

Supplementary materials

SQSTM1^{L341V} variant that is linked to sporadic ALS exhibits impaired association with MAP1LC3 in cultured cells

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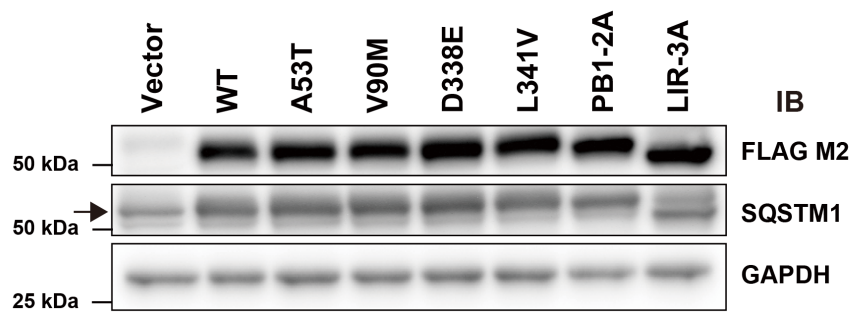


Fig. S1. Expression levels of SQSTM1_WT and its mutant/variant in PC12 cells. PC12 cells were transfected with FLAG-tagged pCIneo_SQSTM1 constructs. Expression levels of SQSTM1_WT and its mutant/variant were analyzed by Western blotting using anti-FLAG M2 and anti-SQSTM1 (p62-C) antibodies (IB: immunoblotting). Arrow indicates the position of endogenous SQSTM1. GAPDH was used for a loading control.

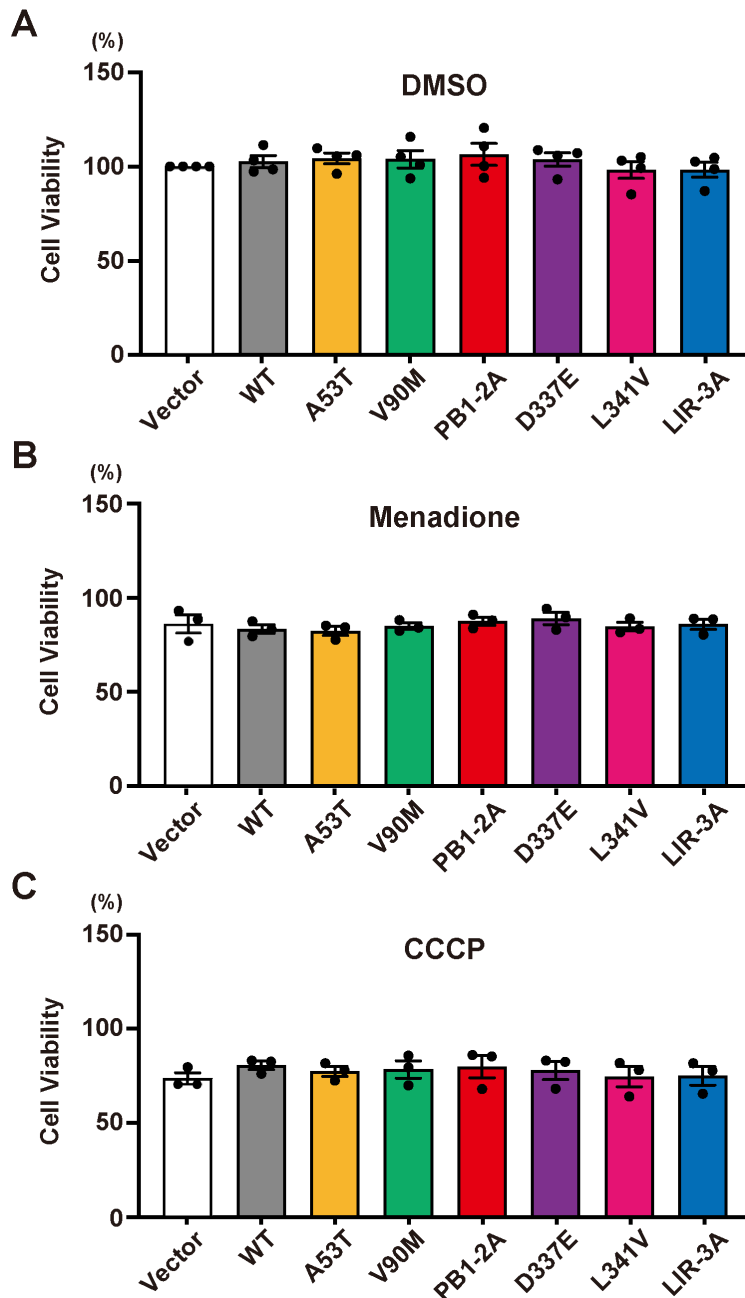


Fig. S2. Effects of overexpression of wild-type SQSTM1 or its mutant/variant on viability in PC12 cells under either normal or stressed conditions. After 24 h of transfection with FLAG-tagged SQSTM1_WT or mutant/variant-expressing construct, PC12 cells were incubated under following conditions: (A) non-treated (DMSO), (B) 10 μ M of menadione for 4 h and (C) 750 μ M of carbonyl cyanide 3-chlorophenylhydrazone (CCCP) for 10 h. Alamar Blue Reagent was used to assess the cell viability. PB1 mutants/variants include A53T and V90M variations identified in ALS patients, and PB1-2A (K7A/D69A) artificial mutation. LIR mutants/variants include D337E and L341V variations identified in ALS patients, and LIR-3A (D335A/D336A/D337A) artificial mutation. Values for the cell viability represent mean percentage relative to control cells that are transfected with pCIneo-vector (Vector) under non-treated conditions [\pm S.E.M.; $n = 3 \sim 4$ (biological replicates)]. Individual data points are also shown. Statistical significance was evaluated by one-way ANOVA with Tukey's multiple comparison test.

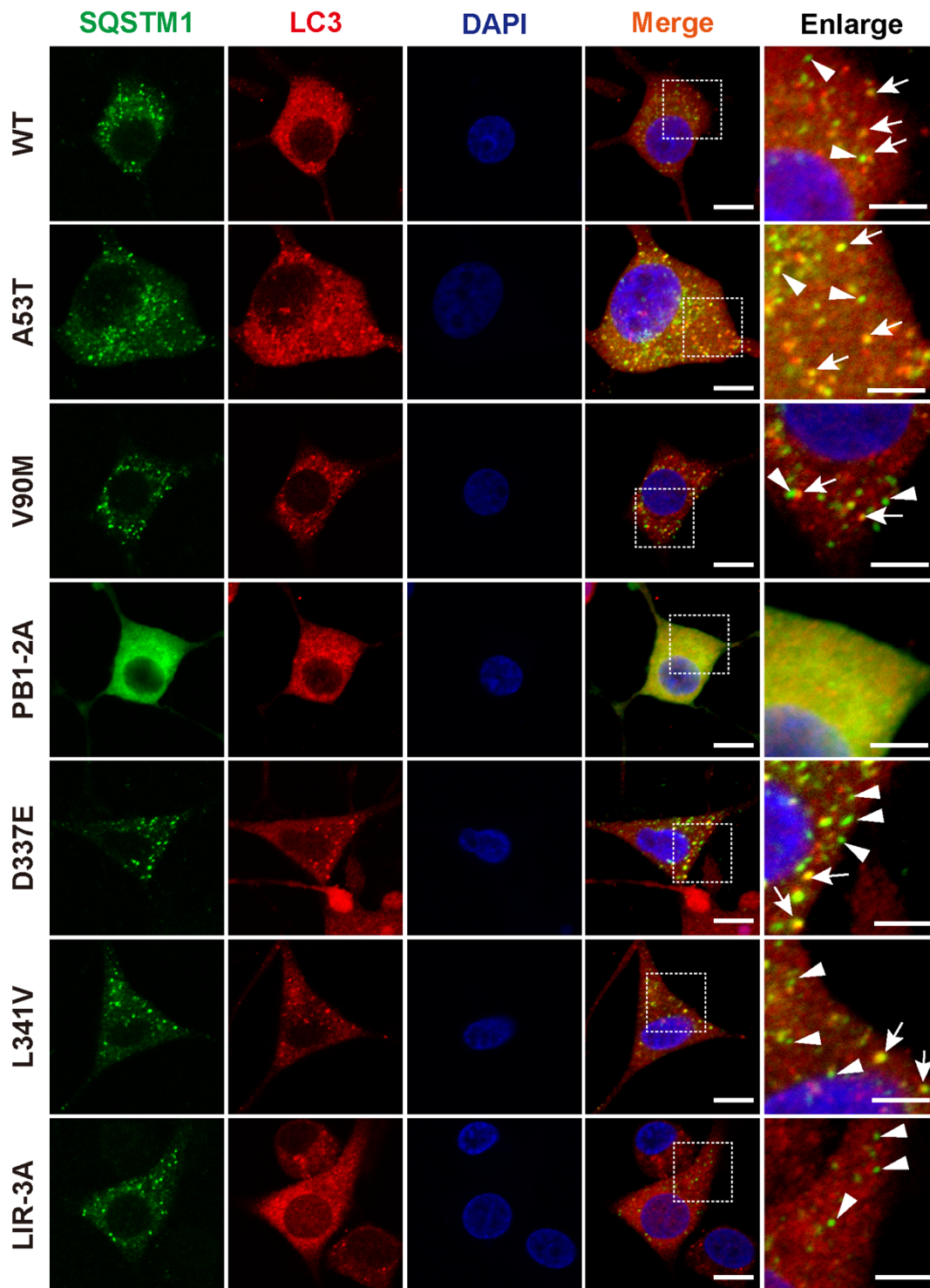


Fig. S3. Subcellular distribution of SQSTM1 mutants in PC12 cells. FLAG-tagged SQSTM1_WT (WT), PB1-domain ALS-linked variants (A53T and V90M), PB1-domain artificial mutant (PB1-2A), LIR ALS-linked variants (D337E and L341V) and LIR artificial mutant (LIR-3A) were expressed in PC12 cells, and their subcellular distributions were analyzed. Images for SQSTM1 and LC3 were obtained by staining with anti-FLAG M2 and anti-LC3 antibodies, respectively. Nuclei were counterstained with DAPI. High-resolution magnified images are shown on the right. Arrows and arrowheads indicate LC3-positive and -negative SQSTM1-bodies, respectively. Scale bars for merged and enlarged images indicate 20 μ m and 10 μ m, respectively.

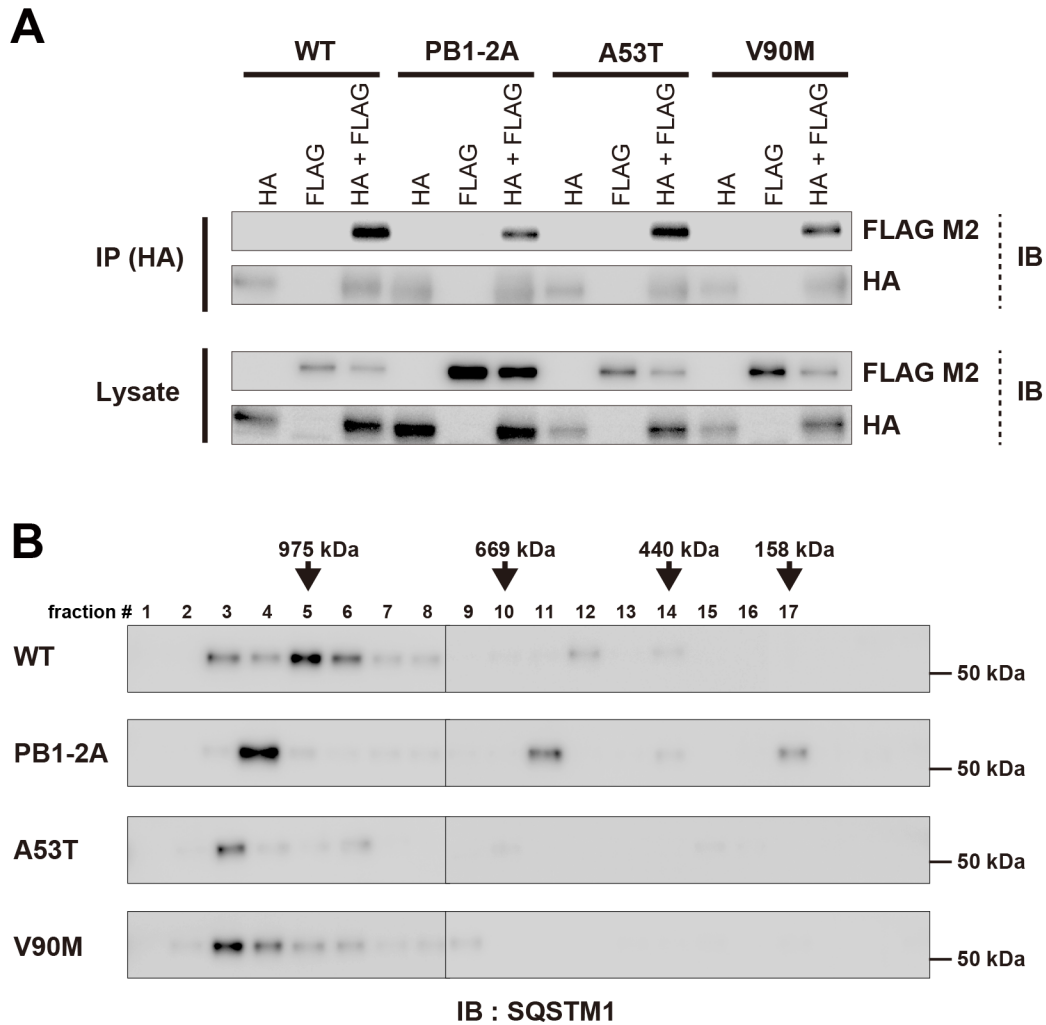


Fig. S4. Analysis of self-oligomerization of the SQSTM1 PB1 mutants. **(A)** Co-immunoprecipitation analysis. COS-7 cells expressing HA-tagged SQSTM1 and FLAG-tagged SQSTM1 were immunoprecipitated by monoclonal anti-HA antibody (IP: immunoprecipitation). Both precipitated samples and cell lysates were analyzed by Western blotting using anti-FLAG M2 and anti-HA antibodies (IB: immunoblotting). **(B)** Gel filtration analysis of the SQSTM1 proteins. SQSTM1 purified from transformed BL21 *E. coli* were applied to the Superose6 10/300 column, and fractions were analyzed by Western blotting using anti-SQSTM1 (p62-C) antibody (IB: immunoblotting). Arrows indicate the positions of molecular mass markers.

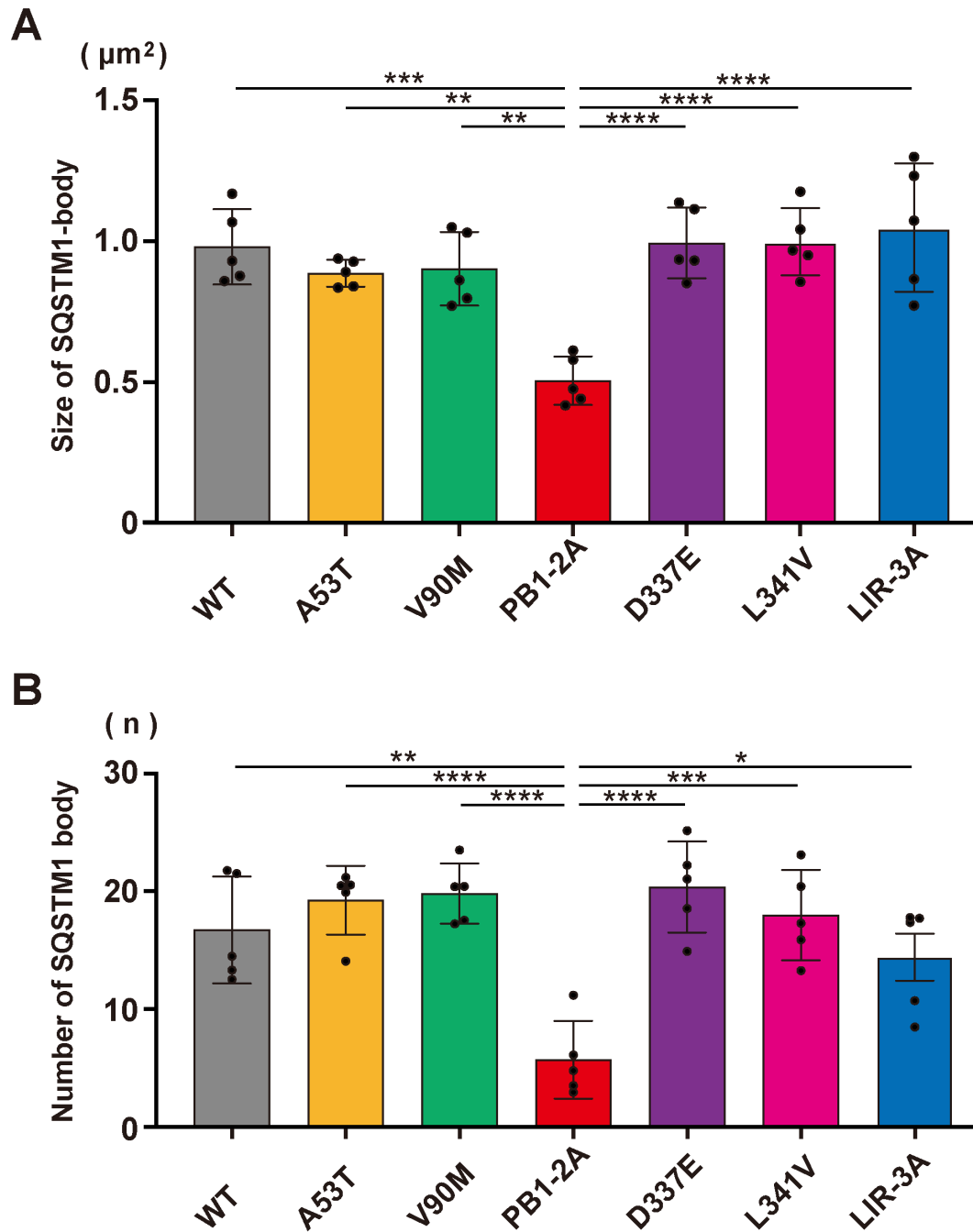


Fig. S5. Quantitative analysis of the size and number of SQSTM1-positive bodies in *Sqstm1* deficient mouse embryonic fibroblast. *Sqstm1* deficient mouse embryonic fibroblasts (*Sqstm1*-KO MEFs) were transfected with pCIneoFLAG-SQSTM1 constructs. The size of each SQSTM1-body in each cell was measured. We also counted and normalized the number of SQSTM1-body with the adjusted area of cell body (per 1,000 μm^2). Mean values of the size [\pm S.D.; n = 5 biological replicates (total number of cells = 26 ~ 28)] (A) and the number [\pm S.D.; n = 5 biological replicates (total number of cells = 21~ 22)] (B) for “SQSTM1-body” are shown. Statistical significances were evaluated by one-way ANOVA with Tukey’s multiple comparison test (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$).