

Supplemental Figures

Supplemental Figure 1: cDNA and protein sequence of human hnRNP G. Start and stop codons are shown in bold. The protein sequence is shown underneath the cDNA sequence in one letter code. The RRM domain is shown as a green box with the two RNP boxes as dark grey ovals. The proline rich region is shown in a pink box. SR residues are indicated in red, tyrosine residues in blue. The RGG and RG motifs are boxed.

Supplemental Figure 2: Alignment of hnRNP G family members. Rat hnRNP G, human hnRNP G, G-T and RBMY were aligned with Clustal W.

Supplemental Figure 3: Sequences of exons that are regulated by hnRNP G. Exons that showed a dependency on hnRNP G expression, both in array analysis and RT-PCR are listed. Exons that did not show this dependency in both assays are shown as controls. CCC and CCA triplets are indicated by shading. The per cent exon usage in transfection assays is indicated.

Supplemental Figure 4: Longer exposure of a Western blot with lysates from different tissues analyzed with an antiserum against hnRNP G (Similar to Figure 1C).

1 cttcctagttgggggtgcattaacccttgaccagcagctgtcacctgagctacttg
 61 gaaggccctttggcgagctttagaggagcttgagaccttcaccgtcctgagactctt
 121 cagcgggaaggaaag**ATG**GTTGAAGCAGATCGCCAGGAAAG**CTCTTCATTGGTGGGCTC**
 M V E A D R P G K **L F I G G L** 15
 44 AATACAGAAACAAATGAGAAAGCCCTGGAAGCAGTATTTGGCAAGTATGGACGGATAGTG
 N T E T N E K A L E A V F G K Y G R I V 35
 104 GAAATACTTTTGGATGAAAGACCGTGAGACCAACAAATCAAGAGGATTTGCTTTTGTACC
 E I L L M K D R E T N K S **R G F A F V T** 55
 164 TTCGAAAGCCAGCAGATGCTAAAGATGCAGCTAGAGATATGAATGGAAAGTCTTTGGAT
 F E S P A D A K D A A R D M N G K S L D 75
 224 GGAAAAGCCATTAAGGTAGAGCAAGCTACCAAACCATCTTTTGAAGTGGCAGGCGTGGAG
 G K A I K V E Q A T K P S F E S **G R R G** 95
 284 CCACCTCCACCTCCAAGAAGCAGAGGCCCTCCCAGAGGTCTTCGAGGAGGAAGTGGAGGA
 P P P P P R **S R G** P P **R G** L **R G G** S G G 115
 334 ACTAGGGGACCCCTTCACGTGGAGGATACATGGATGACGGTGGTTATTCCATGAACCTTT
 T **R G** P P **S R G G** Y M D D G G Y S M N F 135
 394 AACATGAGTTCTTCCAGGGGACCACTTCCAGTAAAAAGAGGACCACCACGAAGCGGG
 N M S S **S R G** P L P V K **R G** P P P **R S** G 155
 454 GGTCCCCCTCCTAAGAGATCAACACCTTCAGGACCAGTTTGAAGCAGCAGTGGAAATGGGT
 G P P P K **R S** T P S G P V **R S** S S G M G 175
 514 GGAAGAACGCCAGTGTCCCGTGGAAAGAGATAGCTATGGAGGCCACCAAGAAGGGAACCC
 G R T P V **S R G R** D S Y G G P P R R E P 195
 574 CTGCCATCTCGCAGAGATGTTTATTTGTCCCCAAGAGATGATGGATATTCTACAAAAGAC
 L P **S R** R D V Y L S P R D D G Y S T K D 215
 634 AGCTATTCAAGCAGAGATTACCCAAGTTCTCGAGACACCAGAGATTATGCACCACCACCA
 S Y S **S R** D Y P S **S R** D T R D Y A P P P 235
 694 AGAGATTATACTTACCGGATTACAGTCATTCCAGTTCCCGAGATGACTATCCGTCAAGA
 R D Y T Y R D Y S H S S **S R** D D Y P **S R** 255
 754 GGCTATGGTGATAGAGATGGATATGGTCGGGATCGTGAGTATTCAGATCATCCAAGTGGC
 G Y G D R D G Y G R D R E Y S D H P S G 275
 814 GGTTCTACAGAGATTCATATGAGAGCTATGGAAATTCGCGCAGTGCGCCCCCTACTCGT
 G S Y R D S Y E S Y G N **S R S** A P P T R 295
 874 GGGCCACCACCATCTTATGGAGGAAGCAGCCGCTATGATGATTACAGCAGCTCACGTGAT
 G P P P S Y G G S **S R Y** D D Y S S **S R** D 315
 934 GGATATGGTGGAAAGTCGAGACAGTTACTCAAGCAGCAGAAGTGATCTCTACTCAAGTGGC
 G Y G G **S R** D S Y S S **S R S** D L Y S S **G** 335
 994 CGTGATCGCGTCGGCAGACAAGAACGAGGGCTTCCCCCGTCTATGGAAAGGGGGTACCCT
 R D R V **G R** Q E **R G** L P P S M E **R G** Y P 355
 1054 CCTCCACGTGATTCCTACAGCAGTTCAAGCCGTGGAGCACCAAGAGGAGGTGGCCCGTGGAG
 P P R D S Y S S S **S R** G A P **R G G G** **R G** 375
 1114 GGGAGCCGATCTGATAGAGGGGAGGCAGAAGCAGATACT**TAG**aaacaaataagacttttg
 G S R S D **R G G G R S R Y** * 388
 1174 atcaaggctccatgcagagaaacacaagatggaaagtctctgtcataactatcaaggac
 1234 taataagagaagttgtgttaccttttttaattttctgttttaagttccccttcatttttg
 1294 tgttcttgtaagaaaaagtaaacatgattaattttgatattatgaattgctttcaaca
 1354 agcaaatgttaaatgtgtaagacttgacttgtactagtgttgtaattttccaagtaaaag
 1414 tgtccctaaaggcaa

Supplemental Figure 2

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rat hnRNP G      MVEADRPGLKFIGGLNLETNEKALEAVFGKYGRIVEILLMKDRETNKSRGFVTFESPA 60
human hnRNP G    MVEADRPGLKFIGGLNLETNEKALEAVFGKYGRIVEVLLMKDRETNKSRGFVTFESPA 60
human hnRNP G-T  MVEADRPGLKFIGGLNLETDEKALEAEVFGKYGRIVEVLLMKDRETNKSRGFVTFESPA 60
human RBMY       MVEADHPGLKFIGGLNRETNEKMLKAVFGKHGPISEVLLIKDR-TSKSRGFVTFESPA 59
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rat hnRNP G      DAKDAARDMNGKSLDGKAIKVEQATKPSFESG-RRGPPPPPSRGPPRGLRGG---SGGT 116
human hnRNP G    DAKDAARDMNGKSLDGKAIKVEQATKPSFESG-RRGPPPPPSRGPPRGLRGGRGSSGGT 119
human hnRNP G-T  DAKAAARDMNGKSLDGKAIKVAQATKPAFESS-RRGPPPP-RRSRGRPRFLRGTTRGGGGGP 118
human RBMY       DAKNAAKDMNGKSLHGKAIKVEQAKKPSFQSGGRRRPPASSRNRSPSGLSRSARGSRGGT 119
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rat hnRNP G      R-GPPSRGGYMDGGYSMNFNMSSSRGPLPVKRGPPPSRGPPPKRSTPSGPVRSSSG-M 174
human hnRNP G    R-GPPSRGGHMDGGYSMNFNMSSSRGPLPVKRGPPPSRGPPPKRSAPSGPVRSSSG-M 177
human hnRNP G-T  R-RSPSRGGPDDDDGGYAADFDLRPSRAPMPMKRGPPRRRVGPPPKRAAPSGPARSSGGGM 177
human RBMY       RGWLPSHEGLDDGGYTPDLKMSYSRGLIPVKRGPPSRSGGPPPKKSAPSAVARNSNSW-M 178
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rat hnRNP G      GGRTPVSRGRDSYGGPPRREPLPSRRDVYLSRDDGYSTKDS----- 216
human hnRNP G    GGRAPVSRGRDSYGGPPRREPLPSRRDVYLSRDDGYSTKDS----- 219
human hnRNP G-T  RGRALAVRGRDGYSGPPRREPLPRRDYLGPRDEGYSSRDG----- 219
human RBMY       GSQGPMSQRRENYGVPPRRATISSWRNDRMSTRHDGYATNDGNHPSCQETRDIYAPPSRGY 238
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rat hnRNP G      -----YSS----- 219
human hnRNP G    -----YSS----- 222
human hnRNP G-T  -----YSS----- 222
human RBMY       AYRDNGHSNRDEHSSRGYRNHRSSRETRDIYAPPSRGHAYRDYGHSSRRDESYSRGYRNRRS 298
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rat hnRNP G      -----RDYSSRDTRDIYAPPRDYTYRDYSHSS 247
human hnRNP G    -----RDYSSRDTRDIYAPPRDYTYRDYGHSS 250
human hnRNP G-T  -----RDY---REPRGFAPSPGEYTHRDYGHSS 247
human RBMY       SRETREYAPPSRGHGYRDYGHSSRRHESYSRGYRNHPSSRETRDIYAPPHRDYAYRDYGHSS 358
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rat hnRNP G      SRDDYPSRGYSDRDYGG--RDREYSDHPSGGSYRDSYESYGNRSRAPSPTRGPPPSYGGSS 305
human hnRNP G    SRDDYPSRGYSDRDYGG--RDRDYSDHPSGGSYRDSYESYGNRSRAPSPTRGPPPSYGGSS 308
human hnRNP G-T  VRDDCPLRGYSDRDYGG--RDRDYGDHLSRGSHPFESYGELRGAAPGRGTPPSYGGGG 306
human RBMY       -WDEHSSRGYSYHDGYGEALGRDHSEHLSGSSYRDALQRYGTSHGAPPARGPRMSYGG-S 416
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rat hnRNP G      RYDDYS-SSRDYGGSRDSYSSS--RSDLYSSGRDRVGRQERGLPPSMERGYPPPRDSYS 362
human hnRNP G    RYDDYS-SSRDYGGSRDSYSSS--RSDLYSSGRDRVGRQERGLPPSMERGYPPPRDSYS 365
human hnRNP G-T  RYEEYRGYSPDAYSGGRDSYSSSYGRSDRYSRGRHRVGRPDRGLSLSMERGCPPQRDSYS 366
human RBMY       TCHAYS-NTRDRYGRSWESYSSC---GDFHYCDREHVCRKDQRNPPSLGRVLPDPREACG 472
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rat hnRNP G      SSSRGAPRGGGRGGSRSRDRGGGRSRY 388
human hnRNP G    SSSRGAPRGGGRGGSRSRDRGGGRSRY 391
human hnRNP G-T  RSGCRVPRGGGRGGRLEGGGRSRY 392
human RBMY       SSSYVASIVDG-GESRSEKGD-SRY 496
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Supplemental Figure 3

Gene	Exon sequence	% exon inclusion	
		EGFP-C2	hnRNP G-C2
Casp7 Mus musculus caspase 7 NM_007611	GTATGGACGTCCGGAATGGGACGGACAAAGATGCAGGGGCCCTCTTCAAGTGCTTCCAAAA CCTGGGTTTTGAAGTAACCGTCCACAATGACTGCTCTTGTGCAAAGATGCAAGATCTGCTT AGAAAAG	2%	20%
NOL5A 127.3.1 Homo sapiens nucleolar protein 5A (56kDa with KKE/D repeat) NM_006392	ACCTGAATGCAGTTGTTCCCATGGCTGGGCCAGGCTTTGCAGTGATGACTTGCGAATCAAA TCTGTCAATCCCCTGAGTGCAATCACTGATGTCTCCATGTCTCTGAGCAATGCCTGATGGG GAGGGATCTAG	2.4%	5.1%
CPSF4 Homo sapiens Cleavage and polyadenylation specific factor 4, 30kDa 136.4.1 NM_006693	GAGACTCTTCCCACTCCATCCTGAGACCTCCTCTTCTGGATCCCGGGACGCTCCCCTTGGT TTCAGGACTCCTGACTCCCAGGCCCCCATTTCCACCGTCTGGGGACTCCTTTTACCCTCAC TCGGACTCAGGAGTTCCTGCTCGGATCTTTGGCCCTCTGCGGCTGTTCAAAG	1.9%	4%
Fyn Homo sapiens FYN oncogene related to SRC, FGR, YES 907.002.002 NM_002037	AAAGCTGATGGTTTGTGTTTTAACTTAACTGTGATTGCATCGAGTTGTACCCCAAACTT CTGGATTGGCTAAAGATGCTTGGGAAGTTGCACGTCGTTCTGTTGTCTGGAGAAGAAGCT GGGTCAGGGGTGTTTCGCTGAAGTGTGGCTT	17,5%	28%
USP39 Homo sapiens Ubiquitin specific protease 39 134.7.1 NM_006590	GGGACAGGCAAATGGTATGAATTACAAGACCTCCAGGTGACTGACATCCTTCCCCAGATGA TCACACTGTGAGAGGCTTACATTCAG	6%	9.3%
SRRM1 110.3.1 Homo sapiens serine/arginine repetitive matrix 1 NM_005839	GATGCAGATGGGAAAGCGATGGCAATCGCCAGTGACTAAAAG	51%	60%
CPSF6 Homo sapiens Cleavage and polyadenylation specific factor 6, 68kDa 148.1.1 NM_007007	CTGGACAGACTCCACCACGTCCACCCTTAGGTCCTCCAGGCCACCTGGTCCACCAGGTCC TCCACCTCCTGGTCAGGTTCTGCCTCCTCCTTAGCTGGGCCTCCTAATCGAGGAGATCGC CCTCCACCACAGTTCTTTTTCTGGACAACCTTTTGGGCAGCCTCCATTGGGTCCACTTC CTCCTGGCCCTCCACCTCCAGTTCAGGCTACGGCCCCCTCCTGGCCCACCACCTCCACA ACAGGGACCACCTCCACCTCCAGGCCCTTTCCACCTCGTCCACCCGGTCCACTTGGGCCA CCCCTTACACTAGCTCCTCCTCCGCATCTTCTGGACCACCTCCAGGTGCCCCACCGCCAG CTCCGCATGTGAACCCAGCTTTCTTTCTCCACCAACTAACAGTGGCATGCCTACATCAGA TAGCCGAGGTCCACCACCAACAGATCCATATGGGCGACCTCCACCATATGATAGGGGTGAC TATGGCCCCCTGGAAG	97%	87%
SFRS 6 Homo sapiens splicing factor, arginine/serine-rich 6 122.4.1 NM_006275	GTATGTTTTGTAATCAAGATAGAAATGATATGACTAATGCTTTAAAGTAAACTC CTTTTATATTCTTATTTCTGGGAATTTATTATGGTATATAGATGTTTTAAGATTT CCGAGTCTGACCAATCTTGTCTTTCAG	25%	18%
Casp9 Mus musculus caspase 9 NM_015733	GTTTTGTCTCCTGGAGGGACAAGAAAAGTGGCTCCTGGTACATCGAGACCTTGGATGGCAT TCTGGAGCAGTGGGCTCGCTCTGAAGACCTGCAGTCCCTCCTTCTCAGG	99%	70%
SF3A2 Homo sapiens splicing factor 3a, subunit 2, 66kDa 150.2.1 NM_007165	GTGAGATCAGGGACTTGGGCGTGGGGGGCGGCCAAAGGCACCCAAGAGGCGGCTCTGCCAC CCGGCCGTGTCCCTGCAG	9.9%	6%
U5-15kD Mus musculus thioredoxin-like 4A (Txnl4a) NM_025299	GTGGTGGCATAAACATCGGGTGGTGTTCAGATCCTGCTGCCGGCAGCTCGAGGCTAGGATG GCTGGAGATGTGAGGGCCTTTGTCTCATCACATCCGAGCACAGCTCAGCAAGATGCTCTTA GCTAGAAAACAGATTTTATGTGTTAAT	24.1%	16.9%
SFRS3 Homo sapiens Splicing factor, arginine/serine-rich 3 39.5.1 NM_003017	AGTCACCATCATGTCTCTTCTCACACCCTCTGAATCTGCAT	24%	11%

Supplemental Figure 3

<p>SC35 NM_011358 Mus musculus splicing factor, arginine/serine-rich 2 (Sfrs2)</p>	<p>GTAATGTCTGGGAATCCGAGACACATAACCCTAATTCATAAATGGGATTTGGGGTAGGTCT TTTTGAGTCGTGTTAATGTAAGAATGACTCCTATCATTAGGAGTGCTGCTCGGAGGTTACT CACCTTTGGGAGTAATACTGAAGAGAGGGGTCTGCAGAAAGGATGTGTATGAAGCTTAGAT AATAATGGCTGTTTCGTAAACTGTTTGAGACCTATTAATGAAAATGACTATTTCTTGCTGT TTTTATCCAACGTCTGCATTTTCCCCCTTTAAAGCTGCGGTCTCCTGTTTGATAAAAAGAAT ATTGGCCAGTATTGCAGATTTTAACTGATTTGGCTGATCCTCCAGGGACCAGTTTCTGTGG GCGTGTATTGGAGCAGGTTTGTCTTTAAATGTTAAAGATGCACTATCCTCTTAGAGAAAACA ATCAGTTCAACTATTGTTGACTGACTGGGACTTCATATTCTAATGGATGTGGCAAAAGAA TTGCAATAAGAAGCAGTGAACATTTGGAACCCAAAAGAAAGTTACAGGTATTGCACTGGG TGGGGAAAGGATAGTGTGTCTTTAACTCTTAAATTGTTTGGTCTATTTTTTAAAAAGGAA AGGGCCCTAAGTAGCTCAGATATTAAGTAGTATTCTCAATTAACAATGTTTCATTTGAA ACAATTTATCTTAATGAAATATAGACCAATTTCTGATCTCGAGTTGTTTTTGTGGATA CAGCCCTTTTTTTTTTCTTTTTTTTTCTTCCCCTTACCTTTCTTACCTTGGTTATTTGGC CAGGAATACGTAAATCAAACCTGTACATGCTGATGGTAGCCTTTGTGAAATTTTCTAAT TGGGCCTTTTTAAAAACATGGCTGGGTGGAACATTTCTGTACCCTACTGGTTTGACCAGAGC CTTAGTAAGTACGTGCCTGAAACTGAAACCATGTGCACTTTAATGGAAGGTAAGCTGAACT TCTTTCTTTTCAAACCTAG</p>	<p>22.5%</p>	<p>6.2%</p>
<p>SF2/ASF NM_173374 Mus musculus splicing factor, arginine/serine-rich 1</p>	<p>GGAGAACTGCCTACATCCGGGTAAAGTTGATGGGCCCAAGAGTCCAAGTTATGGAAGAT CTCGATCTCGAAGCCGTAGTCTGTAGCAGAAGCCGTAGCAGAAGCAACAGCAGGAGTCCGAG TTACTCCCCAAGGAGAAGCAGAGGATCACCCAGCTATTCTCCCCGTATAGCAGATCTCGC TCTCGTACATAA</p>	<p>12%</p>	<p>2%</p>

Control exons

Gene	Exon sequence		
hnRNP M	ATGGCCTTGGTGGTATTGGCATGGGGTTAGGACCAGGAGGGCAACCCATTGATGCCAATCA CCTGAATAAAGGCATCGGAATGGGAAACATAGGTCCCGCAG		
Fe65	TGTTTTCGCCGTGCGCTCCCTAGGCTGGGTAGAGATGACCGAGGAGGAGCTGGCCCCCTGGAC GCAGCAGTGTGGCAGTCAACAATTGCATCCGTGAGCTCTTTACCAAAAAACAACCTGCA TGACCCCATGTCTGGGGGCTGGGGGGAA		
SFRS14	GGGAACCCCTCGGAAGGGGAAGGGTTGGGTGCTGACGGGCAGGAGCACAAAGAAGACACA TTTCGATGTGTTCCGACAGAGGATGATGCAGATGTACAGACACAAGCGGGCCAACAAATAG		
Ku antigen	GAGACTATAAATATTCAGGAAGAGATAGTTTTGATTTTTTTGGTTGATGCCTCCAAGGCTAT GTTTGAATCTCAGAGTGAAGATGAGTTGACACCTTTTGACATGAGCATCCAG		
SNRPD1	GTGTGGATGTCAGCATGAATACACATCTTAAAGCTGTGAAAATGACCCCTGAAGAACAGAGA ACCTGTACAGCTGGAAACGCTGAGTATTCCAGGAAATAACATTCGGTATTTTATTCTACCA G		
hnRNP C	ATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGTGAAACGATCTGC AGCGGAGATGTACGGGTGAGTAACAGAACCCCTTCTCCGTCCCCCTCTACTCAG		
hnRNPA2B1	GCAACTTTGGCTTTGGGGATTACGTTGGTGGCGGTGGAATTTTCGGACCAGGACCAGGAAG TAACCTTAGAGGAGGATCTG		
Caspase 2	GTGCTATTGGATCCCTTGGGCACCTCCTTCTGTTCACTGCTGCCACCGCCTCTCTTGCTCT		
hnRNP K	GTTGGGTTCAAGTGTGATGAAACTTGGGATTCTGCAATTGACACATGGAGCCCATCAGAAT GGCAAATGGCTTATGAACCACAG		

Supplemental Figure 4

