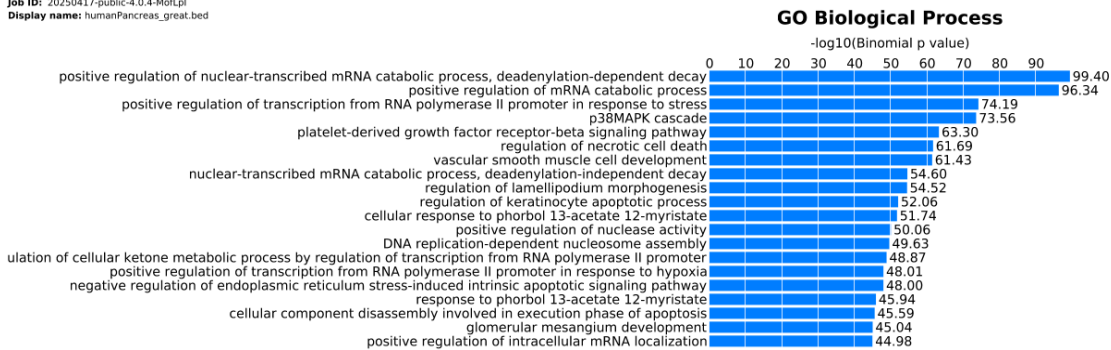
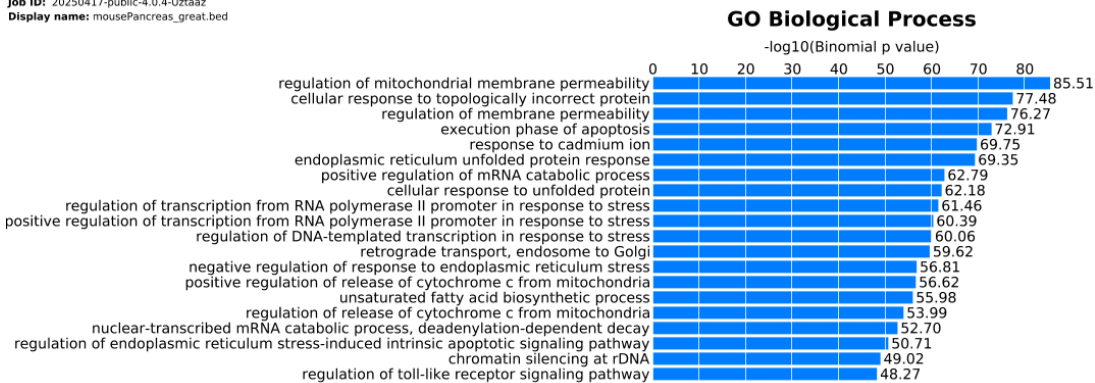


Step 4 (GREAT) figures:

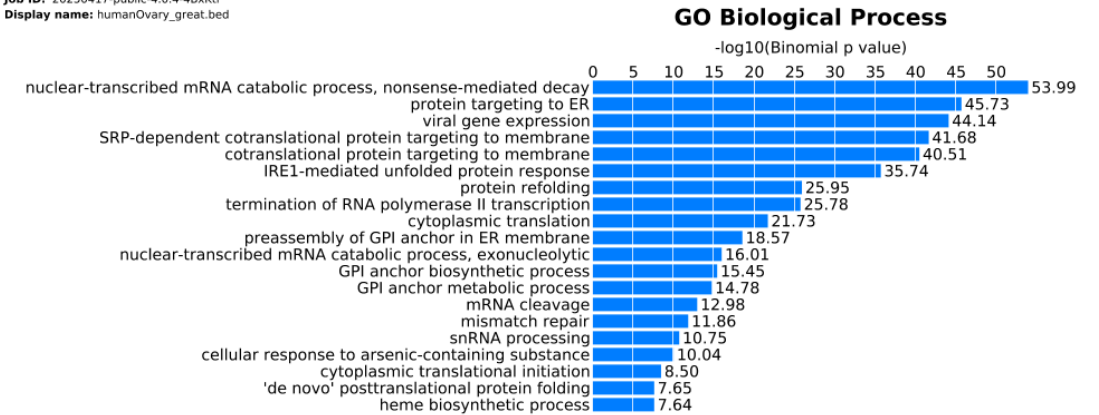
Job ID: 20250417-public-4.0.4-Mofl.pl
Display name: humanPancreas_great.bed



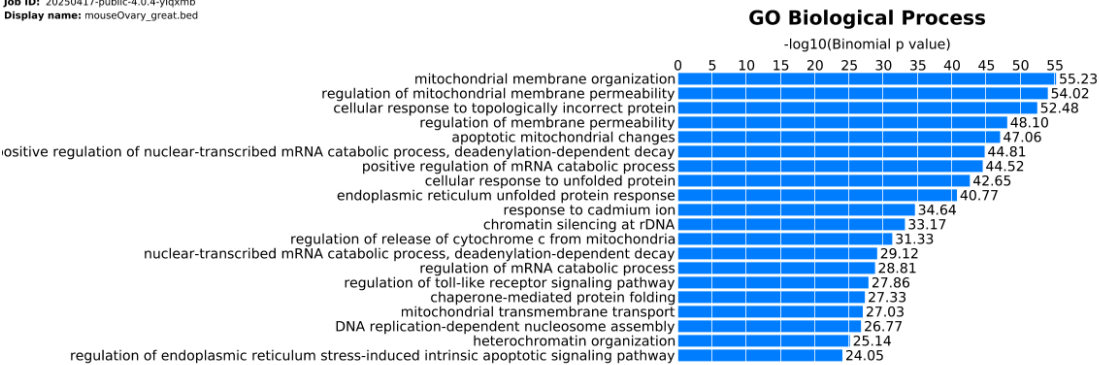
Job ID: 20250417-public-4.0.4-Uztaaz
Display name: mousePancreas_great.bed



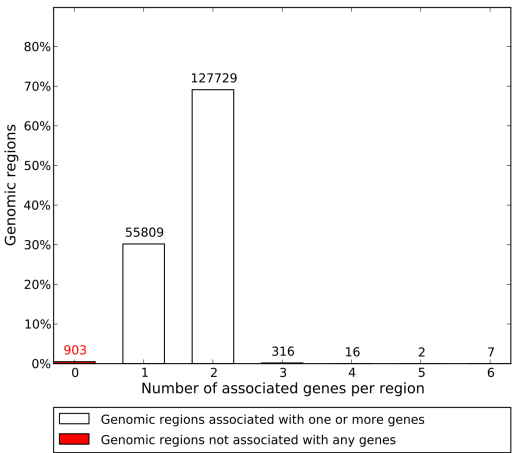
Job ID: 20250417-public-4.0.4-4BxKtl
Display name: humanOvary_great.bed



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



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



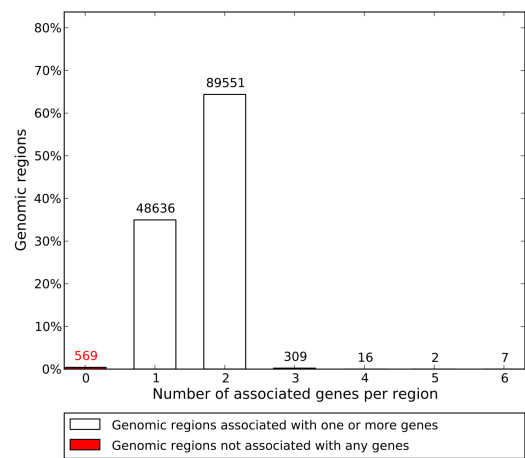
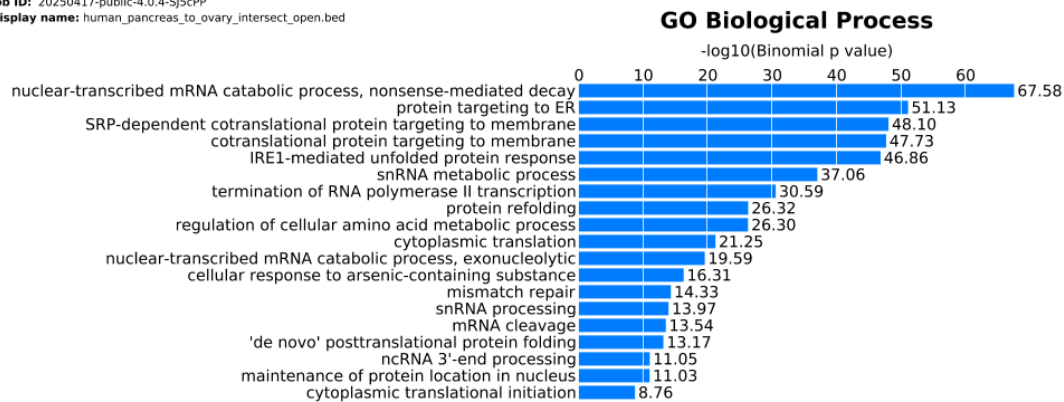
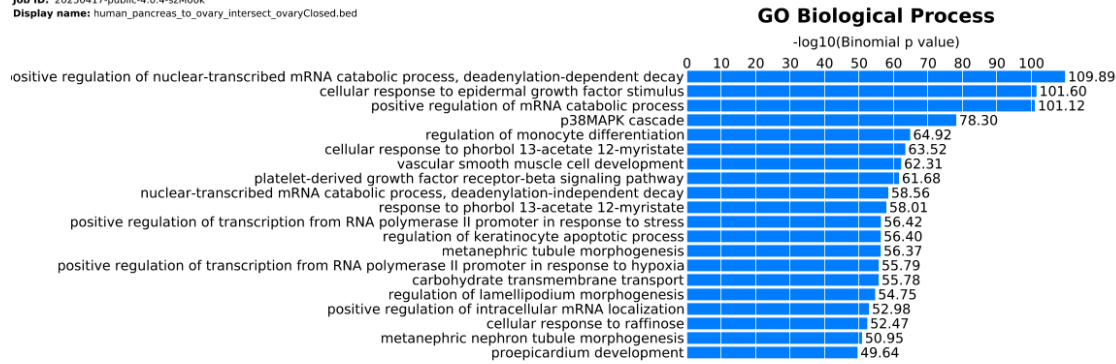


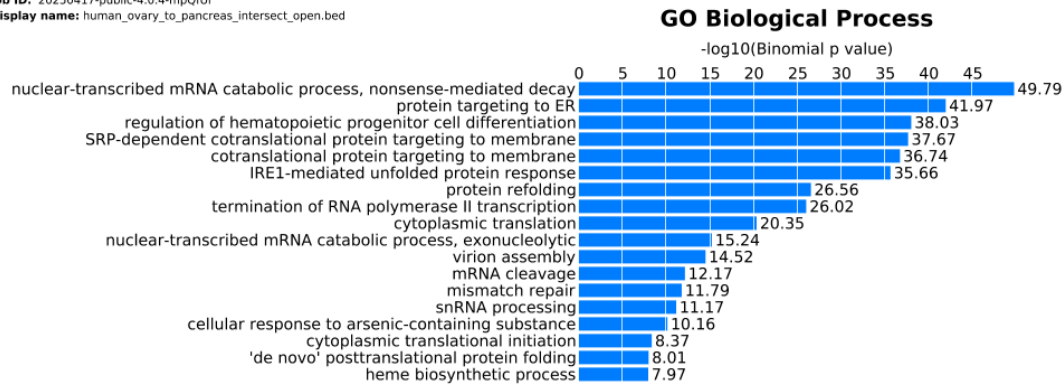
Figure 1: candidate biological processes regulated by open chromatin regions from each species and tissue combination. For humanPancreas_great.bed, the default view failed to produce any GO terms, so a bar chart was generated using the Significant By Region-based Binomial view. Also included are graphs 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.



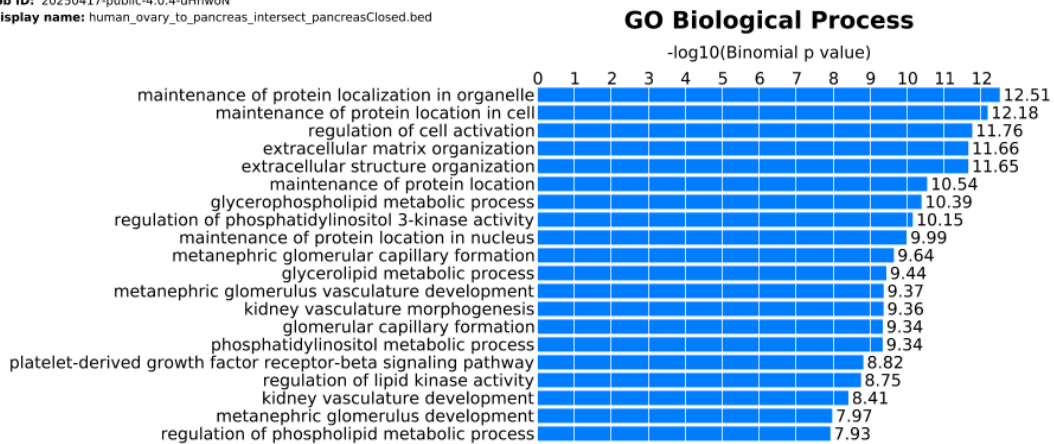
Job ID: 20250417-public-4.0.4-szM00k
Display name: human_pancreas_to_ovary_intersect_ovaryClosed.bed



Job ID: 20250417-public-4.0.4-mpQfUI
Display name: human_ovary_to_pancreas_intersect_open.bed



Job ID: 20250417-public-4.0.4-uHhwoN
Display name: human_ovary_to_pancreas_intersect_pancreasClosed.bed



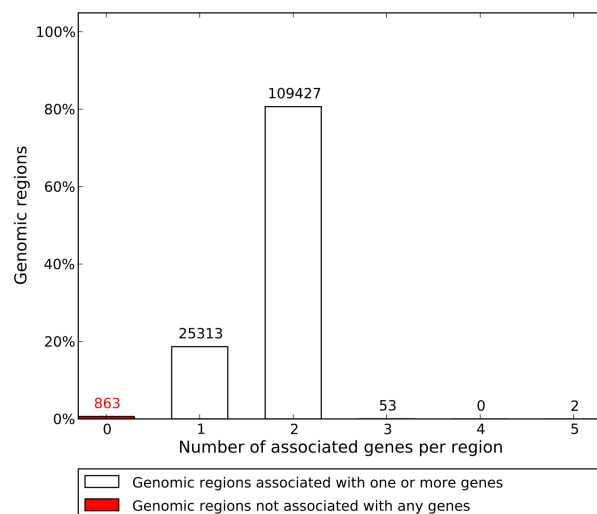
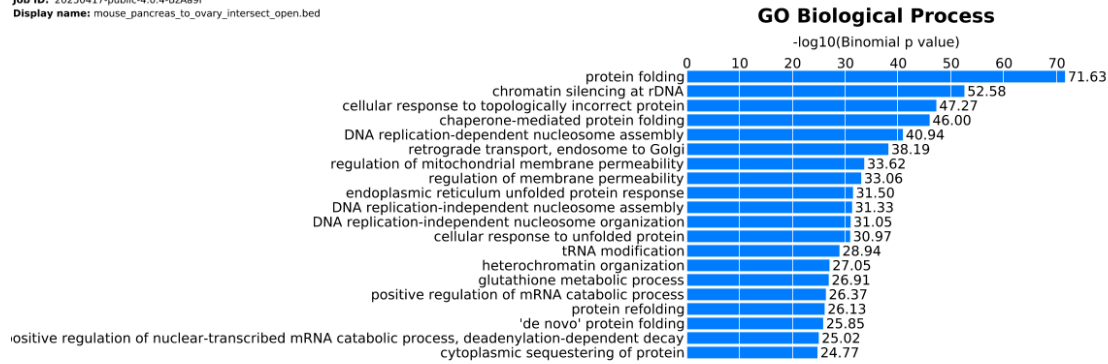
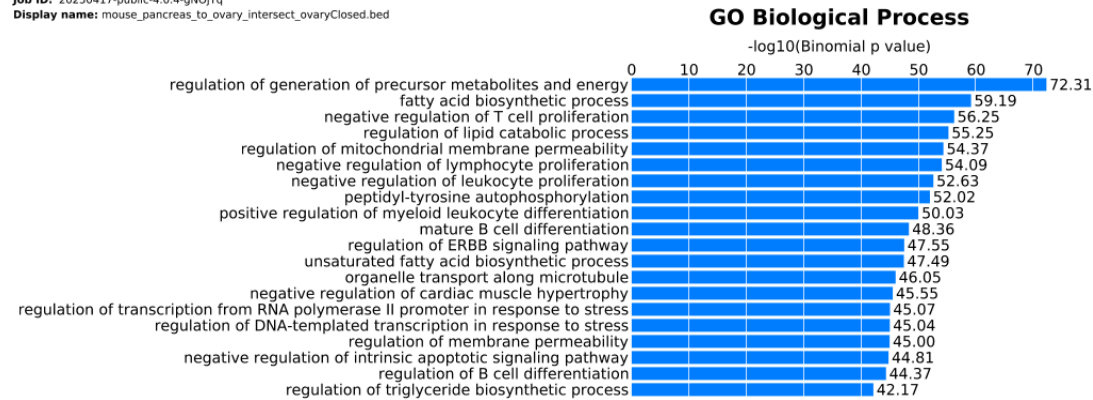


Figure 2: candidate biological processes regulated by open chromatin regions in different human tissues. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is measured by $-\log_{10}$ p-value, with higher 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.

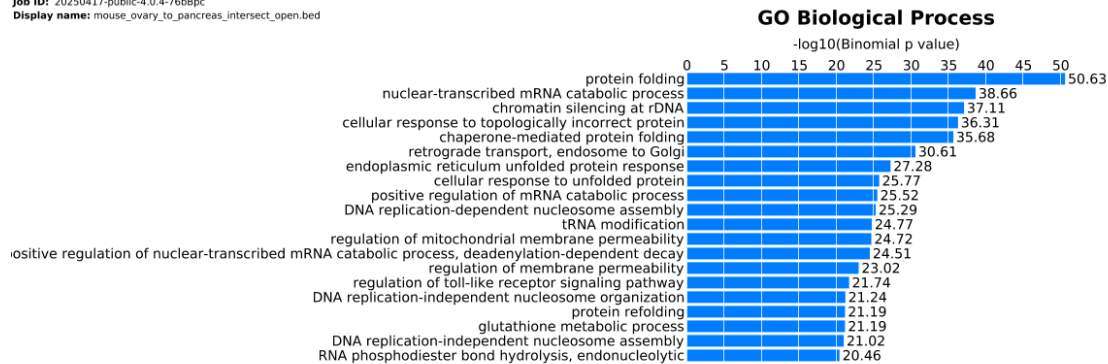
Job ID: 20250417-public-4.0.4-BzAa9l
Display name: mouse_pancreas_to_ovary_intersect_open.bed



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



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



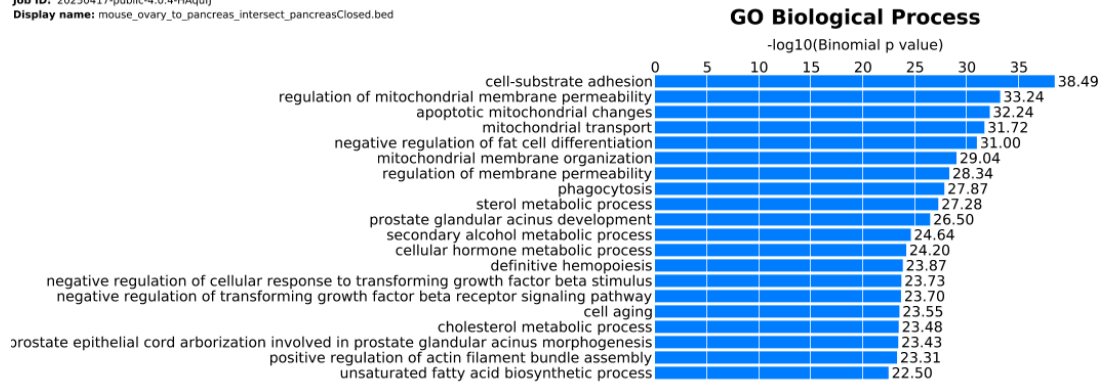
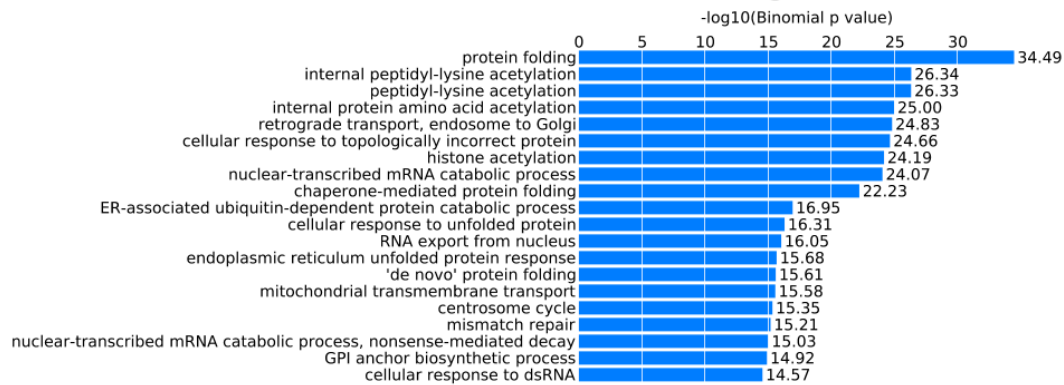


Figure 3: candidate biological processes regulated by open chromatin regions in different mouse tissues. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is measured by $-\log_{10}$ p-value, with higher 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

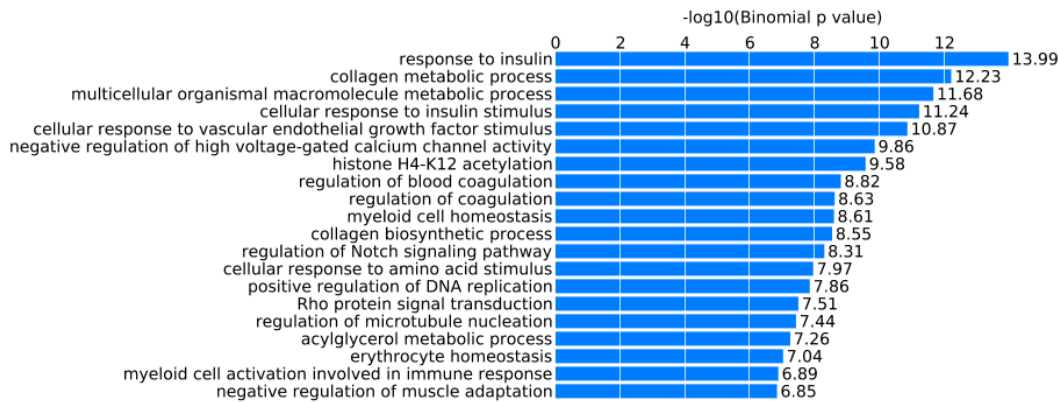
GO Biological Process



Job ID: 20250417-public-4.0.4-Fx9Ax

Display name: ovary_intersect_human_peaks_to_mouse_coords_mouseClosed_great.bed

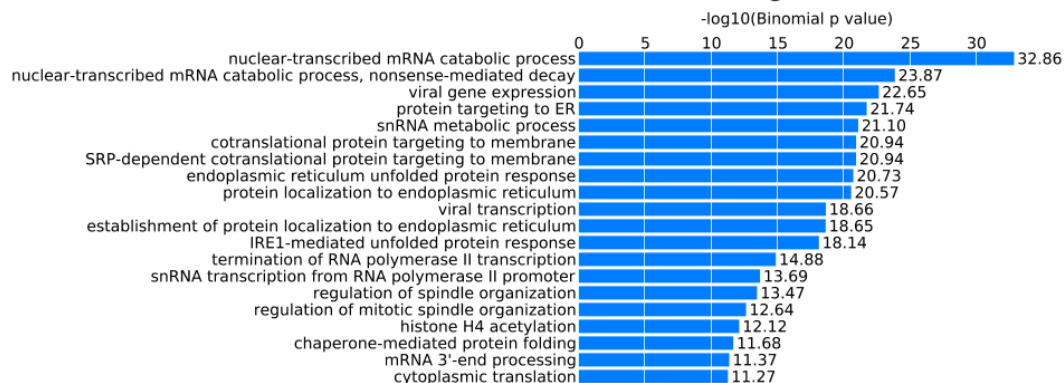
GO Biological Process



Job ID: 20250417-public-4.0.4-nceDYw

Display name: ovary_intersect_mouse_peaks_to_human_coords_open_great.bed

GO Biological Process



Job ID: 20250417-public-4.0.4-hZy96T
 Display name: ovary_intersect_mouse_peaks_to_human_coords_humanClosed_great.bed

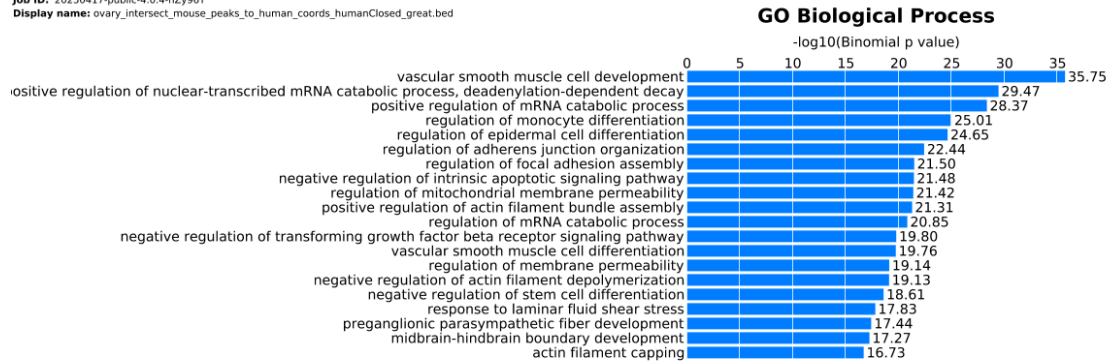
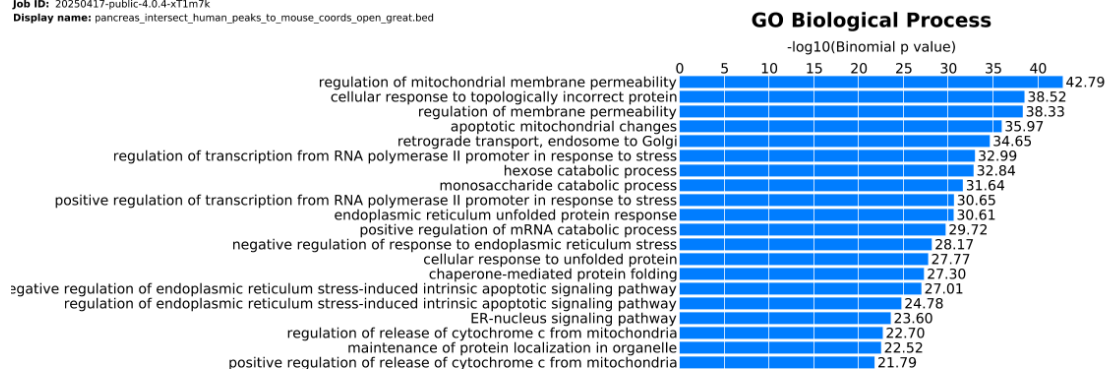
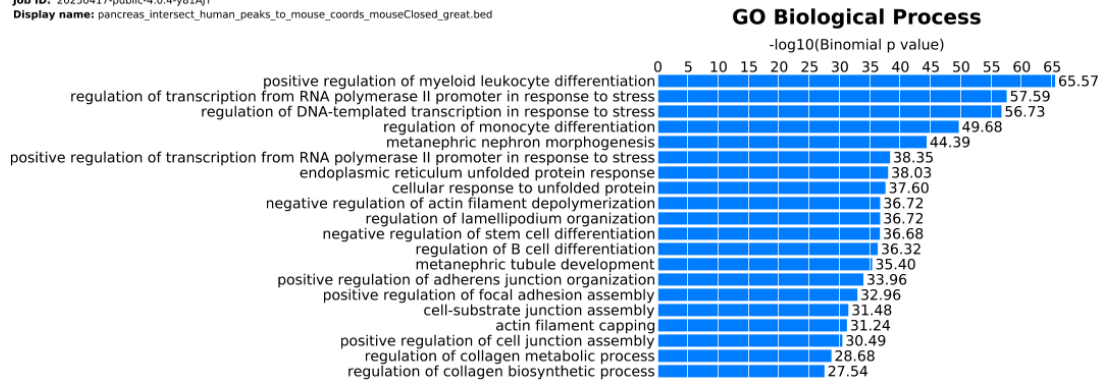


Figure 4: candidate biological processes regulated by open chromatin regions in human and mouse ovaries. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is measured by $-\log_{10}$ p-value, with higher 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.

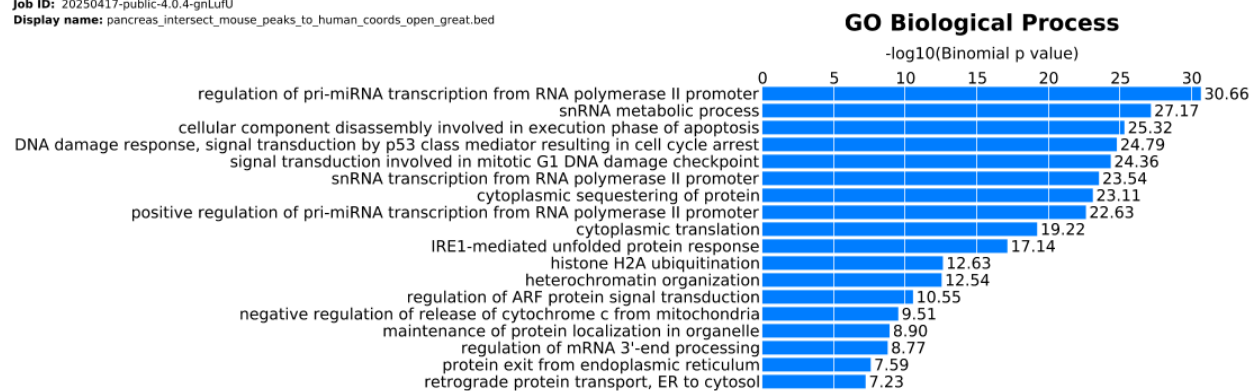
Job ID: 20250417-public-4.0.4-xT1m7k
 Display name: pancreas_intersect_human_peaks_to_mouse_coords_open_great.bed



Job ID: 20250417-public-4.0.4-y81AJY
 Display name: pancreas_intersect_human_peaks_to_mouse_coords_mouseClosed_great.bed



Job ID: 20250417-public-4.0.4-gnLufU
 Display name: pancreas_intersect_mouse_peaks_to_human_coords_open_great.bed



Job ID: 20250417-public-4.0.4-vnqyB0
 Display name: pancreas_intersect_mouse_peaks_to_human_coords_humanClosed_great.bed

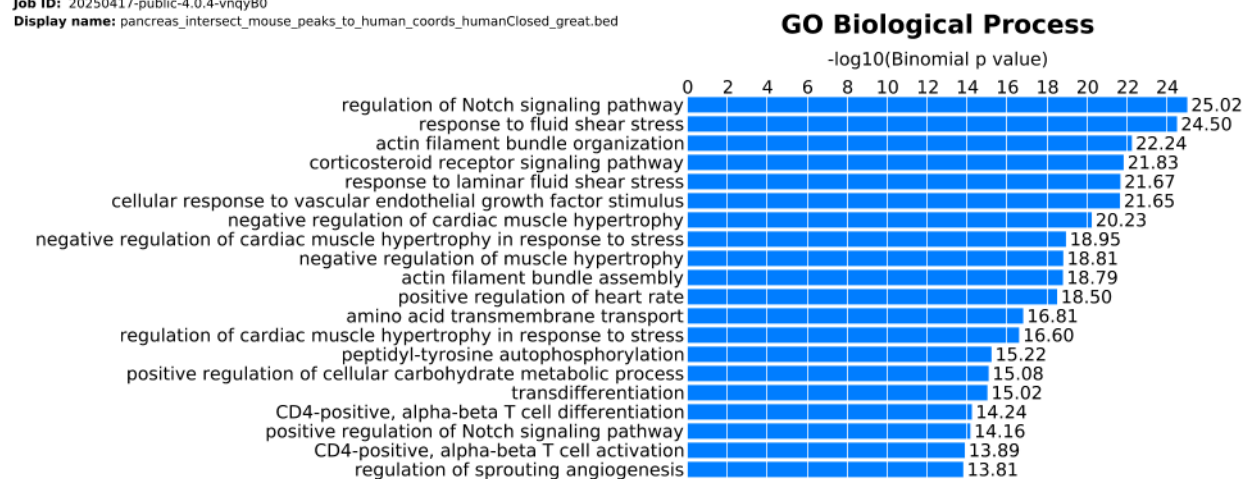


Figure 5: top candidate biological processes regulated by open chromatin regions in human and mouse pancreases. Bar plots show the top Gene Ontology (GO) Biological Process terms significantly enriched in open chromatin regions from ATAC-seq data. Enrichment is

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.