SUPPLEMENTARY FIGURES AND TABLES



Supplementary Figure S1: Effects of miR-558 on the 3'-UTR activity of HIF-2 α in NB cells. A. and B. real-time qRT-PCR showing the miR-558 levels in NB cells transfected with empty vector (mock), miR-558 precursor, anti-NC (100 nmol/L) or anti-miR-558 (100 nmol/L) inhibitors. C. and D. dual-luciferase assay indicating the activity of HIF-2 α 3'-UTR luciferase reporter in NB cells transfected with mock, miR-558 precursor, anti-NC (100 nmol/L) or anti-miR-558 (100 nmol/L) inhibitors. * P<0.01 vs. mock or anti-NC.



Supplementary Figure S2: Endogenous expression of AGO2 and eIF4EBP1 in NB cells. Immunofluorescence assay revealing the co-localization of AGO2 and eIF4EBP1 in cultured SH-SY5Y and IMR32 cells.



Supplementary Figure S3: Effects of eIF4E on HIF-2\alpha translation in NB cells. A. RIP and real-time qRT-PCR assay showing the binding of eIF4E to *HIF-2\alpha* 5'-UTR in NB cells transfected with sh-Scb or sh-AGO2. **B.** and **C.** sucrose gradient sedimentation assay indicating the distribution of *HIF-2\alpha* transcripts to the polysome fractions in NB cells transfected with sh-Scb or sh-eIF4E. * *P*<0.01 vs. sh-Scb.



Supplementary Figure S4: Expression of HIF-2\alpha, AGO2, and eIF4E in public datasets. A. the expression of HIF-2 α , AGO2, and eIF4E in normal dorsal ganglia (DG) and NB tissues derived from GEO database and R2 microarray analysis and visualization platform (http://r2.amc.nl). **B.** and **C.** mining the GEO database and R2 microarray analysis and visualization platform (http://r2.amc.nl) showing the expression of HIF-2 α , AGO2, and eIF4E in NB tissues with different INSS stages or *MYCN* amplification status.



Supplementary Figure S5: Patients' survival analysis. Kaplan–Meier survival plots of NB cohorts (stratified by the scan method and adjusted by Bonferroni correction) derived from GEO database and R2 microarray analysis and visualization platform (http://r2.amc. nl) showing the survival probability of patients with high or low expression of AGO2 **A.** or eIF4E **B.**

| Primer set | Primers | Sequence | Product size (bp) | Application |
|---------------|---------|-----------------------------|-------------------|--------------|
| HIF-2a | Forward | 5'-AAAGCCTTGGAGGGTTTCATT-3' | 292 | qRT-PCR |
| | Reverse | 5'-AGGTGGCTGACTTGAGGTTGA-3' | | |
| HIF-2a 5'-UTR | Forward | 5'-AGGCGGCCGTACAATCCT-3' | 187 | qRT-PCR, RIP |
| | Reverse | 5'-TGTCAGACCCGAAAAGAG-3' | | |
| β-actin | Forward | 5'-ATCTACGAGGGGTATGCC-3' | 227 | qRT-PCR |
| | Reverse | 5'-TAGCTCTTCTCCAGGGAG-3' | | |
| miR-558 | Forward | RiboBio | | qRT-PCR |
| | Reverse | RiboBio | | |
| U6 | Forward | RiboBio | | qRT-PCR |
| | Reverse | RiboBio | | |

| Sunnlementary | Table S1. | Primer sets | used for | aRT_PCR | and RIP |
|----------------|-----------|-----------------|----------|----------|---------|
| Supplemental y | Table S1. | I I IIIICI Sets | useu ioi | 4NI-I UN | anu KII |

HIF-2 α , hypoxia-inducible factor 2 alpha; 5'-UTR, 5'-untranslated region.

| Oligo set | Sequences |
|-----------------------------|--|
| pre-miR-558 | 5'-TGCTGTGAGCTGCTGTACCAAAATGTTTTGGCCACTGACTG |
| | 5'-CCTGTGAGCTGCTGTACCAAAATGTCAGTCAGTGGCCAAAACATTTTGGTACAGCAGCTCAC-3' (antisense) |
| pre-miR-NC | 5'-TGCTGAAATGTACTGCGCGTGGAGACGTTTTGGCCACTGACTG |
| | 5'-CCTGAAATGTACTGCGTGGAGACGTCAGTCAGTGGCCAAAACGTCTCCACGCGCAGTACATTTC-3' (antisense) |
| HIF-2a 5'-UTR mut (miR-558) | 5'-AGACTGTATGTTAGTACAGGCCCGGCCTCCGACTCCTTCCGACTCCCAGC-3' (sense); |
| | 5'-GGAGGCCGGGCCTGTACTAACATACAGTCTCAGGACACTGCCGAGGATTG-3' (antisense) |
| Anti-NC | RiboBio |
| Anti-miR-558 | RiboBio |
| sh-Scb | 5'-CCGGGCGAACGATCGAGTAAACGGACTCGAGTCCGTTTACTCGATCGTTCGCTTTTT-3'(sense); |
| | 5'-AATTCAAAAAAGCGAACGATCGAGTAAACGGACTCGAGTCCGTTTACTCGATCGTTCGC-3' (antisense) |
| sh-AGO2-1 | 5'-CCGGGCACAGCCAGTAATCGAGTTTCTCGAGAAACTCGATTACTGGCTGTGCTTTTTG-3' (sense); |
| | 5'-AATTCAAAAAAGCACAGCCAGTAATCGAGTTTCTCGAGAAACTCGATTACTGGCTGTGC-3' (antisense) |
| sh-AGO2-2 | 5'-CCGGCGTCCGTGAATTTGGAATCATCTCGAGATGATTCCAAATTCACGGACGTTTTTG-3' (sense); |
| | 5'-AATTCAAAAAACGTCCGTGAATTTGGAATCATCTCGAGATGATTCCAAATTCACGGACG-3' (antisense) |
| sh-eIF4E-1 | 5'-CCGGCAGAGAGGAGGAAGGAGAAGTCTCGAGACTTCTCCTTCCT |
| | 5'-AATTCAAAAAACAGAGAGGAGGAAGGAAGGAGAAGTCTCGAGACTTCTCCTTCCT |
| sh-eIF4E-2 | 5'-CCGGCAGACCAGCAGATGGACAACTCTCGAGAGTTGTCCATCTGCTGGTCTGTTTTTG-3' (sense); |
| | 5'-AATTCAAAAAACAGACCAGCAGATGGACAACTCTCGAGAGTTGTCCATCTGCTGGTCTG-3' (antisense) |
| sh-HIF-2α-1 | 5'-CCGGGCGCAAATGTACCCAATGATACTCGAGTATCATTGGGTACATTTGCGCTTTTTG-3' (sense); |
| | 5'-AATTCAAAAAAGCGCAAATGTACCCAATGATACTCGAGTATCATTGGGTACATTTGCGC-3' (antisense) |
| sh-HIF-2α-2 | 5'-CCGGCAGTACCCAGACGGATTTCAACTCGAGTTGAAATCCGTCTGGGTACTGTTTTTG-3' (sense); |
| | 5'-AATTCAAAAAACAGTACCCAGACGGATTTCAACTCGAGTTGAAATCCGTCTGGGTACTG-3' (antisense) |

Supplementary Table S2: Oligonucleotide sets used for constructs, inhibitors and short hairpin RNAs

pre-miR-NC, negative control miRNA precursor; HIF-2α, hypoxia-inducible factor 2 alpha; 5'-UTR, 5'-untranslated region; Anti-NC, negative control inhibitor; sh-Scb, scramble short hairpin RNA; AGO2, Argonaute 2; eIF4E, eukaryotic translation initiation factor 4E.