Supplementary Information

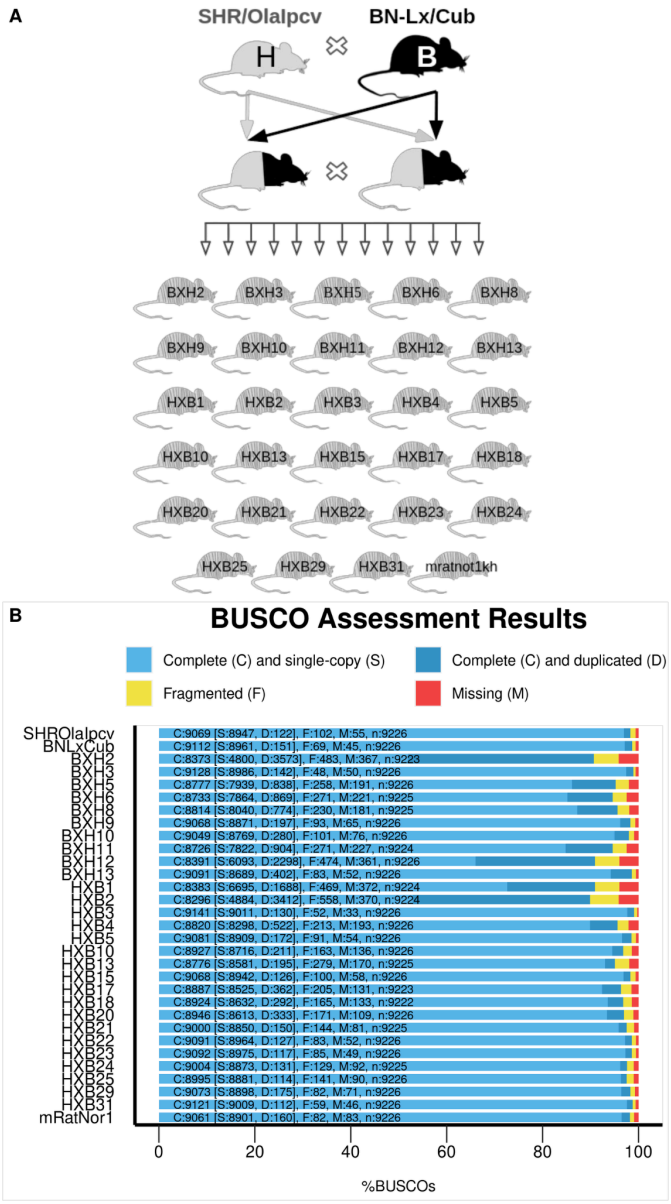

Figure S1. Description of rats used in this study and quality of the genome assembly. **(A)** Overview of the HXB/BXH recombinant inbred rat family describing the origins and breeding history of the HXB/BXH rats. **(B)** BUSCO completeness of the genome assembly used to build the pangenome for genomics data quality control. Bar charts show proportions classified as complete (C, blues), complete single-copy (S, light blue), complete duplicated (D, dark blue), fragmented (F, yellow), and missing (M, red).

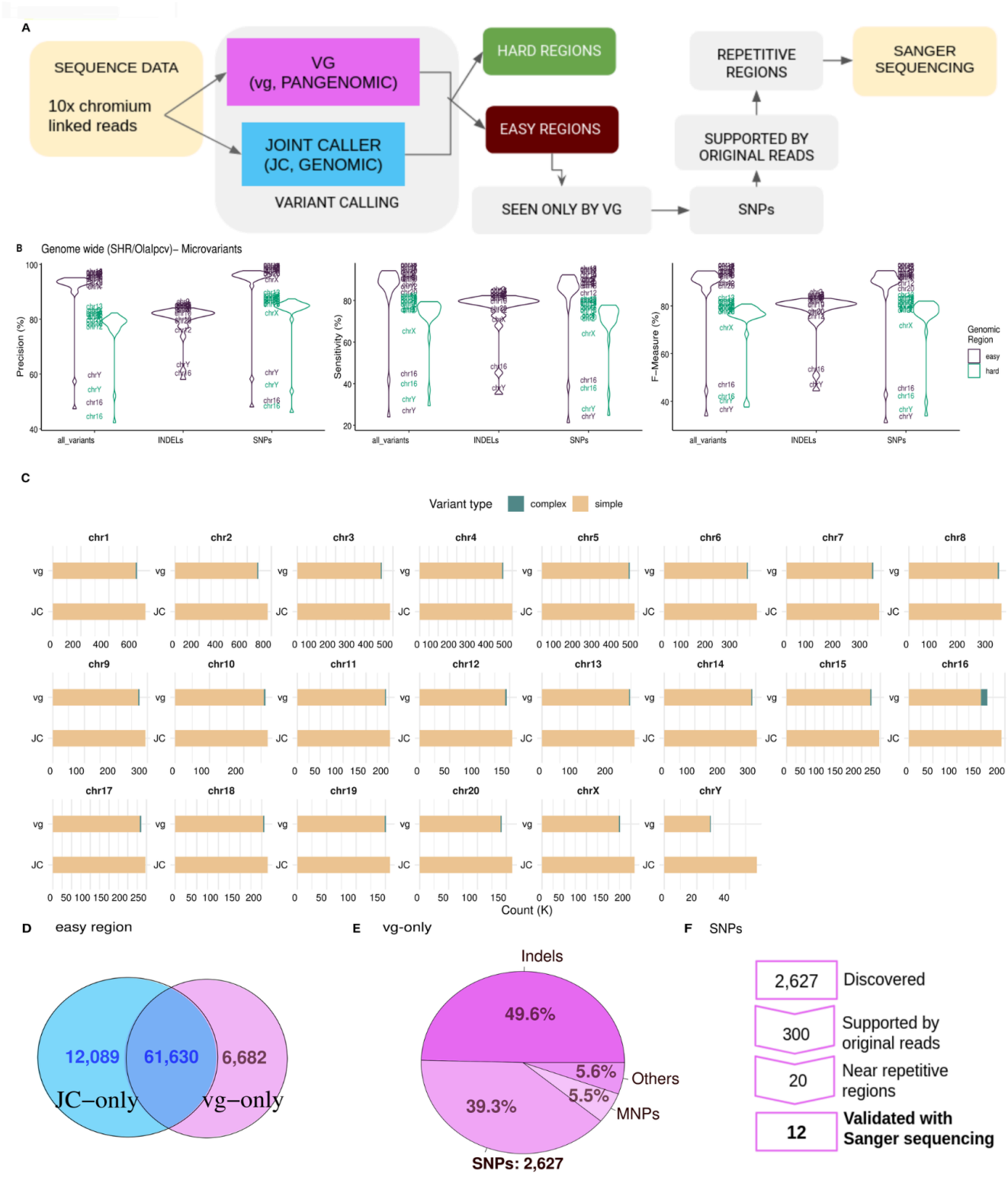

Figure S2. Validation in the SHR/Olapavic sample of the small variants called from the genome graph using vg. Small variants were validated over the JC call set (gold standard) in the SHR/Olalpcv sample according to the scheme in **(A). (B)** Genome-wide accuracy of vg calls is ~100% in the easy regions for SNPs, ~90% in the easy regions and ~80% in the easy regions for Indels and hard regions of the genome. Exceptions are seen for chromosomes 16 and Y, which are enriched for complex variation **(C)**. Validation through Sanger sequencing was restricted to easy regions **(D)**, to SNPs **(E)** supported by original reads and in challenging, repetitive regions **(F).**

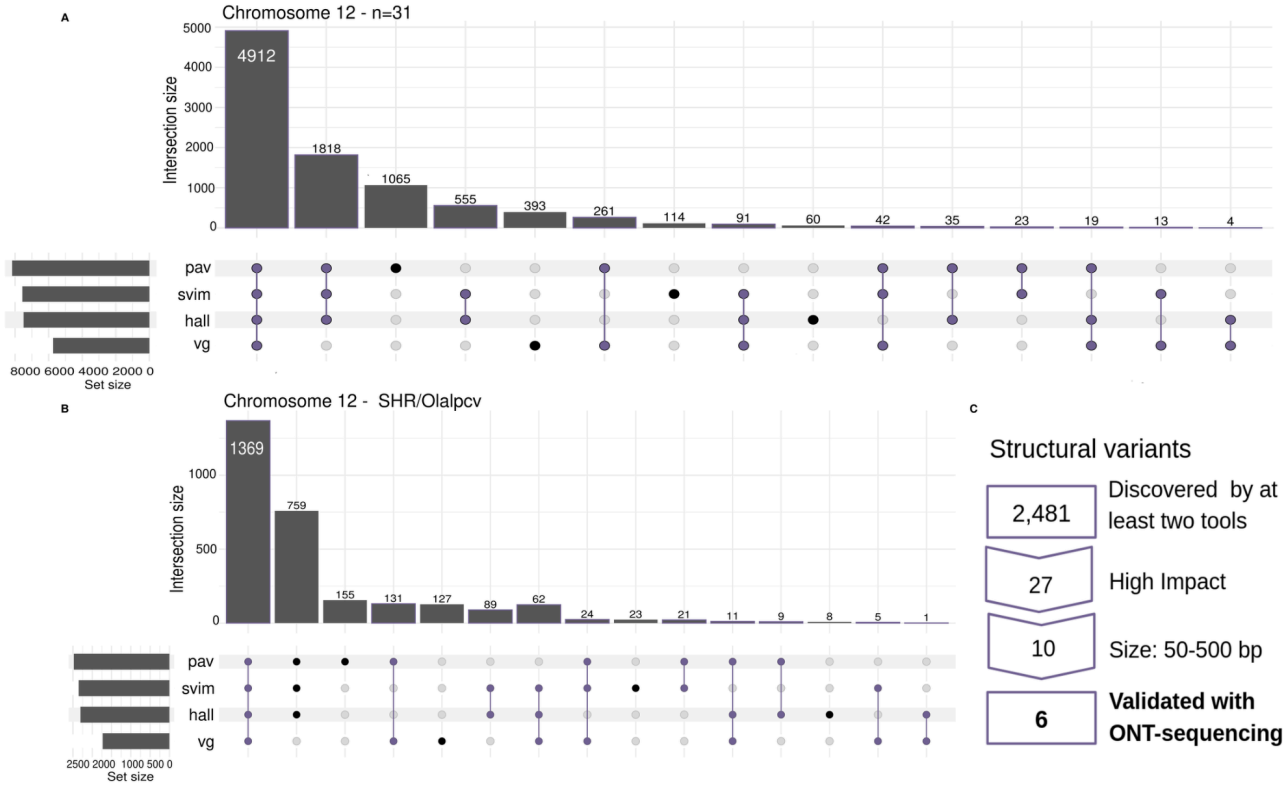

Figure S3. Validation in the SHR/Olapavic sample of the Structural Variants (SVs) called from the genome graph using vg. (A) Overlap of the call sets obtained by the three assembly-based methods (pav, svim, hall), and the graph-based method (vg) for chromosome 12 using the data from all rats. **(B)** Same as (A) for SHR/Olalpcv only. **(C)** Scheme of the validation for SVs

Figure S4. Integrated Genomic View of the validated SVs. For each SV gray bars are validated reads mapped against the mRatBN7.2/rn7.fa reference genome, red bars define the boundaries of the SV.

Supplementary tables: Supplementary Tables