***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

* To investigate the dysregulation of progenitor genes in postmitotic MNs of *IG-DMRmatΔ*. 8~11 E11.5 *IG-DMRmatΔ* and wild type embryos were used. Statistics of p-value was analysis by Student’s *t*-test (Figure 5A~D, page 16).
* To investigate the ectopic expansion of caudal Hox (ie., Hoxc8) and downstream Pea3on and Scipon MN pools in the rostral brachial segment, with a concomitant decrease of Hoxa5on MNs. Five embryos from control and *IG-DMRmatΔ* were used to quantify from serial sections along the rostrocaudal axis. Statistics of p-value were analysis by Student’s *t*-test (Figure 6A~D, page17).
* To investigate axonal branching and nerve trajectories 6 *IG-DMRmatΔ;Hb9GFP*mutants and 6 Ctrl;Hb9GFP embryos were use. Statistics of p-value were analysis by Mann–Whitney U test (Figure 7, page 17~18).

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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All experiments are shown with independent biological samples, typically performed at least 3~6 times. *Meg3* KD ES cell lines were established by three independent retrovirus-based short hairpin RNAs (shRNAs). All microarray, RNA-seq, ChIP-seq data have been deposited in GEO under accession codes GSE114283, GSE114285 and GSE114228.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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Statistical analysis methods are described throughout the MATERIALS AND MEHTODS section (page 40), and more details (N number, p value, the statistical method performed) can be found in the Figure legend in each figure.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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Samples in this manuscript were randomized and objectively selected, no outliers are were excluded .

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

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The information on the total relevant additional are provided in MATERIALS AND MEHTODS section