| PFC | Dist. To 3' gene | Length | Sequence |
|---|---|---|---|
| LmeA$_{AB}$2 | 71,523 | 139 | TCTGGGAGGGATCACCATTGCCCCTTCTTTCTAAACTGTCATTCTTAATGGTGCAGTCGTCATTACAGTACCACTGGTGACGCCACTCATTGATTGCAAGTGGATAAATAGAAACGTCTGCCACCGTAAAGATGAAAGG |
| LmeA$_{AB}$29 | 25,959 | 245 | TCCTGGAACCAAAATGGCCTGTACAGTTCGCCAAACACTCGCTGAGCTGCTGGAGCTGCCTGGGGACCTGCGGCTGCAGCGTCCCTGGGTCTTCCAGGATGAGAGGGGGCGGCGCTGGGCCGCCTATATGGAGAGGGTAAGTACCCAAGATGTCTGCTGTGTGTGTGTGTGTGTGCCTGCTGTGTGTGTGCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACTGCATGATCGGGG |
| LmeA$_{BC}$30$_{b}$ | 2,389 | 24 | CAACTTTCAACTTGACCTTGGCCT |
| LmeA$_{CE}$38 | 14,071 | 24 | GAATGAACCACCTTTGTGCTGAAA |
| LmeA$_{CE}$57$_{abcd}$ | 3,121 | 173 | AAGCTGAAGTTGACTGCCAAATGTGCTATAAAACCGCAGGTCAGTCTAGAGCTGGTTTGGTTCTCCTGGACGCACTGCATTCAATTATAGCTTAAAAGCCCTAATACAAGTGCAAGAATTTGTCTGCGTTCAAGCAGAGGCGGGGCAAGCCTCTGTGATGGTGGCGCCTTTGT |
| LmeA$_{CE}$60$_{abcde}$ | 171 | 168 | TGTCAATTTCAGCATCTGATCATGTGACATGCACCTCCCTGAGATGGCTGTAGATGGATCTCCACGTCAGCTTACGTCTCCAAATTTCTACTTCGGGGATCTGCTTCAAAGAGGCAGCAGCATAGAGAATCATGTTGAGCTCAGCTAAAGTGGAGATCCAAAGGTAGC |
| LmeA$_{EF}$62 | 6,797 | 40 | TTGAACTTCTGGATTTATACGGACATCACCTATAACCTTG |
| LmeA$_{EF}$69 | 4,536 | 38 | CCTACAACAAGCAGTGTCCTCAGGTCATACATTGTTTA |
| LmeA$_{EF}$75$_{bcde}$ | 118 | 105 | ATTGGCTTTAAACTCTTGCTGTGGTATGGGGTATCTCTAATCATATTCAGCATGTTTTGCACAAGAAATGTCAGCCAGAAAGGGCTATCTTCTCCGTTCGCCAAA |
| LmeA$_{FG}$78$_{abc}$ | 4,812 | 170 | ATCTATTTAAATATTACCTAGACAGTCGTAATTTGTCTGGGCCATATAGCAATGGTGCTCTAAGGTTTGTCGGCTTTTGTTCAGTTTTATGACTTGCTAGTATAGCTGGATTGTAGCTGTCTTGGACGAGAGGTTTCAGTTGAGTGAAGAGCTGGAAAGACAGAGGAAGC |
| LmeA$_{FG}$79$_{bc}$ | 4,124 | 55 | AGGTAGTTTCATGTTGTTGGGGCTCCAAATTTATCTCTATAACAAGAAACTGCCT |
| LmeA$_{FG}$85 | 3,504 | 44 | GGGCGCCAGCATTCCATTGAGCCTGAATGCACAACAGCGACCTC |
| LmeA$_{FG}$92$_{abcef}$ | 247 | 213 | CATAAAATAATAATAAAAAATATGGCTTCTACATTGAAATTATGACTGCAAAACATTGACCCTCTAATAGACTGCGGACTGATTTATACTTTATTGTTCTGTTTTACAATCACGTGACACCCCTAACCAATTGAATGGTAGGCAGTACTGAACTTAATAGCTGACTCCACTTGTTCACGCGGCCAAGTTGTTACATGAAATCCGCTGTTTCAT |
| LmeA$_{GI}$97 | 7,064 | 23 | TACCTCGTTGCCTATTGACCAAA |
| LmeA$_{GI}$103$_{ace}$ | 5,638 | 207 | ACGCCCTCTGTTGTTGCAGATAGAAGGAACTTCAAAGACTTAGCCCAGAGACTGCAATAAATGAAGGGTCTGGCATGTTGTCTGGAATTCAGCTTTTAATTAGTTTACAACAGCCTAGCTTCACTTAAGATTTTCTAGAGAAAGCTATTCATTTGTTTTGTCTGACTGTTTCAGACAAAGGGTCCGCGGAAATAACTGTCTTTATTG |
| LmeA$_{GI}$110 | 1,514 | 33 | GTTTATGGTGTGTAATATAGCACGGCAGTAAA |

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|---|---|---|---|
| LmeA$_{GI}$111$_{ab}$ | 181 | 168 | CACCTGAAATGCAAGAAGAGATTGGGTGAAACGGTCATATGGTATATCACGTGTATAAAACGGCTCAGACCAAAAGAAAATGGGGTTTGGTGTAAATCTGGGGTGTAATGCTATCATATATCAAGCTACCTCGTAAAACCGACACTGAAGCGTCCTGGCCAACAAATC |
| LmeA$_{IJ}$119$_{abcd}$ | 4,898 | 190 | ATGGCGCCTCTCAAAGAACGACTCTTCACAGGGAAGAGGAAAACGCCATAAATCCGTTGTTGTTTATGAAAATTTACAACTTTGTAATACAAGTTTATGAGTTGTTCAGTTTCTCCATTGGCCGCCGCTGGTCATGTGGATTGTAACCGTGAACATGAACTTTTTATAATTTCCCTTACGAGAATAGAGC |
| LmeA$_{IJ}$122 | 4,510 | 77 | CCTGGCTAATTTCCTGCTTCTCTTGGCATGCAGAGGAAAGGTTTCTTTCTGAGTACAACCAACAGGACAGCTGTCAG |
| LmeA$_{IJ}$130$_{ab}$ | 135 | 110 | GATCAGCTGATTGTATTTGCTGTCGTCGCTTTTGGCGTTACGCCATCTAGAAACAAACCATTTCGATGACTACTAATAGTTATAGCTAGATGTACTAATACACAACAAAT |
| LmeA$_{JK}$132$_{ac}$ | 329 | 293 | TGGCGCAAAAGTATAATTCAAAACTAGAACTTTAAGGCGGGGACGCGCCACTAGTACGCGCTTCTTCCCTCCGGCATCAACCCTGCCTTCTCATTTGTGCACGAGTTTACCTCCAGAGGTCATCAGGCAGGATTTACGACTGGACAACAAACGCACGTGATTCAAAGTCGTACCCCATATTTGGGTGCCTACGTAGGAGGGAACCAAGTACATGTCCCAGTCATTTCCATAATTCATCATAAATTGTGCAAGGGTGCTATAGACGCACAAAACGACCAAGAGTCACAAATCAA |
| LmeA$_{KL}$133 | 16,559 | 45 | AATAGCTCCAAGCTGTCAGGAAATAATTTACTTTTAAACTACCTA |
| LmeA$_{KL}$134 | 16,393 | 72 | GTGCCTTTGTATAGCTCTTTGCACGAACTTCAATAAGTGTCTCTTATAAGCGCAGCTTCAGTGATGTATGTT |
| LmeA$_{KL}$136$_{abc}$ | 15,637 | 207 | AAACTTTATTACCCCGAGTTCCGGCTATATGACATTTGGGTGCCAAATGAATAGGGTTTTGCCTTTGGATAAGATCGTAAAATCATCCATAGCAGAGATAGATAGGCTCACTGGCTATAAAATGTCACGTGGTGCCATTAAAGTAAGTTTTATGGTTTTGGGGAGTTGACATCCAACAGTATATGCCACATAACATATAATCACTGA |
| LmeA$_{KL}$137 | 15,105 | 13 | AAGGCAAAGCAAA |
| LmeA$_{KL}$140$_{bcde}$ | 9,436 | 56 | AAGATAAATCTGCACACCCTGGGAGCCACCAGCAGAGCTCGCTTTAGACCAAGTTC |
| LmeA$_{KL}$143$_{ab}$ | 8,950 | 27 | AGGTCAGAGTTGAGGGTCAAAAGTTTA |
| LmeA$_{KL}$149$_{abc}$ | 3,004 | 151 | CTTTTAGAAAAAGCTAAGTCCAAGGCCGAGGTGAATTTCAGGTCACTATGTCTAACAAATATGAAAATGTCGCCTGCTGAACGGCACGCCTTGTTATTTAACAAAGACTGTCAATGTGTAAGATTAATAAGAAACAAAGTGCACAGTGTCA |
| LmeA$_{KL}$150 | 6,987 | 31 | ACATTTCTGAAGTGTCTTTCTTTTTTTCTCA |
| LmeA$_{KL}$156 | 4,887 | 13 | TTCTACATTAGCT |
| LmeA$_{KL}$157$_{bc}$ | 75 | 69 | GGAGGGTTTTACATAGACCAGAAAAACTACAACGCGAGAAAAATTAGTATTTTTGCACTTCACAAATTA |

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|---|---|---|---|
| LmeA$_{LM}$160 | 20,895 | 254 | AAAGTTAAGTACTTGCTGAAGATAGCAATCACTTACAAAGGAATAACGGAATAATAAACTGCACACTCAGAAAAGTTTTAAAGTATTCACATGCACGAATGCACTGTATTGTTACAAGTGACTTTTTAAAAGTATTTTTTCTCTTTCATAATGACCTTTTGGACTTCAATGAGCAGCACAATATCCTTGCAAACTCTTTAAAGCAACTCTTTATGATTCTAAAGAAACTATTTTATTTTCTTGTTCCTAACTAC |
| LmeA$_{LM}$162 | 19,007 | 18 | CCAACTCCTGCTTTGATT |
| LmeA$_{LM}$184 | 8,692 | 38 | TCCTTTTTTTCCTTCTTTATCGTAGTTTCCTAAAAGAT |
| LmeA$_{LM}$179$_{abc}$ | 6,986 | 70 | AAATAAAAGGGTTTAAGTTGACGTATGACCACGTGAGCACATAATACAGCGCATTATTGTAGCATTTGGA |
| LmeA$_{LM}$181$_{bcde}$ | 6,749 | 76 | ATGGATTTTATTTTGAGGTATTTCCGTTGATTGTTCATTAATGTGGTGAGTTATTGCTGTTCAAGGCAAAGGTCAG |
| LmeA$_{LM}$188 | 4,048 | 114 | GCAATATGCCGTAAGGAGCTAGTGTTTTCTGTTTTAGTGCTCTGTTTACAGCTTTGGTGCATGAAGCCATAAATCTTGCGTAGCCATAAATGACAAAAATGCATTGGTATGCAT |
| LmeA$_{LM}$194$_{bcde}$ | 2,874 | 149 | TCGTCAGAAACTAAGGTAAGCAGGCCAGAAATAGGCAATCAGTTGTGAATGGCGGAGTTTATGTCCTAGTGATTTATAGCCATATGACTAAAATCTCGGTTCAAGAAGAGTTCACAAGCTATAGCTTCCTTTCACGCAGTGACTGATAC |
| LmeA$_{LM}$198$_{abc}$ | 1,238 | 155 | TGACCCCCATACATCAAATTACAGAGCAGTTTCAGAGACAGAACCTATTATCGCTAGGTTGAGAGAAAAGTTCAAGCCGTGGTCATGGAGATGATCGCCAGTTTTTCAGGTTCCTGGTGTTTTCCCCAATCCATCTTGTTTTAACAGGTAGAATT |
| LmeA$_{LM}$199$_{acd}$ | 228 | 222 | AATATTGATGGCCTTTTTTTTCTTTTATGGCTTTCATGTCACTTAGCTATTGAGACTAAGATGGATTTGTAGTTCTATTTCTCCACTATAGTAAGCGTCTTGTAATTCCAGGTCTAGCCGAAGAGGCCATTGGAGGAAAGACGTCACGTGAAAGGGGGGTGCCAATGTTATTCTATAAGGGTGTCAAGACCCTGTCAGCTTGTGAAATAAATATTGGGAAAC |
| LmeA$_{MN}$201 | 4,657 | 284 | AACAGGGTATATGAACACATTTTAAAGGTTATATAAATGTGAATTTCTTCGAACTTTATTTATCCCATGAAACCAATTAATTTGATTTTATTGCACTTCTCTGGTTTTAAATGGACAGAACAAACTGAAAGGCGCTTGAACAGGGTCCCTGGACAATTATGGATATTTGTACGTCTTTCATTGTGTGTATGCTGGTGAACATTCAGATTTATTTATTTGTCCTTGCATAAATAGAATATTCTAAGTGTTTAAAGTATTATTTATCCCCATCTGATCATATTTAT |
| LmeA$_{MN}$210$_{abc}$ | 567 | 161 | TTCTCCTGGTGTGTTGGTTCTTATGTGGCTAGGATGTGGGGGTCTGGGTGTCAAAACTTTGAAGATTAATGGATTACTTTGTTAATGACTCAAGGCGTCAGATTTAGGTGCTTAAATGATTTGTGAGGTGTAAAGCGTCTTCCCGACAGTCAGAAACAATG |
| LmeA$_{MN}$211$_{abcdef}$ | 306 | 209 | TGTAAATAAAGCACTGCTGGTCCAGAATGAGGCGTTCCTTCCTGACTTTTTTTTGGATCAATCACACAGACAGTGGCTTCTTTTGATTAAACCCCAAATTGTCATTGGGCAGAGGCAATCATGTGACAACCAATTCGGTCCAATTTCAACCTTGTCTCCATGAATTCAATAGTTTAATAGTAGCACGGTCCCCATACGGCTGTAATCAG |

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| Lme$_{NO}$219 | 3,061 | 32 | CTCATAAATCAAATTGCTTTTTATGAATGAGA |