

PFC	Dist to 3' gene	Length	Sequence
LmeD _{AD} 1 _{ab}	59,957	331	CTGGTCAAAATGACCCATGCATCCTTTCTAGCCCGAAATGTCA TTCATCAAAAAGTTGTGCTCGTCATTAAGGTAGGAATGACGCT GTTGGAATAATCATTTATTGTAACAGCTTTATAAGCAAATAAAT ACAAGCGGCTGTCAGTGGATGATAAAAGCGGCCTTTGTGCAGA CAAATACATCCAGGTAGAGACAGAATAGAAGTGAATACTAGAT CTCTGTCTTAAGCTTGATCACTGCTTGGCTGGATTGTTCTGGG GTTTGGCCTCTGGGGTGAATGACAGTCTGATTAATAAAAATG AGCATTGCAACGCTTCCCTCTTCATTTA
LmeD _{DE} 10 _{bcd}	2,950	145	CTTGCAACACTGGCGGTAATAAATGGAATGACTCAAGACACTC TTCTCTTGCCCTGCTATTTTTACGAGAGCTGTCAGACAGTGTCT GTTTCATGTTCTCCAGATACTGGGGGCGCCACAACAAAGTTAAG GTCAAGTTAGTGTCT
LmeD _{DE} 9 _{bcd}	191	70	TATGGTAATTTCTACATTGAGACACGTGACGCAATTACTCCTAG AATCGATCAAGATGCATTACACGTCA
LmeD _{EF} 11 _{ab}	5,450	28	TGTTTATAAAACCTTGAAGTGTCTAGAC
LmeD _{EF} 19 _{abc}	207	177	GTCGCTGTTCCACATATTTGAGGTGAAAGTCAACCATCAACAA CCACGTGACTCCTAACGAGGTAGTGTCTCAAGGCCATTTTCAA ATTTCAATGGCTTCTCTGTCATGTGGGTCTGTAGAGACACTCAC AATTATACAGAGAATATTTTCTAGAGATGTCAGCCTACAAAG GACA
LmeD _{FG} 21 _{ab}	726	46	TTTTATTAGGGAGGCATTATAGTATAATCAAATGCACCTCATAA AA
LmeD _{FG} 23 _{abce}	160	130	AGCGGATTGGTTTACTCCTCATATCGGTAAATATAACCAGTG AGCTCCGTAACCAATGGTTGAAAGTCGCTATCTGCAAAATACTA TGATTGTTGAGAGTGGAACGTATCTTTACTCTAACAGTGTAA
LmeD _{GH} 25	5,468	235	GAAGGTGTTGGTGCTGTATCACTATTTTACGCGTTTACCTATA ATGCAATTAAGCAGGAAGTAACGGGTACAATAAACCCATAG AATTGGCTAGACGTCTGGAGCTAATGAGTTTATGAGTTGTAAGT TGGAATTGCACTGTGCTTTGAAACCGTCTTATTGGATGTTTGT GTCTGCTGGCGACAAGCAACGATGCAAAACACAAATTATTGCAA GGAAATCTAGACAATAAA
LmeD _{GH} 28	3,362	33	AAAATCCATTGGTCTTCCATTAAGGTACAAACA
LmeD _{HL} 35 _{ab}	19,854	52	AAATCCACAAGGAATTGCAGTAAATTCCTTTTTTGTGTTGAAGAA AATTTACA
LmeD _{HL} 37 _b	6,869	46	CACGTGATCGCAATAAAACTTGTTTTATGACAAGGGAGTTGAC AAG
LmeD _{HL} 46 _{abcde}	2,687	81	AATAACTCTGGCTTTGACCTGTCTGAGCAAGTCGCACAATAAG GTGAAATTCAGTCCACAACGTCTAACAAATTTGAAAAAT
LmeD _{HL} 47 _{abc}	2,053	86	TGAACTTTTGTACTTCTTTGCGTGGTTGTCGGCAAAGTAAAAAT AATGAAACTTTGTGATATGTTTGTAAATGATTTAGTATGACC
LmeD _{HL} 48 _{abcde}	1,286	82	GTCTATATATACCCTGTAGAACCGAATTTGTGTGATGTTATCAG AATCACAGATTCAATTCTAGGGGAGTATATGGTCGATG
LmeD _{HL} 49 _{abc}	153	147	TGATAAACTCCTGGATTTTTATTGGCTATCTCTGTCACATGGG TACCTAACTTTATTAGTTGACAGCAAGTAGGAGGGCTCTATGT AGGGAGAGAAAAAAAAGACAACCTCGAGAAAAATTAGTATTT TCTACCTTCAGAAATTA

LmeD _{LM} 56 _{abcde}	12,504	203	ATTGTTTGTATGACAAAAAGCACAGAATTCACGCATAGCAAAG ACGACTTCTTTTTGACGCCTTCACGTTGAGAAGCTGAAAAGGT ATTTACTGAAGTTCGGCTAAACTGCAGAAACAGGTTCAACTA GGGGACAAATTTCTATTTCGATTAGTTGTATTTAGCCGGGAGA GCTGACCTCTAAACCCTTGACCTTTTGGAC
LmeD _{LM} 58 _{bcd}	10,151	198	CACGTGATTTACTAAATAATTAATTCAGTACGTCCCCTAAGAA ACACGGCGTCGTCATTAATCGACCAAGCAAAGGACTCTATCAG ACTTGAAAACGAAAGAGATCCCAAGAATATAATATACAAACGG TGCAGTATCCTAATTCTACTCTTGAAGCTCTTTGGTAACATTGG GACAAATGGAAGCTTGGTAGGTA
LmeD _{LM} 64	9,650	149	GACAATGCCGACTGTCAGTGCATCTGCTCCTATTCTTAAAGA CGGTGAGAAAAGGGCTGGACTTCTTTTCAATCACGGGTAGTA AATTTTTCTTTGGCTCATTAGAGAAAAGGCTATAAAACTGAGTCG AATGTTTCCCAAGGCAGGT
LmeD _{LM} 65	9,074	143	AAAGTTTCTTTTTAGAGCTACATTAGGATAATAAACCATTA TTAGAGGTTCAAAGATGACATATACTTTCCAGTTTCAGTAGTGA TTGGGGAAATAATTCATTGGTTGCTCATAGCTGCTCATTTTGT TGACCAGAATC
LmeD _{LM} 67 _{abc}	8,770	116	TGACAATAGCCAGAATTGTTATAAATCATTCTAAGTAATTCATG AAACAGTGCGAGGCTGTTGGGGCCGGGCGAAGATTGTAATC TTTCAGTTTTATTGCCCGTGAACATATG
LmeD _{LM} 68	8,090	21	ATATTTTACTGTAAAATATA
LmeD _{LM} 69 _{abcd}	7,246	92	CTCAATCAGAACAATCTGGTATACAGATCAGTGAACAAATAT GCTTGTATTTAAGGCAGCGCCTATATTTGTGATTATAAAAGGT TTCCG
LmeD _{LM} 70 _{ab}	7,026	233	TTTATTGGTAGTTGAGCCTGAGACTGTTTCCATTCTATCGGGAA TACTGTCTGCACTGGTATATGGAAATGTCTGTAAAACGCAAG ATCAGGTTTAGGACAGTATTGTCCGACACAAAGGGTGAAGGA TATACACAAGCAACCGCAGGCGAAGAACTGAGTCTGAGAAG CGCAGGTTTATGATAAATTGATATACAGGTAAGCTATAGCATG ACAAAATGGAACCTTAA
LmeD _{LM} 61 _{ab}	4,621	42	GTTCAATTAAGGGGTGAGTTATTGCTGTATAAGCCAAAGGTCA GTCATAAATTTTGTGCAAACCCAATGACAGGTGCATTGATAT
LmeD _{LM} 62 _{ab}	2,302	45	G
LmeD _{MO} 71	19,338	474	TTAATTTATGTACTTTTTCAATAATGTCCGAATTGCATTAAACT CGATATGTATTTATTTTAAATAAGAGCATTTTGTATCACTT ATTTATCCTTGTCTTAATGTATTTATGTGAACATTTGTAGA CTACAGCATGACGTGGACGGGTGATTTCAGATCCATGGTCATT AAATTTTCTCTTTAGTAAACTTGGTTTGAATAGTTCCGAAA GTAGTTCTGAACAATTGTATCAGTGGCTGGTGTGTGAGTTTAT GTAAGGGTACTTCTGGCAGCAGATTGTAAGTTTATAGTGAATC AAAAATGTGGCATTATACACAATAGATTTTGCAGCATTCTGAA AGAATATTTTATTTCAATTGTCTAGTACTATTTCAAAAAGTTTA GAATAAAAATATTGTCTCTGAATGAAGGTGTATCTTTTATTCAT ACTAAAATGTTGAATAAACAGATCACTCAATGCCT
LmeD _{MO} 72	9,621	30	AAAAATGAAAGAACTGAGCATGTTACAGT

LmeD_{MO}73

7,631

27 AAAAAAAAAAGAAAAAAAAACTATT