

1 **Supplementary Figure 1:**

A. Wild type (normal control) ACKR1 amino acid sequence

MGNCLHRAELSPSTENSSQLDFEDVWNSSYGVNDSFPDGDYGANLEAAAPCHSCN
LLDDSA LPFFILTSVLGILASSTVLFMLFRPLFRWQLCPGWPVLAQLAVGSALFSIVVPV
LAPGLGSTRSSALCSLGYCVWYGSAFAQALLGCHASLGHRLGAGQVPGLTLGLTVG
IWGVAALLTLPVTLASGASGGLCTLIYSTE LKALQATHTVACLAIFVLLPLGLFGAKGLK
KALGMGP GPWMNILWAWFIFWWPHGVVLGLDFLVR SKLLLLSTCLAQQALD LLLNLA
EALAILHCVATPLLLALFCHQATR TLLPSLPLPEGWSSHLDTLGSKS

Amino acid inserted in altered sequence

B. Altered ACKR1 amino acid sequence

MGNCLHRAELSPSTENSSQLDFEDVWNSSYGVNDSFPDGDYGANLEAAAPCHSC
NLLDDSA LPFFILTSVLGILASSTVLFMLFRPLFRWQLCPGWPVLAQLAVGSALFSIVVP
VLAPGLGSTRSSALCSLGYCVWYGSAFAQALLGCHASLGHRLGAGQVPGLTLGLTV
GIWGVAALLTLPVTLASGASGGLCTLIYSTE LKALQATHTVACLAIFVLLPLGLFGAKGLK
KALGMGP GPWMNILWAWFIFWWPHGVVLGLDFLVR SKLLLLSTCLAQQALD LLLNLA
ALAILHCVATPLLLALFCHQATR TLLPSLPLPEGWSSHLDTLGSKS

2
3
4
5 **Supplementary Figure 2:**

PROVEAN Prediction - Job ID: 2365908446991770

- Query sequence ([fasta](#))
- Supporting sequence set used for prediction
 - Number of sequences: 215 ([fasta](#), [E-values](#))
 - Number of clusters: 30
- Score thresholds for prediction
 - (1) Default threshold is -2.5, that is:
 - Variants with a score equal to or below -2.5 are considered "deleterious,"
 - Variants with a score above -2.5 are considered "neutral."
 - (2) [How to use a more stringent threshold.](#)

Variant	PROVEAN score	Prediction (cutoff= -2.5)
A49dup	-5.021	Deleterious

6
7
8

Supplementary Figure 1: Alignment of ACKR1 antigen (amino acid) of wild-type and altered sequences. The upper shows amino acid sequences of wild-type (control) ACKR1 antigen. The lower panel shows ACKR1 antigen with an altered sequence. The yellow bold amino acid A highlighted in the sequence is inserted in the sequence. The online Expasy translate tool was used to deduce the amino acid sequence from wild-type and altered *ACKR1* nucleotide sequences (ACKR1(NM_002036.4):c.144_146dup)

Supplementary Figure 2: *In silico* analysis of altered amino acid sequence by online platforms. **A.** Protein prediction by PROVEAN. The single amino acid deleted variant was predicted to be deleterious. **B.** Virtual gel electrophoresis generated by NEBcutter V2.0. **a:** Gel image generated upon digestion of wild type sequence with *Ban I*; **b:** Gel image generated upon digestion of variant sequence with *Ban I*. The horizontal red line helps to illustrate the difference in band size on the gel.