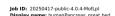
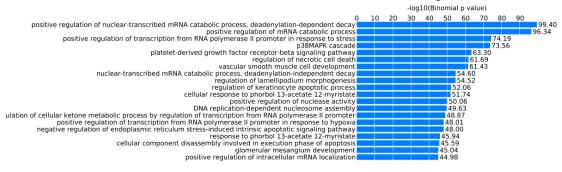
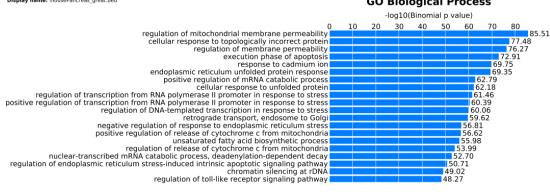
Step 4 (GREAT) figures:



GO Biological Process



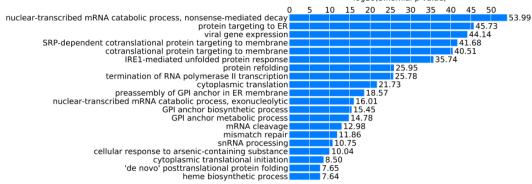
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Job ID: 20250417-public-4.0.4-4BxKtl

GO Biological Process

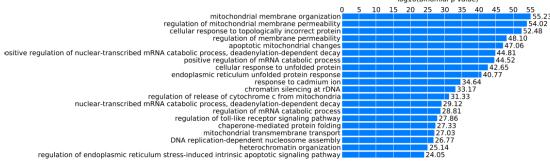




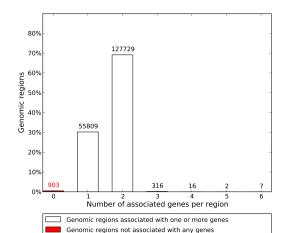
Job ID: 20250417-public-4.0.4-ylqxmb Display name: mouseOvary_great.bed

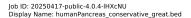
GO Biological Process

-log10(Binomial p value)



Job ID: 20250417-public-4.0.4-MofLpl Display Name: humanPancreas_great.bed





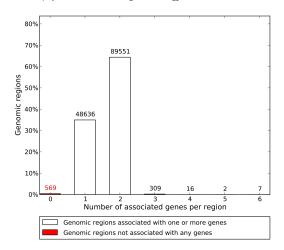
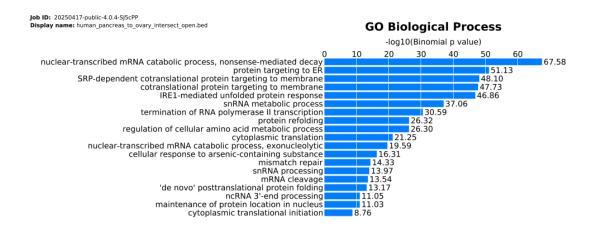
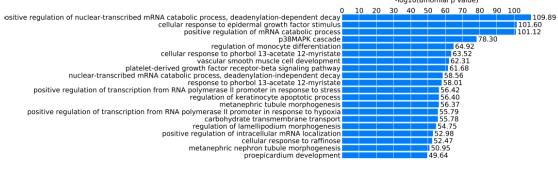


Figure 1: candidate biological processes regulated by open chromatin regions from each species and tissue combination. For humanPancreas_great.bed, the default view failed to produce any GO terms, so a bar chart was generated using the Significant By Region-based Binomial view. Also included are graphs of the number of associated genes per region for humanPancreas_great.bed and humanPancreas_conservative_great.bed. The total number of genomic regions in these two files, as reported by GREAT: 184,782 genomic regions for humanPancreas_great.bed, and 139,090 genomic regions for humanPancreas conservative great.bed.



GO Biological Process

-log10(Binomial p value)



b ID: 20250417-public-4.0.4-mpQfUi

Display name: human ovary to pancreas intersect open.bed

GO Biological Process

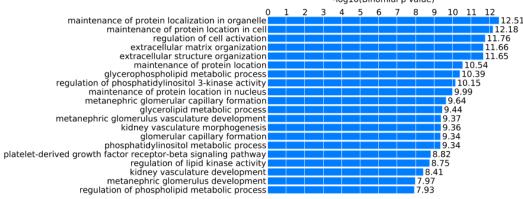
-log10(Binomial p value) 40 45 nuclear-transcribed mRNA catabolic process, nonsense-mediated decay protein targeting to ER regulation of hematopoietic progenitor cell differentiation 49.79 41.97 38.03 SRP-dependent cotranslational protein targeting to membrane cotranslational protein targeting to membrane 37.67 36.74 IRE1-mediated unfolded protein response protein refolding termination of RNA polymerase II transcription 35.66 26.56 26.02 20.35 15.24 14.52 26.56 cytoplasmic translation nuclear-transcribed mRNA catabolic process, exonucleolytic virion assembly mRNA cleavage mismatch repair 14.52 12.17 11.79 snRNA processing cellular response to arsenic-containing substance cytoplasmic translational initiation 'de novo' posttranslational protein folding heme biosynthetic process 11.17 10.16 8.37 7.97

Job ID: 20250417-public-4.0.4-uHhwoN

isplay name: human_ovary_to_pancreas_intersect_pancreasClosed.bed

GO Biological Process

-log10(Binomial p value)



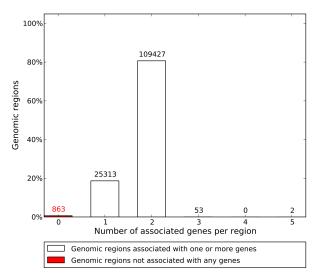
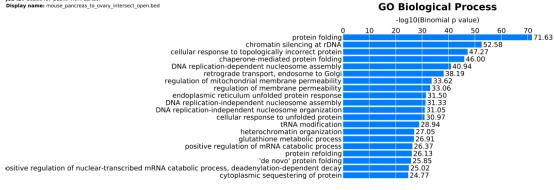


Figure 2: candidate biological processes regulated by open chromatin regions in different human tissues. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is measured by $-log_{10}$ p-value, with higher bars indicating stronger statistical significance. GO terms are displayed for peaks that are shared between species, and for peaks that are unique to species. The reference genome for annotations is chosen based on which species' coordinates were used for the intersection. For

human_pancreas_to_ovary_intersect_ovaryClosed.bed, the default view failed to produce any GO terms, so a bar chart was generated using the Significant By Region-based Binomial view. Also included are graphs of the number of associated genes per region for human_pancreas_to_ovary_intersect_ovaryClosed.bed. The total number of genomic regions in human_pancreas_to_ovary_intersect_ovaryClosed.bed as reported by GREAT: 135,658.

Job ID: 20250417-public-4.0.4-BzAa9I
Display name: mouse_pancreas_to_ovary_intersect_open.bed

GO Biological Process

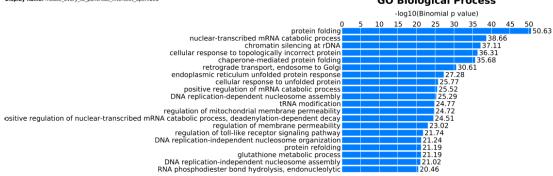


Job ID: 20250417-public-4.0.4-gNOJYq
Display name: mouse_pancreas_to_ovary_intersect_ovaryClosed.bed

GO Biological Process

-log10(Binomial p value) regulation of generation of precursor metabolites and energy fatty acid biosynthetic process negative regulation of T cell proliferation regulation of lipid catabolic process regulation of mitochondrial membrane permeability negative regulation of lymphocyte proliferation peptidyl-tyrosine autophosphorylation peptidyl-tyrosine autophosphorylation positive regulation of myeloid leukocyte differentiation mature B cell differentiation regulation of ERBB signaling pathway unsaturated fatty acid biosynthetic process organelle transport along microtubule negative regulation of cardiac muscle hypertrophy regulation of transcription from RNA polymerase II promoter in response to stress regulation of DNA-templated transcription in response to stress regulation of membrane permeability negative regulation of intrinsic apoptotic signaling pathway regulation of B cell differentiation regulation of triglyceride biosynthetic process 60 59.19 56.25 54.09 52.63 52.02 50.03 48.36 47.55 47.49 46.05 45.55 45.07 45.00 42.17

Job ID: 20250417-public-4.0.4-76bBpc
Display name: mouse_ovary_to_pancreas_intersect_open.bed





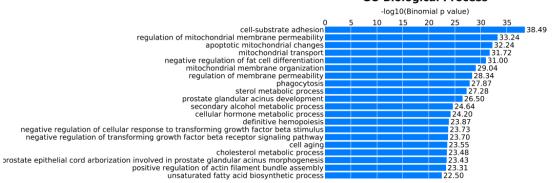
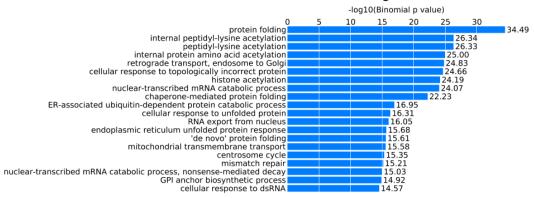


Figure 3: candidate biological processes regulated by open chromatin regions in different mouse tissues. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is measured by $-\log_{10}$ p-value, with higher bars indicating stronger statistical significance. GO terms are displayed for peaks that are shared between species, and for peaks that are unique to species. The reference genome for annotations is chosen based on which species' coordinates were used for the intersection.

Job ID: 20250417-public-4.0.4-1Xc8h9
Display name: ovary intersect human peaks to mouse coords open great.bed

Job ID: 20250417-public-4.0.4-Fxf9Ax

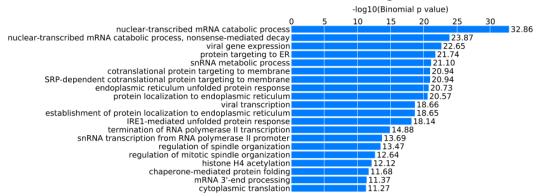
GO Biological Process



Display name: ovary_intersect_human_peaks_to_mouse_coords_mouseClosed_great.bed **GO Biological Process** -log10(Binomial p value) response to insulin 13.99 collagen metabolic process multicellular organismal macromolecule metabolic process 12.23 11.68 cellular response to insulin stimulus cellular response to vascular endothelial growth factor stimulus 11.24 10.87 9.86 negative regulation of high voltage-gated calcium channel activity histone H4-K12 acetylation 9.58 regulation of blood coagulation regulation of coagulation 8.82 8.63 8.61 8.55

regulation of Coagulation myeloid cell homeostasis Collagen biosynthetic process regulation of Notch signaling pathway cellular response to amino acid stimulus positive regulation of DNA replication Rho protein signal transduction regulation of microtubule nucleation regulation of microtubule nucleation acylglycerol metabolic process erythrocyte homeostasis myeloid cell activation involved in immune response negative regulation of muscle adaptation 6.89

Job ID: 20250417-public-4.0.4-nceDYw
Display name: ovary intersect mouse peaks to human coords open great.bed



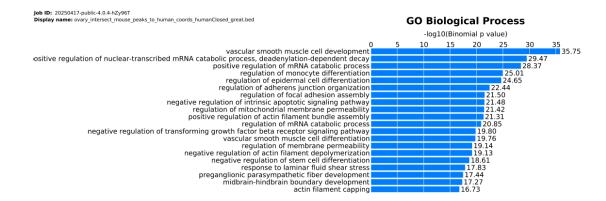
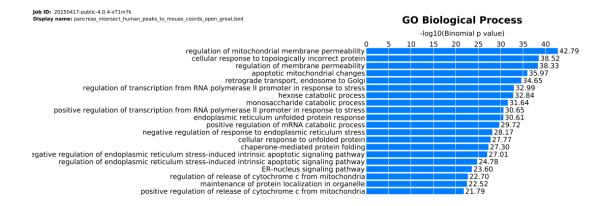
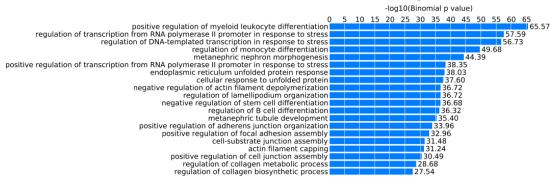
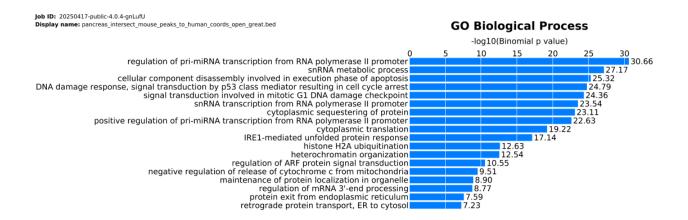


Figure 4: candidate biological processes regulated by open chromatin regions in human and mouse ovaries. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is measured by $-\log_{10}$ p-value, with higher bars indicating stronger statistical significance. GO terms are displayed for peaks that are shared between species, and for peaks that are unique to species. The reference genome for annotations is chosen based on which species' coordinates were used for the intersection.









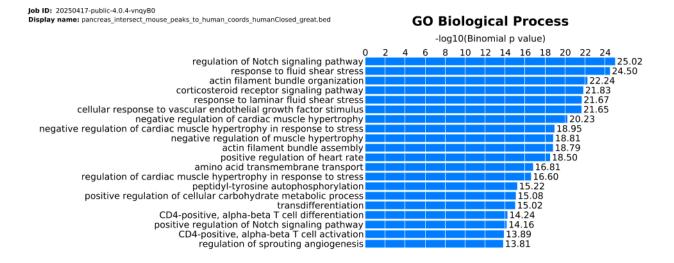


Figure 5: top candidate biological processes regulated by open chromatin regions in human and mouse pancreases. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is

measured by $-\log_{10}$ p-value, with higher bars indicating stronger statistical significance. GO terms are displayed for peaks that are shared between species, and for peaks that are unique to species. The reference genome for annotations is chosen based on which species' coordinates were used for the intersection.