

RRM zf-RanBP mutations				
HsFUSa	MASNDYTQQATQSYGAYPTQPGQGYQQSSQPYGQQSYSYGSQSTDTSY	YGQSSYS-SVG	59	
BtFUS	MASNDYTQQATQSYGAYPTQPGQGYQQSSQPYGQQSYSYGSQSTDTSY	YGQSSYSYGSY	60	
MnFUS	MASNDYTQQATQSYGAYPTQPGQGYQQSSQPYGQQSYSYGSYGSAD	TSG YGQSSYSYGSY	60	
RnFUS	MASNDYTQQATQSYGAYPTQPGQGYQQSSQPYGQQSYSYGSYGSAD	TSG YGQSSYSYGSY	60	
DmCaz	-----	-MERGG YG-----	7	
CeC27H5.3	-----	MAAYDQSQPDYSTPEGQQATWAYQQQQQQPQGGQPDQ-----	38	*
HsFUSa	QSQTNTG YGTQSTPQGYGS TGGYGS SSSQSSYGGQSSYPGYQ	QGQFAPSSTSG SYGSSSQS	119	*
BtFUS	QTQNS-YSTQSAPQGYGSAGGYGS SSSQSSYGGQSSYPGYQ	QGQFAPSSTSG SYGSSSQS	119	*
MnFUS	QTQNTG YGTQSAPQGYGS TGGYGS SSSQSSYGGQSSYPGYQ	QGQFAPSSTSG SYGSSSQS	120	*
RnFUS	QTQNTG YGTQSAPQGYGS TGGYGS SSSQSSYGGQSSYPGYQ	QGQFAPSSTSG SYGSSSQS	120	*
DmCaz	-----	GGSGQCYTMNFAVPPPNIQQMPNKTGNYNEPPN-----	40	*
CeC27H5.3	-----	DPYAAAAAYGGHDQAAQPQNPYAPPFGADPYQGSGGQSGGS-----	80	*
HsFUSa	SSYGQPQSGSYSQQPSYCGQQQSYGQQQS-YNPPQCGYQ	QGQNNQYNSSSGGGGGGGGNYG	178	*
BtFUS	SGYQPQGGGYGQQQSYGQQQS-YNPPQCGYQ	QGQNNQYNSSSGGGGGGGG-SYG	176	*
MnFUS	SSYGQPQSGCGYGQQQSYGQQQS-YNPPQCGYQ	QGQNNQYNSSSGGGGGGGG-NYG	179	*
RnFUS	SSYGQPQSGGYGQQQSYGQQQS-YNPPQCGYQ	QGQNNQYNSSSGGGGGGGG-NYG	179	*
DmCaz	--YGK-QGGYD SGSGHRG-----	SGGSGNGGGGG-----	68	*
CeC27H5.3	DPYQGSRGGRGGFGG SRC-----	GGGYDGGRRGGSRGGYD-----	116	*
HsFUSa	QDQSSMS SGGGSGGGYGNQDQSGGGGS-GGYQ	QDQGRGGRGGRGGSGGGGGG YNRSSG	237	*
BtFUS	QDQSPSMS SGGG-YGQNDQSGG-----	YGGQQDRGGRGRGG-----	223	*
MnFUS	QDQSSMSGGGG-GGGYGNQDQSGGGGG-YGGQQDRGGRGRGG-----	YGGYNRSSG	230	*
RnFUS	QDQSSMSGGGG-GGGYGNQDQSGGGGG-YGGQQDRGGRGRGG-----	YGGYNRSSG	230	*
DmCaz	-----	SWNDRGG-----NS YGN-----GG ASKD-----SY NKHG-----	93	*
CeC27H5.3	RGGGYGGDRGGGRGGYDGEERRGGSRWDGNSDRQGGPPGG-----	RGGYDQDRGP	168	*
HsFUSa	GYEPGRGRRGGRRGGMCGSDRGGFNMFKFGGPRDQGSRHD	SEQDNDSNN TIFWQGLGENVT	297	*
BtFUS	GYEPGRGRRGGRRGGMCGSDRGGFNMFKFGGPRDQGSRHD	SEQDNDSNN TIFWQGLGENVT	283	*
MnFUS	GYEPGRGRRGGRRGGMCGSDRGGFNMFKFGGPRDQGSRHD	SEQDNDSNN TIFWQGLGENVT	290	*
RnFUS	GYEPGRGRRGGRRGGMCGSDRGGFNMFKFGGPRDQGSRHD	SEQDNDSNN TIFWQGLGENVT	290	*
DmCaz	GYSGGGGGGGGGGGGGGGSGGND-----	MITQED TIFVWSGMDPSTT	132	*
CeC27H5.3	RRDGPPSSGGYGGGG AASGNREFG-----	SDGRVELKE TVFWQGISTTAN	213	*
HsFUSa	IIESVADYPKQIG IIKTNKKTGQMINLYTDRE	TGKLKEATVSFDDPPSAKAAIDWFDGK	357	*
BtFUS	IIESVADYPKQIG IIKTNKKTGQMINLYTDRE	TGKLKEATVSFDDPPSAKAAIDWFDGK	343	*
MnFUS	IIESVADYPKQIG IIKTNKKTGQMINLYTDRE	TGKLKEATVSFDDPPSAKAAIDWFDGK	350	*
RnFUS	IIESVADYPKQIG IIKTNKKTGQMINLYTDRE	TGKLKEATVSFDDPPSAKAAIDWFDGK	350	*
DmCaz	EQDIETHEGAIG IIKTKDKRTMVKIWL YKNKE	TGAKSGEATVYTDNTNAQSAIEWFDRG	192	*
CeC27H5.3	EAYIADVFSTOGDIAKNDRG-----PRIK IYIDRN TGEPKGECLTFVDAASQQAI TMYNQ	271	*	
HsFUSa	: * * * * : * : * * : * * : * * : * * : * : * : * : * :	: * * * * : * : * : * : * : * : * : * : * : * : * : * :		*
BtFUS	EFSG--NP IKVSFATRADFN--RGGGNRGCGRGRGGPMG-RGGYGG--GGSGGGGRG	408	*	
MnFUS	EFSG--NP IKVSFATRADFN--RGGGNRGCGRGRGGPMG-RGGYGG--GGSGGGGRG	394	*	
RnFUS	EFSG--NP IKVSFATRADFN--RGGGNRGCGRGRGGPMG-RGGYGG--GGSGGGGRG	401	*	
DmCaz	DFNG-NAIKVSLAQRQNNWN-KGGGGGG-GGRGGFGG-RRGGGG-GGGGGGGGG	243	*	
CeC27H5.3	PFPGGSSPMISLAKFRADAGGERGGRGGFRRGGFPMGRRGGFGGGDRGGYGGGGGR	331	*	
HsFUSa	G-FPSGGGGGG-----	QQRAGDWKCPNP TCEMMNF SWRNECNQCKAP	450	*
BtFUS	G-FPSGGGGGG-----	QQRAGDWKCPNP TCEMMNF SWRNECNQCKAP	436	*
MnFUS	G-FPSGGGGGG-----	QQRAGDWKCPNP TCEMMNF SWRNECNQCKAP	443	*
RnFUS	G-FPSGGGGGG-----	QQRAGDWKCPNP TCEMMNF SWRSECNQCKAP	443	*
DmCaz	GRFDRGGGGGGGGRYDRGGGGGGGGNVQPRDGDVKCN-----SCMTINF AWRNECNRCKTP	301	*	
CeC27H5.3	GFGDGGGGGG-----	FRGGDRGGFRGGDRGGFRGGDRGGFRGGD	372	*
HsFUSa	KPD-----GP GGGPGG SHMGGNY-GDDRGGGRGGYD-----RGGYRGRGGDRGGFRRGGR	498	*	
BtFUS	KPD-----GP GGGPGG SHMGGNY-GDDRGGGRGGYD-----RGGYRGRGGDRGGFRRGGR	484	*	
MnFUS	KPD-----GP GGGPGG SHMGGNY-GDDRGG-RGGYD-----RGGYRGRGGDRGGFRRGGR	490	*	
RnFUS	KPD-----GP GGGPGG SHMGGNY-GDDRGG-RGGYD-----RGGYRGRGGDRGGFRRGGR	490	*	
DmCaz	KGDDEGSSGGGGGGYGGGGGGGGYDRGNDRG SGGGGYHNDRDG NSQGGGGGGGGGGY	361	*	
CeC27H5.3	RGG-----DRGGFRG GRGVGG NANMBQ KNDWPCEQ-----CGNSNFAFRRECNCQCA	421	*	
HsFUSa	G-----GGDRGGFPGKMDSR-----GEHRQDR-----RERPF	526	*	
BtFUS	G-----GGDRGGFPGKMDSR-----GEHRQDR-----RERPF	512	*	
MnFUS	G-----GGDRGGFPGKMDSR-----GEHRQDR-----RERPF	518	*	
RnFUS	G-----GGDRGGFPGKMDSR-----GEHRQDR-----RERPF	518	*	
DmCaz	SRFNDNNNGGGGRGGGGGGGNRDGGPMRNDGGMRSRPF	399	*	
CeC27H5.3	P-----RPDGGSGGGGERR-GGPGGDR-----RPF	448	*	
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Figure S1. Peptide sequence alignments of FUS proteins from different species, including human (Hs), bovine (Bt), mouse (Mm), rat (Rn), fly (Dm) and worm (Ce). The amino acid residues that are identical across all species are in red (*). RNA recognition motif (RRM) and zinc finger (zf-) Ran-BP domain are highlighted in yellow and blue, respectively.

Table S1. Published ALS cases with FUS mutations: the age of onset and duration

		Subject	Age of onset (years)	Duration (months)	Reference
Sporadic	1		13	20	Huang et al., 2010
	2		22	10	Bäumer et al., 2010
	3		18	11	
P525L	1		21	<12	
	2		32	<12	Chiò et al., 2009
	Familial	3	16	<12	
		4	27	<24	
		5	22	6	Kwiatkowski et al., 2009
R524S	Familial	1	34	39	Kwiatkowski et al., 2009

ALS, amyotrophic lateral sclerosis.

References

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