

**Human canonical CD157/Bst1 is an alternatively spliced isoform
masking a previously unidentified primate-specific exon included in a
novel transcript**

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SUPPLEMENTARY INFORMATION

Figure legends

Supplementary Figure 1. Genomic nucleotide sequence of human *BST1* from exon 1 to exon 2, encompassing exon 1b. Nucleotide sequence of human *BST1* from the 5' end of exon 1 to the 3' end of exon 2. Exons 1 and 2 are shaded in blue; exon 1b is shaded in orange. GT/AG splice sites are shaded in yellow. The branch point (open box) and polypyrimidine tract (grey box) associated with exon 1b are indicated. The nucleotide sequence was analysed for splicing signals using Human Splicing Finder¹ and the SROOGLE program².

Supplementary Figure 2. Quantification of *BST1* transcripts. Expression levels of *BST1-001* (top panel) and *BST1-002* (lower panel) in ten PMN samples purified from peripheral blood of healthy subjects. Transcript expression was calculated relative to the *GUSB* endogenous control, using the $\Delta\Delta C_t$ method. Bars represent the fold change of each sample relative to the mean of all samples analysed. Each PMN sample was examined in triplicate (n = 3).

Supplementary Figure 3. Uncut gels for *BST1* expression profiles by RT-PCR.

Supplementary Figure 4. Original gels for western blotting. Top panel show gels from which band images were obtained for CD157 detection by western blotting; bottom panel shows original gel strips for phosphorylation analyses by western blot.

Supplementary Figure 5. Original blot showing CD157 in PMN and U937.

Supplementary References

1. Desmet, F. O. *et al.* Human Splicing Finder: an online bioinformatics tool to predict splicing signals. *Nucleic acids research* **37**, e67, doi:10.1093/nar/gkp215 (2009).
2. Schwartz, S., Hall, E. & Ast, G. SROOGLE: webserver for integrative, user-friendly visualization of splicing signals. *Nucleic acids research* **37**, W189-192, doi:10.1093/nar/gkp320 (2009).

Exon 1

1 GAGAAGGGGA GTGGAGGAAG CACGGGACTG GAGGGACCAA AGTTCCCCGA TGGCGGCCCA
61 GGGGTGCGCG GCATCGCGGC TGCTCCAGCT GCTGCTGCAG CTTCTGCTTC TACTGTTGCT
121 GCTGGCGGCG GGCGGGGCGC GCGCGCGGTG GCGCGGGGAG GGCACCAGCG CACACTTGCG
181 GGACATCTTC CTGGGCCGCT GCGCCGAGTA CCGCGCACTG CTGAGTCCCC AGCAGCGGTG
241 AGGCAGTCGG CCGGGTGGAA GGGGAGCCGG AAAGAGGCAA CCGTGGGGAG GGCCTGGGGA
301 GGGGAAAAC TGGCGTAAAG TTCGGGGTGA GGGGGCAATG AGAGAGGCCT TGAGGGGAGA
361 GGTGAGTGTG GAGACAGCGA TGGTCTGAA CGATGGGGGC GAGTGAGGAG GGGGCTGTGA
421 AGTGTGTCTG CAGGTGAGGG GTGCGCTGTG CGGGGTCTAG AGATGAGTGT GTGTGTGTGC
481 GCGCACACAC AACTGTAGA GGTGAGGGGT GTGTGCGTGT GTTCTAGAGG TGAGGGGGGT
541 GTGTGTGTGC GCGCCTCTA GAGGTGGGAG GTGTGTGTGT GCTCTAGAGG TGGATGTGTG
601 TGTGTGTGCT CTAGAGGTGG GGTGTGTGT GTGTGTGTGT GCTCTAGAGG TGAGGGGTGT
661 GTGTGTGTGT TCTAAAGGTG AGATGTGTGT GTGTGTTCTA GAGGTAAGGG GTGTGTGTGT
721 TCCAGAGGTG AGGTGTCTGT ATGTGTGTTT TAGAGGTGAG GGGTGTGTGC ATGTGTGTTC
781 TAGAGGTGAA GGGGTGTGT GTGCGTGC GC TCTAGAGGTG AGGGGTGTGT GTATTCTAGA
841 GGTGAGGGGT GTGTGTGTTT TAGAAGTGAG GGGTGTGTGT GTTCTGGAGG TGAGATGTGT
901 GTGTGTGTGT TCTAGAGGTG AGGGGTGCGT GCATGTGTTC TAGAGGTGTG TGTGTATCTG
961 TGTTCTAGAG GTGAGGGGTG TGTGTGTGTA GTCTAGAGGT GACAGGTGTG TGTGTGTGGT
1021 CTATAGGTGA GGGATGTGTG TGTGGTCTAG AGGTGAGGGA TGTGTGTGTG GTCTAGAGGT
1081 GAGGGGTGTG TGTGTTCTAG AGGTGAGGGG GTGTATGTGT ATTCTAGAGC TGAGGAGAGT
1141 GTGTGTTCTA GAGATGAGGT GTGTATGTGT GTTCTAGAGG TGAGGGGTGT GTGTGTGTTT
1201 TGGAGTTGAG GGGTGTGTGT TCTAGAGGTG AGATGTGTGT GTTCTAGAGA TGATGGGTGT
1261 GTGTGTTCTA GAAGTGAGAG GTGTGTGTGT TCTAGAGGTA AGGGATGTGT GTGTGTGTGT
1321 GTTCTAGAGG TGAGTTGTGT GTGTGTTCTA GAGGTGAGAT GTGTGTGTGT TTGTTCTAGA
1381 GGTGAGGGGT GTGTGTGTGT AGTCTAGAGG TGACAGGTGT GTGTGTGTGG TCTATAGGTG
1441 AGGGATGTGT GTGTGGTCTA GAGGTGAGGG ATGTGTGTGT GGTCTAGAGG TGAGAGGTGT
1501 GTGTGAGTGT GAAGGAGGGT GGAGAGGTAT CCCTCTAGAA GTGAGGGTGG GGTAGAGGTG
1561 AACTGGGTAA CAGCCCATTC CCACCCAGCA GATGTTTAGT CTGAATACTC AGAACCCAGA
1621 ATGTGATCTC AGGTTGGAAT TCCTGAGTC CAGTCCTTCC AGAATTCAA TTTAGATCC
1681 CCTAAATCTG GAGGATTTCT GAAGTTTGGG TCTTTCTTGC CAGTGC TGCA TTTCTTACTG
1741 ATTTTTGTTC CTTCTGTGGC CCCCTTTTTC TTATGTTTGT GATGCTTTC TTGTTGCTGAT

← Branch point

Polypyrimidine Tract

Exon 1b

1801 CTTTTTATT GTGCACATT TCAGGCAAAT AAGAAACAGC AGAGAACCAC CTGTGTTACA
1861 CACCACCCAG TATGAGAAAC AAAGTTACAA ATGCTATGGG AAATATTTTT TGA AAACTAG
1921 CATGGACCTC AAGAGGGGCT TGCACTGGAG GGTGCACCTG CTTTGCCAGA GGTGGAAGCC
1981 TTTTGCAGCA TTGGGCTCC CTCTAACAC TACACATCCT GCTGGCTGGC CTGGCCTCAC
2041 CTGGTCCCG AGCTCCACAC TGA AACTGGA CTATGAGACT GGCCCAACCG TTAGTCTAA
2101 ATGAAGAGGC ACCTGCTGTA TAGTTGACTG AATTTGTCAC CTCCTGCTCG GTGCCATTTT
2161 TGCTTGCTC CGTGAGCCTG GGCAAGGCT GTATTCCTTA GCTCTGAGAA ATCTGTGCAG
2221 TGCCTT CAGA GAGACAATTC CAGTGCAGA TTTCTGAATC TGTCACCTAA GCCATGACAA
2281 TTCGTTGTCT TTTTGTAAAG C TACTTCTG CAGTTACTAT ATGAAAAATC TCTGTAAAG
2341 CTCTTAGACA AATGGGCATA CTT CACAACA CATTATGATG TGCATGTGTG TGTCTTCC
2401 AACTTG TACT TTTGCACAGG AACAAGA ACT GCACAGCCAT CTGGGAAGCC TTTAAAGTGG
2461 CGCTGGACAA GGATCCCTGC TCCGTGCTGC CCTCAGACTA TGACCTTTTT ATTA ACTTGT
2521 CCAGGCACTC TAT TCCAG A GATAAG

Exon 2







