

<i>abl-D</i>	MTLVLSRSGSLSS LS SSLSTIATPTTTRTSPPPPHSSLPTGCTSSASASASNHTPRPLQEE
<i>ABL</i>	MTLVLSRSGSLSSISSLSTIATPTTTRTSPPPPHSSLPPGCTSSASASASNHTPRPLQEE
<i>abl-D</i>	KTEPYYADDSYKDPPPPAH VL TG EFGVKIRDFAYEKGGVEVRRVKKYVRPEGQGIGRRRE
<i>ABL</i>	KTEPYYADDSYKDPPPPAHVLASEFGVKIRDFAYEKGGVEVRRVKKYVRPEGQGIGRRRE
<i>abl-D</i>	PVLVQRQPTPPGQRGWMWGVGVGGGGGCENAEASTSSGLTRQRVVQDIEDLEFHSQSQ
<i>ABL</i>	PVLVQRQPTPPGQRGWMWGVGVGGGGVGGGYENAEASTSSGLTRQRVVQDIEDLEFHSQSQ
<i>abl-D</i>	SQSQSQSQSQPQSLPPFEHI SFSE SDGEPYIETPAVTPNGSLQWKTTTAAEEELTLPSLHN
<i>ABL</i>	SQSQSQSQSQPQSLPPFEHITFSDSDGEPYIETPAVTPNGSLQWKTTTAAEEELTLPSLHN
<i>abl-D</i>	LPSSKRAFHPDD DEDE EQHHTTPPQPPTKKQRVVSPiKRYNLRERRPPATT TTTT LLPP
<i>ABL</i>	LPSSKRAFHPDD-----EQHHTTPPQPPTKKQRVVSPiKRYNLRERRPPTTT----LLPP
<i>abl-D</i>	SRLRNILSVQSSQSQLSTGPKGRRKGKARTTRV
<i>ABL</i>	SRLRNILSVESSQSQLSTGPKGRRKGKARTTRV

Supplementary Figure S1. Amino acid sequence alignment of *abl-D* and *ABL*. Amino acid residues were expressed in one-letter codes and gaps in the aligned sequences were introduced to maximize similarities. Sites where mutation has been identified in *abl-D* are highlighted by colors. Blue, synonymous mutation; Red, missense mutation; yellow, insertion.