Supplemental Figure 2

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                       *        20         *        40         *        60         *
TOM-1    : MDRAKKKFASAIDGLRSLHNRT--------------EINVDEKIQSEHCRFTRVVRHGLPEDPRCFAYDPVQRLIAI :  63
hTomosyn : --MRKFNIRKVLDGLTAGSSSASQQQQQQ-HPPGNREPEIQETLQSEHFQLCKTVRHGFPYQPSALAFDPVQKILAV :  74
rTomosynS : --MRKFNIRKVLDGLTAGSSSASQQQQQQQHPPGNREPEIQETLQSEHFQLCKTVRHGFPYQPSALAFDPVQKILAV :  75


              80         *        100        *        120        *        140        *
TOM-1    : GTGRGHIRIIGDAGVDYLLKHESGEPVLHMQFLVNEGGLITSCGTDSIHLWNYRQKTAEIVHTVQLSKESVSCIHLP : 140
hTomosyn : GTQTGALRLFGRPGVECYCQHDSGAAVIQLQFLINEGALVSALADDTLHLWNLRQKRPAILHSLKFCRERVTFCHLP : 151
rTomosynS : GTQTGALRLFGRPGVECYCQHDSGAAVIQLQFLINEGALVSALADDTLHLWNLRQKRPAVLHSLKFCRERVTFCHLP : 152


              160        *        180        *        200        *        220        *
TOM-1    : VAGKWLFIGTDKGNVYFLCLNSFLLSPYVINWNKAIDLSCRVHPGPVRQLAVSPAENTKLLIVYDKGIVVQWNLGTR : 217
hTomosyn : FQSKWLYVGTERGNIHIVNVESFTLSGYVIMWNKAIELSSKSHPGPVVHISDNPMDEGKLLIGFESGTVVLWDLKSK : 228
rTomosynS : FQSKWLYVGTERGNIHIVNVESFTLSGYVIMWNKAIELSSKSHPGPVVHISDNPMDEGKLLIGFESGTVVLWDLKSK : 229


              240        *        260        *        280        *        300
TOM-1    : EVD-RYPLDPPIKSVNWHFDGRQILTGNVDGSISLYNHKKSTEAIQRTTPHGSG--------PCRPIQQVEWKHMSE : 285
hTomosyn : KADYRYTYDEAIHSVAWHHEGKQFICSHSDGTLTIWNVRSPAKPVQTITPHGKQLKDGKKPEPCKPILKVEFKTTRS : 305
rTomosynS : KADYRYTYDEAIHSVAWHHEGKQFICSHSDGTLTIWNVRSPTKPVQTITPHGKQLKDGKKPEPCKPILKVEFKTTRS : 306


           *        320        *        340        *        360        *        380
TOM-1    : TESIIMFSGGMPTDDGLPMPALTILKGGKSATVLEMDWPIIQFIPLNQNIWNSIPQCPHSVAVLLKHDFMVLDLNQN : 362
hTomosyn : GEPFIILSGGLSYDTVGRRPCLTVMH-GKSTAVLEMDYSIVDFLTLCETPYPNDFQEPYAVVVLLEKDLVLIDLAQN : 381
rTomosynS : GEPFIILSGGLSYDTVGRRPCLTVMH-GKSTAVLEMDYSIVDFLTLCETPYPNDFQEPYAVVVLLEKDLVLIDLAQN : 382


           *        400        *        420        *        440        *        460
TOM-1    : GHPVIESPHAMNIHESPVTCMAYYSDCPLDLIGALTLVGTKQRNKEFSARSWPVTGGLGRECATGHQELVVTGHKDG : 439
hTomosyn : GYPIFENPYPLSIHESPVTCCEYFADCPVDLIPALYSVGARQKRQGYSKKEWPINGGNWGLGAQSYPEIIITGHADG : 458
rTomosynS : GYPIFENPYPLSIHESPVTCCEYFADCPVDLIPALYSVGARQKRQGYSKKEWPINGGNWGLGAQSYPEIIITGHADG : 459


           *        480        *        500        *        520        *        54
TOM-1    : SLKFWQETGEHLQILYKLKSSSHFERL---EEMETS---DKVSHAVKYIELCLESRQLLVAGISGQVTLFRFTKQE- : 509
hTomosyn : SVKFWDASAITLQVLYKLKTSKVFEKSRNKDDRPNTDIVDEDPYAIQIISWCPESRMLCIAGVSAHVIIYRFSKQEV : 535
rTomosynS : SIKFWDASAITLQVLYKLKTSKVFEKSRNKDDRQNTDIVDEDPYAIQIISWCPESRMLCIAGVSAHVIIYRFSKQEV : 536


           0        *        560        *        580        *        600        *
TOM-1    : ICGTIAVVNIPLLGNLSSNLPNNDFDKSPVPNGPGKEIRRQRKIVSRESTNSLDTSDSGDERIVPFKVRGAPVKRPP : 586
hTomosyn : ITEVIPMLEVRLLYEINDVETPEGEQPPLPTPVGGSNPQPIPPQSHPSTSS-SSSDGLRDNVPCLKVKNSPLKQSP : 611
rTomosynS : VTEVIPMLEVRLLYEINDVETPEGEQPPLSTPVGGSTSQPIPPQSHPSTSS-SSSDGLRDNVPCLKRVLPSTARSN : 612


              620        *        640        *        660        *        680        *
TOM-1    : GFVPELACFVPWHSHAKV-DQITTICLNSSYGIIAIGTSSGLALVDTTQCALIYSWTTNELYGSDPTPAIQLSMQLS : 662
hTomosyn : GYQTELVIQLVWVGGEPPQQITSLAVNSSYGL-VVFGNCNGIAMVDYLQKAVLLNLGTIELYGSN-DPYRREPRSPR : 686
rTomosynS : TSRTQDS-DFYILGNLVLFPVSRYSCMTTYDLTVVFGNSNGIAMVDYLQKAVLLNLSTIELYGSN-DPYRREPRSPR : 687


              700        *        720        *        740        *        760        *
TOM-1    : DAASPLESPIS--------------------LEAPKRIISEQKQRSFDAR---RPQLFKTQSVVENGSLSRGDSQRES : 717
hTomosyn : KSRQPSGAGLCDISEGTVVPEDRCKSPTS-------------------------------------AKMSRKLSLPTD : 727
rTomosynS : KSRQPSGAGLCDITEGTVVPEDRCKSPTSGSSSPHNSDDEQKVNNFIEKVKTQSRKFSKMVASDLAKMSRKLSLPTD : 764
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                780         *         800         *         820         *         840
TOM-1     : PSSGRQLNTSSPSTSSQSLERSMSTQPQESITSLSFIHSYSKKNDSKMSPCLWVGTSAGASLALNLILP---EDRFT :  791
hTomosyn  : LKPDLDVKDNSFSRSRSSSVTSIDKESREAISALHFCETFTRKTDSSPSPCLWVGTTLGTVLVIALNLPPGGEQRLL :  804
rTomosynS : LKPDLDVKDNSFSRSRSSSVTSIDKESREAISALHFCETFTRKADSSPSPCLWVGTTVGTAFVITLNLPLGPEQRLL :  841

             *         860         *         880         *         900         *         920
TOM-1     : STIVVAPSGTVVRLKGQVISQSFMDNTFCIISPASESYKEAAKEQSATSPDRSLLNRVNTKASLAPQYSSSIDSNDE :  868
hTomosyn  : QPVIVSPSGTILRLKGAILRMAFLDTTGCLIPPAYEPWREHNVPEEKDEKEKLKKRR---PVSVSPSSSQEISEN-- :  876
rTomosynS : QPVIVSPSGTILRLKGAILRMAFLDAAGCLMPPAYEPWTEHNVPEEKDEKEKLKKRR---PVSVSPSSSQEISEN-- :  913

             *         940         *         960         *         980         *         1000
TOM-1     : ISQILIVAAENEVKVVALPTFSQLYVQKFDEIPLV-KATPTHIRGYPCLMCLSAAGQIIMLSLPSLRILQTSTIFPH :  944
hTomosyn  : --QYAVICSEKQAKVISLPTQNCAYKQNITETSFVLRGDIVALSNSICLACFCANGHIMTFSLPSLRPLLDVYYLPL :  951
rTomosynS : --QYAVICSEKQAKVISLPTQNCAYKQNITETSFVLRGDIVALSNSVCLACFCANGHIMTFSLPSLRPLLDVYYLPL :  988

             *         1020        *         1040        *         1060        *         10
TOM-1     : SVEIDDPLCQKTAFSDHGLGVYMASQTEMEKYTMCSEIAEQTGESLGELFVPCEMPEQPKNNSFLKGVSSIFGGTPR : 1021
hTomosyn  : T---NMRIARTFCFTNNGQALYLVSPTEIQRLTYSQETCENLQEMLGELFTPVETPEAP-NRGFFKG---LFGGGAQ : 1021
rTomosynS : T---NMRIARTFCFANSGQALYLVSPTEIQRLTYSQETCENLQEMLGELFTPVETPEAP-NRGFFKG---LFGGGAQ : 1058

           80          *         1100        *         1120        *         1140        *
TOM-1     : NDPNDIDAILSENMGVKNSSGVNPMRSVARTIPGPS-VQMDRAQAGGVSAGQAAAMALQNLNERTEKLNATVDATEN : 1097
hTomosyn  : S--------LDREELFGESSSGKASRSLAQHIPGPGGIEGVKGAASGVVGELARARLA--LDERGQKLGDLEERTAA : 1088
rTomosynS : S--------LDREELFGESSSGKASRSLAQHIPGPGGIEGVKGAASGVVGELARARLA--LDERGQKLSDLEERTAA : 1125
SNARE-helix:
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           1160        *         1180
TOM-1     : LKNNAMSLSSRTGKLVEKYEKKKWYNF : 1124
hTomosyn  : MLSSAESFSKHAHEIMLKYKDKKWYQF : 1115
rTomosynS : MMSSADSFSKHAHEMMLKYKDKKWYQF : 1152
SNARE-helix:
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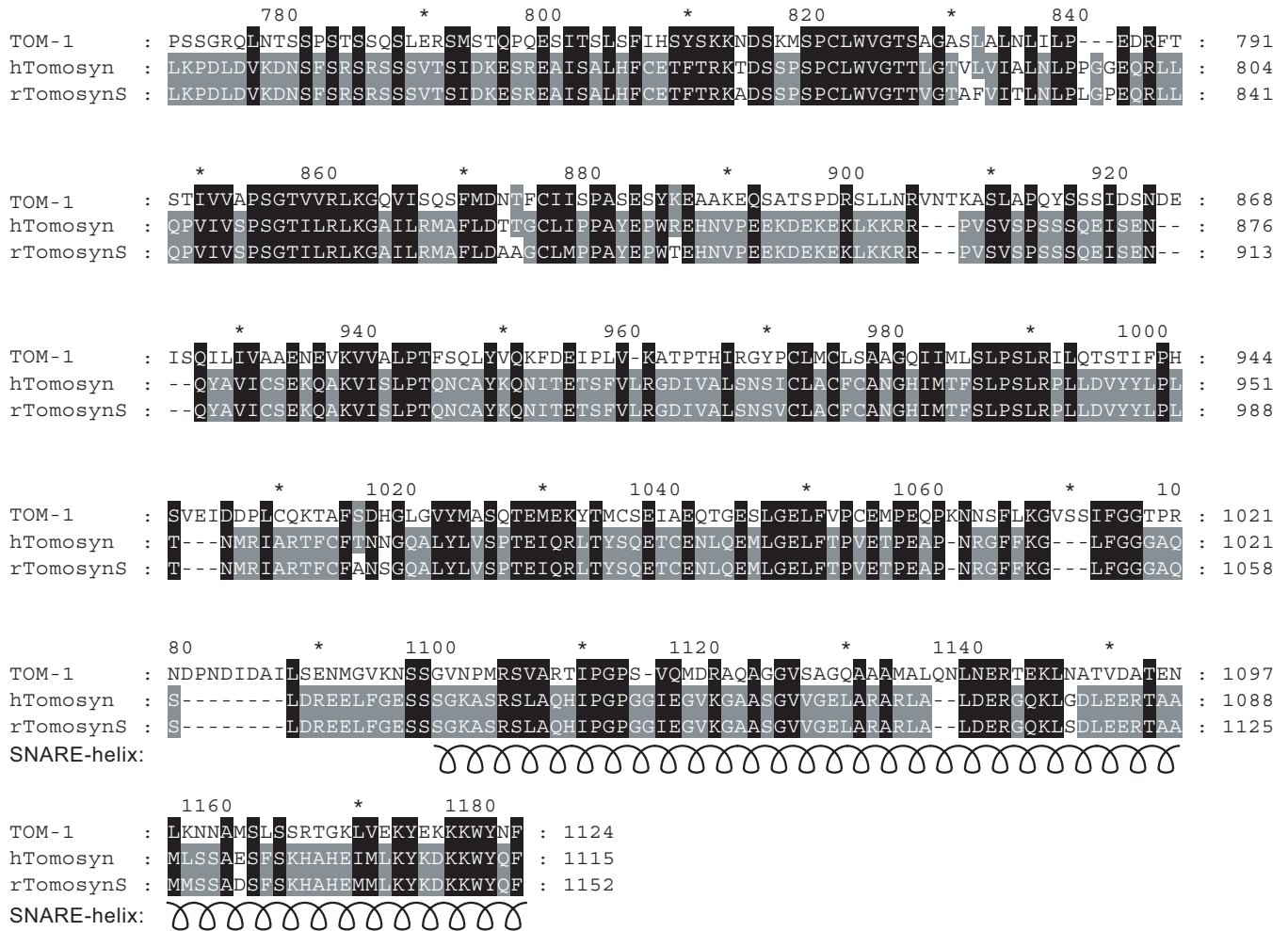
Figure S2. Alignment of TOM-1 to human and rat Tomosyn. Sequences of human and mouse

tomosyn were downloaded from Ensembl (www.ensembl.org/), accession numbers

ENSP00000179882 and ENSRNOP00000018806 respectively. The multiple sequence alignment

was performed using T-Coffee (http://www.ch.embnet.org/software/TCoffee.html). Alignment

output was produced using GeneDoc (www.psc.edu/biomed/genedoc).