

| PFC | Dist to 3' gene | Length | Sequence |
|---------------------------------------|-----------------|--------|--|
| | | | TCTGGGAGGAAGCCCCATTGCCCTCTTCTTTCTAAGCTGTCAT CCTCCTGCTGCAATCGTCATTACAGTACCGCTGGTGACGCCA CTCGGCGAGCGCAAGTGGATAAATAGAAACGTCTGCCACAG |
| HsaA _{AC} 2* | 42,727 | 139 | CGAAGATGAAAGG |
| HsaA _{AC} 3 | 42,243 | 14 | CATTATTACAACCTG |
| HsaA _{AC} 4 | 41,350 | 21 | TTCAAACCTGACCCTTTTTTGAG TTATTGAGAAGAGATTGGAGTGGGGTCAGGGGAGGATATGTT TTCAGGATCTTTTGTGTTGTTTTAATAGATTTTGTCCAGGCAC AAATCCTTTCCAAGCACTGGGCTATCCAAGGGCCAGACAAAC CTGACCACCTTGCTCCCCCTACTCCCAGTCCCCTGCCATGGG GCACCATCTCCACCCTCTCCACCCTGCACTGTAAGAGGGA |
| HsaA _{AC} 5 | 36,891 | 227 | ACCTGCCCCACTGCAGC |
| HsaA _{AC} 6 | 32,134 | 26 | TTTTGTAAAGAATTCTACAGAATGAA GAAAAAGAAAAATCCCATGTGCTCTGGCTCTAAGTCTTATAA |
| HsaA _{AC} 8 | 30,093 | 45 | CAA |
| HsaA _{AC} 9 | 29,255 | 20 | ATAAATAACTACAGAGCAA |
| HsaA _{AC} 10 | 29,122 | 32 | TCCAGGATTTTGTGTCCTTTTTGCAAAAGACA |
| HsaA _{AC} 11 | 28,926 | 20 | TACTTAAATTAGACTGCTTG |
| HsaA _{AC} 14 | 28,729 | 18 | ACTGAAAGGAAGAGGAAT |
| HsaA _{AC} 15 | 27,827 | 28 | AAATGTAAGTTTCCAAGTCTTTCTGAG |
| HsaA _{AC} 16 | 27,563 | 26 | AATAAACGTTTTTCTGGAGATAGAA |
| HsaA _{AC} 22 | 23,227 | 16 | TATTATCACTCTTTT TCTCTGGCTAATAGAAAACAGAAAGCCAAAGAATGAGCACA AGACTTCTAGGAAAAGATTTAAATGAGGCTCCAATTTTCTTA |
| HsaA _{AC} 23 | 15,760 | 106 | GGCAGGCAAACCAATCTGGAAA GATTAAAGTTAATCCGAGGTGTGTGCTCAGACTTGCCATGTT |
| HsaA _{AC} 24 | 10,752 | 54 | ATTTAAACACAT |
| HsaA _{AC} 25 | 10,451 | 13 | CATCTAGTGGGAA |
| HsaA _{AC} 26 | 8,804 | 16 | CAGGTAGGAAGACTCC |
| HsaA _{AC} 27 | 7,466 | 25 | TGTA AAAAGCATCCAGATATTTAAT |
| HsaA _{AC} 28 | 7,033 | 35 | TAGTTTAATCATTAGAAATTTCTTTTGTGTTTCTA TCCTGGGTGGCACGGGCCCTGCAGTCCAGCAAGCCGGTGTG CCCCGCGGGCTGGCCGCGCACTGCGAGAAGGCGTTTCTCCT TCCAGCCGAGCCCTTACCAAGCTCCCTCTGCTTCTAACGCA TGCTCCGGTCTTTCCGCGAAGGCTGTTCCAGCTCCAGTGA |
| HsaA _{AC} 29 | 5,150 | 193 | AGAGCGATCAGTGGCACTGTCGGGG |
| HsaA _{AC} 30 _{bc} * | 2,062 | 31 | CAACTTTCAACTTGACCTTGGCCTCCAGCCG CTGCTCAGGTAAATCTTAGTGAAATTCCTACCGTTGTTGTACG |
| HsaA _{CE} 35 | 12,608 | 59 | TTCTGCAAAACATTTT |
| HsaA _{CE} 36 | 12,393 | 26 | CCGGGTCCGTAATGTCTTTTTAAGAA |
| HsaA _{CE} 37 | 12,360 | 20 | TAATTGCTTATAACAAGCAT |
| HsaA _{CE} 38 | 12,082 | 24 | GAATGAAAATTCATTCCCCTGAAA |

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| | | | TATTAAGGGATTAGTATTTTTCCATGTTTATTGTGTTATCAGA GTGCATTAGAAAAGATTAGTGATTCATCTTCACAGCACATTTTT AATCAAGCAGTTATTTCAACCAGCACATTTCGTTTTGTTCATAT TCACTATAGAATGATATCTTGTAATAAAGACATTCAGCACA CTGTGAAAAATGTATTTGTGCACCTGCTTTTTAAATATTTCTAC |
| HsaA _{CE} 39 | 12,027 | 218 | TAAA |
| HsaA _{CE} 40 | 11,961 | 31 | CATCTTCACAGCACATTTTTAATCAAGCAGT |
| HsaA _{CE} 42 | 11,632 | 23 | ATTATTATTCAGTACTTCTTTTG TTAAACCTTGACCTTGACGAAAAAAAAGACAATTTGTGACCT TGACTTTTGACAGCTCATGAATTGGCCTTAGCTGGATTAGTAG |
| HsaA _{CE} 43 _{ab} | 11,330 | 101 | ATCAAGGGGCGCCACCT |
| HsaA _{CE} 47 | 10,585 | 80 | ACCACAGGATTGGATACAGAACGAGAGTTATCCTGGATAACT CAGAGCTGAGTACTGCTCCAGGGTGGTGTGCAATCTTA |
| HsaA _{CE} 48 | 10,227 | 26 | TAATTTTATCTTTACGTTAGAGGAAA |
| HsaA _{CE} 49 | 10,007 | 21 | AGAAATTC AATTATATTTTGC |
| HsaA _{CE} 51 | 9,807 | 23 | TGTGTGTTTAAGAACAGCTCCAA |
| HsaA _{CE} 52* | 9,292 | 24 | GATTAAGTATTTTTTTCTAAAAA |
| HsaA _{CE} 53 | 9,037 | 35 | TTAAAACAACCTAGTTGAAATCTTTTCTTAAAAAT |
| HsaA _{CE} 54 | 4,355 | 40 | GCCTGTCAAGTGACGATCCTTGCAGCTCACGTCCCTTGAA AAGCTGAAGTTGACTGCCAAAAGTCTATAAAAACCGCAGGTC TGTCTAGAACTGTTTTTCGGTTTTCTAGACGCCCCCGGGTTCA ATTATGGTCTTAAAAGCCCTAATACAAGTGCAAGAATTTGTTT GCCTTCACCCAGGGGCGGGGCGAGCCCCGCAATGGTGGCGC |
| HsaA _{CE} 57 _{abcd} * | 2,744 | 175 | CTTTGT |
| HsaA _{CE} 59 | 2,045 | 21 | GTGGTGGGGGGAGGTGGAGAG TGTC AATTTC AACATCGGGTCACATGACCAGCACCTCCCTGC TAAGGATGGGGATAGATTTCCACGTCAGCTTACGTCTCCAAA TTTCTACTTCACGGATCCGCTTCAAAGAGGCAGCTGCAGTGG AGAATCATGTAAAGCTCGGCTACTGCGGAGAGCCCAAGGTAG |
| HsaA _{CE} 60 _{abcde} * | 175 | 169 | C |
| HsaA _{EF} 62 | 6,367 | 41 | TTGAACCTCTGCCTTAAAATTGGACATCACCCATAACCTTG |
| HsaA _{EF} 63 | 5,802 | 35 | GATTTCTTAGATGTAAAAATGAGATCTCAATAGCA CCTACAATGCCAGAGCCGCCTCCAGTTCTAAGGCCAGAGGCT |
| HsaA _{EF} 69 | 4,319 | 47 | GTTTA |
| HsaA _{EF} 70 | 3,537 | 16 | AGAAATTTAGTAGCTG |
| HsaA _{EF} 71 | 3,041 | 20 | TTTATTACAAGGGGGAAAAA CTCTGAAGCTTTTCTGCACTCAGGTTCTGTCCTCATGGGCC |
| HsaA _{EF} 72 | 2,150 | 65 | TAGAGGGTAGAGAATTTGCCTT |
| HsaA _{EF} 73 | 1,158 | 20 | GGGAGGGGAAGAGGGGAGGG ATTGGCTGCGGGCGCCCGCGGTGCGGGGGATTGCTAAT CGTATTCAGCATGTTTTGCACAAGAAATGTCAGCCAGAAAGG |
| HsaA _{EF} 75 _{bcd} * | 119 | 106 | GCTATCTGCTCCCTTCGCCAAA GACAAGCACACCACAATTCTCCCTATCTTGTGAAGTTGTTTTT |
| HsaA _{FG} 77 | 5,580 | 70 | TTAAATCGCCTTGAACAAAAAGTTTTT |

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| | | | ATCTATTTAAATATTACCTAGACGGTCGTAATTTGTCTGGGCC CTATAGCCCTGGTGCCGTAAGGTTTTGTCGGCTTTTGTTCAGTT TTATGGCTTGCTAGTATATCTGGATTGTGGCTGTCTTGGACCA |
| HsaA _{FG} 78 _{abc} * | 5,037 | 170 | GTGATTTTCAGTTGAGAGGGGAGCTACATAGACAGAGGAAGC AGGTAGTTTCTGTTGTTGGGATCCACCTTTCTCTCGACAGCA |
| HsaA _{FG} 79 _{bc} | 4,091 | 54 | CGACACTGCCT GGGCGCCCGCTTCCATCCTGAGCCTCCCACTGGAGGCCTGCG |
| HsaA _{FG} 85 | 3,758 | 58 | CCTGCCAGGGACCTC |
| HsaA _{FG} 86 | 3,176 | 14 | CAAGGCCTCGGTTA ATACAGCACCTTTGTGCAGCTGGGTGCTGGAGAAGGGGACCC |
| HsaA _{FG} 88 | 2,843 | 66 | TTCCAAGAGCCAGTATGTTTTAAA |
| HsaA _{FG} 89 | 2,226 | 16 | GTAACCTCTTATTTT |
| HsaA _{FG} 90 | 1,921 | 28 | CAGGACGGGGCCATTTCCGGAGTTCATTG |
| | | | TTTTATGTGAGGGGCTCCGCTGGCCGCACTCGCACGCGGGAC CCGCGCCTTCTTGATGGCGTGATTAATTGTGATATAAAA |
| HsaA _{FG} 91 | 461 | 80 | |
| | | | CATAAAAACATATGGCTTTTGTCTATAAAAATTATGACTGCAA AACATCGGACCATTAATAGCGTGCGGAGTGATTTACGCGTTA TTGTTCTGCTGGACGGGCACGTGACGCGCACGGCCAATGGGG GCGCGGGCGCCGCAACTTATTAGGTGACTGTACTTCCCCC CGGTGCCACCAAGTTGTTACATGAAATCTGCAGTTTCAT |
| HsaA _{FG} 92 _{abcdef} * | 252 | 207 | |
| HsaA _{GI} 96 | 6,293 | 16 | CTATATAGTCTGTCT |
| HsaA _{GI} 97 | 5,974 | 23 | TACCTCAAGGCCTACTGACCAAA |
| HsaA _{GI} 98 _b * | 5,246 | 37 | ATAAAAAGAAAATGAGGGCTGTTACCGTTTTATGGGGTG |
| | | | ACGCCCTCTGTTGTTGCAGACAGAAGGAACCTCAAAGAATAG GCAGTAAGAGTGTGCCATAAAGGCCGGGTCTGCGAACTGTCT GGAATTTCGTCCTTAATGAGTTTACAACTGTCCAGCCCAATT AGGATATTCACCAAAGCCCTTTCATTTGTTTATTTGTTCTGT CTGCCGCCGATAAAGCGGGTGCAGAAACACCTCTTTTATTG |
| HsaA _{GI} 103 _{acde} * | 4,970 | 211 | |
| HsaA _{GI} 104 | 3,880 | 32 | TTAATGTGATGTTAATATAACAATCACACC |
| HsaA _{GI} 105 | 2,428 | 18 | TTGAAAGCCTGATTTTAT |
| HsaA _{GI} 106 | 2,014 | 43 | CCTTGGTCTTTTCTCTTTGCGTCTTGCTGTGTGTCACCCAGG |
| HsaA _{GI} 107 | 1,896 | 20 | TAACCTTCTGGGTTTTAT |
| HsaA _{GI} 110 | 1,448 | 33 | GTTTATGGTGTGTAATCGAGCTGAGCAGTAAAA CACCTGTGAGGACTGCTGAGATTGGCGGAGGCGGTCATGTGG GCGGTCACGTGCTGCGGCGAGCTCCGTCCAAAAGAAAATGG GGTTTGGTGTAAATCTGGGGGTGTAATGTTATCATATATCACT CTACCTCGTAAAACCGACACTGAAAGCTGCCGACAACAAAT |
| HsaA _{GI} 111 _{ab} * | 182 | 169 | C CAAAATACTACCTAGCACAGGCCTCTGCTCGAGGCACCCCCA |
| HsaA _{IJ} 114 | 6,864 | 52 | AACTACCTAT |
| HsaA _{IJ} 117 | 5,835 | 18 | TGTCATGTATCTTTTAA |
| HsaA _{IJ} 118 | 5,711 | 36 | CATAATTGGGTGCATGTGTTTTTGTGTGCCATAAT |

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| HsaA _{IJ} 119 _{abcd} | 5,027 | 192 | ATGGCGCCGGTGTAAAGAGCTGCCTCCTCTCAGTGATGGGGAA AGGGTCATAAAATCCGTTGTGTTTATGAAAATTTACAACCTTG CAATACAACCTTATGAGTTGTTCCGGCCCTTCCATTGGCCGCTG TCGGTCATGTGGATGAGAACCCTGAACATGAACTTTTTTATA ATTTCCCTTGCAGAGAATAGAGC |
| HsaA _{IJ} 122 | 4,651 | 79 | CCTGGCTAATTTCTGCGTCTCTGGCACCAGGAAAGAGGAC AATTCTTCTCTCGGGCTGCCAAGCGACAGCTGTCAG |
| HsaA _{IJ} 123 | 3,943 | 24 | GAAAACTTACTAATTCAGCCAGA |
| HsaA _{IJ} 124 | 3,822 | 29 | TGTTGGAGGAGAGGATGGGATTAATTGGG TTCCCCAACTTGAGACAATATCTTGGTATGGATTGATAAAT |
| HsaA _{IJ} 125 | 3,428 | 44 | AG |
| HsaA _{IJ} 126 | 2,663 | 14 | CCCTCCAGGCTGGC |
| HsaA _{IJ} 127 | 2,401 | 17 | GGCTAACATGTAAAGAT |
| HsaA _{IJ} 129 | 2,016 | 55 | TTTTAAAAGTCCCTTTTAATTTTTTGACTCGAGTTTTCATTTTC ACCTATTGAAT TGGCGCTCGAGTCCGGCTGAACGGCGGCAACTGGCGGCGGG CACGCGCCCGGGGCGCGCGCCACCCCTCGCTCCACC CAACTCCCCTATTAGTGCACGAGTTTACCTCTAGAGGTCATC AGGCAGGATTTACGACTGGACAACAAAAGCACGTGATTCGA AGTCGTACCCATATTTGGGTGCCTACGTAGGAGGGAACCAA GTACATGTCCAGTCATTTCCATAATTCATCATAAATTGTGCA AGGGTGCTATAGACGCACAAACGACCGCGAGCCACAAATCA |
| HsaA _{JK} 132 _{ac} * | 312 | 292 | A GTGCCTTTATAGGACCCTTTGCACGAACTCTGGAAGTGGCTC |
| HsaA _{KL} 133 | 10,536 | 71 | TTATAAGCGCAGCTTCAGTGATGTATGTT |
| HsaA _{KL} 134 | 10,696 | 43 | AATAGCTCCAAGCTGTTAAAGATATTTTTATTCAAACCTACCTA AACTTTTATAAGCCCCAGTTCGGCTATATGACATTTGGGTG CCAAATGAATAGGGTTTTGTCTATGAATTAGATCGTAAAATC ATCCATAGCACAGACAGATCGGCTCACTGGCTATAAAACGTC ACGTGGGGCCATTAAAGTAAGTTTTATGGTTTTGGGGAGTTG ACATCCAACATTATATACCACATAACATATAAT |
| HsaA _{KL} 136 _{ab} * | 9,690 | 201 | AAGGCAGAGCAAA CTGTTTGCTGCATGTTCTTTTTATTTTCGGCGGGACTGTTCTC AGCCGCTTGTGAGTCTGAAGCAATAAACTTTATGGCCGGATT |
| HsaA _{KL} 137 | 9,235 | 13 | TAACT |
| HsaA _{KL} 138 _{abc} | 8,556 | 90 | CAAATTCCTACTGCATTCAGAAATGAAACAAAA AAGATAAATCTGCACACCCTAGGAATCGCCAGCAGAGCAGC |
| HsaA _{KL} 139 | 7,803 | 35 | CTTTAGTACAAGTTC |
| HsaA _{KL} 140 _{bcd} * | 5,879 | 56 | AGGTCAAAAAGTTGAGGGTCAAAAGTTTACATTGTGCAGTGC TCTTAGTCATCTGCCAGACAGAGTTTGATGTCAATGTTAGA GCTGTGATCTTGACTATCAGCACAAAAGATAAAATGGCTCAG AGTGACGCGTGTATCACGGTATGGACTCCAGGTGAAC |
| HsaA _{KL} 143 _{abc} * | 5,424 | 163 | ACTGAAGAGCTAAACAATATTTTA |
| HsaA _{KL} 145 | 4,340 | 24 | TAAGTGTTGGTGCTGTAAGAATCTATTTTC |
| HsaA _{KL} 146 | 4,292 | 30 | GGATCAGTATAGGAAAACA |
| HsaA _{KL} 147 | 4,222 | 19 | AATTAATTGGTCAAAT |
| HsaA _{KL} 148 | 3,518 | 16 | |

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| | | | CTTTTAGAAGCGCAAAGTCCAAGGCCGAGGTGAACTTCAGGT CAGTGCCTCTAACAAATATGAAAATGTCGGCTAGTGAAGGGC GCGCCTTGTGATTTAACAAAGACTGTCAATGTGTAAGATTA |
| HsaA _{KL} 149 _{abc} * | 3,214 | 152 | TAAGAAACAAAATGCACACGGTGTC |
| HsaA _{KL} 150 | 2,707 | 28 | ACATTTACAGGCATCCCATCTTTTCTCA TTATTAATTGAGTTAGTTTCTCTCTGGCTTACTTTGGTGTCTT |
| HsaA _{KL} 151 | 2,648 | 46 | GG |
| | | | TTTGATTCAATGGAATGATGCTATGGTTTGCAAAGGGAGATT GAGGAAGGTTGAGAAAAGGACTGAGATTGTTTATTACAGCC ATAAATCTTGAGTAAAATGTCAAATGTCGGTGTGAGATA |
| HsaA _{KL} 152 | 2,551 | 159 | ACACTTGGTGGTCTGGCTCCGTTTGTGTTTAT |
| HsaA _{KL} 153 | 1,927 | 26 | TAAAGATTACACTCAGTGTGATTTC |
| HsaA _{KL} 154 | 1,756 | 18 | CCTTTTAACTCTTTTC AGAAGGCTGTTTATACTGCTCTTTGAAAAATCAACTAAGGTG |
| HsaA _{KL} 155 | 1,536 | 46 | CACC |
| HsaA _{KL} 156 | 1,026 | 14 | TTCTACCCTTAGCT GGAGGGGCTCGGCAAGCCAGAAAAACGACAACGCGAGA |
| HsaA _{KL} 157 _{bc} * | 71 | 71 | AAAATTAGTATTTTTGCACTTCACAAATTA |
| | | | AAAGTTGAAACCATGCAGTGCTGTGGGCCAGGAGTTTCTGC AGCTGTTCTACACTGAACTCTGAGCACACTTGGAAAGAAG TGGTCTCTTGGTATTTGGTATTTGTTGCACCTTCACACTTAAT CTGCCTGTTTCCAGGAGATAAAAAATAGTTTGTGCAAAGGG TTGAGATTAGTTTTTGTTCCTGGCTGTTCTTAAGGTCCTCTTC |
| HsaA _{LM} 160 | 17,551 | 223 | ACTAACTAC |
| | | | GAATCATTAAATCACCTCAAACAATAAATACTTCTTTGTAATTC |
| HsaA _{LM} 161 | 16,478 | 77 | AACAGCAATTCTGAAAGGCATTCTCTGGGAAAAGT |
| HsaA _{LM} 162 | 16,053 | 15 | CCAAGTGTATTGATT |
| | | | TGCCCTTTGCTAGGGCAACCATAAGAGTTCACCGAGAGGACA AATTTTCTATCTCATTAAATTGTTTTTTTTTTTAAAGCAAACCTT |
| HsaA _{LM} 163 | 15,877 | 113 | ACTGGCCCCCAAAATCCCTTGACCTTA |
| HsaA _{LM} 164 | 15,767 | 35 | TTAAAGACAGTATTTTGTGTAAGCTCTATAATTTT |
| | | | GATAAAGGTGTAGCGCCTGTGCAAGGGAGATATTGAAATGT AATCTTTGAGGTCACGTGACTCATTAAATAATTAATGCAGAT CGTCAGGAATGGATCGGAGTCGTCAGGGCCTACTAG |
| HsaA _{LM} 166 | 14,125 | 121 | ATGTTCTGATTCACGCTGGGAAGGCTGCAGAGATACCACAG GACGGGCGCGCGCTTTGTTCAATTTTCCGGCGTTCATAAA TCACCCGCGCCGGGCGAGCGAGGGAGCAAGCGAGCGCCAAA AACCGGAGAGAGAGGCCACGGCGGCGGCGGAGCCATTGT AAAGTGAGAGACCTGGGCAGCATCTCTCTGTGACTCATTAGT |
| HsaA _{LM} 167 | 13,715 | 220 | CTGAACGATTTA |
| HsaA _{LM} 168 | 12,807 | 20 | CAAGAGAGGGTTGCAAATAC |
| HsaA _{LM} 169 | 12,405 | 19 | ATTCACATTCTCCAAGTTG |
| HsaA _{LM} 170 | 11,622 | 26 | CAAACAAACCACTACACTGAACTTCA |
| HsaA _{LM} 173 | 11,280 | 16 | TCCTATTTGAAACAAG |
| HsaA _{LM} 174 | 9,462 | 19 | CAGTGTGAATGATTGGTGA |
| HsaA _{LM} 175 | 8,495 | 25 | CAATTAGATCATTTCCTCTGATATT |

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| HsaA _{LM} 176 | 8,462 | 50 | TTAGAAACTTATAAATCCATGTATCACTCAGTTGTGCACTGAG GAAATGC |
| | | | AATTCATGTATCACTCAGTTGTGCACTGAGGAAATGCTTAA GTGCAAGTTTAGTCAGGGCACTAGGTTTCTCTAGATTTTGCAA AACCCGGACCCACCACTCTATAGCCAAGCACATCTTTCCTAG TGGGCTCCCACTGAACAAAACCACTGGACTTGGAGGAGATG CTTTAACCTTTTGTGAGGTAATTATGTGCCTTTTGGTGTTCCT TGCGTCTGTAGTGTATGGTGTGGGTGTAGCAAACCTCCATAC |
| HsaA _{LM} 177 | 8,450 | 258 | AAT |
| HsaA _{LM} 178 | 8,391 | 23 | GCACTAGGTTTCTCTAGATTTTG AAATAAAAGGATTTAAGTTGACGTATGACCACGTGAGCACAT |
| HsaA _{LM} 179 _{abc} * | 7,797 | 70 | AATACAGCGCATTATTGTGGCATTGGGA TATTTTAAAGTATTTCCGCCGATTGTTTCATATCTAGAGTGAGT TATGGCTGTGAGAGACAAAGGTCAG |
| HsaA _{LM} 181 _{ce} * | 7,515 | 68 | GGAAGAGGGAAATCGATGAGGGAAATGTGCAGATGCGCTGC CATTTTATTGATGATGCTTCCAGGCACTTT |
| HsaA _{LM} 182 | 7,025 | 71 | |
| HsaA _{LM} 184 | 7,403 | 40 | TCCTTTGTTTCTCTTTTAGAACCAGAAACCATTTGAAAGAT TTTAATTGCTGTTCAATTACTTGTGAGCATTTTCATATGATTTAT GACCTAGTTCTGGCGCATTTTGGACCCAGTTAAAGACTCATA |
| HsaA _{LM} 185 | 6,153 | 93 | AATAATA |
| HsaA _{LM} 186 | 5,530 | 13 | CGGGGATTTGGGG |
| HsaA _{LM} 187 | 5,051 | 34 | GTTTTGCCCGGCAGGGTCTTGGCGCCAGTGAAAA GCAATATGCCATAAGGAGCAAGTGTGCTGTTTTGTGCTCTG TTACAGCTTTGGGGCGCGAGTCATAAATCTTGCCAGCCA TAAATGACAAAAACCAATTGGTATGCAT |
| HsaA _{LM} 188 | 4,714 | 112 | |
| HsaA _{LM} 190 | 4,555 | 13 | GGCTTTGTTTTTG CTCAGCGTACTCCATCCCACTAATGAGGAAAATATGTATAT |
| HsaA _{LM} 191 | 4,284 | 50 | ACATATAT |
| HsaA _{LM} 192 | 3,609 | 28 | GCATAATTTTCTGGACTTTCGTGACGC AATATTCATAAGAAACATACCCAAGTCGGTGCCACTAGCCCA |
| HsaA _{LM} 193 _{cd} | 3,373 | 74 | GGCAGAGCCCGGCCCGCACTAGCGCTTATCT TCGTCAGAAGTTAAGGTAAGCAGGGCCGCAACCGGCCGCTCC CGGCGCTGAATGGCGGAGTTTACGTCTCGGTGATTTATGGCT GCAGACTTAAATCTCGGTTCAAGAAGAGTTCACAAGCCGGAG CTTCTTCCCGGCAGTACTGATAC |
| HsaA _{LM} 194 _{bcd} * | 2,999 | 151 | |
| | | | TGACCCCATACATCAAATTACATAGCAGTTTCTAAGACAGA ACCTATTATCGTTAAGTTGGAAGGAGAGTTCAAACCTGTGGTC ATGGAGATGAACGCTGGTTTTTTCAGGTTCTGGAGGGGTTTTT TTTCCCTCTAATCCATCATGTTTTAACAGGTAGAATT |
| HsaA _{LM} 198 _{abc} * | 1,245 | 166 | |
| | | | AATATTGCTGACCACTTTTTCTTTTATGGCTTTCATGTCACTTA GCTATTGAGAGTAAGATGGATTTGCGCGGAGCCCTCACCCGCG CTGCGCTTCTCGCCCCACAGGTCTGCGGGGGCGGCCATTG GCGGGGAGTGTACGTGACCGCGGGGGCGTCCAATGTGC GCCCTCACGGGTGTCAAACCCCTGTGTCAG |
| HsaA _{LM} 199 _{ac} * | 227 | 197 | |

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| | | | AACAGGGTATATGAACAAATTTCTAGTCGAGTTTTCAATGTG AATTTGTTCTTACATTATGGCTCCCGAGGGGAAGCGACTT TTTTAATTTAAATTTTTTTTTAATTGCACTTCTTGTAAGA GTGAGAAAAAATCAAAGGCGCTTTGAAACAGGGGCTCTCT GTGCAAGGATGACTAAGTGTACGTCTTCCGTGTGTATGCT GGTGAACAGTCAGATTTATTTATTTTTTTGCAAGCATTGAA TAATCTAAGTTTTAAATATTATTATCCCCATCCGTTCTATTT |
| HsaA _{MN} 201* | 5,116 | 304 | AT TGCTGCGGAGGCAGGCTGAGGGCGCAGGGGCTGCCGAGTGC |
| HsaA _{MN} 202 | 4,273 | 56 | TGTGCACGGAAGAAA |
| HsaA _{MN} 203 | 3,403 | 40 | CAGAGACAGAAGTGAAAAATGTCGCCATTTTGTGCAAT |
| HsaA _{MN} 204 _{bcd} * | 2,238 | 84 | AAATGTGTTCTTAAGGGCTAGAAGCTGTCAAGGCTTTGGTG AGCAAGATTGATCGCGCCAGACTTCCTTTGGAGCTTTGTTT |
| HsaA _{MN} 208 | 1,377 | 42 | ACAGACTTCCTGGAAATCGGAAATACTCACCGACCCGAGCC |
| HsaA _{MN} 209 | 1,752 | 16 | TTAAAAATTATTTTTT |
| HsaA _{MN} 210 _{abc} | 726 | 162 | TTCTCCTGCTTTAACAGAACTTATGTGGCTGGGACGCAGGGC CCTCGGGTGTCAAACTTTGAAGATTAATGGATTACTTTGTTA ATGACTGCAGGCGTCAGACTGAGGTGCTTAAATGATTTGTGA GGTGCGAGGCGTCTTCCCGACAGTCCCAAACAATG |
| HsaA _{MN} 211 _{abcdef} * | 351 | 207 | TGTAAATAAAGCCTCGCTGGCCCCAATGAGGCGTTCCTTCC CGACTTTTTGGATCAATCAAACAGACAGTGGCTTCTTTGAT TAAAGCCCAAATTGTCAATTGGGCAGAAGCAATCATGTGACAG CCAATTCGGTCCAATTTCAACCTTGTCTCCATGAATCAATAG TTAATAGTAGCGGGTCCCATACGGCTGTAATCAG |
| HsaA _{NO} 215 | 4,771 | 12 | TGCCTTCTTTA |
| HsaA _{NO} 218 | 4,385 | 51 | AATAAAATTCGTCACAATTTATCCTCTTTTTTCAATTTAATA CATTTATT |
| HsaA _{NO} 219 | 3,195 | 31 | CTCATAAATCAAACGCTTCTATGAATGAGA |
| HsaA _{NO} 220 | 1,579 | 22 | TAAACAACAATTTAACGACCTC |
| HsaA _{NO} 221 | 826 | 32 | GAAGTTTCTTTTCTTGCCCTCGTCTCCTCAC |