CCTGAGTCGCCGTTCTTAGCC	CCGCGTACCCTTCGCCGGGCACACCCACGCGG
<i>papA5</i> (rv2939)	GCCCGATCTCAGCGAGGTAAGA	ATGAGATCCCTGCCACCGAGAC GAACGCCATGAGGTCCGATGT	ACCGGCTCGCGCATCCTGGGCTGCCCGCCGGT
<i>pks2</i> (rv3825c)	GTC GGC GTG CTG CTG TAT CCA	GCGGGCGGCAGTGTGCTCT CGAGGAAGCGGACAGCGTGAA	ACCGCGACCGAAGCCCAGCCCCACGCGCGGGT
<i>plsC</i> (rv2483c)	TCTTTGTAGCCGCTTCGTC	ATCTTCAACCACCGCAACCAG CGGGTCGCTCGCCAGT	ACCGCCGCGACAACCTGGGTTGGGGTGGGCGGT

SI Table 8 (continued)

Gene	RT primers	PCR primers	Molecular beacons
<i>rv2182c</i>	ACGTACTCCTGACCCGAGAGC	CCATCGACCGCACCAATG CCTTTGTAGAGCCGACCGTCC	AGCGGCACGGCAGTGGTGTGCTGGGTCAGGCCGCT
<i>tgs1</i> (<i>rv3130c</i>)	AGGGACCTTTGCTGCGCTGTA	GCTAGCTGGGCTCTCCGATGAA AACGCCTCGCTTGGATTGACA	AGGCCCGCAAGCAACATCCACACGACCATGGGCCT
<i>rv3734c</i>	CAAACCGGCCGTCGTTCCAGC	TCCAGCCCATGTTCCGAAAGCA CCGAGCGGCGAACGTGGTAATC	AGCGCCCCGTGTGGCATGGGCTTATGACGGCGCT
<i>rv3371</i>	GCGCCACACCCAGTTCGATA	CATCCCGCCACCGCACT CGGCGTCATAGTCAGCGGTGA	AGCCGGGGATCGCGGTCCTCAGCTACGGCCGCT

Nucleotide sequences were obtained from <http://genolist.pasteur.fr/TubercuList/>. RT and PCR primers (shown in the 5' to 3' direction, one primer per line) were designed by using the software Oligo 6.6 (Molecular Biology Insights, Cascade, Colo.) and were purchased from Integrated DNA Technologies (Coralville, Iowa). Molecular beacons, which are hairpin-shaped oligonucleotide probes that become fluorescent upon hybridization to their target sequence (Tyagi & Kramer 1996), were synthesized by Biosearch Technologies (Novato, Calif.). Hairpin stability of molecular beacons was estimated by using the DNA folding program available at <http://www.bioinfo.rpi.edu/zukerm>. Molecular beacons are labeled at 5' with FAM (iodoacetamide derivative of fluorescein (5-iodoacetamidofluorescein)) and at 3' with Dabcyl (4-(4'-dimethylaminophenylazo)-benzoic acid) succinimidyl ester). The nucleotide sequences of primers and molecular beacon for *M. tuberculosis* 16S rRNA were published previously (Shi et al., 2003).

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