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Genetic variation within 90 inbred rat strains mapped to mRatBN7.2

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The new rat reference genome has provided much needed improvements to the research community. To fully utilize this new resource we have analyzed a whole-genome sequencing datasets of 168 samples representing 90 strains. We utilized 10X linked-read sequencing data for 72 samples (60 unique strains, including the full HXB/BXH panel, 19 FXLE/LEXF strains, and the 8 founders of outbred heterogeneous stock) and Illumina short-read sequencing data for 96 samples (40 strains), including 39 samples downloaded from the Sequence Read Archive. Some strains overlapped between the technologies. Variants were called using Deepvariant, and joint-calling was performed with GLNexus, leading to the discovery of >16 million variant sites. We found 131,941 variants were shared by more than 160 samples, including BN, suggesting these are errors remaining in mRatBN7.2 or genotypes unique to the reference BN sample. The remaining variants included 5,879 with a high predicted functional impact on 4,431 genes. The most frequent high-impact variants included frameshift variants, splice acceptor and donor variants, and stop-gained variants. Annotation with disease ontology revealed that the human homolog of 897 of these genes are associated with 1,575 known diseases, such as cardiomyopathy, diabetes, and depression. The rat is a complex organism with a wide range of behavioral traits and a body large enough for easy phenotyping analysis. With the large set of variants and disease annotation provided, we have created a springboard for future research, including function and gene mapping studies using the hybrid rat diversity panel.