

**S1 Figure. Alignment of the SmCBX chromo domain (CD) to other CD-containing proteins reveal conservation of critical residues required for H3K9me3 binding.** The chromo domain (CD) from *Homo sapiens* Suv39h1, labelled HsSUV39H1 in the alignment (GenBank accession number: CAG46546) and *Drosophila melanogaster* HP1, labelled DmHP1 in the alignment (GenBank accession number: ACI96784.1) were aligned against that of SmCBX. Invariant residues are highlighted in blue and presented in upper case. Partially conserved residues (i.e. among pairs with similar physico-chemical properties) are shaded grey and presented in upper case. Non-conserved residues are shown in lower case and are not shaded. Residues known to form the aromatic cage that interacts with the methylammonium group of H3K9me3 are indicated below by “\*”. Residues indicated by “#” are involved in direct interactions and recognition of histone H3 [55, 56].