Description of Additional Supplementary Files

Supplementary Movie 1 and 2: *Mettl14* deletion leads to slower growth cone dynamics. Outgrowing growth cones of WT (Supplementary Movie 1) and *M14* cKO (Supplementary Movie 2) mouse primary neuron were monitored over 3 hours at DIV6 (scale bar: 20 μm). Related to **Fig. 1i-k.**

Supplementary Movie 3 and 4: *Mettl14* deletion reduces anterograde RNA dynamics. MS2 system visualize BFP-Actb-3'UTR-MS2x24 reporter on WT (Supplementary Movie 3) and *M14* cKO mouse primary neuron (Supplementary Movie 4), acquired for 5minutes with 500ms intervals (scale bar: 10 μm). Related to **Fig. 3i-k.**

Supplementary Movie 5 and 6: m^6A point mutation in the reporter construct reduces anterograde RNA dynamics. MS2 system visualize BFP-Actb-3'UTR-MS2x24 reporter (Supplementary Movie 5) and BFP-Actb-3'UTRΔm^6A-MS2x24 reporter (Supplementary Movie 6) mouse primary neuron, acquired for 5minutes with 500ms intervals (scale bar: 10 μm). Related to **Fig. 3l-n.**

Supplementary Movie 7 and 8: *Mettl14* depletion does not affect to lysosome transport. Lysotracker live imaging of WT (Supplementary Moive 7) and Mettl14 cKO (Supplementary Movie 8) were observed for 30 minutes with 10 seconds intervals at DIV6 (scale bar: 10μm). Related to **Supplementary Fig 5.e-h**

Supplementary Movie 9 and 10: *Ythdf2* deletion leads to slower growth cone dynamics. Outgrowing growth cones of *DF2 Het* control (Supplementary Movie 9) and *DF2* cKO (Supplementary Movie 10) mouse primary neuron were monitored over 3 hours at DIV6 (scale bar: 20 μm). Related to **Fig. 4d-f**

Supplementary Movie 11 and 12: *Ythdf2* deletion reduces anterograde RNA dynamics. MS2 system visualize BFP-Actb-3'UTR-MS2x24 reporter on WT (Supplementary Movie 11) and *DF2* cKO mouse primary neuron (Supplementary Movie 12) acquired for 5minutes with 500ms intervals (scale bar: 10 μm). Related to **Fig. 4l-n**

Supplementary Data 1. The list of Mettl14-dependent m^{6}A peaks identified by m^{6}A-SAC-seq. The table includes the chromosome, chromosomal position, original genome sequence, mutated sequence, mutation ratio among transcripts, gene symbol, and the genomic location of m^{6}A peaks identified using m^{6}A-SAC-seq by comparing P0 WT and *M14* cKO mouse forebrain.

Supplementary Data 2. The results of the RNA stability assay in *Mettl14* and *Ythdf2* cKO primary cortical neurons. The table includes the gene symbol, the log2 fold-change ratio in the 0-hour sample, the log2 fold-change ratio in the 5-hour sample, the difference between the 0-hour and 5-hour samples, and the presence of m^{6}A from the m^{6}A-SAC-seq results. The first sheet shows the stability assay results for the *M14* cKO condition compared to the control. The second sheet shows the stability assay results for the *DF2* cKO condition compared to the control. The third sheet compares the *M14* cKO and *DF2* cKO stability assay results. Results were filtered according to the standard described in the Methods section (provided as a separate Excel spreadsheet).

Supplementary Data 3. The list of mRNAs with significantly altered abundances between the corpus callosum of WT and *M14* cKO mice. The table includes the Ensembl transcript ID, gene symbol, baseMean count, log2 fold-change ratio, and adjusted p-value. Results were filtered according to the standard described in the Methods section (provided as a separate Excel spreadsheet).

Supplementary Data 4. The list of protein interactors of YTHDF2 identified by Co-IP LC-MS/MS experiments. The table includes the gene symbol, the normalized PSM values for WT and *M14* cKO

with IgG pull-down samples, and the log2 fold-change of PSM values in WT compared to *M14* cKO (provided as a separate Excel spreadsheet).

Supplementary Data 5. Summary of statistical analyses for all experiments. The table includes p-values, sample sizes, statistical tests used, and additional parameters (provided as a separate Excel spreadsheet).