

Supplement Fig. S4

	622	630	640	648	660	670
human RBM10v2 (622)	KGALAERQHTSM	DLPKLASD	DRPSPP	RGLVAA	YSGESD	SEEEQERGGPERE
human RBM10v1 (700)	KGALAERQHTSM	DLPKLASD	DRPSPP	RGLVAA	YSGESD	SEEEQERGGPERE
human RBM5 (589)	KGALAERQQLIPEL	LVRNGDE	ENP-LK	RGLVAA	YSGDSD	NEEELVERLESEE
	673	680	690	700	710	720
human RBM10v2 (673)	EKLTDWQK	LACLL	CRRQFPSKEALIRHQQLSGLHKQN	LEIH	RRRAHLSENEL	
human RBM10v1 (751)	EKLTDWQK	LACLL	CRRQFPSKEALIRHQQLSGLHKQN	LEIH	RRRAHLSENEL	
human RBM5 (639)	EKLADWKK	MACLL	CRRQFPNKDALVRHQQLSDLHKQN	MDIY	RRSRLSEQEL	
	724	730	740	750	759	770
human RBM10v2 (724)	EALE	KNDMEQMKYRDRAAE	RREKYGIPEPPEP	KRRK	YGGISTASVDFEQPT	
human RBM10v1 (802)	EALE	KNDMEQMKYRDRAAE	RREKYGIPEPPEP	KRRK	YGGISTASVDFEQPT	
human RBM5 (690)	EALE	LRERE-MKYRDRAAE	RREKYGIPEPPEP	KRRK	Q--FDAGTVNIEQPT	
	775	780	790	800	810	820
human RBM10v2 (775)	RDGLGSDNIGSRMLQAMGW	KEGSGLGRKKQ	GI	VTPIEAQ	TRVRGSGLGAR	G
human RBM10v1 (853)	RDGLGSDNIGSRMLQAMGW	KEGSGLGRKKQ	GI	VTPIEAQ	TRVRGSGLGAR	G
human RBM5 (738)	KDGI	DHSNIGNKMLQAMGW	REGSGLGRKKQ	GI	TAPIEAQ	VRLKGAGLGAK
	826	830	930	852		
human RBM10v2 (826)	SSYGVTSTESYK	ETLHK	TMVTRFNEAQ			
human RBM10v1 (904)	SSYGVTSTESYK	ETLHK	TMVTRFNEAQ			
human RBM5 (789)	SAYGLSGADSYK	DAVRK	AMFARFTEME			