

| PFC | Dist to 3' gene | Length | Sequence |
|---|-----------------|--------|---|
| HsaB _{CG} 22 | 96,213 | 23 | CCACTGGGAGGCTGAAACCTTTA |
| HsaB _{CG} 23 | 95,483 | 28 | TATTTATACAATAAAAATTTTTTAAAAA |
| | | | TAAAGGGGAGATCTAAGCAAATGATATGAACGGTCAGGTCAA GAATTGGCCACACAATTGAACGAAGTACATTTTTAGCATGTTG GTAGATATCCCATTTGAAAATGCTTGGCATGGAAGCATGGGAAT |
| HsaB _{CG} 24 | 84,917 | 159 | TGAGGAAACTGGTTAGAGATCCCCCTACGGA |
| HsaB _{CG} 25 | 80,145 | 36 | TTGATTTCCCAAGGCAGGTACCCCTTGGCAGCCTGA |
| HsaB _{CG} 26 | 78,392 | 21 | GAGCTCGTTGACTTTAATAAG |
| HsaB _{CG} 28 | 51,295 | 31 | CATAAAGAAGCTTCTAGTGCATCCTTGGGCC |
| HsaB _{CG} 29 | 46,437 | 29 | GAAAATTTTTAAAAGCATCTTTTGCTGCT |
| HsaB _{CG} 30 | 44,661 | 21 | CTTATTGATGAGTTGGATAAA |
| HsaB _{CG} 31 | 43,671 | 16 | CACTGTGCCTGGCCTG |
| HsaB _{CG} 32 | 14,496 | 29 | GTCAGTTTACGTAGGTCTTCACCCTTTCT TTAAATTTAATTTAAAAAACAGGATACATTTTCAGTAATCCATT AAACATCAGGGGTGAATTGTAACAGAATCCAATCCATATTTG |
| HsaB _{CG} 33 | 30,201 | 89 | AT |
| HsaB _{CG} 34 | 14,496 | 29 | GTCAGTTTACGTAGGTCTTCACCCTTTCT |
| HsaB _{CG} 35 | 11,355 | 23 | GGCCTGGACGTTTCTGAGGGGC |
| HsaB _{CG} 36 | 3,545 | 22 | GTAAATTTTCAGCTAAGCTTATT |
| HsaB _{CG} 37 | 1,319 | 24 | AGTACAGGAGGGCTGAAAACCTCAG |
| | | | CCGATTGATTTATGTCGGAGCTGACGCTTTATCAGGCAGTCGG AAAAACTTTGACCAATCATTTTGCAAGGAGAGCTGAGACGGGG |
| HsaB _{CG} 38* | 264 | 118 | TGCTCCACTGTACTTTGTTGGCTGAGAAGTTG |
| HsaB _{GH} 43 | 8,164 | 15 | TCTTCCCCATCTCAC |
| HsaB _{GH} 44 | 5,323 | 19 | TCATTAGGGATGCAAAATG |
| | | | GCAATAAAATAATATGACCGCTATAAAAGTTTATAGCGTATAA |
| HsaB _{GH} 45* | 4,945 | 84 | ATTTCTGAAGTTAAGAACTAAACAGCAGCAAAGCAAACA |
| HsaB _{GH} 46 | 4,502 | 38 | AGACGTCTGGGCGGGCAGCCTCTTGATTCTTTTACA |
| HsaB _{GH} 49 | 2,390 | 35 | TTTGTAAGCCTCCACTTTTGTGCTCAAAATTTT |
| | | | CTCGTAAAATGCTAACAGCTTTTATGCGCTGCGGCATAAACAA CAACAGACTCCGGCTTTATTGCGTTTTATAGTTTCTTAAAGAGT TTACAGCCGTTTTTTGGGGGGCCGGTTATCCAGCCAATCCCTC CACACGATAGTTAAACCTTTATCAATAATAAGGAAATTGATCA TTAAAGCTTTAAATATGACTACCTCGTTTGTGAAAATACGTT TAGGAGAGGAAGCTGTATGATTTGATAACTTGTATTTAAATAC CAATTACATTTATAGGACCTTTTAAACTCGGCGCAATTAAC CGTGTCTTTTACATTTTCCGAAGCGACCCTGACATT |
| HsaB _{GH} 50 _{abcdef} * | 1,227 | 342 | TGATTTGTTGTGAGGCGAGAGATATCTCATTAAATGTAGGTAGTT |
| HsaB _{GH} 51 _{abc} | 748 | 71 | AAACAGATTTAATCCGTATTCATTCTC |
| | | | CCAATAGGATGCGGGTCTCTAATGGATGCAAATGATCATGAA AAGACAGTGCAAAATATGAAACAACCTATTTGCAGGGAAGTA AATCACCGAAAACGTTTATGAACTGGCATCCCTTCTTCGAAA |
| HsaB _{GH} 52 _{bcd} * | 480 | 153 | TGTAAGCGAGGACCTCTTTAAGTG |
| HsaB _{Hl} 57* | 1,889 | 34 | ATTTCTGCTAAGTTCTCCAACAACATGAAAACCTG |

| | | | |
|---|--------|-----|---|
| HsaB _{Hl} 60 _a | 1,868 | 17 | CAACATGAAACTGCCTA AGCATGCGCGCTGTGGGCAATTGTTACAAGTGTTCCTTAGGTTT ACTGTGAAGAGAATGTATTCTGTATCCGTGAATTGCTTTATGGG GGGGAGGGAGGGCTAATTATATAATTTGTGTTCCTCTATACTT TGTTCTGTTGTCTGCGCTGAAAAGGGCGGAAGAGTTACAATA AAGTTTACAAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTC |
| HsaB _{Hl} 62 _{abc} | 1,623 | 223 | CTCATTT ATTATTGATCATATTTTATAAAATCCAACGCCACACAATTTTTTC CACATTACCGGGAGCCGTGGGGAGACGGCCCGCCATTGGCG GAGGGGACGTCACGTGGGCGGGGTCACGTGGTCCGGAGAGGA AAAAGGGGTCCCTTTTGGTGTAATCTGGACTCTAATCTGT ATATATCAAGGAATCTCGTAAAACCGACACTAAAACGTCCCTG CCTACAAATCATCCGGCCAAATT |
| HsaB _{Hl} 63 _{ab} | 238 | 238 | |
| HsaB _{Ij} 64 | 9,547 | 23 | TTAAATGAAAGGAGTTTAAAAAC AGATGGCGACTGAGAAAAGGGTTGCTGGTGGAGCAGCCATGA AGAAATGCAATAAAATTCCTTGTGTTTTATGAAAATTTACAAC TTGTGATAGAAGTTTATGAGTGGTTGAATCCAGCGATTGGCCG GCGCCGGTCATGTGGCCGGGCGATCGTGAACATGAACTTTTTA TCATTTCCCTGGTGGTTATAATGCAGCATTCTTTTGG |
| HsaB _{Ij} 65 _{abcd} * | 7,032 | 209 | |
| HsaB _{Ij} 66 | 5,717 | 15 | ATTTTTGAAATTA CCAACTCGGATATACTACTAATAGGCGCGGCTCGGACTAT |
| HsaB _{Ij} 70 _{ab} * | 103 | 61 | AAAACACAACAAATCATA |
| HsaB _{Ij} 71 | 2,259 | 87 | ACTACCTAGAAGTAAGAAGAGGAGCCTCAGAAGAAAACAAAG TTCTATTTTATTAATTTTCTATGTGTTGTGTTTGTAGTCTTGTCT CCTAACGATTCTCGGATCGTCATTATTTGTAACCATAGAGCAT GAATTACCTCTTGAGGTCATCAGCGAGAATTTACGACTGGTCA ACAAAAGCACGTGATCCCTAACGCCCCCACCCTTCCAA CCCCCCCCCATAATTTGGCCGCATACATAGCAAAACGAAGTAC AGTGCATCGCTATAATTCATTAATACATCATAAATCGTGAAGC ACAGGGTTATAACGACCACGATCCACAAATC GCATGTTTAAATGTGAACTCTCCCCTCCCCATCTGTGTTCTAACT |
| HsaB _{Jk} 79 _{abc} * | 267 | 246 | |
| HsaB _{Kl} 80 | 13,558 | 53 | TATTTATAA |
| HsaB _{Kl} 84 | 13,483 | 19 | GTTTCAGCTGGAACTTCT AAAAGTCGCTATGACATTTAGATGTCAAATGGATAGGGGTTTT ATCTCGAAGTTAGATCGTAAAAATCGCCGAGAAGTCAGACAG ATACCCCTCACTGGCTCGAGAAAGTCACGTGAGGTCCATAAAG TTAGTTTTATGGTTTTGGGGAGTTGACACCGCGCAGTATATTT ACATTTCTCCAGAATGTTAAGTGACACTTTAAC |
| HsaB _{Kl} 87 _{abcdef} * | 12,115 | 204 | |
| HsaB _{Kl} 88 | 12,418 | 40 | CCAAGTATCTCCCTCTGATTAGGAGTTAGGGTCCTTT |
| HsaB _{Kl} 89 | 11,577 | 35 | GGGAAAAGGGTTTTGTGTGGGGATCCATGCTCCCT |
| HsaB _{Kl} 96 | 9,043 | 18 | CATTTTTGGAGTTTTTCA |
| HsaB _{Kl} 90 _{abcd} | 8,297 | 84 | ATAATGGAGTTTGCATCCTGAAAAGGGGAAATCAACGCTCATAT CTCATCAATAATTCATAGAGTCCGGGATCATGCAGAGGTCA TTTGCATCCTGAAAGGGGAAATCAACGCTCATATCTCATCAAT AATTCATAGAGTCCGGGATCATGCAGAGGTCCAGCAGACGGG |
| HsaB _{Kl} 98* | 8,288 | 84 | |
| HsaB _{Kl} 99 | 7,273 | 23 | CGCTGCTCTGGACCAGAGGCAGA |

| | | | |
|---|--------|-----|--|
| HsaB _{KL} 100* | 7,248 | 51 | CTGTAACATCCCGGAGCTGCCAGTAGAGTCCGCCTTAGACCAA GTTCACAG |
| HsaB _{KL} 101 | 4,511 | 55 | ATGGAAAATCAAAAACAGGGGCGTGGCCGACTGACTCCTATCC GAATGGGACTTTT |
| HsaB _{KL} 102 _{ab} * | 4,357 | 200 | AAGTAATGACCTACGCAAAATTCAATATGACCCAGCGAACTGC GCGAGCATATTATAGTAACTGCCTGCTCGTGGGGGAGGCTGGG AGAGAGGTGAACCGCAGGTCACGGCGTCTAAAAATTATTTAA ATGTTTGAGAGCCTCGTGACGCGCTAGCTGTTTAACAAAAGAC TGCCAAAAGTATGAGATTAACACGAAAACT |
| HsaB _{KL} 104 _{bcd} e | 1,606 | 69 | TACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCACA AATTCGTATCTAGGGGAATATGTAGT |
| HsaB _{KL} 107 | 1,472 | 34 | TTTCTGAATGAGGACAGTCTGGTGACTGGCCACA AAACGAGTCAGGGGTCGGAATAAAATTTTAGTATATTTTGTGGG |
| HsaB _{KL} 108* | 59 | 58 | CAATCCCAGAAATF |
| HsaB _{LM} 110 _b * | 23,888 | 13 | CATCTTTAATCAC |
| HsaB _{LM} 111 | 23,080 | 26 | TGTACAGAGTGACAATAGAAATAAAT TTGTGTGTGGTTGAAGATTTTTTTCAAAGAGTCTGATGGGAATT TTTATCTCAGAGGACTCCAAATTGTGGTGGCTGGTTTGTTCCTC |
| HsaB _{LM} 112 | 22,942 | 90 | TT |
| HsaB _{LM} 113 _{ab} * | 22,517 | 156 | ACAGATGTTTCTGGGTGTTTGCAGGTTTTTCAGAGTATTTTTATA TTACAAAAGAAGCTAGCCAGTGCCATAGCTCAAACCTCTGACAAG CAAAATAGATAATCAAGAAGACAAATGGCCTCTTTTGTGAAGCC TTGCTCCAGTATTAATTTTCATTTTC |
| HsaB _{LM} 114 _{ab} * | 21,660 | 72 | AAAGTTCACAGCCATTCTGTGTAGACAAGAGCTAAGAAAAATG TGAGAATTATACAGAAAACCATTAATCAC |
| HsaB _{LM} 115 | 21,308 | 20 | CACAACTGAAAGAAGAAACA |
| HsaB _{LM} 116 | 20,477 | 79 | CACGTTTTCTAGGCGATTAGCTCAGTATTAGAACCACAAAATG ACCTCGGAAGCCCCTTGACCTCGCTGAGACTGGACA |
| HsaB _{LM} 117 | 19,434 | 26 | TTGGTTTGCATTTTGTAAATTGTTTC |
| HsaB _{LM} 118 _{abcde} * | 16,792 | 393 | GGTCATAGTGGTCCTTTGAGCCTGAAATCGAAAAGACCCCTTC CCCCTCCCGTACGTGATTCATTAATAATTAATGCCGAGGT TGCAGAATAGATATGTATTCTGTCAGGAAAATCGCAGGCTCGGT CTCCCTGTTTCTGACGTGCAATTCAACTGTCCTTTGAAAAACAA GCCTGTACCCCGAGAAAAAAAAGAGAGGGGGGAGAGAGAG AGGGAGAGAGAGAGAGAGAAAAGAAAGGGAGACAGCAATAAA ACAGCCCCCGCAGCCGAGCCACACCGCGGCTGGGGTATTGT AAGTAGAAGGGATTTCTCACTACCTACCGCTTATATGTCC ATGTAATTTATTGTTTGTATTAATGTTATTGTCGTAAAAATGT GACAAATAG |
| HsaB _{LM} 128 | 12,557 | 22 | TCCTCCCTCAAACCTCCAGCCT |
| HsaB _{LM} 129 | 10,193 | 27 | TAATTTAATTGATTTTATCATAAATCA TTTTATAATTTGGAGGCAATTCGGAAGGCCTTTCGCTGATTGGTC ATTAATCCACTGAGTTATTGTCTGTAAACAGAGGTCACTGGG |
| HsaB _{LM} 130 | 7,873 | 108 | AGAGAAAACATCCAGTCTGTCA |
| HsaB _{LM} 131 | 7,665 | 20 | TGCAGCCTCCCTTCTCTGC |
| HsaB _{LM} 132* | 4,597 | 36 | TGCAGACACCTACATTTTGGCTCCTGTCTTCTCC CAGAGGCCATTGTTACGGAGAGTAGGGCGTACCAGTCTTATAG |
| HsaB _{LM} 133 | 3,473 | 51 | GGCAACCA |

| | | | |
|--|--------|-----|---|
| | | | CTCGTCGGTGGCTAAGGTAAGCTGGACTGAAATAGGCTATCAG TTTGTGAATGCGGAGAGTATGTCTCAATGATTTATGGCCAT ATGACTCCAATCTCGGTTCAAGAAAGAGTTCACAAGCTTTAAGC |
| HsaB _{LM} 134 _{abcd} * | 3,072 | 133 | TTCC |
| HsaB _{LM} 135* | 248 | 40 | CCTATTGATGTCAGTTCCTTTTCAGTTCCTAAGATGGAT |
| HsaB _{MN} 139 _{abcd} * | 4,581 | 38 | TCTTGACTTAACGTGAAAACAGGGTATATTTGAACAAA |
| | | | TTGCACTTAGAATTTACATTTTAAATGGATGTAAAAACAACCTGTG AGAGATGTCTGGGCCTGCAGAAGTCCAGCATTGCTCAAAAAA GCGTGTGTTCTAGTGAACATTTTCATATATATTTATTGGTTATA GCCTGTAAAAATATTTCTTTTTTTGTATTATTTATCCCCCTACAT TATGTATTTATATGAGGGAAAAAAGGAAAAAATTGTACTTTT |
| HsaB _{MN} 140 _{bc} * | 4,478 | 232 | TTAGTATTTACCTG |
| HsaB _{MN} 141* | 3,994 | 17 | AACAATTCTTGAATAAA TCACGTGACCCGAAGCCCAACCACCATTGGGTCTAAAATGAAA |
| HsaB _{MN} 150 | 3,495 | 52 | ACAAAGAAA |
| HsaB _{MN} 151 | 3,013 | 33 | AATTGTAAGCGATGTGCCCGCATGCTTAATTA TATAATTTAAAGGCATAAGAGCGTGCAAAGTTTGATTGGGATC AAATAACGCTCAAGGGTTTTTCTTTCTTTCTCTTCTTCTT |
| HsaB _{MN} 152* | 2,732 | 107 | CCTTGAATAACATTTTCTG CTCTGGTGTTTTTGAATCAATTAACCAAATAATGCTCTCTGTT TTCCACCAGGCCAGACGAGCGATTGGCGGAGGCCGGTCCCG TGACCACGAATCCCTGTAATTTGCTGGAGTCTGGGGTTAAT AGAGAGAGTCCCCATACGCTTGTATTTATCAGCAATATACAAT |
| HsaB _{MN} 153* | 328 | 180 | TATAAAG |
| | | | TATTTATTAATAATTTAATAATAGGAAAAGGGGAAAGTATT |
| HsaB _{NO} 154 _{abc} * | 11,844 | 73 | TATTGTACATTATTTTCATAGATTAATAA |
| HsaB _{NO} 159 | 5,635 | 20 | CCTTCAGGTTAGAAGAAAAT |
| HsaB _{NO} 160 | 2,483 | 25 | CCTCCTCCCATCTCAATTTTCCTTT TCAGATGGATGGGCTGCGGGTGATTGAAGTGTCTTTGTATGC |
| HsaB _{NO} 161 _{abc} * | 289 | 64 | TAATGCTTGGGGGTGATGGA |