

## **SUPPLEMENTAL FILES LEGEND.**

- A. Supp Fig 1. Estimated sequencing error rate for HiSeq and SOLiD platforms based on concurrent analysis of the PhiX genome.** Sequencing error rate is shown for each of the individual flow cell lanes on the Illumina HiSeq, as well as for the cumulative SOLiD dataset.
- B. Supp Tables. Detailed coverage statistics for all analyses where summarized data is presented in Figures 1 through 5.**
- C. Supp File 1. 101 Nuclear Mitochondrial Disease Panel commercially available as of October 2012 at GeneDx (Gaithersburg, MD).**
- D. Supp File 2. mtDNA genome regions targeted by eArray.**
- E. Supp File 3. Target coding and UTR regions of 16 Mitocarta genes having suboptimal coverage on standard 50 Mb exome capture kit.**
- F. Supp File 4. Numt regions analyzed in standard 50 Mb exome capture kit.**

**SUPP FIG 1.**

