Supplementary Figure S1

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            1                                                                            90
JIP3        MMEIQMDEGGGVVVYQDDYCSGSVMSERVSGLAGSIYREFERLIHCYDEEVVKELMPLVVNVLENLDSVLSENQEHEVELELLREDNEQL
JIP4
Consensus

            91                                                                           180
JIP3        LTQYEREKALRKQAEEKFIEFEDALEQEKKELQIQVEHYEFQTRQLELKAKNYADQISRLEERESEMKKEYNALHQRHTEMIQTYVEHIE
JIP4                                                                               ..HN.M..L.
Consensus                                                                            MI  Y EH E

            181                                                                          265
JIP3        RSKMQQVGGSGQTESSLPGRSRKERPTSLNVFPL--ADGMVR--AQMGGKLVPAGDHWHLSDLGQLQSSSSYQCPNDEMSESGQ-SSAAA
JIP4        .T.LH.LS..D.L.ATAHS.I.....I..GI...PAG..LLTPDT.K..E-T.GSEQ.KFQE.S.PR.HT.LK---..L.DIS.GG.K.T
Consensus   R K  Q GS Q E     R RKERP SL  FPL DG    Q GG  P   W   LQ S S    DES  Q  SA

            266                                                                          355
JIP3        TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYVSVTKNNKQAREKRNSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELDVC
JIP4        ..AS.---A.SDV.AI.PD--..SK.------.NEGFV.GTDTSNKSEI.KHI....A..T....TES.ENE.K.E..A..E......MD
Consensus   TP T  N  S P   TP E      D    K        S  EVQV QE RNVS  G  E S VQ II STPELD

            356                                                                          445
JIP3        PETRLERTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGDVDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIAKVDQ
JIP4        KDLSGYKGS.T..K..E....DR..E..FE...S...GL...........----...R..E..I...T................E
Consensus          S PT GI NKAF  NT SL  ELS AGS  IGDVDEGADLL   GMG EV NL LEN QLLETKNALNVVKNDLIAKVD

            446                                                                          536
JIP3        LSGEQEVLKGELEAAKQAKVKLENRIKELEEELKRVKSEAVTARREPREEVEDDKIPMAQRRRFTRVEMARVLMERNQYKERLMELQEAV
JIP4        .TC.KD..Q.....V....L...DKNR......RKARA..ED..QKAKDD-D.SD..T...K............................
Consensus    L  E  VL GELEA KQAK KLE   ELEEEL   EA AR    D  IP AQR RFTRVEMARVLMERNQYKERLMELQEAV

            537                                                                          622
JIP3        RWTEMIRASREHPSVQEKKKSTIWQFFSRLFSSSSSPPPAKRSYPSVNIHYKSPTA--AGFSQRRSHALCQISAG-SRPLEFFPDD-DCT
JIP4        ...........N.AM....R.S..............N--AT.KPE.P..LK.NA...SHVTPSVKK..ST.S.LPGDK.KAFD.LSEETEAS
Consensus   RWTEMIRASRE P  QEKK S IWQFFSRLFSSSS    K  P VN Y  PT      RS  L Q    S   F

            623                                                                          712
JIP3        SSARREQKREQYRQVREHVRNDDGRLQACGWSLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPSTKLWCAAGVNLSGWKPHEEDS
JIP4        LAS............KA..QKE...V..F.....Q....VA--N..GE.K...L.....L...D...A.M.....V.......G.TRDGG.
Consensus      RREQKREQYRQV HV  DGR QA GWSLP KYKQ    GQ  T MKN PVPVY RPL EKD S KLWCA GVNLSG K    S

            713                                                                          796
JIP3        SNGPKPVPGRDPLTCDREGEGEPKSTHPSPE------KKKAKETPEADATSSRVWILTSTLTTSKVVIIDANQPGTIVDQFTVCNAHVLC
JIP4        VV.AS-.FYK.IAGL.T..SKQRSASQS.LDKLDQEL.EQQ..FKNQEEL..Q...C...HS.T..I....V...N.L.S.....S....
Consensus    G  V  D   D EG      S       K  KE     SS VWI TST  K KV IIDA QPG I D FTVCN HVLC

            797                                                                          874
JIP3        ISSIPAASDSDYPPGEMFLDS-DVN--------PEDSGA--DGVLAGITLVGCATR-CNVPRSNCSSRGDTPVLDKGQGDVATTANGKVN
JIP4        .A.V.G.RET...A..ELSE.GQ.DKASLCGSMTSN.S.EM.SLLG...V...S.EGLTGAATSP.TN.AS..IE.--PPEME.E.SE.D
Consensus   I S PA  DYP GE   S V            S A  D  L GIT VGC T        S  G PV K        T N V

            875                                                                          957
JIP3        PSQST-EEATEATEVPDPGPSESEATTVRPGPLTEHVFTDPAPTP-SSSTQPASENGSESNGTIVQPQVEP-----SGELSTTTSSAAPT
JIP4        ENIP.A.........-GNA.ST.DTVDISQ..VY........LGVQIPEDLS.VFQSSND.DVYKD.IS.L.NEQDLAR.EAQKM..LL..
JIP3           T EEATEATE   G E      PG TEHVFTDP         P    S   Q V P       E    SS  PT

            958                                                                          1047
JIP3        MWLGAQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALADGTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVNDRVW
JIP4        .........C......S..Q.R...........I..I.....I.................V...........L.............T..H.K..
Consensus   MWLGAQNG LYVHS VA W KCLHSIKLKDS LS VHVKG VLVALADGTLAIFHRG DGQWDLSNYHL DLG PHHSIRCM VV D VW

            1048                                                                         1137
JIP3        CGYKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIRLDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
JIP4        ...R..IY.V...A.K..........K.........V....................Y................................
Consensus   CGY NK  V QPK M IEKSFDAHPR ESQVRQLAW GDGVWVSIRLDSTLRLYHAHT QHLQDVDIEPYVSKMLGTGKLGFSFVRITAL

            1138                                                                         1226
JIP3        LIAGNRLWVGTGNGVVISIPLTETVVLHRGQLLGLRANKTSPTSGEGTRPGGIIHVYGDDSSDKAA-SSFIPYCSMAQAQLCFHGHRDAV
JIP4        MVSC..........I.........--------------....G.--P.N...SV.R....EN...VTPGT........H.............
Consensus     NRLWVGTGNGV ISIPLTET           NKTS T  G RPG  I VYGD SDK    FIPYCSMA AQLCFHGHRDAV

            1227                                                                         1315
JIP3        KFFVSVPGNVLATLNGS-VLDSPSEGPGPAAPAADAEGQKLKNALVLSGGEGYIDFRIGDGEDDETEECAGDVNQTKPSLSKAERSHIIV
JIP4        ....A...Q.ISPQSS.GGA.LTADKA.SS.QEPSSQ-TP..SM..I.........M..-.GG.S.LLGE.L-PLE..VT......LI.
Consensus   KFFV VPG V    S  D     G A     LK  LV SGGEGYIDFR GD E  E  D     PS KAERSH IV

            1322
JIP3        WQVSYTPE#
JIP4        ...MCGN.#
Consensus   WQV   E#
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Supplementary Figure S1. Primary structure of JIP3 and JIP4

Comparison of deduced amino acid sequence of JIP3 and JIP4. The numbering is based on the sequence of JIP3α (3).

Residues identical with JIP3 (.), deletions (-) and termination codon (#) are indicated. The consensus sequence is also

presented. Conserved domains are highlighted in color, including the JNK binding domain (blue), JNK

phosphorylation domain (pink), Leucine zipper domain (turquoise), and a putative transmembrane domain (green).