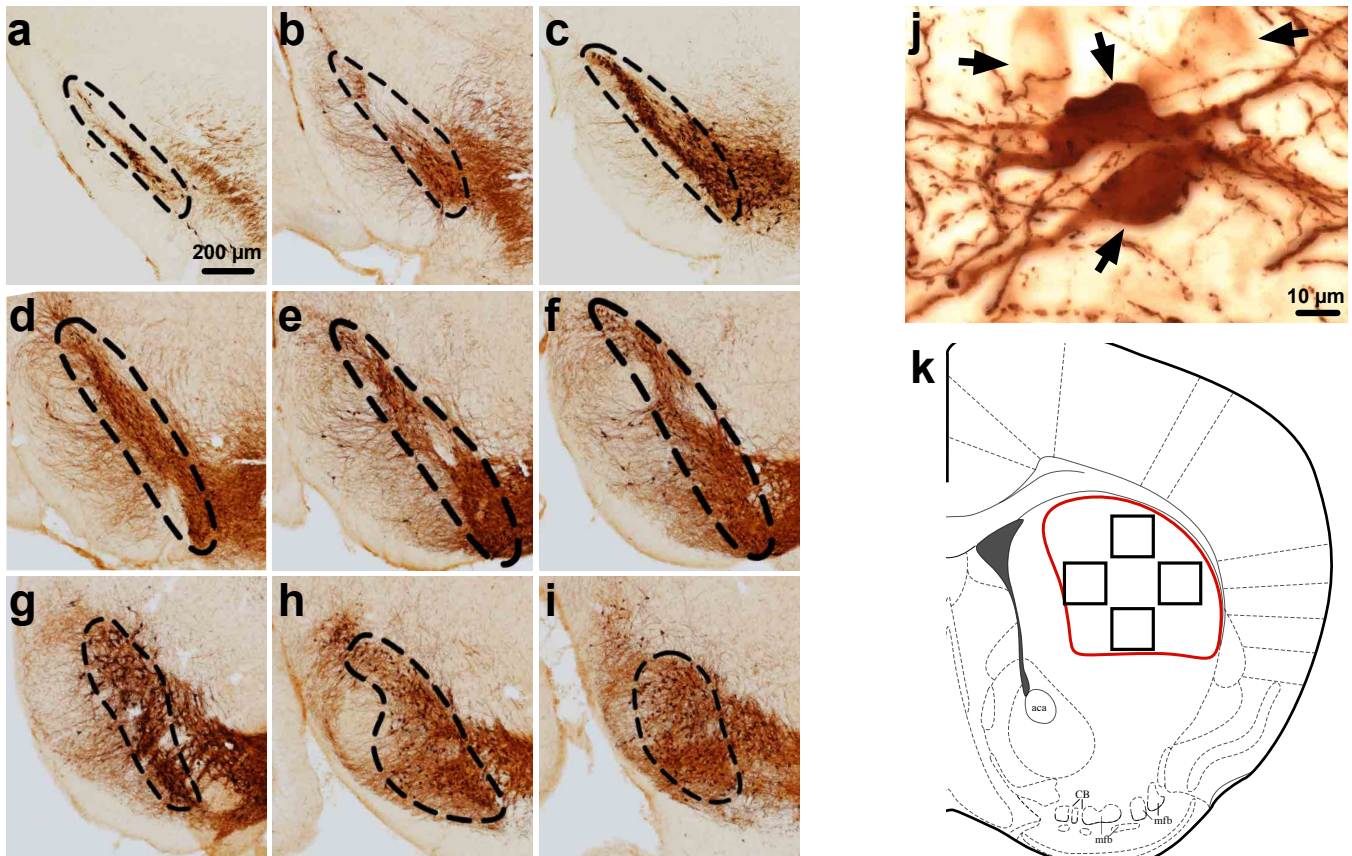


Identification of Multiple QTLs Linked to Neuropathology in the *Engrailed1* Heterozygous Mouse Model of Parkinson's Disease

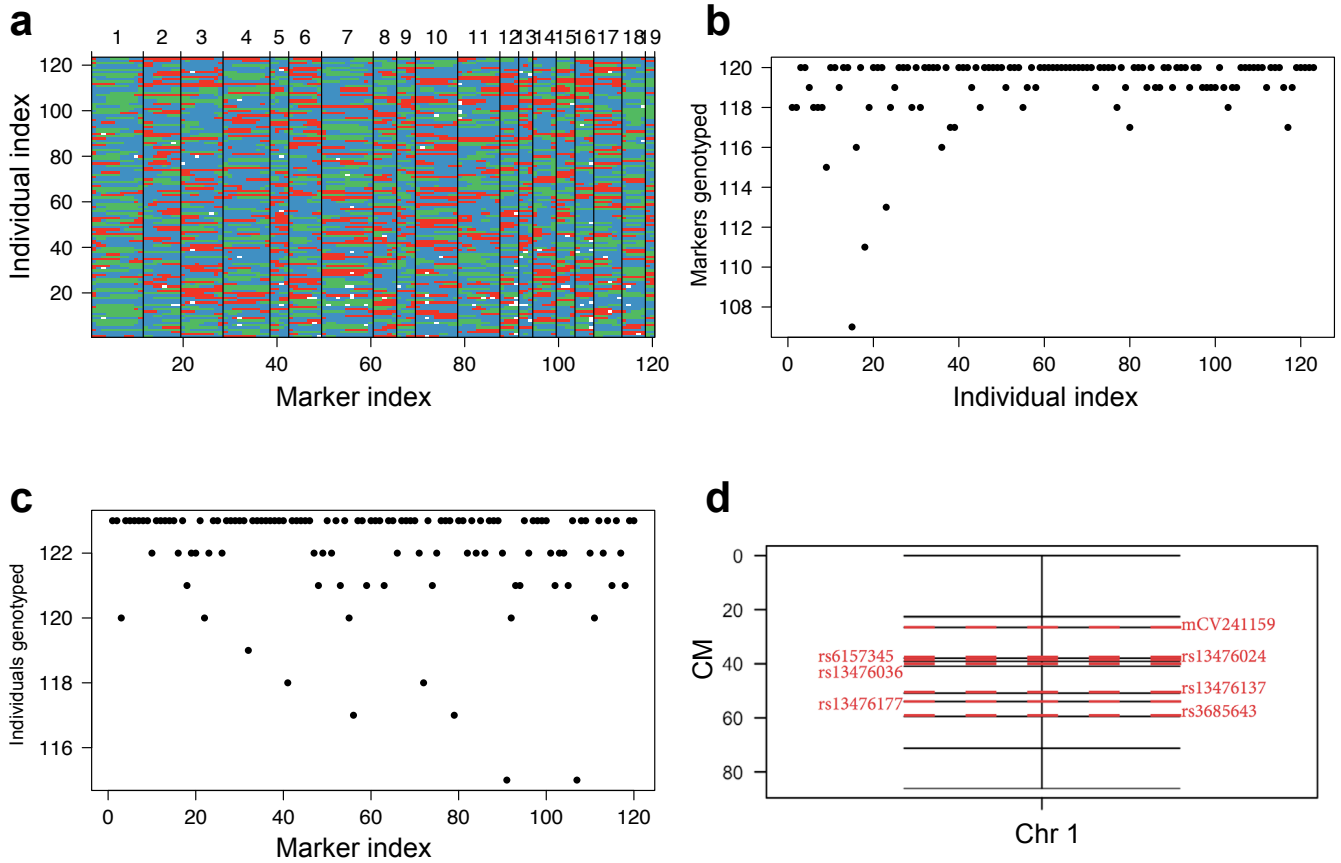
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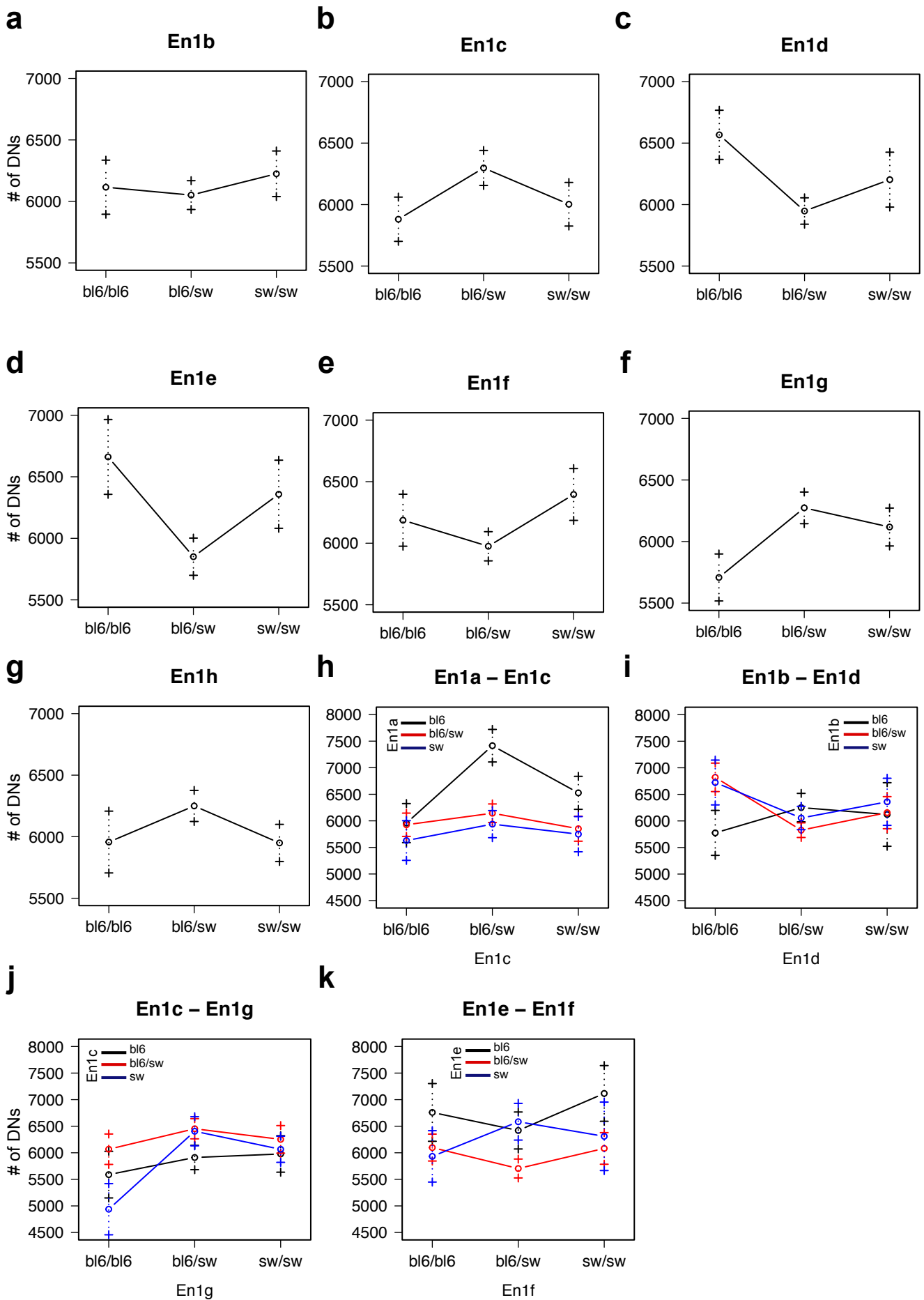
Supplementary Information



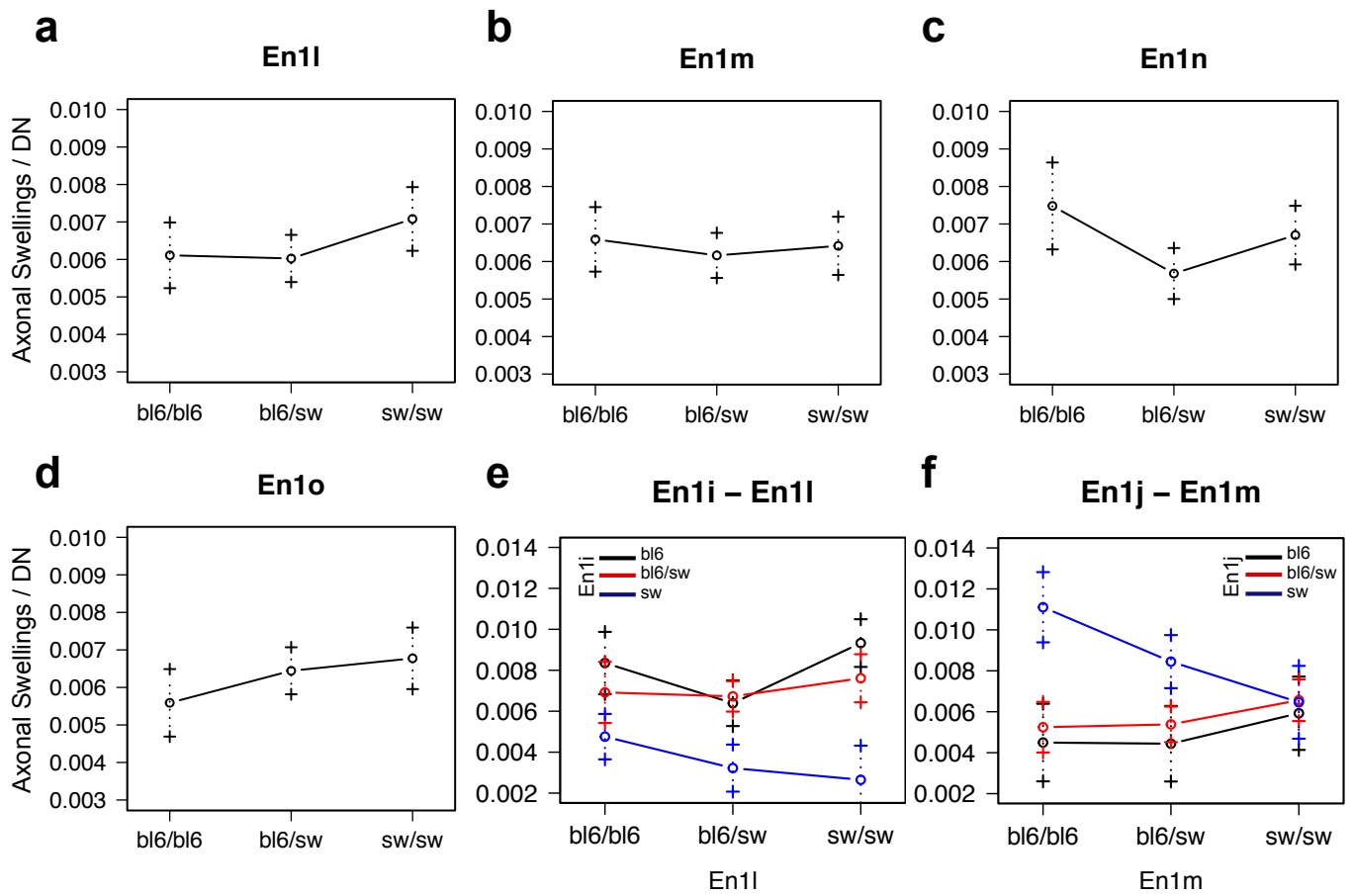
Supplementary Figure S1. Representative sampling areas for the analyses of TH-stained DNs and axonal swellings. A-I. Representation of every 3rd coronal section, spanning the SNpc region (-3.78 to -2.7 mm from bregma), organized rostro-caudally. SNpc region used for stereological estimation of total number of TH-positive DNs is marked in red. J. Examples of nigral TH-positive neurons included (black arrows) in the counting. K. Representation of the sampling scheme for the quantification of the axonal swellings in the dorso-lateral caudate putamen of striatum. Red line shows the dorso-lateral part where the 4 images (black rectangles) were taken.



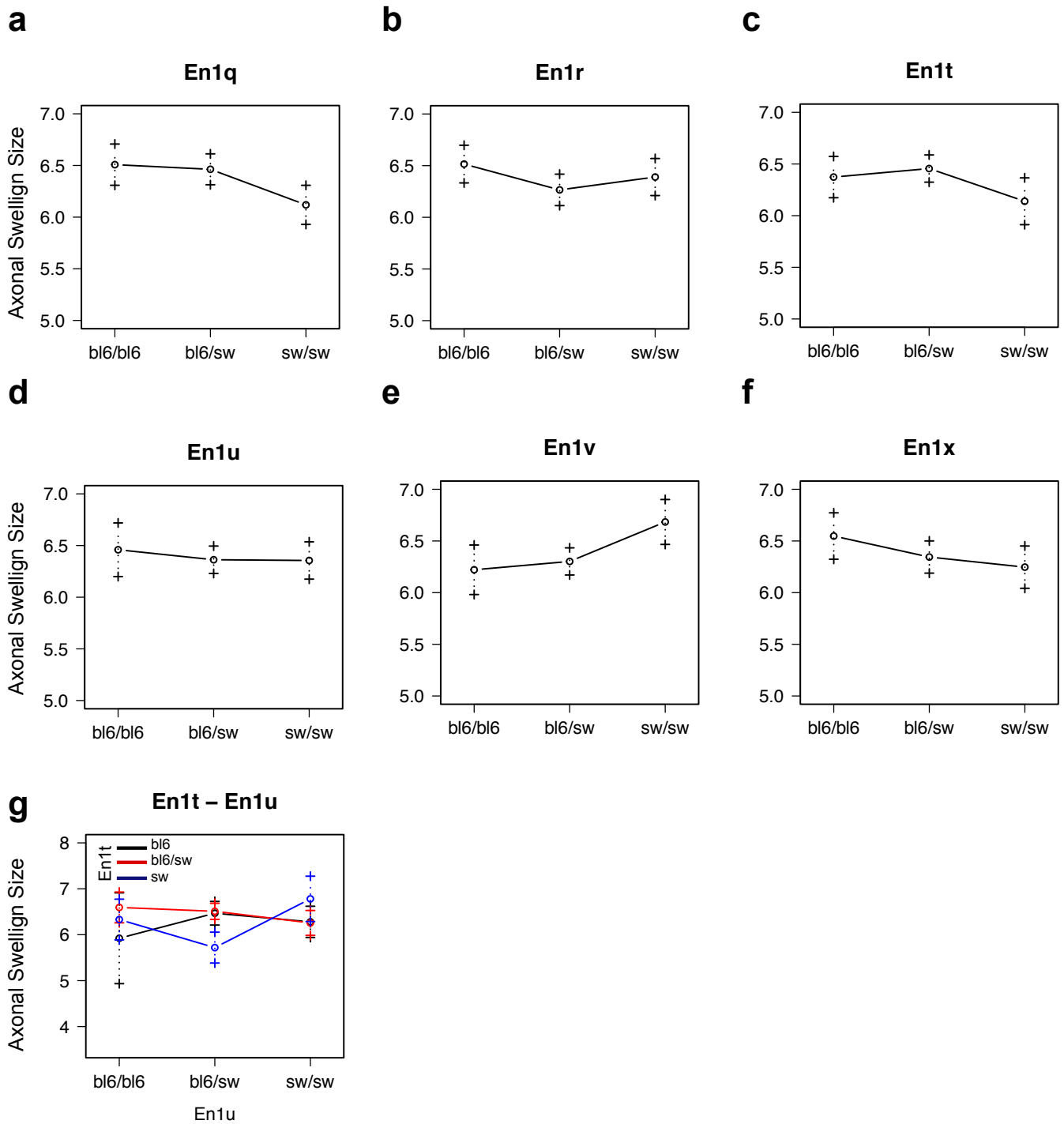
Supplementary Figure S2. Genomic coverage. A. Genotype data for each individual and each marker in the SNP genotyping. Red: Bl/Bl; Blue: Bl6/Sw; Green: Sw/Sw; B. Number of markers genotype for each genotyped individual; C. Number of individuals genotyped at each marker; D. Genetic map of chromosome 1. Red markers were removed from the analysis due to significantly distorted segregation patterns.



Supplementary Figure S3. QTLs linked to number of DNs. A-G. Effectplots for En1b – En1h; H-K. Interaction plots for the significant interactions for DN counts.



Supplementary Figure S4. QTLs linked number of axonal swellings per number of remaining DNs. A-D. Effectplots for En1l, m, n and o. E-F. Interaction plots for significant interactions between En1i-En1l and En1j-En1m.



Supplementary Figure S5. QTLs linked to size of axonal swellings. A-F. Effectplots for En1q, r, t, u, v and x; G. Interaction plot for En1t-En1u.