

### Average conservation fraction of all identical bases

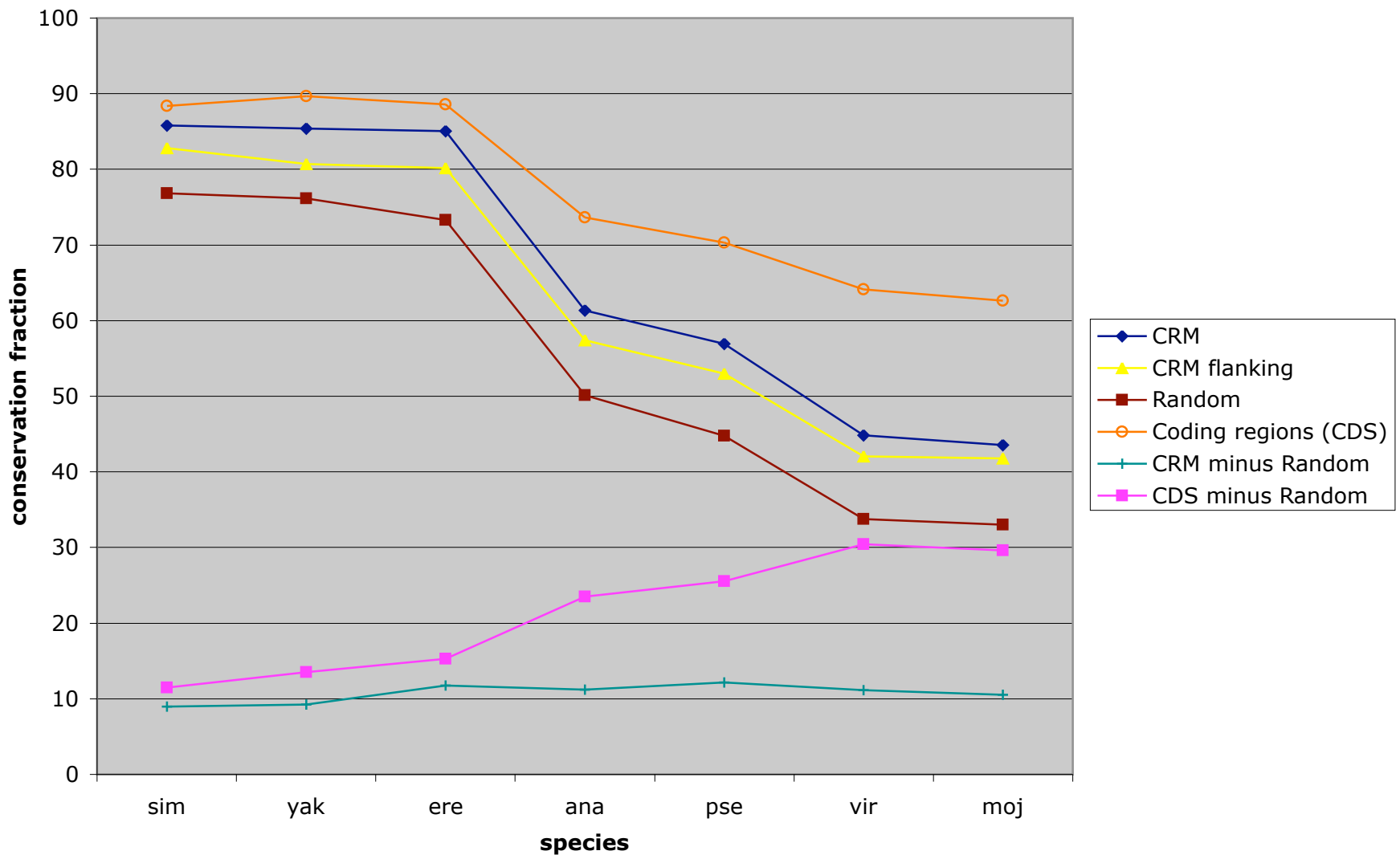
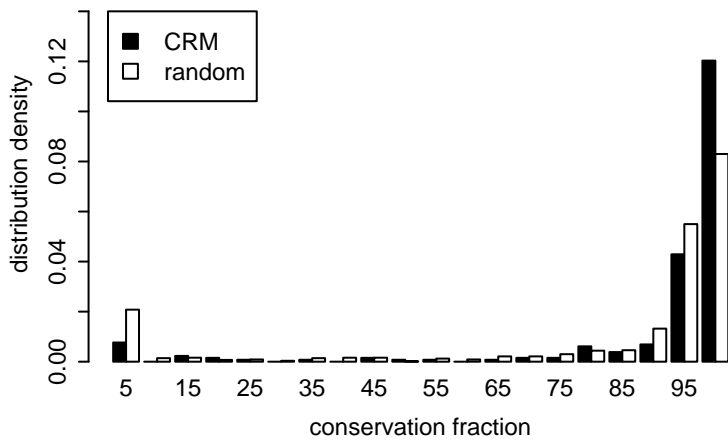
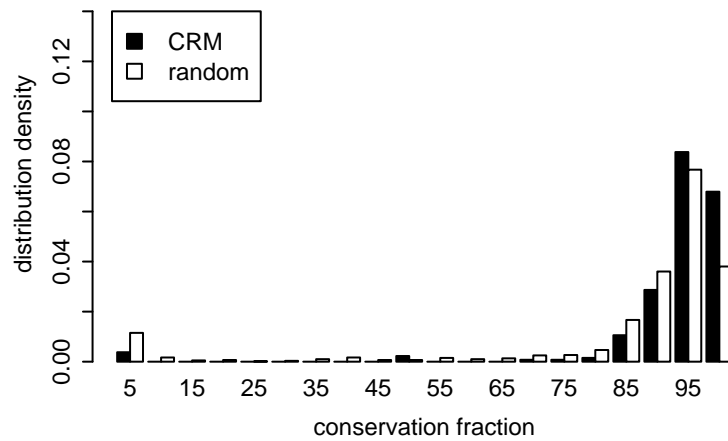


Figure S3-1: Average conservation fraction of all identical bases. See Fig. 3A and legend for details of each data type.

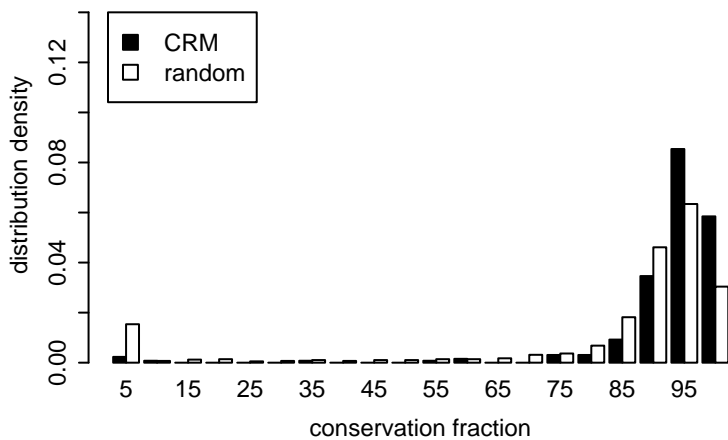
**The distribution of conservation fraction mel/sim**



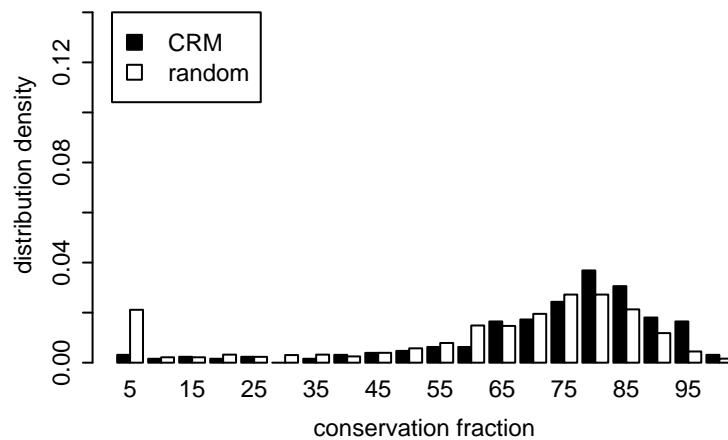
**The distribution of conservation fraction mel/yak**



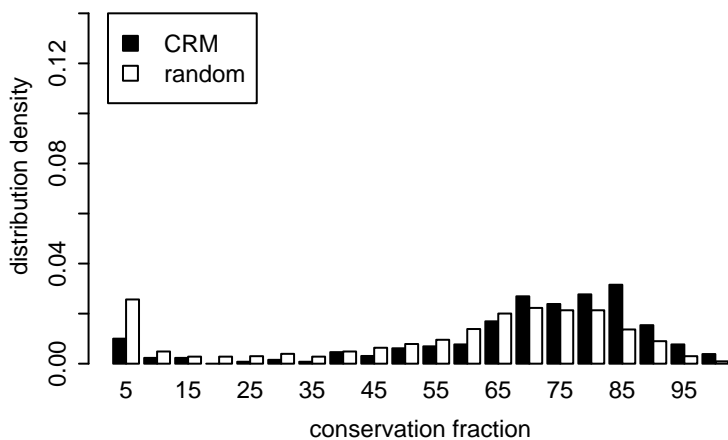
**The distribution of conservation fraction mel/ere**



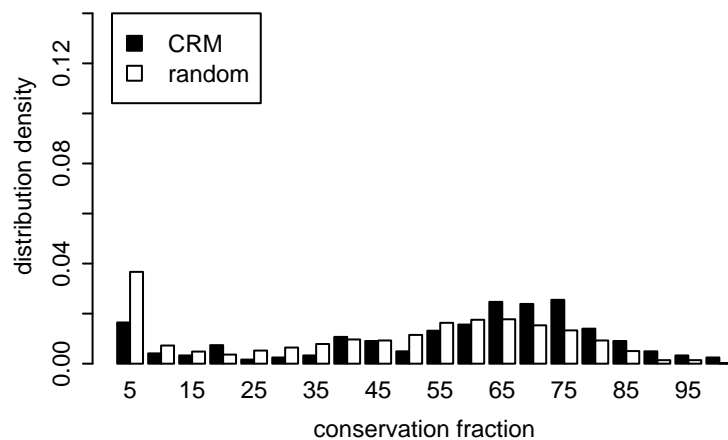
**The distribution of conservation fraction mel/ana**



**The distribution of conservation fraction mel/pse**



**The distribution of conservation fraction mel/vir**



**The distribution of conservation fraction mel/moj**

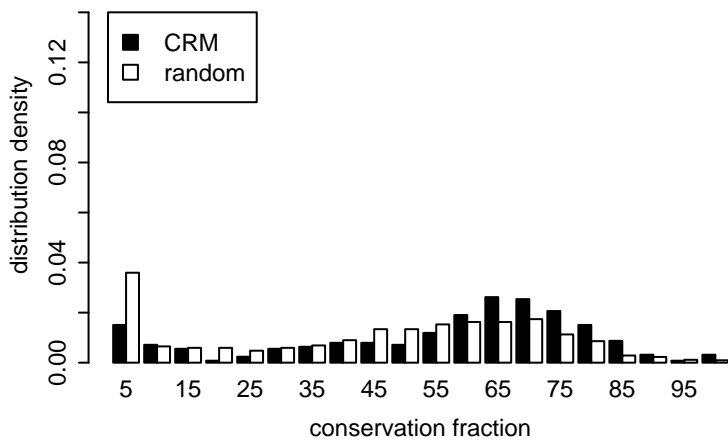


Figure S3-2. Histogram of the conservation fraction for CRMs (black bars) and random non-coding sequences (white bars) for *D. melanogaster* aligned with each of the other species.

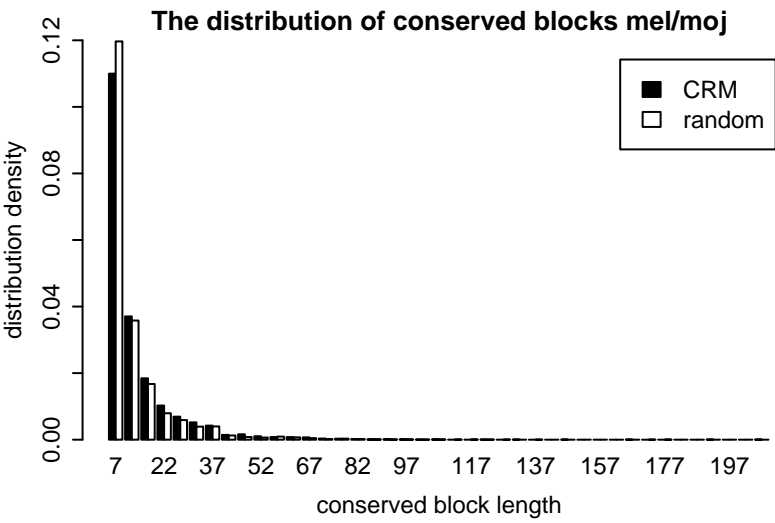
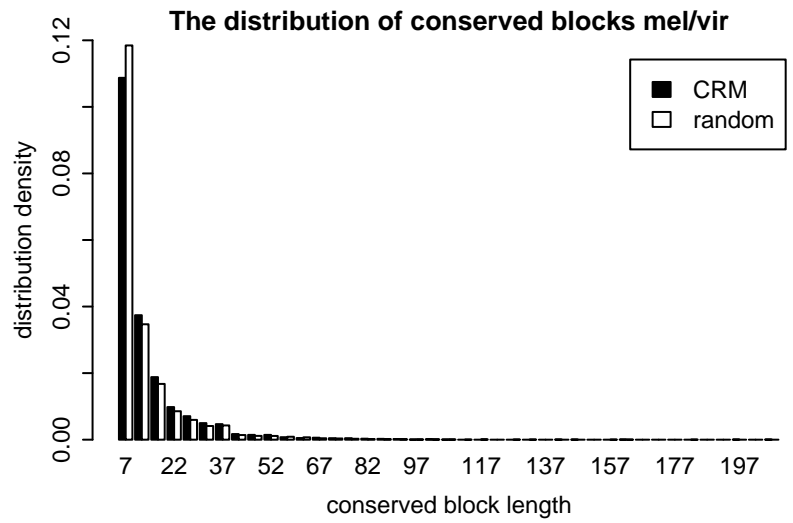
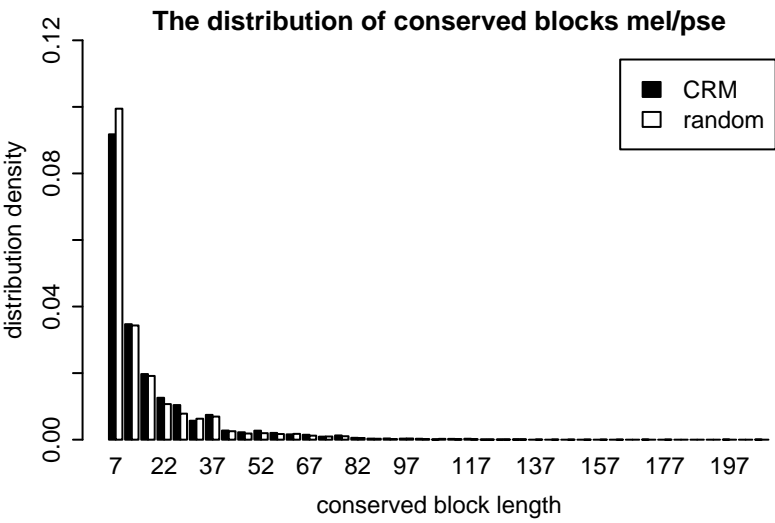
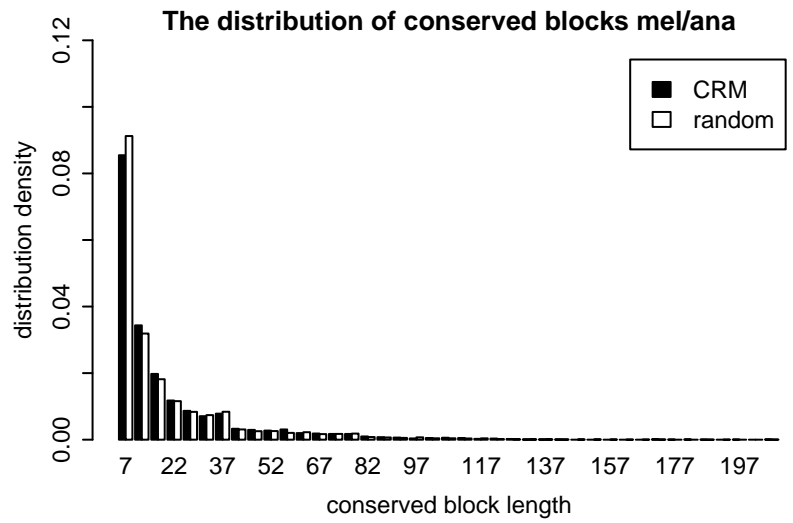
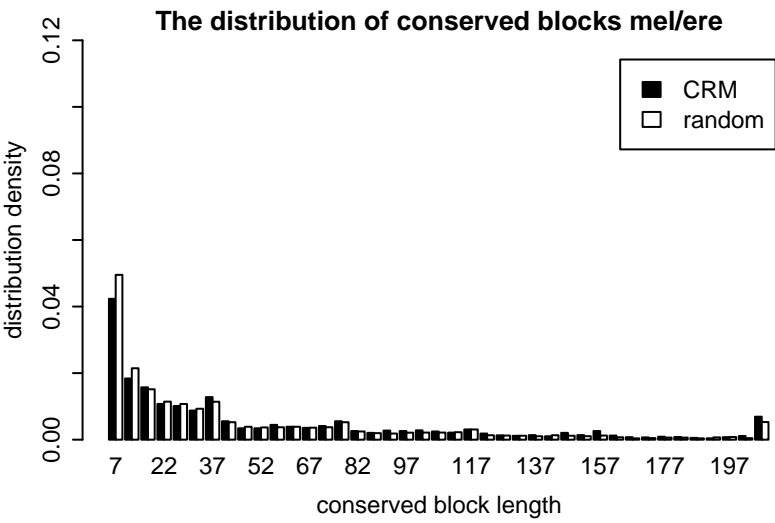
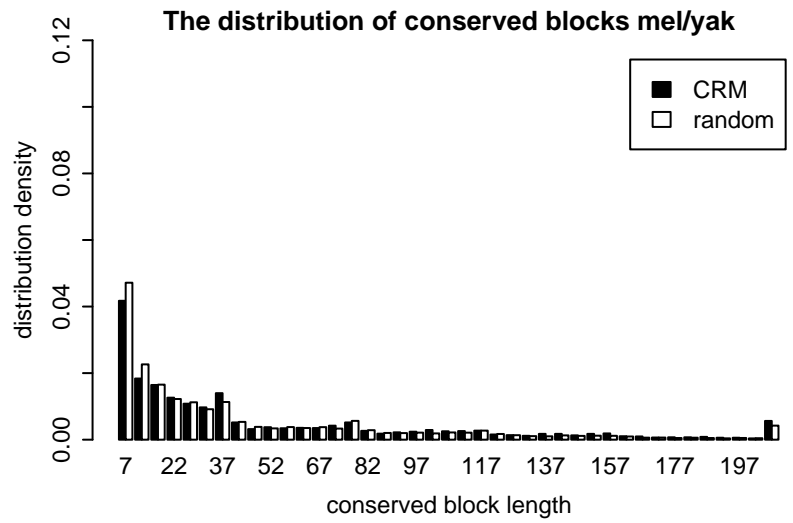
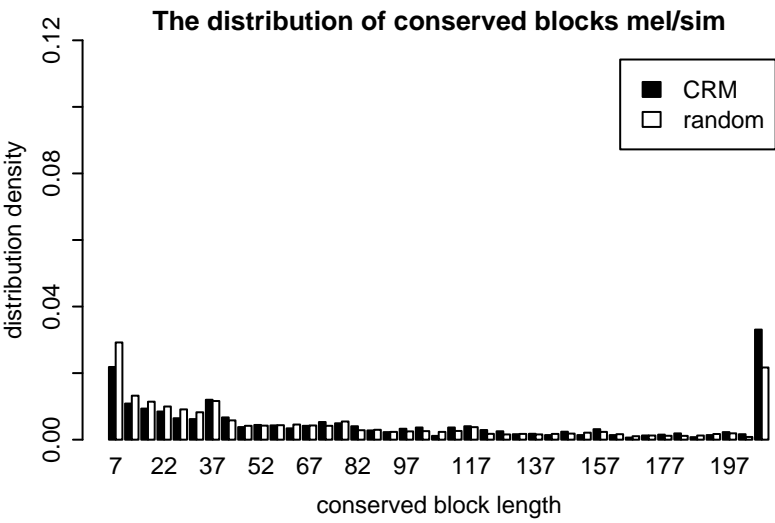


Figure S3-3. Histogram of the conserved block length for CRMs (black bars) and random non-coding sequences (white bars) for *D. melanogaster* aligned with each of the other species.

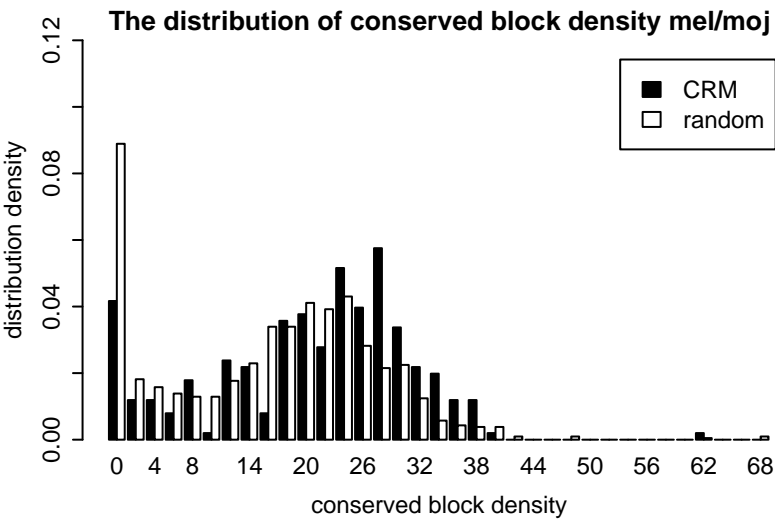
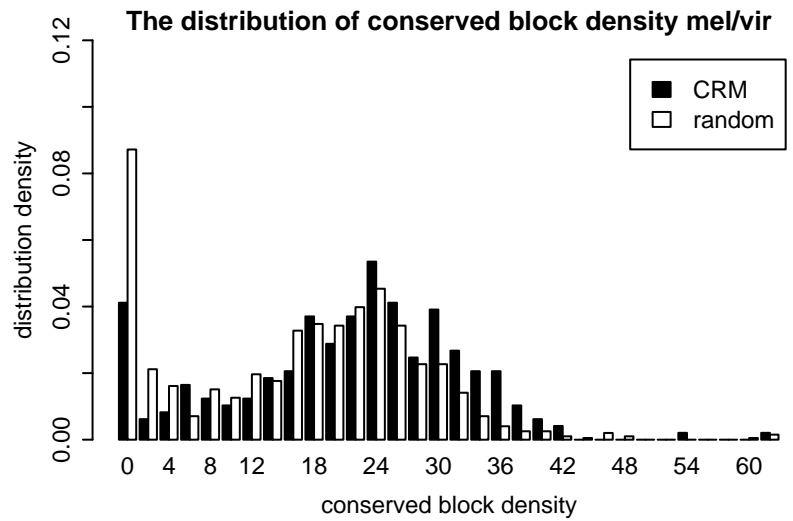
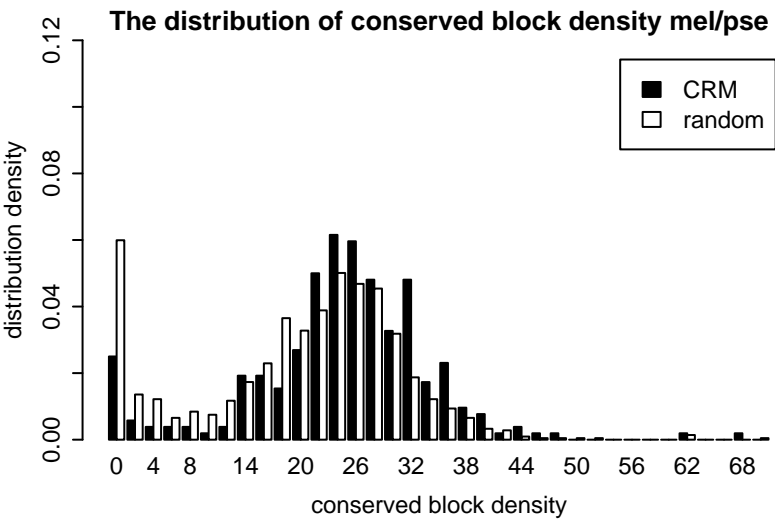
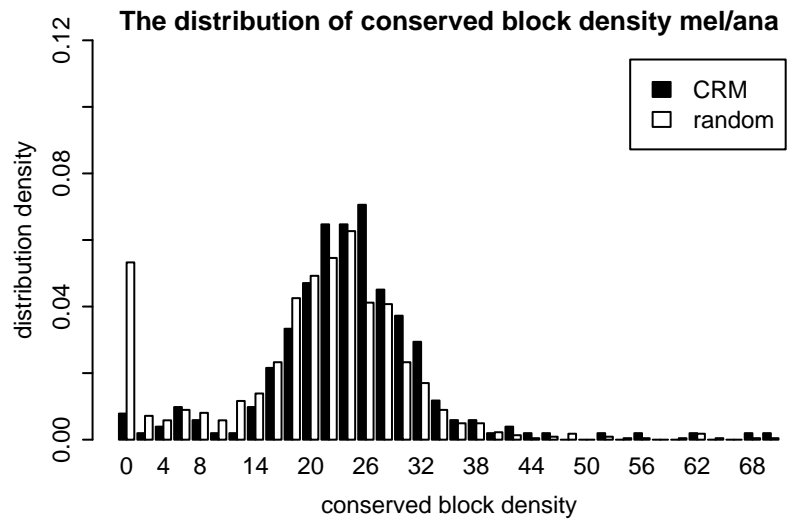
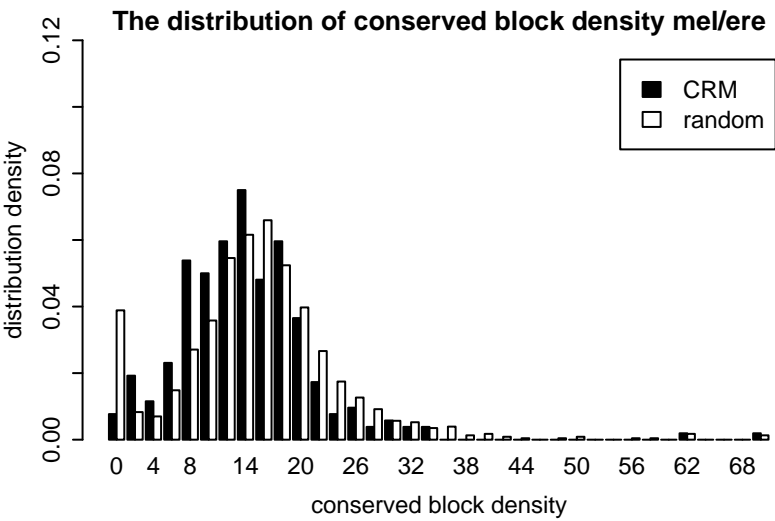
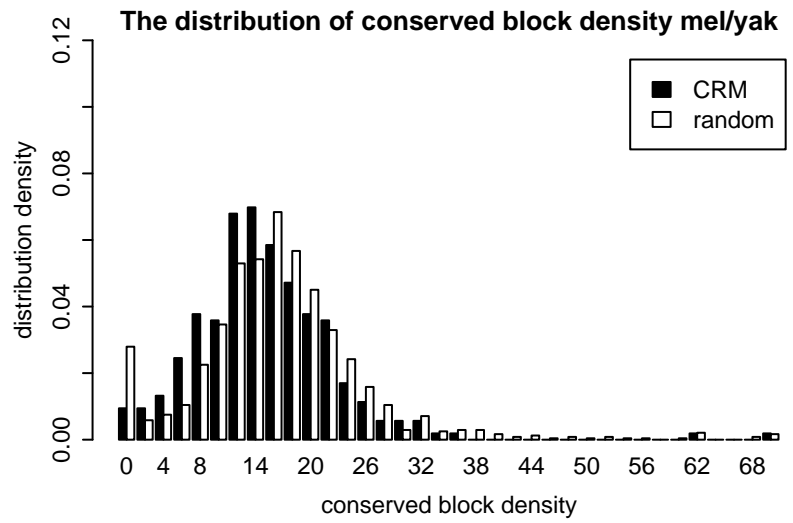
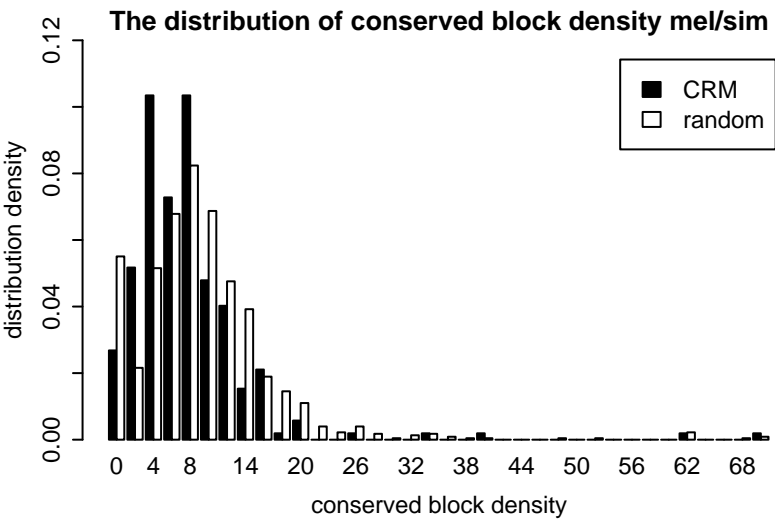


Figure S3-4. Histogram of the conserved block density for CRMs (black bars) and random non-coding sequences (white bars) for *D. melanogaster* aligned with each of the other species.