PFC	Dist to 3' gene	Length	Sequence
HsaD$_{AC}$1$_{ab}$*	8,977	339	CTGGTCAAAATGACCCATACATCCTTCCGATCCCGAGATGTCATTCATCAAAAAGTAGCGCCCGCTCGTCATTAAGGTACGAATGACGCTGTTCGAATAATCATTTATTGTAACAGGTTTATAAGCAAATAAATACACCCTCCTGTCAGTGGGTAATGAAGGCAGCTTCAGAGCAGACAAATAGATCCAGGTAGGAGGCGAGAAGAGACAAGTGAGGAGGAAGGCTCCGGTCCTTTGCCCGCTCCGAGCCAGTTCTGCTCGCCCGGGGGTTTGGCCTCGGGGGTGAAATTGACAGTCTGATTAATAGAGCGCGCCGCGGCACATTTCCCCCTTCATTTA
HsaD$_{AC}$3	3,006	55	TAATGCACCCACACACAAACACAAGGCTTGGTCTGTGTTCCTGGCCACCTAAAGA
HsaD$_{CD}$5	2,973	26	TTGAGGGGGAGGGACAGAGACAGAGA
HsaD$_{CD}$6	783	39	TTGGCCACGATTGGTGGATCGAGCTGATGGGTTCCCTGG
HsaD$_{DE}$8	4,835	25	ATGTTTTGGATTCCACCTTAATGTT
HsaD$_{DE}$10$_{abcde}$*	3,031	142	CTTGCAGAACTGTAGTGGCAATAAATGAAATGACTCAGAATCCCTTCCCCAGTCAGCTTTTACGAGAGCTGCCAGACAGTGTCTGTTCACGTTCTCCAGATACCAGGGGCGCCCTGACAAAGTTAAGGTCAAGTTAGTGTCT
HsaD$_{EF}$11$_{ab}$*	6,554	28	TGTTTACAAAACCTTGAACTGTCTAGAC
HsaD$_{EF}$12	6,463	32	CCCAAAAGAGATTTCCGCAATGTGCAATAAAC
HsaD$_{EF}$13	6,226	49	TTTGAACTTCCAAAATGTCAAGGTCATCACCTTTAACCTTTCTGAATAA
HsaD$_{EF}$14	5,739	39	GGAACAAAAGGAAATATAGTTATAATGCTTTTAAAAGCA
HsaD$_{EF}$15	5,278	25	TGAGAAGTTGTATAGAGACAGAAAA
HsaD$_{EF}$16	5,360	43	TGCAAAAGAATACCTTGGTATAACCAGATGGTGTGGAGCAGAG
HsaD$_{EF}$17	3,266	29	TTTATTCCATTTGTCTCACCTCAGCCTTA
HsaD$_{EF}$18	1,464	387	ATTTGTATTAAAACAAAAATGACCTTCTTGGTTAGCAGCGAAGGGAAAAAAATCAATAGTATAATTTTCAATAATTCATAAAGCGAACGCCATTATGGTAAATTTAACTATTAATCTTATCCTTTACAAAGTCTCGATTGATTTGTTAATAAAGTATCTTCCCGTGTGTGGCAACAGCGGGCATAACTCTTTAAAAACCTTCAGAAGCAAGAAAATTACCAAGTAGCCCAAGAATGTAGATGAGAATTTTATTGATCGCCCTGATTCTTCTTAATATGTATTAATAAATTCCACAACCTTTTGTACCTTGCACTTGTCAGAAACCAGTGCTTTTACAAAATCCATAAAAGGAAAACATTTTTCTTTGCAGAAGAACCAAAATGACAC
HsaD$_{EF}$19$_{abc}$*	208	178	GTCGCTGTTGTCCGTGCTTACCCGGCCGGCCGGCCAGGCTCTGGAGCACGTGACCCGAGAGGAGGCTGCGGCTCAAGGCCATTTTCAAATCTCATTGGCTTGGTTGTCATGTGGTCGGCAGAGGCATCCACAATTACACGGGGAATGTTTTCCTAGAGATGTCAGCCTACAAAGGACA
HsaD$_{FG}$20*	2,906	33	TGCATGTTCTGGTCGCATGTATAATGCAATAAA
HsaD$_{FG}$21$_{ab}$*	691	46	TTTTATTAGGGACACATTAATCTATAATCAAATACACCTCATAAAA
HsaD$_{FG}$23$_{abe}$*	162	133	AGCGGACTGATTTACTCCCGGTATTGGTAAATATGATCACGTGGGCCGCGCGACCAATGGTGGAGGCTGCAGCCTGCGAACTAGTCGGTGGCTCGGGCGCCGGCGGGGAGCTGCTCGGCGGCGGACAGTGTAA

HsaD$_{GH}$24	6,120	23	TTTGGTGCTTGATTTCCAGAAAC
HsaD$_{GH}$25	4,591	228	GAAGGTGCTGCGCACCCCTGCCACTGTGGCCAGCTGGGTACCTAGGGCTCTTTGAAAACAGGAAGAGCCGAGGTGTCATAAAGCCATCTAGCGGGCCAGACGTCTGGAGGTAATGAGTTTACGACAGGCCCAGTGCTTTGCTTTGAAACCATCTCATTTTGATGTTTGTGTTTGTGGGAGAAAAGGAAAAATGCAGACAAAACTGGGTCTTAAAATCTAGACAATAAA
HsaD$_{GH}$26	4,157	17	TAGAAACAAACAAACAA
HsaD$_{GH}$27	3,022	19	CTATTAATTTCTGTGTTTG
HsaD$_{GH}$28	2,631	31	AAAATCCACTCATTTATCCAGGGTTCAAACA
HsaD$_{HL}$30	17,402	29	ATGTGTCAACATCCAAGCATTGAGGCAAC
HsaD$_{HL}$31	16,788	34	TAATTTAAAATATTGTTTTATTCTGTAACACAGA
HsaD$_{HL}$33	15,895	31	GTATTTCGGAGAGGTTGACAAGTACCTAAAA
HsaD$_{HL}$34	15,588	40	AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT
HsaD$_{HL}$35$_{abcd}$*	15,223	177	AAATCCGCAAGGAATTGCAGTAAATTCCTTTTTGTTTGAAGAAAATTTACAACTTGGTAATAGACCTTTTTATGACCTATTTGCGGTCGTCATTGGCTGCGGCTGGTCATGTGCAGGCGCCGCTCGCCTTCACGGCCTTTTTCCTGATTTCCCCGGCGAATTTCCCCCCGCATTCTG
HsaD$_{HL}$36	13,285	33	AATAAGAAACTTGAGTGATTGTTATTTTATTTG
HsaD$_{HL}$37$_{bc}$*	5,380	60	CACGTGATTCCAATAAACTTTGTTTTATGGCTTGAGAGTTGACAAGCCAAAATATAATTC
HsaD$_{HL}$39	12,554	27	GAGAAAGACGAAGCTCGAAATTATAAA
HsaD$_{HL}$40$_{ab}$*	12,419	73	GAACAAAGACAGTATTTCACCCTGGGCTGGCAGGCAGCTGTTAGAGGTATTTACGGCCTTGCCGCAGTGCGGC
HsaD$_{HL}$41	9,512	18	AAAAGACCCCTGGTTCAC
HsaD$_{HL}$42	6,519	22	CGTTTTTACACTGTTTGGTGGC
HsaD$_{HL}$46$_{abcde}$*	2,614	83	AATAACTCGTTGGCTTTGACCTGTCTGAACAAGTCGAGCAATAAGGTGAAATGCAGGTCACAGCGTCTAACAAATATGAAAAT
HsaD$_{HL}$47$_{abc}$*	2,005	86	TGAACTTTTGTACTCTTGTGTGCTGCTGTCGGCAAAGCAAAAATAATGAAAGTTTGTGATATGTTTGTAAATGATTTCGAATGACC
HsaD$_{HL}$48$_{abcde}$	1,314	82	GTCTATATATACCCTGTAGAACCGAATTTGTGTGGTATCCGTATAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATG
HsaD$_{HL}$49$_{abc}$*	143	143	TGATAAACTTGCTCCCTCGCCATTGGCTGGCCTGGTCACATGGCTGCCCAACTTTATTCAGTTGACAGCAAGTAGGAGGGCCCTATGGAAGGAGAAAAAAAGACAACACGAGAAAAATTAGTATTTTCTACCTTCTGAAATTA
HsaD$_{LM}$56$_{abcde}$*	14,261	203	ATTGTTTCTATGACAAAAAGCACAGAGTTCATACATAGTCAAGACGTCTTTTTTCTGACGCCCTCACGTTGAGAAGCTGAAAAGGTATTTTACCGAAGTTCGGGTAAATTACAGAATCAGGTTCATCCAGAGGACAAATTTTCTATTTGATTAGCTGTATTTCAGCCGGGAGGACTGACCTCTAAACCCCTAACCTTTTGGAC

HsaD$_{LM}$57	13,480	372	CCACTTAGGGCAGGGAAGGAAATGGGTTTCCATCTGAGAACGTGCTTTGGAGAAAGCTAGGTGTGGAAAAGCTCCAATGCCCATTTGCTATTATTTGTTTCCAGTTTGTTCCTTTAAATATGAGCCAGAAGTGTTTGTGTTGGTGTTTTAAAAACAAAAACAAAAACCGTGTTGGGGTCCTGACTGGGGGAGGGGGAGAGTGAAGTGTTTGCTGAGGACATTGCTCCTCTGACTCCCATCTCACTTTGTCCATCGCAGCCTTTTGTTGGGAGATGACACTGTCAGTCAGCCCATGATGTCTGTTCACACGAGATGCTTTTTTAATAGAATTGACCAATGTTTTGCTGCCACTGATTAAAGTATTATTTATAC
HsaD$_{LM}$58$_{bd}$*	11,855	198	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAAACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCTCCGACTTGGAAAGTGCAGGGATCCCAAGAATATCACCCGTCCAGGGGGGCCGCGCGGTGCCCCCGGCCCTCCACCCCCGGCCCCCGGCGGGCGCGGGAGCGCGGCCGCAGGTAAA
HsaD$_{LM}$61$_{abc}$*	5,973	57	GTTCATTAAGGGGTGAGTTATTGCGGTGCGAGCCAAAGGTCACTTCAAAGGCTTATG
HsaD$_{LM}$62$_{ab}$*	3,899	45	GTCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATATG
HsaD$_{LM}$64	11,225	149	GAACAATGGTCGCTGTCACGGCATCTGCCGCCTATTCTTAAACCGGTGAGAAAAGGCCCTGGCCCTCTTTTCAAGCGAGGGTCGTAAATTTTTCTTTGCGTCATAATAGAAGGCTATAAAATCGAGTTGAAATTTTACCCCAGGCAGGT
HsaD$_{LM}$65	10,461	151	AAAGTTTCCCCCATTATGAATTATACATTCAAACAATAACACATTAATTCAATTATTCAAAGATGACAAATGTTTATGTGCTTTGCGAGTGACTCGGGCGCAGATTCCAGGCGCTTTCTCTGAGCTGCTTGCATTTTTCTCAATGAGAATC
HsaD$_{LM}$66	10,176	24	CGGCTTGGCGGGCACTGGCCCGGG
HsaD$_{LM}$67$_{abc}$*	10,138	119	TGACAATTGCCCGGGTTGGTGTGATAAATCATCGTAAGTAATTCCTGAAAGGGTGCGAGACTGTTGGGGGCCGGGCGAGGACTGTAAATCTTTCCGGTTTATTGCTCTATGAACATATG
HsaD$_{LM}$68	9,398	17	ATATTTCTAAAATATAA
HsaD$_{LM}$69$_{abd}$	8,541	94	CTCAATCAGTACAAGCTTCCCTCGGGGTCACGTGAACAAATATGCTTGCATTTGAAGGCAGCGTCTGTATTTCCCGACTATGAGGGGGTTTCCG
HsaD$_{LM}$70$_{a}$*	8,233	204	TTTATTGGTAGTTGAACCTCAGCCTGGTTCCGTTCTACCGGGAATTCCGTGTGCTCGAGTATATGGCCGTGTCTGCGAGCGCGCAAGACCAGGGTTGGGACAGTGTTGTCTGCAGACAAAGGGGGAAGGCTAGCTCTGCCCCCCACTGGCGCCCACTCTGAGGCCGAGGACACCAGGTTTATGATAAATTGGGATCCAGGTAAG

HsaD$_{MO}$71	16,143	491	TTAATTTATATTCTCCTTCCTGTGCCGTAAGGATTGCATCGGACTAAACTATCTGTATTTATTATTTGAAGCGAGTCATTTCGTTCCCTGATTATTTATCCTTGTCTGAATGTATTTATGTGTATATTTGTAGATTTATCCAGCCGAGCTTAGGAATTCGCTTCCAGGCCGTGGGGGCCACATTTCACCTCCTTAGTCCCCCTGGTCTGAACTAGTTGAGAGAGTAGTTTTGAACAGTCGTAACCGTGGCTGGTGTTTGTAGTTGACATAAAGGATTAAGACCGCAAATTGTCCTTCATGGGTAGAGTCAGGAAGCCCGGTGGCGTGGCACAACACACTTTGGTCATTTCTCAAAAACCACAGTCCTCACCACAGTTTATTGATTTCAAATTGTCTGGTACTATTGGAACAAATATTTAGAATAAAAAAATTTCCCAGTCGGAACTGTATCTGTGTTAATCATGCACACTTGCAAGCAGATCACTATGCCT
HsaD$_{MO}$72	6,777	25	AAAAATAAAAGAAGTCGGGCACAGT
HsaD$_{MO}$73	4,912	27	AAAAAAAAATTCCTGAGTCAGACTATT
HsaD$_{MO}$74	2,912	18	AAAACAAAACAAAACAAA