Hi Carl,

A visiting scientist in our group (Tomasz Stokowy) has extensive expertise in identifying harmful variants in extremely rare disorders from whole genome sequencing data. Dr. Stokowy had previously developed a tool ("RareVariantVis") to do exactly that.

We decided to analyze your genome using this tool. As expected, the results look very "normal" in that, as far as we can tell, no major chromosomal abnormalities were detected. You may view some of the results below, and a short legend is provided as a document in the same directory containing these images:

Chromosomes 1:

http://archive.gersteinlab.org/proj/zimmerome/part05/data/rarevariantvis/chr1.png

Chromosomes 6:

http://archive.gersteinlab.org/proj/zimmerome/part05/data/rarevariantvis/chr6.png

Chromosomes 7:

http://archive.gersteinlab.org/proj/zimmerome/part05/data/rarevariantvis/chr7.png

Figure legend:

http://archive.gersteinlab.org/proj/zimmerome/part05/data/rarevariantvis/RareVariantVis\_Legend\_160615.docx

Whole genome archive:

http://archive.gersteinlab.org/proj/zimmerome/part05/data/rarevariantvis/RareVariantVis\_Variants\_160613.zip

Certainly feel free to let us know if you have any questions. Many thanks.

best,

declan