

Figure 1 – figure supplement 4

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|-------------|------|---|------|
| Human_TRPC3 | 1 | -----MREKGRRAVRGPAFMFNDGRGSLTAEERFLDAAEYGNIPVVRKMLEE | 49 |
| Human_TRPC6 | 56 | CFRGS-----DNRLAHRRTVLRKGRRLANRGPAYMFSDRSTSLSEERFLDAAEYGNIPVVRKMLEE | 120 |
| Human_TRPC7 | 1 | MLRNS-----TFKNMQRRTHTLREKGRRAIRGPAYMFNEKGTSLTPEERFLDSEYGNIPVVRKMLEE | 65 |
| Human_TRPC1 | 8 | STDL-----GASSSLSPSSSSSPN-----EVMALKDVRVEKEENTLNEKFLFLCKDGQYVMKKILEE | 69 |
| Human_TRPC4 | 7 | KRNVN-----APYRD-----RIPLRIVRAESELSPSEKAYLNAVKEGQDYAVKKSLEE | 54 |
| Human_TRPC5 | 7 | KKVNY-----SPYRD-----RIPLQIVRAETELSAEKAFLNAVKEGQDYATVKQALQE | 54 |
| Mouse_TRPC2 | 241 | IETLPQHAATCGESPQQPASPASLSSESVLRRRHHVALTVP-PL--VPKQPWNTEIVNKKLKFPPTLRLAIQEGQLGLVQQLLES | 324 |
| Human_TRPC3 | 50 | SK---TLNVN-----CVDYMGQNALQAVGNEHLEVTELLK--KENLARIGDALLAISKGYVRIEAILNHPGFAASKR | 120 |
| Human_TRPC6 | 121 | CH---SLNVN-----CVDYMGQNALQAVANEHLEITELLK--KENLSRVGDALLAISKGYVRIEAILSHPAFAEGKR | 191 |
| Human_TRPC7 | 66 | SK---TLNFN-----CVDYMGQNALQAVANEHLEVTELLK--KENLARVGDALLAISKGYVRIEAILNHPAFAQQGR | 136 |
| Human_TRPC1 | 70 | NS-SGDLNIN-----CVDVLRGNVITITENENLDILQLLLDY---GCQSADALLVAIDSEVVGAVDILLNHRPKRSSRP | 140 |
| Human_TRPC4 | 55 | AEIYFKININ-----CIDPLGRSALLIAIENENLEIMELLNH---SVYVGDALLVAIRKEVVGAVELLNHHKPSGEKQ | 126 |
| Human_TRPC5 | 55 | AEIYVNVNIN-----CMDPLGRSALLIAIENENLEIMELLNH---SVYVGDALLVAIRKEVVGAVELLNHHKPSGEKQ | 126 |
| Mouse_TRPC2 | 325 | SS---DASGAGGGPLRNVEESEDRSWREALNAILRGHEVITDVLINLVKDFFRQIHEALLVAVDTNQPAVRLRLARLEREKGR | 408 |
| Human_TRPC3 | 121 | LTLSPECEQLQDDDFYAYDEGTRFSPDITPIILAAHCQKQYEVVHMLLMKGARIERPHDYFCKGDCMEKQRHDSFHSRSRINAYK | 207 |
| Human_TRPC6 | 192 | LATSPSQSEQLQDDDFYAYDEGTRFSDVTPPIILAAHCQYEVIVHTLLRRKGARIERPHDYFCKCNDCKQKQKHSFHSRSRINAYK | 278 |
| Human_TRPC7 | 137 | LTLSPELEQLRDDDFYAYDEGTRFSDITPIILAAHCQYEVIVHTLLLRKGARIERPHDYFCKCNECTEKQRKDSFHSRSRINAYK | 223 |
| Human_TRPC1 | 141 | TIVKLME-----RIQNPEYSTTMDVAPVILAAHRRNVEITLMLLKQDVSLPKPHAVGCECTLCSAKNKKDSLHRSRFLDIYR | 218 |
| Human_TRPC4 | 127 | VPP-ILL-----DKQFS--EFTPDITPIILAAHTNNEYIKLLVQKGVSVPRPHEVRNCNCECVSSSDVDSLHRSRSLNIYK | 201 |
| Human_TRPC5 | 127 | VPT-LMM-----DTQFS--EFTPDITPIILAAHTNNEYIKLLVQKGVSVPRPHEVRNCNCECVSSSDVDSLHRSRSLNIYK | 201 |
| Mouse_TRPC2 | 409 | VD-----TKSFSLAFDSSIDGSRFAPGVTPITLACQKDYELIAQLLMDQGHVITARPHVSCALECNSNARYDILLKFLSLRINTYR | 490 |
| Human_TRPC3 | 208 | GLASPAYLSLSSDPVLTALSELNLAKEFKNDRKLSMOCKDFVVGVLDLCDRDEEVEAILNGDLESAEP-----LE | 286 |
| Human_TRPC6 | 279 | GLASPAYLSLSSDPVMTALELSNELAVLANIEKEFKNDRKLSMOCKDFVVGVLDLCDRNTTEEVEAILNGDVTFLQ-----S | 355 |
| Human_TRPC7 | 224 | GLASAAVLSLSSDPVLTALSELNLAKEFKNDRKLSMOCKDFVVGVLDLCDRTEEVEAILNGDVNFQV-----W | 300 |
| Human_TRPC1 | 219 | CLASPALIMTEEDPILRAFELSADLKLSEVEFRNDYEELARQCKFAKADLLAQARNSRELEVLNHTSDFEPD-----KRG | 299 |
| Human_TRPC4 | 202 | ALASPSLIASSDEPFLTAFLQSWELQELSKVNEFKSEYELSRQCKFAKADLLDQTRSSRELEIILNRRDNDNL-I----- | 278 |
| Human_TRPC5 | 202 | ALASPSLIASSDEPILTAFLRLGWELELSKVENFKSEYELLSQCKFAKADLLDQARSSRELEIILNHRDDSEEL----- | 279 |
| Mouse_TRPC2 | 491 | GIASRAHLSLASEDAMLAFLSLRELRRLARKEPEFKPQYIALESLCQDYGFELLMGCRNQSEVTAVIDLGEDSETEPEAELGGA | 577 |
| Human_TRPC3 | 287 | VHRHKASLSRVKLAIKYEVKKFVAHPNCCQQLTIWYENLSGLREQTIAIKCLVLVLVALGLFLAIGYWIAPCSRLGKILRSPFMK | 373 |
| Human_TRPC6 | 356 | GDHGRPNLSRLKLAIKYEVKKFVAHPNCCQQLLSIWYENLSGLRQQTMAVKKFLVLVAIGLFLALAIYWFAPCSKMGKIMRGPFMK | 442 |
| Human_TRPC7 | 301 | SDHHRPSLSRIKLAIKYEVKKFVAHPNCCQQLTMWYENLSGLRQQTIAVKKFLAVFGVSI GLFLALAIYWIAPCSKLGRTLRSPFMK | 387 |
| Human_TRPC1 | 300 | LEERMNLSRLKLAIKYQKQEFVQSNCQQLNTVWFGQMSGYRRKPTCKIMTVLTGIFWVLSLCYLIAPKSQFGRIIHTPFMK | 386 |
| Human_TRPC4 | 279 | EEQSGNDLARKLKLAIKYRQKEFVAQPNCCQLLASRWYDEFPGWRRRHWAVMKMTCFIIGLLFPVFSVCYLIAPKSPLGLFLIKPFPIK | 365 |
| Human_TRPC5 | 280 | DPQKYHDLAKLKVAIKYHQKEFVAQPNCCQLLATLWYDGFPGWRRKHVVKLLTGMTIGFLFPLMSIAYLISPRSNLGLFIKPFPIK | 366 |
| Mouse_TRPC2 | 578 | FEEGIPNLRRLRLAVNQNQKFVAHPICQQLSSIWCGNLGWRGSTTIWKLFAVFLITLMPFLCIGYWLAPKSQGLRLLKIPVLK | 664 |
| Human_TRPC3 | 374 | FVAHAASFTIFLGLLVFNASDRFEGITTLPNITVTDYPKQIFRVKTTQFTWTEMLIMVWV LGMMWSECKELWLEGPREYILQLWNVL | 460 |
| Human_TRPC6 | 443 | FVAHAASFTIFLGLLVFNASDRFEGITTLPNETSTDNAKQLFRMKTSCFSWMEMLIISWVIGMIWAECKEIWTPGPKKEYLELWNML | 529 |
| Human_TRPC7 | 388 | FVAHVSFTIFLGLLVFNASDRFEGVKTLPNETFTDYPKQIFRVKTTQFTWTEMLIMKVV LGMIWSECKEIWEGEPREYVILHWNML | 474 |
| Human_TRPC1 | 387 | FIIHGASYFTFLLLNLYSLVYNEDKKN-----TMGPALERIDYLLILWIIGMIWSDIKRLWYEGLEDLEESNRQL | 458 |
| Human_TRPC4 | 366 | FICHTASYLTFLFLLLASQHIDRSDLN-----VQGGPPTIVVWMLIPWV LGFIWGEIKQMWDGGLQDYIHDWNNLM | 437 |
| Human_TRPC5 | 367 | FICHTASYLTFLFMLLASQHIVRTDLH-----VQGGPPTIVVWMLIPWV LGFIWGEIKEMWDGGLFTEYIHDWNNLM | 438 |
| Mouse_TRPC2 | 665 | ELLHSASYLWFLIFLLGESLVM-----E-----TQLSTF-KGRSSVWETS LHMIVWVTRGLWFECKEWGIEGLFSYLLDWNML | 737 |
| Human_TRPC3 | 461 | DFGMLSIFIAAFTARFLAFLQATKAQYVDSVYQESDLSEVTLPPETIYQF-TYARDKWLPSDPQIISEGLYAI AVVLSFSRIAYILP | 546 |
| Human_TRPC6 | 530 | DFGMLAIFAASFIAEFMAFWHASKAQSII DANDTLKDLTKVTLGDNVVKY-NLARIKWDPSDPQIISEGLYAI AVVLSFSRIAYILP | 615 |
| Human_TRPC7 | 475 | DFGMLSIFVASFARFMAFLKATEAQLYVDQHVQDDTLHNVS LPPVAYF-TYARDKWLPSDPQIISEGLYAI AVVLSFSRIAYILP | 560 |
| Human_TRPC1 | 459 | SPVMNSLYLATFALKVVAHNK-----FHDFAKDKWDAFHTPLVAEGLFAFANVLSYRLFFMYT | 518 |
| Human_TRPC4 | 438 | DFVMNSLYLATISLKIIVAVK-----YALANPRESDWMWHTPLVAEALFANISLSSRLISLFT | 497 |
| Human_TRPC5 | 439 | DFAMNSLYLATISLKIIVAVK-----YNGSRPRESEWEMWHTPLIAEALFANISLSSRLISLFT | 498 |
| Mouse_TRPC2 | 738 | DVVILSLYLASFARLLLAGLA-----YMHCRD-----ASDSTTCRYFTTAERSEWRTEDPQLAEVLFAYTSMLSFTRLAYILP | 812 |
| Human_TRPC3 | 547 | ANESFGPLQISLGRTVKDIKFKFMVIFIMVFAFMIGMFIYSYLLGA-----KVNAAFTTVEESFKTLFWSIFGLSE | 618 |
| Human_TRPC6 | 516 | ANESFGPLQISLGRTVKDIKFKFMVIFIMVFAFMIGMFIYSYLLGA-----KQNEAFTTVEESFKTLFWAIFGLSE | 687 |
| Human_TRPC7 | 661 | ANESFGPLQISLGRTVKDIKFKFMVIFIMVFAFMIGMFIYSYLLGA-----KYNPAFTTVEESFKTLFWSIFGLSE | 632 |
| Human_TRPC1 | 519 | TSSILGLPLQISMGQMLQDFGKFLGMYLFLFSFTIGLTQLYDK--GYTSKEQKDCVGFCEQSQNDTHFSFIGTCFALFWYIFSLAH | 603 |
| Human_TRPC4 | 498 | ANSHLGLPLQISLGRMLLDILKFLFIYCLVLLAFANGLNQLYFYYETRAIDEPNNCKGIRCEKQNN-AESTLFTLQSLFWSYFGLL- | 579 |
| Human_TRPC5 | 499 | ANSHLGLPLQISLGRMLLDILKFLFIYCLVLLAFANGLNQLYFYYETRAIDEPNNCKGIRCEKQNN-AESTLFTLQSLFWSYFGLL- | 583 |
| Mouse_TRPC2 | 813 | AHESLGLTQISIGKMIDDMIRFMFILMIILTAELCGLNNIYVPYQES-----E---KLGNFNETFQFLFWTFMGME | 881 |
| Human_TRPC3 | 619 | --VTSVVLKYDHHKFIENIGYVLYGIVNVTMVVLLNMLIAMINSSYQETEDDSVVEWKFARSKLWLSYFDDGKTLPPFPFLVPSPKS | 703 |
| Human_TRPC6 | 698 | --VKSIVYNNHFIENIGYVLYGVNVTMVIIVLLNMLIAMINSSYQETEDDAVVEWKFARAKLWLSYFEGRTLPVPFNLPVSPKS | 772 |
| Human_TRPC7 | 633 | --VTSVVLKYDHHKFIENIGYVLYGVNVTMVVLLNMLIAMINSSYQETEDDAVVEWKFARAKLWLSYFDEGRTPLPFPFNLPVSPKS | 717 |
| Human_TRPC1 | 604 | VAIFVTRFSYGEQLQSFVGAIVGTNYVVVIVLTLLKVLAMLHKSQFLIANHEDKEWKFARAKLWLSYFDDKCTLPFPFNIPSPKT | 690 |
| Human_TRPC4 | 580 | -NLYVTNVKAKHEFTEFVGATMFGTYNVISLVVLLNMLIAMMNSYQLIADHADIEWKFAKTLWMSYFEEGGTLPTFPFNIPSPKS | 665 |
| Human_TRPC5 | 584 | -NLYVTNVKAKHEFTEFVGATMFGTYNVISLVVLLNMLIAMMNSYQLIADHADIEWKFAKTLWMSYFEEGGTLPTFPFNIPSPKS | 669 |
| Mouse_TRPC2 | 882 | --HTVVDN-PQLVPVEFVGARMYGIETIVMVIIVLLNMLIAMINTSFQKIETDDAVVEWKFARSKLWLSYFDEGTLPTFPFNIPSPKA | 965 |
| Human_TRPC3 | 704 | FVYFIMRIVN---FPKCRRRRLQKDIEMGMGNSKSRN-----LFTQSNRSRVFESHFSNISLNQPTTRYQQIM | 767 |
| Human_TRPC6 | 773 | LFYLLLLKLLKWI SELFQGHKKGFQEDAEMNKINEEKKLGILGSHEDLSKLSLDKKQVGHNKQPSIRSSDFHLNNSFPNPPQYQKIM | 859 |
| Human_TRPC7 | 718 | FYLLIMRIKMLIKLKCKSKAKSCNDLEMGMLNSKFKKT-----RYQ-AGMRNSENLTANNTLSKPTRYQKIM | 784 |
| Human_TRPC1 | 691 | ICYMISLSLKWICSHTSKGVKVRQNSLKE-----WRNLKQKRDENYQKVM | 735 |
| Human_TRPC4 | 666 | LWYLIKWIWTHLCKKKM---RRKPESFGT-----IGR-----RAADNLRHHQYQEVIM | 710 |
| Human_TRPC5 | 670 | FLYLGNWFNNTFCPRDPGRRRRRNLGS-----FTE-----RNADSLIQNHQYQEVIM | 717 |
| Mouse_TRPC2 | 966 | AFYLVLRNIFRFLCCGSSCCKAKKSDYPPI-----GTFTNPGARAGSAGEGE---RVSYRLRYI | 1020 |
| Human_TRPC3 | 768 | KRLIKRYVLKAQVDKENDEV--NEGELKEIKQDISSSLRYELLE-----DKSQATEELA-----ILIHKLSE--K | 827 |
| Human_TRPC6 | 860 | KRLIKRYVLKAQIDKESDEV--NEGELKEIKQDISSSLRYELLE-----EKSQNTEDLA-----ELIRELGE--K | 919 |
| Human_TRPC7 | 785 | KRLIKRYVLKAQVDREDEV--NEGELKEIKQDISSSLRYELLE-----EKSQATGELA-----DLIQQLSE--K | 844 |
| Human_TRPC1 | 736 | CCLVHRYLTL SMRQKMQSTDQ-ATVENLNLRLQDL SKFRNEIRDLLGRTSKYAMFYPRN----- | 793 |
| Human_TRPC4 | 711 | RNLVKRYVAAMIRDAKTEEG-LTEENFKEKQDISSFRFEVLGLHRSKSLT IQSANASKESNSADSDEKSDSEGNKDKKKNFSL | 796 |
| Human_TRPC5 | 718 | RNLVKRYVAAMIRNSKTHEG-LTEENFKEKQDISSFRFEVLGLHRSKSLT IQSANASKESNSADSDEKSDSEGNKDKKKNFSL | 798 |
| Mouse_TRPC2 | 1021 | KALVQRYIETARREFEETRRKDLGNRLTELTKTVSRQLQSEVASVQKNLAAGGAPRPPDGASIL--S-----RYITVRNRSFNQ | 1096 |
| Human_TRPC3 | 828 | LNP SML-----RCE----- | 836 |
| Human_TRPC6 | 920 | LSMEPN-----QEETNR----- | 931 |
| Human_TRPC7 | 845 | FGKNLN-----KDLRLVNKGKDI----- | 862 |
| Human_TRPC1 | | | |
| Human_TRPC4 | 797 | FDLTTLIHPSRAAIA-SERHNISNGSALVVQE--PP-----REKQ | 833 |
| Human_TRPC5 | 799 | FNLGCK-----KKTCHGAPLIRTM--PRSSGAQGKSKAESSS | 833 |
| Mouse_TRPC2 | 1097 | LGPPTSDTPAELTMPGIVETEVSLGDLGDLGTGEAGAPAPGEGSSSS-- | 1143 |