The mRNA sequencing was conducted by the Clinical Genomics Center at the Oklahoma Medical Research Foundation (Oklahoma City, OK). Prior to mRNA-seq analysis, quality control measures were implemented. Concentration of RNA was ascertained via fluorometric analysis on a Thermo Fisher Qubit 4 fluorometer. Overall quality of RNA was verified using an Agilent Tapestation 4200 instrument. Following initial QC steps, mRNA was isolated and libraries were generated using the Watchmaker Genomics mRNA kit according to the manufacturers protocol. Briefly, mature mRNA was enriched total RNA via pull down with beads coated with oligo-dT homopolymers. The mRNA molecules were then chemically fragmented and the first strand of cDNA was generated using random primers followed by second strand synthesis and adapter ligation. Libraries were then indexed using IDT xGen Unique Dual Indexing primers. Final libraries for each sample were assayed on the Agilent Tapestation 4200 for appropriate size and quantity. These libraries were then pooled in equimolar amounts as ascertained via fluorometric analyses. Final pools were absolutely quantified using qPCR on an ABI QuantStudio 5 instrument with NEB Illumina Library Quantification reagents. Sequencing of the libraries was performed on an Illumina NovaSeq X Plus with PE150 reads.