



Figure S11 (preceding page): Examples of ChIP-seq datasets with high cross-correlation scores, which, however, seem to contain an unexplained source of read clustering other than specific immunoprecipitation enrichment of the targeted protein as measured by cross-correlation. (A,B) Cross-correlation plots for Nanog and Smad1 ChIP-seq in mESC cells from Chen et al. 2008. Each dataset receives extremely high RSC scores (356.86 and 298.50, respectively), but the cross-correlation profiles are very atypical, displaying an strikingly narrow peak and a very small phantom peak. (C,D,E). RAP1 ChIP-seq in wild type (WT) and RAP1 knock out (KO) cells as well as a corresponding input sample from Martinez et al. 2010. Here both the input and the KO sample ChIP (which should exhibit no immunoprecipitation enrichment) have a very high enrichment peak and high RSC scores. Thus the observed enrichment in the WT RAP1 ChIP-seq sample likely contains a significant contribution from a source different from actual RAP1 binding events. (F,G) A similar situation in a ChIP-seq dataset targeting p53 phosphorylated at Ser18 (p53-pS18) (Li et al. 2012).).