**Supporting Information Table S1**: **Probe-sets uniquely present in PC I serotype 1/2a**

|  |  |
| --- | --- |
| **Probe ID** | **Annotation** |
| AARI\_0068\_s\_at | 99% similar to LMHCC\_2375 |
| AARI\_0069\_s\_at | NK |
| AARI\_0075\_s\_at | NK |
| AARI\_0221\_x\_at | 99% similar to lmo0897 |
| AARI\_0239\_at | 98% similar to lmo0901 |
| AARI\_0244\_s\_at | 98% similar to LMHCC\_2380 |
| AARI\_0309\_s\_at | 98% similar to lmo0723 |
| AARI\_0318\_s\_at | NK |
| AARI\_0325\_s\_at | 98% similar to LMHCC\_2378 |
| AARI\_0328\_s\_at | 99% similar to LMHCC\_0054 |
| AARI\_0334\_s\_at | NK |
| AARI\_0337\_x\_at | NK |
| AARI\_0338\_x\_at | NK |
| AARI\_0346\_at | NK |
| AARI\_0431\_s\_at | 99% similar to lmo2760 |
| AARI\_0449\_s\_at | 100% similar to lmo2446 |
| AARI\_0469\_s\_at | NK |
| AARI\_0479\_s\_at | 99% similar to lmo1838 |
| AARI\_0502\_s\_at | NK |
| AARI\_0510\_x\_at | 98% similar to lmo2470 |
| AARI\_0553\_s\_at | 99% similar to LMHCC\_0760 |
| AARI\_0615\_x\_at | 100% similar to LMOf2365\_0491 |
| AARI\_0622\_s\_at | 99% similar to lmo1811 |
| AARI\_0629\_x\_at | NK |
| AARI\_0692\_x\_at | 99% similar to lmo1479 |
| AARK\_0198\_s\_at | 99% similar to LMOf2365\_0095 |
| AARK\_1185\_s\_at | 100% similar to LMOf2365\_0510 |
| AARK\_1755\_s\_at | 100% similar to LMOf2365\_1702 |
| AARK\_1862\_s\_at | NK |
| AARK\_1905\_s\_at | 100% similar to LMOf2365\_1498 |
| AARL\_0186\_x\_at | NK |
| AARL\_0257\_x\_at | 98% similar to LMHCC\_2123 |
| AARL\_0284\_s\_at | NK |
| AARL\_0295\_x\_at | NK |
| AARL\_0356\_x\_at | NK |
| AARL\_0602\_at | NK |
| AARL\_0669\_at | NK |
| AARL\_0669\_x\_at | NK |
| AARL\_0702\_x\_at | NK |
| AARL\_0704\_x\_at | NK |
| AARL\_0707\_x\_at | NK |
| AARL\_0808\_at | 98% similar to LMHCC\_0399 |
| AARL\_0816\_at | NK |
| AARL\_0868\_s\_at | 99% similar to lmo0678 |
| AARM\_0092\_s\_at | NK |
| AARM\_0100\_at | NK |
| AARM\_0103\_x\_at | NK |
| AARM\_0295\_s\_at | 99% similar to lmo2138 |
| AARM\_0410\_at | NK |
| AARM\_0472\_at | 98% similar to lmo1927 |
| AARM\_0539\_x\_at | 98% similar to lmo2693 |
| AARM\_0824\_s\_at | 99% similar to lmo1728 |
| AARM\_0844\_s\_at | NK |
| AARM\_0875\_at | NK |
| AARM\_0875\_x\_at | NK |
| AARM\_0959\_at | 98% similar to lmo1675 |
| AARM\_0988\_s\_at | 98% similar to lmo0489 |
| AARM\_1125\_s\_at | 100% similar to lmo1838 |
| AARM\_1323\_s\_at | NK |
| AARM\_1327\_x\_at | NK |
| AARM\_1422\_s\_at | 99% similar to LMHCC\_1448 |
| AARM\_1482\_at | NK |
| AARM\_1557\_s\_at | NK |
| AARM\_1630\_s\_at | NK |
| AARM\_1652\_at | NK |
| AARM\_1658\_x\_at | 98% similar to lmo1987 |
| AARM\_1665\_at | 100% similar to lmo1360 |
| AARM\_1775\_s\_at | NK |
| AARO\_0227\_s\_at | NK |
| AARO\_0227\_x\_at | NK |
| AARO\_1102\_s\_at | 100% similar to LMOf2365\_1391 |
| AARO\_1143\_s\_at | 99% similar to LMOf2365\_0063 |
| AARO\_1671\_s\_at | 100% similar to LMOf2365\_2417 |
| AARO\_1687\_x\_at | 100% similar to LMOf2365\_1628 |
| AARO\_1738\_at | NK |
| AARO\_1857\_s\_at | NK |
| AARY\_0088\_s\_at | 99% similar to lmo2121 |
| AARY\_0114\_s\_at | 100% similar to lmo1821 |
| AARY\_0115\_s\_at | 99% similar to lmo1820 |
| AARY\_0176\_s\_at | 99% similar to lmo1913 |
| AARY\_0201\_s\_at | 99% similar to lmo1759 |
| AARY\_0549\_s\_at | 100% similar to lmo0199 |
| AARY\_0684\_s\_at | 99% similar to lmo0401 |
| AARY\_0715\_s\_at | 99% similar to lmo2172 |
| AARY\_0854\_x\_at | 100% similar to lmo2766 |
| AARY\_0860\_s\_at | 100% similar to lmo1165 |
| AARY\_0864\_s\_at | 99% similar to lmo0327 |
| AARY\_0961\_x\_at | 99% similar to lmo1135 |
| AARY\_0964\_s\_at | 100% similar to lmo2591 |
| AARY\_1136\_s\_at | 99% similar to lmo2561 |
| AARY\_1157\_s\_at | 100% similar to lmo0841 |
| AARY\_1177\_x\_at | 100% similar to lmo1431 |
| AARY\_1222\_s\_at | 100% similar to lmo1360 |
| AARY\_1354\_x\_at | 100% similar to lmo2023 |
| AARY\_1408\_s\_at | 100% similar to lmo1764 |
| AARY\_1409\_s\_at | 100% similar to lmo1764 |
| AARY\_1417\_at | 100% similar to lmo1286 |
| AARY\_1545\_s\_at | 100% similar to lmo1559 |
| AARY\_1570\_s\_at | 100% similar to lmo1660 |
| IGLm4b\_00274\_x\_at | intergenic region |
| IGLm4b\_00397\_at | intergenic region |
| IGLm4b\_00397\_x\_at | intergenic region |
| IGLm4b\_00488\_x\_at | intergenic region |
| IGLm4b\_01128\_at | intergenic region |
| IGLm4b\_01489\_x\_at | intergenic region |
| IGLm4b\_02138\_x\_at | intergenic region |
| IGLm4b\_02207\_x\_at | intergenic region |
| IGLm4b\_02290\_x\_at | intergenic region |
| IGLMHCC\_0098\_s\_at | intergenic region |
| IGLMHCC\_0287\_at | intergenic region |
| IGLMHCC\_0300\_at | intergenic region |
| IGLMHCC\_0401\_at | intergenic region |
| IGLMHCC\_0534\_x\_at | intergenic region |
| IGLMHCC\_0575\_s\_at | intergenic region |
| IGLMHCC\_0583\_x\_at | intergenic region |
| IGLMHCC\_1058\_at | intergenic region |
| IGLMHCC\_1092\_at | intergenic region |
| IGLMHCC\_1114\_s\_at | intergenic region |
| IGLMHCC\_1316\_at | intergenic region |
| IGLMHCC\_1318\_s\_at | intergenic region |
| IGLMHCC\_1333\_at | intergenic region |
| IGLMHCC\_1333\_x\_at | intergenic region |
| IGLMHCC\_1387\_at | intergenic region |
| IGLMHCC\_1387\_x\_at | intergenic region |
| IGLMHCC\_1434\_at | intergenic region |
| IGLMHCC\_2069\_x\_at | intergenic region |
| IGLMHCC\_2079\_at | intergenic region |
| IGLMHCC\_2165\_x\_at | intergenic region |
| IGLMHCC\_2168\_x\_at | intergenic region |
| IGLMHCC\_2169\_at | intergenic region |
| IGLMHCC\_2169\_x\_at | intergenic region |
| IGLMHCC\_2181\_at | intergenic region |
| IGLMHCC\_2182\_at | intergenic region |
| IGLMHCC\_2230\_at | intergenic region |
| IGLMHCC\_2385\_at | intergenic region |
| IGLMHCC\_2419\_x\_at | intergenic region |
| IGLMHCC\_2862\_at | intergenic region |
| IGLMHCC\_2862\_x\_at | intergenic region |
| IGlmo0081\_at | intergenic region |
| IGlmo0082\_at | intergenic region |
| IGlmo0115\_at | intergenic region |
| IGlmo0142\_at | intergenic region |
| IGlmo0143\_at | intergenic region |
| IGlmo0144\_at | intergenic region |
| IGlmo0145\_at | intergenic region |
| IGlmo0145\_x\_at | intergenic region |
| IGlmo0146\_s\_at | intergenic region |
| IGlmo0146\_x\_at | intergenic region |
| IGlmo0175\_at | intergenic region |
| IGlmo0281\_at | intergenic region |
| IGlmo0293\_at | intergenic region |
| IGlmo0293\_x\_at | intergenic region |
| IGlmo0295\_s\_at | intergenic region |
| IGlmo0296\_at | intergenic region |
| IGlmo0296\_s\_at | intergenic region |
| IGlmo0296\_x\_at | intergenic region |
| IGlmo0324\_x\_at | intergenic region |
| IGlmo0334\_at | intergenic region |
| IGlmo0339\_at | intergenic region |
| IGlmo0424\_at | intergenic region |
| IGlmo0452\_at | intergenic region |
| IGlmo0452\_x\_at | intergenic region |
| IGlmo0459\_at | intergenic region |
| IGlmo0460\_at | intergenic region |
| IGlmo0464\_x\_at | intergenic region |
| IGlmo0662\_x\_at | intergenic region |
| IGlmo0792\_x\_at | intergenic region |
| IGlmo0866\_at | intergenic region |
| IGlmo0900\_at | intergenic region |
| IGlmo0981\_x\_at | intergenic region |
| IGlmo1014\_at | intergenic region |
| IGlmo1014\_x\_at | intergenic region |
| IGlmo1190\_at | intergenic region |
| IGlmo1479\_x\_at | intergenic region |
| IGlmo1571\_at | intergenic region |
| IGlmo1572\_at | intergenic region |
| IGlmo1604\_at | intergenic region |
| IGlmo1648\_at | intergenic region |
| IGlmo1649\_at | intergenic region |
| IGlmo1659\_at | intergenic region |
| IGlmo1660\_at | intergenic region |
| IGlmo1762\_x\_at | intergenic region |
| IGlmo2034\_at | intergenic region |
| IGlmo2256\_at | intergenic region |
| IGlmo2272\_at | intergenic region |
| IGlmo2310\_at | intergenic region |
| IGlmo2444\_at | intergenic region |
| IGlmo2500\_at | intergenic region |
| IGlmo2500\_x\_at | intergenic region |
| IGlmo2538\_at | intergenic region |
| IGlmo2538\_x\_at | intergenic region |
| IGlmo2560\_at | intergenic region |
| IGlmo2760\_x\_at | intergenic region |
| IGLMOf2365\_0151\_s\_at | intergenic region |
| IGLMOf2365\_0156\_s\_at | intergenic region |
| IGLMOf2365\_0161\_at | intergenic region |
| IGLMOf2365\_0161\_s\_at | intergenic region |
| IGLMOf2365\_0163\_x\_at | intergenic region |
| IGLMOf2365\_0188\_x\_at | intergenic region |
| IGLMOf2365\_0266\_s\_at | intergenic region |
| IGLMOf2365\_0267\_s\_at | intergenic region |
| IGLMOf2365\_0272\_s\_at | intergenic region |
| IGLMOf2365\_0274\_s\_at | intergenic region |
| IGLMOf2365\_0285\_s\_at | intergenic region |
| IGLMOf2365\_0330\_s\_at | intergenic region |
| IGLMOf2365\_0372\_s\_at | intergenic region |
| IGLMOf2365\_0481\_at | intergenic region |
| IGLMOf2365\_0482\_s\_at | intergenic region |
| IGLMOf2365\_0493\_x\_at | intergenic region |
| IGLMOf2365\_0498\_x\_at | intergenic region |
| IGLMOf2365\_0505\_s\_at | intergenic region |
| IGLMOf2365\_0696\_x\_at | intergenic region |
| IGLMOf2365\_0860\_x\_at | intergenic region |
| IGLMOf2365\_0921\_x\_at | intergenic region |
| IGLMOf2365\_1162\_x\_at | intergenic region |
| IGLMOf2365\_1257\_s\_at | intergenic region |
| IGLMOf2365\_1275\_at | intergenic region |
| IGLMOf2365\_1275\_x\_at | intergenic region |
| IGLMOf2365\_1365\_at | intergenic region |
| IGLMOf2365\_1498\_x\_at | intergenic region |
| IGLMOf2365\_1573\_x\_at | intergenic region |
| IGLMOf2365\_1621\_x\_at | intergenic region |
| IGLMOf2365\_1733\_x\_at | intergenic region |
| IGLMOf2365\_2176\_x\_at | intergenic region |
| IGLMOf2365\_2177\_at | intergenic region |
| IGLMOf2365\_2177\_x\_at | intergenic region |
| IGLMOf2365\_2253\_x\_at | intergenic region |
| IGLMOf2365\_2366\_at | intergenic region |
| IGLMOf2365\_2537\_x\_at | intergenic region |
| IGLMOf2365\_2796\_x\_at | intergenic region |
| IGLMOf2365\_2797\_at | intergenic region |
| IGLMOf2365\_2797\_x\_at | intergenic region |
| Lm4b\_01128\_at | GI=225876187 |
| Lm4b\_01270\_s\_at | proB gamma-glutamyl kinase/GI=225876325 |
| Lm4b\_01815\_s\_at | Putative peptidoglycan bound protein (LPXTG motif)/GI=225876864 |
| Lm4b\_02041\_s\_at | Hypothetical protein of unknown function/GI=225877088 |
| Lm4b\_02459\_x\_at | Putative CsbA protein/GI=225877500 |
| LMBG\_01686\_at | phage protein |
| LMBG\_01686\_x\_at | phage protein |
| LMBG\_02156\_x\_at | thiaminephosphate pyrophosphorylase/Pfam=PF02581.9 |
| LMFG\_00724\_s\_at | D-alanine-D-alanine ligase |
| LMFG\_02515\_at | predicted protein |
| LMFG\_02674\_at | predicted protein |
| LMFG\_02675\_at | conserved hypothetical protein |
| LMFG\_02675\_x\_at | conserved hypothetical protein |
| LMFG\_02953\_s\_at | conserved hypothetical protein |
| LMFG\_03116\_s\_at | predicted protein/Pfam=PF00746.13 |
| LMFG\_03220\_x\_at | predicted protein |
| LMFG\_03225\_s\_at | conserved hypothetical protein |
| LMFG\_03235\_s\_at | predicted protein |
| LMHCC\_0008\_s\_at | alkaline phosphatase synthesis transcriptional regulatory proteinphoP/GI=217332580 |
| LMHCC\_0010\_at | ABC transporter, permease protein/GI=217332582 |
| LMHCC\_0098\_s\_at | membrane protein, putative/GI=217332666 |
| LMHCC\_0260\_s\_at | L-cystine import ATP-binding protein TcyN/GI=217332826 |
| LMHCC\_0348\_s\_at | oligopeptide transport system permease protein OppC/GI=217332914 |
| LMHCC\_0401\_at | mannose-6-phosphate isomerase, class I, putative/GI=217332966 |
| LMHCC\_0401\_s\_at | mannose-6-phosphate isomerase, class I, putative/GI=217332966 |
| LMHCC\_0537\_x\_at | nadB L-aspartate oxidase/GI=217333100 |
| LMHCC\_0832\_x\_at | glutamate synthase (NADPH) small chain/GI=217333390 |
| LMHCC\_0833\_s\_at | ABC transporter permease protein/GI=217333391 |
| LMHCC\_0834\_s\_at | ABC transporter, permease protein/GI=217333392 |
| LMHCC\_1056\_s\_at | cysteine desulfurase/GI=217333610 |
| LMHCC\_1057\_x\_at | trmU tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase/GI=217333611 |
| LMHCC\_1091\_s\_at | lepA GTP-binding protein LepA/GI=217333645 |
| LMHCC\_1117\_s\_at | S-adenosylmethionine/GI=217333671 |
| LMHCC\_1156\_s\_at | conserved hypothetical protein/GI=217333710 |
| LMHCC\_1199\_s\_at | 2-oxoisovalerate dehydrogenase subunit alpha (branched-chain alpha-keto acid dehydrogenase e1 component alpha chain)/GI=217333752 |
| LMHCC\_1223\_s\_at | gcvT glycine cleavage system T protein/GI=217333776 |
| LMHCC\_1315\_s\_at | hydrolase, alpha-beta fold family/GI=217333866 |
| LMHCC\_1333\_x\_at | conserved hypothetical protein/GI=217333884 |
| LMHCC\_1489\_s\_at | propanediol utilization protein PduM/GI=217334039 |
| LMHCC\_1774\_s\_at | small multidrug resistance protein/GI=217334321 |
| LMHCC\_2150\_x\_at | MutTnudix family protein/GI=217334694 |
| LMHCC\_2164\_x\_at | transposase OrfA, IS3 family, putative/GI=217334708 |
| LMHCC\_2167\_s\_at | conserved hypothetical protein/GI=217334711 |
| LMHCC\_2182\_s\_at | PBP 5 synthesis repressor/GI=217334726 |
| LMHCC\_2211\_x\_at | pts system fructose-specific eiibbc component (eiibbc-fru)/GI=217334755 |
| LMHCC\_2333\_s\_at | PRDPTS system IIA 2 domain regulatory protein/GI=217334876 |
| LMHCC\_2497\_s\_at | hypothetical protein/GI=217335038 |
| LMHCC\_2520\_s\_at | ABC transporter, ATP-bindingpermease protein/GI=217335061 |
| LMHCC\_2600\_s\_at | glyoxylate reductase (Glycolate reductase)/GI=217335141 |
| LMHCC\_2600\_x\_at | glyoxylate reductase (Glycolate reductase)/GI=217335141 |
| LMHCC\_2771\_s\_at | hydrolase, CocENonD family/GI=217335311 |
| LMHCC\_2803\_s\_at | HAD-superfamily hydrolase, subfamily IA, variant 1/GI=217335342 |
| LMHCC\_2836\_x\_at | phosphosugar-binding transcriptional regulator, RpiR family/GI=217335374 |
| LMHCC\_2859\_at | hydrolase, alphabeta fold family/GI=217335396 |
| LMHCC\_2859\_x\_at | hydrolase, alphabeta fold family/GI=217335396 |
| LMHCC\_2860\_x\_at | ImpBMucBSamB family protein/GI=217335397 |
| LMHCC\_2861\_s\_at | conserved hypothetical protein/GI=217335398 |
| LMHCC\_2889\_s\_at | conserved hypothetical protein/GI=217335426 |
| LMHCC\_3006\_s\_at | lipoprotein, putative/GI=217335543 |
| LMHG\_00214\_at | ABC transporter/Pfam=PF01497.10 |
| LMHG\_00237\_at | hisA/Pfam=PF00977.13 |
| LMHG\_00512\_at | conserved hypothetical protein/Pfam=PF07006.3 |
| LMHG\_00512\_x\_at | conserved hypothetical protein/Pfam=PF07006.3 |
| LMHG\_00893\_s\_at | ImpBMucBSamB family protein/Pfam=PF00817.12 |
| LMHG\_00894\_x\_at | hydrolase/Pfam=PF00561.12 |
| LMHG\_00906\_s\_at | hypothetical protein |
| LMHG\_00908\_at | Nacetylmuramoyl-L-alanine amidase/Pfam=PF01832.12 |
| LMHG\_00908\_s\_at | Nacetylmuramoyl-L-alanine amidase/Pfam=PF01832.12 |
| LMHG\_00910\_x\_at | thymidylate kinase/Pfam=PF02223.9 |
| LMHG\_01289\_at | alsS/Pfam=PF02776.10 |
| LMHG\_01437\_x\_at | hydrolase/Pfam=PF00561.12 |
| LMHG\_01678\_x\_at | Disomer specific 2hydroxyacid dehydrogenase/Pfam=PF02826.11 |
| LMHG\_01684\_at | CBS domaincontaining protein/Pfam=PF07085.4 |
| LMHG\_01923\_x\_at | MutTnudix family protein/Pfam=PF00293.20 |
| LMHG\_02484\_at | conserved hypothetical protein/Pfam=PF04055.13 |
| LMHG\_02678\_s\_at | propanediol utilization protein PduM |
| LMHG\_03094\_at | conserved hypothetical protein |
| LMHG\_03149\_at | PTS system protein |
| LMHG\_03157\_x\_at | peptidoglycan binding protein/Pfam=PF00746.13 |
| LMIG\_00006\_at | crisprassociated protein/Pfam=PF09711.2 |
| LMIG\_00007\_at | crisprassociated protein cas2 |
| LMIG\_00333\_s\_at | DHH family protein/Pfam=PF02272.11 |
| LMIG\_00411\_s\_at | EAL domaincontaining protein/Pfam=PF00563.12 |
| LMIG\_00413\_x\_at | conserved hypothetical protein/Pfam=PF06902.3 |
| LMIG\_00630\_s\_at | acetolactate synthase 3 regulatory subunit/Pfam=PF01842.17 |
| LMIG\_00662\_at | alphaDmannosidase/Pfam=PF09261.3 |
| LMIG\_01005\_s\_at | septum sitedetermining protein MinC/Pfam=PF03775.8 |
| LMIG\_01364\_s\_at | trehalose6phosphate hydrolase/Pfam=PF00128.16 |
| LMIG\_01517\_at | glycosyl hydrolase/Pfam=PF03422.7 |
| LMIG\_01913\_x\_at | conserved hypothetical protein/Pfam=PF00356.13 |
| LMIG\_01920\_s\_at | phosphoglucomutasephosphomannomutase/Pfam=PF02879.8 |
| LMIG\_01940\_s\_at | protoporphyrinogen oxidase/Pfam=PF01593.16 |
| LMIG\_01965\_s\_at | phosphoglycerate mutase/Pfam=PF00300.14 |
| LMIG\_02175\_s\_at | conserved hypothetical protein |
| LMIG\_02249\_x\_at | conserved hypothetical protein/Pfam=PF05675.4 |
| LMIG\_02280\_at | GTPbinding protein TypA/Pfam=PF08477.5 |
| LMIG\_02564\_s\_at | betaglucosidase/Pfam=PF01915.14 |
| LMIG\_02570\_s\_at | transcriptional regulator GltC/Pfam=PF03466.12 |
| LMIG\_02662\_at | NADH:flavin oxidoreductase/Pfam=PF00724.12 |
| LMIG\_02662\_x\_at | NADH:flavin oxidoreductase/Pfam=PF00724.12 |
| LMIG\_02677\_s\_at | alcohol dehydrogenase/Pfam=PF08240.4 |
| LMIG\_02826\_s\_at | conserved hypothetical protein/Pfam=PF01841.11 |
| LMIG\_02843\_x\_at | conserved hypothetical protein/Pfam=PF01527.12 |
| LMIG\_02887\_s\_at | predicted protein |
| LMIG\_02909\_s\_at | predicted protein |
| LMIG\_02910\_s\_at | predicted protein |
| LMIG\_02939\_at | predicted protein |
| LMIG\_02947\_s\_at | predicted protein |
| LMIG\_02948\_s\_at | conserved hypothetical protein |
| LMJG\_02806\_s\_at | predicted protein |
| LMKG\_00453\_s\_at | predicted protein |
| LMKG\_01576\_at | predicted protein |
| LMKG\_01623\_x\_at | predicted protein |
| LMKG\_01740\_at | predicted protein |
| LMKG\_01740\_x\_at | predicted protein |
| LMKG\_02495\_x\_at | conserved hypothetical protein |
| LMLG\_00020\_x\_at | conserved hypothetical protein |
| LMLG\_00205\_at | major facilitator family transporter/Pfam=PF07690.8 |
| LMLG\_00210\_x\_at | conserved hypothetical protein |
| LMLG\_00291\_at | glycosyl hydrolase/Pfam=PF01074.14 |
| LMLG\_00315\_at | conserved hypothetical protein/Pfam=PF00881.16 |
| LMLG\_00377\_x\_at | pantetheinephosphate adenylyltransferase/Pfam=PF01467.18 |
| LMLG\_00453\_at | glucose6phosphate 1dehydrogenase/Pfam=PF02781.8 |
| LMLG\_00524\_at | glutamate dehydrogenase/Pfam=PF02812.10 |
| LMLG\_00527\_s\_at | imidazoleglycerol phosphate synthase/Pfam=PF00977.13 |
| LMLG\_00570\_at | conserved hypothetical protein/Pfam=PF01554.10 |
| LMLG\_00741\_x\_at | conserved hypothetical protein |
| LMLG\_00754\_s\_at | transcriptional regulator |
| LMLG\_00790\_at | internalin D/Pfam=PF09479.2 |
| LMLG\_00804\_at | RTCB proteinlike protein/Pfam=PF01139.9 |
| LMLG\_00804\_x\_at | RTCB proteinlike protein/Pfam=PF01139.9 |
| LMLG\_00815\_x\_at | RNA polymerase sigma30 factor/Pfam=PF08281.4 |
| LMLG\_00838\_s\_at | iron compound ABC transporter/Pfam=PF01032.10 |
| LMLG\_00951\_at | conserved hypothetical protein/Pfam=PF03466.12 |
| LMLG\_00991\_at | conserved hypothetical protein |
| LMLG\_00991\_x\_at | conserved hypothetical protein |
| LMLG\_00992\_at | glutamate 5kinase/Pfam=PF00696.20 |
| LMLG\_00993\_at | gammaglutamyl phosphate reductase |
| LMLG\_00994\_x\_at | hydrolase/Pfam=PF00561.12 |
| LMLG\_00996\_at | MutTnudix family protein/Pfam=PF00293.20 |
| LMLG\_00996\_x\_at | MutTnudix family protein/Pfam=PF00293.20 |
| LMLG\_00997\_s\_at | PTS system/Pfam=PF02378.10 |
| LMLG\_00998\_s\_at | trehalose6phosphate hydrolase/Pfam=PF00128.16 |
| LMLG\_01200\_at | conserved hypothetical protein/Pfam=PF00425.10 |
| LMLG\_01200\_s\_at | conserved hypothetical protein/Pfam=PF00425.10 |
| LMLG\_01200\_x\_at | conserved hypothetical protein/Pfam=PF00425.10 |
| LMLG\_01203\_at | conserved hypothetical protein/Pfam=PF02574.8 |
| LMLG\_01283\_at | ribose 5phosphate isomerase B/Pfam=PF02502.10 |
| LMLG\_01395\_at | glutathione reductase/Pfam=PF07992.6 |
| LMLG\_01402\_s\_at | succinatesemialdehyde dehydrogenase/Pfam=PF00171.14 |
| LMLG\_01532\_at | methionine aminopeptidase/Pfam=PF00557.16 |
| LMLG\_01718\_s\_at | pyruvate formatelyase activating enzyme/Pfam=PF04055.13 |
| LMLG\_01752\_at | DHH subfamily protein/Pfam=PF02272.11 |
| LMLG\_02001\_at | sigma70 region 2 family protein/Pfam=PF08281.4 |
| LMLG\_02001\_x\_at | sigma70 region 2 family protein/Pfam=PF08281.4 |
| LMLG\_02040\_at | thiaminepyrophosphaterequiring enzyme/Pfam=PF02775.13 |
| LMLG\_02575\_at | conserved hypothetical protein/Pfam=PF04095.8 |
| LMLG\_02607\_at | transcriptional regulator/Pfam=PF08279.4 |
| LMLG\_02617\_at | conserved hypothetical protein/Pfam=PF00232.10 |
| LMLG\_02625\_at | conserved hypothetical protein/Pfam=PF03239.6 |
| LMLG\_02654\_at | major facilitator family transporter/Pfam=PF07690.8 |
| LMLG\_02829\_at | propanediol utilization/Pfam=PF08841.2 |
| LMLG\_02829\_x\_at | propanediol utilization/Pfam=PF08841.2 |
| LMLG\_02853\_x\_at | glutamine amidotransferase/Pfam=PF07722.5 |
| lmo0079\_s\_at | GI=16409438 |
| lmo0080\_at | GI=16409439 |
| lmo0081\_at | GI=16409440 |
| lmo0082\_at | GI=16409441 |
| lmo0140\_s\_at | GI=16409499 |
| lmo0143\_s\_at | GI=16409502 |
| lmo0145\_s\_at | GI=16409504 |
| lmo0241\_s\_at | GI=16409606 |
| lmo0242\_at | GI=16409607 |
| lmo0242\_x\_at | GI=16409607 |
| lmo0256\_x\_at | GI=16409621 |
| lmo0281\_s\_at | GI=16409646 |
| lmo0294\_s\_at | GI=16409659 |
| lmo0317\_s\_at | GI=16409681 |
| lmo0335\_x\_at | GI=16409713 |
| lmo0336\_x\_at | GI=16409714 |
| lmo0337\_s\_at | GI=16409715 |
| lmo0338\_s\_at | GI=16409716 |
| lmo0342\_s\_at | GI=16409720 |
| lmo0369\_s\_at | GI=16409747 |
| lmo0427\_x\_at | GI=16409804 |
| lmo0458\_s\_at | GI=16409835 |
| lmo0461\_s\_at | GI=16409838 |
| lmo0463\_s\_at | GI=16409840 |
| lmo0487\_s\_at | GI=16409863 |
| lmo0488\_s\_at | GI=16409864 |
| lmo0636\_at | GI=16410025 |
| lmo0645\_s\_at | GI=16410034 |
| lmo0861\_at | GI=16410264 |
| lmo0861\_x\_at | GI=16410264 |
| lmo0865\_at | GI=16410268 |
| lmo0915\_at | GI=16410318 |
| lmo0923\_s\_at | GI=16410326 |
| lmo0947\_s\_at | GI=16410349 |
| lmo1135\_s\_at | GI=16410551 |
| lmo1168\_at | AckA2 GI=16410584 |
| lmo1179\_s\_at | GI=16410595 |
| lmo1217\_s\_at | GI=16410633 |
| lmo1280\_s\_at | codY GI=16410696 |
| lmo1402\_s\_at | GI=16410831 |
| lmo1472\_s\_at | dnaJ heat shock protein DnaJ/GI=16410901 |
| lmo1573\_s\_at | accD GI=16411002 |
| lmo1604\_s\_at | GI=16411033 |
| lmo1647\_s\_at | GI=16411083 |
| lmo1648\_at | GI=16411084 |
| lmo1659\_at | GI=16411095 |
| lmo1685\_s\_at | gsaB glutamate-1-semialdehyde aminotransferase/GI=16411121 |
| lmo1735\_s\_at | gltC transcription activator of glutamate synthase operon GltC/GI=16411189 |
| lmo1765\_s\_at | purH Bifunctional phosphoribosylaminoimidazole carboxy formyl formyltransferase and inosine-monophosphate cyclohydrolase/GI=16411219 |
| lmo1837\_s\_at | pyrC GI=16411291 |
| lmo1913\_s\_at | GI=16411366 |
| lmo1917\_at | pflA GI=16411370 |
| lmo1922\_s\_at | GI=16411375 |
| lmo1954\_s\_at | drm GI=16411407 |
| lmo2046\_x\_at | GI=16411516 |
| lmo2049\_s\_at | GI=16411519 |
| lmo2228\_s\_at | GI=16411698 |
| lmo2312\_x\_at | GI=16411782 |
| lmo2430\_s\_at | GI=16411918 |
| lmo2447\_s\_at | GI=16411935 |
| lmo2475\_s\_at | GI=16411963 |
| lmo2536\_x\_at | atpI GI=16412024 |
| lmo2537\_s\_at | GI=16412025 |
| lmo2558\_at | ami "autolysin, amidase"/GI=16412046 |
| lmo2561\_s\_at | argS arginyl tRNA synthetase/GI=16412049 |
| lmo2593\_at | GI=16412081 |
| lmo2634\_s\_at | GI=16412122 |
| lmo2662\_s\_at | GI=16412162 |
| lmo2683\_at | GI=16412183 |
| lmo2689\_x\_at | GI=16412189 |
| lmo2695\_at | GI=16412195 |
| lmo2695\_x\_at | GI=16412195 |
| lmo2721\_s\_at | GI=16412221 |
| lmo2748\_at | GI=16412248 |
| lmo2760\_at | GI=16412260 |
| lmo2812\_s\_at | GI=16412312 |
| LMOf2365\_0019\_s\_at | qoxD quinol oxidase AA3, subunit IV/GI=46879506 |
| LMOf2365\_0135\_s\_at | lmaB prophage LambdaLm01, antigen B/GI=46879621 |
| LMOf2365\_0159\_s\_at | conserved hypothetical protein/GI=46879644 |
| LMOf2365\_0160\_s\_at | hypothetical protein/GI=46879645 |
| LMOf2365\_0162\_s\_at | conserved hypothetical protein/GI=46879647 |
| LMOf2365\_0267\_s\_at | sugar ABC transporter, sugar-binding protein/GI=46879752 |
| LMOf2365\_0269\_s\_at | sugar ABC transporter, permease protein/GI=46879754 |
| LMOf2365\_0270\_s\_at | malL2 oligo-1,6-glucosidase/GI=46879755 |
| LMOf2365\_0271\_s\_at | gtfA sucrose phosphorylase/GI=46879756 |
| LMOf2365\_0272\_s\_at | hypothetical protein/GI=46879757 |
| LMOf2365\_0273\_s\_at | hypothetical protein/GI=46879758 |
| LMOf2365\_0284\_s\_at | peptidase, M20M25M40 family/GI=46879770 |
| LMOf2365\_0304\_s\_at | metN D-methionine ABC transporter, ATP-binding protein/GI=46879790 |
| LMOf2365\_0316\_s\_at | nitroreductase family protein/GI=46879802 |
| LMOf2365\_0336\_s\_at | thiE thiamine-phosphate pyrophosphorylase/GI=46879821 |
| LMOf2365\_0346\_x\_at | conserved hypothetical protein/GI=46879831 |
| LMOf2365\_0354\_s\_at | conserved domain protein/GI=46879839 |
| LMOf2365\_0355\_at | conserved hypothetical protein/GI=46879840 |
| LMOf2365\_0444\_s\_at | PTS system, fructose-specific, IIC component/GI=46879927 |
| LMOf2365\_0474\_s\_at | putative ytfG protein/GI=46879956 |
| LMOf2365\_0481\_s\_at | conserved domain protein/GI=46879963 |
| LMOf2365\_0496\_s\_at | hypothetical protein/GI=46879978 |
| LMOf2365\_0497\_s\_at | hypothetical protein/GI=46879979 |
| LMOf2365\_0499\_s\_at | putative transposase OrfA, IS3 family/GI=46879981 |
| LMOf2365\_0664\_s\_at | HAD-superfamily hydrolase, subfamily IA, variant 1/GI=46880146 |
| LMOf2365\_0712\_s\_at | fliP flagellar biosynthesis protein FliP/GI=46880193 |
| LMOf2365\_0733\_s\_at | putative flagellar hook protein FlgE/GI=46880214 |
| LMOf2365\_0828\_s\_at | HD domain protein/GI=46880308 |
| LMOf2365\_0854\_s\_at | ABC transporter, ATP-binding protein/GI=46880334 |
| LMOf2365\_0929\_s\_at | phosphoglycerate mutase family protein/GI=46880409 |
| LMOf2365\_0942\_s\_at | putative ABC transporter, permease protein/GI=46880422 |
| LMOf2365\_1020\_s\_at | putative membrane protein/GI=46880498 |
| LMOf2365\_1256\_s\_at | conserved hypothetical protein/GI=46880733 |
| LMOf2365\_1257\_s\_at | hypothetical protein/GI=46880734 |
| LMOf2365\_1269\_s\_at | conserved hypothetical protein/GI=46880746 |
| LMOf2365\_1274\_s\_at | conserved hypothetical protein/GI=46880751 |
| LMOf2365\_1348\_s\_at | pnp polyribonucleotide nucleotidyltransferase/GI=46880825 |
| LMOf2365\_1363\_s\_at | general secretion pathway protein F/GI=46880840 |
| LMOf2365\_1364\_s\_at | general secretion pathway protein E/GI=46880841 |
| LMOf2365\_1376\_s\_at | nusB N utilization substance protein B/GI=46880853 |
| LMOf2365\_1446\_s\_at | opuCB glycine betaineL-proline ABC transporter, permease protein/GI=46880923 |
| LMOf2365\_1497\_s\_at | transcriptional regulator, MerR family/GI=46880975 |
| LMOf2365\_1563\_x\_at | minD septum site-determining protein MinD/GI=46881041 |
| LMOf2365\_1595\_s\_at | accD acetyl-CoA carboxylase, carboxyl transferase, beta subunit/GI=46881073 |
| LMOf2365\_1617\_s\_at | GAF domain protein/GI=46881095 |
| LMOf2365\_1624\_s\_at | putative aminopeptidase/GI=46881102 |
| LMOf2365\_1761\_s\_at | alcohol dehydrogenase, iron-dependent/GI=46881237 |
| LMOf2365\_1787\_s\_at | conserved hypothetical protein/GI=46881262 |
| LMOf2365\_1793\_s\_at | purF amidophosphoribosyltransferase/GI=46881268 |
| LMOf2365\_1836\_s\_at | fabD malonyl CoA-acyl carrier protein transacylase/GI=46881310 |
| LMOf2365\_1889\_s\_at | conserved hypothetical protein/GI=46881363 |
| LMOf2365\_1982\_s\_at | lysA diaminopimelate decarboxylase/GI=46881456 |
| LMOf2365\_2018\_x\_at | deoC deoxyribose-phosphate aldolase/GI=46881493 |
| LMOf2365\_2027\_s\_at | transcriptional regulator, GntR family/GI=46881502 |
| LMOf2365\_2032\_s\_at | putative ABC transporter, permease protein/GI=46881507 |
| LMOf2365\_2066\_s\_at | cell division protein FtsQ/GI=46881541 |
| LMOf2365\_2092\_s\_at | conserved hypothetical protein/GI=46881567 |
| LMOf2365\_2118\_s\_at | DNA-binding protein/GI=46881592 |
| LMOf2365\_2176\_s\_at | transcriptional regulator, GntR family/GI=46881648 |
| LMOf2365\_2342\_s\_at | ABC transporter, permease protein/GI=46881814 |
| LMOf2365\_2517\_s\_at | thymidine kinase/GI=46881988 |
| LMOf2365\_2565\_s\_at | morA morphine 6-dehydrogenase/GI=46882036 |
| LMOf2365\_2658\_s\_at | kdpE DNA-binding response regulator KdpE/GI=46882130 |
| LMOf2365\_2794\_s\_at | conserved hypothetical protein/GI=46882266 |
| LMOf2365\_2795\_s\_at | conserved hypothetical protein/GI=46882267 |
| LMOf6854\_0085\_at | gp32, putative/GI=47016488 |
| LMOf6854\_0093\_s\_at | conserved hypothetical protein/GI=47016496 |
| LMOf6854\_0134\_at | membrane protein, putative/GI=47016537 |
| LMOf6854\_0146\_x\_at | conserved hypothetical protein/GI=47016549 |
| LMOf6854\_0152\_x\_at | conserved hypothetical protein/GI=47014045 |
| LMOf6854\_0248\_s\_at | gltX glutamyl-tRNA synthetase/GI=47014205 |
| LMOf6854\_0263\_x\_at | conserved hypothetical protein/GI=47015102 |
| LMOf6854\_0315\_at | glycosyl hydrolase, family 1/GI=47015263 |
| LMOf6854\_0323\_at | conserved hypothetical protein/GI=47015193 |
| LMOf6854\_0324\_x\_at | thiM hydroxyethylthiazole kinase/GI=47015194 |
| LMOf6854\_0443\_s\_at | phosphate transporter family protein/GI=47015056 |
| LMOf6854\_0493\_s\_at | hypothetical protein/GI=47016826 |
| LMOf6854\_0494\_x\_at | hypothetical protein/GI=47016827 |
| LMOf6854\_0496\_s\_at | conserved domain protein/GI=47016829 |
| LMOf6854\_0505\_s\_at | conserved hypothetical protein/GI=47016838 |
| LMOf6854\_0522\_at | NADH:flavin oxidoreductase/GI=47016855 |
| LMOf6854\_0522\_x\_at | NADH:flavin oxidoreductase/GI=47016855 |
| LMOf6854\_0615\_s\_at | glycosyl hydrolase, family 1/GI=47016948 |
| LMOf6854\_0744\_s\_at | flagellar hook protein FlgE, putative/GI=47016334 |
| LMOf6854\_0770\_at | methyl-accepting chemotaxis protein, putative/GI=47016360 |
| LMOf6854\_0840\_s\_at | rarD protein/GI=47014306 |
| LMOf6854\_0882\_s\_at | ABC transporter, ATP-binding protein/GI=47016725 |
| LMOf6854\_0896\_s\_at | conserved hypothetical protein/GI=47016739 |
| LMOf6854\_0911\_at | hypothetical protein/GI=47016754 |
| LMOf6854\_0946\_s\_at | conserved hypothetical protein/GI=47016789 |
| LMOf6854\_0992\_s\_at | lipoprotein, putative/GI=47015377 |
| LMOf6854\_1178\_at | conserved hypothetical protein/GI=47016599 |
| LMOf6854\_1178\_x\_at | conserved hypothetical protein/GI=47016599 |
| LMOf6854\_1179\_s\_at | siroheme synthase subunit, putative/GI=47016600 |
| LMOf6854\_1180\_at | PduS protein/GI=47016601 |
| LMOf6854\_1317\_s\_at | topA DNA topoisomerase I/GI=47014084 |
| LMOf6854\_1624\_s\_at | accA acetyl-CoA carboxylase, carboxyl transferase, alpha subunit/GI=47014818 |
| LMOf6854\_1656\_s\_at | aminopeptidase, putative/GI=47014550 |
| LMOf6854\_1701\_x\_at | helicase, Snf2 family/GI=47014621 |
| LMOf6854\_1928\_at | conserved hypothetical protein/GI=47014723 |
| LMOf6854\_1928\_x\_at | conserved hypothetical protein/GI=47014723 |
| LMOf6854\_2147\_at | DNA-binding protein/GI=47015799 |
| LMOf6854\_2147\_x\_at | DNA-binding protein/GI=47015799 |
| LMOf6854\_2558\_s\_at | phosphate ABC transporter, ATP-binding protein/GI=47015550 |
| LMOf6854\_2656\_at | holin, phage phi LC3 family/GI=47014863 |
| LMOf6854\_2657\_s\_at | conserved hypothetical protein/GI=47014864 |
| LMOf6854\_2749\_s\_at | prenyltransferase, UbiA family/GI=47013953 |
| LMOf6854\_2766\_s\_at | PTS system, IIA component, putative/GI=47014502 |
| LMOf6854\_2846\_s\_at | conserved hypothetical protein/GI=47016144 |
| LMOf6854\_2874\_s\_at | hydrolase, CocENonD family/GI=47015993 |
| LMOf6854\_2897\_s\_at | ychF GTP-binding protein YchF/GI=47016016 |
| LMOf6854\_2948\_s\_at | beta-phosphoglucomutase/GI=47014256 |
| LMOG\_00590\_x\_at | predicted protein |
| LMOG\_00709\_at | predicted protein |
| LMOG\_00709\_x\_at | predicted protein |
| LMOG\_01542\_at | predicted protein |
| LMOG\_01819\_x\_at | predicted protein |
| LMOG\_01925\_s\_at | conserved hypothetical protein |
| LMOG\_02612\_at | predicted protein |
| LMOG\_03106\_at | DNAmethyltransferase/Pfam=PF00145.9 |
| LMOh7858\_0100\_s\_at | pentapeptide repeats domain protein/GI=47019472 |
| LMOh7858\_0417\_s\_at | conserved hypothetical protein/GI=47020192 |
| LMOh7858\_0538\_x\_at | conserved hypothetical protein/GI=47019134 |
| LMOh7858\_0804\_at | conserved hypothetical protein/GI=47020058 |
| LMOh7858\_0870\_s\_at | HD domain protein/GI=47017728 |
| LMOh7858\_1192\_x\_at | conserved hypothetical protein/GI=47019636 |
| LMOh7858\_2276\_at | hypothetical protein/GI=47019882 |
| LMOh7858\_2276\_s\_at | hypothetical protein/GI=47019882 |
| LMPG\_02651\_x\_at | predicted protein |
| LMPG\_03082\_s\_at | conserved domaincontaining protein/Pfam=PF06860.3 |
| LMSG\_01585\_x\_at | phosphomethylpyrimidine kinase/Pfam=PF08543.4 |
| LMSG\_01821\_s\_at | conserved hypothetical protein/Pfam=PF05043.5 |
| LMSG\_02793\_at | phage protein/Pfam=PF05565.3 |
| LMSG\_03161\_s\_at | conserved hypothetical protein |