

PFC	Dist to 3' gene	Length	Sequence
			ATTCATCAAAGTGCCGGCGCTTCGCTGGTAAAACGCAGGCT GACGTTGCTCCAATGATCATTTATTGTAACAGGTTTATAAGCA AATAAATAGGAGAGGGCTGTCACCTTGATGATGGAGGCGGCCT TCGGTCAGACGAATATTATCCAAGTGGAGAGGAGGAGAGGA GTGAGGAGCGCGCTGCTCGTCCCTGAGTTGATATCTGAGTCT GTTTTAGATTGCTCTTGGGTTTGGCCTCATGGGCGAAATTGAC AGTCTGATTAATAAAAACGAGCGCGCAGCATTTCCTCTTCA
OlaDA _{AD} 1 _b	9,694	299	TTTA
OlaDA _{AD} 2	4,918	27	ATTTTAAGTTCATTAAGTTCATAAGTT TAATGCATTACACAAACAAGTCACATTGGTTTAAATATAATG
OlaDA _{AD} 3	3,333	57	ATTATCAATTAAGA
OlaDA _{DE} 8	3,353	24	ATGTTTGCATGTTTATTAATGTT
OlaDA _{DE} 10 _d	1,910	16	CAAAGTTAAGGTCAAG
			TAATGACTGATATTGATGTATGGTAATTCCTTAGCTCGATCAC ATGACACAATTACCTCAAGAATCGATCAAGATGTATTGCAGG TCTGCCTGCGTTTCTCTATTTTTTCTCCCTCGTGGGCTTTCC
OlaDA _{DE} 9 _{abce}	218	153	ACACGCGCGCCGTGCTATAGATGG
OlaDA _{EF} 11 _{ab}	2,657	28	TGTTTACTAAACCTTGAACCGTCTAGAC
OlaDA _{EF} 17	1,738	30	TTTATTGCTTCTAAATTGCAATAGCCTTA
			GTCGCTGTTGACCACGTCTGCATCCGCAGTGGGAACGCGTGC GTGGCGAGGAGGCTGCGTCTCAAGGCCATTTTCAAATCTCAT TGGTGGGTTTGTATGTGGTCTGGAGGCATCCTGACTTACAGA
OlaDA _{EF} 19 _{ac}	193	162	TTGTTTTTCTAGATATGTCAGCTTACAAAGGACA
OlaDA _{FG} 20	1,409	33	TGCATGTTTGTTCATGTATATAATGCAATAAA
OlaDA _{FG} 22	434	33	TTTACAGCATGTTATTACATCTCATTACGAGG
			GTAAATATGATCACGTGATCCACGTAACCAATCCCTGTAGAT GCAGGCCAGCAAAAATACTATGATTGTTTACAGAGGGAAGCT TCCCGTACGAGTGCCTGTATTTTATGAGT
OlaDA _{FG} 23 _{bcd}	128	113	GAACAAAGACAGTATTTCACTGGTGCCTGACAGGCAGCTGCC AAAGTATTTACAGCCAACCTGCAATGCGGC
OlaDA _{GL} 40 _{ab}	5,098	71	CTATTAATTTTGTTG
OlaDA _{GL} 27	4,754	16	
			CAGGAAGGAGCGTGGTCCAATAAAGCTAAAGAAATGGCCAG ACGTCTGGTCTAAATTAGTTTATGACTCTTTCAGTAATT
OlaDA _{GL} 29	11,025	80	
OlaDA _{GL} 32	3,631	24	GGATTGGCCTAAAAGAAGGAATGA AATTTACAACCTTGGAATAGAGGTTTTTATGTGCCTCCATCGC CTGTCATTGGATGCCACTGGTCATGTGTGAGAGGCAAACGTC TTCATGGCCCTTTTCTGATTTCCCAGGCGATTTCCCCCCT GCATTCTG
OlaDA _{GL} 35 _{bcd}	7,177	136	TATTGAATAAGTGCAACTTCGGGGATTATTTATGGGCCAGTGC GGGGTTGTGAATGGCTGCGAGGAAAACAGTGACGCCATTA GTTTGTTTTATGGCTTGGACTTGACAAGCCAAAATATAATTC
OlaDA _{GL} 37 _{abcd}	3,308	135	TCATTGT
			TTATTGATTCCCAGAAGCTGTTGCCACTGACCAATGGGCTCCC GAAACACTTTTCTTCTCTTTTTTTCAAAGGGACAGGGGACAG TGAAGAGATGAGAGTCATGTAACCTTTTGGATGACCCCATCTT GACAAAGACAGTGTCCATCACTGTCTCCTCAGTCATTCTTCCCT GCTTTTATGCCAAAGGGCTTTTTGTGCTTTTGT
OlaDA _{GL} 38	641	205	

OlaDA _{GL} 46 _{cde}	2,326	41	AAGGTGAAAGACAGGTCAGGGCGTCTAACAAATATCAAAAT GTCTATATATACCCTGTAGAACCGAATTTGTGTGAAGAACGC
OlaDA _{GL} 48 _{abcde}	980	82	TCAATCACAGATTTCGATTCTAGGGGAGTATATGGTCGATG ATTGGCCGATCTGGTCACATGGTTCGCTAACTTTATTTCAGTTG ACACCAAGTAGGAGGGCTTTATGGAGGGAGGAAAAAAGAC
OlaDA _{GL} 49 _{bc}	123	123	AACTCGAGAAAAATTAGTATTTTCTACCTTCAGAAATTA TGTTTTAACTTATTTTGTACAAAAATAACTAGCTTGGAATCT CCTTAACCCAAATTTCTATTCCCACACGGAAGACATTCCTGC GCGCATTCTGGTCTGAGCGCCTTATAAATCTCCTCTGACATC TCTGTAAACAGTGTACATTTTCAGTGGGCTCTCTTATTCTATA TGAAACTCACATGAATGATCATTCGATCCTGCATGGCTCAA TTGATTTTGGCCGTTTTTACCCCATCGGACATAATCGAATAT TTAGGATTAAGTGGTTATTTTACGAAGTTACGTGGTTATT
OlaDA _{LM} 52	7,599	307	TATTTGTT ATATTTTTGTTTTATATGGTCATTGTGCACGAATAGAAAAAG CCCAGAAGCTTTTTAGTACAAGGAGGTCTCTACTCTAAAAGTG ATGAGAGGGTTGAAAAGGTATTCATCCGAAGGTCGACAAAAG GCAGCTGAGGCAGGTTTCGTCGCGGGGACACATTCAGCCCGG AGGACTGACCCAGCACCCCTGACCCGCCGACAGGCAGCA TTTTCTCTCCAGGCGCTACTCGCTTTGGTTTGAAGACTGTT GTGCTGTTAAAAAACCTAAAGCCATTCAAAGTAAAGAGTCA CTTAATCCACATTTTACACGTGTTGAGCTGTATTTATA
OlaDA _{LM} 53	7,101	336	
OlaDA _{LM} 54	6,678	15	TTTTTTATCTTGAT AGACAAAGTGATGCTTCCAGTTCAGCGTCCTGTCAAAAGTGA
OlaDA _{LM} 55	5,731	60	TCCGGATATTGATGCTGA TGACCTACATGTCTGAACAGCAATAAATGAGAGCCAAAGGCA GTGCCATTTCAATGACACTGCACCCAGTGCATGAACACAAC AGCCTTGCTCTCCATCCGGCCATGTTTGATTTCCAGCTGTTTT TTCGCAGAAACCTCTCCGAGCCAGACAACCCCTAAGATATA TTAAAGTGCCTGTCTGCATTTCAGAGATATAATCCAGAGACT ATGCCACTCCGCTCTCTATTCTCGACCACGTGATTGTCTAAAT AATTAATGCAGCACGTCCCCCTAGAAACACGGCGTCGTCATT AATCGCAAGGACTCTATCAGACTTGAAAACCTGAAGAGATCCC CCAAGAAAATAATATCCGATTCTCGGCGCAACTGTAGCCCCG CATTGTAGCTGCGCATCTGAGCCGATGGATGTTCCGGGTAGGT
OlaDA _{LM} 58 _{abcd}	5,413	425	AAA
OlaDA _{LM} 59	4,045	16	GTCATTTTCCCCATAA
OlaDA _{LM} 60	2,310	29	CAAACTTACCGTAACAGCGCGTAGGGCAA
OlaDA _{LM} 62 _a	916	36	GTCATAAATTTTGCCACGGTCCACACTGACAGGTGC
OlaDA _{LM} 63	2,423	22	CATTTTTGGACAAAAGCATATA TAAATCAGTGTAAGTAATCCTTAAGTGTGCGAGGCTGTGGG GGCCGGGCGAAAACCTGTAATCTTTCACTTTTATTACCCTCCG
OlaDA _{LM} 67 _{bc}	4,439	93	AACATATG TCACGTGAACAAATATGCTTGTATCTAAAGGCAGCGCCTTTAT
OlaDA _{LM} 69 _{bc}	3,614	47	TTGT

OlaDA_{LM}70_{ab}

3,430

235

TTTATTGGTAGTTGAATGCAAGTCCTTCCATTCTTTCGGGAAT
ACTGTCTCCACTGGTGTATGGAAATGTCTGAAAAACAGCAAG
ATCAGGTTTAGGACAACCTCTGTCTGCAGACAAAAGGGTGAAGG
ATTTATTCTAGAGACTGCGTGGAAAGGAACCCATGCTCAGAG
GAAACTTGCTTTATATGATGAATTGATTCCAGGTAAGAAACT
GCACGGCGGAAAGCAACCTTAA