Supplementary Figure 1 Cartilage genes are significantly up-regulated in calvaria over-expressing ERRα. SigPathway analysis of expression profiling in calvaria infected with ERRα or GFP and cultured for 4 days before RNA isolation demonstrates up-regulation of genes involved in cartilage development. This empirical cumulative distribution plot shows the distribution of t-statistic values for all genes on the array (light blue), or genes in the given functional categories (dark blue). N represents the total number of genes in the category. The false discovery rate based on randomized permutation of gene labels is FDR=0.