

Cheerathodi *et al.* Supplementary Figure 1

Exon:	1↓2		
Mm_C3G_isoform2	MSSGLGRRSPMSGKIEKADSRSHLSSTMKLMDKFHSPKIKRTPSKKGGKPAEVSKI	59	
Mm_C3G_isoform3	MSSGLGRRSPMSGKIEKADSRSHLSSTMKLMDKFHSPKIKRTPSKKGGKPAEVSKI	59	
Exon:	2↓3		
Mm_C3G_isoform2	PEKFSV-----KNCWLEEKEKEVVS	81	
Mm_C3G_isoform3	PEKFSVKEARDRFLPEGYPPLDLEQQAVFMSTSAVASRSQRQKNCWLEEKEKEVVS	119	
Exon:	3↓4		
Mm_C3G_isoform2	LRYFKTIVDKMAIDKKVLEMLPGSASKVLEAILPLVQTDPRIQHSSALSSCYSRVYQSLA	141	
Mm_C3G_isoform3	LRYFKTIVDKMAIDKKVLEMLPGSASKVLEAILPLVQTDPRIQHSSALSSCYSRVYQSLA	179	
Exon:	4↓5		
Mm_C3G_isoform2	NLIRWSDQVMLEGVNSEDKEMVTTVKGVIKAVLDGVKELVRLTIEKQGRPSPTSVVKFSS	201	
Mm_C3G_isoform3	NLIRWSDQVMLEGVNSEDKEMVTTVKGVIKAVLDGVKELVRLTIEKQGRPSPTSVVKFSS	239	
Exon:	5↓6		
Mm_C3G_isoform2	PASKPDGQPELPLTDREMEILNKTTSVSPSAELLDPDSTSEEVAPPKPELPGIRVVDNSPP	261	
Mm_C3G_isoform3	PASKPDGQPELPLTDREMEILNKTTSVSPSAELLDPDSTSEEVAPPKPELPGIRVVDNSPP	299	
Exon:	7↓8		
Mm_C3G_isoform2	ALPKKQRQAPSPTRVAVVAPMSRATSGSSLVPGINRQDFDVECYTQRRLSGGSRSCGGE	321	
Mm_C3G_isoform3	ALPKKQRQAPSPTRVAVVAPMSRATSGSSLVPGINRQDFDVECYTQRRLSGGSRSCGGE	359	
Exon:	8↓9		
Mm_C3G_isoform2	SPRLSPCSSTGKLSRSDEQLSSLDLDRDSGQCSRNTSCETLDHYDDPYEFLQDLSNADQIP	381	
Mm_C3G_isoform3	SPRLSPCSSTGKLSRSDEQLSSLDLDRDSGQCSRNTSCETLDHYDDPYEFLQDLSNADQIP	419	
Mm_C3G_isoform2	PQAACNLSPLPESLGESEPPFLGHPFQLPLGSLCQQEGQQTDTPALPKKRRSAVSQTT	441	
Mm_C3G_isoform3	PQAACNLSPLPESLGESEPPFLGHPFQLPLGSLCQQEGQQTDTPALPKKRRSAVSQTT	479	
Mm_C3G_isoform2	DSSGCRVSYERHPSQYDNISEGDLQNPVQVPPFAAVLFFQQGASSASAEFVGDFFS	501	
Mm_C3G_isoform3	DSSGCRVSYERHPSQYDNISEGDLQNPVQVPPFAAVLFFQQGASSASAEFVGDFFS	539	
Exon:	9↓10		
Mm_C3G_isoform2	VPFLAGDTEKPELPEKKNKHMLAYMQLLEDYSEPPSMFYQTPQSEHIYQQKNKMLMEV	561	
Mm_C3G_isoform3	VPFLAGDTEKPELPEKKNKHMLAYMQLLEDYSEPPSMFYQTPQSEHIYQQKNKMLMEV	599	
Exon:	10↓11		
Mm_C3G_isoform2	YGFSEFCGSDSTQELAPPALPKKQRQQLQASYAASSFSVYCVQQTVAFTPEDGSAAQ	621	
Mm_C3G_isoform3	YGFSEFCGSDSTQELAPPALPKKQRQQLQASYAASSFSVYCVQQTVAFTPEDGSAAQ	628	
Exon:	11↓12		
Mm_C3G_isoform2	GLSVSVNSFLNRHGSGLPVPSYKSVFRYSQDFMPHHQASVQFLPPTSSSHFPPVHT	681	
Mm_C3G_isoform3	-----	628	
Exon:	12↓13		
Mm_C3G_isoform2	SQSSDLAVPTVSSPPSTVDGPLSSQDSSFHGNPVRPLPSETSF7DSSEKASSEAGGDE	741	
Mm_C3G_isoform3	-----	628	
Exon:	13↓14		
Mm_C3G_isoform2	YVSLYSSGQTSEELAPCRGEPSPGKDGHRDPSVSSASGKDSRENGERSPKSLDGLESAQ	801	
Mm_C3G_isoform3	-----EPPSGKDGHRDPSVSSASGKDSRENGERSPKSLDGLESAQ	669	
Exon:	15↓16		
Mm_C3G_isoform2	SEEEVDELSLIDHNEIMARLTLLKQEGDDGPDVRRGGSDILLVHATETDRKDLVLYCEAFL	861	
Mm_C3G_isoform3	SEEEVDELSLIDHNEIMARLTLLKQEGDDGPDVRRGGSDILLVHATETDRKDLVLYCEAFL	729	
Exon:	17↓18		
Mm_C3G_isoform2	TTYRTFISPEELIKKLQYRYEKFSFPADTFKKRVSKNTFFVLRVVDELCLVELTEEILK	921	
Mm_C3G_isoform3	TTYRTFISPEELIKKLQYRYEKFSFPADTFKKRVSKNTFFVLRVVDELCLVELTEEILK	789	
Exon:	19↓20		
Mm_C3G_isoform2	LLMELVFRVLCVSGELSLARVLRKNIIDKVDQKLLRCAHSDQPLAARGVAARPGTLHDFH	981	
Mm_C3G_isoform3	LLMELVFRVLCVSGELSLARVLRKNIIDKVDQKLLRCAHSDQPLAARGVAARPGTLHDFH	849	
Exon:	20↓21		
Mm_C3G_isoform2	SHEIAEQTLTLLDAELFYKIEIPEVLLWAKEQNEEKSPNLTQFTEHFNNMSYWVRSIIMLQ	1041	
Mm_C3G_isoform3	SHEIAEQTLTLLDAELFYKIEIPEVLLWAKEQNEEKSPNLTQFTEHFNNMSYWVRSIIMLQ	909	
Exon:	22↓23		
Mm_C3G_isoform2	EKAQDRERLLKFKIKIMKHLRKLNNFNLSYLAISALDSAPIRLEWQRQTSEGLAEYCTL	1101	
Mm_C3G_isoform3	EKAQDRERLLKFKIKIMKHLRKLNNFNLSYLAISALDSAPIRLEWQRQTSEGLAEYCTL	969	
Exon:	24↓25		
Mm_C3G_isoform2	IDSSSFRAARAALSEVEPPCIPYLGILLQDLTFVHLGNPDYIDGKVNFSKRWQDFNILD	1161	
Mm_C3G_isoform3	IDSSSFRAARAALSEVEPPCIPYLGILLQDLTFVHLGNPDYIDGKVNFSKRWQDFNILD	1029	
Exon:	25↓26		
Mm_C3G_isoform2	SMRCFQAQAHYEIRRNDDIINFNFDSHDLAEALWELSLKIKPRNITRRTKDREKKT	1218	
Mm_C3G_isoform3	SMRCFQAQAHYEIRRNDDIINFNFDSHDLAEALWELSLKIKPRNITRRTKDREKKT	1086	

Cadherin Binding Domain
 EXXEXX (Crk/CrkL-SH3 Binding Motif)
 █ Activating Phosphorylation Site
Ras Family Exchanger Motif
Ras Family GEF Domain

Alignment of the two most characterized proteins species variants of murine C3G (Rapgef1 isoform 2 and 3: http://www.ncbi.nlm.nih.gov/gene?cmd=Retrieve&dopt=full_report&list_uids=107746). Indicated are the functional domains and exon boundaries as presented in Figure 5.

