**Supporting Information Table S2: Probe-sets uniquely present in PC III and IV strains serotype 1/2a**

|  |  |
| --- | --- |
| **Probe ID** | **Annotation** |
| AARI\_0190\_s\_at | 98% similar to lmo1117 |
| AARI\_0343\_s\_at | 99% similar to lmo0444 |
| AARI\_0426\_at | 98% similar to lmo0774 |
| AARI\_0438\_s\_at | 100% similar to lmo2500 |
| AARI\_0440\_at | 100% similar to lmo0444 |
| AARI\_0504\_s\_at | 99% similar to lmo2237 |
| AARI\_0522\_s\_at | NK |
| AARI\_0545\_at | 99% similar to lmo1825 |
| AARI\_0551\_s\_at | 99% similar to lmo0446 |
| AARI\_0571\_s\_at | 100% similar to lmo2734 |
| AARI\_0643\_s\_at | 100% similar to LMHCC\_1725 |
| AARI\_0695\_x\_at | 99% similar to lmo0107 |
| AARK\_0177\_s\_at | 99% similar to LMHCC\_2322 |
| AARK\_0874\_s\_at | NK |
| AARK\_1149\_s\_at | 99% similar to LMOf2365\_0299 |
| AARK\_1531\_s\_at | 99% similar to LMOf2365\_1024 |
| AARK\_1677\_at | 99% similar to LMHCC\_2212 |
| AARK\_1780\_x\_at | 100% similar to LMOf2365\_0394 |
| AARK\_1899\_s\_at | 99% similar to LMOf2365\_1790 |
| AARK\_1928\_s\_at | 99% similar to LMOf2365\_2050 |
| AARL\_0174\_x\_at | NK |
| AARL\_0331\_at | NK |
| AARL\_0491\_s\_at | NK |
| AARL\_0520\_s\_at | NK |
| AARL\_0588\_s\_at | NK |
| AARL\_0679\_s\_at | NK |
| AARL\_0701\_s\_at | 98% similar to LMHCC\_1450 |
| AARL\_0833\_at | NK |
| AARL\_0900\_s\_at | NK |
| AARL\_0900\_x\_at | NK |
| AARM\_0062\_s\_at | NK |
| AARM\_0105\_x\_at | NK |
| AARM\_0157\_s\_at | 99% similar to lmo2720 |
| AARM\_0206\_s\_at | 99% similar to lmo0269 |
| AARM\_0408\_s\_at | 100% similar to lmo0030 |
| AARM\_0645\_s\_at | 98% similar to LMHCC\_0797 |
| AARM\_0699\_s\_at | 99% similar to lmo1512 |
| AARM\_0845\_s\_at | 100% similar to lmo1453 |
| AARM\_0869\_s\_at | NK |
| AARM\_1167\_x\_at | NK |
| AARM\_1201\_x\_at | 98% similar to LMOf2365\_1121 |
| AARM\_1413\_s\_at | 98% similar to lmo2444 |
| AARM\_1440\_s\_at | NK |
| AARM\_1460\_s\_at | 100% similar to lmo1258 |
| AARM\_1461\_s\_at | 99% similar to lmo1259 |
| AARM\_1501\_s\_at | NK |
| AARM\_1646\_x\_at | 98% similar to lmo1861 |
| AARM\_1650\_x\_at | NK |
| AARM\_1717\_x\_at | NK |
| AARM\_1737\_x\_at | 98% similar to lmo1985 |
| AARO\_0340\_s\_at | 99% similar to LMOf2365\_1597 |
| AARO\_0378\_at | NK |
| AARO\_1179\_at | NK |
| AARO\_1417\_s\_at | 99% similar to LMOf2365\_1784 |
| AARO\_1609\_s\_at | 100% similar to LMOf2365\_2475 |
| AARO\_1820\_x\_at | 99% similar to lmo0304 |
| AARO\_1856\_s\_at | 99% similar to lmo0448 |
| AARY\_0032\_x\_at | 100% similar to lmo0107 |
| AARY\_0039\_s\_at | 100% similar to lmo0121 |
| AARY\_0142\_x\_at | 100% similar to lmo0458 |
| AARY\_0249\_s\_at | 100% similar to lmo0915 |
| AARY\_0260\_at | NK |
| AARY\_0261\_at | NK |
| AARY\_0262\_at | NK |
| AARY\_0316\_s\_at | 100% similar to lmo0563 |
| AARY\_0361\_s\_at | 100% similar to lmo1606 |
| AARY\_0396\_s\_at | 100% similar to lmo2143 |
| AARY\_0644\_x\_at | 100% similar to lmo0520 |
| AARY\_0668\_s\_at | 99% similar to lmo0535 |
| AARY\_0777\_s\_at | 100% similar to lmo1116 |
| AARY\_0821\_s\_at | 100% similar to lmo2839 |
| AARY\_0880\_s\_at | 98% similar to lmo1689 |
| AARY\_1012\_s\_at | 100% similar to lmo1513 |
| AARY\_1056\_s\_at | 99% similar to lmo1666 |
| AARY\_1084\_s\_at | 100% similar to lmo0444 |
| AARY\_1294\_s\_at | 100% similar to lmo1798 |
| AARY\_1307\_s\_at | 100% similar to lmo1479 |
| AARY\_1352\_x\_at | 100% similar to lmo2674 |
| AARY\_1544\_s\_at | 100% similar to lmo1513 |
| IGLMHCC\_0060\_at | intergenic region |
| IGLMHCC\_0060\_x\_at | intergenic region |
| IGLMHCC\_0212\_x\_at | intergenic region |
| IGLMHCC\_0407\_at | intergenic region |
| IGLMHCC\_0512\_at | intergenic region |
| IGLMHCC\_0575\_at | intergenic region |
| IGLMHCC\_0575\_x\_at | intergenic region |
| IGLMHCC\_0803\_at | intergenic region |
| IGLMHCC\_0997\_at | intergenic region |
| IGLMHCC\_0997\_x\_at | intergenic region |
| IGLMHCC\_0999\_at | intergenic region |
| IGLMHCC\_1462\_at | intergenic region |
| IGLMHCC\_1513\_s\_at | intergenic region |
| IGLMHCC\_1663\_x\_at | intergenic region |
| IGLMHCC\_1703\_x\_at | intergenic region |
| IGLMHCC\_1841\_at | intergenic region |
| IGLMHCC\_1996\_x\_at | intergenic region |
| IGLMHCC\_2144\_x\_at | intergenic region |
| IGLMHCC\_2146\_x\_at | intergenic region |
| IGLMHCC\_2323\_at | intergenic region |
| IGLMHCC\_2325\_at | intergenic region |
| IGLMHCC\_2326\_at | intergenic region |
| IGLMHCC\_2350\_at | intergenic region |
| IGLMHCC\_2351\_at | intergenic region |
| IGLMHCC\_2834\_at | intergenic region |
| IGlmo0105\_at | intergenic region |
| IGlmo0105\_x\_at | intergenic region |
| IGlmo0133\_at | intergenic region |
| IGlmo0133\_x\_at | intergenic region |
| IGlmo0135\_at | intergenic region |
| IGlmo0149\_s\_at | intergenic region |
| IGlmo0258\_at | intergenic region |
| IGlmo0304\_at | intergenic region |
| IGlmo0304\_x\_at | intergenic region |
| IGlmo0363\_at | intergenic region |
| IGlmo0363\_x\_at | intergenic region |
| IGlmo0364\_x\_at | intergenic region |
| IGlmo0365\_x\_at | intergenic region |
| IGlmo0378\_at | intergenic region |
| IGlmo0407\_x\_at | intergenic region |
| IGlmo0444\_at | intergenic region |
| IGlmo0445\_at | intergenic region |
| IGlmo0446\_at | intergenic region |
| IGlmo0447\_at | intergenic region |
| IGlmo0448\_at | intergenic region |
| IGlmo0449\_at | intergenic region |
| IGlmo0510\_at | intergenic region |
| IGlmo0559\_at | intergenic region |
| IGlmo0801\_at | intergenic region |
| IGlmo0908\_x\_at | intergenic region |
| IGlmo1031\_at | intergenic region |
| IGlmo1031\_x\_at | intergenic region |
| IGlmo1117\_x\_at | intergenic region |
| IGlmo1122\_x\_at | intergenic region |
| IGlmo1125\_at | intergenic region |
| IGlmo1125\_x\_at | intergenic region |
| IGlmo1140\_at | intergenic region |
| IGlmo1140\_x\_at | intergenic region |
| IGlmo1243\_at | intergenic region |
| IGlmo1243\_x\_at | intergenic region |
| IGlmo1253\_at | intergenic region |
| IGlmo1256\_at | intergenic region |
| IGlmo1256\_x\_at | intergenic region |
| IGlmo1257\_at | intergenic region |
| IGlmo1258\_at | intergenic region |
| IGlmo1258\_x\_at | intergenic region |
| IGlmo1261\_at | intergenic region |
| IGlmo1261\_x\_at | intergenic region |
| IGlmo1276\_s\_at | intergenic region |
| IGlmo1348\_at | intergenic region |
| IGlmo1600\_x\_at | intergenic region |
| IGlmo1613\_x\_at | intergenic region |
| IGlmo1796\_at | intergenic region |
| IGlmo2085\_x\_at | intergenic region |
| IGlmo2116\_x\_at | intergenic region |
| IGlmo2145\_at | intergenic region |
| IGlmo2145\_x\_at | intergenic region |
| IGlmo2365\_s\_at | intergenic region |
| IGlmo2392\_x\_at | intergenic region |
| IGlmo2394\_at | intergenic region |
| IGlmo2408\_at | intergenic region |
| IGlmo2411\_at | intergenic region |
| IGlmo2565\_x\_at | intergenic region |
| IGlmo2926\_at | intergenic region |
| IGLMOf2365\_0314\_s\_at | intergenic region |
| IGLMOf2365\_0383\_s\_at | intergenic region |
| IGLMOf2365\_0485\_s\_at | intergenic region |
| IGLMOf2365\_0500\_s\_at | intergenic region |
| IGLMOf2365\_0501\_x\_at | intergenic region |
| IGLMOf2365\_0502\_s\_at | intergenic region |
| IGLMOf2365\_0517\_x\_at | intergenic region |
| IGLMOf2365\_0638\_x\_at | intergenic region |
| IGLMOf2365\_0810\_at | intergenic region |
| IGLMOf2365\_0897\_x\_at | intergenic region |
| IGLMOf2365\_1000\_at | intergenic region |
| IGLMOf2365\_1121\_x\_at | intergenic region |
| IGLMOf2365\_1129\_s\_at | intergenic region |
| IGLMOf2365\_1751\_at | intergenic region |
| IGLMOf2365\_1906\_x\_at | intergenic region |
| IGLMOf2365\_2019\_x\_at | intergenic region |
| IGLMOf2365\_2159\_at | intergenic region |
| IGLMOf2365\_2234\_x\_at | intergenic region |
| IGLMOf2365\_2236\_x\_at | intergenic region |
| IGLMOf2365\_2289\_at | intergenic region |
| IGLMOf2365\_2381\_s\_at | intergenic region |
| IGLMOf2365\_2556\_x\_at | intergenic region |
| IGLMOf2365\_2564\_s\_at | intergenic region |
| IGLMOf2365\_2616\_x\_at | intergenic region |
| IGLMOf2365\_2626\_x\_at | intergenic region |
| IGLMOf2365\_2749\_x\_at | intergenic region |
| IGLMOf2365\_2848\_s\_at | intergenic region |
| Lm4b\_00080a\_s\_at | Hypothetical protein of unknown function |
| Lm4b\_00080b\_s\_at | Hypothetical protein of unknown function |
| Lm4b\_01119\_x\_at | Hypothetical protein of unknown function/GI=225876179 |
| Lm4b\_02561\_s\_at | Hypothetical protein of unknown function/GI=225877602 |
| LMBG\_00131\_x\_at | conserved hypothetical protein |
| LMBG\_02371\_s\_at | predicted protein |
| LMFG\_01868\_x\_at | phage protein |
| LMFG\_02839\_at | conserved hypothetical protein |
| LMFG\_02936\_s\_at | predicted protein |
| LMFG\_03054\_s\_at | predicted protein |
| LMFG\_03054\_x\_at | predicted protein |
| LMHCC\_0718\_s\_at | pyrB aspartate carbamoyltransferase/GI=217333279 |
| LMHCC\_0798\_s\_at | purN phosphoribosylglycinamide formyltransferase/GI=217333356 |
| LMHCC\_0798\_x\_at | purN phosphoribosylglycinamide formyltransferase/GI=217333356 |
| LMHCC\_0924\_s\_at | muramoyl-tetrapeptide carboxypeptidase family/GI=217333479 |
| LMHCC\_0959\_s\_at | 2-Cys peroxiredoxin BAS1, (Thiol-specific antioxidant protein)/GI=217333513 |
| LMHCC\_0960\_s\_at | aminopeptidase protein/GI=217333514 |
| LMHCC\_0995\_s\_at | accD acetyl-CoA carboxylase, carboxyl transferase, beta subunit/GI=217333549 |
| LMHCC\_0996\_s\_at | accA acetyl-CoA carboxylase, carboxyl transferase, alpha subunit/GI=217333550 |
| LMHCC\_0997\_s\_at | hypothetical protein/GI=217333551 |
| LMHCC\_1074\_at | transcription elongation factor GreA (Transcript cleavage factor greA)(General stress protein 20M) (GSP20M)/GI=217333628 |
| LMHCC\_1212\_s\_at | nusB transcription antitermination factor NusB/GI=217333765 |
| LMHCC\_1319\_s\_at | treC alpha,alpha-phosphotrehalase/GI=217333870 |
| LMHCC\_1319\_x\_at | treC alpha,alpha-phosphotrehalase/GI=217333870 |
| LMHCC\_1346\_at | gp30/GI=217333897 |
| LMHCC\_1347\_s\_at | gp29/GI=217333898 |
| LMHCC\_1348\_s\_at | gp28/GI=217333899 |
| LMHCC\_1401\_s\_at | conserved hypothetical protein/GI=217333952 |
| LMHCC\_1512\_s\_at | conserved hypothetical protein/GI=217334062 |
| LMHCC\_1675\_s\_at | inner membrane transport protein YeaN/GI=217334223 |
| LMHCC\_1677\_s\_at | late competence protein/GI=217334225 |
| LMHCC\_1815\_x\_at | HD domain protein/GI=217334362 |
| LMHCC\_2177\_s\_at | membrane protein, putative/GI=217334721 |
| LMHCC\_2190\_s\_at | YtfG protein, putative/GI=217334734 |
| LMHCC\_2254\_x\_at | DNA-binding protein IolR/GI=217334798 |
| LMHCC\_2323\_s\_at | conserved hypothetical protein/GI=217334866 |
| LMHCC\_2324\_s\_at | conserved hypothetical protein/GI=217334867 |
| LMHCC\_2350\_s\_at | hypothetical protein/GI=217334893 |
| LMHCC\_2351\_s\_at | membrane protein, putative/GI=217334894 |
| LMHCC\_2489\_s\_at | conserved hypothetical protein/GI=217335030 |
| LMHCC\_2505\_s\_at | EAL domain protein/GI=217335046 |
| LMHCC\_2718\_s\_at | conserved hypothetical protein/GI=217335259 |
| LMHCC\_2784\_s\_at | general stress protein 26 (GSP26)/GI=217335324 |
| LMHCC\_2872\_x\_at | rpiB ribose 5-phosphate isomerase B/GI=217335409 |
| LMHCC\_2899\_s\_at | 1,4-dihydroxy-2-naphthoate octaprenyltransferase/GI=217335436 |
| LMHG\_02050\_s\_at | PTS system protein/Pfam=PF02378.10 |
| LMHG\_02326\_x\_at | acetylCoA carboxylase |
| LMHG\_02578\_x\_at | conserved hypothetical protein/Pfam=PF02618.8 |
| LMHG\_02630\_s\_at | formate dehydrogenase/Pfam=PF04879.8 |
| LMHG\_02651\_x\_at | phosphoribosylaminoimidazolecarboxamide formyltransferase/Pfam=PF00551.11 |
| LMHG\_02737\_s\_at | conserved hypothetical protein |
| LMIG\_00094\_s\_at | hydrolase/Pfam=PF00561.12 |
| LMIG\_00113\_s\_at | conserved hypothetical protein/Pfam=PF02733.9 |
| LMIG\_00356\_s\_at | Disomer specific 2hydroxyacid dehydrogenase/Pfam=PF02826.11 |
| LMIG\_00397\_s\_at | antigen B |
| LMIG\_00412\_s\_at | inositol5monophosphate dehydrogenase/Pfam=PF00571.20 |
| LMIG\_00640\_s\_at | deoxyribosephosphate aldolase/Pfam=PF01791.1 |
| LMIG\_01617\_s\_at | peptide chain release factor 1/Pfam=PF03462.10 |
| LMIG\_01642\_s\_at | transcriptional regulator/Pfam=PF00532.13 |
| LMIG\_01855\_x\_at | conserved hypothetical protein/Pfam=PF04794.4 |
| LMIG\_02087\_x\_at | conserved hypothetical protein |
| LMIG\_02163\_s\_at | conserved hypothetical protein/Pfam=PF09375.2 |
| LMIG\_02166\_s\_at | conserved hypothetical protein/Pfam=PF01709.12 |
| LMIG\_02311\_x\_at | glyoxalase/Pfam=PF00903.17 |
| LMIG\_02689\_x\_at | conserved hypothetical protein/Pfam=PF06993.4 |
| LMIG\_02874\_s\_at | truB |
| LMIG\_02875\_s\_at | predicted protein |
| LMJG\_00033\_s\_at | conserved hypothetical protein |
| LMJG\_00766\_x\_at | ABC transporter/Pfam=PF01061.16 |
| LMKG\_00550\_x\_at | conserved hypothetical protein/Pfam=PF07301.3 |
| LMKG\_00871\_at | predicted protein |
| LMKG\_00871\_x\_at | predicted protein |
| LMKG\_00998\_s\_at | phage protein |
| LMKG\_01388\_s\_at | predicted protein |
| LMKG\_01598\_at | 6phosphobetaglucosidase |
| LMKG\_01598\_x\_at | 6phosphobetaglucosidase |
| LMKG\_01794\_at | predicted protein |
| LMKG\_01813\_s\_at | conserved hypothetical protein |
| LMKG\_02058\_s\_at | predicted protein |
| LMKG\_02149\_s\_at | autolysin/Pfam=PF01832.12 |
| LMKG\_02734\_at | predicted protein |
| LMKG\_02734\_s\_at | predicted protein |
| LMKG\_02734\_x\_at | predicted protein |
| LMLG\_00022\_s\_at | predicted protein |
| LMLG\_00088\_at | conserved hypothetical protein |
| LMLG\_00089\_s\_at | predicted protein |
| LMLG\_00089\_x\_at | predicted protein |
| LMLG\_00419\_s\_at | conserved hypothetical protein/Pfam=PF06824.3 |
| LMLG\_00739\_s\_at | conserved hypothetical protein |
| LMLG\_00751\_s\_at | PRDPTS system IIA 2 domain-containing protein/Pfam=PF08280.3 |
| LMLG\_00788\_at | conserved hypothetical protein/Pfam=PF07687.6 |
| LMLG\_00805\_x\_at | conserved hypothetical protein/Pfam=PF08242.4 |
| LMLG\_01061\_s\_at | precorrin3B C17methyltransferase |
| LMLG\_01313\_s\_at | conserved hypothetical protein |
| LMLG\_01353\_at | predicted protein |
| LMLG\_01501\_s\_at | alcohol dehydrogenase |
| LMLG\_01504\_s\_at | glutamate synthase/Pfam=PF04898.6 |
| LMLG\_01956\_s\_at | 2oxoisovalerate dehydrogenase E3/Pfam=PF07992.6 |
| LMLG\_02051\_s\_at | malonyl CoAacyl carrier protein transacylase/Pfam=PF00698.13 |
| LMLG\_02080\_s\_at | dihydroorotase/Pfam=PF01979.12 |
| LMLG\_02235\_s\_at | conserved hypothetical protein |
| LMLG\_02292\_s\_at | formate acetyltransferase |
| LMLG\_02461\_s\_at | conserved hypothetical protein/Pfam=PF03466.12 |
| LMLG\_02500\_x\_at | conserved hypothetical protein |
| LMLG\_02550\_s\_at | conserved hypothetical protein/Pfam=PF01370.13 |
| LMLG\_02587\_s\_at | conserved hypothetical protein |
| LMLG\_02609\_s\_at | conserved hypothetical protein |
| LMLG\_02754\_s\_at | conserved hypothetical protein/Pfam=PF00293.20 |
| LMLG\_02857\_x\_at | conserved hypothetical protein/Pfam=PF00746.13 |
| LMMG\_03049\_x\_at | conserved hypothetical protein |
| lmo0107\_s\_at | GI=16409466 |
| lmo0147\_s\_at | GI=16409506 |
| lmo0179\_s\_at | GI=16409536 |
| lmo0243\_x\_at | sigH RNA polymerase sigma-30 factor (sigma-H)/GI=16409608 |
| lmo0265\_s\_at | GI=16409630 |
| lmo0284\_s\_at | GI=16409649 |
| lmo0318\_s\_at | GI=16409682 |
| lmo0362\_x\_at | GI=16409740 |
| lmo0363\_s\_at | GI=16409741 |
| lmo0364\_s\_at | GI=16409742 |
| lmo0366\_s\_at | GI=16409744 |
| lmo0370\_s\_at | GI=16409748 |
| lmo0377\_x\_at | GI=16409755 |
| lmo0378\_s\_at | GI=16409756 |
| lmo0379\_s\_at | GI=16409757 |
| lmo0382\_x\_at | GI=16409760 |
| lmo0445\_s\_at | GI=16409822 |
| lmo0447\_s\_at | GI=16409824 |
| lmo0495\_s\_at | GI=16409871 |
| lmo0635\_s\_at | GI=16410024 |
| lmo0676\_s\_at | GI=16410065 |
| lmo0697\_s\_at | GI=16410086 |
| lmo0758\_s\_at | GI=16410147 |
| lmo0800\_s\_at | GI=16410189 |
| lmo0809\_s\_at | GI=16410198 |
| lmo0854\_s\_at | GI=16410257 |
| lmo0862\_s\_at | GI=16410265 |
| lmo0907\_s\_at | GI=16410310 |
| lmo0945\_x\_at | GI=16410347 |
| lmo0973\_s\_at | dltB DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid/GI=16410375 |
| lmo1117\_x\_at | GI=16410519 |
| lmo1120\_s\_at | GI=16410522 |
| lmo1122\_s\_at | GI=16410524 |
| lmo1141\_s\_at | GI=16410557 |
| lmo1203\_s\_at | cbiL GI=16410619 |
| lmo1242\_s\_at | GI=16410658 |
| lmo1243\_s\_at | GI=16410659 |
| lmo1255\_s\_at | GI=16410671 |
| lmo1256\_s\_at | GI=16410672 |
| lmo1257\_s\_at | GI=16410673 |
| lmo1260\_s\_at | proB gamma-glutamyl kinase/GI=16410676 |
| lmo1261\_s\_at | GI=16410677 |
| lmo1346\_s\_at | comGB GI=16410762 |
| lmo1347\_s\_at | comGA GI=16410763 |
| lmo1348\_s\_at | GI=16410764 |
| lmo1372\_s\_at | GI=16410788 |
| lmo1407\_s\_at | pflC pyruvate-formate lyase activating enzyme/GI=16410836 |
| lmo1427\_s\_at | opuCB GI=16410856 |
| lmo1453\_s\_at | GI=16410882 |
| lmo1479\_s\_at | lepA GI=16410908 |
| lmo1512\_s\_at | GI=16410941 |
| lmo1595\_s\_at | GI=16411024 |
| lmo1598\_s\_at | tyrS tyrosyl-tRNA synthetase/GI=16411027 |
| lmo1737\_s\_at | GI=16411191 |
| lmo1803\_s\_at | GI=16411257 |
| lmo1985\_s\_at | ilvN GI=16411438 |
| lmo1985\_x\_at | ilvN GI=16411438 |
| lmo2018\_s\_at | GI=16411471 |
| lmo2036\_s\_at | murD GI=16411506 |
| lmo2061\_s\_at | GI=16411531 |
| lmo2143\_s\_at | GI=16411613 |
| lmo2144\_s\_at | GI=16411614 |
| lmo2345\_s\_at | GI=16411833 |
| lmo2362\_s\_at | GI=16411850 |
| lmo2364\_s\_at | Hypothetical protein/GI=16411852 |
| lmo2371\_s\_at | GI=16411859 |
| lmo2374\_s\_at | GI=16411862 |
| lmo2405\_x\_at | GI=16411893 |
| lmo2408\_at | GI=16411896 |
| lmo2409\_at | GI=16411897 |
| lmo2410\_at | GI=16411898 |
| lmo2497\_s\_at | GI=16411985 |
| lmo2503\_s\_at | GI=16411991 |
| lmo2583\_s\_at | GI=16412071 |
| lmo2592\_s\_at | GI=16412080 |
| lmo2755\_s\_at | GI=16412255 |
| LMOf2365\_0253\_s\_at | RNA methyltransferase, TrmH family, group 3/GI=46879738 |
| LMOf2365\_0313\_s\_at | hypothetical protein/GI=46879799 |
| LMOf2365\_0480\_s\_at | putative transcriptional regulator/GI=46879962 |
| LMOf2365\_0500\_s\_at | hypothetical protein/GI=46879982 |
| LMOf2365\_0501\_s\_at | hypothetical protein/GI=46879983 |
| LMOf2365\_0504\_x\_at | HD domain protein/GI=46879986 |
| LMOf2365\_0519\_s\_at | NADH:flavin oxidoreductase/GI=46880000 |
| LMOf2365\_0651\_x\_at | conserved hypothetical protein/GI=46880133 |
| LMOf2365\_0670\_s\_at | putative transcriptional regulator/GI=46880151 |
| LMOf2365\_0828\_x\_at | HD domain protein/GI=46880308 |
| LMOf2365\_0883\_s\_at | hypothetical protein/GI=46880364 |
| LMOf2365\_0904\_s\_at | acpS holo-(acyl-carrier-protein) synthase/GI=46880385 |
| LMOf2365\_0919\_s\_at | conserved hypothetical protein/GI=46880399 |
| LMOf2365\_0920\_s\_at | hypothetical protein/GI=46880400 |
| LMOf2365\_1065\_s\_at | moaE molybdenum cofactor biosynthesis protein E/GI=46880543 |
| LMOf2365\_1126\_s\_at | conserved hypothetical protein/GI=46880603 |
| LMOf2365\_1127\_s\_at | conserved hypothetical protein/GI=46880604 |
| LMOf2365\_1170\_s\_at | pduM propanediol utilization protein PduM/GI=46880647 |
| LMOf2365\_1172\_s\_at | PduO protein/GI=46880649 |
| LMOf2365\_1228\_s\_at | conserved hypothetical protein/GI=46880706 |
| LMOf2365\_1298\_s\_at | transcriptional regulator CodY/GI=46880775 |
| LMOf2365\_1466\_s\_at | zurA2 zinc ABC transporter, ATP-binding protein/GI=46880943 |
| LMOf2365\_1759\_s\_at | gltC transcriptional regulator GltC/GI=46881235 |
| LMOf2365\_1789\_s\_at | purD phosphoribosylamine--glycine ligase/GI=46881264 |
| LMOf2365\_2227\_s\_at | oligopeptide ABC transporter, permease protein/GI=46881699 |
| LMOf2365\_2261\_s\_at | putative membrane protein/GI=46881733 |
| LMOf2365\_2381\_s\_at | conserved hypothetical protein/GI=46881853 |
| LMOf2365\_2469\_s\_at | phosphate ABC transporter, ATP-binding protein/GI=46881940 |
| LMOf2365\_2567\_at | hypothetical protein/GI=46882039 |
| LMOf2365\_2567\_x\_at | hypothetical protein/GI=46882039 |
| LMOf2365\_2607\_s\_at | cobalt transport protein/GI=46882079 |
| LMOf2365\_2714\_s\_at | conserved hypothetical protein/GI=46882186 |
| LMOf2365\_2724\_s\_at | transcriptional regulator, LacI family/GI=46882196 |
| LMOf6854\_0134\_s\_at | membrane protein, putative/GI=47016537 |
| LMOf6854\_0152\_s\_at | conserved hypothetical protein/GI=47014045 |
| LMOf6854\_0154\_s\_at | conserved hypothetical protein/GI=47014091 |
| LMOf6854\_0157\_x\_at | conserved hypothetical protein/GI=47014094 |
| LMOf6854\_0158\_at | conserved hypothetical protein/GI=47014095 |
| LMOf6854\_0193\_x\_at | oligo-1,6-glucosidase/GI=47015425 |
| LMOf6854\_0401\_s\_at | Iron permease FTR1 family family/GI=47014950 |
| LMOf6854\_0416\_at | hypothetical protein/GI=47015029 |
| LMOf6854\_0416\_x\_at | hypothetical protein/GI=47015029 |
| LMOf6854\_0417\_x\_at | conserved hypothetical protein/GI=47015030 |
| LMOf6854\_0502\_x\_at | conserved hypothetical protein/GI=47016835 |
| LMOf6854\_0597\_x\_at | phosphoglycerate mutase family protein/GI=47016930 |
| LMOf6854\_0618\_s\_at | membrane protein, putative/GI=47014735 |
| LMOf6854\_0856\_s\_at | HD domain protein/GI=47016699 |
| LMOf6854\_0909\_x\_at | conserved hypothetical protein/GI=47016752 |
| LMOf6854\_0977\_x\_at | conserved hypothetical protein/GI=47015362 |
| LMOf6854\_1105\_s\_at | pdhB pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit/GI=47015491 |
| LMOf6854\_1155\_s\_at | conserved hypothetical protein/GI=47016577 |
| LMOf6854\_1294\_x\_at | hypothetical protein/GI=47014581 |
| LMOf6854\_1295\_at | conserved hypothetical protein/GI=47014582 |
| LMOf6854\_1295\_x\_at | conserved hypothetical protein/GI=47014582 |
| LMOf6854\_1582\_s\_at | L-lactate dehydrogenase/GI=47013917 |
| LMOf6854\_1592\_s\_at | ribonuclease G/GI=47014890 |
| LMOf6854\_1628\_s\_at | CBS domain protein/GI=47014822 |
| LMOf6854\_1789\_s\_at | ABC transporter, permease protein/GI=47015942 |
| LMOf6854\_1795\_s\_at | alcohol dehydrogenase, iron-dependent/GI=47015948 |
| LMOf6854\_1854\_s\_at | glutamine amidotransferase, class-I/GI=47014031 |
| LMOf6854\_1941\_at | hypothetical protein/GI=47013989 |
| LMOf6854\_1972\_s\_at | conserved hypothetical protein/GI=47015149 |
| LMOf6854\_1990\_s\_at | hepB heptaprenyl diphosphate synthase, component II/GI=47013897 |
| LMOf6854\_2065\_s\_at | transcriptional regulator, GntR family/GI=47014968 |
| LMOf6854\_2111\_s\_at | conserved hypothetical protein/GI=47014353 |
| LMOf6854\_2405\_s\_at | amino acid ABC transporter, ATP-binding protein/GI=47015641 |
| LMOf6854\_2688\_s\_at | gp55/GI=47014132 |
| LMOf6854\_2712\_s\_at | cas2 CRISPR-associated protein Cas2/GI=47014481 |
| LMOf6854\_2713\_s\_at | cas1 CRISPR-associated protein Cas1/GI=47014482 |
| LMOf6854\_2715\_s\_at | conserved hypothetical protein/GI=47014484 |
| LMOf6854\_2759\_s\_at | conserved hypothetical protein/GI=47014495 |
| LMOf6854\_2817\_s\_at | phosphosugar-binding transcriptional regulator, RpiR family/GI=47016115 |
| LMOf6854\_2849\_s\_at | HAD-superfamily hydrolase, subfamily IA, variant 1/GI=47016147 |
| LMOf6854\_2953\_s\_at | alcohol dehydrogenase, zinc-dependent/GI=47014261 |
| LMOG\_00938\_s\_at | hypothetical protein similar to internalin |
| LMOG\_01931\_s\_at | hypothetical protein similar to internalin/Pfam=PF08191.3 |
| LMOG\_03220\_x\_at | conserved hypothetical protein/Pfam=PF00746.13 |
| LMOh7858\_0339\_s\_at | conserved hypothetical protein/GI=47020119 |
| LMOh7858\_0850\_s\_at | rarD protein/GI=47017830 |
| LMOh7858\_1186\_s\_at | conserved hypothetical protein/GI=47019631 |
| LMOh7858\_1187\_s\_at | conserved hypothetical protein/GI=47019632 |
| LMOh7858\_1833\_s\_at | map methionine aminopeptidase, type I/GI=47017382 |
| LMOh7858\_2088\_s\_at | iron compound ABC transporter, permease protein/GI=47017007 |
| LMOh7858\_2508\_at | hypothetical protein/GI=47019248 |
| LMPG\_03052\_s\_at | conserved hypothetical protein/Pfam=PF00746.13 |
| LMRG\_00002\_at | threonine aldolase family protein/Pfam=PF01212.13 |
| LMRG\_00003\_at | conserved hypothetical protein/Pfam=PF07252.3 |
| LMRG\_00004\_at | conserved hypothetical protein |
| LMRG\_00006\_at | conserved hypothetical protein/Pfam=PF07510.3 |
| LMRG\_00007\_x\_at | conserved hypothetical protein/Pfam=PF04794.4 |
| LMRG\_00011\_at | thiaminephosphate pyrophosphorylase/Pfam=PF02581.9 |
| LMRG\_00021\_at | conserved hypothetical protein/Pfam=PF06458.4 |
| LMRG\_00022\_x\_at | conserved hypothetical protein |
| LMRG\_00029\_at | conserved hypothetical protein/Pfam=PF06860.3 |
| LMRG\_00033\_x\_at | transketolase/Pfam=PF02780.12 |
| LMRG\_00058\_at | ywbM/Pfam=PF09375.2 |
| LMRG\_00058\_x\_at | ywbM/Pfam=PF09375.2 |
| LMRG\_00059\_s\_at | ipa29d/Pfam=PF04261.4 |
| LMRG\_00075\_x\_at | IolR/Pfam=PF08279.4 |
| LMRG\_00094\_at | glycosyl hydrolase/Pfam=PF07748.5 |
| LMRG\_00151\_at | predicted protein |
| LMRG\_00152\_at | predicted protein |
| LMRG\_00170\_x\_at | NADH:flavin oxidoreductase/Pfam=PF00724.12 |
| LMRG\_00270\_at | deoxyribodipyrimidine photolyase/Pfam=PF03441.6 |
| LMRG\_00325\_at | conserved hypothetical protein |
| LMRG\_00325\_x\_at | conserved hypothetical protein |
| LMRG\_00366\_at | fliR/Pfam=PF01311.12 |
| LMRG\_00386\_at | flagellar hook protein FlgE/Pfam=PF07559.6 |
| LMRG\_00397\_at | conserved hypothetical protein/Pfam=PF02561.6 |
| LMRG\_00397\_x\_at | conserved hypothetical protein/Pfam=PF02561.6 |
| LMRG\_00457\_s\_at | conserved hypothetical protein |
| LMRG\_00499\_at | conserved hypothetical protein |
| LMRG\_00560\_x\_at | predicted protein/Pfam=PF00903.17 |
| LMRG\_00561\_x\_at | conserved hypothetical protein |
| LMRG\_00567\_s\_at | conserved hypothetical protein |
| LMRG\_00605\_x\_at | conserved hypothetical protein |
| LMRG\_00629\_at | conserved hypothetical protein |
| LMRG\_00645\_at | precorrin3B C17methyltransferase/Pfam=PF00590.12 |
| LMRG\_00650\_x\_at | cbiM/Pfam=PF01891.8 |
| LMRG\_00651\_at | cobalt transport protein CbiN/Pfam=PF02553.7 |
| LMRG\_00663\_at | conserved hypothetical protein/Pfam=PF05343.6 |
| LMRG\_00930\_at | oxidoreductase family protein/Pfam=PF01370.13 |
| LMRG\_00931\_at | transcription regulator/Pfam=PF00376.15 |
| LMRG\_01008\_at | conserved hypothetical protein |
| LMRG\_01008\_x\_at | conserved hypothetical protein |
| LMRG\_01022\_at | ABC transporter/Pfam=PF00005.19 |
| LMRG\_01061\_at | conserved hypothetical protein/Pfam=PF00563.12 |
| LMRG\_01069\_at | conserved hypothetical protein/Pfam=PF07719.9 |
| LMRG\_01070\_at | 3phosphoshikimate 1carboxyvinyltransferase/Pfam=PF00275.12 |
| LMRG\_01132\_at | ilvB/Pfam=PF02776.10 |
| LMRG\_01133\_at | ilvN/Pfam=PF01842.17 |
| LMRG\_01172\_at | Laspartate oxidase/Pfam=PF07992.6 |
| LMRG\_01182\_x\_at | ftsA/Pfam=PF02491.12 |
| LMRG\_01275\_at | glycosyl transferase/Pfam=PF03636.7 |
| LMRG\_01294\_x\_at | menB/Pfam=PF00378.12 |
| LMRG\_01301\_at | predicted protein/Pfam=PF02494.8 |
| LMRG\_01308\_s\_at | predicted protein |
| LMRG\_01710\_s\_at | UDPNacetylglucosamine 2epimerase/Pfam=PF02350.11 |
| LMRG\_01712\_x\_at | ATP synthase protein I/Pfam=PF05468.3 |
| LMRG\_01751\_x\_at | phosphate ABC transporter/Pfam=PF00528.14 |
| LMRG\_01790\_at | phosphoglycerate kinase/Pfam=PF00162.11 |
| LMRG\_01796\_at | est2 |
| LMRG\_01801\_s\_at | conserved hypothetical protein/Pfam=PF01381.14 |
| LMRG\_01804\_at | 6glucosyltransferase/Pfam=PF03422.7 |
| LMRG\_01837\_at | FeS assembly protein SufB/Pfam=PF01458.9 |
| LMRG\_01841\_at | conserved hypothetical protein |
| LMRG\_01872\_at | major facilitator family transporter/Pfam=PF07690.8 |
| LMRG\_01873\_at | phosphoserine aminotransferase/Pfam=PF00266.11 |
| LMRG\_01876\_at | conserved hypothetical protein |
| LMRG\_01876\_x\_at | conserved hypothetical protein |
| LMRG\_01890\_x\_at | conserved hypothetical protein/Pfam=PF07006.3 |
| LMRG\_01891\_at | conserved hypothetical protein/Pfam=PF07006.3 |
| LMRG\_01892\_at | conserved hypothetical protein |
| LMRG\_01962\_at | alphamannosidase/Pfam=PF01074.14 |
| LMRG\_02005\_at | conserved hypothetical protein |
| LMRG\_02020\_s\_at | conserved hypothetical protein/Pfam=PF03773.5 |
| LMRG\_02080\_s\_at | ABC transporter/Pfam=PF01061.16 |
| LMRG\_02114\_at | glycine betaineL-proline ABC transporter/Pfam=PF00571.20 |
| LMRG\_02118\_s\_at | CutC family protein/Pfam=PF03932.6 |
| LMRG\_02134\_x\_at | conserved hypothetical protein |
| LMRG\_02138\_at | conserved hypothetical protein/Pfam=PF01844.15 |
| LMRG\_02193\_x\_at | phosphotriesterase family protein/Pfam=PF02126.10 |
| LMRG\_02206\_s\_at | ribulosephosphate 3epimerase family protein/Pfam=PF00834.11 |
| LMRG\_02207\_x\_at | ribose 5phosphate isomerase B/Pfam=PF02502.10 |
| LMRG\_02219\_at | rpiB/Pfam=PF02502.10 |
| LMRG\_02220\_at | conserved hypothetical protein |
| LMRG\_02220\_x\_at | conserved hypothetical protein |
| LMRG\_02221\_at | ImpBMucBSamB family protein/Pfam=PF00817.12 |
| LMRG\_02221\_s\_at | ImpBMucBSamB family protein/Pfam=PF00817.12 |
| LMRG\_02278\_at | D-alanine-D-alanine ligase/Pfam=PF07478.5 |
| LMRG\_02287\_x\_at | conserved hypothetical protein/Pfam=PF04041.5 |
| LMRG\_02380\_at | EAL domaincontaining protein/Pfam=PF00563.12 |
| LMRG\_02380\_x\_at | EAL domaincontaining protein/Pfam=PF00563.12 |
| LMRG\_02404\_at | surface anchored protein/Pfam=PF05738.5 |
| LMRG\_02419\_at | Lrhamnose isomerase/Pfam=PF06134.3 |
| LMRG\_02481\_x\_at | conserved hypothetical protein/Pfam=PF02272.11 |
| LMRG\_02503\_s\_at | amidophosphoribosyltransferase/Pfam=PF00310.13 |
| LMRG\_02572\_at | conserved hypothetical protein |
| LMRG\_02573\_at | transcriptional regulator/Pfam=PF03466.12 |
| LMRG\_02574\_at | acetyltransferase/Pfam=PF00583.16 |
| LMRG\_02575\_at | conserved hypothetical protein/Pfam=PF04851.7 |
| LMRG\_02576\_at | N6 DNA methylase/Pfam=PF02384.8 |
| LMRG\_02577\_at | type I restriction enzyme S protein/Pfam=PF01420.11 |
| LMRG\_02578\_at | hypothetical protein/Pfam=PF02590.8 |
| LMRG\_02578\_x\_at | hypothetical protein/Pfam=PF02590.8 |
| LMRG\_02593\_at | conserved hypothetical protein |
| LMRG\_02594\_at | conserved hypothetical protein/Pfam=PF00005.19 |
| LMRG\_02597\_at | ABC transporter/Pfam=PF08402.2 |
| LMRG\_02708\_at | arginyltRNA synthetase/Pfam=PF05746.7 |
| LMRG\_02710\_at | CTP synthase/Pfam=PF06418.6 |
| LMRG\_02759\_s\_at | glutamate1semialdehyde 2,1aminomutase/Pfam=PF00202.13 |
| LMRG\_02784\_x\_at | scrK/Pfam=PF00480.12 |
| LMRG\_02794\_s\_at | conserved hypothetical protein/Pfam=PF00999.13 |
| LMRG\_02837\_at | dihydrouridine synthase family protein/Pfam=PF01207.9 |
| LMRG\_02837\_x\_at | dihydrouridine synthase family protein/Pfam=PF01207.9 |
| LMRG\_02862\_at | conserved hypothetical protein |
| LMRG\_02863\_at | conserved hypothetical protein/Pfam=PF06860.3 |
| LMRG\_02864\_at | conserved hypothetical protein |
| LMRG\_02864\_s\_at | conserved hypothetical protein |
| LMRG\_02872\_x\_at | conserved hypothetical protein |
| LMRG\_02887\_at | predicted protein |
| LMRG\_02891\_at | conserved hypothetical protein/Pfam=PF08937.3 |
| LMRG\_02892\_at | predicted protein |
| LMRG\_02893\_at | predicted protein |
| LMRG\_02893\_x\_at | predicted protein |
| LMRG\_02907\_at | conserved hypothetical protein |
| LMRG\_02908\_at | conserved hypothetical protein |
| LMRG\_02910\_at | conserved hypothetical protein |
| LMRG\_02933\_at | conserved hypothetical protein |
| LMRG\_02934\_at | resolvase |
| LMRG\_02935\_at | cassette chromosome recombinase B/Pfam=PF07508.5 |
| LMRG\_02937\_at | predicted protein |
| LMRG\_02937\_s\_at | predicted protein |
| LMSG\_00232\_x\_at | tRNA uridine 5carboxymethylaminomethyl modification enzyme GidA/Pfam=PF01134.14 |
| LMSG\_02867\_x\_at | naphthoate synthase/Pfam=PF00378.12 |