## Supplementary Information

# Characterization of gene regulation and protein interaction networks for Matrin 3 encoding mutations linked to amyotrophic lateral sclerosis and myopathy

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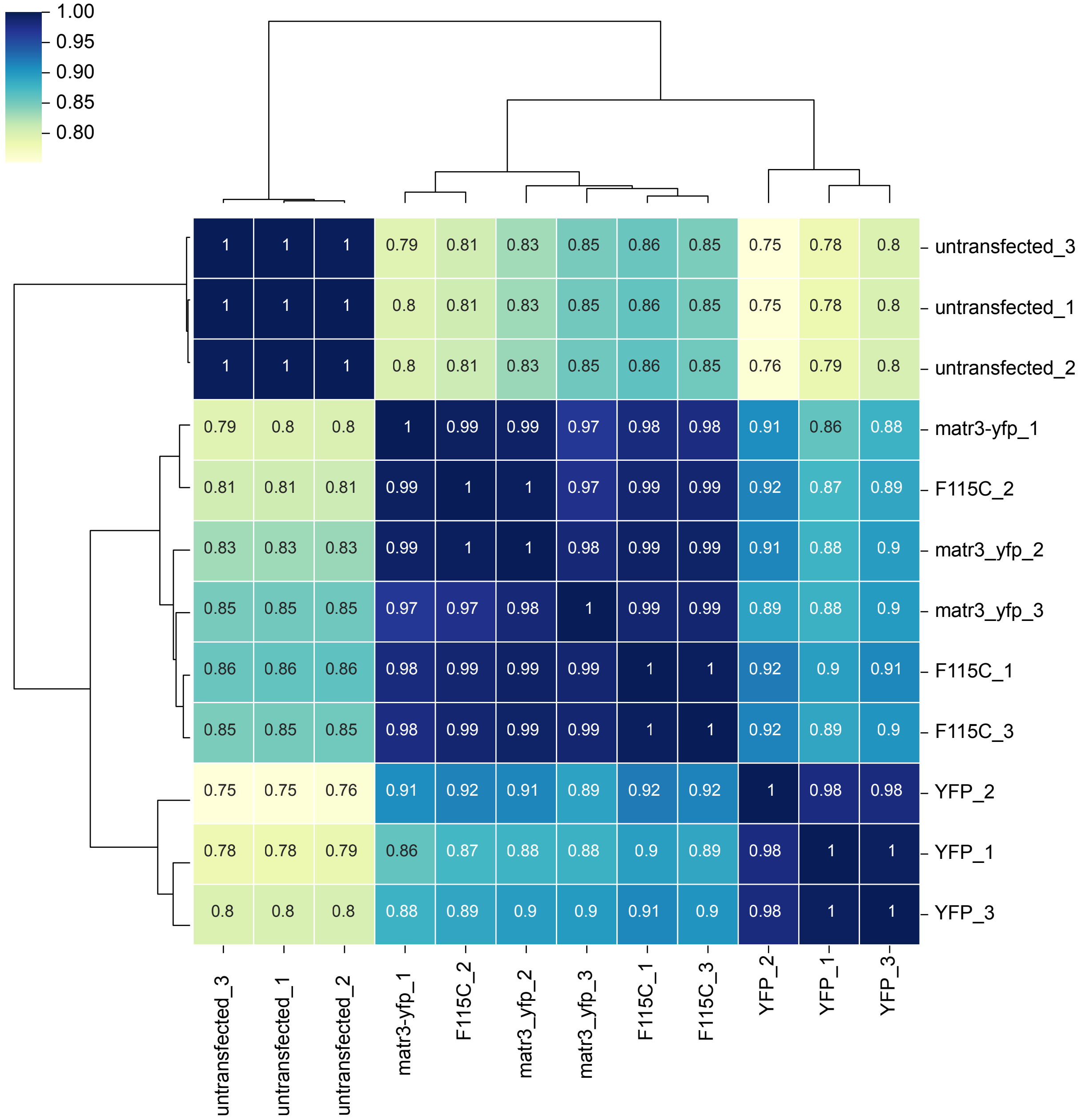
**Supplementary Figures S1 – S17**

**Supplementary Tables S2, S3, S4, S6, and S7.**

**Supplementary Tables S1 and S5 are provided as separate Excel Files**

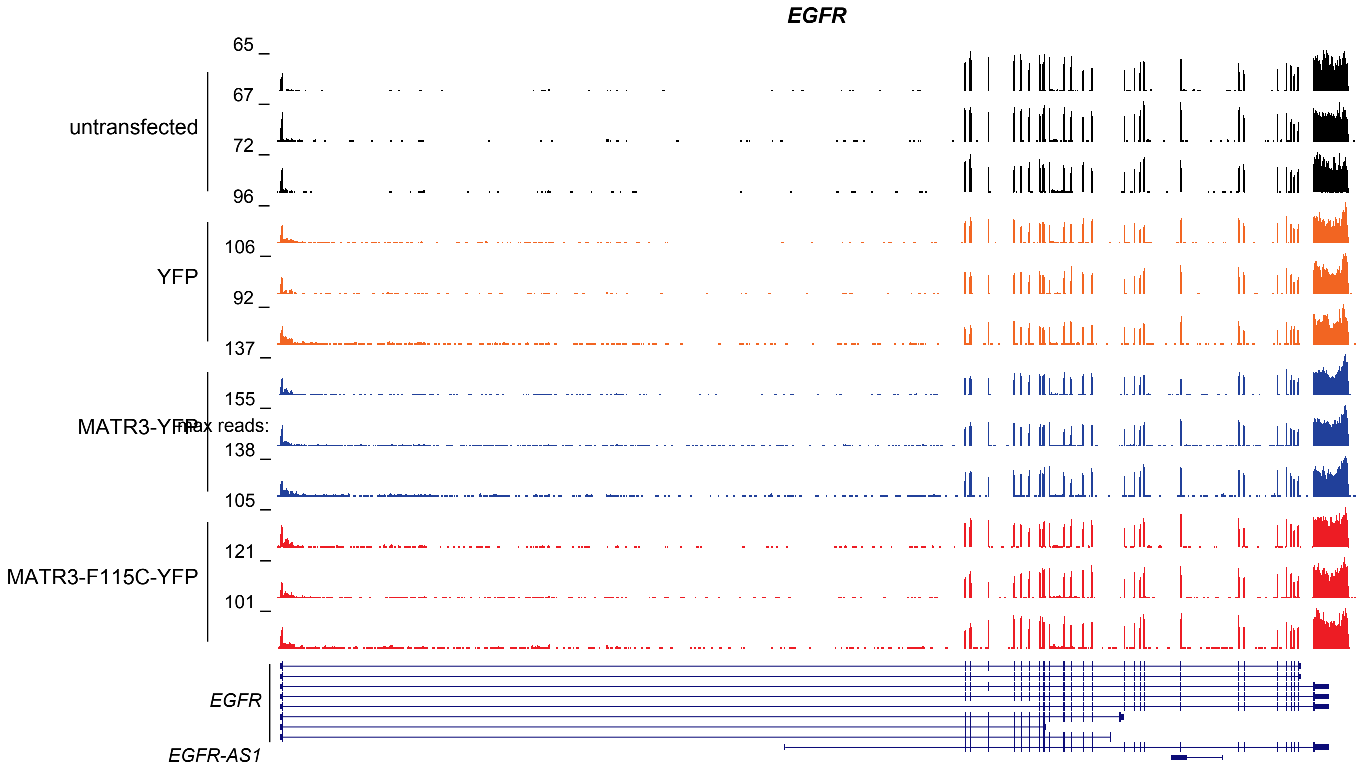
Supplemental Fig. S1



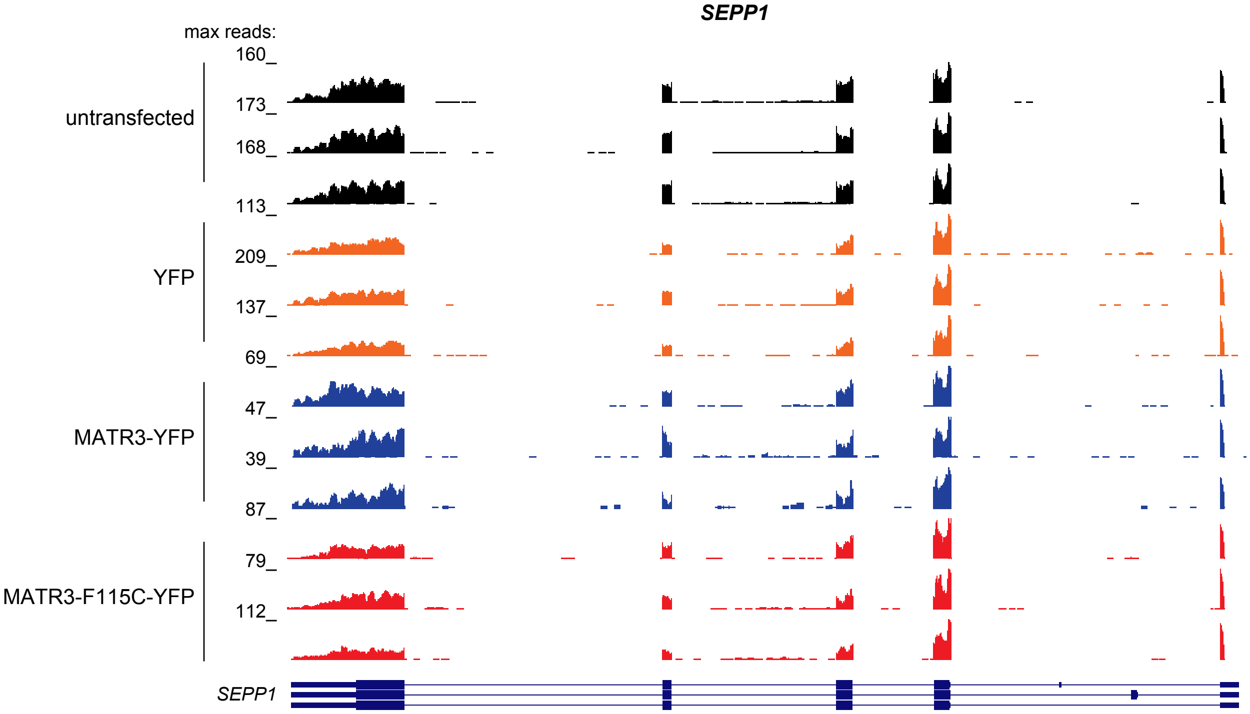
| | untransfected_3 | untransfected_1 | untransfected_2 | matr3-yfp_1 | F115C_2 | matr3_yfp_2 | matr3_yfp_3 | F115C_1 | F115C_3 | YFP_2 | YFP_1 | YFP_3 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| untransfected_3 | 1 | 1 | 1 | 0.79 | 0.81 | 0.83 | 0.85 | 0.86 | 0.85 | 0.75 | 0.78 | 0.8 |
| untransfected_1 | 1 | 1 | 1 | 0.8 | 0.81 | 0.83 | 0.85 | 0.86 | 0.85 | 0.75 | 0.78 | 0.8 |
| untransfected_2 | 1 | 1 | 1 | 0.8 | 0.81 | 0.83 | 0.85 | 0.86 | 0.85 | 0.76 | 0.79 | 0.8 |
| matr3-yfp_1 | 0.79 | 0.8 | 0.8 | 1 | 0.99 | 0.99 | 0.97 | 0.98 | 0.98 | 0.91 | 0.86 | 0.88 |
| F115C_2 | 0.81 | 0.81 | 0.81 | 0.99 | 1 | 1 | 0.97 | 0.99 | 0.99 | 0.92 | 0.87 | 0.89 |
| matr3_yfp_2 | 0.83 | 0.83 | 0.83 | 0.99 | 1 | 1 | 0.98 | 0.99 | 0.99 | 0.91 | 0.88 | 0.9 |
| matr3_yfp_3 | 0.85 | 0.85 | 0.85 | 0.97 | 0.97 | 0.98 | 1 | 0.99 | 0.99 | 0.89 | 0.88 | 0.9 |
| F115C_1 | 0.86 | 0.86 | 0.86 | 0.98 | 0.99 | 0.99 | 0.99 | 1 | 1 | 0.92 | 0.9 | 0.91 |
| F115C_3 | 0.85 | 0.85 | 0.85 | 0.98 | 0.99 | 0.99 | 0.99 | 1 | 1 | 0.92 | 0.89 | 0.9 |
| YFP_2 | 0.75 | 0.75 | 0.76 | 0.91 | 0.92 | 0.91 | 0.89 | 0.92 | 0.92 | 1 | 0.98 | 0.98 |
| YFP_1 | 0.78 | 0.78 | 0.79 | 0.86 | 0.87 | 0.88 | 0.88 | 0.9 | 0.89 | 0.98 | 1 | 1 |
| YFP_3 | 0.8 | 0.8 | 0.8 | 0.88 | 0.89 | 0.9 | 0.9 | 0.91 | 0.9 | 0.98 | 1 | 1 |

Supplemental Figure S1. Pearson coefficient analysis of RNAseq data.
To assess the variance in RNAseq data from the 3 replicate samples for each condition of transfection, we performed an unsupervised clustering of Pearson correlation values for all pair-wise comparsions.

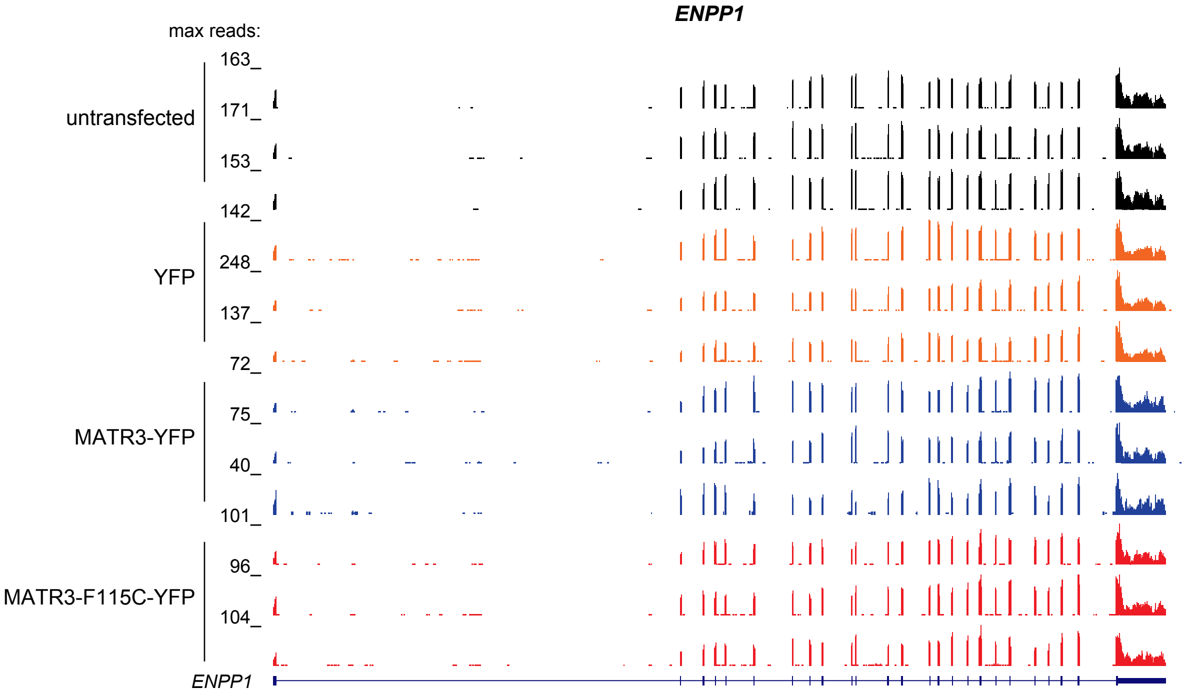
Supplemental Fig. S2



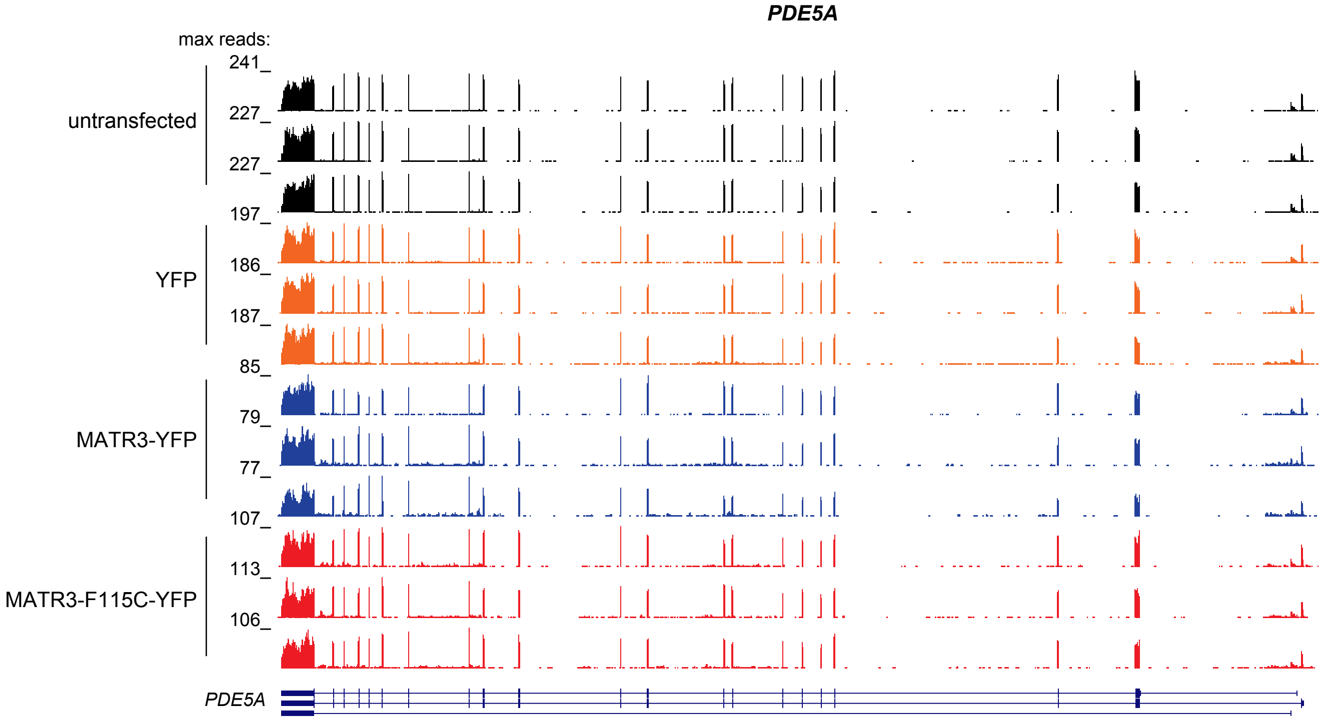
# Supplemental Fig. S3



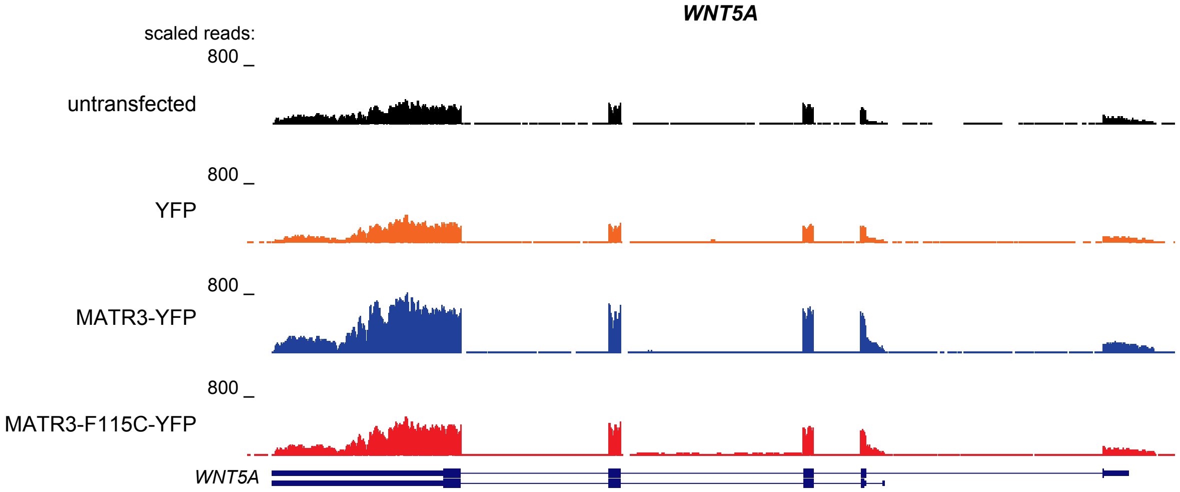
# Supplemental Fig. S4

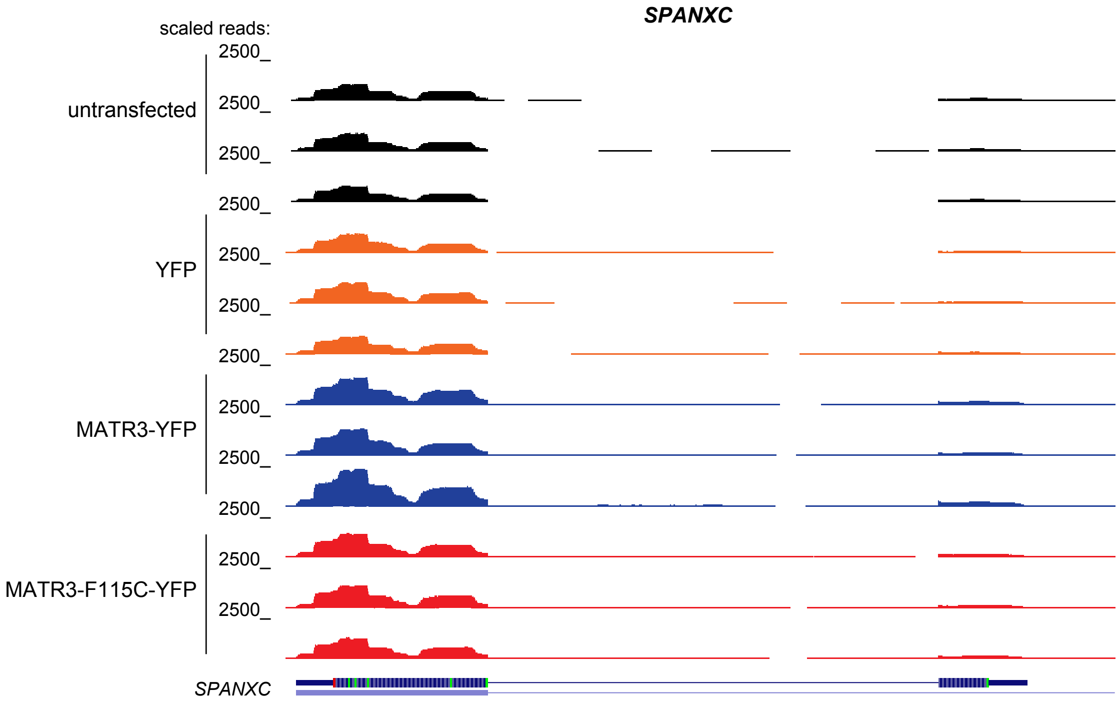


# Supplemental Fig. S5

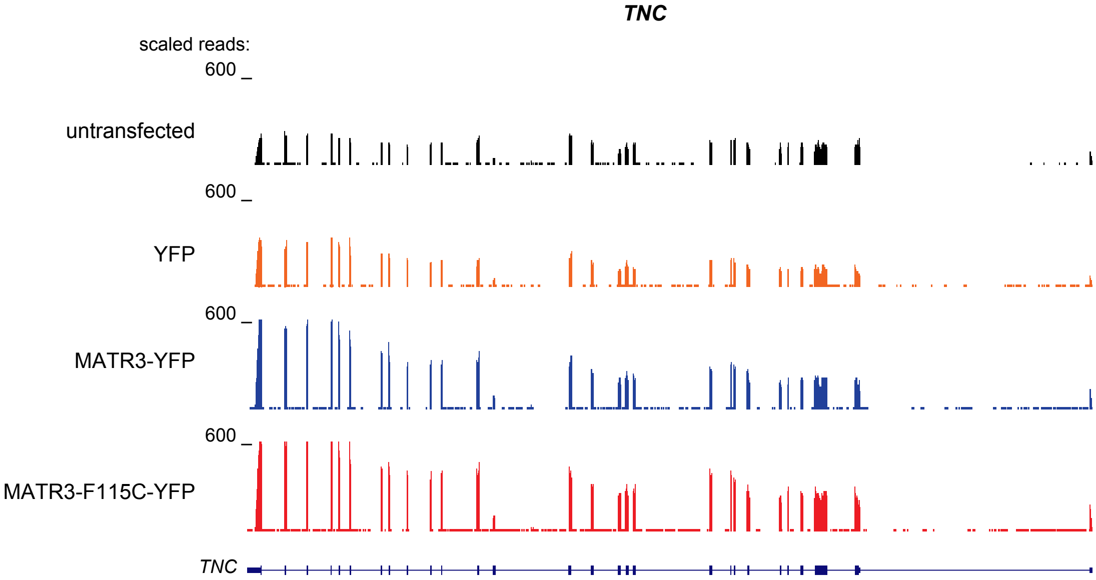


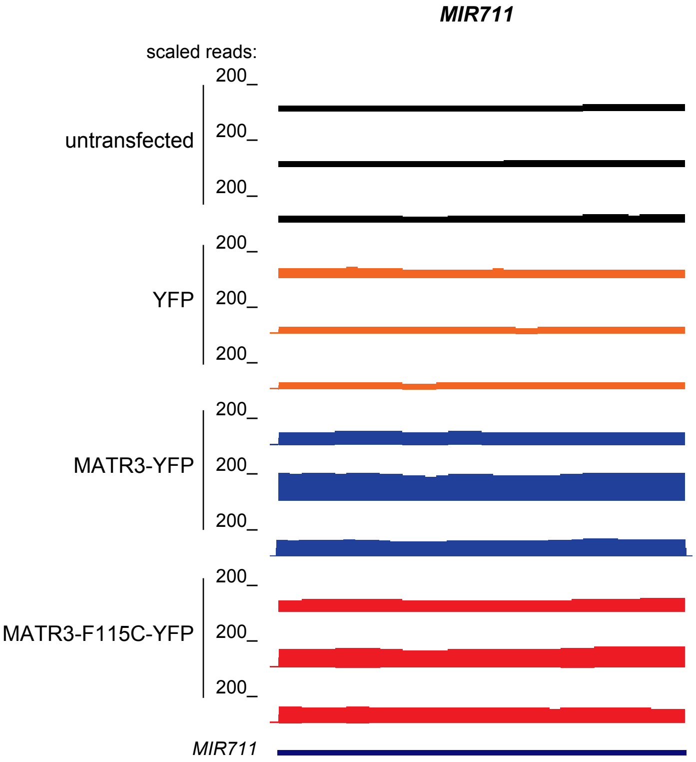
# Supplemental Fig. S6



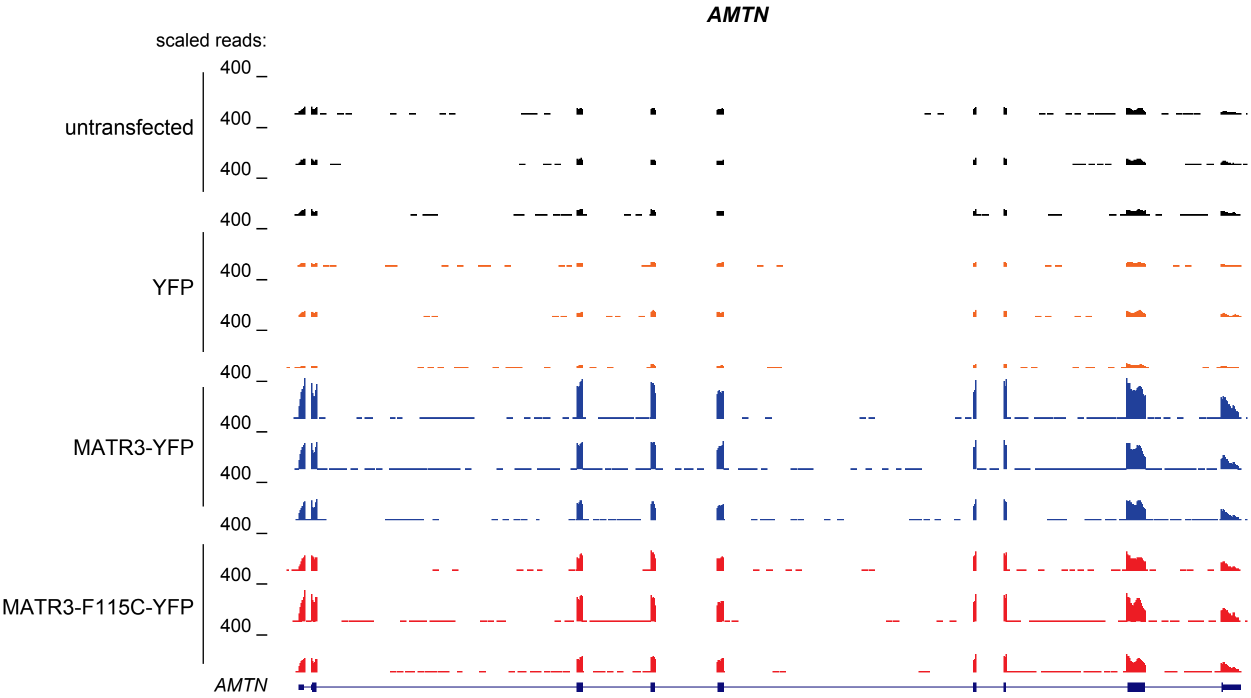

SPANXC
scaled reads:
2500_
2500_
2500_
2500_
2500_
2500_
2500_
2500_
2500_
2500_
2500_
2500_
untransfected
YFP
MATR3-YFP
MATR3-F115C-YFP
SPANXC

Supplemental Fig. S8

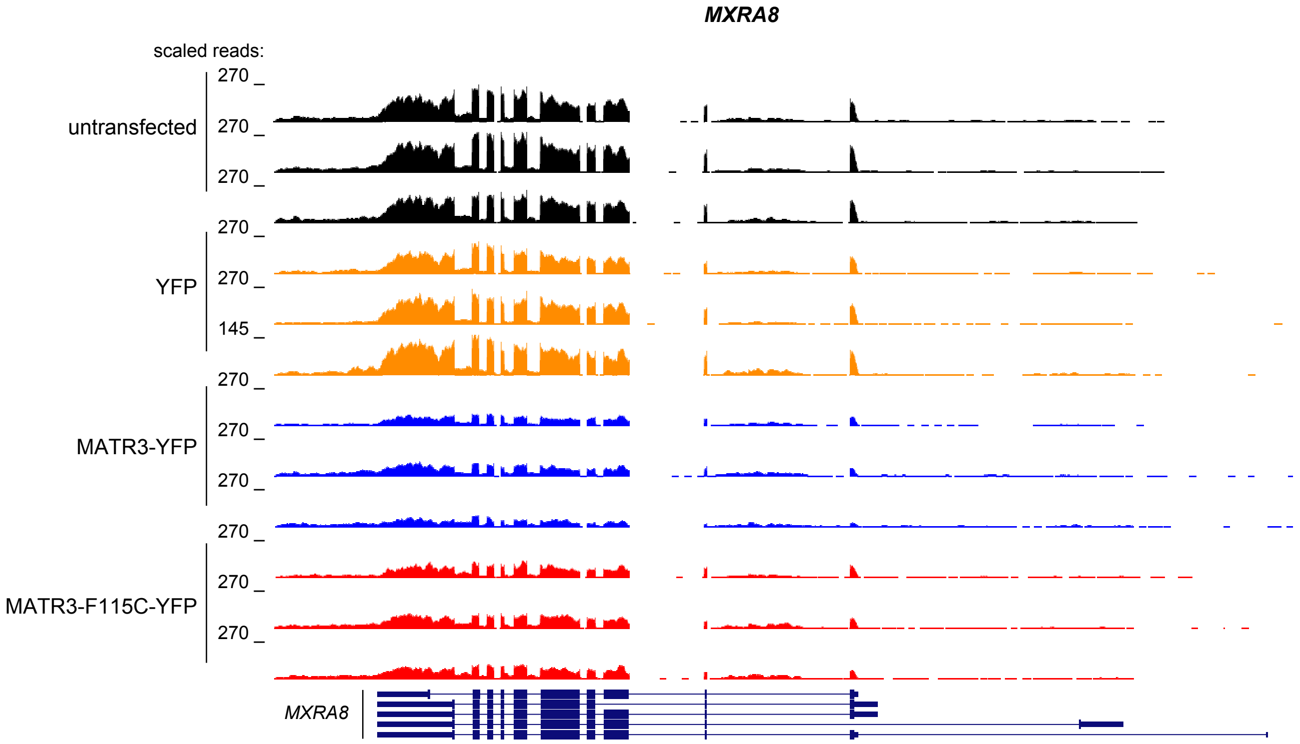



MIR711
scaled reads:
200_
untransfected
200_
200_
200_
YFP
200_
200_
200_
MATR3-YFP
200_
200_
200_
MATR3-F115C-YFP
200_
200_
MIR711

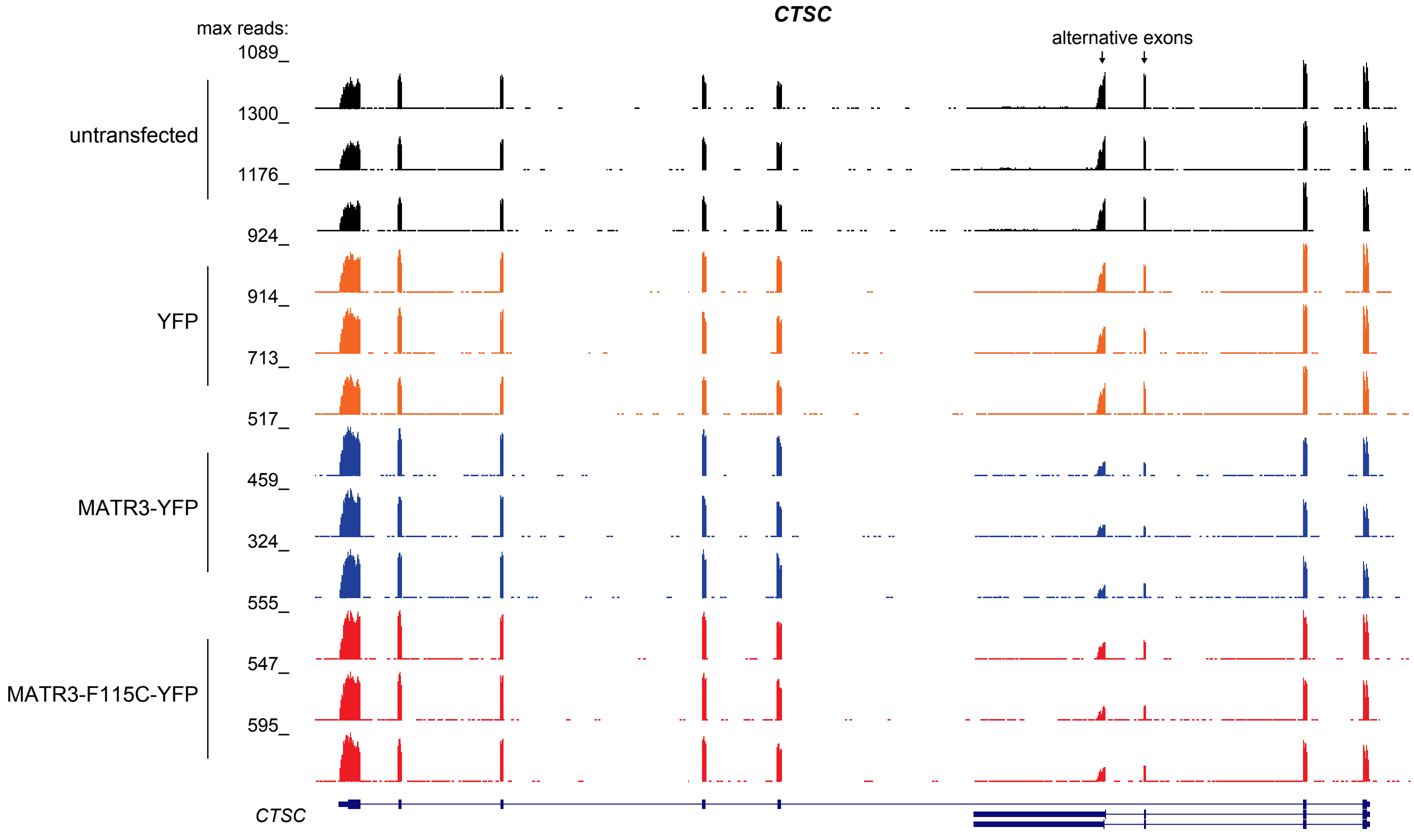
Supplemental Fig. S10



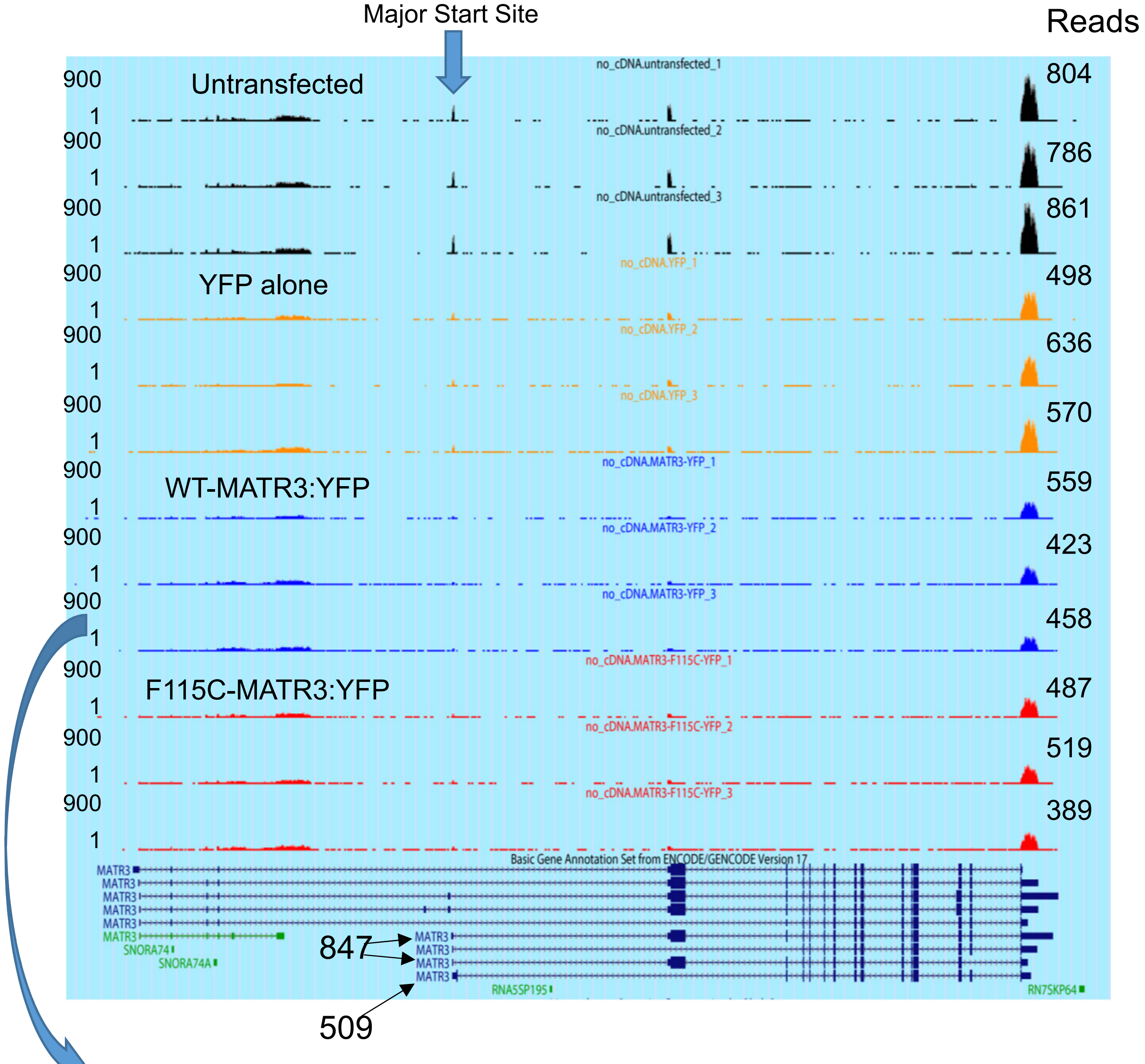
Supplemental Fig. S11



Supplemental Fig. S12



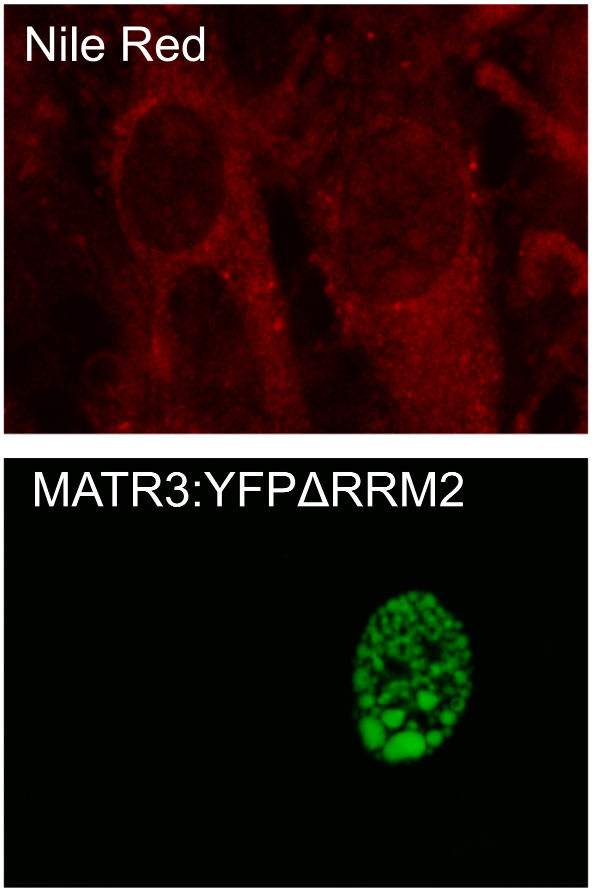
Endogenous MATR3 transcripts



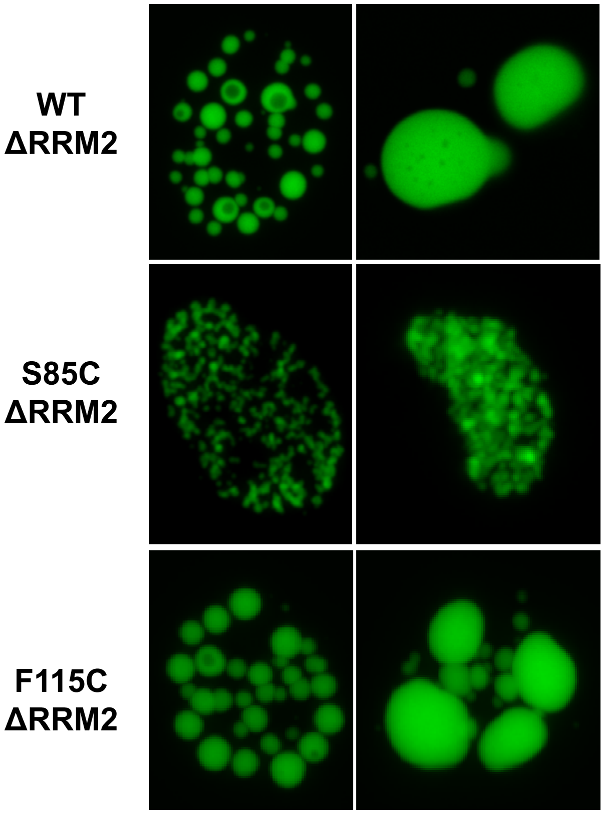
Sample with most reads for WT-MATR3:YFP

**Supplemental Fig S13. Image captured from Genome Browser that shows the read mapping with maximum RPKM for endogenous MATR3 after removal of the reads that would map to the coding exons that overlap with the cDNA for MATR3:YFP.**

Supplemental Fig. S14

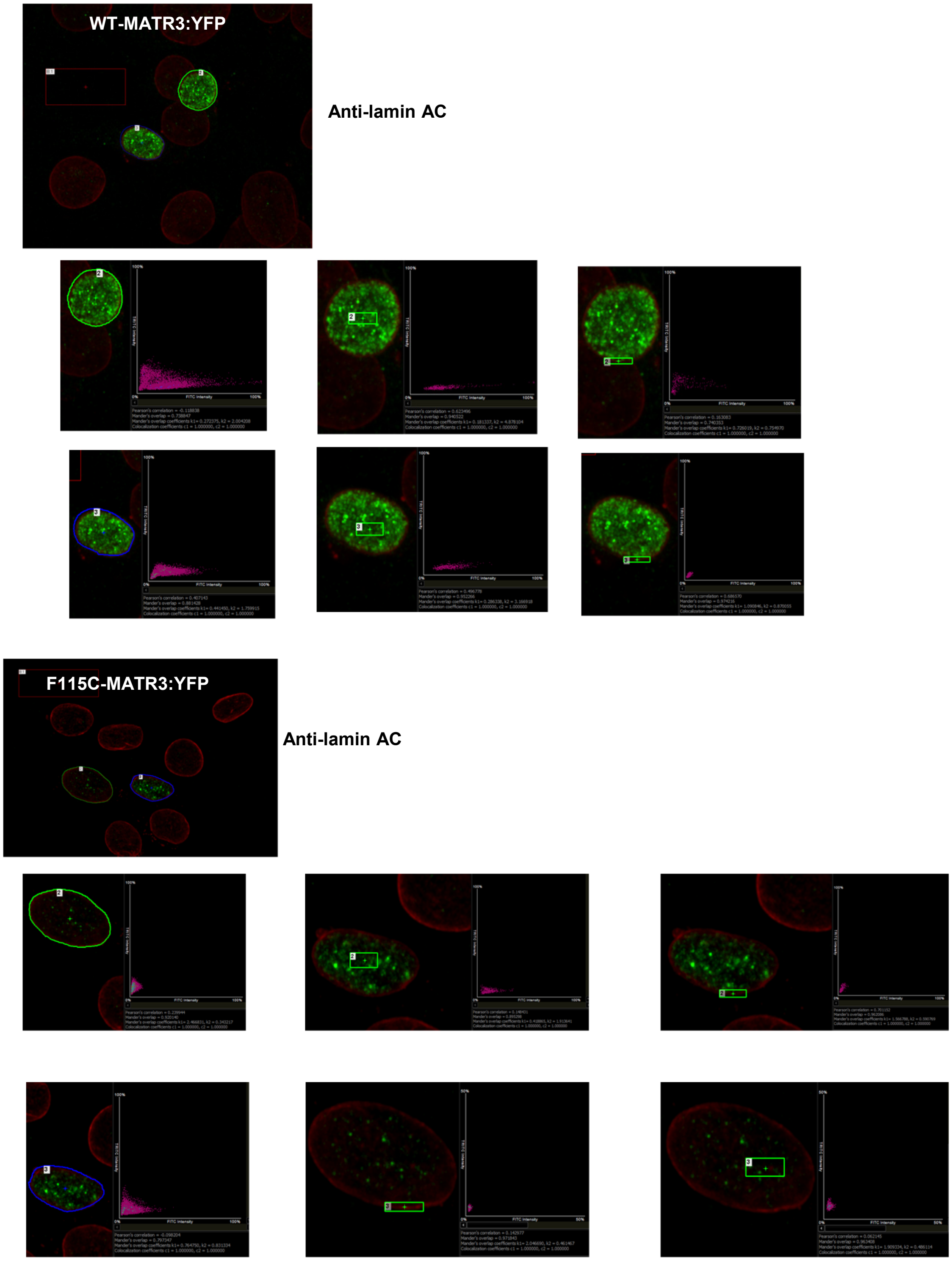


**Supplemental Figure S14. Representative example of cells stained with Nile Red.** C2C12 cells were transiently transfected with expression plasmids for MATR3:YFPΔRRM2 and then 24 hours later the cells were fixed in 4% paraformaldehyde for 10 minutes before washing in PBS. The cells were stained with Nile Red prepared by diluting a 1 mg/ml stock solution (in Acetone) 1 to 10,000 in PBS before applying to the cells for 5 minutes. After 2 washes in PBS, the cells were imaged on a Nikon Eclipse Ti-E Inverted Fluorescent fluorescence microscope image system as described in Methods at 40X magnification. The image shown is representative of what was observed in 2 independent transfection experiments, visualizing 20-50 cells in each experiment.



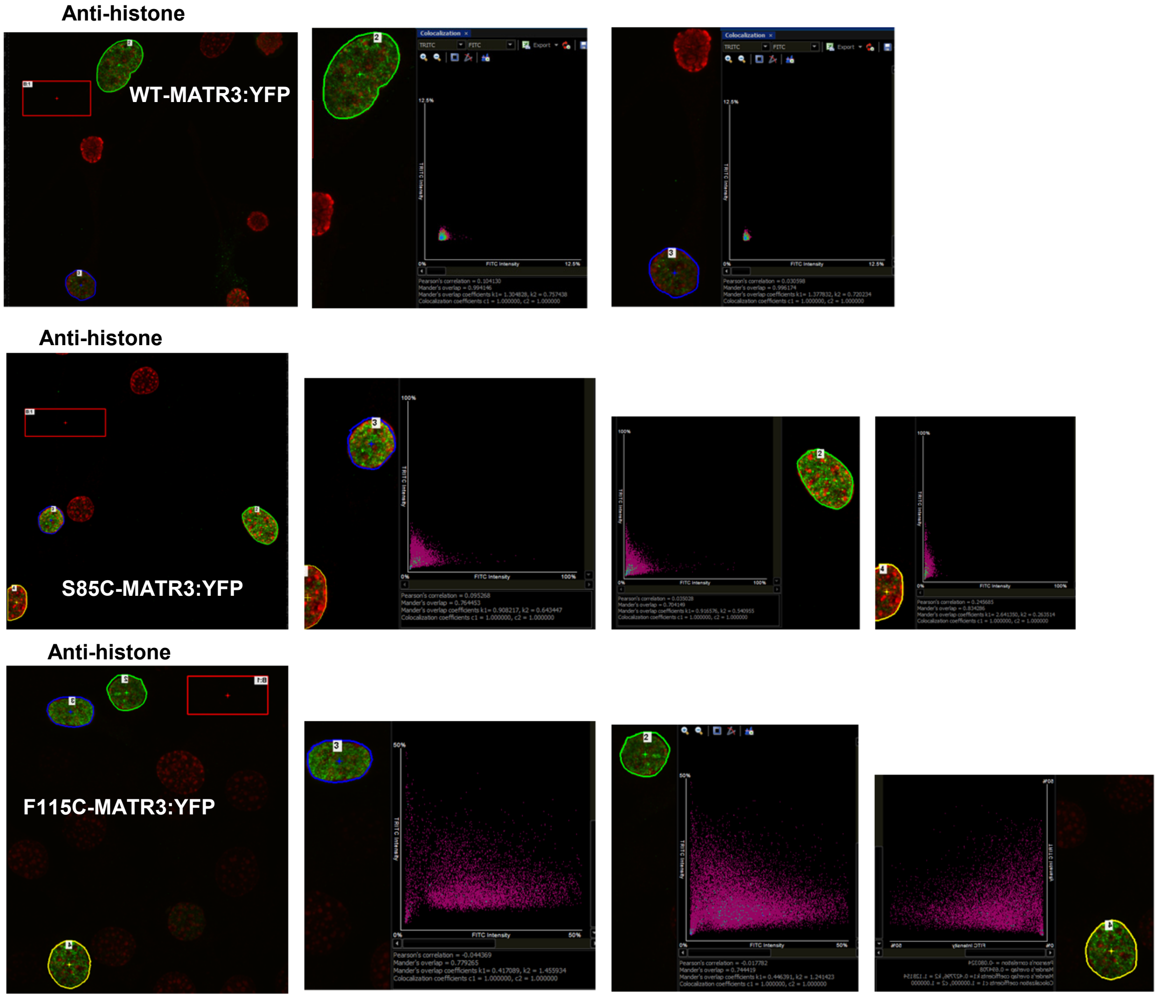
**Supplemental Figure S15. Disease mutations produce different effects on the formation of spheres by MATR3:YFPΔRRM2**. Representative images of C2C12 cells expressing WT, S85C, and F115C MATR3:YFPΔRRM2. The number of cells analyzed in 3 separate transfection experiments is provided in Table 2. In a single Z-plane, some spheres appear as ring-like structures, or contain a relatively large vacuole. Larger spheres contain small vacuoles, or bubbles. The original magnification of image capture was 60x, with some digital enlargement.

Supplemental Fig. S16



**Supplemental Figure S16. Analysis of MATR3:YFP co-localization with lamin A/C.** Representative images of C2C12 cells expressing WT and F115C MATR3:YFP co-stained with antibodies to lamin AC (red). The degree of fluorescence co-localization in a single Z-plane was assess using Nikon elements software. The original magnification of image capture was 60x, with some digital enlargement.

Supplemental Fig. S17



Pearson's correlation = 0.104130
Mander's overlap = 0.994146
Mander's overlap coefficients k1= 1.304828, k2 = 0.757438
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = 0.030598
Mander's overlap = 0.996174
Mander's overlap coefficients k1= 1.377832, k2 = 0.720234
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = 0.095268
Mander's overlap = 0.764453
Mander's overlap coefficients k1= 0.908217, k2 = 0.643447
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = 0.035028
Mander's overlap = 0.704149
Mander's overlap coefficients k1= 0.916576, k2 = 0.540955
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = 0.245685
Mander's overlap = 0.834286
Mander's overlap coefficients k1= 2.641350, k2 = 0.263514
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = -0.044369
Mander's overlap = 0.779265
Mander's overlap coefficients k1= 0.417089, k2 = 1.455934
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = -0.017782
Mander's overlap = 0.744419
Mander's overlap coefficients k1= 0.446391, k2 = 1.241423
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

Pearson's correlation = -0.080324
Mander's overlap = 0.694708
Mander's overlap coefficients k1= 0.427796, k2 = 1.128154
Colocalization coefficients c1 = 1.000000, c2 = 1.000000

**Supplemental Figure S17. Analysis of MATR3:YFP co-localization with histone.** Representative images of C2C12 cells expressing WT and F115C MATR3:YFP co-stained with antibodies to histone (red). The degree of fluorescence co-localization in a single Z-plane was assess using Nikon elements software. The original magnification of image capture was 60x, with some digital enlargement.

**Supplemental Table S2. Genes influenced by over-expression of MATR3:YFP**

| Gene Name | Log 2 fold change WT MATR3:YFP vs YFP | Fold change F115C MATR3:YFP vs YFP |
|---|---|---|
| *Genes induced by YFP expression with further induction by WT or F115C MATR3 expression* (log FC relative to untransfected) | | |
| ORM1 | 3.50 (6.49) | 2.48 |
| SERPINB2 | 3.23 (4.69) | 1.70 |
| FDCSP | 2.87 (7.12) | 2.22 |
| CSF2 | 2.59 (11.32) | 2.04 |
| SPRR2D | 2.32 (6.30) | 2.05 |
| EID3 | 2.30 (4.09) | 1.90 |
| OLR1 | 2.08 (3.93) | 1.68 |
| SAA1 | 1.96 (9.40) | 1.68 |
| TNFAIP6 | 1.95 (8.59) | 1.42 |
| TNFAIP2 | 1.91 (5.13) | 1.81 |
| C15orf48 | 1.87 (8.73) | 1.16 |
| SAA2 | 1.68 (10.51) | 1.56 |
| SERPINA1 | 1.63 (2.79) | 1.09 |
| CXCL11 | 1.63 (12.66) | 1.20 |
| CCL2 | 1.62 (7.03) | 1.40 |
| CX3CL1 | 1.54 (4.63) | 1.48 |
| SERPINE2 | 1.54 (2.43) | 1.15 |
| COL7A1 | 1.51 (2.03) | 1.36 |
| SLC2A6 | 1.45 (3.21) | 1.39 |
| IL8 | 1.42 (8.85) | 1.13 |
| IL32 | 1.41 (7.27) | 1.18 |
| IL6 | 1.28 (10.99) | 1.04 |
| TNFRSF9 | 1.26 (6.04) | 1.29 |
| DNER | 1.25 (2.02) | 0.90 |
| INHBA | 1.24 (6.43) | 0.84 |
| KLHDC7B | 1.23 (9.41) | 1.23 |
| CCL20 | 1.21 (10.64) | 0.98 |
| SPANXE | 1.16 (2.17) | 0.65 |
| ELF3 | 1.16 (1.88) | 1.14 |
| CXCL3 | 1.11 (8.99) | 1.02 |
| EDN1 | 1.07 (4.02) | 0.50 |
| C3 | 1.07 (4.04) | 1.18 |
| MT1X | 1.06 (2.26) | 0.60 |
| CCL3 | 1.04 (12.08) | N.S. |
| CXCL10 | 1.03 (11.68) | 0.99 |
| BIRC3 | 1.02 (3.65) | 0.91 |
| CD82 | 0.99 (3.65) | 0.64 |
| IL7R | 0.98 (1.92) | 0.74 |
| RAB27B* | -0.97 (2.43) | -0.83 |
| RARRES3* | -0.98 (1.90) | -0.92 |
| HIST1H2BC* | -0.99 (1.00) | N.S. |
| CTGF* | -1.01 (2.87) | -0.69 |
| CA9* | -1.02 (4.65) | -0.82 |
| TDO2* | -1.03 (2.78) | N.S. |
| IL1R1* | -1.06 (0.81) | -0.68 |
| VWA5A* | -1.08 (2.15) | -0.64 |
| LOX* | -1.08 (1.56) | -0.67 |
| LGALS9* | -1.09 (4.91) | -0.97 |
| TIMP3* | -1.18 (0.45) | -0.82 |
| A2M* | -1.18 (3.11) | -0.88 |
| TGFA* | -1.18 (0.88) | -0.93 |
| AGT* | -1.20 (2.42) | -0.96 |

| | | |
|---|---|---|
| TGM2* | -1.22 (1.38) | -1.06 |
| IFNB1* | -1.30 (9.44) | -0.91 |
| FOS* | -1.34 (4.36) | -0.72 |
| IL18BP* | -1.40 (2.18) | -1.30 |
| MGP* | -1.47 (0.73) | -1.33 |
| PLAT* | -1.73(2.5) | -1.33 |
| CD74* | -2.33(4.14) | -2.25 |
| Genes suppressed by YFP expression | | |
| HBE1 | 1.13 (0.53) | 0.98 |
| | | |
| *Genes suppressed by WT or F115C MATR3 Overexpression* | | |
| Genes induced by YFP expression | | |
| TRIB2 | -1.20 (-0.62) | -0.84 |
| Genes suppressed by YFP | | |
| UNC13D | -0.96 (-0.59) | 0.79 |
| CRISPLD1 | -0.96 (-3.38) | -0.45 |
| ARHGAP28 | -0.99 (-2.70) | N.S. |
| CAT | -1.00 (-1.55) | -0.72 |
| ENPP2 | -1.03 (-2.16) | N.S. |
| FLJ22447 | -1.07 (-1.54) | -0.61 |
| COLEC12 | -1.08 (-2.58) | -0.56 |
| EGLN3 | -1.14 (-1.97) | -0.73 |
| RASL11A | -1.23 (-3.96) | N.S. |
| PDGFRA | -1.35 (-1.73) | -0.92 |
| VAV3 | -1.39 (-2.26) | -1.93 |
| PI15 | -1.47 (-4.42) | -0.43 |
| AKAP6 | -1.57 (-2.84) | -0.89 |
| ITGA8 | -1.59 (-2.72) | -0.90 |
| PBX1 | -1.72 (-2.90) | -1.12 |
| CBLN2 | -2.20 (-4.88) | -1.40 |
| *Suppressed by WT and F115C MATR3 relative to YFP expressing cells but induced relative to untransfected cells. | | |

| **Supplemental Table S3. Non-coding RNA detected in RNA-seq dataset** | | |
|---|---|---|
| **Non coding RNAs** | **Untransfected vs YFP** | **Untransfected vs WT MATR3:YFP** |
| tRNAs | 1 | 1 |
| mt-tRNAs | 21 | 21 |
| rRNAs | 1 | 1 |
| miRNAs | 64 | 64 |
| Piwi RNAs | 0 | 0 |
| SCARNA | 23 | 23 |
| Small nucleolar RNAs (SNORD) | 189 | 191 |
| Small nucleolar RNAs (SNORA) | 76 | 76 |
| Long non coding RNAs | 105 | 105 |
| Linc RNAs | 0 | 0 |
| ERV | 4 | 4 |
| DNA transposon derived genes transposable | 21 | 21 |
| Gag like LTR retrotransposon | 55 | 55 |
| Competing endogenous long non coding RNAs (CERNA) | 8 | 8 |
| Transcribed pseudogenes | 10 | 10 |
| Pseudoautosomal region 1 | 20 | 20 |
| Non coding RNA Ro associated Y | 0 | 2 |
| Non coding RNA 7sl cytoplasmic (RN7SL) | 0 | 0 |
| Small nuclear RNAs non coding | 20 | 20 |
| Cytoplasmic transfer RNAs (TR) | 103 | 103 |
| Mitochondrially encoded tRNAs (MT-T) | 1 | 1 |
| Nuclear encoded mitochondrial tRNAs | 0 | 0 |
| Vault RNAs (VTRNA) | 6 | 6 |

## Supplemental Table S4. Proteins binding WT MATR3 and MATR3 deletion mutants.

| Protein (location/pathway) | MW kDa | RRM | PrLD | Avg # spectra control | Avg # spectra WT | Fold Change vs Control | p Value | Ratio ΔRRM1 vs WT | Ratio ΔRRM2 vs WT | Ratio ΔZnf1 vs WT | Ratio ΔZnf2 vs WT | SAINT Score | SAINT Fold Change |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MATR3 | 100 | 2 | LC | 5.4 | 375 | 69 | 0.02316 | - | - | - | - | - | - |
| **HNRNPM (N,No,I)** | 40 | 2 | LC | 4 | 157 | 40 | 0.03967 | 1.22 | 0.62 | 1.30 | 1.76 | 1 | 39.4 |
| SFRS14 (N,S) | 120 | other[†] | LC | 1* | 26 | 26 | 0.00018 | 0.32 | 0.38 | 0.32 | 0.76 | 1 | 262.5 |
| **PTBP3(N,S,SG)** | 57 | 4 | - | 1* | 25 | 25 | 0.00518 | 0.69 | 0.51 | 0.98 | 0.78 | 1 | 61.3 |
| M0QYT0 Unc | 36 | 1 | - | 1* | 24 | 24 | 0.00015 | 0.59 | 0.74 | 0.45 | 0.97 | 1 | 29.7 |
| **ADAR (N,P,SG)** | 138 | other[†] | - | 1* | 23 | 23 | 0.01720 | 0.13 | 0.38 | 0.05 | 0.40 | 1 | 55.6 |
| PRPF8 (N,No,S) | 274 | other[†] | - | 1 | 20 | 20 | 0.00693 | 0.28 | 2.60 | 0.15 | 1.15 | 1 | 20.0 |
| A0A024R8A7 Unc | 62 | other[†] | Y | 2 | 39 | 19 | 0.0000003 | 0.55 | 0.52 | 0.37 | 0.77 | 1 | 19.4 |
| **PTBP1 (N,S)** | 59 | 4 | - | 2.8 | 52 | 19 | 0.01502 | 0.90 | 2.32 | 1.23 | 1.45 | 1 | 18.7 |
| **ZNF326 (N,S)** | 66 | - | - | 1* | 18 | 18 | 0.000011 | 0.38 | 0.11 | 0.49 | 0.38 | 1 | 182.5 |
| PABPC1 (N,P,SG) | 71 | 4 | Y | 1.4 | 25 | 18 | 0.00599 | 0.58 | 0.80 | 0.62 | 1.32 | 1 | 17.9 |
| **ILF3 (N,No,I)** | 96 | other[†] | Y | 1.8 | 32 | 18 | 0.000001 | 0.61 | 1.03 | 0.53 | 1.16 | 1 | 17.8 |
| PABPC4 (N,P) | 70 | 4 | Y | 1* | 18 | 18 | 0.00002 | 0.48 | 0.51 | 0.34 | 0.90 | 1 | 44.4 |
| SNRNP200 (N,S) | 245 | other[†] | LC | 1* | 17 | 17 | 0.02466 | 0.24 | 3.15 | 0.07 | 1.03 | 1 | 20.6 |
| MYBBP1A (N,No,T) | 149 | - | LC | 1* | 16 | 16 | 0.00057 | 0.37 | 3.45 | 0.52 | 1.48 | 1 | 81.3 |
| B2R959 *HNRNPL sim* | 60 | 3 | LC | 2 | 31 | 16 | 0.00026 | 0.61 | 0.77 | 0.68 | 1.03 | 1 | 15.5 |
| **HNRNPA2B1 (N,P,SG)** | 37 | 2 | Y | 5.8 | 88 | 15 | 0.00826 | 0.62 | 1.79 | 1.09 | 0.94 | 1 | 15.1 |
| DHX30 (M,R,SG) | 134 | other[†] | - | 1* | 15 | 15 | 0.01069 | 0.13 | 0.77 | 0.20 | 0.40 | 1 | 150.0 |
| IGF2BP3 (N,P,SG) | 64 | 2 | - | 1* | 15 | 15 | 0.00005 | 0.28 | 1.45 | 0.17 | 0.41 | 1 | 72.5 |
| BCLAF1 (N,P) | 106 | - | LC | 1* | 14 | 14 | 0.000001 | 1.05 | 1.93 | 0.87 | 1.82 | 1 | 34.4 |
| **HNRNPA3 (N,S,SG)** | 40 | 2 | Y | 2.4 | 32 | 13 | 0.00003 | 0.63 | 1.41 | 0.86 | 1.69 | 1 | 13.3 |
| SYNCRIP (N,No,S,SG) | 70 | 3 | LC | 1.2 | 16 | 13 | 0.00022 | 0.22 | 1.31 | 0.60 | 0.63 | 1 | 13.3 |
| A0A024RC46 Unc | 34 | 2 | Y | 3.6 | 48 | 13 | 0.00114 | 0.48 | 2.58 | 0.95 | 1.47 | 1 | 13.3 |
| **HNRNPA1 (N,S,SG)** | 34 | 2 | Y | 4.4 | 57 | 13 | 0.00191 | 0.57 | 2.34 | 1.06 | 1.57 | 1 | 13.0 |
| MOV10 (SG) | 114 | other[†] | - | 1* | 13 | 13 | 0.01766 | 0.08 | 0.27 | 0.14 | 0.15 | 1 | 130.0 |
| ATAD3B (M) | 73 | - | LC | 1 | 13 | 13 | 0.01226 | 0.76 | 0.88 | 1.49 | 2.08 | 1 | 15.6 |
| **HNRNPUL1 (N,S,SG)** | 90 | other[†] | Y | 1* | 13 | 13 | 0.00465 | 0.08 | 0.84 | 0.10 | 0.16 | 1 | 62.5 |
| THRAP3 (N,S) | 109 | other[†] | Y | 1* | 12 | 12 | 0.000003 | 0.92 | 0.92 | 0.45 | 1.08 | 1 | 120.0 |
| DDX1 (N,No,P,T) | 82 | other[†] | - | 1* | 12 | 12 | 0.01004 | 0.13 | 0.04 | 0.05 | 0.68 | 1 | 29.4 |
| **HNRNPR (N,S,P)** | 71 | 3 | Y | 1.6 | 18 | 11 | 0.00006 | 0.27 | 1.81 | 0.56 | 1.10 | 1 | 11.4 |
| RPL13A (R,I) | 24 | - | LC | 1* | 11 | 11 | 0.00047 | 0.91 | 2.41 | 1.75 | 2.82 | 1 | 13.8 |
| RPL15 (N,No,R) | 24 | - | LC | 1* | 11 | 11 | 0.00014 | 0.57 | 2.48 | 0.74 | 2.00 | 1 | 52.5 |
| RPL6 (N,No,R) | 33 | - | LC | 2 | 21 | 10 | 0.00043 | 0.48 | 2.39 | 1.07 | 2.12 | 1 | 10.4 |
| GTPBP4 (N,No,R) | 74 | - | LC | 1* | 10 | 10 | 0.00054 | 0.20 | 1.61 | 0.06 | 1.07 | 1 | 51.3 |
| **HNRNPUL2 (N)** | 85 | - | Y | 1* | 10 | 10 | 0.00052 | 0.10 | 0.59 | 0.12 | 0.29 | 1 | 102.5 |
| RSL1D1 (N,No,P,SG) | 55 | - | LC | 1* | 10 | 10 | 0.00263 | 0.15 | 4.40 | 0.42 | 2.20 | 1 | 25.0 |
| SMC1A (N,No,Ch) | 143 | - | LC | 1 | 10 | 10 | 0.01218 | 0.30 | 3.15 | 0.24 | 0.50 | 0.99 | 10.0 |
| B0AZQ4 (N,Ch) | 142 | - | LC | 1* | 10 | 10 | 0.02789 | 0.15 | 3.03 | 0.06 | 0.21 | 1 | 48.8 |
| MYEF2 (N,T) | 64 | 3 | LC | 1* | 10 | 10 | 0.00366 | 0.10 | 0.36 | 0.31 | 0.21 | 1 | 97.5 |
| SMCHD1 (N,No,Ch) | 226 | - | - | 1* | 10 | 10 | 0.03239 | 0.15 | 3.23 | 0.25 | 1.85 | 1 | 24.4 |
| IGF2BP1 (N,P,SG) | 63 | 2 | - | 3.5 | 33 | 10 | 0.000003 | 0.55 | 1.06 | 0.49 | 0.79 | 1 | 9.7 |
| EPPK1 (SG) | 556 | - | - | 2.2 | 21 | 10 | 0.00753 | 0.56 | 1.22 | 0.51 | 2.26 | 0.99 | 8.9 |
| **KHDRBS1 (N,No,S,P,SG)** | 48 | other[†] | LC | 1.6 | 15 | 9.5 | 0.00016 | 0.56 | 0.98 | 0.71 | 1.38 | 1 | 9.5 |
| DHX15 (N,No,S) | 91 | other[†] | LC | 2 | 19 | 9.5 | 0.000008 | 0.24 | 1.13 | 0.32 | 1.11 | 1 | 9.5 |
| B3KY60 (N,T) ***CDC5L sim*** | 92 | - | LC | 1* | 9.5 | 9.5 | 0.00718 | 0.42 | 1.26 | 0.06 | 0.21 | 1 | 11.9 |
| PRPF6 (N,S) | 107 | - | LC | 1* | 9.5 | 9.5 | 0.00914 | 0.11 | 0.84 | 0.06 | 0.63 | 1 | 47.5 |
| **ILF2 (N,No,I)** | 39 | - | LC | 1.8 | 17 | 9 | 0.00049 | 0.36 | 1.46 | 0.64 | 0.96 | 1 | 9.3 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LRPPRC (N,M,P) | 158 | other† | - | 1* | 9 | 9 | 0.01603 | 0.16 | 1.78 | 0.06 | 0.43 | 1 | 11.6 |
| A8K4T9 (N,S,P)<br>***RALY sim*** | 30 | 1 | Y | 1* | 9 | 9 | 0.00004 | 0.44 | 1.22 | 1.20 | 1.56 | 1 | 9.0 |
| EIF3S8 | 105 | - | LC | 1* | 9 | 9 | 0.02137 | 0.06 | 0.57 | 0.07 | 0.23 | 1 | 87.5 |
| B2RCM2<br>*LARS sim* | 134 | - | LC | 1* | 9 | 9 | 0.00893 | 0.06 | 0.46 | 0.41 | 0.46 | 1 | 87.5 |
| RPS9 (N,No,R) | 23 | other† | LC | 2.2 | 19 | 8.5 | 0.00378 | 0.72 | 0.96 | 1.54 | 1.97 | 1 | 8.5 |
| **HNRNPK<br>(N,T,S,P,SG)** | 49 | other† | LC | 5.2 | 44 | 8.5 | 0.01622 | 0.75 | 1.72 | 1.00 | 1.08 | 1 | 8.5 |
| Q59GX6<br>helicase | 75 | - | Y | 5.6 | 48 | 8.5 | 0.00266 | 0.72 | 1.49 | 0.73 | 1.45 | 1 | 8.5 |
| RPL7A (R) | 30 | - | LC | 3 | 25 | 8.5 | 0.0004 | 0.77 | 1.37 | 1.52 | 2.30 | 1 | 8.4 |
| RPL28 (R) | 16 | - | LC | 1.2 | 10 | 8 | 0.0349 | 0.90 | 1.30 | 1.44 | 2.10 | 0.96 | 8.3 |
| **RTCB (N,P)** | 55 | - | - | 1.6 | 13 | 8 | 0.00007 | 0.34 | 1.17 | 0.95 | 1.21 | 1 | 8.3 |
| **HNRPH3 (N,S)** | 37 | 2 | Y | 1 | 8 | 8 | 0.00014 | 0.36 | 2.18 | 0.44 | 0.85 | 1 | 8.3 |
| SF3B2 (N,S) | 100 | other† | LC | 1 | 8 | 8 | 0.01897 | 0.12 | 0.18 | 0.15 | 0.24 | 0.96 | 8.3 |
| **RPL7 (R)** | 30 | - | LC | 3.2 | 26 | 8 | 0.00005 | 0.54 | 1.62 | 1.15 | 2.19 | 1 | 8.1 |
| **SRSF9 (N,S)** | 26 | 2 | - | 1* | 8 | 8 | 0.00007 | 0.58 | 1.74 | 1.86 | 2.06 | 1 | 19.4 |
| Q59G75 (*Unc*) | 146 | - | - | 1.2 | 9 | 8 | 0.03206 | 0.22 | 1.03 | 0.32 | 0.86 | 0.98 | 7.7 |
| RPL18 (N,No,R) | 22 | - | LC | 1.2 | 9 | 8 | 0.00574 | 0.76 | 3.24 | 1.75 | 3.89 | 0.99 | 7.7 |
| RPL4 (N,No,R) | 48 | - | LC | 4.4 | 34 | 8 | 0.00109 | 0.73 | 1.93 | 0.96 | 2.40 | 1 | 7.7 |
| ATAD3A (M,SG) | 66 | - | LC | 2.2 | 17 | 8 | 0.00742 | 0.69 | 1.01 | 1.22 | 1.91 | 0.99 | 7.6 |
| A8KAP3<br>*EFTUD2 sim* | 109 | - | LC | 1.8 | 13 | 7 | 0.02806 | 0.15 | 1.89 | 0.14 | 0.75 | 0.97 | 7.4 |
| Q2VIN3<br>*RBM1 sim* | 41 | 1 | LC | 3.2 | 23 | 7 | 0.00213 | 1.05 | 0.92 | 1.21 | 1.63 | 1 | 7.1 |
| **SAFB (N,T)** | 103 | 1 | Y | 1* | 7 | 7 | 0.00064 | 0.71 | 0.21 | 0.26 | 0.43 | 1 | 70.0 |
| **YBX1 (N,S,SG)** | 36 | other† | LC | 1* | 7 | 7 | 0.00128 | 0.36 | 1.00 | 0.43 | 0.57 | 1 | 35.0 |
| DDX21<br>(N,No,P,SG) | 87 | other† | LC | 3.6 | 25 | 7 | 0.00008 | 0.34 | 2.44 | 0.74 | 2.64 | 1 | 6.9 |
| NOP2 (N,No,R) | 89 | - | LC | 1.6 | 11 | 7 | 0.01063 | 0.32 | 1.55 | 0.44 | 1.73 | 0.99 | 6.9 |
| RPS2 (R) | 31 | other† | LC | 2.6 | 18 | 7 | 0.00215 | 0.70 | 1.52 | 1.22 | 2.82 | 1 | 6.8 |
| ABCF1 | 96 | - | LC | 1* | 7 | 7 | 0.02019 | 0.37 | 2.22 | 0.27 | 0.89 | 0.98 | 8.4 |
| EIF4G1 (SG) | 172 | - | Y | 1* | 7 | 7 | 0.02074 | 0.52 | 1.33 | 0.27 | 0.30 | 1 | 33.8 |
| RBM4 (N,No,S,P) | 40 | 2 | - | 1* | 7 | 7 | 0.00595 | 0.07 | 0.59 | 0.27 | 0.30 | 1 | 67.5 |
| SRSF7 (N,S) | 26 | 1 | LC | 1* | 7 | 7 | 0.00995 | 1.26 | 1.70 | 1.16 | 2.22 | 0.99 | 11.3 |
| A8K622<br>*STAU sim* | 63 | other† | - | 1* | 7 | 7 | 0.01229 | 0.15 | 0.96 | 0.27 | 0.44 | 1 | 33.8 |
| **DDX17<br>(N,No,S,P)** | 80 | other† | Y | 8.4 | 56 | 9 | 0.00184 | 0.80 | 1.20 | 0.96 | 1.72 | 1 | 6.7 |
| **HNRNPA0<br>(N,No,P,I)** | 31 | 2 | Y | 2 | 13 | 7 | 0.00308 | 0.42 | 2.11 | 1.09 | 1.89 | 0.99 | 6.6 |
| ELAVL1<br>(N,No,P,SG) | 39 | 3 | - | 3 | 20 | 6.5 | 0.00593 | 0.79 | 0.95 | 1.20 | 1.54 | 0.99 | 6.5 |
| A8K588 (N,S)<br>*SFRS6 sim* | 39 | 2 | LC | 1* | 6.5 | 6.5 | 0.00324 | 0.85 | 1.46 | 1.29 | 2.15 | 1 | 16.3 |
| **HNRNPC<br>(N,S,P)** | 32 | 1 | LC | 8 | 51 | 6 | 0.00631 | 0.79 | 1.32 | 0.93 | 1.73 | 0.99 | 6.3 |
| RPS3A (N,No,R) | 30 | - | - | 5 | 32 | 6 | 0.00373 | 0.73 | 0.83 | 1.09 | 1.97 | 0.99 | 6.3 |
| RPS13 (N,No,R) | 17 | - | - | 2.6 | 16 | 6 | 0.00108 | 0.58 | 1.05 | 1.51 | 2.28 | 1 | 6.3 |
| SMC2L1<br>(N,No,C) | 136 | - | LC | 1.4 | 9 | 6 | 0.02893 | 0.17 | 2.97 | 0.27 | 0.69 | 0.96 | 6.3 |
| SFRS3<br>(N,S,P,SG) | 19 | 1 | LC | 1.2 | 8 | 6 | 0.00368 | 0.93 | 3.07 | 1.52 | 2.27 | 0.99 | 6.3 |
| B4DMY3<br>*HNRNPAB sim* | 35 | 2 | Y | 1* | 6 | 6 | 0.00007 | 0.48 | 2.80 | 0.77 | 0.80 | 1 | 62.5 |
| TSR1 (N,No,R) | 92 | - | LC | 1* | 6 | 6 | 0.00353 | 0.16 | 0.08 | 0.19 | 0.48 | 1 | 62.5 |
| **SFPQ (N,S,P,SG)** | 76 | 2 | Y | 9.4 | 59 | 6 | 0.00367 | 0.68 | 1.79 | 0.90 | 1.52 | 1 | 6.2 |
| **DDX5 (N,No,S)** | 69 |  | Y | 9.2 | 57 | 6 | 0.00540 | 0.89 | 1.10 | 1.11 | 1.88 | 0.99 | 6.2 |
| **RBMX (N,T,I)** | 42 | 1 | LC | 5.6 | 34 | 6 | 0.00309 | 1.22 | 1.01 | 1.23 | 1.57 | 1 | 6.2 |
| RPL26L1 (R) | 17 |  | LC | 1.8 | 11 | 6 | 0.00664 | 0.64 | 1.73 | 1.69 | 2.73 | 0.99 | 6.1 |
| ZC3HAV1<br>(N,SG) | 101 | - | - | 1* | 6 | 6 | 0.01979 | 0.08 | 0.83 | 0.20 | 0.33 | 1 | 60.0 |
| **HNRNPU (N,P)** | 91 | other† | Y | 10 | 60 | 6 | 0.00147 | 0.75 | 1.74 | 1.01 | 1.62 | 1 | 6.0 |
| HNRNPCL1 (N) | 32 | 1 | LC | 3.2 | 19 | 6 | 0.00044 | 0.66 | 1.53 | 0.82 | 1.53 | 1 | 5.9 |
| RPL3 (N,No,R) | 46 | - | LC | 3 | 18 | 6 | 0.00004 | 0.42 | 2.20 | 0.61 | 1.52 | 1 | 5.9 |
| RPL14 (N,No,R) | 24 | - | LC | 1.4 | 8 | 6 | 0.00037 | 0.61 | 2.42 | 1.09 | 2.06 | 0.99 | 5.9 |
| RRBP1 (R) | 152 | - | LC | 1* | 6 | 6 | 0.01043 | 0.26 | 2.87 | 0.31 | 2.26 | 1 | 57.5 |
| HSPA1B | 70 | - | - | 1.4 | 8 | 6 | 0.0201 | 0.52 | 6.58 | 0.31 | 0.77 | 0.95 | 5.5 |
| ZFR (N,No) | 117 | - | LC | 1* | 5.5 | 5.5 | 0.00212 | 0.09 | 0.45 | 0.11 | 0.36 | 1 | 55.0 |
| RPS4X (N,No,R) | 30 | other† | - | 4.8 | 26 | 5.5 | 0.01078 | 0.76 | 0.70 | 1.55 | 2.44 | 0.99 | 5.5 |
| HCG26523 Unc | 17 | - | LC | 1.6 | 9 | 5.5 | 0.03222 | 0.74 | 1.49 | 1.85 | 3.54 | 0.97 | 5.5 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SRSF1 (N,S,P) | 28 | 2 | LC | 2.2 | 12 | 5 | 0.01679 | 1.49 | 2.30 | 2.55 | 4.51 | 0.97 | 5.3 |
| RPL10A (R) | 25 | - | - | 2.6 | 14 | 5 | 0.00387 | 0.51 | 1.42 | 1.00 | 2.18 | 0.99 | 5.3 |
| RPL8 (N,No,R) | 28 | - | - | 3.4 | 18 | 5 | 0.015837 | 0.68 | 1.32 | 1.62 | 1.97 | 0.95 | 5.2 |
| **RBM14 (N,No,T)** | 69 | 2 | Y | 5.2 | 27 | 5 | 0.00030 | 0.87 | 1.00 | 0.86 | 1.74 | 1 | 5.1 |
| RPL10 (N,R) | 25 | - | - | 2.2 | 11 | 5 | 0.00510 | 0.36 | 2.14 | 1.20 | 2.18 | 0.99 | 5.0 |
| SF3B1 (N,S) | 146 | - | LC | 2 | 10 | 5 | 0.03394 | 0.15 | 0.45 | 0.30 | 0.20 | 0.96 | 5.0 |
| B3KMC9 Unc | 109 | - | LC | 1* | 5 | 5 | 0.00502 | 0.60 | 0.70 | 0.72 | 0.80 | 1 | 50.0 |
| SRPK1 (N,S) | 74 | - | LC | 1* | 5 | 5 | 0.04555 | 0.20 | 0.50 | 0.24 | 0.20 | 1 | 50.0 |
| **DHX9 (N,No,T)** | 141 | other[†] | Y | 9.2 | 43 | 4.5 | 0.00022 | 0.55 | 1.95 | 0.65 | 1.27 | 1 | 4.6 |
| EPRS (I) | 171 | - | - | 3 | 14 | 5 | 0.01973 | 0.22 | 0.51 | 0.31 | 0.80 | 0.94 | 4.6 |
| RPL13 (N,R) | 24 | - | LC | 4.4 | 20 | 4.5 | 0.0081 | 0.71 | 1.34 | 1.70 | 2.58 | 0.95 | 4.5 |
| RPS6 (N,No,R) | 29 | - | LC | 3.2 | 14 | 4.5 | 0.0075 | 0.91 | 1.09 | 1.26 | 1.96 | 0.97 | 4.5 |
| HNRPF (N,S,P) | 46 | 2 | Y | 3 | 13 | 4.5 | 0.00155 | 0.62 | 2.69 | 0.92 | 2.38 | 0.99 | 4.3 |
| RPL27 (N,No,R) | 16 | - | LC | 3.4 | 14 | 4 | 0.01033 | 0.69 | 0.84 | 1.53 | 2.55 | 0.94 | 4.0 |
| **HNRNPH1 (N,No,S,P)** | 51 | 3 | Y | 7 | 28 | 4 | 0.02574 | 0.64 | 2.00 | 1.10 | 2.30 | 0.93 | 3.7 |
| RPS3A (N,No,R) | 27 | other[†] | - | 6.6 | 27 | 4 | 0.02574 | 0.89 | 1.08 | 1.15 | 1.55 | 0.99 | 6.3 |
| **HNRNPH2 (N,No,S,P,SG)** | 49 | 3 | Y | 5 | 20 | 4 | 0.00591 | 0.56 | 1.62 | 1.09 | 2.38 | 0.94 | 4.0 |
| RPS11 (N,No,R) | 18 | - | LC | 4.2 | 16 | 4 | 0.01174 | 0.29 | 1.02 | 1.18 | 1.84 | 0.95 | 3.8 |
| FBL (N,No,R,SG) | 34 | - | Y | 3.6 | 14 | 5 | 0.00560 | 0.30 | 2.22 | 1.11 | 2.89 | 0.93 | 3.8 |
| **TARDBP (N,S,P,SG)** | 45 | 2 | Y | 1.2 | 4 | 3.5 | 0.00324 | 0.35 | 1.53 | 0.71 | 1.18 | 0.96 | 3.5 |

[†]other: utilizes another RNA binding motif.

PrLD predicted by PLAAC: Prion-like amino acid composition plaac.wi.mit.edu (46); LC- low complexity sequences are present such as Arg/Ser (RS domain), Arg-rich, Gly-rich Glu-rich, or elements >50aa with a low folding index.

*Peptide counts avg of 0 to 1 rounded to 1.

Bold – match data on MATR3 interactors available in public databases; https://thebiogrid.org/115126, https://www.ebi.ac.uk/intact/, http://string-db.org.

Green highlight – match with (19)

Location and function annotations derived from {uniport.org}(44, 45), (N = nuclear; No = nucleolar; S = mRNA splicing; P = RNA processing; R = ribosomal; Ch = chromatin; I = inflammation; SG = stress granule).

**Supplemental Table S6. Proteins that show significantly different spectral counts for F115C-MATR3:AviTag capture.**

| Protein (isoform) | MW kDa | RRM | PrLD | Avg # spectra control | Avg # spectra WT | Fold Change | p Value vs Control | Avg # spectra F115C | Fold Change vs WT | p Value vs WT | G-Test vs WT | SAINT F115C | SAINT Fold |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MYBBP1A (N,N,T) | 149 | - | - | 1* | 16.25 | 16.25 | 0.0006 | 31.67 | 1.95 | 0.04978 | 0.02780 | 1 | 158.3 |
| MKI67 (N,N,C) | 359 | - | LC | 2.20 | 15.50 | 7.05 | 0.09146 | 39.33 | 2.54 | 0.04945 | 0.00132 | 1 | 17.9 |
| DDX21 (N,N,T) | 87 | other[†] | LC | 3.60 | 25.00 | 6.94 | 0.00008 | 45.33 | 1.81 | 0.01357 | 0.01608 | 1 | 10.1 |
| RPL5 (N,N,R) | 34 | - | LC | 1.00 | 6.25 | 6.25 | 0.10384 | 16.67 | 2.67 | 0.03526 | 0.03406 | 1 | 16.7 |
| RPL32 (R) | 16 | - | LC | 1* | 3.50 | 3.50 | 0.00999 | 13.67 | 3.90 | 0.02761 | 0.01717 | 1 | 34.2 |
| CKAP4 | 66 | - | Y | 3.20 | 11.00 | 3.44 | 0.08359 | 25.00 | 2.27 | 0.03732 | 0.02155 | 1 | 7.8 |
| Q53HW2 (R) | 34 | - | - | 1* | 3.00 | 3.00 | 0.29235 | 18.00 | 6.00 | 0.04108 | 0.00111 | 1 | 180.0 |
| HMGB2 (N,T,C) | 24 | - | LC | 1* | 2.50 | 2.50 | 0.22817 | 12.67 | 5.07 | 0.02557 | 0.01119 | 1 | 21.1 |
| **ALYREF (N,S,P)** | 28 | 1 | LC | 1* | 2.00 | 2.00 | 0.22745 | 10.67 | 5.33 | 0.04306 | 0.01933 | 1 | 13.3 |

[†] other: utilizes another RNA binding motif.

PrLD predicted by PLAAC: Prion-like amino acid composition plaac.wi.mit.edu (46); LC- low complexity sequences are present such as Arg/Ser (RS domain), Arg-rich, Gly-rich Glu-rich, or elements >50aa with a low folding index.

*Peptide counts avg of 0 to 1 rounded to 1.

Bold – match data on MATR3 interactors available in public databases; https://thebiogrid.org/115126, https://www.ebi.ac.uk/intact/, http://string-db.org.

Green – match with (19)

Location and function annotations derived from {uniport.org}(44, 45), (N = nuclear; No = nucleolar; S = mRNA splicing; P = RNA processing; R = ribosomal; Ch = chromatin; I = inflammation; SG = stress granule).

## Supplemental Table S7. Proteins binding to MATR3ΔRRM2 with >3-fold enrichment relative to WT-MATR3 that are low abundance in control or WT-MATR3 samples.

| Protein (location) | MW kDa | RRM | PrLD | Avg # Spectra Control | Avg # spectra WT | Avg # spectra ΔRRM2 | Fold Change vs WT* | p Value vs WT | G-test Vs Control | SAINT ΔRRM2 | SAINT Fold |
|---|---|---|---|---|---|---|---|---|---|---|---|
| HSPA5 (Cy) | 72 | - | LC | 1* | 1* | 35.50 | 35.50 | 0.0000001 | 0.0000001 | 1 | 177.5 |
| EZR (Cy) | 69 | - | LC | 1.00 | 1* | 28.00 | 28.00 | 0.0004464 | 0.0000038 | 1 | 28.0 |
| PNPT1(Cy) | 86 | other[†] | n | 1* | 1* | 25.50 | 25.50 | 0.0000001 | 0.0000006 | 1 | 127.5 |
| PA2G4 (Cy) | 44 | other[†] | n | 1* | 1* | 23.50 | 23.50 | 0.0004719 | 0.0000002 | 1 | 235.0 |
| B7Z4V2 HSPA9 sim (N) | 72 | - | LC | 1* | 1* | 20.00 | 20.00 | 0.0003250 | 0.0000023 | 1 | 33.3 |
| Q59GW1 (N) | 20 | - | LC | 1* | 1.50 | 27.50 | 18.33 | 0.0000058 | 0.0000001 | 1 | 137.5 |
| RDX (Cy) | 69 | - | LC | 1* | 1* | 17.50 | 17.50 | 0.0045524 | 0.0004229 | 1 | 43.8 |
| MYL6 (Cy) | 17 | - | n | 1* | 1.75 | 30.00 | 17.14 | 0.0010307 | 0.0000002 | 1 | 37.5 |
| MSN (Cy) | 68 | - | LC | 1* | 1* | 17.00 | 17.00 | 0.0018334 | 0.0005652 | 1 | 28.3 |
| CYFIP1 (Cy) | 145 | - | n | 1* | 1.25 | 19.00 | 15.20 | 0.0001182 | 0.0001758 | 1 | 47.5 |
| RPLP1 (Cy) | 12 | - | n | 1* | 1* | 15.00 | 15.00 | 0.0000424 | 0.0004304 | 1 | 75.0 |
| NCKAP1 (Cy) | 130 | - | n | 1* | 1* | 14.50 | 14.50 | 0.0000001 | 0.0000903 | 1 | 145.0 |
| NOLC1 (N,Cy) | 75 | - | LC | 1* | 1* | 14.50 | 14.50 | 0.0000186 | 0.0000903 | 1 | 36.3 |
| CYFIP2 (N,Cy) | 143 | - | n | 1* | 1.25 | 17.00 | 13.60 | 0.0000066 | 0.0005652 | 1 | 42.5 |
| D3DQY9 (N) | 22 | - | LC | 1* | 1* | 13.50 | 13.50 | 0.0000001 | 0.0001760 | 1 | 135.0 |
| HEL-S-2a | 22 | - | n | 1* | 1* | 13.50 | 13.50 | 0.0000014 | 0.0001760 | 1 | 22.5 |
| PSPC1 (N,Cy) | 59 | 2 | Y | 1* | 1.25 | 16.50 | 13.20 | 0.0009990 | 0.0066882 | 1 | 20.6 |
| A8K245 (N,Cy) | 45 | - | LC | 1.00 | 1* | 12.50 | 12.50 | 0.0038108 | 0.0440165 | 1 | 12.5 |
| EIF5A (N,Cy) | 16 | - | n | 1* | 1* | 12.50 | 12.50 | 0.0000393 | 0.0019814 | 1 | 31.3 |
| FEN1 (N) | 43 | - | LC | 1.00 | 1.00 | 12.50 | 12.50 | 0.0015825 | 0.0440165 | 1 | 12.5 |
| NME1 (N,Cy) | 33 | - | n | 1* | 1* | 12.50 | 12.50 | 0.0010837 | 0.0003423 | 1 | 125.0 |
| CBX3 (N) | 21 | - | LC | 1* | 1.00 | 12.00 | 12.00 | 0.0000933 | 0.0004771 | 1 | 120.0 |
| SSBP1 (Cy) | 17 | - | n | 1* | 1* | 12.00 | 12.00 | 0.0005500 | 0.0251027 | 1 | 20.0 |
| B4DNN4 (N) | 86 | - | LC | 1* | 1* | 11.50 | 11.50 | 0.0000001 | 0.0006647 | 1 | 115.0 |
| CFL1 (N,Cy) | 19 | - | n | 1* | 1* | 11.50 | 11.50 | 0.0000459 | 0.0006647 | 1 | 57.5 |
| ALDOA (Cy) | 40 | - | n | 1* | 1* | 11.00 | 11.00 | 0.0000594 | 0.0161880 | 1 | 13.8 |
| EIF2S2 (Cy) | 38 | - | LC | 1* | 1.50 | 16.50 | 11.00 | 0.0002966 | 0.0000237 | 1 | 165.0 |
| HCFC1 (N,Cy) | 213 | - | n | 1* | 1* | 11.00 | 11.00 | 0.0034757 | 0.0009255 | 1 | 110.0 |
| H0YHG0 (N) | 59 | - | LC | 1* | 1* | 10.50 | 10.50 | 0.0000023 | 0.0012881 | 1 | 52.5 |
| MTHFD1L (Cy) | 99 | - | LC | 1* | 1.25 | 13.00 | 10.40 | 0.0007487 | 0.0002455 | 1 | 32.5 |
| **ALYREF (N,Cy)** | 28 | 1 | LC | 1* | 2.00 | 20.50 | 10.25 | 0.0000066 | 0.0002808 | 1 | 25.6 |
| DNM3 (Cy) | 97 | - | n | 1* | 1* | 10.00 | 10.00 | 0.0025635 | 0.0274882 | 1 | 25.0 |
| FKBP3 (N,Cy) | 25 | - | LC | 1* | 1* | 9.50 | 9.50 | 0.0016671 | 0.0024909 | 1 | 23.8 |
| KIF4A (N,Cy) | 128 | - | LC | 1* | 1* | 9.50 | 9.50 | 0.0000718 | 0.0024909 | 1 | 95.0 |
| I6TRR8 (N) | 109 | - | n | 1* | 1* | 9.00 | 9.00 | 0.0028852 | 0.0158264 | 1 | 45.0 |
| IFIT1 (Cy) | 52 | LC | n | 1* | 1.00 | 9.00 | 9.00 | 0.0000129 | 0.0034605 | 1 | 90.0 |
| LBR (N) | 71 | - | LC | 1* | 1.75 | 15.50 | 8.86 | 0.0013488 | 0.0108830 | 1 | 19.4 |
| VDAC1 (Cy) | 31 | - | n | 1.60 | 1.75 | 15.50 | 8.86 | 0.0003094 | 0.0108830 | 1 | 9.7 |
| FLNC (Cy) | 287 | - | n | 1* | 1* | 8.50 | 8.50 | 0.0013559 | 0.0048041 | 1 | 85.0 |
| MRE11A (N) | 81 | - | LC | 1* | 1* | 8.50 | 8.50 | 0.0001230 | 0.0048041 | 1 | 85.0 |
| DKFZp586K0821 unc | 22 | - | - | 1* | 1* | 8.00 | 8.00 | 0.0009005 | 0.0066643 | 1 | 40.0 |
| DYNC1LI1 (Cy) | 57 | - | - | 1* | 1* | 7.50 | 7.50 | 0.0003758 | 0.0374259 | 1 | 37.5 |
| IMPDH2 (N,Cy) | 51 | - | - | 1* | 1* | 7.50 | 7.50 | 0.0000010 | 0.0092372 | 1 | 75.0 |
| MAP1B (Cy) | 271 | - | LC | 1* | 1* | 7.50 | 7.50 | 0.0000125 | 0.0374259 | 1 | 37.5 |
| A0A024RB41 (Cy) | 23 | - | LC | 1* | 1* | 6.50 | 6.50 | 0.0000021 | 0.0176967 | 1 | 65.0 |
| SMARCC2 (N) | 133 | - | Y | 1* | 1* | 6.50 | 6.50 | 0.0004417 | 0.0176967 | 1 | 65.0 |
| Q69YJ6 unc | 84 | - | LC | 1* | 1* | 6.00 | 6.00 | 0.0000933 | 0.0244555 | 1 | 60.0 |
| RCN2 (Cy) | 39 | - | LC | 1* | 1.25 | 7.50 | 6.00 | 0.0000010 | 0.0092372 | 1 | 75.0 |
| DDOST (Cy) | 51 | - | n | 1* | 1.75 | 10.00 | 5.71 | 0.0001073 | 0.0274882 | 1 | 16.7 |
| SND1 (N,Cy) | 102 | - | n | 1* | 2.25 | 12.50 | 5.56 | 0.0010837 | 0.0003423 | 1 | 125.0 |
| ENAH (Cy) | 66 | - | LC | 1* | 1* | 5.50 | 5.50 | 0.0000048 | 0.0337546 | 1 | 60.0 |
| PECI (Cy) | 40 | - | n | 1* | 1* | 5.50 | 5.50 | 0.0000048 | 0.0337546 | 1 | 55.0 |
| DDX6 (N,Cy) | 54 | LC | Y | 1* | 2.75 | 14.00 | 5.09 | 0.0000767 | 0.0092042 | 1 | 23.3 |
| ACSL3 (Cy) | 80 | - | n | 1* | 2.50 | 12.50 | 5.00 | 0.0016593 | 0.0071805 | 1 | 31.3 |

[†] other: utilizes another RNA binding motif.

PrLD predicted by PLAAC: Prion-like amino acid composition plaac.wi.mit.edu (46); LC- low complexity sequences are present such as Arg/Ser (RS domain), Arg-rich, Gly-rich Glu-rich, or elements >50aa with a low folding index.

*Peptide counts avg of 0 to 1 rounded to 1.

Bold – match data on MATR3 interactors available in public databases; https://thebiogrid.org/115126, https://www.ebi.ac.uk/intact/, http://string-db.org.

Green – match with (19)

Location annotations derived from {uniport.org} (N = nuclear; Cy = cytoplasmic).