

Figure S2. Post-injury gene expression changes correlate with histone modification levels for H3K27Ac and H3K4me3 - but not H3K27me3 – for all genes when compared to Control. (A-I) These scatterplots show all genes with associated active regions for each histone modification. Changes for both genes and histone modifications are in log2 fold-change (LFC). Correlation is represented by Pearson's r and p-values are from correlation tests (0.05 significance level). Blue lines represent linear regressions.