Figure S1 *(preceding page)*: **Examples of cross-correlation plots and QC score assignments for both ChIP-seq and control datasets.** Successful ChIP-seq is expected to show a very high cross-correlation peak relative to the read length "phantom peak". Failed ChIP-seq experiments lack such a peak. Control libraries (sonicated inputs or IgG input) are also expected to lack this peak; the presence of a high cross-correlation peak is most likely due to a very strong Sono-seq effect (Auerbach et al. 2009). (A). Example of a ChIP-seq dataset with QC score of -2 (from Visel et al. 2009; Gotea et al. 2010; Blow et al. 2010). (B). Example of a ChIP-seq dataset with QC score of -1 (from Ho et al. 2009). (C). Example of a ChIP-seq dataset with QC score of 0 (from Yuan et al. 2009). (D). Example of a dataset with QC score of 1 (from He et al. 2011). (E). Example of a ChIP-seq dataset with QC score of 2 (from Handoko et al. 2011). (F). Example of a control dataset with QC score of -2 (from Lee et al. 2010). (G). Example of a control dataset with QC score of -1 (from GSE15844). (H). Example of a control dataset with QC score of 0 (from GSE23581). (I). Example of a dataset with QC score of 1 (from Vermeulen et al. 2010). (J). Example of a control dataset with QC score of 2 (from He et al. 2011).