

PFC	Dist to 3' gene	Length	Sequence
OlaAA <sub>AC</sub> 1	5,762	16	CTGTCCTTGTGCGCCC
			TGTTAATTATCTTGATTTCAAAACAATCTGAATCAAATCATA CCATACAAAAATCAAAGCAAAAACGCAAGACTTAGCATA AAAACAACGTTCTAGCTTTTATAATTCTAATCCTAAAGTTGG TTTACTTAATTTAAAAATTATGAGATTGTCTATTGTTTATATGT TTTCCTGAAACCGCAATAAATATGTTTTTTTTACTTGTGCTG TCTTCCAATTTTTCTGTAACAATATGTTTCTAATTTTATGGG
OlaAA <sub>AC</sub> 20	1,772	287	GATGTGTATATTTATTATACTTATTTGGATGTT TGGCTAGACAGCAACTTTCAACTTGACCTTGGCCTCCAGCC
OlaAA <sub>AC</sub> 30 <sub>ab</sub>	921	42	G
			CTTTGCATAGTGCGGTCACGTGCCGGCGCCCTGACCAATCA GAGCGCGAGCTGCGCGCTCTTGTGCGCGTCAGAGTGGCTTT ACTCTCTGAGAAGCAGTGCCTTTTTTTCAGTCAGTGGGCT TTTTAAAAAAGAGCCAGAAGCTTCAATGTTGGA
OlaAA <sub>AC</sub> 31 <sub>acdef</sub>	167	157	ACCAAACTCCAGACAGAATCTTTGCTTGTGTTTTGTTCAT TATTTACCACGGTGGTTAATCTTA
OlaAA <sub>CE</sub> 47	6,877	66	
OlaAA <sub>CE</sub> 49	6,475	17	AGAAATAAAGATTTTGC
			GCTATAAAAACGCAGTTCAGTGCAGAGCTGGCTTTGGTTTTTC CTGAGCATCCTGTCTCAATTACAGCTTAAAAGCCTCAGTA CAACTCGTAGAATTTGCCTGGATTGACTAAGAGGCGG
OlaAA <sub>CE</sub> 57 <sub>bc</sub>	2,146	120	
OlaAA <sub>CE</sub> 50	1,266	23	CTTGAGACCATTTTTTAGGCAGA
			TGTC AATTTCTGCCGCGTGATCACGTGACCCTCCTCCTCAGT GGAGTGGATGGAGATGGCTCTCCACGTCAGCTTACGTCTCC AAATTTCTGCTTAGCGAACCTGCTTCAAAGAG
OlaAA <sub>CE</sub> 60 <sub>abcd</sub>	204	115	CCTAATTATGGGACATCCTCCCCGTTGCCGAGCAACGCCG CCATAAAAGCTGTCTGAGAGTCTGGAGCATTGTACAATTG GAGTGCAGTGCAATAAACCGTCTGAGACCCAAGTTATTAA
OlaAA <sub>EF</sub> 65 <sub>bcd</sub>	3,082	128	CTGTG GGGAGGGACCTCCTTTTTCCAGTCTTTTCATTGGTCTGGGG CCTACCCTGGAGAGGGGGTGCCTTAATCATATCCAGCATG TTTTGTACGAGAAATGTGAGCCAGAAAGGGCTATCTTCTTCC
OlaAA <sub>EF</sub> 75 <sub>acde</sub>	147	134	TTCGCCAAA GACTGTGAGTGGTTTAGGTAGTTTCATGTTGTTGGGGTCCA TTTCTAACTCTGCAACACGAAACTGCCTTAATTGCCACAGTT
OlaAA <sub>FG</sub> 79 <sub>abcde</sub>	2,645	85	A
OlaAA <sub>FG</sub> 89	904	17	GTAAGTGTTTTTATTTT
			CACGTGACTCTGCTGACCAATGGCAGGGGCGTCTGTCTCCC CATTACTTTCCACTGTAGTTCTGTGTGGGGCCAAGTTGCTA CTTGATTTCTCCACATTGTTATTTGTGAGGCTGGGTTTACTG
OlaAA <sub>FG</sub> 93 <sub>abcdef</sub>	223	127	C
OlaAA <sub>GI</sub> 94	3,952	19	ACTACCTTCATTTTGCACA
			TGTTAGTTGTATGCAGTCATAAAAGACAATTACGCCATAA CCTTTTATTGGGTGCAAAGCGCCGCAAGGCCGA
OlaAA <sub>GI</sub> 98 <sub>abcd</sub>	3,113	73	

OlaAA <sub>GI</sub> 103 <sub>bcd</sub>	2,638	288	GCAGATGGACCCAACTTCAAAGACTCGGCCAGAGACAGT GCAATAAACGCCTGGTCTGCTATACTGTCTGGCATTCCAG TTTTAATGACTTTATGGCAGTCCAGACACAATTAGGCCGTTT CCAGAATGACACCCATTTGTTTCTTCTTTCTGTGTGA CTGAGATTTCCACAAAAGGCTGGGCGGAAATGATCAGCTTT ATTGGATCCTGCCCGCCGGGACGCGCAGGACTCACGGTCA TTCTGAGCAATCCTTTGTTTCTACCTGGGAACCTTCCGCC GTTTGGTGTAAATCTAGGGTGTATTGCTGTAATATATCACAC TACCTCGTAAAAACGACACTGGGGATTCTGGGCCAACAAAT
OlaAA <sub>GI</sub> 111 <sub>b</sub>	98	84	C ATGGCGCCTCACCCCTCCCTTCTCCCTCCCCCTTCTCCCTC TCCCAGCACCGGGTCATAAATCCGTTGTGTTTATGAAAAT TTACAACGTAGCGGTCCAACCTTACGACGCGCCTCGGCTGC CTATTGGCCACAGCGCATCACGTGGGAGGGACCCGTGAACA
OlaAA <sub>IK</sub> 119 <sub>abc</sub>	3,725	170	TGAA
OlaAA <sub>IK</sub> 120	2,375	21	TTAAATAAAAAACACAACCTT
OlaAA <sub>IK</sub> 126	1,416	14	GGCTAATAAAAAGAT
OlaAA <sub>IK</sub> 132 <sub>abcd</sub>	384	382	TGGCGCAGCGCACAATTCAAACAGCAAAGCCCTGCCTTC TCGCTCGCCTTAGCCCAGAGCGGAGAGGGCGCGCCCTT TACATCCCACCCAGTATTTCTGCGTGCAGGTTTACCTCT GGAGGTCACCGAGCAGGATTTACGACTGGTCAACAAAAGCA CGTGATTTCCCGCCGTACCCCATATTTGGGTGCCTACGTAA GAGAGAATCAAGTCCATGTCCACTCATTTCATAAATTCATC ATAAATTGTCAAGGGTGCTATAGGACGCACTAAGCCATAA GAGCCACAAATCAAGAGCGCAGGTTTATGCTGTTTGCTTTC CACAAATAATCATAAAAAGCAACAAAAGCTACAAAACGGA GGAAGTGTCAAC
OlaAA <sub>KL</sub> 136 <sub>ab</sub>	6,756	199	AACTTTATTAAGGGGTTGATTCTGGCTCCCTGACATTTAGG TGCTAAATGAATGGGGTTTTGTCTATGAATTAGATCGTAAA AATCATCCGGAGACCGGCCAGATAGGCTCACTGGCCATAAA CGGTCACGTGGTAGCCATTAAGTAAGTTTTATGGTTTTGGG GAGTTGACAGTATATTGCACATAACATATAAT GGTTCATCGGGAGGTCAGCCGCAGCAGCAAGATAAATCTGC ATCCTCTCGGAGCCACCAGCAGAGCTCGCTTAGGCCAAGT
OlaAA <sub>KL</sub> 140 <sub>abcde</sub>	5,016	84	TC GGTCAAAAGTTTACGCACTGAACAAGTCTCAGTCATCTGTT CACTCAGAGCCTGATGCCAGCTTTATAATAGGGATCTTGAC TCTCCACACAAAAGGCAGAATAGCTTTGCATTACATATGTT GCACGGTGCCTCCAGGTGAACCCCTGGAAGCGCGATGACCT CGCGTTTGGGACCGGGGGGGGCAACAAGATTGAGTGGT TGCGTTTTATTAGGGAGGTTGATTGGTGAATTTCTTTGAAT AAATTGCATTTGATATGTTTAGGGACCAGGGCAAAATTTGC
OlaAA <sub>KL</sub> 143 <sub>bcd</sub>	4,450	292	ATTT
OlaAA <sub>KL</sub> 146	2,512	19	TAAGTGTTCTGTTATTTTC TCCAAGGCCGGGGTGAACCCCGGTCCTGCGTCTAACAGA TATGAAAATGTCGCTCTTTGGGGAAAAAAGGGAGGGCAAA CGCCTTGTGTTTAAACAAAGACTGTCAATGAGTAAGATTAAT CAGAAAACAAATGGAAACGGTGTCACTTTAGGGTCAGGCAG AAGTTATCTCTGT
OlaAA <sub>KL</sub> 149 <sub>bcd</sub>	1,744	178	

			CCATTGGTTCCTGTTTACATGATGCCACAGGACAGCCGGT GATTGGTGGCTCCTCACACGTGACCAGGCAACTTTGTACAT TTGACAGGGAGTAGGAGGGTTTTGTGGAGATCAGAAAAACG
OlaAA <sub>KL</sub> 157 <sub>abc</sub>	164	164	ACAGCGCGATAAAAAATTAGTATTGTTGCACTTCACAAATTA
OlaAA <sub>LM</sub> 165	5,943	15	TGACGGAAAAACAAGC TTAATGATTCACGGACTCAAATAAAAAGGGATTTAAGTTGAC
OlaAA <sub>LM</sub> 172	5,117	57	GTTGCGTCACGTGAGC AAATAAAAAGGGATTTAAGTTGACGTTGCGTCACGTGAGCAG
OlaAA <sub>LM</sub> 179 <sub>ab</sub>	4,878	53	GGCGCATAATAC
			CTGTCAGGGACGGATATGTTTTTCCACGCGGACAGAGTCGG AGCCCAAGCTATGGGAGGATGGATTTTATTTTGAGGTATTTT
OlaAA <sub>LM</sub> 181 <sub>abcd</sub>	4,625	115	CGCCGATTGTTTCGTTACTGTCGTGAGTTATTG GGAAGAAAACCGGAGCCCTGGTCTGGCCATACGATGCAGAT
OlaAA <sub>LM</sub> 182	5,026	64	TATATGCTGGTTACCCCACTT
OlaAA <sub>LM</sub> 189	3,199	14	GGATTTTATTTTTT
			AAGGCGCGACTTCATTTGCATAATTTTTCTTGTCTATGGTGA CGCTCTGGTCTGGGCAGTTCCTGGTGTCTGCATGGTACTG GTGAAGGATCTCATAGTCAAGCATCGCCTTGGCTGACGTTA ATATTGCTATGAAGCACTGTCCACTGCTCCATAGCATGACG
OlaAA <sub>LM</sub> 193 <sub>abcd</sub>	2,249	201	ATACATTCAGTCTTCAGGCCAGATAAATCTTATCT ATCGATTTTCGTCGCTGAATGAGAAAAGTATTGCACGGTGCTTT GCATTCATCGTGAGAGGATAAGGTAAGCAGGCCAGAAATAG GCTCCCTCAGTTGTAATGGTGGAGTTTGTGTGTCGCGCAGT GATTTATCACCGTATGACTTAGATCTCGGTTCAAGGAAGATT
OlaAA <sub>LM</sub> 194 <sub>acd</sub>	1,819	169	CA
			AAAGTTCCTCCATGGTCATGAGAATGCGAAAACACCCGTC TGGTTTTTCTGGTTTTCTTTGGTAATTTCTT
OlaAA <sub>LM</sub> 196	826	72	
OlaAA <sub>LM</sub> 197	784	17	GGTTTTTCTGGTTTTCT
			TGTCAGGTCTGTATTGAAAAGTAAGATGGATCGCCACCATT TCTCCTCCTCACAGTGCTTCTTGTAACCCAGGTTACCCAG GGAAGCCATTGGAGGAGAGGCGTCACGTGACCACGGGGTG CCAATGTTATTCTACAAGGGTGTCAAGACCCTGTCAGTTTCT
OlaAA <sub>LM</sub> 199 <sub>bcd</sub>	190	184	AAAATAAATATTGGGAAAC AGAAGCCTTAAATGTGTTGCGAGGGCACCGAGCTGTCAGAC CTTTGGCGAGTAAGATTGATCGCGCACAGGCTTCCAGGAC
OlaAA <sub>MN</sub> 204 <sub>abcd</sub>	1,403	91	TCTTTGTTT
OlaAA <sub>MN</sub> 216	1,369	25	GTCAGACCTTTTGGCGAGTAAGATT TGTAATAAAAAGCAGTCGTGCCCCAGCTGAGAGAGGCGATA TTCACCAGAGTTTTTGGATCAATCAGGCAGACAGTAGCTTCT TTTGATTAACCCCAAATTGTCATTGGGCAGAAGTAATCAT GTGACAGGCAATTCGGTCCAATTTCAACCTTGTCTCCATGA ATCAATAGTTAATGGTAGCTCGGTCCCCACAGGCCGTA
OlaAA <sub>MN</sub> 211 <sub>abcdef</sub>	334	211	ATCAG
OlaAA <sub>NO</sub> 219	3,083	30	CTCATAAATCACTCCGTGGCATGAATGAGA
OlaAA <sub>NO</sub> 217	1,840	29	TTTATGTATCTCTTGAAAACCTTGAAAAA
OlaAA <sub>NO</sub> 220	1,434	24	TAAACATCAAGTCTGCTTGACCTC
OlaAA <sub>NO</sub> 222	283	36	GCGTCACCTTGATCGACGAGCGCTTGAATTTAAAT

OlaAA<sub>NO</sub>223

194

ACTGGCTGACCCTGGCCCACGTGACAGCACCCGTTTCATTGA  
74 TATCACCCACGCGCCCTCCTTCCTTACTGAT