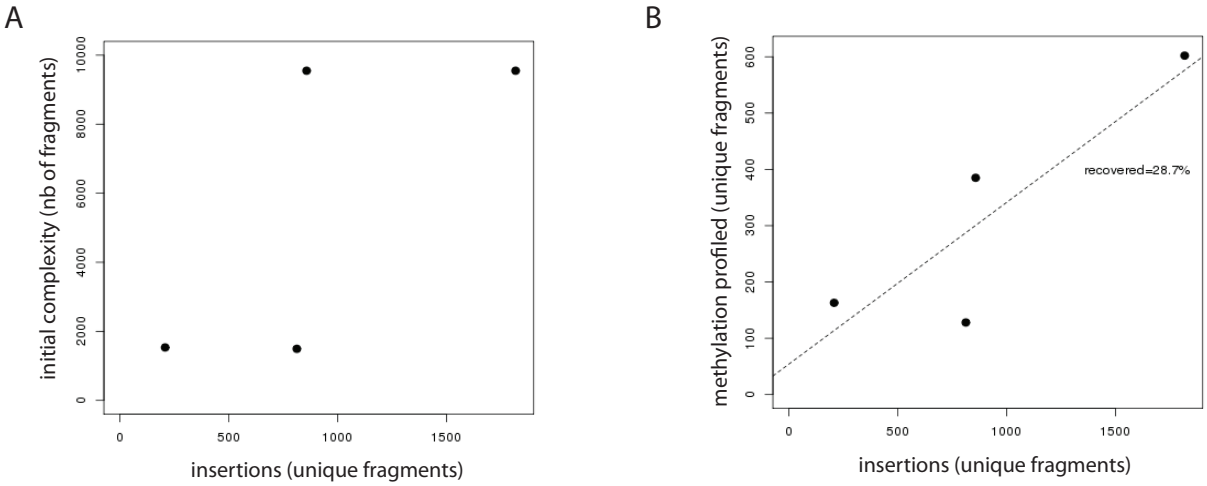

Figure 1-figure supplement 1:
(A) Evaluation of the library insertion efficiency for four of the tested libraries shows up to 1,800 insertions per experiment. Compared are the numbers of unique fragments in the initially cloned pool as determined by sequencing of the native PCR performed on the library containing plasmid and the number of unique fragments inserted in the mESC genome as detected by sequencing of the native PCR performed using the universal primers flanking the fragments. The number of uniquely detected fragments depends on the initial library complexity. (B) Evaluation of the proportion of inserted fragments recovered during the methylation profiling as measured by sequencing of the PCR performed on the bisulphite converted gDNA. This reveals that around 30% of the initially inserted fragments are efficiently covered suggesting that bisulphite PCR is the limiting step of the experiment.