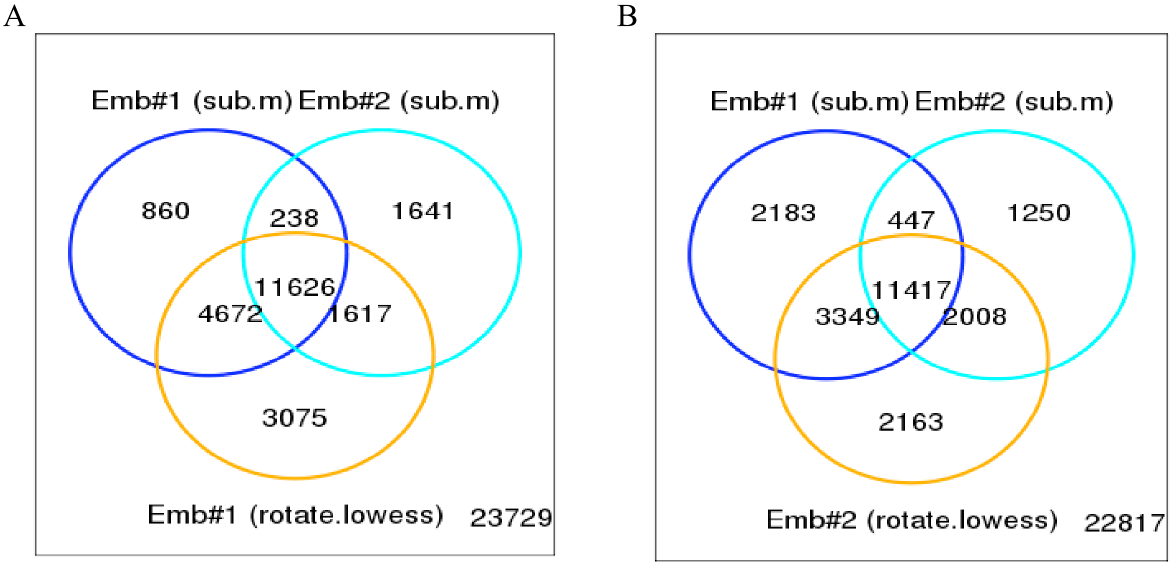
Adaptation of the Peng *et al.* normalisation method: validation



Supplemental Fig. S1: As we readapted the implementation of a previously described normalisation method (Peng *et al*., 2007), we went through the validation method described in the original paper, which consisted in studying whether there was a change in results between this normalisation method and the standard mock subtraction. We used *Drosophila melanogaster* embryo male specific lethal complex ChIP-on-chip data from the above-mentioned paper. In these supplemental figures, we display Venn diagrams that show overlap of clusters obtained between two replicates using mock subtraction (Emb#1 sub.m, dark blue and Emb#2 sub.m, light blue) and the new normalisation method implemented in CoCAS (Emb#1 rotate.lowess and Emb#2 rotate.lowess, orange) for each embryo, A and B. Overall, these Venn diagrams show more overlap between results of each mock subtraction method and that of the new normalisation method implemented in CoCAS than between the mock subtraction groups themselves, as well as the same trend in results as in (Peng *et al*., 2007). This is an additional argument for the consistency of the new method implemented in CoCAS.

References:

Peng,S. et al. (2007) Normalization and experimental design for ChIP-chip data. *BMC Bioinformatics,* 8, 219.