Supplementary File 1

Primers used to get HLAB-5801 PCR product:

Forward Primer: 5′-GGCGGGGGCGCAGGACCTGA-3′

Reverse Primer: 5′-GGAGGCCATCCCCGGCGACCTAT-3′

Sequence of HLAB-5801-Patient DNA using Forward primer:

5′-
GTCTCAGCCCCTCCTCGCCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCCGGCCGCGGG
GAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAG
GACGGAGCCCCGGGCGCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAACATGAAGGCCT
CCGCGCAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGTGAGTGACCCCGG
CCCGGGGCGCAGGTCACGACTCCCCATCCCCCACGTACGGCCCGGGTCGCCCCGAGTCTCCGGGTCCGAGATCCGCC
TCCCTGAGGCCGCGGGACCCGCCCAGACCCTCGACCGGCGAGAGCCCCAGGCGCGTTTACCCGGTTTCATTTTCAGT
TGAGGCCAAAATCCCCGCGGGTTGGTCGGGGCGGGGCGGGGCTCGGGGGACGGGGCTGACCGCGGGGCCGGGGCCAG
GGTCTCACATCATCCAGAGGATGTATGGCTGCGACCTGGGGCCCGACGGGCGCCTCCTCCGCGGGCATGACCAGTCC
GCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGAGCTCCTGGACCGCGGCGGACACCGCGGCTCAGAT
CACCCAGCGCAAGTGGGAGGCGGCCCGTGTGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGC
TCCGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCA-3′

Sequence of HLAB-5801-Patient DNA using Reverse primer:

5′-
CGCCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATC
GCAGTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAGGACGGAGCCCCGGGC
GCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAACATGAAGGCCTCCGCGCAGACTTACC
GAGAGAACCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGTGAGTGACCCCGGCCCGGGGCGCAGGTC
ACGACTCCCCATCCCCCACGTACGGCCCGGGTCGCCCCGAGTCTCCGGGTCCGAGATCCGCCTCCCTGAGGCCGCGG
GACCCGCCCAGACCCTCGACCGGCGAGAGCCCCAGGCGCGTTTACCCGGTTTCATTTTCAGTTGAGGCCAAAATCCC
CGCGGGTTGGTCGGGGCGGGGCGGGGCTCGGGGGACGGGGCTGACCGCGGGGCCGGGGCCAGGGTCTCACATCATCC
AGAGGATGTATGGCTGCGACCTGGGGCCCGACGGGCGCCTCCTCCGCGGGCATGACCAGTCCGCCTACGACGGCAAG
GATTACATCGCCCTGAACGAGGACCTGAGCTCCTGGACCGCGGCGGACACCGCGGCTCAGATCACCCAGCGCAAGTG
GGAGGCGGCCCGTGTGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGCTCCGCAGATACCTGG
AGAACGGGAAGGAGACGCTGCAGCGCGC-3′

The DNA sequence blasted with the NCBI nucleotide blast and showed 100% matching to *HLA-B*58:01* (Forward primer) as shown below (Supplementary File 1):

Homo sapiens HLA-B gene for HLA class I histocompatibility antigen B alpha chain precursor, complete cds, allele: B*58:01:01:03

Sequence ID: LC257744.1 Length: 4571 Number of Matches: 1

Range 1: 1037 to 1857 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1517 bits(821)	0.0	821/821(100%)	0/821(0%)	Plus/Plus

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Query  1     GTCTCAGCCCCTCCTCGCCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1037  GTCTCAGCCCCTCCTCGCCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGT  1096

Query  61    CCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1097  CCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGT  1156

Query  121   TCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAGGACGGAGCCCCGGGCGCCATGGATAG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1157  TCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAGGACGGAGCCCCGGGCGCCATGGATAG  1216

Query  181   AGCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAACATGAAGGCCTCCGCGCAGA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1217  AGCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAACATGAAGGCCTCCGCGCAGA  1276

Query  241   CTTACCGAGAGAACCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGTGAGT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1277  CTTACCGAGAGAACCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGTGAGT  1336

Query  301   GACCCCGGCCCGGGGCGCAGGTCACGACTCCCCATCCCCCACGTACGGCCCGGGTCGCCC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1337  GACCCCGGCCCGGGGCGCAGGTCACGACTCCCCATCCCCCACGTACGGCCCGGGTCGCCC  1396

Query  361   CGAGTCTCCGGGTCCGAGATCCGCCTCCCTGAGGCCGCGGGACCCGCCCAGACCCTCGAC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1397  CGAGTCTCCGGGTCCGAGATCCGCCTCCCTGAGGCCGCGGGACCCGCCCAGACCCTCGAC  1456

Query  421   CGGCGAGAGCCCCAGGCGCGTTTACCCGGTTTCATTTTCAGTTGAGGCCAAAATCCCCGC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1457  CGGCGAGAGCCCCAGGCGCGTTTACCCGGTTTCATTTTCAGTTGAGGCCAAAATCCCCGC  1516

Query  481   GGGTTGGTcggggcggggcggggctcgggggacggggctgaccgcggggccggggccagg  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1517  GGGTTGGTCGGGGCGGGGCGGGGCTCGGGGGACGGGGCTGACCGCGGGGCCGGGGCCAGG  1576

Query  541   gTCTCACATCATCCAGAGGATGTATGGCTGCGACCTGGGGCCCGACGGGCGCCTCCTCCG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577  GTCTCACATCATCCAGAGGATGTATGGCTGCGACCTGGGGCCCGACGGGCGCCTCCTCCG  1636

Query  601   CGGGCATGACCAGTCCGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGAG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1637  CGGGCATGACCAGTCCGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGAG  1696

Query  661   CTCCTGGACCGCGGCGGACACCGCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCG  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1697  CTCCTGGACCGCGGCGGACACCGCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCG  1756

Query  721   TGTGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGCTCCGCAGATA  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1757  TGTGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGCTCCGCAGATA  1816

Query  781   CCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCA  821
             ||||||||||||||||||||||||||||||||||||||||
Sbjct  1817  CCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCA  1857
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The DNA sequence blasted with the NCBI nucleotide blast and showed 100% matching to *HLA-B*58:01* (Reverse primer) as shown below (Supplementary File 2):

Homo sapiens HLA-B gene for HLA class I histocompatibility antigen B alpha chain precursor, complete cds, allele: B*58:01:01:03
Sequence ID: LC257744.1 Length: 4571 Number of Matches: 1

Range 1: 1052 to 1849 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1474 bits(798)	0.0	798/798(100%)	0/798(0%)	Plus/Plus

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Query  1     CGCCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCCGGCCGCG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1052  CGCCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCCGGCCGCG  1111

Query  61    GGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTCGACA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1112  GGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTCGACA  1171

Query  121   GCGACGCCGCGAGTCCGAGGACGGAGCCCCGGGCGCCATGGATAGAGCAGGAGGGGCCGG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1172  GCGACGCCGCGAGTCCGAGGACGGAGCCCCGGGCGCCATGGATAGAGCAGGAGGGGCCGG  1231

Query  181   AGTATTGGGACGGGGAGACACGGAACATGAAGGCCTCCGCGCAGACTTACCGAGAGAACC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1232  AGTATTGGGACGGGGAGACACGGAACATGAAGGCCTCCGCGCAGACTTACCGAGAGAACC  1291

Query  241   TGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGTGAGTGACCCCGGCCCGGGG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1292  TGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGTGAGTGACCCCGGCCCGGGG  1351

Query  301   CGCAGGTCACGACTCCCCATCCCCCACGTACGGCCCGGGTCGCCCCGAGTCTCCGGGTCC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1352  CGCAGGTCACGACTCCCCATCCCCCACGTACGGCCCGGGTCGCCCCGAGTCTCCGGGTCC  1411

Query  361   GAGATCCGCCTCCCTGAGGCCGCGGGACCCGCCCAGACCCTCGACCGGCGAGAGCCCCAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1412  GAGATCCGCCTCCCTGAGGCCGCGGGACCCGCCCAGACCCTCGACCGGCGAGAGCCCCAG  1471

Query  421   GCGCGTTTACCCGGTTTCATTTTCAGTTGAGGCCAAAATCCCCGCGGGTTGGTcggggcg  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1472  GCGCGTTTACCCGGTTTCATTTTCAGTTGAGGCCAAAATCCCCGCGGGTTGGTCGGGGCG  1531

Query  481   gggcggggctcgggggacggggctgaccgcggggccggggccaggg TCTCACATCATCCA  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1532  GGGCGGGGCTCGGGGGACGGGGCTGACCGCGGGGCCGGGGCCAGGGTCTCACATCATCCA  1591

Query  541   GAGGATGTATGGCTGCGACCTGGGGCCCGACGGGCGCCTCCTCCGCGGGCATGACCAGTC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1592  GAGGATGTATGGCTGCGACCTGGGGCCCGACGGGCGCCTCCTCCGCGGGCATGACCAGTC  1651

Query  601   CGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGAGCTCCTGGACCGCGGC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1652  CGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGAGCTCCTGGACCGCGGC  1711

Query  661   GGACACCGCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGTGTGGCGGAGCAGCT  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1712  GGACACCGCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGTGTGGCGGAGCAGCT  1771

Query  721   GAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAA  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1772  GAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAA  1831

Query  781   GGAGACGCTGCAGCGCGC  798
             ||||||||||||||||||
Sbjct  1832  GGAGACGCTGCAGCGCGC  1849
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