Supplementary information for

RUNX3 negatively regulates autophagic degradation of aggregated α-synuclein

Ikumi Tomizawa[1], Yung-Wen Chiu[1], Yutaka Tatenuma[1], Norikazu Hara[2], Mai Hasegawa[2], Masataka Kikuchi[2], Tatsuo Mano[3,4], Maiko Ono[5], Maho Morishima[6], Shigeo Murayama[6], Yuko Saito[6], Makoto Higuchi[7,8], Mari Tada[9], Akiyoshi Kakita[9], Tatsushi Toda[3,10], Atsushi Iwata[3,11], Akinori Miyashita[2], Takeshi Ikeuchi[2], Yukiko Hori[1], Taisuke Tomita[1]

[1] Laboratory of Neuropathology and Neuroscience, Graduate School of Pharmaceutical Sciences, The University of Tokyo, Tokyo, Japan 113-0033

[2] Center for Bioresources, Brain Research Institute, Niigata University, Niigata, Japan 951-8122

[3] Department of Neurology, The University of Tokyo Hospital, Tokyo, Japan 113-8655

[4] Department of Degenerative Neurological Diseases, National Institute of Neuroscience, National Center of Neurology and Psychiatry, Tokyo Japan 187-8551

[5] Institute for Quantum Life Science, National Institutes for Quantum Science and

Technology, Chiba, Japan 263-0024

[6] Department of Neuropathology (Brain Bank for Aging Research), Tokyo Metropolitan Institute for Geriatrics and Gerontology, Tokyo, Tokyo, Japan 173-0015

[7] Advanced Neuroimaging Center, Institute for Quantum Medical Science, National Institutes for Quantum Science and Technology, Chiba, Japan 263-0024

[8] Department of Neuroetiology and Diagnostic Science, Graduate School of Medicine, Osaka Metropolitan University, Osaka, Japan 545-8585

[9] Department of Pathology, Brain Research Institute, Niigata University, Niigata, Japan 951-8122

[10] National Center Hospital, National Center of Neurology and Psychiatry, Tokyo Japan 187-8551

[11] Department of Neurology, Tokyo Metropolitan Institute for Geriatrics and Gerontology, Tokyo, Japan 173-0015

*Correspondence: Y.H., yukiko-hori@mol.f.u-tokyo.ac.jp

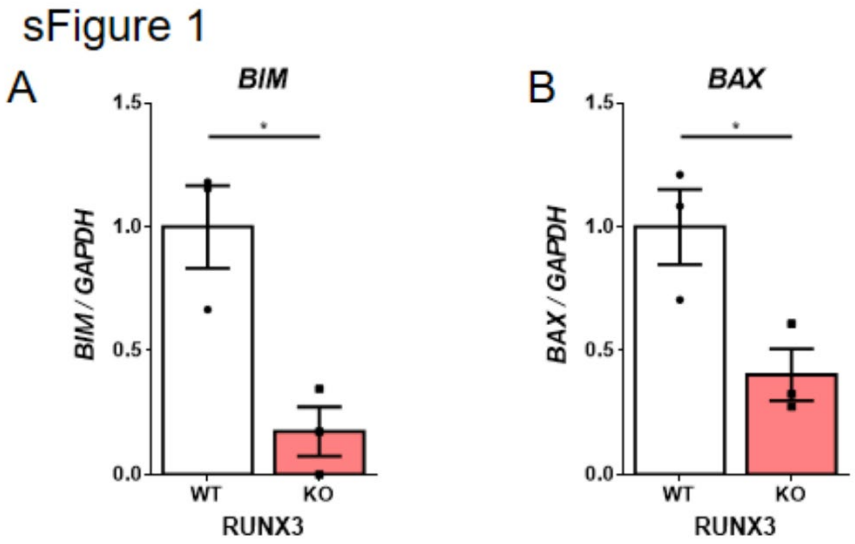
*Correspondence: T.T., taisuke@mol.f.u-tokyo.ac.jp

Supplementary table 1

Summary of patient derived samples used for the single nucleus RNA sequencing

ID	Clinical diagnosis	Age at death	Sex	Brain Region	Provided from
Control_AMG_1	Control	66	M	Amygdala	Department of Pathology, Brain Research Institute, Niigata University
Control_AMG_2	Control	67	F	Amygdala	Department of Pathology, Brain Research Institute, Niigata University
Control_AMG_3	Control	74	M	Amygdala	Department of Pathology, Brain Research Institute, Niigata University
MSA_AMG_1	MSA	64	M	Amygdala	Department of Pathology, Brain Research Institute, Niigata University
MSA_AMG_2	MSA	74	F	Amygdala	Department of Pathology, Brain Research Institute, Niigata University
MSA_AMG_3	MSA	78	M	Amygdala	Department of Pathology, Brain Research Institute, Niigata University

Supplementary figure 1



sFig. 1. Expression of RUNX3 downstream factors in RUNX3 KO cells.

(A) qRT-PCR analysis of *BIM* mRNA levels in RUNX3 KO cells normalized by *GAPDH* (n=3, mean ± SEM, Student's t-test, *: $p<0.05$).

(B) qRT-PCR analysis of *BAX* mRNA levels in RUNX3 KO cells normalized by *GAPDH* (n=3, mean ± SEM, Student's t-test, *: $p<0.05$).