

PFC	Dist to 3' gene	Length	Sequence
OniA _{AC} 30 _{ab}	1,073	35	TGGCTAGACAGCAACATTCAACTTGACCTTGGCCT
OniA _{CE} 36	10,037	24	CCGGGTCTTATCGACGTGGAAGAA
OniA _{CE} 42	9,408	23	ATTATTATTATTATTTTCTTTTG
OniA _{CE} 54	3,540	38	GCCTGTAGTAAAGCTTTGAGCTTTTTCTTTTCCTTGAA GCTATAAAAACCCAGGTCTGTGCAGTGTGGCTTTGGTTTTCTG GGCATCCTGTCTCAATTACAGCTTAAAAGCTTCGGCACAACCTCT TAGAATTTGTCTGGATTGACCGAGAGGCGG
OniA _{CE} 57 _{bc}	2,236	120	TGTCAATTTCTGCCGTGTGGTCCGGTACGTGACCTCCTCCTCCGT GGAGTGGATGGAGATGACTCTCCACGTACGCTACGTCTCCCAA TTTCTGCTTAGCGAACCTGCTTCAAAGAG
OniA _{CE} 60 _{abcd}	206	118	CCTAATTACGGGACATCCTCCCCGTTGCCGAGCAACGCGGCCA TAAAAGCTGTCTGAGAGTCTGGAGCATTGTACAATTGGAGTGCA GTGCAATAAACCGTCTGAGACCCAAGGTTATTAAGTGTG CTCTGAAATTTTATGCACACAGGTTTTATATAAAAATTAAGAAAGT GCCTT
OniA _{EF} 65 _{bcd}	3,627	128	GGGAGGGACTGCCCATCTTCCAGCTTTTCCATTGGTTTCACAGTC TGCTCGGCGGAGAGGGGGTGCCTCTAATCATATCCAGCATGTTTT GCACAAGAAATGTCAGCCAGAAAGGGCTACCTTCTCTCTCGCC
OniA _{EF} 72	1,161	50	GCCTT GGGAGGGACTGCCCATCTTCCAGCTTTTCCATTGGTTTCACAGTC TGCTCGGCGGAGAGGGGGTGCCTCTAATCATATCCAGCATGTTTT GCACAAGAAATGTCAGCCAGAAAGGGCTACCTTCTCTCTCGCC
OniA _{EF} 75 _{acde}	150	137	AAA
OniA _{FG} 76	3,273	12	AGTTTTATGACT AGGTAGTTTCATGTTGTTGGGGTCCATTTCTAACTCTGCAACATG
OniA _{FG} 79 _{bde}	2,879	69	AAACTGTCTTAATTGCCCCAGTTA
OniA _{FG} 83	1,374	20	AAGAATTATGCATTTAATTT ATACAGTATATTAATGTATCCTGGTGCAGGCCATTCCCCGCGCC
OniA _{FG} 88	1,721	58	ATTTCTTTTAAA CACGTGTGTCTGCTACCCAATGGCATGGCAGCCTGTCTCCCCATT ACTTTCCCACTGTAGTTCTCTGTGGAGCGAAGTTGCTACTTGATTT CTCCACATTGTTATTTTGTGAGGCTGGGTTTACTGC
OniA _{FG} 93 _{abdef}	219	127	ACTACCTTTATATTGCACA
OniA _{GK} 94	10,308	19	CTATATTTGTTGTCTGTCT
OniA _{GK} 96	10,146	19	TGTTAGCTGTATACAGCCATAAAAGACAATTACCGCTATAACCTT TTATGGGGTGCAAAGCGCTGCGAGGCGA
OniA _{GK} 98 _{abcd}	9,217	73	GCAGATGGACCCAAACTTCAAAGACTCGGCCAGAGACAGTGCAA TAAAACGCCTGGTCTGCTATACTGTCTGGCATTCCAGTTTTAATG GCTTTATGGCCGTCCAGACACAATTAGGCCGCTTCCAGAATGGC ACCCATTTGTTTTTCTTCTTTCTGTGAGACTGCGGTCTGGACA AAAGGCCCGAGCGGAAATGATCAGTTTTTATTGGATTCTCCTCGAC GGGGACGCGCAGGACTCACGGTCATTTGGAGGGATCCTTTGTTTC TACCTGGGAACCTTCCGCC
OniA _{GK} 103 _{bcddef}	8,610	289	GTTTGGTGTAATCTAGGGTGTATTGCTGTACATCTATCACACTAC CTCGTAAAAACGACACTGAGGATTCTGGGCAACAAATC
OniA _{GK} 111 _b	6,657	84	ATGGCGCCTGACGCTGACCTGCCCTCCTCCTCCTCCTTTTTTCT GTCTCTCTCTCCCCCGTCCCTCTCCCTCCAGCTCTGGGCCAT AAATCCGTTGTTGTTTATGAAAATTTACAACATAGCCATACAAGT TTACGACGCGCCCGGGTTCCCATTTGGCCGAGCTTGTACAGTGG CTGGGAGCCATGAACATGAA
OniA _{GK} 119 _{abc}	3,871	200	

			TGGCGCACCACGACAATCCAAAACACCCAAAGCCCCGGCTCAGA GTTTGCCCTAGCCACGAGCGCAGGGAAAGCGCGCACCCCTTATA TCCCACCCAGTATTTCTGCGTGCACGAGTTTACCTCTGGAGGTC ACCGAGCAGGATTTACGACTGGTCAACAAAAGCACGTGATTCTT CGCCATACCCCATATTTGGGTGCCTACGTAAGAGAGAATCAAGT CCATGTCCCACTATTTCCATAATTCATCATAAAATTGTGCAAGGG TGCTATAGGACGCGCTAAAGCATAAGAGCCACAAATCAAGAACA CAGGTTATGCTATTTTACCTCTAAAAATAACCATCAAAAACAAGA GCAATACCTACAACAAGCAAACGGTGGAACTGTCAAC
OniA _{GK} 132 _{abcd}	484	392	
			AAACTTTATTAGGGCCGTTTCTGGCTCTCTGACATTTGGGTGCTA AATGAATGGGGGTTTGTCTATGAATTAGATCGTAAAAATCATCC GGAGAGCGGCCAGATAGGCTCACTGGCCATAAACGGTCACTGG TAGCCATTTAAAGTAAGTTTTATGGTTTTGGGGAGTTGACAGTATA TTGCACATAACATATAATCGCACTGA
OniA _{KL} 136 _{abc}	7,537	205	
			GGTTCATCTGGAGGTCAGCCACAGCACCAAGATAAATCTGCATC CTCTCTGAGCCACCAGCAGAGCTCGCTTAGGCCAAGTTC
OniA _{KL} 140 _{abcde}	5,596	84	
			GGTCAAAAGTTTACGCGCTGAACAACCTCTCCGTCATCTGTTCACT CGGAGCCTGATGCCAGCCTTATAATAGCGATCTTACTCTCCACA CAAAAGACAGAATAGCTTTGCATTACATATGTTGCATGGTGCCT CCAGGTGAACCCTGGATGCGCAGTGACCTCGCGTTTGAACCCGG GGGAGGAGACCCCCACCCGTCCCAGCAACAAGATTGAGTGGT TGGCGTTTTATTAGGGCGGCTGATTGGTGAATTTCTTTGAATAA ATTGCATTTGATATGTTTGGGGACGAGGGCAAAATTAGCATT
OniA _{KL} 143 _{bcd}	4,958	311	
OniA _{KL} 145	2,825	21	ACTGAATACTTTGACATTTTA
			TCCAAGTCCGGGTGAACCCCGGGTCACTGCGTCTAACAGATAT GAAAATGTGCGCTTTTGAAAAAGGGCACGCTTGTGTTTAAAC AAAGACTGTCAATGGGCAAGATTAATCAGAAACAAAATGGAAAC GGTGTCACTATGGGGTCAGGCAGAAGTTATCTCTGT
OniA _{KL} 149 _{bcde}	1,758	169	
			TTATTATTACTATTATTATTATTATTATTATTATAGGTTTCTTGG
OniA _{KL} 151	1,254	45	
OniA _{KL} 154	497	17	CCTTTTCTTTTCTTTTC
			CCATTGGTTCCTGTTTACATGATGCCCACAGGACACGCCGTGATT GGTGGCTCTTACACGTGACCAGGCAACTTTGTACATTTGACAGG GAGTAGGAGGGTTTTGTGGAGATCAGAAAAACGACAGCGCGATA AAAATTAGTATTGTTGCATTCACAAATTA TTAATGATTACGGGCTCAAATAAAAGGGATTTAAGTTGACGTTG CGTCACGTGAGC
OniA _{KL} 157 _{abc}	164	164	
			TCCTATGGACAACAAG
OniA _{LM} 172	5,729	57	
			CAATTAGGACTTGGGGGCGATATT
OniA _{LM} 173	8,368	16	
			AAATAAAAGGGATTTAAGTTGACGTTGCGTCACGTGAGCGCGGC
OniA _{LM} 175	6,224	24	
			GCATAATAC
OniA _{LM} 179 _{ab}	5,711	53	
			CTGTCACGGACGGATATGTTTTCCACGCGGACGGAGTCAGAGCT CGAGCTTTGGGAGGATGGATTTTATTTTGGAGTATTTCCGCTGAT TGTTCACTACTGTCGTGAGTTATTGCTGCGCGAGGCAGAGGTCAG
OniA _{LM} 181 _{abcde}	5,469	135	
			GGCTTTCTTTTGG
OniA _{LM} 190	3,178	13	
			CTCAGCTATTTGAAAGCACAACTATATATACATATAT
OniA _{LM} 191	2,978	37	

OniA _{LM} 192	2,438	28	GCATAATTTTTCTTGTCTATGGTGACGC AAGGCGCTACTTCATTTGCATAATTTTTCTTGTCTATGGTGACGCT CTGGTTCGGGGCAGTTCACTGGTGA CTGCATGGTACTAGTGAAGG ATCACATACACCAGCATAGCCTTGGCCGACTTTAATATTGCTATG AAGCCCTGGTCATTGCTCTATAGCAGGACGATACATTTCAATCTTG
OniA _{LM} 193 _{abcd}	2,455	201	GGGCCAGATAAGTCTTATCT ATCGATTTTCGTCGCTGAATGAGAAAATATTGCTTGGTGCTCTGCA TTCGTCGTAAGAGGATAAGGTAAGCAGGCCAGGAATAGGCTCCC TCGGTTGTAATGGCTGAGTTTGTATGTCGCGCGGTGATTTATCA CCGTATGACTTAGATCTCGGTT CAGGAAGAGTTCA TGTCAGGGCTGCATTGAAAAGTAAGATGGATCGCCACCATTTCTT CTCCTCACAGTGCTTCTGTAAACCCTAGGTTACCCAAGGAGGCC ATTGGCGGAGAGGCGTCACGTGACCACGGGGTGCCAATGTTATT CTACAAGGGTGTCAAGACCCTGTCAGTTTCTGAAATAAATATTGG
OniA _{LM} 194 _{acd}	2,028	169	GAAAC CAGAGACACAGCTGGAGCTAAAAGACTACACTTTGGGTGTGCAA
OniA _{LM} 199 _{bcd}	190	184	T AGAAGCCTTAAATGTGTTGTGAGGGCACCGAGCTGTCAGACCTTT TGGCGAGTAAGATTGATCGCGCAGGCTTCCAGGACTCTTGT
OniA _{MN} 203	2,658	45	T TAAACCCCAAATTGTCATTGGGCAGAGTAATCATGTGACAGG CAATTCGGTCCAATTTCAACCTTGTCTCCATGAATTC AATAGTTT
OniA _{MN} 204 _{abcd}	1,720	91	T
OniA _{MN} 216	1,686	25	GTCAGACCTTTTGGCGAGTAAGATT TGTAATATAAACAGTCGTCCCCCCCAGCTGAGCGAGGGCTTCT TCACCAGAGTTTTGGATCAATCAGGCAGACAGTGGCTTCTTTTGA TTAAACCCCAAATTGTCATTGGGCAGAGTAATCATGTGACAGG CAATTCGGTCCAATTTCAACCTTGTCTCCATGAATTC AATAGTTT
OniA _{MN} 211 _{abcdef}	344	213	AATAGCAGCTCGGTCCCCATACGGCCGTAATCAG
OniA _{NO} 212	3,601	16	TACAATTA ACTTGCTA
OniA _{NO} 213	3,472	20	AAAATAATTTTTAAAAAGTA
OniA _{NO} 219	2,919	30	CTCATAAATCACTCCGTGGCATGAATGAGA
OniA _{NO} 221	784	30	GAAGTTTTCTGTCTTTTGCTTCTCCTCAC
OniA _{NO} 222	282	36	GCGTCACCTTGATCGACGAGTGCTTGG AATTTAAAT