EXHIBIT AD

Genomic Variant Filtering Process for Hypothesis-free WGS Testing

based on data from Patrick Folbigg

- The number of variants in every persons genome
- Variants that lie within genes
- Exclude variants at high frequency in normal population, and any with a CADD score of less than 10
- Exclude variants in non-protein coding transcripts, in an inhouse database of AGRF variants, & homozygous in population
- Exclude variants that were sequencing artefacts
- Analyse each variant to determine if the gene it is located in has a known disease association, and whether that is related to the phenotype under investigation in this family