PFC	Dist to 3' gene	Length	Sequence
TruAA$_{\mathrm{AC}}$5	7,175	193	TTATTGGCCTCCCCTTTCGGGTTTGCGGGTTACGTGGAAACCCTGCATCTTTGGCGCATGCAAATTTACATCCAGGCTGATATGCTATGTGAGGGACTCATTATCCAAGTGGAGCAGAAACATTCTTGGTTAGATTTACCACAGCGAGGCTCCAGCCGGCACCGTGTTCAATGGAGAGACACAGCTCTGCAGC
TruAA$_{\mathrm{AC}}$1	5,423	16	CTGTCCTTGTGCGCCC
TruAA$_{\mathrm{AC}}$8	1,704	34	GAAAAAGAGAAGTCATATCAACAGTAAATAACAA
TruAA$_{\mathrm{AC}}$14	625	15	ACTGAAAAAAGGAAT
TruAA$_{\mathrm{AC}}$21	1,030	235	AAAATAAAGGGTAAAAACATAATGATTGTAAAAGTTAATGTCCTTCAATCGCTCTCAATGGGGCAGGAATTCTCACCCCTCTTCCGCTCCTTTCAAGCATTCAGACAGTTCCTTTAAAGCCTGAATTGCCCGACAGCCTGGATGGCTAGACGGCAACTTTCAACTTGACCTTGGCCTCCAGCCGCGTCCTATGGAGGAAAAAAGCAGTATTTTCAGTGTTTGCATGCTGTAAACA
TruAA$_{\mathrm{AC}}$30$_{\mathrm{abc}}$	888	42	TGGCTAGACGGCAACTTTCAACTTGACCTTGGCCTCCAGCCG
TruAA$_{\mathrm{AC}}$31$_{\mathrm{abdef}}$	165	156	CTTTGCATAGTCGGGTCACGTGGTACAACCCTGGCCAATGACGGCGCGTCCTCGGCGCTCCTGTGCACGTCAGAGTGGCAATACTCCCTGGGAACCAGTATCTCTTTTTTCAGTCCCTGGGCTTTTTAAAAAAGAGCCACAAGCCTCAATGTTGGA
TruAA$_{\mathrm{CE}}$48	7,169	26	TAATTTAGTTCTATGGTTGTAGGAAA
TruAA$_{\mathrm{CE}}$53	6,132	29	TTAAAATAATGCATGTTTTTAACAAAAAT
TruAA$_{\mathrm{CE}}$55	2,572	23	ATAAACGACCAACCAGGATTAAA
TruAA$_{\mathrm{CE}}$57$_{\mathrm{bc}}$	1,889	120	GCTATAAAAACGCAGGTCTGTGCAGAGCTGCCTTTGGTTTTCCTGGGCATCCTGTGCTCAATTACAGCTTAAAAGCTTCAGCACAACTCGTAGAATTTGTCTGAATTGACTGAGAGGCGG
TruAA$_{\mathrm{CE}}$60$_{\mathrm{abcd}}$	203	114	TGTCAATTTCTACCGCGCGGTCACGTGATCTCCTCCTCCATGGAGTGGATGGAGATGGCTCTCCACGTCAGCTTACGTCTCCAAATTTCAGCATAGCAAACCTGCTTGAAAGAG
TruAA$_{\mathrm{EF}}$65$_{\mathrm{bcd}}$	3,300	128	CCTAATTACGGGACATCCTCCCTGTTGCCCCAGCAACGCGGCCATAAAAGTCGTCTGAGAGTCTGGGGCATTTGTACAATTGGAGTGCAGTGCAATAAACCGTCTGAGAACCAAGGTTATTAACTGTG
TruAA$_{\mathrm{EF}}$71	1,325	15	TTTATTGCGGAAAAA
TruAA$_{\mathrm{EF}}$75$_{\mathrm{acde}}$	150	137	GGGAGGGACCGCTTATCTTCCAGTATTTCCATTGGTTTTACAGTCCGCACAGTGGAGAGGGGGCGCCTCTAATCATATCCAGCATGTTTTGCACAAGAAATGTCAGCCAGAAAGGGCTACCTTCTCCCCTCGCCAAA
TruAA$_{\mathrm{FG}}$79$_{\mathrm{abde}}$	2,700	85	GACTGTCGAGTGGTTTAGGTAGTTTCATGTTGTTGGGGTCCATTTCAAACTCTGCAACATGAAACTGTCTTAATTGCCCCAGTTA

TruAA$_{FG}$93$_{abcdef}$	212	127	CACGTGTGCGCGCTGCCCAATGACATCGCGCCTTGACTCCCCATTACAAGCCCACTGTAGTTCTCTGTGGGGCCAAGTTGCTACTTGATTTCTCCACATTGTTATTTTGTGAGACTGTGTTTACTGC
TruAA$_{GK}$95	7,934	30	TTTATTTATTAAATAAAACAAATTATATCT
TruAA$_{GK}$99$_{bcde}$	7,590	98	ATAAAAGACAATTACCGCCATAACCTTTTATGGGGTGCAAAGCGCTGCGAGGCGAGAGGACACAAAACAAAAAAAGACATCGAGAACGACGACAGCTG
TruAA$_{GK}$100	6,809	20	CCTTTGCTTAGCCAGTCCTA
TruAA$_{GK}$103$_{bcdef}$	7,098	285	GCAGATGGACTCAAACTTCAAAGACGGCCAGAGACAGCGCAATAAAAACGCCTGGTCGGCTGTACTGTCTGGCATTCCAGTTTAAATGGTTTTATGGCCGTCCAGACACAATTAGCCCGTTTCCAGAATGGCACCCATTTGTTTTTTCTCCTCTTTCTGTGAGACAACGCTCTGGACAAAAGGCCCAGCGGAAATGATCAGTTTTATTGGATTCCCCGACGGGGACGCGCATGACTCGTGGTCATTTGTATAGAGCCTTTGTTTCTACCTGGGAACCTTCCGCCC
TruAA$_{GK}$111$_{b}$	5,556	83	GTTTGGTGTAAATCTAGGCTGTATTACTGTCATATATCAAGCTACCTCGTAAAAACGACACTAAGGATTCTGGCCAACAAATC
TruAA$_{GK}$116	4,073	35	TGTTTTATATCAAAATGTCTAAAAAAAAAAAAAAGT
TruAA$_{GK}$119$_{abc}$	3,321	197	ATGGCGCCCGGTGGTGGGTGACCCCCCCTCTTCCTTCTCTCTCCTCCACCCAGTTCTCACCAGCTCTCCCTCCGGCGCTGGCTCATAAATCGGCTGTTGTTTATGAAAATTTACAACACAGCGACGTAACTTTACGAGCGGACTCGTCTCCCTATTGGTCGCAGCCGATCACGTGGCGGAGGAGCCGTGAACATGAA
TruAA$_{GK}$125	3,254	15	CCCTCCGGCGCTGGC
TruAA$_{GK}$132$_{abcd}$	376	374	TGGCGCGCCACGACAATACAAAACAAGCGAGTTTGTCCTGCCTTTGAGCGCACGGAGGCGCGCACCCTCCACATCCCACCCAGTATTTGCTCTGTGCATGAGTTTACCTCTGGAGGTCACCAGGCAGGATTTACGACTGGTCAACAAAAGCACGTGATTCACCGGCGTACCCCATATTTGGTTGCCTACGTAAGAGAGAATCAAGTCTATGTCCCACTCATTTCCATAATTCATCATAAATTGTGCAAGGGTGCTATAGGACGCGCTAAAGCATACGAGCCACAAATCAAGCACACAGGTTTATGCTGTTTAACCTGTAACACAATAAAAGACGACAACAACACTTGAGACCAGTTAGCGGTGGACCTGTCAAC
TruAA$_{KL}$136$_{abc}$	3,673	204	AAACTTTATTAAGGCCGATTCTGGGTCTGACATTTGGACGCTAAATGAATGGGGGGTTTTGTCTATGAATTAGATCGTAAAAAATCATCCGGAGCGCGGCCAGATAGGCTCACTGGCCATAAACGGTCACGTGGTAGCCATTAAAGTAAGTTTTATGGTTTTGGGGAGTTGACAGTATATTGCACATAACATATAATCGCACTGA

TruAA$_{KL}$140$_{abcd}$	2,046	63	GGTTCATGTGGAGGTCATCTCCGGCACGAAGATAAATCTGCATCCTCTCAGAGCCACCAGCAG
TruAA$_{KL}$149$_{bcd}$	1,641	161	TCCAAGTACGGGGTGAACCCCAGGTCAGTGCGTCTAACAGATATGAAAACGTCGCCCCTTAGAAAAATGGCACGCCTTGTTGTTTAACAAAGACTGTCAATGGGCAAGATTAATCAGAAACAAAATGGAAGCAGTGTCACTTTTGGGTCAGGCAGAAGTTA
TruAA$_{KL}$157$_{abc}$	164	164	CCATTGGTTCCTGTTTACATGATGCCCACGGGAGGCGCGGTGATTGGTGGCTTTTCACACGTGACCAGGCAACTTTGTACATTTGACAGGGAGTAGGAGGGTTTTGTGGAGATCAGAAAAACGACAGCGCGATAAAAATTAGTATTGTTGCACTTCACAAATTA
TruAA$_{LM}$172	4,830	57	TTAATGATTCACGGGCTCAAATAAAAGGGATTTAAGTTGACGCTGCGTCACGTGAGC
TruAA$_{LM}$179$_{ab}$	4,812	53	AAATAAAAGGGATTTAAGTTGACGCTGCGTCACGTGAGCGGGGCGCATAATAC
TruAA$_{LM}$181$_{abcde}$	4,567	128	CTGTCACGGACGGATATGCTTGTTCAACGCGGACCGAGTGGGCTTCGGGAGGATGGATTTTATTTTGAGGTATTTCCGCCGATTGTTCATTACCACCGTGAGTTATTGCTGCAGGAGGCAGAGGTCAG
TruAA$_{LM}$183	3,996	171	AGCAGTGAACGTGTTGTGATTGTGTCGCTCCGCCGGGGAAAACGAGCATATAATGGAAGACGGAGTGCCATCTAGGACCGGCCGGCCATGCTGGGGTCACGACGTTCTCGCTTGATTTATGGGCGCGGGGACTTGGGGAAGATGGTGTGCGAGACCTAATGACTATTCGAT
TruAA$_{LM}$186	3,871	13	CGGGGACTTGGGG
TruAA$_{LM}$187	3,520	30	GTTTTGTTCATGTATGGGCGCCGTTGGAAA
TruAA$_{LM}$193$_{abd}$	2,012	199	AAGGCGCTGCTGATTTGCATAATTTTTTTGTTCGTGGTGACGCTCAGGTTCGGGGCAGTTCACTGCTGTCTGCGTGGTACTGGTGAAGGATCACATAGCCCAACATAGCCTTGGCTGAGTTTGATATTTCCATGAAGCCCTGGCCATTGCTCCTTAGCATGACGATACATTCAATCTCGGGCCTAGATAACTCTTATCT
TruAA$_{LM}$194$_{abcd}$	1,591	169	ATCGATTTCGTCGCTGAATGAGAAAATATCGCCAGGTGCCCTGCATTGGTCGTCAGAGGATCAGGTAAGCAGGCCAGAAATAGGCTCCCTCGGTTGTGAATGGCGGAGTTTGTGTGTCGTACGGTGATTTATCACCGTATGACTTAGATCTCGGTTCAGGAAGAGTTCA
TruAA$_{LM}$199$_{bcd}$	190	184	TGTCAGCCCTGTATTGAAAAGTAAGATGGATCGCCACCATTTCTTCTCCTCACAGTGCTTCTTGTAACCCTAGGTTCACCCGAGGAGGCCATTGGAGGAGAGGCGTCACGTGAACACGGGGTGCCAATGTTATTCTACAAGGGTGTCAAGACCCTGTCAGTTTCTGAAATAAATATTGGGAAAC
TruAA$_{MN}$200	3,053	34	CATTCCATGCTGCTCCAGTTCGAAGAAATAAATA

TruAA$_{MN}$204$_{abcd}$	1,431	91	AGAAGCCTTAAATGTGTTGCGAGGGCACCGAGCTGTCAGACCTTTTGGCGAGTAAGATTGATCGCGCACAGGCTTCCAGCACTCTTTGTTT
TruAA$_{MN}$216	1,397	25	GTCAGACCTTTTGGCGAGTAAGATT
TruAA$_{MN}$211$_{abcdef}$	332	212	TGTAAATAAAAGCAGTCGTCCCAGCTGAGCGAGGCGATCTTCATCTGAGTTTTTTTTGGATCAATCATGCAGACAGTGGCTTCTTTTGATTAAACCCCAAATTGTCATTGGGCAGAGGTAATCATGTGACAGCCTATTCGGTCCAATTTCAACCTTGTCTCCATGAATTCAATAGTTTAATAGTAGCTTGGTCCCCACACGACCATAATCAG
TruAA$_{NO}$214	2,735	222	AGAAAACTAAAATGAAATTAGTAGAGTAAATAGAGAGCCGTATGCAAATTTCTCAACAGGTTGGCAATGAATATAATTTGTATAATCGGGTGGCACTGTGATGACACAGGTTTCACTTTTTACAATTCTTTTAATTGCATTGTAAATCTTAATGTCGTACATCGATATATATAGGATGCATATAAAGTAAATACTAAGATAAAAATCTAAGAACGCTAGCATTT
TruAA$_{NO}$222	284	36	GCGTCACCTTGATCGACGAGCGCCTGGAATTTAAAT