



## Supplementary Figure 2

DmGry 347 HPGIYYHKAEE-FVMKRRD-AAMEAYAA--MQASSEATPTI-QNPLSLYTEF--FGIRAVKTKDL-----VAEQQA-----  
HsGry 345 NPGFYQQAAAY-YAQRKQ-LAKTLGNH--EASVMYPPNDPL-ETQTG-VLDF--YQQRSWRQGLSFSLSDPEKBYVG-----  
DrGry 345 NPGFYQQAAAY-YAQRKQ-QAGOLGSH--EPGVGYPADPL-ETTSQ-ALDE--YQQRPMWQGHQSIDPPDEKBYQG-----  
AtGry 365 PPAIYYQLAAH-VLKDKKS-ALELLLSM--SEIAQEIIDSSSA-SITPSVYVGO--FA-QLEKGEAI-TLHSITDEYTT-----  
CeGry 361 NPGTHLDGAAASISAAANTE-IAALKRNA--PQNVPIPSDDPF--ANSS--STVF--FGQRPWRINHEGLA--TAEVAAA-----  
Dm130 371 CAPIW-----N-LAKDKLY-ELGKLCGL--LPG-CTPTSEQL-HIVVQ-LSSG--IGDAPSEQHQFLQATPQLRDRSPN-----  
At130 495 ASLSTGNIPMFDRPSPFTEGSGLEASPRTPSSLKVOAPPMSTRNSS--PGNFESPLDRPMLAEIFVA--A--EHAL-----  
Hs130 385 TVGLW-----S-YATEKIK-SLGLCGL--VSE-KGPNSEDL-NRTVD-LLAG--LGAERPET-----  
Tn130 377 TVGLW-----V-YAIEKIK-SLGLCGL--MSE-KGPNSEDL-NRTVD-LLAG--LGAERPETGEFSD-ETLLSDDTLGLACNHFNRFIHFKLKY

DmGry 412 ---NMQLCDQERSYNHSA-----AIATATLSQMAQFKIYKCLFRK-KLAIDMEEVLKSGDHAKALTLYSLMLPDYRQEKWTTFDVLK  
HsGry 416 ---ILAIQKERNVHSE-----IIITLISNVAQFKKYKCPMKKS-HLMVMGEEYAKDYTKALKLLDYVMCDYRSEGWTLTASVLT  
DrGry 416 ---ILALQVKERDVLHSE-----LIITLISNVAQFKKYKCPMKKS-HLMVMGEEYAKDYTKALKLLDYVMCDYRTERWTLTASVLT  
AtGry 435 ---RTTIS-EAKRVQDS-----QIIATLKRSESTNLKAORMAA-LCAFEVAREFDLADPNNAKFFFDIAANLVROEGWTLTNEVLY  
CeGry 430 ---VTA--IIQRLVVNHE-----GVISLSALAAQYQYKGLRMKK-KVMEMEMANTCYANNEIQRLRFNGLVVKDNAL--PYSIRKDMHHR  
Dm130 436 ---RKPCKS-GAEOLKEAGSNQAFQKLYLELAELATSTYKHVTRLSAR-LVGLDLGNFICALNEPHKAVGFFDILLRELKAGNWHMSSQTLE  
At130 567 ---RLT--ISDHDLLKTSIIQDFENKYLNTKGAAENHRSWWKHGV-VLDGEIAAVCFKHGKYDAAANSYKVCALYAGEGWODLAEVLPN  
Hs130 434 ---ANTAQS-PYKKLKEAASSVEAFEKHYLEDSHATIEMTSISGRIRSAK-FVGKDLAEFMRKKAPQKAEIYLQGALKNYLAEGWALPTHTTRKQ  
Tn130 457 FTVNSLQS-PYKKLKEAASSVEAFERHYLEDSHATIEMTSISGRIRSAK-FVGKDLAEFMRKKAPQKAEIYLQGALKNYLAEGWALPTHTTRKQ

DmGry 495 TLRCALLSGSVAADYIACSVEALSLR-HQSDQSERILILENLWO-----VFQGVPPM--PKTQLT----PEAQAALWTSALANV-KSPIQIDL  
HsGry 499 ALKCSYLMAQLKDYITYSLETLGRA-STLKDDQKSRIEKNLIN-----VLMNESPD--PEPDCDILAVKTAQKLWADRISLAGSNFTIGV  
DrGry 499 ALKCSYLMAQLKDYITYSLETLGRA-STLKDDQKSRIEKNLIN-----VLMNESPD--PEPDCDILAVKTAQKLWADRISLAGSNFTIGV  
AtGry 517 LRECSRNLDAKDFVEFSLMVALP-VTSYENSGNLRNKNYGP--GGPATISGRESIHQEVFFLVCREAEELSSTEG--SGFKLATDSPLHLEI  
CeGry 509 ATWAAYAITSIQDYAVCCMQMCPAY--SEVLPSDCVKGGLD-----VLDGKPPGSPFFPNDDISQEQLHTYQLQWQHVLO--EHFPAVVQA  
Dm130 527 LANCYRKKMCDSLATKTKCSSISCCA-ELET-LVTFYFDEFLLKSLKTLKTLTSLAQPSIE-N-----ANYCVTE--  
At130 656 LAQCOKILDDQAGMSSCVRLSLDKGLFSSKERQAFQSEVVT--LAHSEMKN-----PVPPLDV  
Hs130 525 LAQCOKHLQIENMLQTSLSLASDH-HLT-EEERKHFCQELD-----FASQPSDS--P-----GHKIVLPM  
Tn130 551 VAECKLLCRTLDEYLOTSSALAGDV-NLT-TAERKHFCQELN-----FSGKSGDE-----SNKVTLSM

DmGry 573 DKVND---VVMECATFER--VQLSNDLLQLQLIVRVLTDIPLRIRSFHVILADAGNP  
HsGry 582 QDFVP---FVQCKAKFHA--PSFHVDVVPQFDIYLKADCPHPPIRFSKICVSFNNQ--E  
DrGry 582 QDFVP---FVQCKAKFHA--PSFHVDVVPQFDIYLKADCPHPPIRFSKICVSFNNQ--E  
AtGry 606 DLVSLRPRVLLASVAFHD--QMIKPHALCSFTLSLLSHLELPLVEIDHEVOFQNS--T  
CeGry 591 SKIAE--LFLETRIHFSLDQ-QTVEQDSKVAVRVEIVSKIEQVIRLNDVSVHLKAKKF-  
Dm130 592 DHF-RIL---D--IEVVNQPII-QDDYILVQLKVESLYERGVAENVKLCYELEASS  
At130 713 SSLIT---FSG--NTGPPL--QLCDGDPGNLSVTVMGSGFDDITLDSLSLTIVATNN-  
Hs130 583 HSFQ--LRD--LHSDPSNAVHVGGVLCVEITMYSQMPVPVHVEQTVUNVHFSI-E  
Tn130 608 DNLSH---LSR--ISHPATASVHSGAALQVELVLRCLMEMPVCLQQAASIHFAE-E

DmGry 1175 NPSAVPIFGVFCIRMRANCKEENE-----SKFVIRGLDIAEPFLNIYCTIEEK-MFVKMPMAFKVVLKNPT  
HsGry 973 IEGGV-ATGHYIISWKRTSAMENIPIIT-----TVITPHVIVENIPLHVNADLPSP-GRVRESLPVKYHLQNK  
DrGry 973 GTSTV-ASGHYIISWKRTSAMENIPIIT-----TVITPHVIVENIPLHVNADLPSP-GRVRESLPVKYHLQNK  
AtGry 1033 RTPKL-GLGSIHLKVRREGGNITEAYVS-----TKHKLPEVNVVEASPLVMSLDSPPY-AILGEPFTYAVRICNQ  
CeGry 952 DESET-PLGRMSVEVRRAPV--NSCPVR-----SVAPLCRIPVLACISISSHIKTNPAIVROPIETCFELKSHS  
Dm130 986 HFVIKYASLSQPDVVRTYGCADLV-----DYTLFKLQAQLEP-----NELCRLRTVCNMNLKITKV-  
At130 1123 DHSET-DTEGRDL---VFK--SAIVLQ-----RPVLDPCLTUGFLP-----LPSDGLRUGKLTIMQWRVERLK  
Hs130 1003 SK-QS-VFFVWELKWTTEPPPSLHCRFSVGFSPASEEQLSISLKPYTEFKVENFFLYNVKAEIIP-----PSGMEYCRGSLCSLEVLITRLS  
Tn130 1062 SK-HS-VFCLWEVRWKDNLPSCLQCQVFSTDFSPNLQDV-SV-FKLHHQFQLERVTLLYSVRADILP-----PAGEQHCRCGLLCKLEVFITRLS

DmGry 1241 THVLHL-----IANLS-ISKTDNFIKSGHKQLDI--SIMAYEKEELVYNLYPQVQWQELPVLSTIEYNT--KADPQKK-D-----  
HsGry 1041 DVQD-----VEIS-VEPSDAFMPSGLKQIRL--RILPGTEQEMLYNFYPLMAGYQQLPSLNINLLR--FPNFT-----  
DrGry 1041 DVQD-----VEIS-VEPSDAFMPSGLKQIRL--RILPGTEQEMLYNFYPLMAGYQQLPSLNINLLR--FPNFT-----  
AtGry 1101 QLQD-----AKFG-LADAQSFLVSGSHSNTV--SVLPKSEHVLKYKLVELTCEQQLPKITTSAR--YAA-----  
CeGry 1019 KEAVE-----ISTN-FDLNDVFMPSGERKVTM--TVLPGATRRVTVVVMALSAQRLNFPKISLKSQ--ISDQT-----  
Dm130 1044-----HENPYTDLMEVNLNDQNLWAVCGRSAGVVSVM--KDVDSSHISLDMPLSTGFLPMPISIRTSKYT--AGGKS-----  
At130 1180 EKESEA-----VEQQHDEVLYEVNANSENWMIAGKRGRGHVLSLEEQGSRVVISILCVPLVACVVRPPQLGPNVE--EANVS-----  
Hs130 1091 DLEVDK-DEALTESDEHFTKLMYEVVDNSSNNAVCGKSCGVISMVPAARATHRVHMEVPLFAGLYLPEDVRFFKYLPHHSAHSSQOLDADSWI  
Tn130 1148 EPAEGEMAESRSOLDGLKTTKLMYQVADSSNNAVCGKSSGLVSMVPVATGSSQKVQIEVMPLFAGHLFYPRIINVLRYPHTAGVFNQPPDPSCM

DmGry 1310-----S-----Q-----N-----ALLDELVQRALPKRVFVLPPLKO-----QNK  
HsGry 1105-----NQLLRRFIPSTIFVKPQGRMD-----DTS-IAAA-----  
DrGry 1105-----SOLLRRFLPSRIFVKPQGRNG-----DAS-IEAA-----  
AtGry 1163-----EFQPSAVASSVVFVPSAPQA-----EKAISTSK-----  
CeGry 1083-----LQQLSLRTLGAATFVLKAKD-----L-APHP-----  
Dm130 1111-----K-----TDGHSKVHPFPQGVNSTRKSMQIHVIASVAGDQ-----  
At130 1256-----SN-----PSGHLVCVLPPLSS-----SYC-LPVK-----  
Hs130 1185 ENDSLVSVDKHGDDQPDSSSLKSRGSVHSACSSEH--KGLPMPRLQALPAGQVFNSSSGTQVLVIPSQDDH-----VLE-VSVT-----  
Tn130 1243 ENDSLSSL---LDDQTDATASIRSRGSVHSVSGSEHQQRGIAMPRLDSFGPGEVFNHSHMQQLVLPSTDDH-----IME-VNAT-----

	essential				non-essential			
generic		Gdi1	Sec17	Sec18				
COPII vesicles	Sar1	Sec23	Sec24	Sec13	Sfb3	(Sfb2)	Rer1	
		Sec16	Sec12	Sec31	Erv14	Erv29	Emp24 family	
					Erv41	Erv46	Svp26	Emp47
Sec20 complex		Tip20	Use1	Sec20				
		Ufe1	Dsl1	(Sec39)				
ER Golgi SNAREs			Sly1	Bos1	Sec22	Gos1	Got1	Sft2
		Sed5	Bet1	(Sft1)				
YIP family		Yif1	Yip1	Yos1	Yip2	Yip3		
Ypt1/TRAPP	Ypt1	Trs130	Trs120	Trs31	Gyp8	Trs85	(Trs65)	
	Trs23	Trs20	Bet3	Bet5	Trs33			
COP1 vesicles	Arf1/2	Gea1/2	Sec7	Sec21	Glo3	Gcs1		
	COPI	Sec26	Sec27	Ret2	Sec28			
			Ret3					
Coiled-coil proteins				Uso1	Grh1	Bug1		
					Coy1	Rud3		