



Supplementary Figure S2. SNV description. SNVs were classified based on the consequence at the RNA level (A) and type (B). SNVs class was also quantified, being C>T transition the most frequent (C). The median of variants per sample was 12 (D), missense variants were the most frequent (E). *HSPG2* presented the highest number of variants and variants were found in the 100% of the analyzed individuals (F). *ctl* corresponds to control. *Ddc* corresponds to the individuals with developmental dysplasia of the hip.