

Supplementary Material

Inherited and de novo variation in Lithuanian genomes: introduction to the analysis of the generational shift

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Supplementary Figures

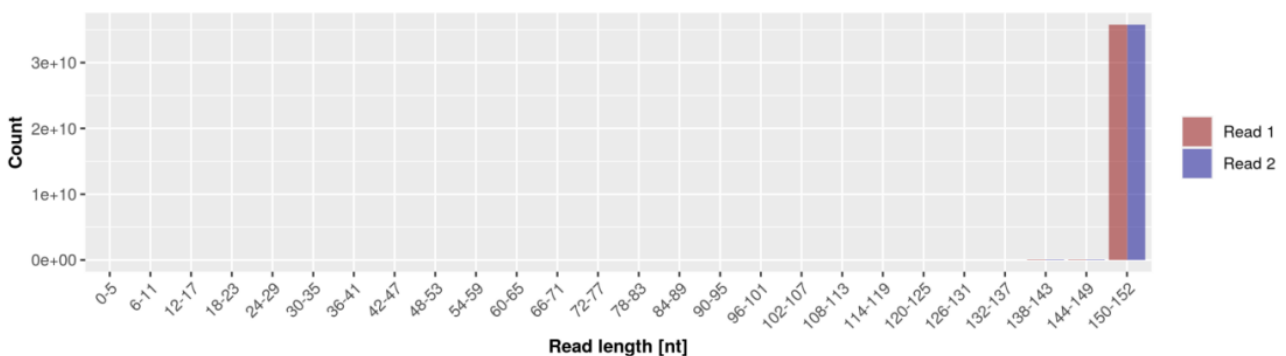


Figure S1. Sequence lengths of trimmed FASTQ reads (average of all samples) (DNA).

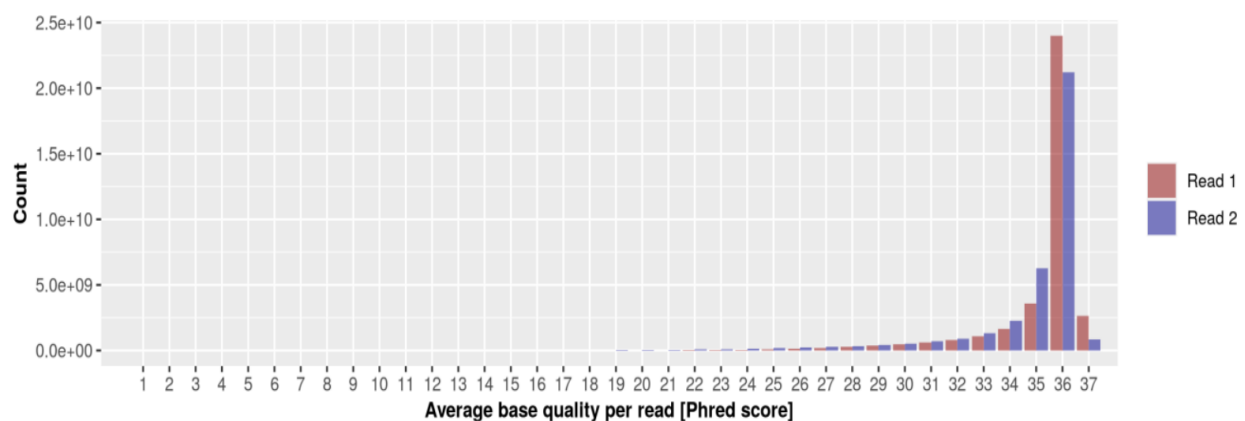


Figure S2. Sequence quality of trimmed FASTQ reads (average of all samples) (DNA).

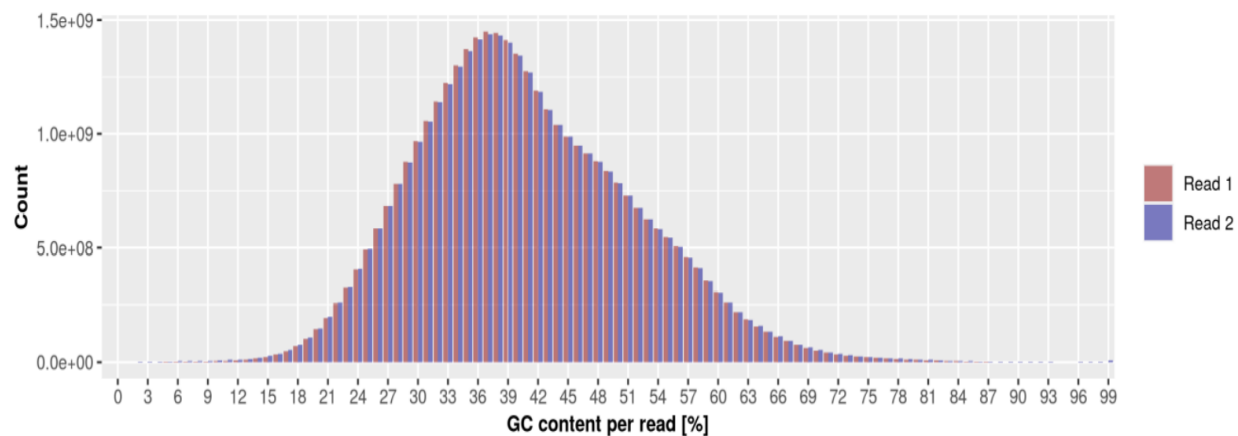
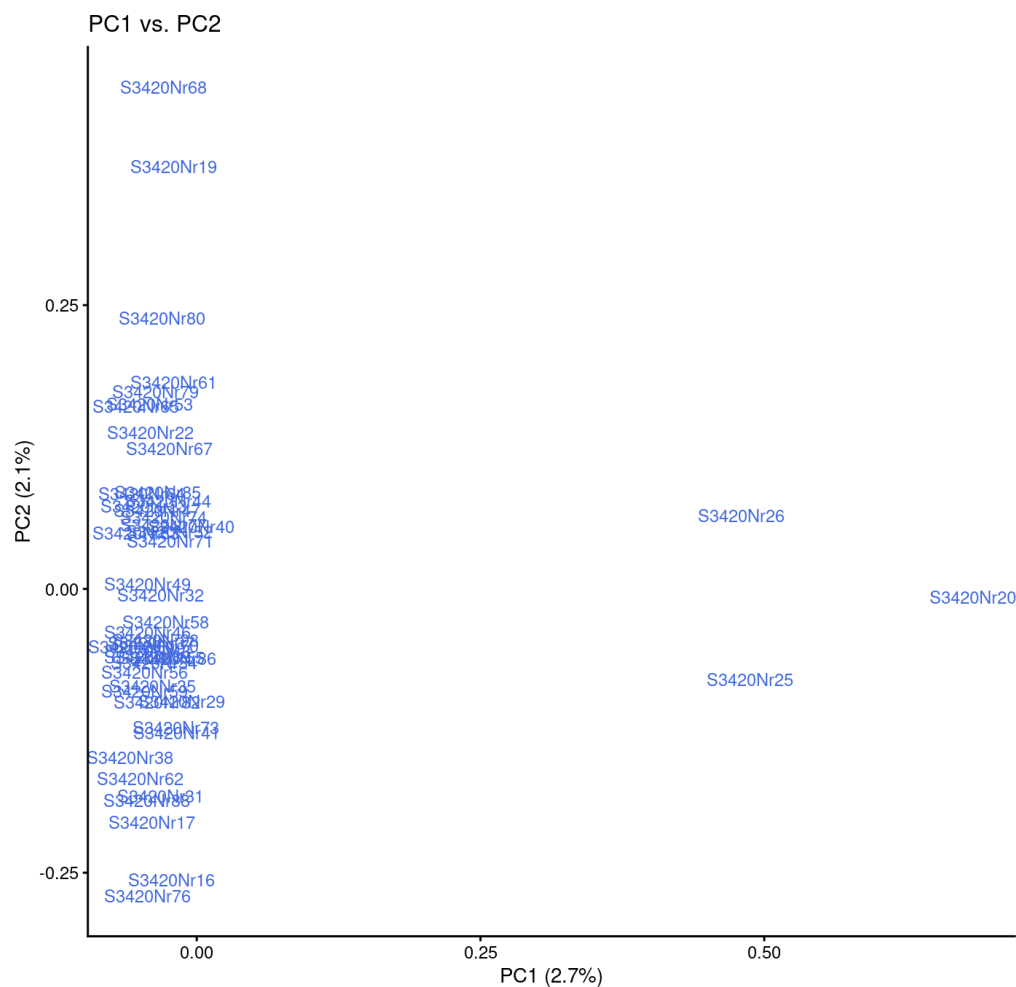


Figure S3. GC content of trimmed FASTQ reads (average of all samples) (DNA).



Figure

Figure S4. Principal component analysis (PCA) of 50 individuals (parents) from Lithuania included in the study.

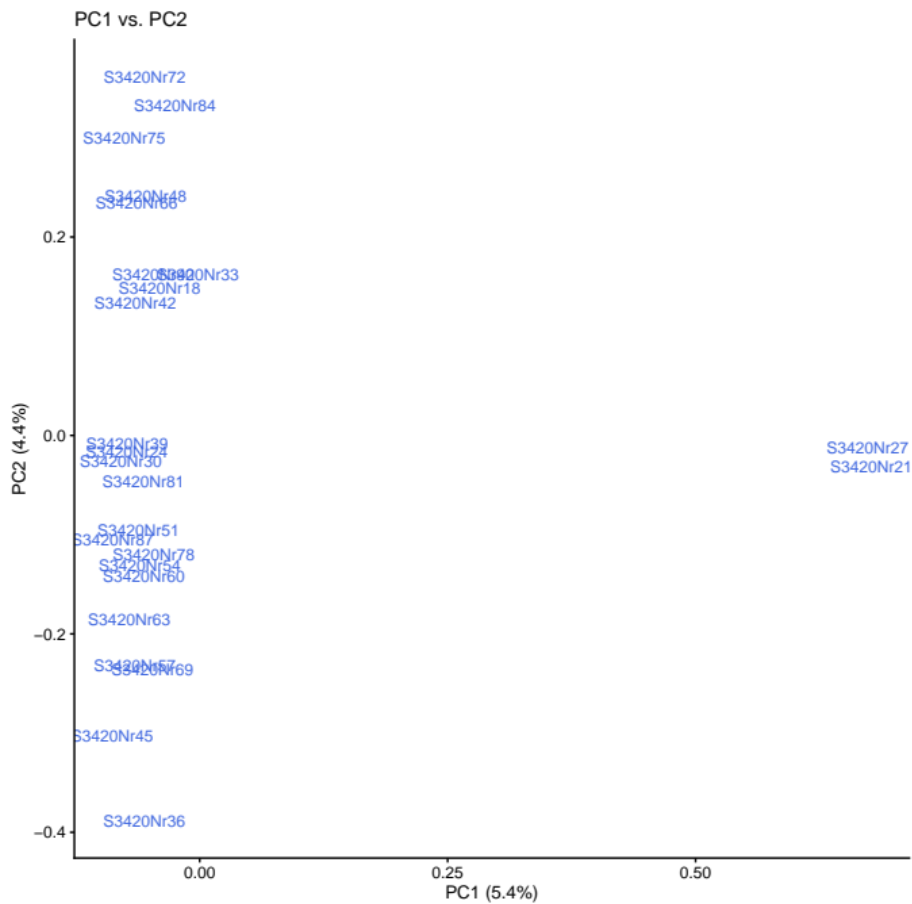


Figure S5. Principal component analysis (PCA) of 25 newborns from Lithuania included in the study.

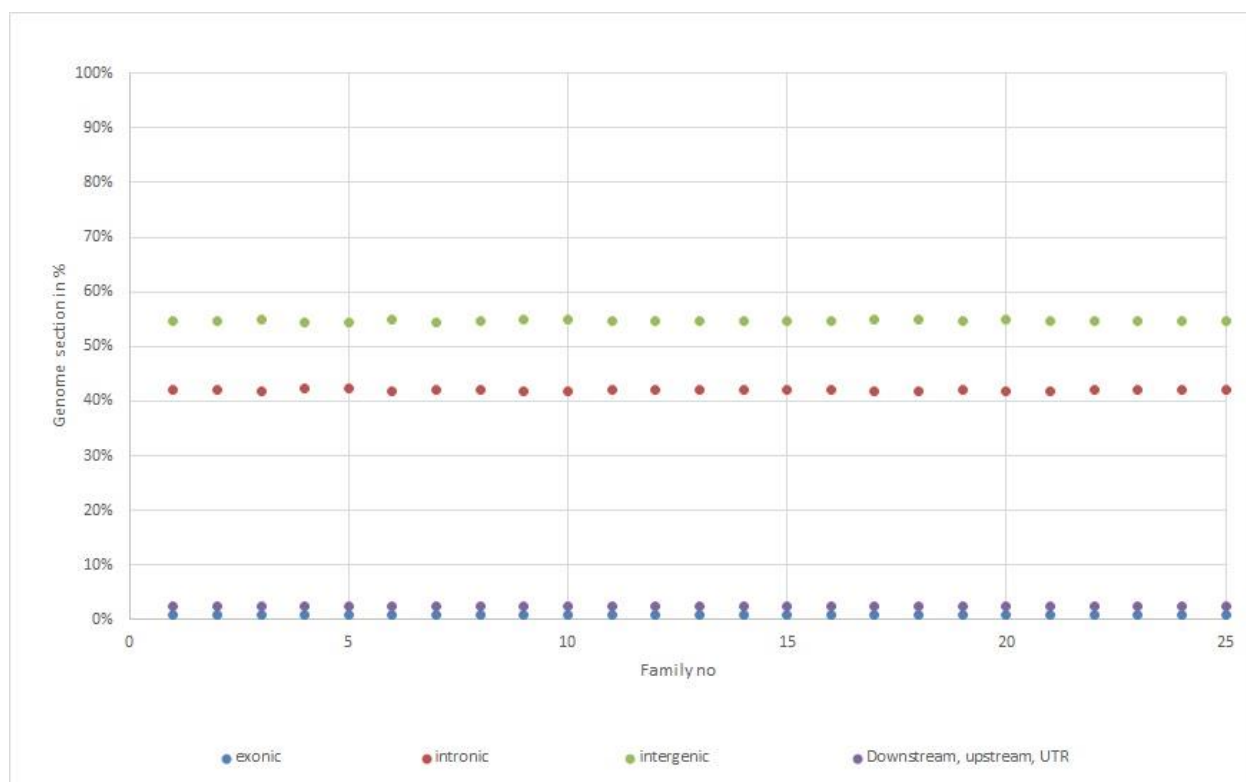


Figure S6. Summary of the identified variants. Distribution of SNPs and indels.

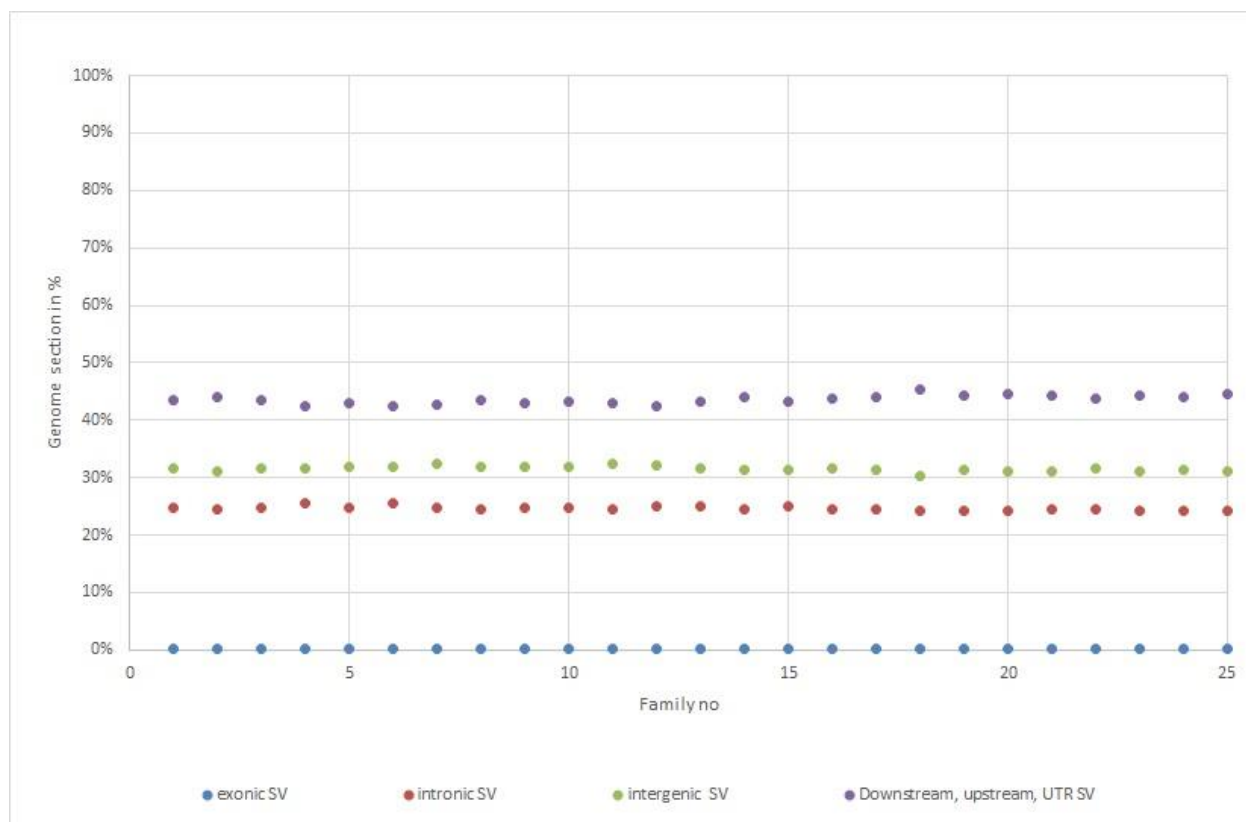
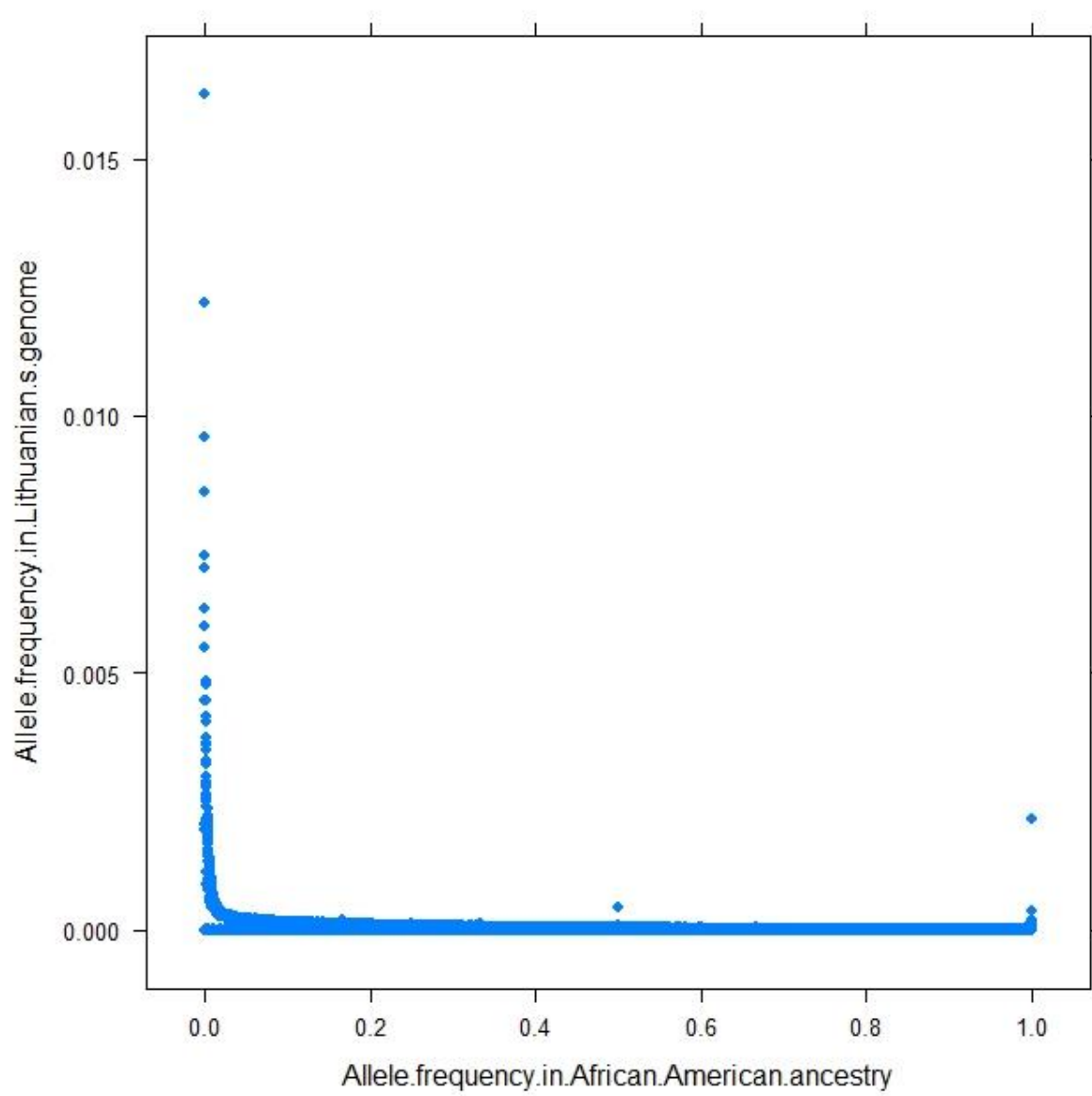
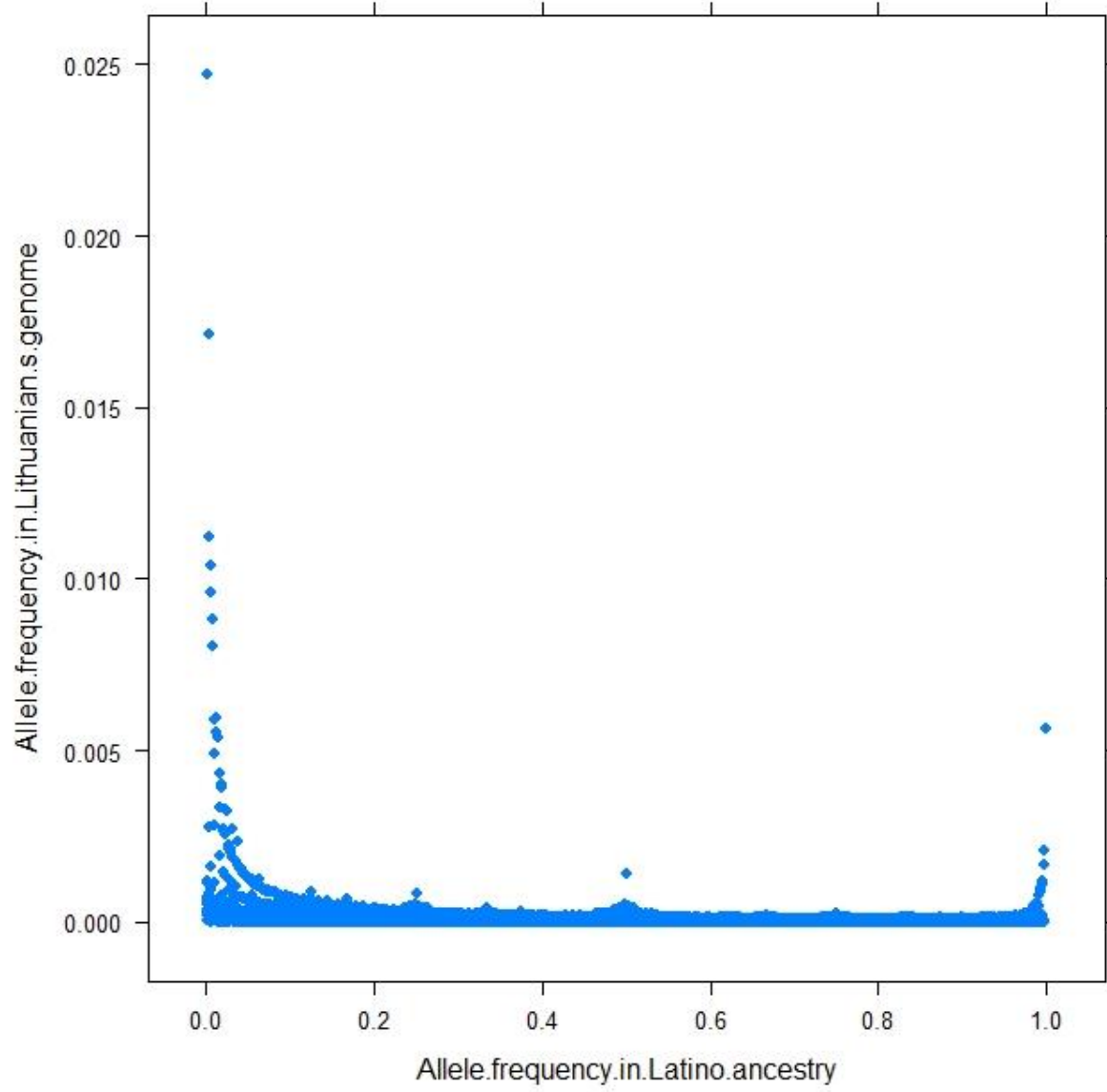
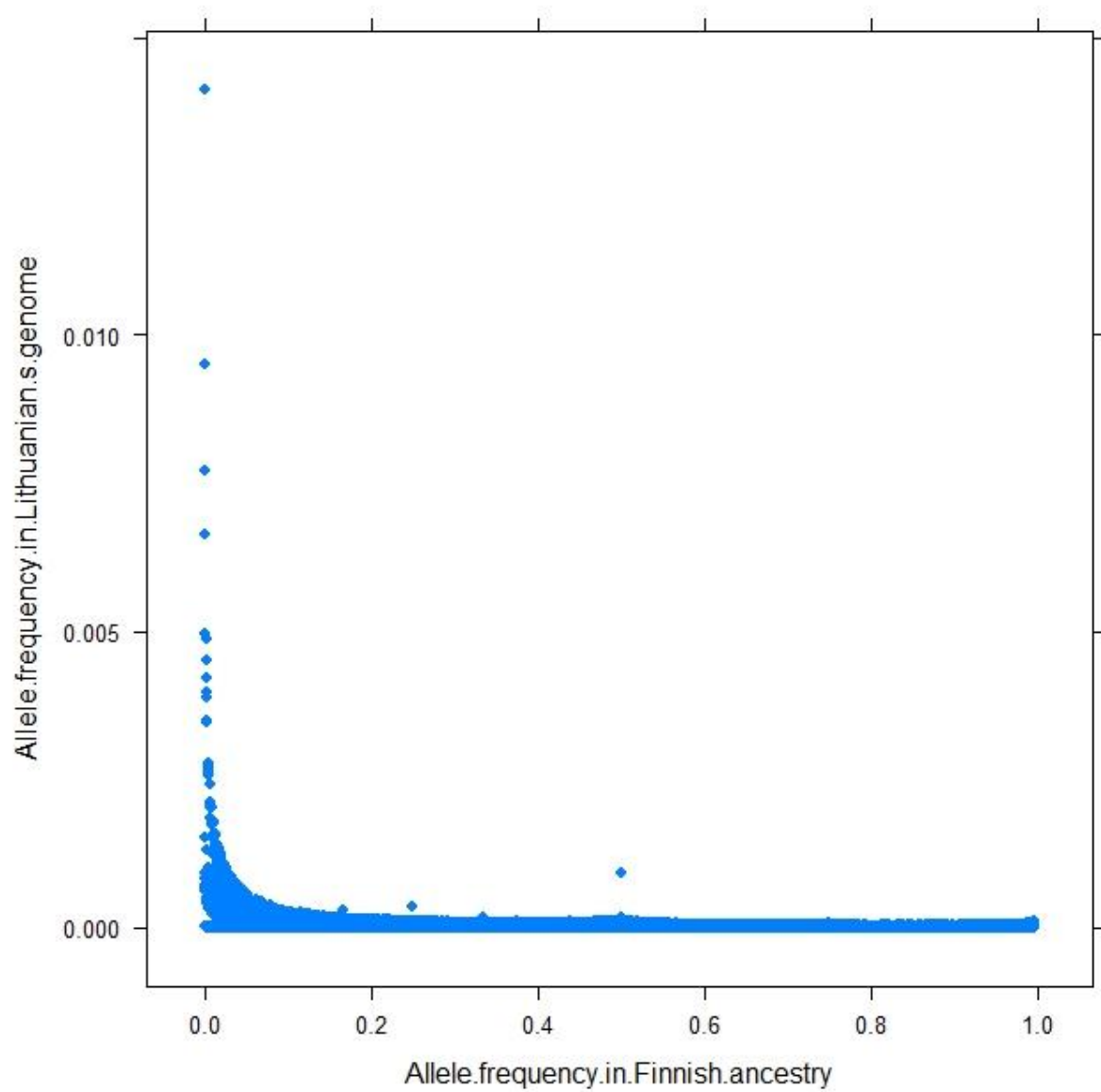
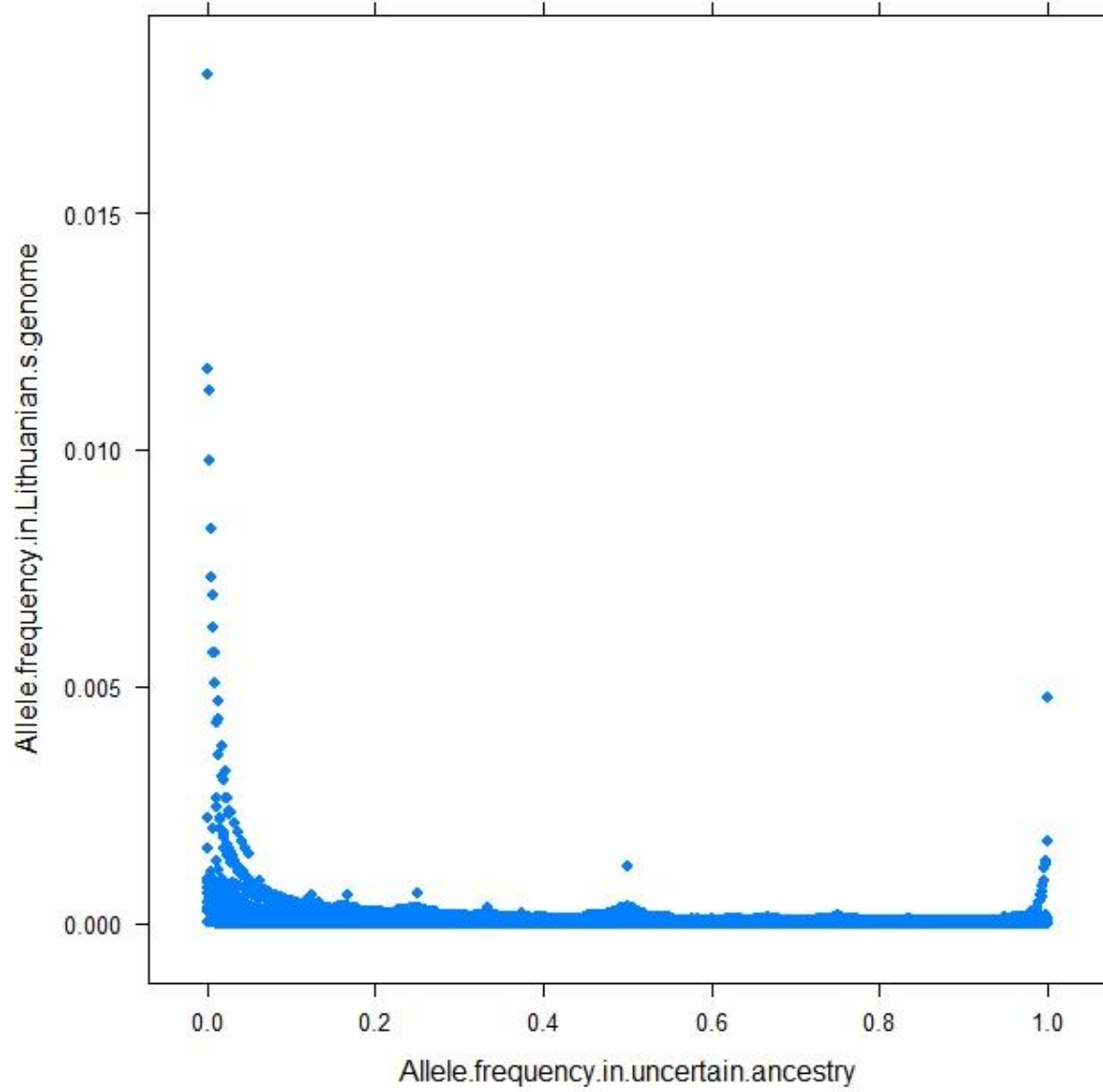


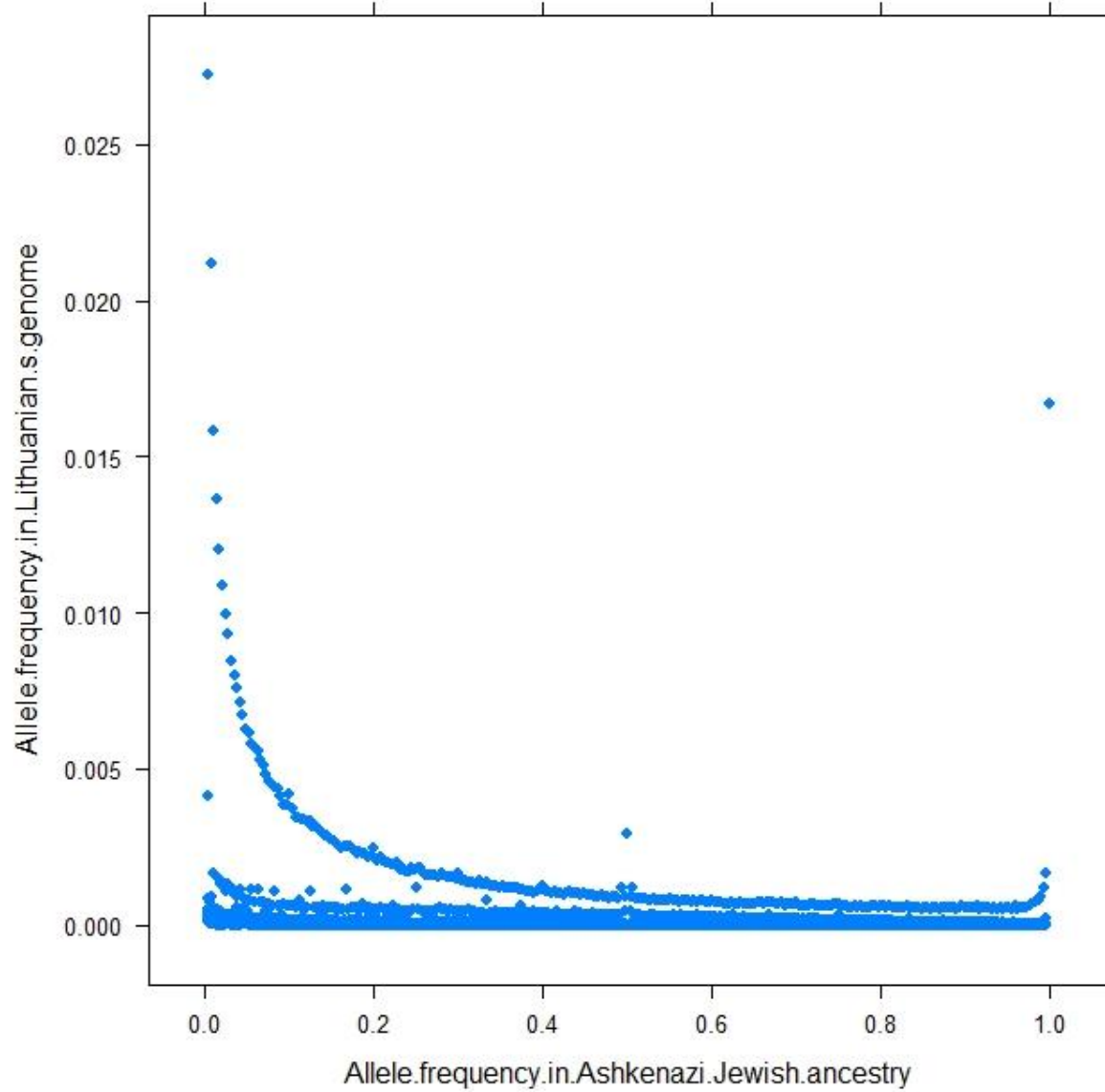
Figure S7. Summary of the identified variants. Distribution of structural variants.

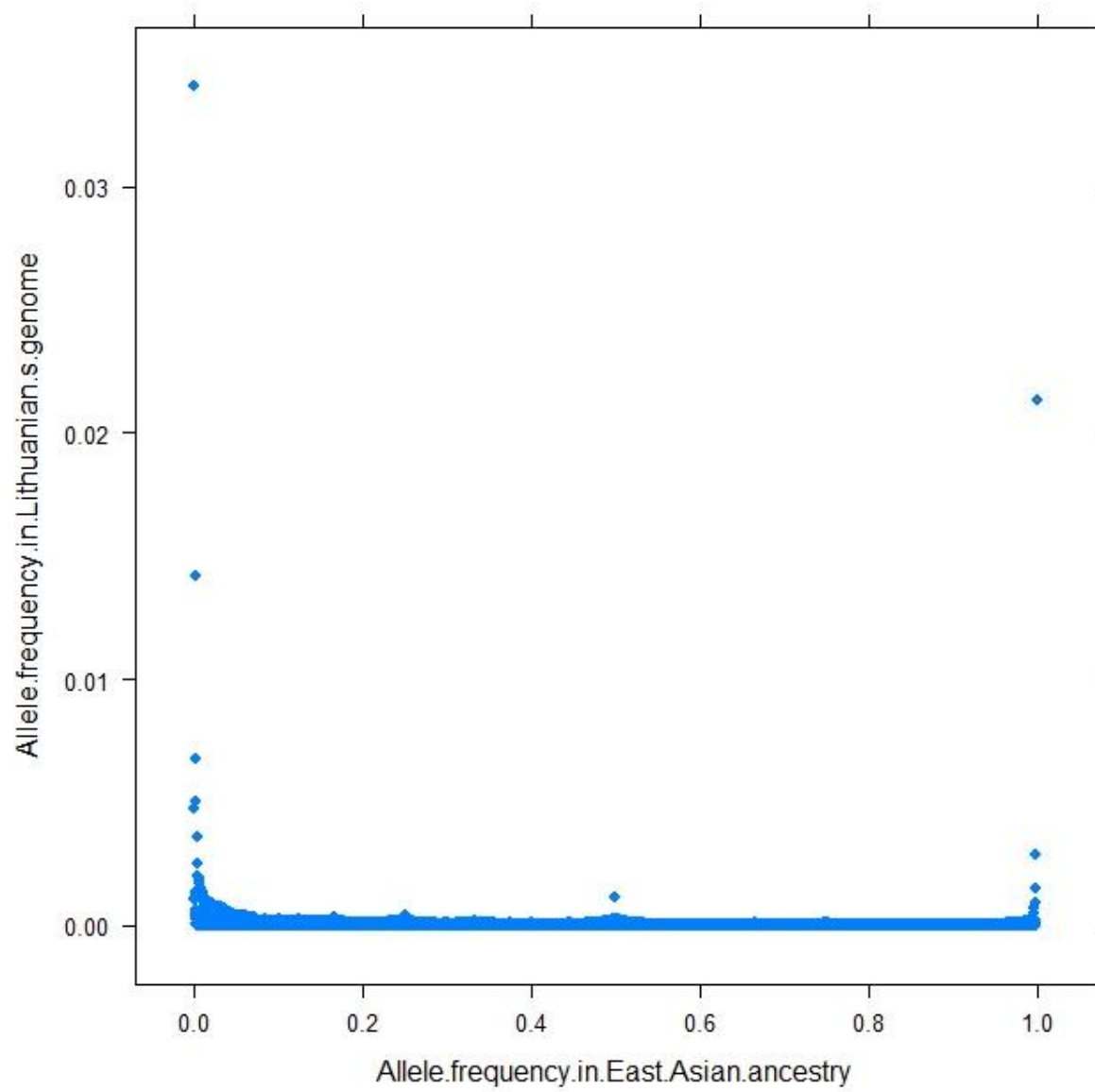












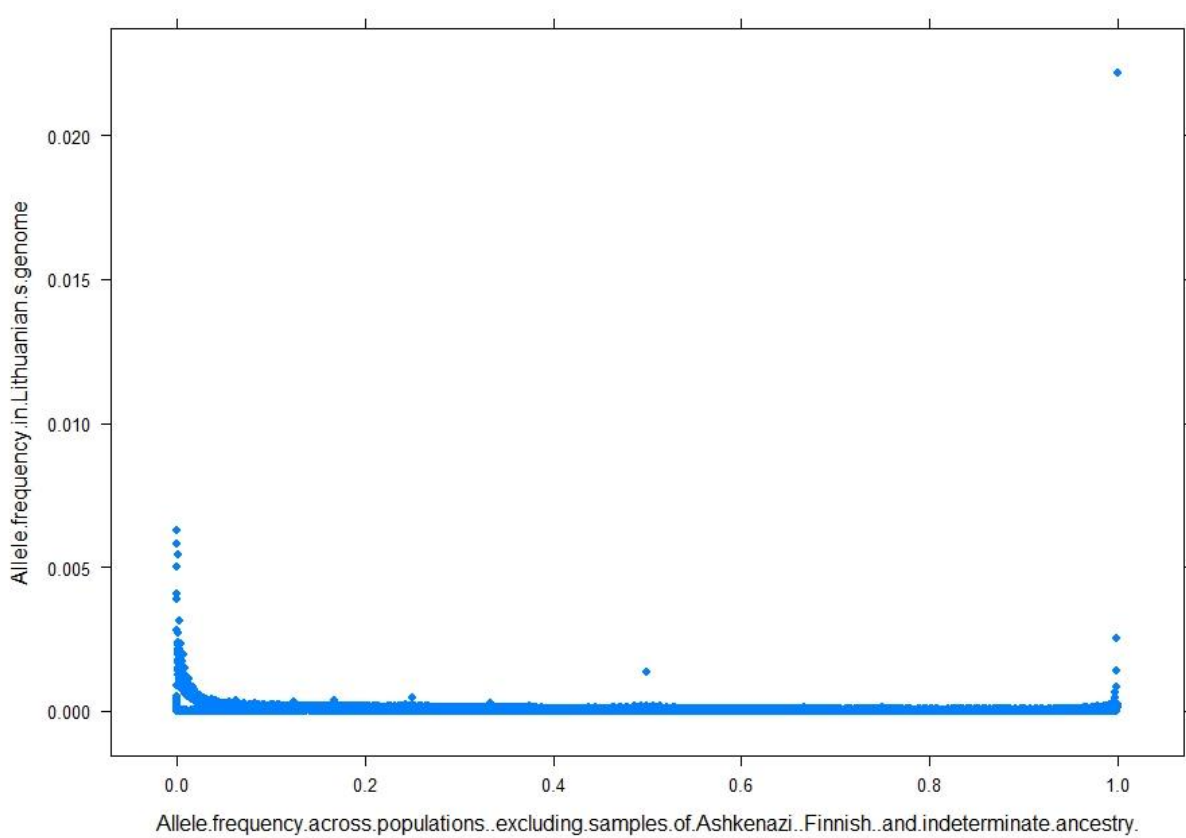


Figure S8. Allele frequency distribution comparison between the Lithuanian and African-American, Latino ancestry, Finish, uncertain, Ashkenazi Jewish, and east Asian ancestry genomes.