CR in vivo screen hit definition:

Primary hits

1. Draw a DESeq pVal cutoff at .75
2. Sort genes based on log2 fold-change and divide list into two groups: positive values and negative values
3. Sort each list based on shRNA symbol.
4. Identify primary hits as any gene with > 2 shRNAs result in a pVal of less than .75 that has a log2 fold-change of the same sign. (For shRNAs in which 2 have positive values, and 2 have negative values, we will consider these “ambiguous”, but don’t them eliminate yet).