

PFC	Dist to 3' gene	Length	Sequence
HsaC _{CD} 9	5,643	23	TTCTTTCCGAGATCCCTCCATG
HsaC _{CD} 10	3,635	22	ACTAGACAGTGACCTTGAAGT GAAGTTAGAGTGCGGGATGGGATGGTGGGGGGGGGGATCGG TTGTCCCCACCCCTCCCCTGGCGGCCGTGCCACGTGAGTGG GGCGGCAATGGGTGACTGGTGCAGATTAACTATGTTTAATG TCAGATAGCAATAAAGTAGAAGCTGCCGGTCGGGCCCCGCGG
HsaC _{CD} 8 _{bde} *	172	172	AA
HsaC _{DE} 11	9,984	13	GTAATTCTTAAAT
HsaC _{DE} 12	6,843	42	AAACGTCATAAAGAAAAGTTCATTACAGCTTAAATGTCTGA
HsaC _{DE} 23	6,264	22	AGAAAGAAGGAGAGGAAAATAA
HsaC _{DE} 24	4,786	17	AAATCTCTGGCGAATCT TTTTATGGTGGCCAGGAATAAACTTTGGTGGTCAAATCAAG
HsaC _{DE} 25*	2,505	65	TGCTCAGTCCAGCAGCTGTCTC AAATCTGCAATGATTTTCATAATGTTCTGCGGTGTTTGCAA CCAATCGCCTGAACGTCCCCGATTTACCTAAGAGAGAACCC TCCTACGTCTGCGAAGTGCTCCGAAGTATATGACAATATC TACTTTGGATCACGTGCTCAGAGAGAGAGAGACTAAGACGGAT AACGCGTCATCTCGCCTTCCCAAATTTTCCCCCTCGTAGAG
HsaC _{DE} 26 _{abcde} *	259	257	CGGGTCCAAAACCTCCATCCGGAGCCGGCAGGAGAGGAGAA
HsaC _{EF} 32	9,811	20	GGAAAATTATTTATTTAT CATTCGTTCATATTTATGATTTTATTTGACCCTTTTATTAACCC
HsaC _{EF} 33	8,852	64	CTCTCCTTAAATCCTC
HsaC _{EF} 34	6,692	17	GTGCACGTGGGAGTTTA CTTTGTTGCGGGGAAGGGCTCCGGTGCCCTACCCCGAGGCA GCTGCTAGATGGCGCTGTACTCCACTCTGCGCGCTCCGCCTG CCGACAACCTGACCCCGTACGTCACGGCCGCTGAATCATC AAGGCCATTTCAAATCCATTGGTCTAGCCGTCACATGGTGA GAACCGAATGCGCGGATAATTACGGAGCTGAT
HsaC _{EF} 35 _{ab} *	330	204	GAACCGAATGCGCGGATAATTACGGAGCTGAT
HsaC _{FG} 36	9,975	30	TTTGCATGTAGCTTCCTTAATGGAGAAAAA ATAACGTTGATTTAAATATTATCCAGGTGACCACAATAAGTCA AGGTCATAAAACAGTAATGTCAGGACGGTCTGGTGCGCGCGA GAGGTGGATTTATGATCTGCAAATATAATGTGGTGTGAGT AAAAGATGCATTTAAAGGTGACTGGAGGAGGG
HsaC _{FG} 38 _{ab} *	9,764	161	CAGCTGATCTGTGGCTTAGGTAGTTTCATGTTGTTGGGATTGAG
HsaC _{FG} 40 _{ac}	8,443	72	TTTTGAACTCGGCAACAAGAACTGCCT
HsaC _{FG} 43	7,032	30	TGTTTTGACTCCCAAGGAAGCTGGAGGAGA
HsaC _{FG} 47	6,650	18	TCTCTGTGCCCCATTTT CTTTCTGTCTGAGACGCCCAAACCCTGAGCTCTCCTTCCCAA GGCTGGAAAAAAATCGGGAAAAACGGCGGAATTTGCACTTT CATTCATTGGGTTATCTGCAACTGAGAGGGGCTGGTTAAGGCG
HsaC _{FG} 48	5,053	129	T
HsaC _{FG} 49	2,076	29	GGGGAAGACAGTGGCGCCAAGGAGCTGAA
HsaC _{FG} 50 _{ab} *	1,183	18	TTTATGAACAATCAAATG
HsaC _{FG} 51	347	34	ATGGGTGGACATGGGCACAGGGGCTTCTCAGATG

HsaC _{FG} 52 _{abc} *	175	164	GCGCATTGATCCGCGCCGTATTTTTGGGTAAATACGATCACGT GGGGGCCGGGAGCCAATGAGCTGTGGGAAAAGGCTGGAAA AATAATTACCTGACTTGATTGTTCTGTGAGCAGATAAAAAGTA CATATACAGTTCATAACAATAATCTTATGTATGTA
HsaC _{GH} 54	5,999	42	TGTTATGGTAGAACAGCCCTGTGTTAATATATTGAAGTCACT GTTTGTCTCCCTGTTCTGGGTTCTCAATGGGGCCGAACAAAAC AGCAGCGGGAGCTGGCTAGACGTCTGGGCTTAATTGTTTTAT GGTTAAATAAGGTGGACTTTCCTTTGAAATCGGATTATAG GAATGTTT
HsaC _{GH} 55*	3,848	137	GCCTGTCTTCATGTCGTGGATTGATGAACGGAATCGCGTGTA AGCGCCGCCACCGCCGGGAGTCTGAGGAATTCGCTGGGCTGT TAGAGGAAAGAGCTAAGTGAGAGAGCGGAGCTCTACCTA
HsaC _{GH} 57	400	126	TGAAGTTTCGTTTTATGGTAGCAGATAAATTGAGAAGTTTACG ACTGTCAATTGCTTTTATAGAGAATAGAATGACACTCACA
HsaC _{HJ} 58	17,102	83	AATTTACAGCTGAGTAATAAAAAGTTTA TTCTCTAAGGTCCCCAAATACCCAGATCTGGTTACTGGATGA ACTGCGTTTTA
HsaC _{HJ} 67 _b *	11,757	27	AGATATAGCATGTCATT
HsaC _{HJ} 74	7,266	54	TATTAATTTAAAAGAGTATCATTGAA
HsaC _{HJ} 75	6,257	17	AATAAACGAGTTTTTCTCAGCATAGTCCCGTTTATGGCTTTAT TGCTACCCATTGATTACTCCGCTTTGTTACACAGAAGGAAAAG ATC
HsaC _{HJ} 76	6,080	27	ATC
HsaC _{HJ} 77	1,717	90	GGGAATCAACAGAAGCAGAAGCGATTTTTTCCCCTTCCTGA CATCTGGCTTGCATTGGCTGGGAGGGGGTCAGCTGACTTGT CATTTTGTCTGTCCCTGGATTGGAGCCGTCCCTATAACCATCTAG TTCCGAGTACAACTGGAGACAGAAATAAATATTAAGAAATC TGGCACAATTGATGTGTTTTGATTCCCTAAAACAAAATTAGGG AGTCAAACGTGGAC
HsaC _{HJ} 78*	200	173	TGTGTGAAGATTTTTAGCTGTATTTGTGGTCTCTGTATTTATATT TATGTTTAGCACCGTCAGTGTTCCTATCCAATTTCAAAAAAGG AAAAAAAAGAGGGAAAATTACAAAAAGAGAAAAAAAAGTG AATGACGTTTGTTTAGCCAGTAGGAGAAAAATAAATAAATAAT AAATCCCTTCGTGTTACCCTCCTGTATAAATCCAACCTCTGGGT CCGTTCTCGAATATTTAATAAAACTGATATT
HsaC _{HJ} 79	3,075	57	ACATATCGAGATGCTTTTCGCCGGCTTCCATCACTAACCTCCC GGAGGTCATCAAGCCAAATTTATGAGTGGCCGCTCGAGTCACG TGACTCTATTTAAGGCTCCCTTATTGGGAAGAGCGCATAGGA TAAAGAAAGAGATATCTCCACCTATAAATTGTCCACTTTGGAG AACAAAAAACCCTCAACTTCAAAGAGTCACAAATCACCTTA ATCAAAAAGGGTGCAGAAATTTT
HsaC _{HJ} 80	2,561	247	AGGTTATTTATGTGAATAGCCTGAAGGCAAGCCCGTGAGTGGC TCTGGGGACCACGTGATATCATTAAACCAAGTTTTATGGTG TAGGGAGAGCTGACAAACCCACAATATTTACATCATATATA ATCTTAACTGTCCAGCCACGCAGCTGCTGGTGAGGTTTAAATGC TAGGACAGAGGGCCTGGCAGTTAGAGGGGATTAC
HsaC _{HJ} 81	255	238	CAAAAAGTGGAGATTTTTTAAAAGTTCTGATTGG GGATTTCAGTGTGAGTTTACATGGATT
HsaC _{KL} 87 _{abcd} *	16,174	206	CAAAAAGTGGAGATTTTTTAAAAGTTCTGATTGG
HsaC _{KL} 88	13,050	33	GGATTTCAGTGTGAGTTTACATGGATT
HsaC _{KL} 89	12,787	29	

HsaC _{KL} 90	10,282	17	TTCTGGAAACTCAAAC
HsaC _{KL} 91	8,173	18	TAGGGAACAAATATATTT
			ACATTATAACTAGTTATTGAACTCGCTGGAAGATCTAAAGGCC
			ATTTGCGAAGAGACAAATTTCAATGGAGTTTCCCATCAATAA
			CCCCATGGCAGTGAAGTATTGGAACAAGTCAAACACCCGAGG
HsaC _{KL} 99 _{ab} *	4,717	164	TGAAATGCAGGTCACCTCTGTCTAACCAATATTAATA
			TCACAGCTCACCTTTCCAGGTGAGGCAGCCGCATCCAGGTACA
HsaC _{KL} 100	2,751	58	GGCCTAGAAGGGAGA
			GCAGCCAGCGGCCGCCAGCCCTGCGCCGCCGCCGACACAAAG
			AGTGCGGGCGATTCCGCGAGACTGATTTATGACGTTTTACAGC
			CCTATAAAAGCTGTAGCGACGAGCAAGCGCTCCTACCACCG
			CTGGCAGATTTAGTCTAATAAAATAAAACATAAACAGTTAACTT
			TATGTGTCACCTTTTATTGTTATCAAGTAAAATATAGCTGAGCCC
			TGGCAAGCTATGATTTTAAACTATAATTGTTATCAAGTACAAC
HsaC _{KL} 101	1,720	262	AAGGG
			GGTTCCTTATCCGGGGACTGGGTTGCTCCGTGTGATTGGCCGG
			AGGAGTCACATGGTGAAAGTAACTTTACAGGGTCGCTAGCTAG
			TAGGAGGGCTTTATGGAGCAGAAAAACGACAAAGCGAGAAAA
HsaC _{KL} 102*	151	151	ATTATTTTCCACTCCAGAAATTA