



Figure S1. The Weddell seal genome annotation was constructed by the following six steps:

1. RNA-seq assembly: RNA-seq reads for each sample were aligned using Tophat and assembled into transcript files using Cufflinks, with one transcript file per sample.
2. Dog annotation liftover: The Weddell Seal genome and the Ensembl dog genome (CanFam3.1) were aligned using the syntenic aligner Satsuma to transfer the dog annotations to the corresponding regions of the seal genome. This initial liftover was fine-tuned using the local alignment program Rum.
3. Transcript Reconciliation: The four RNA-seq assemblies were reconciled with Cuffmerge, which also integrated the NCBI *ab initio* annotation as a reference.
4. Abundance estimation: Cuffnorm estimated normalized abundance values for each transcript across all samples.
5. Coding potential: As a proxy for coding potential, transcripts were compared to existing protein databases. A match in either Pfam or RefSeq was taken to indicate coding potential.
6. Categorization: A custom script read the annotation information into a database and categorizes the transcript loci as follows: high confidence protein coding (if RNAseq evidence); low confidence protein coding (if no RNAseq evidence); spliced anti-sense; unspliced anti-sense; lncRNA; other non-coding; and unclassified.