Table S3. DNaseI-seq data files

Filetype	File Name	Description
BigWig	merged.embryo.ce10.total.bw	Merged Embryo DNase I signal (total)
BigWig	merged.embryo.ce10.positive.bw	Merged Embryo DNase I signal (positive strand)
BigWig	merged.embryo.ce10.negative.bw	Merged Embryo DNase I signal (negative strand)
BigWig	merged.L1.ce10.total.normalized.bw	Merged L1 DNase I signal (total)
BigWig	merged.L1.ce10.positive.normalized.bw	Merged L1 DNase I signal (positive strand)
BigWig	merged.L1.ce10.negative.normalized.bw	Merged L1 DNase I signal (negative strand)
BigWig	merged.embryo.ce10.A.total.bw merged.embryo.ce10.B.total.bw merged.embryo.ce10.D.total.bw merged.embryo.ce10.C.total.bw	Embryo DNase I signal (total) for each replicate A, B, C, D
BigWig	merged.embryo.ce10.A.positive.bw merged.embryo.ce10.B.positive.bw merged.embryo.ce10.C.positive.bw merged.embryo.ce10.D.positive.bw	Embryo DNase I signal (positive strand) for each replicate A, B, C, D
BigWig	merged.embryo.ce10.A.negative.bw merged.embryo.ce10.B.negative.bw merged.embryo.ce10.C.negative.bw merged.embryo.ce10.D.negative.bw	Embryo DNase I signal (negative strand) for each replicate A, B, C, D
BigWig	merged.L1.ce10.Z.total.bw merged.L1.ce10.Y.total.bw merged.L1.ce10.X.total.bw merged.L1.ce10.W.total.bw merged.L1.ce10.V.total.bw	L1 DNaseI signal (total) for each replicate Z, Y, X, W, V
BigWig	merged.L1.ce10.Z.positive.bw merged.L1.ce10.Y.positive.bw merged.L1.ce10.X.positive.bw merged.L1.ce10.W.positive.bw merged.L1.ce10.V.positive.bw	L1 DNase I signal (positive strand) for each replicate Z, Y, X, W, V
BigWig	merged.L1.ce10.Z.negative.bw merged.L1.ce10.Y.negative.bw merged.L1.ce10.X.negative.bw merged.L1.ce10.W.negative.bw merged.L1.ce10.V.negative.bw	L1 DNase I signal (negative strand) for each replicate Z, Y, X, W, V
BED	embryo.ce10.allDHS.bed	All DHSs (post-IDR, filtered)
BED TXT	embryo.ce10.noncodingDHS.bed embryo.ce10.noncodingDHS.geneannot.txt	Embryo Noncoding DHSs + Nearest Gene Annotation
BED	embryo.ce10.DHSfootprints.FDR0.05.bed	Embryo TF Footprints
BED	L1.ce10.allDHS.bed	All DHSs (post-IDR, filtered)
BED TXT	L1.ce10.noncodingDHS.bed L1.ce10.noncodingDHS.geneannot.txt	L1 Arrest Noncoding DHSs + Nearest Gene Annotation
BED	L1.ce10.DHSfootprints.FDR0.05.bed	L1 Arrest TF Footprints
BED TXT	L1arrestassoc.noncodingDHS.bed L1arrestassoc.ncDHS.geneannot.txt	L1 arrest-associated noncoding DHSs + Nearest Gene Annotation
TXT	embryo.DNaseI.novelmotifs.txt	Novel motifs (in MEME format)
TXT	embryo.DNaseI.motifassocgenes.txt	List of motif-associated genes for each motif
TXT	embryo.DNaseI.motifGO.txt embryo.DNaseI.motifanatomy.txt	Enriched Gene Ontology and anatomy terms for each motif