

Supporting Information

Characterization of FUS mutations in amyotrophic lateral sclerosis using RNA-Seq

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Materials and Methods S1. Formulas used for RNA-Seq analysis.

Exon Skipping: Log_2 (Inclusion: Skip + General Ratio) in the two groups, respectively. In formula

$LISGR1 = \text{Log}_2 ((jup1 + ea1 + jdn1) / (eup1 + jsk1 + edn1))$ and analogously for LISGR2.

Intron Retention: Log_2 (Intron: Flank Ratio). Log-Odds-Ratio (Flanking). In formula $LORF = LIFR2 -$

$LIFR1$. The sign convention means that higher value indicates more intron retention (unspliced isoform) in the second group. This indicates the level of the intron relative to the flanking exons.

More detailed information regarding terms and definitions can be found on the ExpressionPlot website (http://www.expressionplot.com/wiki/index.php?title=Project_directory_structure) and corresponding manuscript [17].

Table S1. Summary of RNA-Seq analysis.

Sample	No. Reads	No. Reads Passing QC	% Passing QC	Uniquely Mapping	% Uniquely mapping	No. Ribosomal	% Ribosomal	Splice Junctions	% Splice Junctions
Wild-type	31,051,162	31,022,757	99.91	21,865,318	70.48	446,094	2.04	2,222,084	10.16
R521G	31,077,360	31,057,750	99.94	21,710,924	69.91	488,727	2.25	2,292,605	10.56
R522G	24,491,122	24,476,034	99.94	17,427,598	71.20	474,659	2.72	1,754,345	10.07
siRNA	28,196,024	28,179,703	99.94	20,640,291	73.25	291,210	1.41	2,242,343	10.86
Vector	27,295,832	27,273,639	99.92	19,416,054	71.19	421,688	2.17	1,983,350	10.22
Average	28,422,300	28,401,977	99.93	20,212,037	71.20	424,476	2.12	2,098,945	10.37

Table S2. Functional annotation KEGG pathways.

<i>Analysis</i>	<i>Group</i>	<i>KEGG pathway</i>	<i>Count</i>	<i>P-value</i>	<i>Benjamini</i>
Differential expression	FUS-WT vs. vector	Ribosome	14	5.6E-6	
	siRNA vs. vector	Spliceosome	34	7.1E-11	7.2E-4
		Ribosome	26	1.9E-9	1.2E-8
	R521G vs. vector	Spliceosome	18	4.4E-10	1.6E-7
	R522G vs. vector	Ribosome	15	3.1E-8	4.1E-8
		Spliceosome	15	3.3E-6	3.1E-6
		Mismatch repair	6	2.4E-4	1.7E-4
		DNA replication	7	2.7E-4	8.2E-3
		Cell cycle	11	1.3E-3	6.8E-3
					2.6E-2
Skipped exons	FUS-WT vs. vector	N/A	N/A	N/A	N/A
	siRNA vs. vector	Ribosome	18	8.6E-11	8.9E-9
		Spliceosome	17	2.0E-7	1.1E-5
	R521G vs. vector	Ribosome	6	1.6E-4	6.7E-3
	R522G vs. vector	Spliceosome	6	3.7E-4	1.4E-2
		Ribosome	5	9.0E-4	1.6E-2
Retained introns	FUS-WT vs. vector	Spliceosome	50	1.0E-16	1.9E-14
		Huntington's disease	54	3.9E-12	3.3E-10
		Proteasome	21	2.7E-8	1.5E-6
		Parkinson's disease	37	4.9E-8	2.1E-6
		Oxidative phosphorylation	37	7.6E-8	2.6E-6
		Cell cycle	36	8.6E-8	2.4E-6
		DNA replication	17	3.3E-7	7.9E-6
		Pyrimidine metabolism	29	5.5E-7	1.2E-5
		RNA polymerase	14	2.3E-6	4.4E-5
		Aminoacyl-tRNA biosynthesis	17	2.7E-6	4.6E-5
		Alzheimer's disease	38	9.9E-6	4.6E-5
		Nucleotide excision repair	16	3.8E-5	1.5E-4
		Citrate cycle (TCA cycle)	13	5.4E-5	5.3E-4
		Purine metabolism	33	2.1E-4	7.0E-4
		Mismatch repair	10	4.3E-4	2.5E-3
		RNA degradation	15	2.8E-3	4.9E-3
					2.9E-2
	siRNA vs. vector	Spliceosome	57	1.4E-22	2.4E-20
		Huntington's disease	54	2.4E-12	2.0E-10

	R521G vs. vector	Pyrimidine metabolism	30	1.1E-7	6.4E-6
		Proteasome	20	1.3E-7	5.6E-6
		Cell cycle	35	2.1E-7	7.1E-6
		DNA replication	17	2.8E-7	7.9E-6
		Parkinson's disease	35	3.9E-7	9.5E-6
		Oxidative phosphorylation	35	5.8E-7	1.2E-5
		RNA polymerase	14	2.0E-6	3.9E-5
		Aminoacyl-tRNA biosynthesis	17	2.3E-6	4.0E-5
		Alzheimer's disease	37	1.9E-5	2.9E-4
		Citrate cycle (TCA cycle)	13	4.8E-5	6.8E-4
		Purine metabolism	34	6.9E-5	9.1E-4
		Mismatch repair	10	3.9E-4	4.8E-3
		Nucleotide excision repair	14	5.4E-4	6.2E-3
		Spliceosome	48	4.7E-16	7.5E-14
		Huntington's disease	49	2.9E-10	2.5E-8
		Proteasome	21	1.1E-8	6.0E-7
		DNA replication	18	2.0E-8	8.7E-7
		Cell cycle	36	2.2E-8	7.4E-7
		Pyrimidine metabolism	28	6.7E-7	1.9E-5
		Oxidative phosphorylation	33	2.1E-6	5.2E-5
		Aminoacyl-tRNA biosynthesis	16	7.4E-6	1.6E-4
		RNA polymerase	13	9.2E-6	1.7E-4
		Parkinson's disease	31	1.3E-5	2.2E-4
		Alzheimer's disease	34	1.1E-4	1.8E-3
		Purine metabolism	32	1.8E-4	2.6E-3
		Mismatch repair	10	2.9E-4	3.8E-3
		Nucleotide excision repair	14	3.6E-4	4.4E-3
	R522G vs. vector	RNA degradation	15	1.7E-3	1.9E-2
		Spliceosome	46	4.3E-16	7.3E-14
		Huntington's disease	47	1.5E-10	1.2E-8
		Proteasome	20	1.5E-8	8.4E-7
		Pyrimidine metabolism	29	2.5E-8	1.0E-6
		Cell cycle	34	2.9E-8	9.4E-7
		DNA replication	16	3.3E-7	8.9E-6
		RNA polymerase	14	4.4E-7	1.0E-5
		Purine metabolism	33	1.2E-5	2.5E-4

	Aminoacyl-tRNA biosynthesis	15	1.3E-5	2.4E-4
	Parkinson's disease	29	1.8E-5	2.9E-4
	Oxidative phosphorylation	27	1.7E-4	2.6E-3
	Alzheimer's disease	30	6.1E-4	8.3E-3
	Citrate cycle (TCA cycle)	10	1.8E-3	2.2E-2
	Nucleotide excision repair	12	2.2E-3	2.5E-2
	RNA degradation	14	2.2E-3	2.4E-2

Abbreviations: FUS-WT = cell lines transfected with human FUS wild-type, used as a model for overexpression, siRNA = cell lines transfected with FUS small interfering RNA (siRNA), used as a model for underexpression, R521G = p.Arg521Gly, R522G = p.Arg522Gly, and N/A = not applicable. Significant KEGG pathways are shown for each condition. *Homo sapiens* is used as background, in Table 1 the Vector alone is used as background. Genes are specified in Table S3.

Table S3. Differentially expressed genes present within identified KEGG pathways.

<i>Group</i>	<i>KEGG pathway</i>	<i>Name</i>	<i>Description</i>
FUS-WT vs. vector	Ribosome	RPL13	ribosomal protein L13
		RPL18	ribosomal protein L18
		RPL26	ribosomal protein L26
		RPL29	ribosomal protein L29
		RPL37A	ribosomal protein L37a
		RPL8	ribosomal protein L8
		RPS11	ribosomal protein S11
		RPS16	ribosomal protein S16
		RPS19	ribosomal protein S19
		RPS3	ribosomal protein S3
		RPS4X	ribosomal protein S4X
		RPS6	ribosomal protein S6
		RPLP0	ribosomal protein, large, P0
		RPLP2	ribosomal protein, large, P2
siRNA vs. vector	Spliceosome	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
		DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
		BAT1	HLA-B associated transcript 1
		LSM2	LSM2 homolog, U6 small nuclear RNA associated
		PRP19	PRP19/PSO4 pre-mRNA processing factor 19 homolog
		PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A
		PRPF8	PRP8 pre-mRNA processing factor 8 homolog
		RBM17	RNA-binding motif protein 17
		RBM25	RNA-binding motif protein 25
		THOC2	THO complex 2
		THOC4	THO complex 4
		U2AFBP	U2 small nuclear RNA auxiliary factor 1
		SR140	U2-associated SR140 protein
		ACIN1	apoptotic chromatin condensation inducer 1
		EFTUD2	elongation factor Tu GTP binding domain containing 2
		HSPA1A	heat shock 70kDa protein 1B
		HSPA8	heat shock 70kDa protein 8

	Ribosome	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1-like 3
		HNRNPM	heterogeneous nuclear ribonucleoprotein M
		HNRNPU	heterogeneous nuclear ribonucleoprotein U
		SNRNP200	similar to U5 snRNP-specific protein, 200 kDa
		SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
		SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
		SF3B1	splicing factor 3b, subunit 1, 155kDa
		SF3B2	splicing factor 3b, subunit 2, 145kDa
		SFRS1	splicing factor, arginine/serine-rich 1
		SFRS2	splicing factor, arginine/serine-rich 2
		SFRS4	splicing factor, arginine/serine-rich 4
		SFRS6	splicing factor, arginine/serine-rich 6
		SFRS7	splicing factor, arginine/serine-rich 7, 35kDa
		TXNL4A	thioredoxin-like 4A
		TCERG1	transcription elongation regulator 1
		USP39	ubiquitin specific peptidase 39
		ZMAT2	zinc finger, matrin type 2
		RPL10	ribosomal protein L10
		RPL10A	ribosomal protein L10a
		RPL13	ribosomal protein L13
		RPL14	ribosomal protein L14
		RPL15	ribosomal protein L15
		RPL18	ribosomal protein L18
		RPL23	ribosomal protein L23
		RPL24	ribosomal protein L24
		RPL26	ribosomal protein L26
		RPL28	ribosomal protein L28
		RPL29	ribosomal protein L29
		RPL30	ribosomal protein L30
		RPL35A	ribosomal protein L35a
		RPL36AL	ribosomal protein L36a-like
		RPL38	ribosomal protein L38
		RPL3	ribosomal protein L3
		RPL5	ribosomal protein L5
		RPL7A	ribosomal protein L7a
		RPS11	ribosomal protein S11

R521G vs. vector	Spliceosome	RPS16	ribosomal protein S16
		RPS19	ribosomal protein S19
		RPS20	ribosomal protein S20
		RPS23	ribosomal protein S23
		RPS29	ribosomal protein S29
		RPS3	ribosomal protein S3
		RPS6	ribosomal protein S6
		DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
		PRPF8	PRP8 pre-mRNA processing factor 8 homolog
		RBM25	RNA-binding motif protein 25
		THOC4	THO complex 4
		U2AF2	U2 small nuclear RNA auxiliary factor 2
		SR140	U2-associated SR140 protein
		ACIN1	apoptotic chromatin condensation inducer 1
		CTBL1	catenin, beta like 1
		HSPA8	heat shock 70kDa protein 8
		HNRNPU	heterogeneous nuclear ribonucleoprotein U
		PCBP1	poly(rC) binding protein 1
		PRPF6	similar to U5 snRNP-associated 102 kDa protein
		SNRNP200	similar to U5 snRNP-specific protein, 200 kDa
R522G vs. vector	Spliceosome	SF3A1	splicing factor 3a, subunit 1, 120kDa
		SFRS4	splicing factor, arginine/serine-rich 4
		SART1	squamous cell carcinoma antigen recognized by T cells
		TCERG1	transcription elongation regulator 1
		ZMAT2	zinc finger, matrin type 2
		CDC5L	CDC5 cell division cycle 5-like
		DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
		DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
		DDX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
		FUSIP1	FUS interacting protein (serine/arginine-rich) 1
		PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B
		THOC2	THO complex 2
		HNRNPM	heterogeneous nuclear ribonucleoprotein M
		HNRNPU	heterogeneous nuclear ribonucleoprotein U
		NCBP1	nuclear cap binding protein subunit 1, 80kDa
		RNRPB	small nuclear ribonucleoprotein polypeptides B and B1

	Ribosome	SF3B1	splicing factor 3b, subunit 1, 155kDa
		SFRS2	splicing factor, arginine/serine-rich 2
		SFRS5	splicing factor, arginine/serine-rich 5
		SFRS7	splicing factor, arginine/serine-rich 7, 35kDa
		RPL10	ribosomal protein L10
		RPL11	ribosomal protein L11
		RPL23	ribosomal protein L23
		RPL26	ribosomal protein L26
		RPL29	ribosomal protein L29
		RPL34	ribosomal protein L34
		RPL4	ribosomal protein L4
		RPS16	ribosomal protein S16
		RPS19	ribosomal protein S19
		RPS20	ribosomal protein S20
		RPS24	ribosomal protein S24
		RPS29	ribosomal protein S29
		RPS3	ribosomal protein S3
		RPS4X	ribosomal protein S4, X-linked
		RPS6	ribosomal protein S6
	Mismatch repair	EXO1	exonuclease 1
		MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1
		PCNA	proliferating cell nuclear antigen
		RFC1	replication factor C (activator 1) 1, 145kDa
		RFC5	replication factor C (activator 1) 5, 36.5kDa
	DNA replication	SSBP1	single-stranded DNA-binding protein 1
		MCM4	minichromosome maintenance complex component 4
		MCM6	minichromosome maintenance complex component 6
		MCM7	minichromosome maintenance complex component 7
		PCNA	proliferating cell nuclear antigen
		RFC1	replication factor C (activator 1) 1, 145kDa
		RFC5	replication factor C (activator 1) 5, 36.5kDa
		SSBP1	single-stranded DNA-binding protein 1
	Cell cycle	CDC25A	cell division cycle 25 homolog A (S. pombe)
		HDAC2	histone deacetylase 2
		MCM4	minichromosome maintenance complex component 4
		MCM6	minichromosome maintenance complex component 6

	MCM7	minichromosome maintenance complex component 7
	PLK1	polo-like kinase 1 (Drosophila)
	PCNA	proliferating cell nuclear antigen
	YWHAE	similar to 14-3-3 protein epsilon (14-3-3E)
	PRKDC	similar to protein kinase, DNA-activated, catalytic polypeptide
	STAG2	stromal antigen 2
	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide

Table S4. Significant protein domains present in differentially expressed genes.

<i>Group</i>	<i>INTERPRO</i>	<i>Count</i>	<i>P-value</i>	<i>Benjamini</i>
FUS-WT vs. vector	RNA recognition motif, RNP-1	20	7.2E-7	6.0E-4
	Endoplasmic reticulum, targeting sequence	10	9.2E-7	3.8E-4
	Nucleotide-binding, alpha-beta plait	17	5.2E-5	1.4E-2
siRNA vs. vector	Nucleotide-binding, alpha-beta plait	48	3.2E-14	5.4E-11
	RNA recognition motif, RNP-1	46	4.1E-13	3.5E-10
	Zinc finger, PHD-type	19	1.2E-5	6.6E-3
	Zinc finger, PHD-finger	18	2.1E-5	8.6E-3
	Helicase, superfamily 1 and 2, ATP-binding	20	4.0E-5	1.3E-2
	DEAD-like helicase, N-terminal	20	5.2E-5	1.5E-2
	Actinin-type, actin-binding, conserved site	9	5.4E-5	1.3E-2
	Zinc finger, PHD-type, conserved site	18	6.9E-5	1.4E-2
	K Homology	11	7.4E-5	1.4E-2
	DNA/RNA helicase, C-terminal	19	1.3E-4	2.2E-2
R521G vs. vector	RNA recognition motif, RNP-1	28	1.9E-15	1.2E-12
	Nucleotide-binding, alpha-beta plait	27	2.0E-14	6.3E-12
	DNA/RNA helicase, C-terminal	12	4.3E-6	8.9E-4
	Helicase, superfamily 1 and 2, ATP-binding	12	4.3E-6	8.9E-4
	DEAD-like helicase, N-terminal	12	5.2E-6	8.0E-4
	Zinc finger, PHD-finger	10	2.6E-5	3.2E-3
	Zinc finger, PHD-type	10	4.1E-5	4.2E-3
	DNA-binding SAP	6	5.2E-5	4.6E-3
	SNF2-related	6	2.7E-4	2.1E-2
	K Homology, type 1	6	3.1E-4	2.1E-2
	K Homology, type 1, subgroup	6	4.2E-4	2.5E-2
	K Homology	6	5.4E-4	3.0E-2
R522G vs. vector	Nucleotide-binding, alpha-beta plait	20	9.2E-9	6.3E-6
	RNA recognition motif, RNP-1	19	4.6E-8	1.6E-5
	HEAT	10	5.0E-7	1.1E-4
	Armadillo-like helical	13	3.1E-6	5.3E-4
	RNA helicase, ATP-dependent, DEAD-box, conserved site	7	1.9E-5	2.6E-3
	Chaperonin TCP-1, conserved site	5	1.9E-5	2.2E-3

Helicase, superfamily 1 and 2, ATP-binding	11	2.1E-5	2.1E-3
DNA/RNA helicase, C-terminal	11	2.1E-5	2.1E-3
DEAD-like helicase, N-terminal	11	2.5E-5	2.1E-3
Chaperone, tailless complex polypeptide 1	5	3.0E-5	2.2E-3
Nucleic acid-binding, OB-fold	8	4.1E-5	2.8E-3
RNA helicase, DEAD-box type, Q motif	7	4.5E-5	2.8E-3
DNA/RNA helicase, DEAD/DEAH box type, N-terminal	8	1.0E-4	5.8E-3
Importin-beta, N-terminal	5	1.2E-4	6.1E-3
Chaperonin Cpn60/TCP-1	5	1.2E-4	6.1E-3
DNA-dependent ATPase MCM, conserved site	4	2.9E-4	1.4E-2
DNA-dependent ATPase MCM	4	4.4E-4	2.0E-2
ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain, active site	4	1.1E-3	4.6E-2
Heat shock protein Hsp90	4	1.1E-3	4.6E-2

Table S5. Shared genes with retained introns as identified by Venn diagrams and KEGG pathways.

<u>KEGG pathway</u>	<u>Name</u>	<u>Description</u>
<u>Spliceosome</u>	<u>BUD31</u>	<u>BUD31 homolog (S. cerevisiae)</u>
	<u>DDX23</u>	<u>DEAD (Asp-Glu-Ala-Asp) box polypeptide 23</u>
	<u>DDX5</u>	<u>DEAD (Asp-Glu-Ala-Asp) box polypeptide 5</u>
	<u>DHX38</u>	<u>DEAH (Asp-Glu-Ala-His) box polypeptide 38</u>
	<u>LSM4</u>	<u>LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)</u>
	<u>LSM7</u>	<u>LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)</u>
	<u>PRPF3</u>	<u>PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)</u>
	<u>PRPF31</u>	<u>PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)</u>
	<u>PRPF38B</u>	<u>PRP38 pre-mRNA processing factor 38 (yeast) domain containing B</u>
	<u>PRPF8</u>	<u>PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)</u>
	<u>RBM17</u>	<u>RNA binding motif protein 17</u>
	<u>RBM25</u>	<u>RNA binding motif protein 25</u>
	<u>THOC4</u>	<u>THO complex 4</u>
	<u>U2AF1</u>	<u>U2 small nuclear RNA auxiliary factor 1</u>
	<u>U2AF2</u>	<u>U2 small nuclear RNA auxiliary factor 2</u>
	<u>ACIN1</u>	<u>apoptotic chromatin condensation inducer 1</u>
	<u>CTNBL1</u>	<u>catenin, beta like 1</u>
	<u>EFTUD2</u>	<u>elongation factor Tu GTP binding domain containing 2</u>
	<u>EIF4A3</u>	<u>eukaryotic translation initiation factor 4A, isoform 3</u>
	<u>HSPA8</u>	<u>heat shock 70kDa protein 8</u>
	<u>HNRPM</u>	<u>heterogeneous nuclear ribonucleoprotein M</u>
	<u>SNRPG</u>	<u>hypothetical protein LOC100132425; similar to small nuclear ribonucleoprotein polypeptide G; small nuclear ribonucleoprotein polypeptide G; small nuclear ribonucleoprotein G-like protein</u>
	<u>PQBP1</u>	<u>polyglutamine binding protein 1</u>
	<u>PRPF6</u>	<u>similar to U5 snRNP-associated 102 kDa protein (U5-102 kDa protein); PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)</u>
	<u>ASCC3L1</u>	<u>similar to U5 snRNP-specific protein, 200 kDa; small nuclear ribonucleoprotein 200kDa (U5)</u>

	<u>WDR57</u>	<u>small nuclear ribonucleoprotein 40kDa (U5)</u>
	<u>SNRPA</u>	<u>small nuclear ribonucleoprotein polypeptide A</u>
	<u>SF3B14</u>	<u>splicing factor 3B, 14 kDa subunit</u>
	<u>SF3B1</u>	<u>splicing factor 3b, subunit 1, 155kDa</u>
	<u>SF3B2</u>	<u>splicing factor 3b, subunit 2, 145kDa</u>
	<u>SF3B3</u>	<u>splicing factor 3b, subunit 3, 130kDa</u>
	<u>SFRS1</u>	<u>splicing factor, arginine/serine-rich 1</u>
	<u>SFRS2</u>	<u>splicing factor, arginine/serine-rich 2</u>
	<u>SFRS4</u>	<u>splicing factor, arginine/serine-rich 4</u>
	<u>SFRS5</u>	<u>splicing factor, arginine/serine-rich 5</u>
	<u>SFRS7</u>	<u>splicing factor, arginine/serine-rich 7, 35kDa</u>
	<u>SFRS9</u>	<u>splicing factor, arginine/serine-rich 9</u>
	<u>SART1</u>	<u>squamous cell carcinoma antigen recognized by T cells</u>
	<u>SMNDC1</u>	<u>survival motor neuron domain containing 1</u>
	<u>TCERG1</u>	<u>transcription elongation regulator 1</u>
	<u>TRA2A</u>	<u>transformer 2 alpha homolog (Drosophila)</u>
	<u>SFRS10</u>	<u>transformer 2 beta homolog (Drosophila)</u>
	<u>USP39</u>	<u>ubiquitin specific peptidase 39</u>
<u>Huntington's disease</u>	<u>ATP5G3</u>	<u>ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)</u>
	<u>BAX</u>	<u>BCL2-associated X protein</u>
	<u>CREBBP</u>	<u>CREB binding protein</u>
	<u>NDUFA1</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa</u>
	<u>NDUFA10</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa</u>
	<u>NDUFA2</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa</u>
	<u>NDUFA8</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa</u>
	<u>NDUFB10</u>	<u>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa</u>
	<u>NDUFS1</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS3</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS6</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS7</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)</u>

	<u>NDUFV1</u>	<u>NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa</u>
	<u>AP2A1</u>	<u>adaptor-related protein complex 2, alpha 1 subunit</u>
	<u>AP2A2</u>	<u>adaptor-related protein complex 2, alpha 2 subunit</u>
	<u>AP2M1</u>	<u>adaptor-related protein complex 2, mu 1 subunit</u>
	<u>CLTC</u>	<u>clathrin, heavy chain (Hc)</u>
	<u>CLTA</u>	<u>clathrin, light chain (Lca)</u>
	<u>CLTB</u>	<u>clathrin, light chain (Lcb)</u>
	<u>COX4I1</u>	<u>cytochrome c oxidase subunit IV isoform 1</u>
	<u>COX7B</u>	<u>cytochrome c oxidase subunit VIIb</u>
	<u>COX6B1</u>	<u>cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)</u>
	<u>CYC1</u>	<u>cytochrome c-1</u>
	<u>HDAC1</u>	<u>histone deacetylase 1</u>
	<u>HDAC2</u>	<u>histone deacetylase 2</u>
	<u>IFT57</u>	<u>intraflagellar transport 57 homolog (Chlamydomonas)</u>
	<u>POLR2A</u>	<u>polymerase (RNA) II (DNA directed) polypeptide A, 220kDa</u>
	<u>POLR2B</u>	<u>polymerase (RNA) II (DNA directed) polypeptide B, 140kDa</u>
	<u>POLR2E</u>	<u>polymerase (RNA) II (DNA directed) polypeptide E, 25kDa</u>
	<u>POLR2F</u>	<u>polymerase (RNA) II (DNA directed) polypeptide F</u>
	<u>POLR2G</u>	<u>polymerase (RNA) II (DNA directed) polypeptide G</u>
	<u>POLR2H</u>	<u>polymerase (RNA) II (DNA directed) polypeptide H</u>
	<u>POLR2J</u>	<u>polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa</u>
	<u>NDUFS5</u>	<u>similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)</u>
	<u>SLC25A5</u>	<u>solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5; solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 pseudogene 8</u>
	<u>SDHA</u>	<u>succinate dehydrogenase complex, subunit A, flavoprotein (Fp)</u>
	<u>SDHB</u>	<u>succinate dehydrogenase complex, subunit B, iron sulfur (Ip)</u>
	<u>SOD1</u>	<u>superoxide dismutase 1, soluble</u>
	<u>UCRC</u>	<u>ubiquinol-cytochrome c reductase complex (7.2 kD)</u>
	<u>UQCRC1</u>	<u>ubiquinol-cytochrome c reductase core protein I</u>
	<u>UQCRC2</u>	<u>ubiquinol-cytochrome c reductase core protein II</u>
	<u>VDAC3</u>	<u>voltage-dependent anion channel 3</u>
<u>DNA replication</u>	<u>MCM2</u>	<u>minichromosome maintenance complex component 2</u>
	<u>MCM3</u>	<u>minichromosome maintenance complex component 3</u>
	<u>MCM4</u>	<u>minichromosome maintenance complex component 4</u>

	<u>MCM5</u>	<u>minichromosome maintenance complex component 5</u>
	<u>MCM6</u>	<u>minichromosome maintenance complex component 6</u>
	<u>MCM7</u>	<u>minichromosome maintenance complex component 7</u>
	<u>POLD1</u>	<u>polymerase (DNA directed), delta 1, catalytic subunit 125kDa</u>
	<u>POLD2</u>	<u>polymerase (DNA directed), delta 2, regulatory subunit 50kDa</u>
	<u>POLE</u>	<u>polymerase (DNA directed), epsilon</u>
	<u>POLE3</u>	<u>polymerase (DNA directed), epsilon 3 (p17 subunit)</u>
	<u>PCNA</u>	<u>proliferating cell nuclear antigen</u>
	<u>RFC2</u>	<u>replication factor C (activator 1) 2, 40kDa</u>
	<u>RFC5</u>	<u>replication factor C (activator 1) 5, 36.5kDa</u>
	<u>RPA1</u>	<u>replication protein A1, 70kDa</u>
	<u>RPA2</u>	<u>replication protein A2, 32kDa</u>
	<u>RNASEH2A</u>	<u>ribonuclease H2, subunit A</u>
<u>Proteasome</u>	<u>PSMC3</u>	<u>proteasome (prosome, macropain) 26S subunit, ATPase, 3</u>
	<u>PSMD1</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 1</u>
	<u>PSMD11</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 11</u>
	<u>PSMD13</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 13</u>
	<u>PSMD14</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 14</u>
	<u>PSMD3</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 3</u>
	<u>PSMD7</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 7</u>
	<u>PSMD8</u>	<u>proteasome (prosome, macropain) 26S subunit, non-ATPase, 8</u>
	<u>PSME3</u>	<u>proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)</u>
	<u>PSMA1</u>	<u>proteasome (prosome, macropain) subunit, alpha type, 1</u>
	<u>PSMA5</u>	<u>proteasome (prosome, macropain) subunit, alpha type, 5</u>
	<u>PSMA7</u>	<u>proteasome (prosome, macropain) subunit, alpha type, 7</u>
	<u>PSMB1</u>	<u>proteasome (prosome, macropain) subunit, beta type, 1</u>
	<u>PSMB2</u>	<u>proteasome (prosome, macropain) subunit, beta type, 2</u>
	<u>PSMB4</u>	<u>proteasome (prosome, macropain) subunit, beta type, 4</u>
	<u>PSMB6</u>	<u>proteasome (prosome, macropain) subunit, beta type, 6</u>
	<u>PSMB7</u>	<u>proteasome (prosome, macropain) subunit, beta type, 7</u>
	<u>PSMC4</u>	<u>similar to 26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7); proteasome (prosome, macropain) 26S subunit, ATPase, 4</u>
<u>Pyrimidine metabolism</u>	<u>ITPA</u>	<u>inosine triphosphatase (nucleoside triphosphate pyrophosphatase)</u>

	<u>NME1-NME2</u>	<u>non-metastatic cells 1, protein (NM23A) expressed in; NME1-NME2 readthrough transcript; non-metastatic cells 2, protein (NM23B) expressed in</u>
	<u>NME3</u>	<u>non-metastatic cells 3, protein expressed in</u>
	<u>NP</u>	<u>nucleoside phosphorylase</u>
	<u>POLD1</u>	<u>polymerase (DNA directed), delta 1, catalytic subunit 125kDa</u>
	<u>POLD2</u>	<u>polymerase (DNA directed), delta 2, regulatory subunit 50kDa</u>
	<u>POLE</u>	<u>polymerase (DNA directed), epsilon</u>
	<u>POLE3</u>	<u>polymerase (DNA directed), epsilon 3 (p17 subunit)</u>
	<u>POLR1A</u>	<u>polymerase (RNA) I polypeptide A, 194kDa</u>
	<u>POLR1C</u>	<u>polymerase (RNA) I polypeptide C, 30kDa</u>
	<u>POLR2A</u>	<u>polymerase (RNA) II (DNA directed) polypeptide A, 220kDa</u>
	<u>POLR2B</u>	<u>polymerase (RNA) II (DNA directed) polypeptide B, 140kDa</u>
	<u>POLR2E</u>	<u>polymerase (RNA) II (DNA directed) polypeptide E, 25kDa</u>
	<u>POLR2F</u>	<u>polymerase (RNA) II (DNA directed) polypeptide F</u>
	<u>POLR2G</u>	<u>polymerase (RNA) II (DNA directed) polypeptide G</u>
	<u>POLR2H</u>	<u>polymerase (RNA) II (DNA directed) polypeptide H</u>
	<u>POLR2J</u>	<u>polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa</u>
	<u>POLR3A</u>	<u>polymerase (RNA) III (DNA directed) polypeptide A, 155kDa</u>
	<u>POLR3H</u>	<u>polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)</u>
	<u>POLR3K</u>	<u>polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa</u>
	<u>TXNRD2</u>	<u>thioredoxin reductase 2</u>
	<u>TK1</u>	<u>thymidine kinase 1, soluble</u>
	<u>TYMS</u>	<u>thymidylate synthetase</u>
	<u>UMPS</u>	<u>uridine monophosphate synthetase</u>
	<u>UCK2</u>	<u>uridine-cytidine kinase 2</u>
<u>RNA polymerase</u>	<u>POLR1A</u>	<u>polymerase (RNA) I polypeptide A, 194kDa</u>
	<u>POLR1C</u>	<u>polymerase (RNA) I polypeptide C, 30kDa</u>
	<u>POLR2A</u>	<u>polymerase (RNA) II (DNA directed) polypeptide A, 220kDa</u>
	<u>POLR2B</u>	<u>polymerase (RNA) II (DNA directed) polypeptide B, 140kDa</u>
	<u>POLR2E</u>	<u>polymerase (RNA) II (DNA directed) polypeptide E, 25kDa</u>
	<u>POLR2F</u>	<u>polymerase (RNA) II (DNA directed) polypeptide F</u>
	<u>POLR2G</u>	<u>polymerase (RNA) II (DNA directed) polypeptide G</u>
	<u>POLR2H</u>	<u>polymerase (RNA) II (DNA directed) polypeptide H</u>
	<u>POLR2J</u>	<u>polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa</u>

<u>Cell cycle</u>	<u>POLR3A</u>	<u>polymerase (RNA) III (DNA directed) polypeptide A, 155kDa</u>
	<u>POLR3H</u>	<u>polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)</u>
	<u>POLR3K</u>	<u>polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa</u>
	<u>CDC45L</u>	<u>CDC45 cell division cycle 45-like (S. cerevisiae)</u>
	<u>CREBBP</u>	<u>CREB binding protein</u>
	<u>E2F1</u>	<u>E2F transcription factor 1</u>
	<u>RAD21</u>	<u>RAD21 homolog (S. pombe)</u>
	<u>ANAPC5</u>	<u>anaphase promoting complex subunit 5</u>
	<u>BUB3</u>	<u>budding uninhibited by benzimidazoles 3 homolog (yeast)</u>
	<u>CDC25A</u>	<u>cell division cycle 25 homolog A (S. pombe)</u>
	<u>CCNA2</u>	<u>cyclin A2</u>
	<u>CCNB1</u>	<u>cyclin B1</u>
	<u>CCNB2</u>	<u>cyclin B2</u>
	<u>CDK4</u>	<u>cyclin-dependent kinase 4</u>
	<u>CDKN2A</u>	<u>cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)</u>
	<u>HDAC1</u>	<u>histone deacetylase 1</u>
	<u>HDAC2</u>	<u>histone deacetylase 2</u>
	<u>MCM2</u>	<u>minichromosome maintenance complex component 2</u>
	<u>MCM3</u>	<u>minichromosome maintenance complex component 3</u>
	<u>MCM4</u>	<u>minichromosome maintenance complex component 4</u>
	<u>MCM5</u>	<u>minichromosome maintenance complex component 5</u>
	<u>MCM6</u>	<u>minichromosome maintenance complex component 6</u>
	<u>MCM7</u>	<u>minichromosome maintenance complex component 7</u>
	<u>PLK1</u>	<u>polo-like kinase 1 (Drosophila)</u>
	<u>PCNA</u>	<u>proliferating cell nuclear antigen</u>
	<u>RBX1</u>	<u>ring-box 1</u>
	<u>SMC1A</u>	<u>structural maintenance of chromosomes 1A</u>
	<u>TGFB1</u>	<u>transforming growth factor, beta 1</u>
<u>Parkinson's disease</u>	<u>ATP5G3</u>	<u>ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)</u>
	<u>NDUFA1</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa</u>
	<u>NDUFA10</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa</u>
	<u>NDUFA2</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa</u>

	<u>NDUFA8</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa</u>
	<u>NDUFB10</u>	<u>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa</u>
	<u>NDUFS1</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS3</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS6</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS7</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFV1</u>	<u>NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa</u>
	<u>PARK7</u>	<u>Parkinson disease (autosomal recessive, early onset) 7</u>
	<u>COX4I1</u>	<u>cytochrome c oxidase subunit IV isoform 1</u>
	<u>COX7B</u>	<u>cytochrome c oxidase subunit VIIb</u>
	<u>COX6B1</u>	<u>cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)</u>
	<u>CYC1</u>	<u>cytochrome c-1</u>
	<u>NDUFS5</u>	<u>similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)</u>
	<u>SLC25A5</u>	<u>solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5; solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 pseudogene 8</u>
	<u>SDHA</u>	<u>succinate dehydrogenase complex, subunit A, flavoprotein (Fp)</u>
	<u>SDHB</u>	<u>succinate dehydrogenase complex, subunit B, iron sulfur (Ip)</u>
	<u>UCRC</u>	<u>ubiquinol-cytochrome c reductase complex (7.2 kD)</u>
	<u>UQCRC1</u>	<u>ubiquinol-cytochrome c reductase core protein I</u>
	<u>UQCRC2</u>	<u>ubiquinol-cytochrome c reductase core protein II</u>
	<u>UCHL1</u>	<u>ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)</u>
	<u>UBE2G1</u>	<u>ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)</u>
	<u>UBE2G2</u>	<u>ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)</u>
	<u>VDAC3</u>	<u>voltage-dependent anion channel 3</u>
<u>Purine metabolism</u>	<u>ATIC</u>	<u>5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase</u>
	<u>IMPDH2</u>	<u>IMP (inosine monophosphate) dehydrogenase 2</u>
	<u>APRT</u>	<u>adenine phosphoribosyltransferase</u>
	<u>AK2</u>	<u>adenylate kinase 2</u>
	<u>HPRT1</u>	<u>hypoxanthine phosphoribosyltransferase 1</u>
	<u>ITPA</u>	<u>inosine triphosphatase (nucleoside triphosphate pyrophosphatase)</u>

	<u>NME1-NME2</u>	<u>non-metastatic cells 1, protein (NM23A) expressed in; NME1-NME2 readthrough transcript; non-metastatic cells 2, protein (NM23B) expressed in</u>
	<u>NME3</u>	<u>non-metastatic cells 3, protein expressed in</u>
	<u>NP</u>	<u>nucleoside phosphorylase</u>
	<u>NUDT5</u>	<u>nudix (nucleoside diphosphate linked moiety X)-type motif 5</u>
	<u>PRPS1</u>	<u>phosphoribosyl pyrophosphate synthetase 1; phosphoribosyl pyrophosphate synthetase 1-like 1</u>
	<u>PAICS</u>	<u>phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase</u>
	<u>PFAS</u>	<u>phosphoribosylformylglycinamide synthase</u>
	<u>POLD1</u>	<u>polymerase (DNA directed), delta 1, catalytic subunit 125kDa</u>
	<u>POLD2</u>	<u>polymerase (DNA directed), delta 2, regulatory subunit 50kDa</u>
	<u>POLE</u>	<u>polymerase (DNA directed), epsilon</u>
	<u>POLE3</u>	<u>polymerase (DNA directed), epsilon 3 (p17 subunit)</u>
	<u>POLR1A</u>	<u>polymerase (RNA) I polypeptide A, 194kDa</u>
	<u>POLR1C</u>	<u>polymerase (RNA) I polypeptide C, 30kDa</u>
	<u>POLR2A</u>	<u>polymerase (RNA) II (DNA directed) polypeptide A, 220kDa</u>
	<u>POLR2B</u>	<u>polymerase (RNA) II (DNA directed) polypeptide B, 140kDa</u>
	<u>POLR2E</u>	<u>polymerase (RNA) II (DNA directed) polypeptide E, 25kDa</u>
	<u>POLR2F</u>	<u>polymerase (RNA) II (DNA directed) polypeptide F</u>
	<u>POLR2G</u>	<u>polymerase (RNA) II (DNA directed) polypeptide G</u>
	<u>POLR2H</u>	<u>polymerase (RNA) II (DNA directed) polypeptide H</u>
	<u>POLR2J</u>	<u>polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa</u>
	<u>POLR3A</u>	<u>polymerase (RNA) III (DNA directed) polypeptide A, 155kDa</u>
	<u>POLR3H</u>	<u>polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)</u>
	<u>POLR3K</u>	<u>polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa</u>
	<u>PKM2</u>	<u>similar to Pyruvate kinase, isozymes M1/M2 (Pyruvate kinase muscle isozyme) (Cytosolic thyroid hormone-binding protein) (CTHBP) (THBP1); pyruvate kinase, muscle</u>
<u>Aminoacyl-tRNA biosynthesis</u>	<u>AARS</u>	<u>alanyl-tRNA synthetase</u>
	<u>NARS</u>	<u>asparaginyl-tRNA synthetase</u>
	<u>DARS</u>	<u>aspartyl-tRNA synthetase</u>
	<u>CARS</u>	<u>cysteinyl-tRNA synthetase</u>
	<u>QARS</u>	<u>glutaminyl-tRNA synthetase</u>
	<u>GARS</u>	<u>glycyl-tRNA synthetase</u>
	<u>LARS</u>	<u>leucyl-tRNA synthetase</u>

	<u>LARS2</u>	<u>leucyl-tRNA synthetase 2, mitochondrial</u>
	<u>MARS</u>	<u>methionyl-tRNA synthetase</u>
	<u>FARSA</u>	<u>phenylalanyl-tRNA synthetase, alpha subunit</u>
	<u>FARSB</u>	<u>phenylalanyl-tRNA synthetase, beta subunit</u>
	<u>SARS</u>	<u>seryl-tRNA synthetase</u>
	<u>TARS</u>	<u>threonyl-tRNA synthetase</u>
	<u>YARS</u>	<u>tyrosyl-tRNA synthetase</u>
<u>Oxidative phosphorylation</u>	<u>ATP5G3</u>	<u>ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)</u>
	<u>ATP5I</u>	<u>ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E</u>
	<u>ATP6V1G1</u>	<u>ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1</u>
	<u>ATP6V1F</u>	<u>ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F</u>
	<u>ATP6V1E1</u>	<u>ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1</u>
	<u>NDUFA1</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa</u>
	<u>NDUFA10</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa</u>
	<u>NDUFA2</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa</u>
	<u>NDUFA8</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa</u>
	<u>NDUFB10</u>	<u>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa</u>
	<u>NDUFS1</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS3</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS6</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS7</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFV1</u>	<u>NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa</u>
	<u>COX4I1</u>	<u>cytochrome c oxidase subunit IV isoform 1</u>
	<u>COX7B</u>	<u>cytochrome c oxidase subunit VIIb</u>
	<u>COX6B1</u>	<u>cytochrome c oxidase subunit Vlb polypeptide 1 (ubiquitous)</u>
	<u>CYC1</u>	<u>cytochrome c-1</u>
	<u>NDUFS5</u>	<u>similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)</u>
	<u>SDHA</u>	<u>succinate dehydrogenase complex, subunit A, flavoprotein (Fp)</u>
	<u>SDHB</u>	<u>succinate dehydrogenase complex, subunit B, iron sulfur (Ip)</u>
	<u>UCRC</u>	<u>ubiquinol-cytochrome c reductase complex (7.2 kD)</u>

<u>Alzheimer's disease</u>	<u>UQCRC1</u>	<u>ubiquinol-cytochrome c reductase core protein I</u>
	<u>UQCRC2</u>	<u>ubiquinol-cytochrome c reductase core protein II</u>
	<u>ATP5G3</u>	<u>ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)</u>
	<u>NDUFA1</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa</u>
	<u>NDUFA10</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa</u>
	<u>NDUFA2</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa</u>
	<u>NDUFA8</u>	<u>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa</u>
	<u>NDUFB10</u>	<u>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa</u>
	<u>NDUFS1</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS3</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS6</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFS7</u>	<u>NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)</u>
	<u>NDUFV1</u>	<u>NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa</u>
	<u>APPBP1</u>	<u>NEDD8 activating enzyme E1 subunit 1</u>
	<u>APP</u>	<u>amyloid beta (A4) precursor protein</u>
	<u>APH1A</u>	<u>anterior pharynx defective 1 homolog A (C. elegans)</u>
	<u>CALM3</u>	<u>calmodulin 3 (phosphorylase kinase, delta); calmodulin 2 (phosphorylase kinase, delta); calmodulin 1 (phosphorylase kinase, delta)</u>
	<u>CAPN2</u>	<u>calpain 2, (m/II) large subunit</u>
	<u>COX4I1</u>	<u>cytochrome c oxidase subunit IV isoform 1</u>
	<u>COX7B</u>	<u>cytochrome c oxidase subunit VIIb</u>
	<u>COX6B1</u>	<u>cytochrome c oxidase subunit Vlb polypeptide 1 (ubiquitous)</u>
	<u>CYC1</u>	<u>cytochrome c-1</u>
	<u>HSD17B10</u>	<u>hydroxysteroid (17-beta) dehydrogenase 10</u>
	<u>MAPK1</u>	<u>mitogen-activated protein kinase 1</u>
	<u>NDUFS5</u>	<u>similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)</u>
	<u>SDHA</u>	<u>succinate dehydrogenase complex, subunit A, flavoprotein (Fp)</u>
	<u>SDHB</u>	<u>succinate dehydrogenase complex, subunit B, iron sulfur (Ip)</u>
	<u>UCRC</u>	<u>ubiquinol-cytochrome c reductase complex (7.2 kD)</u>
	<u>UQCRC1</u>	<u>ubiquinol-cytochrome c reductase core protein I</u>

	<u>UQCRC2</u>	<u>ubiquinol-cytochrome c reductase core protein II</u>
<u>Nucleotide excision repair</u>	<u>DDB1</u>	<u>damage-specific DNA binding protein 1, 127kDa</u>
	<u>POLD1</u>	<u>polymerase (DNA directed), delta 1, catalytic subunit 125kDa</u>
	<u>POLD2</u>	<u>polymerase (DNA directed), delta 2, regulatory subunit 50kDa</u>
	<u>POLE</u>	<u>polymerase (DNA directed), epsilon</u>
	<u>POLE3</u>	<u>polymerase (DNA directed), epsilon 3 (p17 subunit)</u>
	<u>PCNA</u>	<u>proliferating cell nuclear antigen</u>
	<u>RFC2</u>	<u>replication factor C (activator 1) 2, 40kDa</u>
	<u>RFC5</u>	<u>replication factor C (activator 1) 5, 36.5kDa</u>
	<u>RPA1</u>	<u>replication protein A1, 70kDa</u>
	<u>RPA2</u>	<u>replication protein A2, 32kDa</u>
	<u>RBX1</u>	<u>ring-box 1</u>
	<u>XPC</u>	<u>xeroderma pigmentosum, complementation group C</u>
<u>Mismatch repair</u>	<u>MSH6</u>	<u>mutS homolog 6 (E. coli)</u>
	<u>POLD1</u>	<u>polymerase (DNA directed), delta 1, catalytic subunit 125kDa</u>
	<u>POLD2</u>	<u>polymerase (DNA directed), delta 2, regulatory subunit 50kDa</u>
	<u>PCNA</u>	<u>proliferating cell nuclear antigen</u>
	<u>RFC2</u>	<u>replication factor C (activator 1) 2, 40kDa</u>
	<u>RFC5</u>	<u>replication factor C (activator 1) 5, 36.5kDa</u>
	<u>RPA1</u>	<u>replication protein A1, 70kDa</u>
	<u>RPA2</u>	<u>replication protein A2, 32kDa</u>
<u>Citrate cycle (TCA cycle)</u>	<u>ACLY</u>	<u>ATP citrate lyase</u>
	<u>IDH3A</u>	<u>isocitrate dehydrogenase 3 (NAD+) alpha</u>
	<u>IDH3B</u>	<u>isocitrate dehydrogenase 3 (NAD+) beta</u>
	<u>IDH3G</u>	<u>isocitrate dehydrogenase 3 (NAD+) gamma</u>
	<u>MDH2</u>	<u>malate dehydrogenase 2, NAD (mitochondrial)</u>
	<u>PDHA1</u>	<u>pyruvate dehydrogenase (lipoamide) alpha 1</u>
	<u>SDHA</u>	<u>succinate dehydrogenase complex, subunit A, flavoprotein (Fp)</u>
	<u>SDHB</u>	<u>succinate dehydrogenase complex, subunit B, iron sulfur (Ip)</u>
	<u>SUCLG1</u>	<u>succinate-CoA ligase, alpha subunit</u>

Figure S1. MA plots per condition comparison.

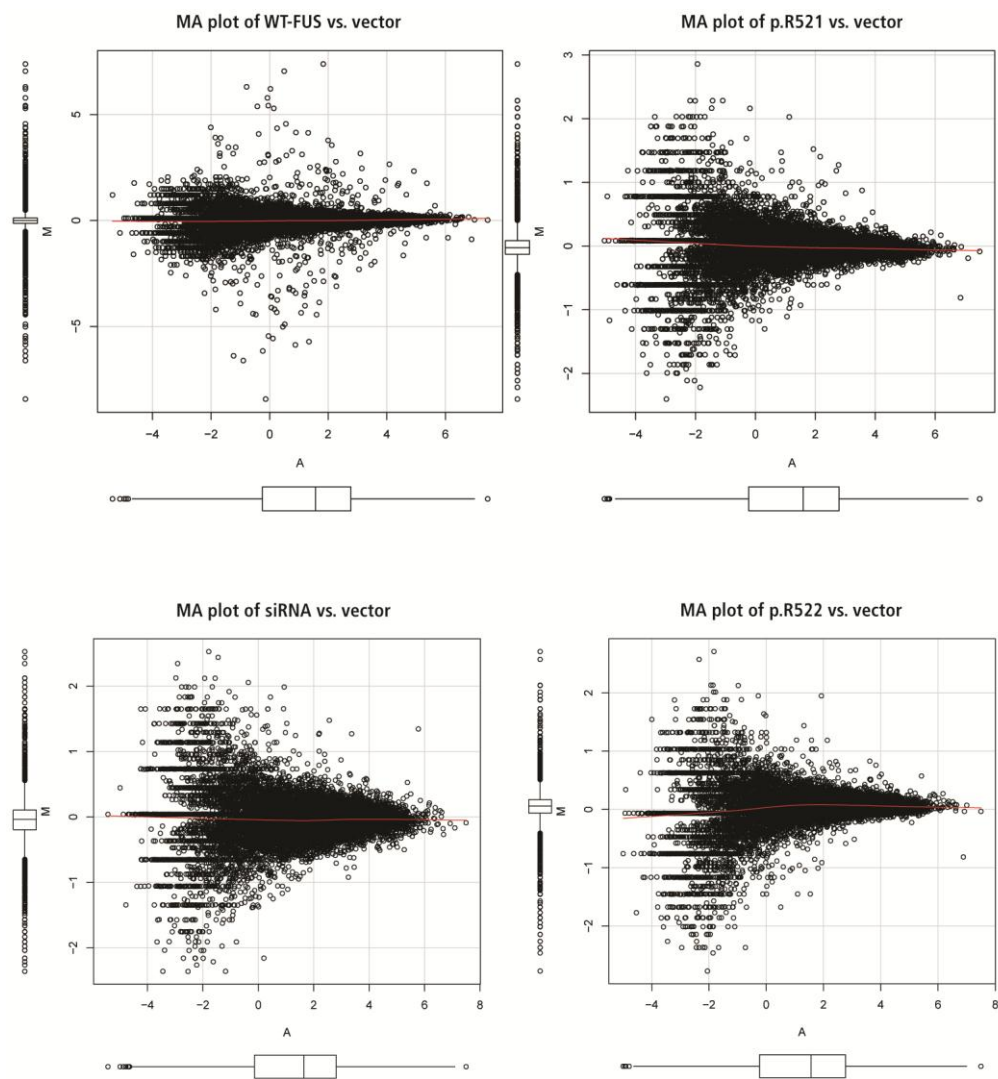


Figure S2. *FUS* gene expression levels measured by RNA-Seq.

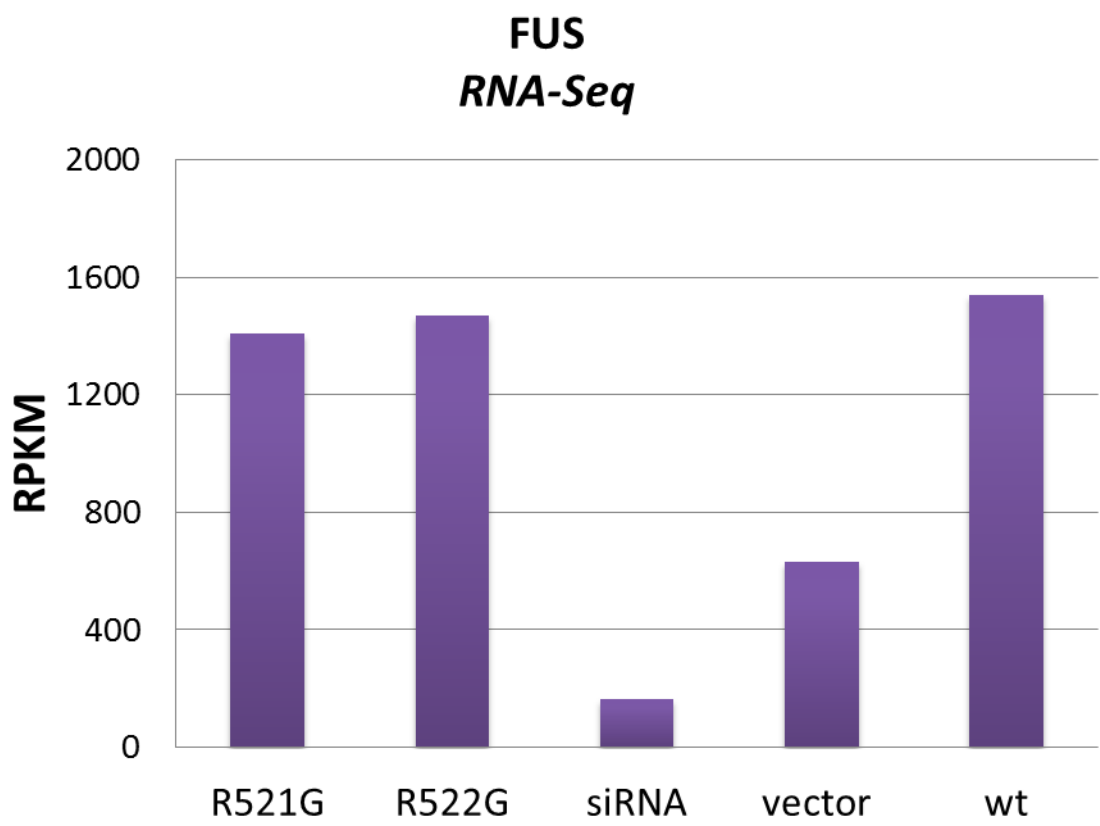


Figure S3. FUS protein levels measured by western blot.

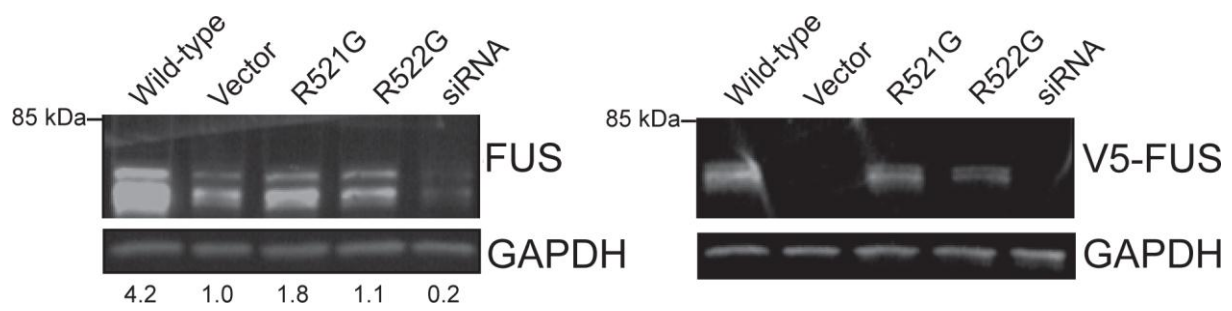


Figure S4. Correlation of RNA-Seq and RT-PCR for *RBM25*, *TAF15*, *TARS*, *TPR*, *APP* and *HN1*. Shown are the p-values for RNA-Seq and RT-PCR.

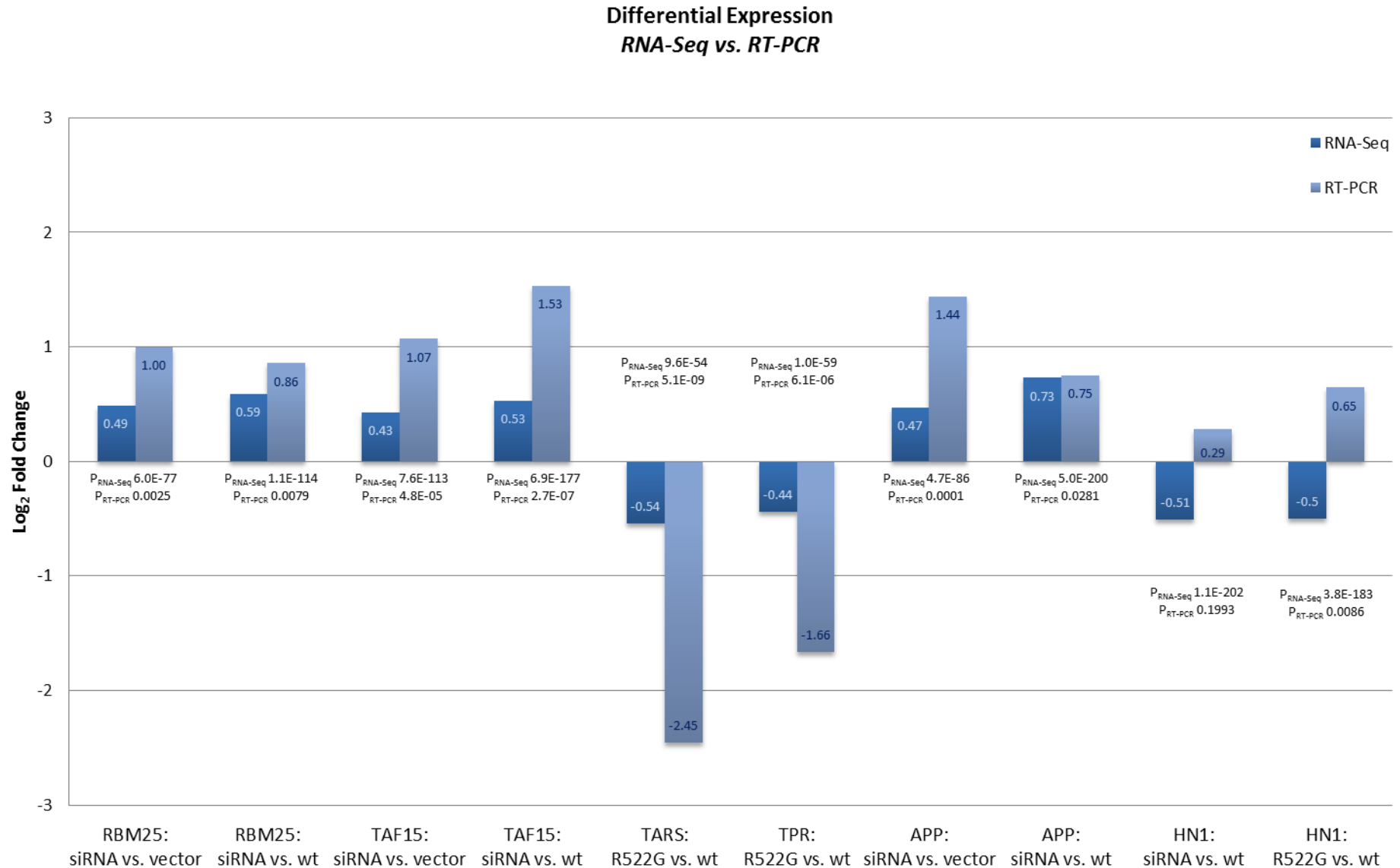


Figure S5. Correlation RNA-Seq and Semi-quantitative PCR for *PRPF8* and *RPS24*. Shown are the p-values for RNA-Seq and RT-PCR.

