

```

B*07:02:01  1 GSHSMRYFYTSVSRPGRGEPRI SVGYVDDTQFVRFDSDAASPREEPRAP 50
B*57:01:01  1 GSHSMRYFYTAMSRPGRGEPRI AVGYVDDTQFVRFDSDAASPRMAPRAP 50

B*07:02:01  51 WIEQEGPEYWD RNTQIYKAQAQT DRESLRNLRGYYNQSEAGSH TLQSMYG 100
B*57:01:01  51 WIEQEGPEYWD GETRNMKASAQTYRENLR IALRYYNQSEAGSH I IQVMYG 100

B*07:02:01  101 CDVGPDGRLLRGHQDYAYDGKDYIALNEDLRSWTAADTAAQITQRKWEAA 150
B*57:01:01  101 CDVGPDGRLLRGHQQSAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAA 150

B*07:02:01  151 REAEQR RAYLEGECVEWLRRYLENGKDKLERADPPKTHVTHHPISDHEAT 200
B*57:01:01  151 RVAEQL RAYLEGLCVEWLRRYLENGKETLQRADPPKTHVTHHPISDHEAT 200

B*07:02:01  201 LRCWALGFYPAEITLTWQRDGEDQTQDTEL VETRPAGDRTFQKWA AVVVP 250
B*57:01:01  201 LRCWALGFYPAEITLTWQRDGEDQTQDTEL VETRPAGDRTFQKWA AVVVP 250

B*07:02:01  251 SGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG 300
B*57:01:01  251 SGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG 300

B*07:02:01  301 AVVAAVMCRRKSSGGKGGSYSQAACSDSAQGS DVSLTA 338
B*57:01:01  301 AVVAAVMCRRKSSGGKGGSYSQAACSDSAQGS DVSLTA 338

```

Supplementary Figure S2. Amino acid sequence alignment of HLA-B*57:01 and the reference sequence HLA-B*07:02. Amino acid 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.