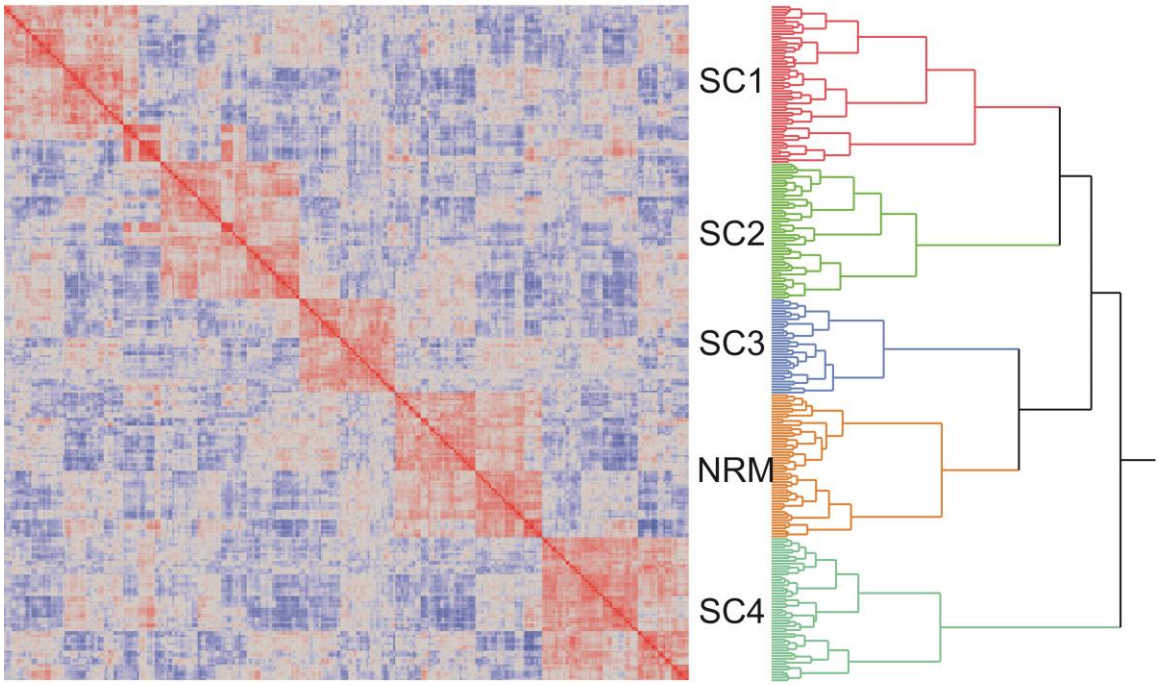
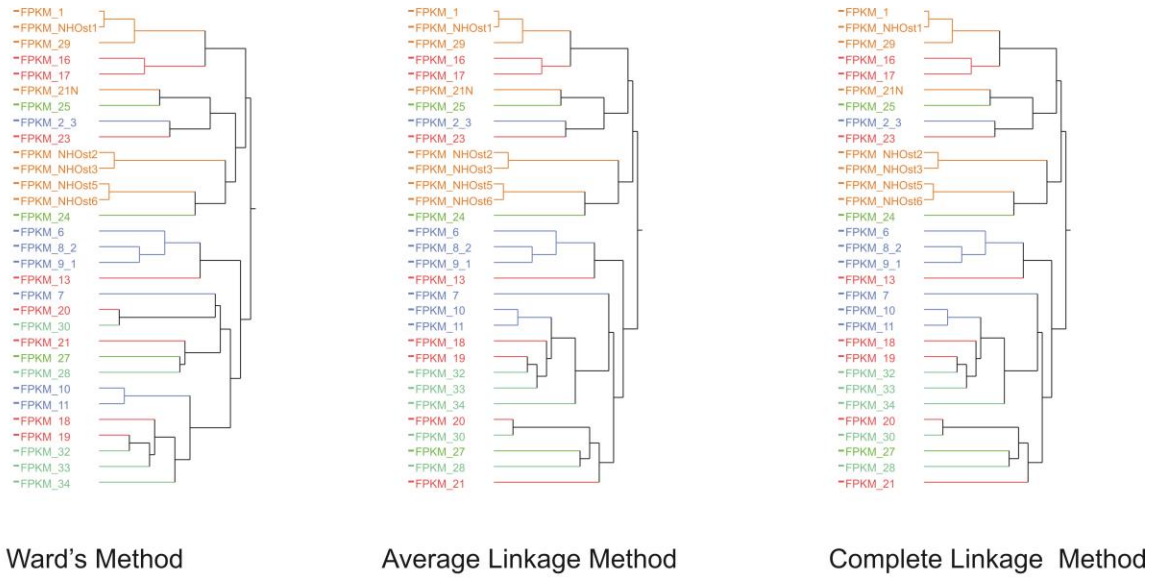
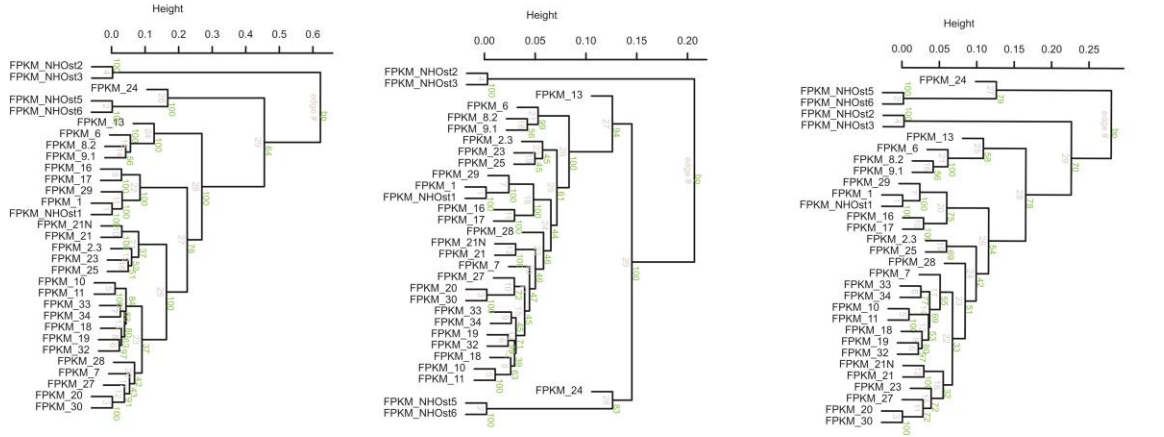
Suppl. Figure 1. Rojas-Peña et al, 2013



Supplementary Figure 1. Initial cluster analysis of the Stamper *et al*. (2011) dataset. GSE27976 was downloaded from GEO and run through the Basic Expression Workflow in JMP-Genomics, generating the clustering of samples based on overall similarity shown in (A). The central cluster highlighted in Bold corresponds to the 50 normal samples, while the other three major clusters correspond to samples GSM692146 to GSM692195 (C1), GSM692196 to GSM692230 (C2), GSM692231 to GSM692289 (C4) and GSM692290 to GSM692387 (C3). After removing the normal samples and normalizing with SNM to remove the four probable batch effects, four new clusters are observed (B), coloring of which by original cluster sub-type shows no correspondence to the original clusters.

Suppl. Figure 2. Rojas-Peña et al, 2013





Supplementary Figure 2. Bootstrap support for sub-types of craniosynostosis samples in the RNA-Seq datasets. (A,B,C) Centroid, Average linkage, and Ward two-way hierarchical clustering of 8,025 transcripts with FPKM > 2 in JMP Genomics confirm the separation between the craniosynostosis types and normal samples. (D,E,F) Hierarchical clustering using pvclust in R generates bootstrap support with 64% of bootstrap samples separating the normal long bone and cranial bone samples, and support for the three craniosynostosis sub-groups ranging from 80% to 100%.