B*07:02:01   1 ATGCTGGTCATGGCGCCCCGAACCGTCCTCCTGCTGCTCTCGGCGGCCCTGGCCCTGACCGAGACCTGGGCC 72
B*57:01:01   1 ATGCGGGTCACGGCACCCCGAACCGTCCTCCTGCTGCTCTGGGGGGCAGTGGCCCTGACCGAGACCTGGGCC 72

B*07:02:01   73 GGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCTCA 144
B*57:01:01   73 GGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCA 144

B*07:02:01   145 GTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAGAGAGGAGCCGCGG 216
B*57:01:01   145 GTGGGCTACGTGGACGACACCCAGTTCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAGGATGGCGCCCCGG 216

B*07:02:01   217 GCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCGGAACACACAGATCTACAAGGCCCAGGCACAG 288
B*57:01:01   217 GCGCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAACATGAAGGCCTCCGCGCAG 288

B*07:02:01   289 ACTGACCGAGAGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGCCGGGTCTCACACCCTCCAG 360
B*57:01:01   289 ACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGCCGGGTCTCACATCATCCAG 360

B*07:02:01   361 AGCATGTACGGCTGCGACGTGGGGCCGGACGGGCGCCTCCTCCGCGGGCATGACCAGTACGCCTACGACGGC 432
B*57:01:01   361 GTGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCCTCCTCCGCGGGCATGACCAGTCCGCCTACGACGGC 432

B*07:02:01   433 AAGGATTACATCGCCCTGAACGAGGACCTGCGCTCCTGGACCGCCGCGGACACGGCGGCTCAGATCACCCAG 504
B*57:01:01   433 AAGGATTACATCGCCCTGAACGAGGACCTGAGCTCCTGGACCGCGGCGGACACGGCGGCTCAGATCACCCAG 504

B*07:02:01   505 CGCAAGTGGGAGGCGGCCCGTGAGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCGAGTGCGTGGAGTGGCTC 576
B*57:01:01   505 CGCAAGTGGGAGGCGGCCCGTGTGGCGGAGCAGCTGAGAGCCTACCTGGAGGGCCTGTGCGTGGAGTGGCTC 576

B*07:02:01   577 CGCAGATACCTGGAGAACGGGAAGGACAAGCTGGAGCGCGCTGACCCCCCAAAGACACACGTGACCCACCAC 648
B*57:01:01   577 CGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGACCCCCCAAAGACACATGTGACCCACCAC 648

B*07:02:01   649 CCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGTTTCTACCCTGCGGAGATCACACTGACC 720
B*57:01:01   649 CCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACC 720

B*07:02:01   721 TGGCAGCGGGATGGCGAGGACCAAACTCAGGACACTGAGCTTGTGGAGACCAGACCAGCAGGAGATAGAACC 792
B*57:01:01   721 TGGCAGCGGGATGGCGAGGACCAAACTCAGGACACCGAGCTTGTGGAGACCAGACCAGCAGGAGATAGAACC 792

B*07:02:01   793 TTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAG 864
B*57:01:01   793 TTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAG 864

B*07:02:01   865 GGGCTGCCGAAGCCCCTCACCCTGAGATGGGAGCCGTCTTCCCAGTCCACCGTCCCCATCGTGGGCATTGTT 936
B*57:01:01   865 GGGCTGCCAAAGCCCCTCACCCTGAGATGGGAGCCATCTTCCCAATCCACCGTCCCCATCGTGGGCATTGTT 936

B*07:02:01   937 GCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTAGGAGGAAGAGT 1008
B*57:01:01   937 GCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTAGGAGGAAGAGC 1008

B*07:02:01 1009 TCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTGCAGCGACAGTGCCCAGGGCTCTGATGTGTCTCTC 1080
B*57:01:01 1009 TCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTGCAGCGACAGTGCCCAGGGCTCTGATGTGTCTCTC 1080

B*07:02:01 1081 ACAGCTTGA   1089
B*57:01:01 1081 ACAGCTTGA   1089

Supplementary Figure S1. **Nucleotide coding sequence alignment of *HLA-B*57:01:01* and the reference sequence *HLA-B*07:02:01***. Nucleotide differences between the two sequences are highlighted in grey. This alignment was generated using the IMGT/HLA Database's alignment tool (www.ebi.ac.uk/imgt/hla/align.html) and visualized in Jalview.