

Supplemental Table S3: Homologs of enzymes of the methylerythritol phosphate pathway are present in all 20 isolates of *Rhodococcus*

	DXPS*	DXPR*	CMS*	CMK*	MCS*	HDS*	IDS*	IDI1*
<i>Nocardia farcinia</i> [^]	YP_119953	YP_120333	YP_116642	YP_121117	YP_116643	YP_120331	YP_121011	YP_118189
GIC26	RFGIC26_02338 72.35; 0.0	RFGIC26_02145 74.13; 0.0	RFGIC26_00763 66.35; 2e-82	RFGIC26_03805 75.90; 5e-161	RFGIC26_00764 81.82; 1e-83	RFGIC26_02147 87.34; 0.0	RFGIC26_01206 84.48; 0.0	RFGIC26_02627 43.40; 2e-29
GIC36	RFGIC36_02362 72.35; 0.0	RFGIC36_02108 73.87; 0.0	RFGIC36_00754 65.71; 4e-81	RFGIC36_03898 76.22; 1e-161	RFGIC36_00755 82.47; 1e-83	RFGIC36_02110 87.34; 0.0	RFGIC36_01284 84.18; 0.0	RFGIC36_02651 43.40; 2e-29
05-561-1	RF05561_02716 72.31; 0.0	RF05561_02520 74.13; 0.0	RF05561_00754 65.40; 2e-80	RF05561_04429 75.90; 7e-161	RF05561_00755 82.47; 1e-83	RF05561_02522 87.34; 0.0	RF05561_01245 84.18; 0.0	RF05561_02957 43.40; 2e-29
LMG3605	RF3605_02508 72.51; 0.0	RF3605_02175 73.87; 0.0	RF3605_04159 65.88; 1e-81	RF3605_03773 76.22; 2e-161	RF3605_04158 82.47; 1e-83	RF3605_02177 87.34; 0.0	RF3605_01317 84.18; 0.0	RF3605_02797 43.40; 1e-29
<i>D188</i>	RFD188_02269 72.51; 0.0	RFD188_02074 73.87; 0.0	RFD188_00725 65.88; 1e-81	RFD188_03538 76.22; 3e-161	RFD188_00726 82.47; 1e-83	RFD188_02076 87.34; 0.0	RFD188_01214 84.18; 0.0	RFD188_02558 43.40; 1e-29
LMG3602	RF3602_03412 72.51; 0.0	RF3602_03060 74.40; 0.0	RF3602_00204 65.71; 2e-81	RF3602_04805 76.22; 1e-161	RF3602_00203 82.47; 1e-83	RF3602_03062 87.34; 0.0	RF3602_02266 84.18; 0.0	RF3602_03698 42.77; 3e-29
LMG3616	RF3616_02691 72.51; 0.0	RF3616_02316 73.87; 0.0	RF3616_00833 66.35; 2e-82	RF3616_03691 76.22; 2e-161	RF3616_00834 82.47; 1e-83	RF3616_02318 87.86; 0.0	RF3616_01325 84.18; 0.0	RF3616_02978 42.77; 3e-29
A3b	RFA3b_02032 72.35; 0.0	RFA3b_01766 74.13; 0.0	RFA3b_00611 66.35; 3e-82	RFA3b_03832 76.22; 3e-161	RFA3b_00612 82.47; 1e-83	RFA3b_01768 87.08; 0.0	RFA3b_01082 83.88; 0.0	RFA3b_02350 42.77; 3e-29
LMG3623	RF3623_02067 72.51; 0.0	RF3623_01470 73.87; 0.0	RF3623_00294 65.88; 2e-81	RF3623_03568 76.22; 2e-161	RF3623_00295 82.47; 1e-83	RF3623_01472 87.34; 0.0	RF3623_04267 84.18; 0.0	RF3623_02356 42.77; 3e-29
A78	RFA78_02580 72.35; 0.0	RFA78_02388 73.87; 0.0	RFA78_00866 65.71; 7e-82	RFA78_03918 76.22; 4e-161	RFA78_00867 81.82; 4e-83	RFA78_02390 87.34; 0.0	RFA78_01369 84.18; 0.0	RFA78_02867 43.40; 2e-29
A21d2	RFA21d2_01886 72.86; 0.0	RFA21d2_01613 74.13; 0.0	RFA21d2_00584 65.88; 2e-81	RFA21d2_04036 75.42; 5e-158	RFA21d2_00585 80.79; 1e-82	RFA21d2_01615 87.60; 0.0	RFA21d2_01116 84.48; 0.0	RFA21d2_02183 40.61; 6e-26
04-516	RF04516_02331 72.70; 0.0	RF04516_02140 73.87; 4e-180	RF04516_05280 66.35; 3e-82	RF04516_01001 75.42; 5e-158	RF04516_05281 80.79; 1e-82	RF04516_02142 87.60; 0.0	RF04516_00530 84.48; 0.0	RF04516_02628 40.61; 6e-26
A25f	RFA25f_02996 73.02; 0.0	RFA25f_02802 74.13; 0.0	RFA25f_00482 65.88; 3e-82	RFA25f_02465 75.08; 2e-157	RFA25f_00483 80.79; 1e-82	RFA25f_02804 87.60; 0.0	RFA25f_01062 84.48; 0.0	RFA25f_03300 40.61; 1e-25
LMG3625	RF3625_04912 73.02; 0.0	RF3625_03926 73.87; 3e-180	RF3625_02426 66.35; 5e-83	RF3625_04242 74.91; 2e-151	RF3625_02427 80.79; 1e-82	RF3625_03928 87.34; 0.0	RF3625_02964 83.88; 0.0	RF3625_05210 40.00; 5e-25
05-339-1	RF05339_02297 72.83; 0.0	RF05339_02107 74.06; 0.0	RF05339_00278 65.07; 1e-77	RF05339_04009 75.42; 3e-157	RF05339_00277 79.87; 4e-83	RF05339_02109 87.60; 0.0	RF05339_01291 84.18; 0.0	RF05339_02591 41.21; 3e-26
A76	RFA76_02494 72.83; 0.0	RFA76_02302 74.40; 0.0	RFA76_05363 65.14; 2e-85	RFA76_03930 75.42; 3e-157	RFA76_05364 79.87; 3e-83	RFA76_02304 87.60; 0.0	RFA76_01654 84.18; 0.0	RFA76_02795 40.34; 4e-27
<i>A44a</i>	RFA44a_02292 74.13; 0.0	RFA44a_02099 74.40; 0.0	RFA44a_00645 65.47; 4e-88	RFA44a_05247 76.55; 5e-162	RFA44a_00646 81.46; 5e-82	RFA44a_02101 89.38; 0.0	RFA44a_01139 83.28; 0.0	RFA44a_01395 41.21; 4e-26
02-815	RF02815_02526 74.13; 0.0	RF02815_02333 74.40; 0.0	RF02815_01093 64.57; 4e-86	RF02815_04653 76.55; 6e-162	RF02815_01094 81.46; 5e-82	RF02815_02335 89.38; 0.0	RF02815_01297 83.28; 0.0	RF02815_02069 40.61; 2e-25
02-816c	RF02816c_02438 74.13; 0.0	RF02816c_02246 74.40; 0.0	RF02816c_00772 65.02; 6e-87	RF02816c_04485 76.55; 6e-162	RF02816c_00773 81.46; 5e-82	RF02816c_02248 89.38; 0.0	RF02816c_01507 83.28; 0.0	RF02816c_01700 40.61; 2e-25
A73a	RFA73a_02592 74.13; 0.0	RFA73a_02400 74.40; 0.0	RFA73a_00558 64.57; 4e-86	RFA73a_01123 76.55; 5e-162	RFA73a_00559 81.46; 5e-82	RFA73a_02402 89.38; 0.0	RFA73a_01858 83.28; 0.0	RFA73a_01567 40.61; 2e-25

*Locus; % identity; BLAST e-value. Column abbreviations: Deoxyxylulose 5-phosphate synthase (DXPS); DXP reductoisomerase (DXPR); isopentenyl diphosphate isomerase (IDI1); 4-diphosphocytidyl-2C-methyl-D-erythriol synthase (CMS); 4-(cytidine 5'-diphospho)-2-C-methyl-D-

erythritol kinase (CMK); 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MCS); hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (HDS); hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (HDR); No homologs of the MEP pathway were identified: 3-hydroxy-3-methylglutaryl-CoA synthase (HMGS; *N. farcinia*; YP_118423); 3-hydroxy-3-methylglutaryl-CoA reductase (HMGR; class I; *N. farcinia*; YP_118422); Mevalonate Kinase (MVK; *N. farcinia*; YP_118418); Phosphomevalonate kinase (PMK; *N. farcinia*; YP_118420); Mevalonate-5-decarboxylase (MDC; *N. farcinia*; YP_118419). YP_118418 identified homologs in isolates of sub-clades i and ii but e-values ranged from $6e-10$ ~ $3e-10$ and CDSs are annotated as galactokinase. ^Genbank ID number of sequence used for BLAST searches.