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Database issue

MouseOmics: a multi-omics database for mouse biological study

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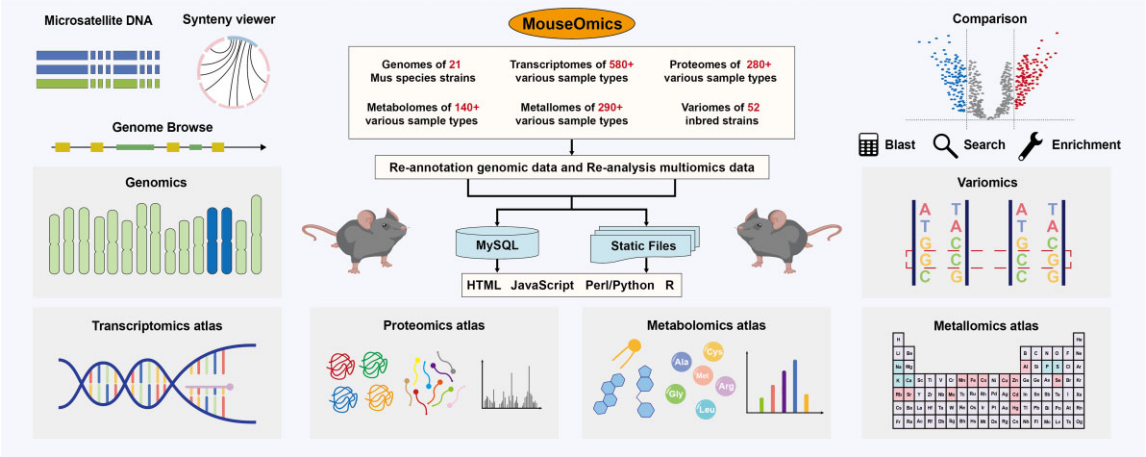
Abstract

Mouse represents a pivotal model and indispensable resource in medical and life sciences, widely used for developmental biology and multi-omics studies. Yet, a comprehensive, integrated mouse multi-omics database remains lacking. Here, we established a mouse multi-omics database, MouseOmics, by integrating 21 genomes distributed among five species within the genus *Mus*, transcriptomes in 584 tissue samples, proteomes in 285 tissue samples, metabolomes in 143 tissue samples, metallomes in 296 tissue samples, and three variomes covering 52 mouse inbred strains. All mouse multi-omics data can be explored through multiple functional modules with user-friendly web interface. Furthermore, we embedded several useful tools, like MISAweb, for the identification of microsatellite DNAs, and specifically developed the enrichment analysis modules of InterPro, Gene Ontology, and Pathway for mouse. The mouse multi-omics data can be downloaded online conveniently. MouseOmics will be updated regularly with the newly released mouse multi-omics data and can be accessed freely via the address https://www.varnatech.cn/MouseOmics.

Graphical abstract



Introduction

Mouse stands as one of the world's most vital model organisms, extensively utilized across diverse research fields. More than 45 species have been identified in the genus *Mus*, and some strains of mouse in *Mus spretus*, *M. caroli*, *M. pahari*, *M. spicilegus*, and *M. musculus* have undergone complete genome

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sequencing [1–5]. With the great progress in sequencing technology and computing power, there have been many studies on mouse genome assembly and multi-omics sequencing [6–11]. This has led to the acquisition of diverse biological information across multiple mouse strains and life stages. Several genomic, transcriptomic, proteomic, metabolomic, and phenomic databases have been constructed and released in the genus *Mus*, such as MGD, GXD, ProteomicsDB, and IMPC. MGD provides comprehensive genomic and genetic data, including reference genomes, gene annotations, mutant alleles, phenotype associations, genetic markers, and germplasm resources for *Mus* genus [12]. GXD integrates spatiotemporal gene expression data, including *in situ* hybridization patterns, RNA-seq/array datasets, and embryonic developmental stage-specific expression profiles for *Mus musculus* [13]. ProteomicsDB contains proteomic information, including protein identification/quantification data, posttranslational modification sites, and mass spectrometry raw data across multiple species, including *M. musculus* [14]. IMPC integrates large-scale phenotypic screening data, including standardized knockout phenotypes, embryo viability analyses, and genotype-phenotype associations for *M. musculus* [15]. These databases offer abundant biological data of the mouse, which assist and consolidate the research progress of life and medical sciences, but their constrained architecture cannot accommodate the multidimensional requirements of advancing multi-omics approaches. Several databases primarily contain one omics data and lack comprehensive multi-omics profiles spanning the entire murine life cycle. Meanwhile the metallomics, which includes the content, speciation, distribution, and functions of metals and metalloids within organisms, has gained significant research interest [16–19]. An increasing number of studies are exploring the changes and functional effects of metal elements across different mouse life stages [20–22]. Meanwhile, the integration of multi-omics databases based on model organisms has been proven to significantly advance scientific research [23–26], but there isn't a systematic database that collects and integrates metallomics data.

In this study, we constructed a mouse multi-omics database (designated as MouseOmics, https://varnatech.cn/MouseOmics) by mining and integrating the data of 21 mouse genomes, 14 transcriptomes, 14 proteomes, 8 metabolomes, 6 metallomes, and 3 variomes. MouseOmics offers extensive multi-omics data covering diverse mouse strains across their entire life cycle and supplies user-friendly visualization tools, which will become a valuable database for future mouse multi-omics research.

Materials and methods

Data collection and preprocess

A total of 21 mouse genomes encompassing five mouse species, including *M. pahari*, *M. spicilegus*, *M. spretus*, *M. caroli*, and *M. musculusis,* are currently available in MouseOmics. The *M. musculusis* species contained 13 laboratory lines (house mouse) and four subspecies, including *M. musculus* subsp. *molossinus* (Japanese wild mouse), *M. musculus* subsp. *castaneus* (southeastern Asian house mouse), *M. musculus* subsp. *domesticus* (western European house mouse), and *M. musculus* subsp. *musculus* (eastern European house mouse). All genomic data are the newly released and high-quality genome assemblies downloaded from public repositories. Several representative projects of transcriptomics, proteomics, metabolomics, metallomics, and variomics data were extracted from the released publications through data-mining technology with in-house pipeline. These data span multiple mouse tissues and organs throughout development and are supplemented by three variomics cohorts representing distinct strains. Finally, 21 mouse genomes, transcriptomes in 584 tissue samples with 2254 replicates, proteomes in 285 tissue samples with 1161 replicates, metabolomes in 143 tissue samples with 1025 replicates, and metallomes in 296 tissue samples with 1920 replicates were parsed and collected in MouseOmics.

A total of 426 844 mouse genes with 1074 098 transcripts in MouseOmics received comprehensive functional annotation via an integrated pipeline that queries premier online web services and public databases (Table 1). The customized InterProScan tool (interproscan-5.52–86.0) was employed to functionally annotate the protein sequences of 21 mouse genomes with parameters: "-f tsv -dp -goterms -pa" [27]. All the protein sequences of 21 mouse genomes were mapped to the non-redundant (nr) (v2025.01.07) and UniProt-SwissProt/TrEMBL (Release_2024_06) protein databases using Diamond Blastp v0.9.24.125 with the parameters: "-e 1e-5 –max-target-seqs 5 –outfmt 6 –more-sensitive" [28], and the top five best hits were curated and collected in the database. Furthermore, eggNOG-mapper [29] software with the latest database was implemented to get the functional annotation of Gene Ontology (GO) [30], MetaCyc [31], and Reactome [32] of all mouse protein sequences. After merging the output files between eggNOG-mapper and InterProScan software, only the mouse annotations were retrieved as the final annotations of GO and pathway. Finally, comprehensive functional annotation information of all protein-coding genes in 21 mouse genomes was obtained and parsed for the downstream functional enrichment analyses (Table 2).

The diamond (v2.1.8.162) with an *E*-value cutoff of 1e-10 was employed to identify homologous gene pairs between any two genomes among the 21 mouse genomes [28]. With the combination of homologous gene pairs and gene location, MCScanX software was used to identify syntenic blocks with default parameters: E_VALUE = 1e-10 and MATCH_SIZE = 5. Finally, 67 967 syntenic blocks and 7 539 681 syntenic gene pairs have been identified for the 21 mouse genomes [33].

Database implementation

MouseOmics was developed with Hyper Text Markup Language (HTML), Cascading Style Sheets (CSS), and LAMP (Linux, Apache, MySQL, and PHP/Perl) system, as well as a high-level, interpreted, multi-paradigm programming language, JavaScript (JS). All the mouse multi-omics data were stored in the relational database management system, MySQL database, and static files. MouseOmics integrated a suite of functional modules and localized third-party software that were user-friendly, allowing for the exploration and visualization of mouse multi-omics data across various mice. R module, Statistics::R, was used to identify the differentially expressed genes between two different tissues and implement function enrichment analysis. D3 (or D3.js) is a JS library for visualizing genomic data using web standards, which will assist in visualizing the genomic data using SVG, Canvas, and HTML, and in designing the right visual interface for genomic

Table 1. Statistics of 21 mouse genome assemblies

Species	English name	Strain	Genome size (GB)	No. Genes	No. mRNA	Released date
M. pahari	shrew mouse	PAHARI/EIJ	2.5	19 164	48 213	28 April 2017
M. spicilegus	steppe mouse	ZRU	2.7	22 907	36 985	14 April 2023
M. spretus	Western wild mouse	SPRET/EiJ	2.6	19 580	49 220	26 April 2016
M. caroli	Ryukyu mouse	CAROLI/EIJ	2.6	19 311	48 738	28 April 2017
M. musculus	house mouse	C3H/HeJ	2.5	20 093	50 368	1 January 2022
M. musculus	house mouse	BALB/cJ	2.5	20 232	50 612	2 January 2022
M. musculus	house mouse	DBA/2J	2.6	20 189	50 499	3 January 2022
M. musculus	house mouse	NOD/ShiLtJ	2.5	20 059	50 193	4 January 2022
M. musculus	house mouse	A/J	2.5	20 165	50 537	30 June 2022
M. musculus	house mouse	129S1_SvImJ	2.5	20 178	50 456	1 July 2022
M. musculus	house mouse	CBA/J	2.5	20 092	50 316	30 June 2022
M. musculus	house mouse	C57BL/6NJ	2.5	20 308	50 769	1 July 2022
M. musculus	house mouse	NZO/HlLtJ	2.8	20 267	50 808	18 December 2022
M. musculus	house mouse	LP/J	2.9	20 164	50 376	18 December 2022
M. musculus	house mouse	AKR/J	2.5	20 170	50 523	1 July 2022
M. musculus	house mouse	FVB/NJ	2.5	20 068	50 246	1 July 2022
M. musculus	house mouse	C57BL/6J	2.7	21 748	65 977	24 June 2020
M. musculus ssp. *musculus*	Eastern European house mouse	PWK_PhJ	2.5	19 532	49 198	5 January 2022
M. musculus ssp. *domesticus*	Western European house mouse	WSB/EiJ	2.5	19 787	49 707	1 July 2022
M. musculus ssp. *molossinus*	Japanese wild mouse	JF1/MsJ	2.7	23 178	70 897	1 July 2022
M. musculus ssp. *castaneus*	southeastern Asian house mouse	CAST/EiJ	2.5	19 652	49 460	1 July 2022

Table 2. Statistics of annotated genes across 21 mouse genomes

Strain	No. Genes	No. mRNA	IPRScan	Gene ontology	MetaCYC	Reactome	nr	Swiss-Prot	TrEMBL
PAHARI/EIJ	19 164	48 213	44 379	40 795	24 036	38 438	48 250	47 514	48 626
ZRU	22 907	36 985	35 212	32 667	19 908	30 820	36 702	35 520	36 858
SPRET/EiJ	19 580	49 220	46 971	43 207	25 500	40 748	51 027	50 211	51 521
CAROLI/EIJ	19 311	48 738	44 846	41 185	24 256	38 832	48 858	48 032	49 313
C3H/HeJ	20 093	50 368	46 383	42 598	25 040	40 200	50 450	49 573	50 952
BALB/cJ	20 232	50 612	46 526	42 767	25 068	40 335	50 619	49 728	51 119
DBA/2J	20 189	50 499	46 401	42 621	50 906	40 232	50 552	49 650	51 046
NOD/ShiLtJ	20 059	50 193	46 337	42 552	25 031	40 148	50 424	49 552	50 929
PWK_PhJ	19 532	49 198	47 310	43 485	25 715	40 965	51 412	50 574	51 908
A/J	20 165	50 537	46 586	42 801	25 133	40 352	50 666	49 785	51 163
129S1_SvImJ	20 178	50 456	46 580	42 787	25 174	40 384	50 680	49 776	51 178
CBA/J	20 092	50 316	46 385	42 596	25 070	40 201	50 468	49 575	50 965
JF1/MsJ	23 178	70 897	63 289	57 421	33 478	54 775	69 326	67 013	70 078
C57BL/6NJ	20 308	50 769	46 701	42 863	25 245	40 461	50 840	49 934	51 351
C57BL/6J	21 748	65 977	59 448	54 364	30 669	51 384	64 653	63 528	65 373
NZO/HlLtJ	20 267	50 808	46 897	43 062	25 367	40 664	50 992	50 094	51 498
LP/J	20 164	50 376	46 430	42 646	25 112	40 267	50 523	49 642	51 025
AKR/J	20 170	50 523	46 556	42 710	25 103	40 347	50 648	49 770	51 152
CAST/EiJ	19 652	49 460	47 607	43 750	/	41 246	51 737	50 886	52 214
FVB/NJ	20 068	50 246	46 257	42 495	25 032	40 113	50 385	49 502	50 888
WSB/EiJ	19 787	49 707	45 924	42 182	24 867	39 783	49 987	49 143	50 482

data. MouseOmics employed D3 library to display the syntenic view between any two mouse genomes. Several R libraries, such as DESeq2 [34], pheatmap [35], ggplot2 [36], and ggrepel [37], were used to display the expression profiles of transcriptome and proteome, as well as the differences of metabolites and ion concentrations in comparisons between two tissues. The SAMtools v0.1.16 and BCFtools v1.20 packages were installed to process SAM and BAM files, and VCF and BCF files to extract the genetic variations in mouse populations [38]. The interactive visualization of mouse multi-omics data was implemented using Apache WWWBLAST and JBrowse2 for the genome browser with views of mouse orthologs and genomic components [39].

Results

Overview of MouseOmics

The MouseOmics database consists of eight functional parts, including six "Omics" data exploration, useful tools, and supplemental information, like statistics, resources, manual, and download. The genomics data were organized through five mouse species, with the remaining six "Omics" data organized through the released projects (Fig. 1). MouseOmics presents basic information for each mouse genome sequencing project and four interactive functional modules: basic search, advanced search, genome browse, and data download, which will assist to retrieve, search, and visualize the information of genomic components in each mouse genome. For the visualization of transcriptomics and proteomics data, the gene and protein expression profiles were displayed through selecting tissues and inputting gene lists, and several projects with equal biological replicates were analyzed through pairwise comparison between any two samples in the transcriptomic and proteomic projects. However, the metabolite values and ion concentration values across various tissues were visualized through selecting target tissues in the metabolome and metallome functional parts. MouseOmics performed the syntenic analysis within five mouse species to identify divergence in the genus *Mus*. MouseOmics supplied user-friendly interface, and key mouse functional genes can be explored through browsing and searching with localized open-resource software, such as

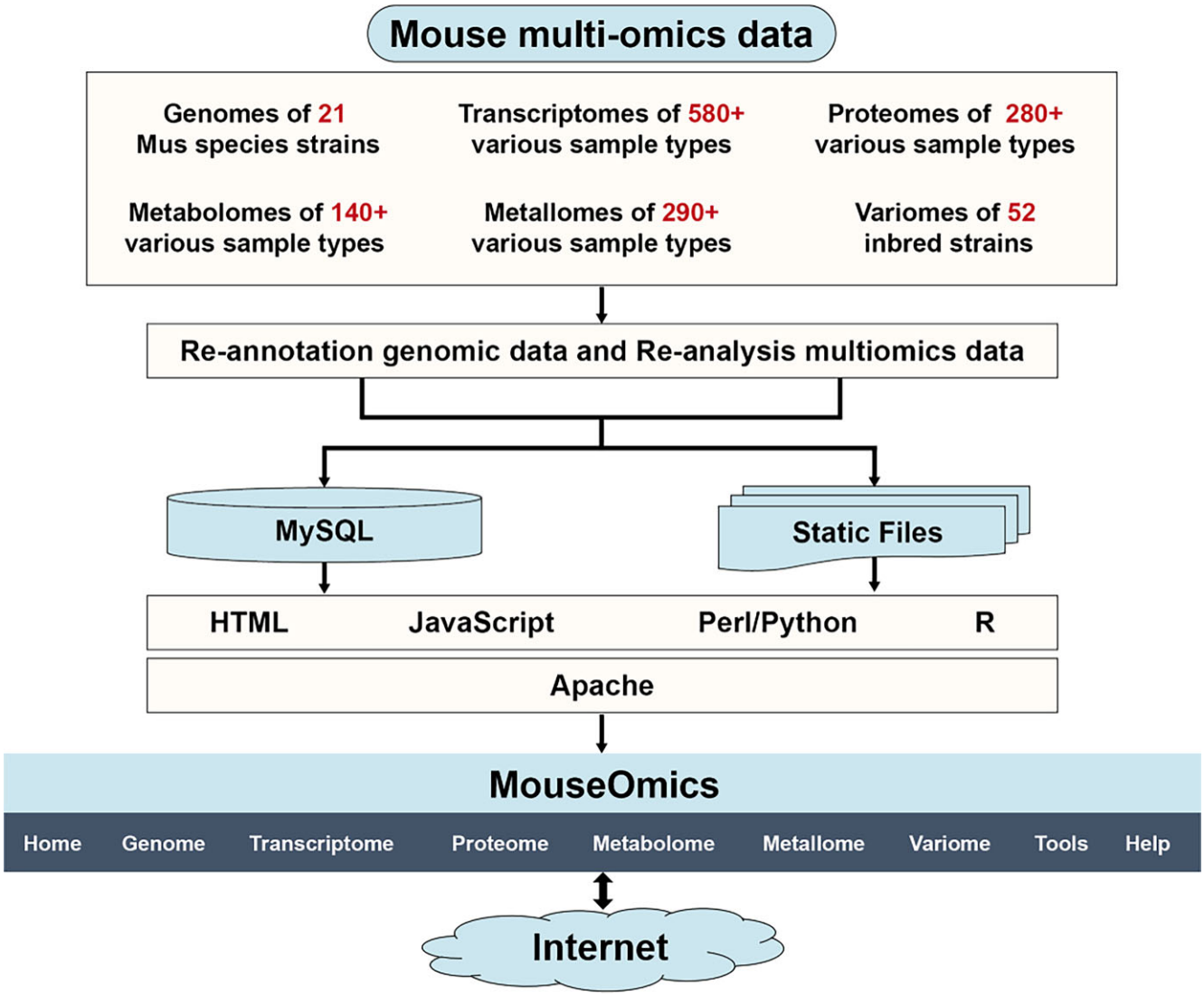

Figure 1. Overview of the MouseOmics database. All mouse multi-omics data collected in the MouseOmics database were downloaded from public databases or resources, which comprise six parts: genome, transcriptome, proteome, metabolome, metallome, and variome. The collected multi-omics data were performed to re-annotate and re-analyze, and then stored in MySQL relational database and static files on server. The programming languages such as HTML, JS, Perl/Python, and R were installed on the server, and parsed and visualize the multi-omics data in back- and front end. Through the Apache, users can access the MouseOmics database with the user-friendly web interface.

keyword search, BLAST, and JBrowse2. Except that, we embedded several useful tools like MISAweb for the identification of microsatellite DNAs and specifically developed the enrichment analysis tools of InterPro, GO, and pathway for mouse.

Web interface and usage

The MouseOmics database presents a user-friendly interface to explore extensive mouse multi-omics data for the community. The current version of the MouseOmics database mainly contains nine main pages, namely Home, Genome, Transcriptome, Proteome, Metabolome, Metallome, Tools, and Help.

The Home page constitutes a synoptic portal that strategically amalgamates the database overview, expedited navigation modules, curated links, real-time announcements, peer-reviewed literature, and direct gateways to all omics repositories, thereby furnishing experimental biologists with an integrated and information-dense portal to the resource. The Genome, Transcriptome, Proteome, Metabolome, and Metallome pages organize multi-omics projects by mouse strain and link each project to the downstream analysis. The Tools page provides both standalone utilities and embedded web services, while the Help pages guide users through every feature of MouseOmics.

Mouse genome components

The Genome page presents detailed information for each mouse species and genome sequencing project, such as basic information, assembly status, genome annotation, and publication (Fig. 2A). For each gene, MouseOmics supplies basic information and location on genome assemblies, and specifically developed the gene and protein expression profiles across the transcriptome and proteome projects for *M. musculus*, strain C57BL/6J (Fig. 2B). As the gene detailed information, the transcripts were supplied with basic information and genomic location on genome assemblies across various mouse species, as well as the functional annotation. Within the panel

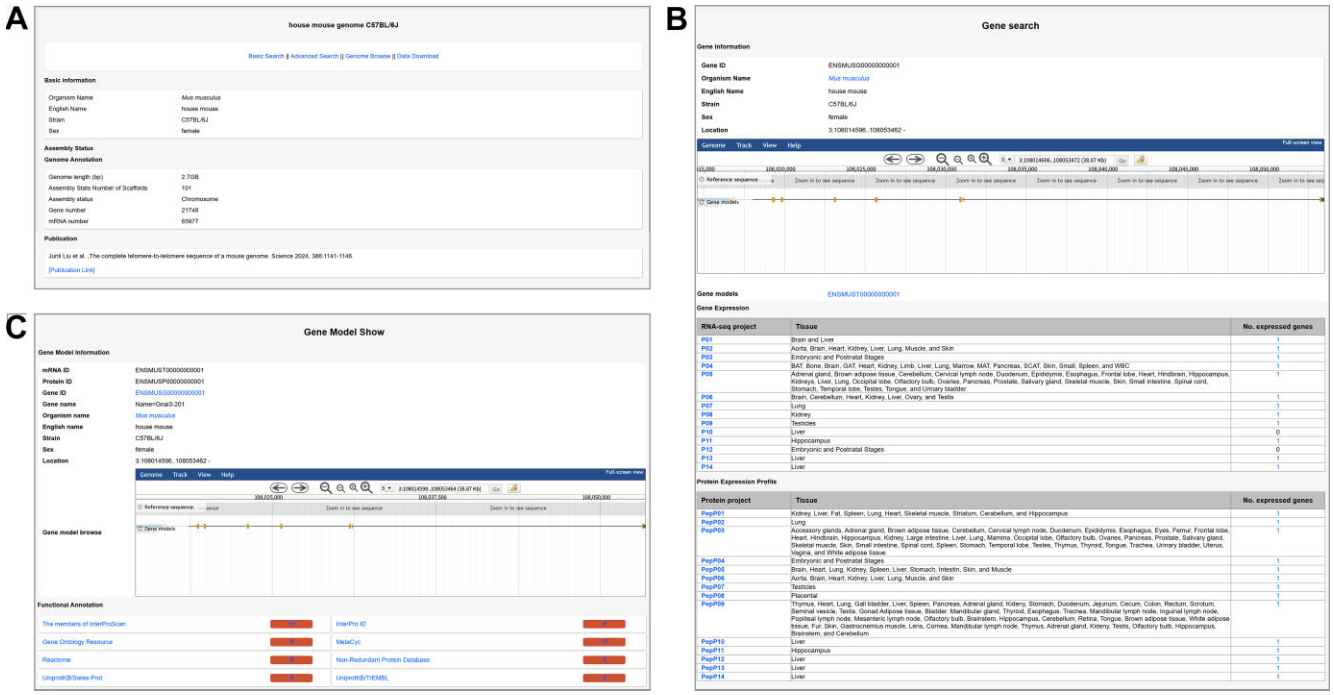

Figure 2. Representative screenshots for genome module. (**A**) The detailed page of mouse species and genome sequencing project. (**B**) The detailed page of mouse genes, including basic information, gene location, and gene and protein expression profiles. (**C**) The detailed page of mouse mRNA or transcripts that included mRNA basic information, corresponding genomic location, and functional annotations.

of functional annotation, each functional unit has the detailed annotation from online web services and public protein function database via the corresponding hyperlinks (Fig. 2C).

Mouse gene expression module

The MouseOmics database systematically organizes representative transcriptome projects spanning different mouse tissues and life periods across an extensive panel of mouse strains (Fig. 3A). For every transcriptome project, MouseOmics presents exhaustive metadata, accession, primary publication, experimental design, tissue source, and treatment regimen, alongside quantitative expression matrices that report mean TPM (or FPKM) across biological replicates and their associated standard deviations (Fig. 3B). Each expressed gene is hyperlinked to a dedicated gene-detail page, enabling one-click retrieval of curated functional annotations within MouseOmics. Each expressed gene is hyperlinked to its dedicated gene-detail page, enabling instant, one-click access to curated functional annotations within MouseOmics. The transcriptome project interface comprises two integrated functional units: "gene expression" and "pairwise comparison." For the functional unit of "gene expression," users obtain an interactive expression heatmap that instantly visualizes the transcriptional profile after selecting a target tissue within the project and entering a gene or gene list of interest (Fig. 3C and D). The pairwise comparison module empowers users to conduct head-to-head transcriptomic analyses between any two samples within a project, instantly revealing differential expression landscapes. Upon selecting query and subject samples together with the treatments of interest, MouseOmics executes differential expression analysis and delivers exhaustive results: a filtered list of DEGs meeting user-defined adjusted *P*-value and fold-change thresholds, accompanied by downloadable tables and high-resolution, interactive heatmaps, and volcano plots (Fig. 3E and F).

MISAweb and synteny viewer modules

Microsatellite DNAs participate in a spectrum of fundamental processes—chromatin architecture sculpting, DNA metabolism, and mismatch-repair fidelity—thereby furnishing mice with an agile, heritable substrate for rapid genomic and phenotypic adaptation to environmental flux. The MouseOmics database integrates MISAweb module, a dedicated online microsatellite discovery engine that enables microsatellite DNA mining across 21 mouse reference genomes. Users simply upload or paste a target genomic sequence; within seconds, MISAweb returns an exhaustive catalogue of microsatellites packaged in two compressed archives, including detailed statistics and tabulated list of microsatellite DNAs in the target mouse genomic sequence.

To illuminate genomic evolution and divergence across the 21 curated mouse genomes, MouseOmics provides an interactive synteny viewer that dynamically renders syntenic blocks and homologous gene pairs between any single chromosome of a reference genome and the complete chromosome complement of any other mouse strain in the collection (Fig. 4A). On the back end, syntenic blocks and homologous gene pairs have been stored in a normalized MySQL relational schema, enabling sub-second retrieval of any requested chromosome-to-genome comparison. Once users designate the query chromosome in target mouse genome, and comparative mouse strain, the submitted job triggers MouseOmics to render high-resolution synteny viewer via Circos software and to deliver a structured table enumerating block ID, query and subject coordinates, score, and *E*-value for every detected syntenic region (Fig. 4B). Within each syntenic block, homologous gene pairs are rendered as collinear cartoon bars in the Circos plot

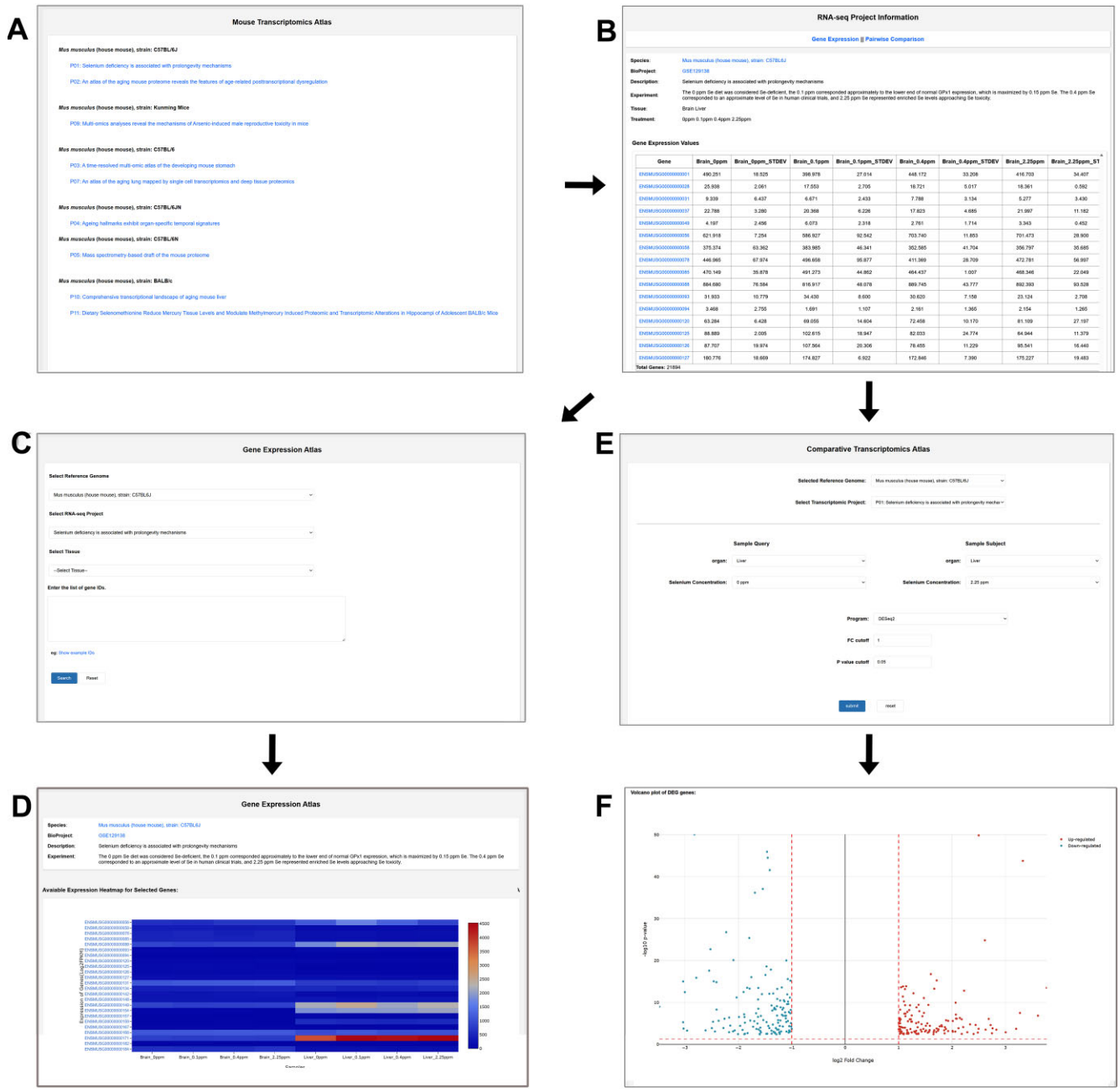

Figure 3. Representative screenshots for transcriptome module. (**A**) The transcriptome project organized by mouse strains. (**B**) The detailed information for each project and expressed genes in the project. (**C**) The functional unit of "gene expression." (**D**) The gene expression of target gene or gene list in single or all tissue(s). (**E**) The functional unit of "pairwise comparison." (**F**) The volcano plot of differentially expressed genes of the pairwise comparison in the project.

and listed in an interactive table; every block ID is hyperlinked to enable instant drill-down into detailed gene-level annotations within MouseOmics (Fig. 4C).

Functional enrichment modules

MouseOmics has three kinds of functional enrichment modules, including InterPro, GO, and Pathway enrichment modules. On the back-end, MouseOmics maintains pre-indexed, genome-specific flat files that house the complete InterPro, GO, and MetaCyc functional annotations for every protein encoded within 21 mouse reference genomes. InterPro and Pathway enrichment modules have the same procedures to perform in MouseOmics. Via the web interface, users first select the desired genome from a dropdown box, then supply a list of protein identifiers in the adjacent textbox, and finally define the statistical significance threshold by entering a *P*-value cutoff derived from the hypergeometric test. Upon submission, the analysis job is dispatched to the server queue for immediate processing. MouseOmics displays each enriched InterPro accession together with its curated description, the corresponding MetaCyc pathway identifier and functional summary, and a concise catalog of all protein identifiers within the selected mouse genome that co-cluster into

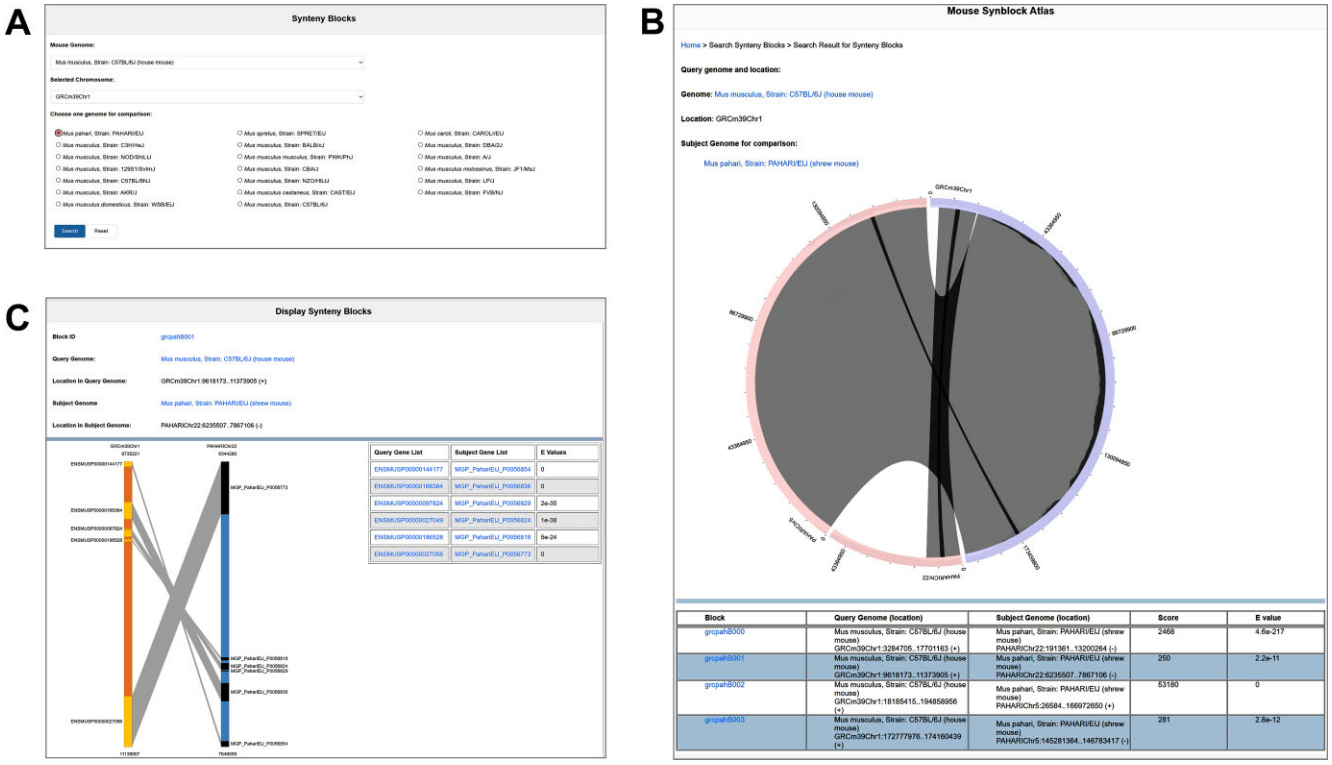

Figure 4. Synteny viewer module in the MouseOmics database. (**A**) The selection of query and subject genomic regions across 21 mouse genomes. (**B**) The comparison between two genomic regions from any two genomes in MouseOmics. (**C**) The display of homologous gene pairs from any two mouse genomes.

the same InterPro entry and pathway. Owing to the tripartite architecture of the GO resource, the GO enrichment module in MouseOmics incorporates a dedicated workflow that discretely evaluates enrichment within the biological process, molecular function, and cellular component ontologies. Following the same streamlined submission used for InterPro and pathway enrichment, users only need to specify the desired ontologies; the back end then executes the GO enrichment and returns the enriched terms together with their full textual descriptions for the queried mouse functional genes.

Case study showing interactions among multi-omic data

The MouseOmics database allows users to search for any gene of interest across genome, transcriptome, and proteome sections. Using *slc11a2* as an example, we demonstrate how to retrieve comprehensive information from MouseOmics. This gene encodes the divalent metal transporter DMT1, which is essential for the absorption and transport of divalent metal ions and for maintaining metal homeostasis, including iron balance [40, 41]. Starting from the homepage, users can enter "slc11a2" in the search box (Fig. 5A). Upon clicking the search button, MouseOmics returns a list of all *slc11a2* genes across various mouse strains. The results are displayed in a visualized table that includes gene models, protein IDs, gene IDs, mouse species, and chromosome numbers (Fig. 5B). By clicking on a gene model hyperlink, users can access detailed information, including basic gene features and functional annotations (Fig. 5C). From this page, clicking on the gene ID hyperlink leads to a comprehensive gene summary that shows all associated gene models, gene expression levels across multiple RNA-seq projects, and protein abundance data from various proteome projects (Fig. 5D). Furthermore, clicking on the hyperlinks within the expression tables allows users to view detailed gene expression values and protein abundances across different tissues or conditions (Fig. 5E and F). Thus, the search function enables users to explore gene information across genomics, transcriptomics, and proteomics. The integrated interface allows intuitive and easy visualization of multi-omics data.

MouseOmics consolidates the available metallome projects—though still limited—into a strain-centric framework that lets users quickly retrieve ion concentrations for any tissue or condition (Fig. 6A). The module offers two complementary views: an overview page summarizing project metadata, plotting aggregate ion levels and supplying a sortable concentration table (Fig. 6B), and a single-tissue query panel where a tissue and either an ion list or an individual ion can be selected (Fig. 6C). One click generates an interactive heatmap plus downloadable table of concentrations for the chosen tissue or condition (Fig. 6D), while clicking an ion symbol (e.g. Fe) opens line or bar charts tracing that ion's abundance across every metallome project in the database (Fig. 6E). The metallome module equips experimental biologists with a clear, data-driven view of how metal content differs among tissues and across mouse strains, deepening their understanding of metal stress and accelerating the advancement of murine metallomics.

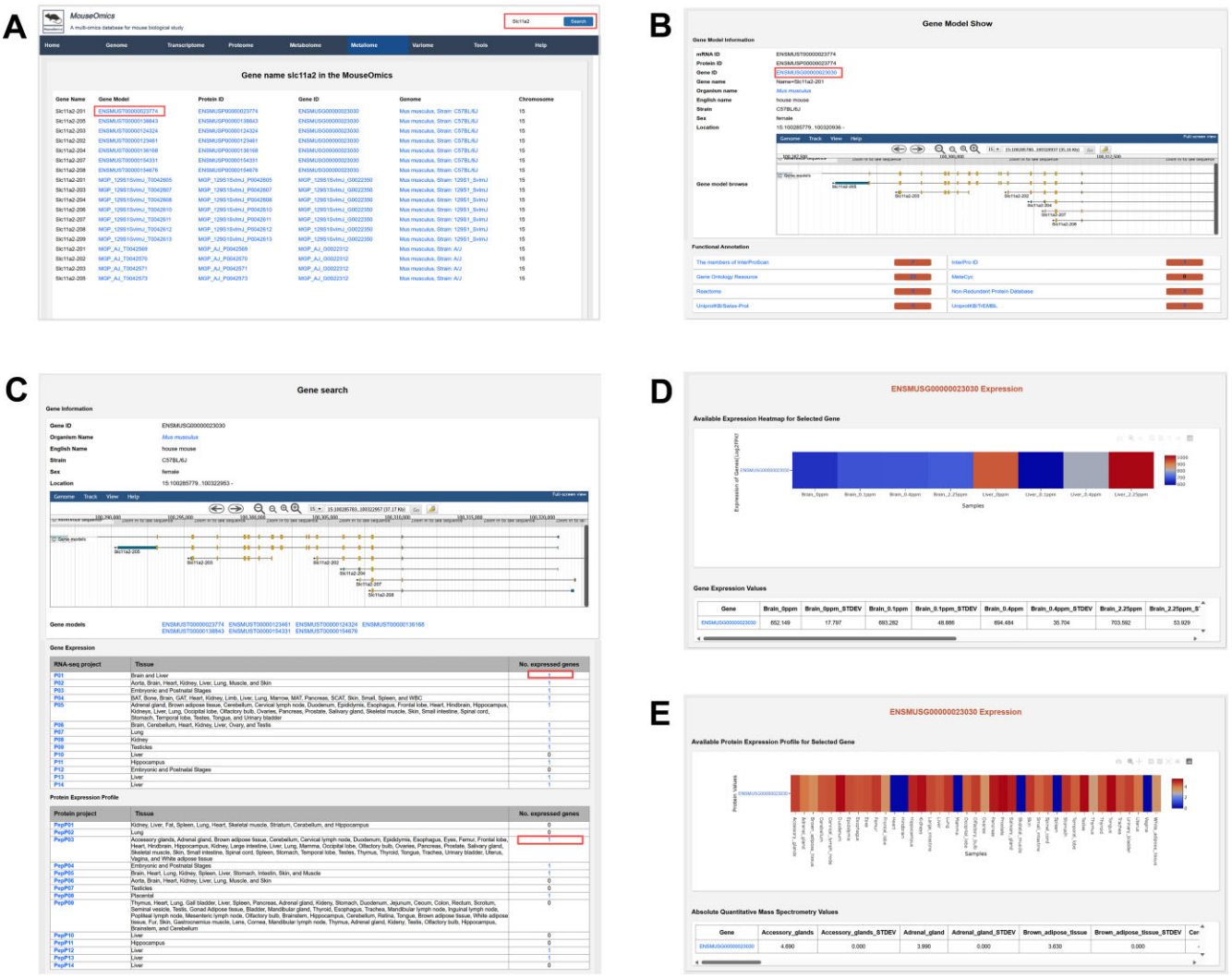

Figure 5. Search case for the *slc11a2* gene. (**A**) Search function on the homepage. (**B**) List of *slc11a2* homologs across mouse strains. (**C**) Gene-model detail (ENSMUST00000023774) for *slc11a2* gene in *M. musculus* C57BL/6J. (**D**) Corresponding gene details (ENSMUSG00000023030) for the target gene model. (**E**) The gene expression values across tissues in the RNA-seq project. (**F**) Protein abundances across tissues from proteome datasets.

Discussion and future perspectives

The MouseOmics database provides an integrated platform for accessing and leveraging multi-omics data consolidated from diverse mouse studies. Recognizing the pivotal role of multi-omics integration in advancing scientific discoveries, this resource consolidates extensive datasets spanning genomic annotations across multiple mouse strains, detailed mutation profiles, and high-throughput data from multi-tissue organs of mice at varying ages.

Relative to other published mouse biological databases, including MGD, GXD, ProteomicsDB, MMMDB, and IMPC, it demonstrates unique capabilities as follows: (i) MouseOmics is the first integrated database for six mouse omics types. Meanwhile, MouseOmics is also the first database to comprehensively collect and assemble mouse metallomics data, enabling researchers to rapidly mine cross-omics biological insights; (ii) MouseOmics collects multi-omics data from mice across the entire lifespan. For example, metallomics data of multiple organs from mice (aged from zero to three years), and proteomic, transcriptomic, and metabolomic data spanning multiple stages and organs, including from embryonic stage to birth, birth to adulthood, and adulthood to aging; (iii) MouseOmics performed the syntenic analysis within five mouse species aiming to detect the divergence in the genus *Mus*; (iv) MouseOmics embedded several useful tools like MISAweb, for the identification of microsatellite DNAs, and specifically developed the enrichment analysis tools of InterPro, GO, and pathway for the mouse; and (v) MouseOmics is not restricted to specific architectures and will continuously update with other advanced omics data, including single-cell transcriptomics and metagenomics.

In summary, MouseOmics serves as a crucial resource and tool for swiftly retrieving mouse—related gene information and understanding mouse multi-omics data. The data coverage in MouseOmics remains comparatively limited. As sequencing technologies advance and become more widespread, more datasets will emerge, and we will continually expand MouseOmics with representative mouse multi-omics datasets, prioritizing developmental multi-omics profiles and metallomic dysregulation datasets. The integration of these data types, combined with the development of database tools, will

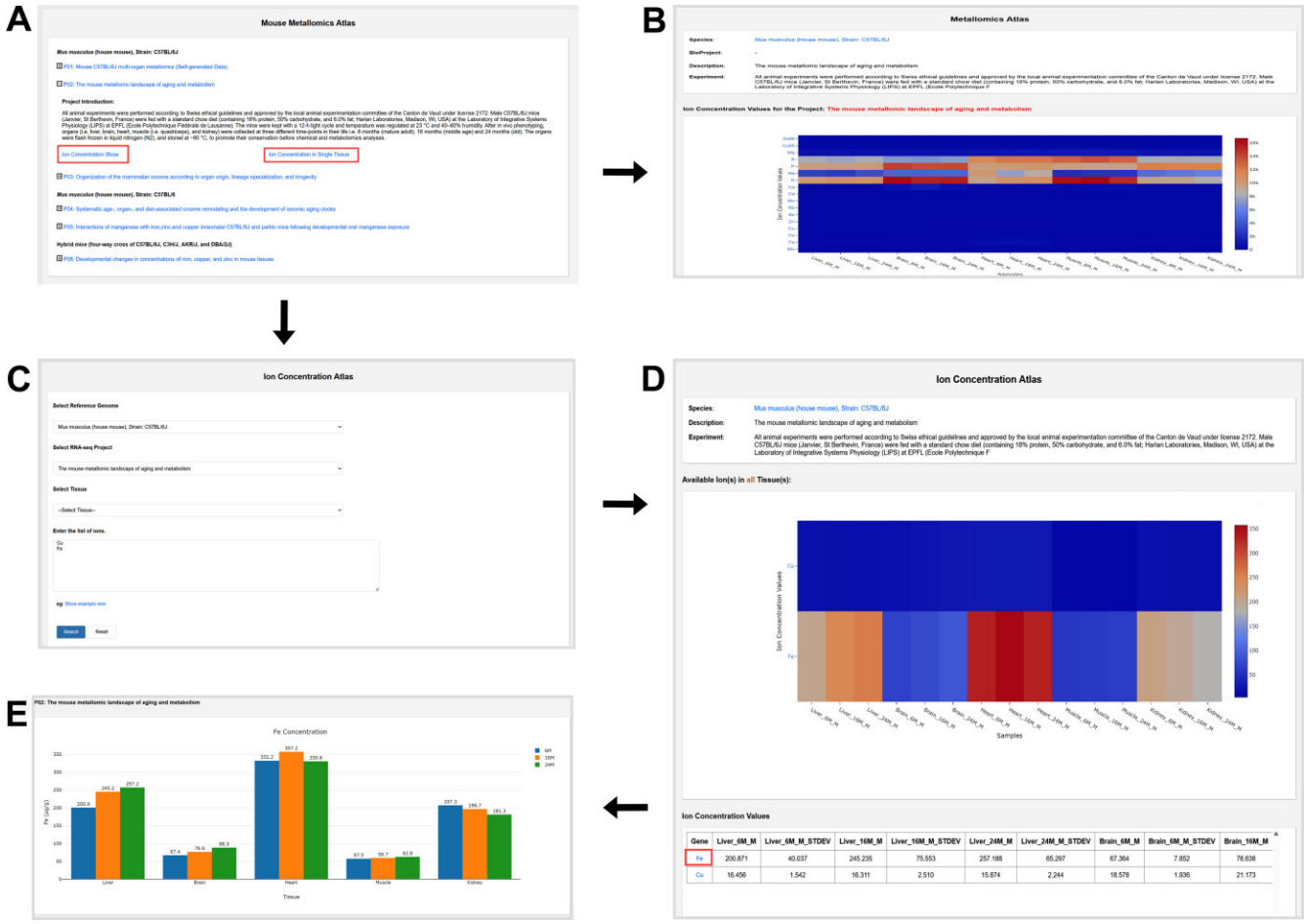

Figure 6. The utilization of metallome modules. (**A**) The overview of metallomic data organized in the database. (**B**) The concentration showing page of all ions in metallome project. (**C**) The search function of ion concentration of single tissue. (**D**) The concentration showing page of target ions in single tissue. (**E**) The display of Fe concentration across various metallome projects.

effectively assist researchers in elucidating the roles of various metal elements throughout the mouse lifespan. Such integration will help pinpoint the imbalances in transporters, proteins, and metabolites resulting from the deficiency or excess of specific metals, thereby facilitating a deeper understanding of the interplay between metallomics and other omics fields. In the future, we will develop more user-friendly analytical tools, including those for cross-omics correlation analysis and protein–protein interaction networks, and gradually build new omics sections such as single-cell transcriptomics, metagenomics, and pangenomics.

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Conflict of interest

None declared.

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Data availability

All the data in MouseOmics are freely available via https://www.varnatech.cn/MouseOmics.

References

1. Couger MB, Arévalo L, Campbell P. A high quality genome for *Mus spicilegus*, a close relative of house mice with unique social

and ecological adaptations. *G3* 2018;**8**:2145–52. https://doi.org/10.1534/g3.118.200318
2. Yarmishyn AA, Kremenskoy M, Batagov AO *et al.* Genome-wide analysis of mRNAs associated with mouse peroxisomes. *BMC Genomics* 2016;**17**:1028. https://doi.org/10.1186/s12864-016-3330-x
3. Harr B, Karakoc E, Neme R *et al.* Genomic resources for wild populations of the house mouse, *Mus musculus* and its close relative *Mus spretus*. *Sci Data* 2016;**3**:160075. https://doi.org/10.1038/sdata.2016.75
4. Macholán M, Baird SJE, Munclinger P, Piálek J (eds.) *Evolution of the House Mouse* Cambridge: Cambridge University Press, 2012. https://doi.org/10.1017/CBO9781139044547
5. Liu M, Yu C, Zhang Z *et al.* Whole-genome sequencing reveals the genetic mechanisms of domestication in classical inbred mice. *Genome Biol* 2022;**23**:203. https://doi.org/10.1186/s13059-022-02772-1
6. Liu J, Li Q, Hu Y *et al.* The complete telomere-to-telomere sequence of a mouse genome. *Science* 2024;**386**:1141–6. https://doi.org/10.1126/science.adq8191
7. Qiu C, Martin BK, Welsh IC *et al.* A single-cell time-lapse of mouse prenatal development from gastrula to birth. *Nature* 2024;**626**:1084–93. https://doi.org/10.1038/s41586-024-07069-w
8. Takasugi M, Nonaka Y, Takemura K *et al.* An atlas of the aging mouse proteome reveals the features of age-related post-transcriptional dysregulation. *Nat Commun* 2024;**15**:8520. https://doi.org/10.1038/s41467-024-52845-x
9. Zhang F, Li R, Liu Y *et al.* Integrative cross-tissue analysis unveils complement-immunoglobulin augmentation and dysbiosis-related fatty acid metabolic remodeling during mammalian aging. *Imeta* 2025;**4**:e70027. https://doi.org/10.1002/imt2.70027
10. Ma S, Ji Z, Zhang B *et al.* Spatial transcriptomic landscape unveils immunoglobin-associated senescence as a hallmark of aging. *Cell* 2024;**187**:7025–44. https://doi.org/10.1016/j.cell.2024.10.019
11. Lilue J, Doran AG, Fiddes IT *et al.* Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nat Genet* 2018;**50**:1574–83. https://doi.org/10.1038/s41588-018-0223-8
12. Ringwald M, Richardson JE, Baldarelli RM *et al.* Mouse genome informatics (MGI): latest news from MGD and GXD. *Mamm Genome* 2022;**33**:4–18. https://doi.org/10.1007/s00335-021-09921-0
13. Baldarelli RM, Smith CM, Finger JH *et al.* The mouse gene expression database (GXD): 2021 update. *Nucleic Acids Res* 2021;**49**:D924–D931. https://doi.org/10.1093/nar/gkaa914
14. Lautenbacher L, Samaras P, Muller J *et al.* ProteomicsDB: toward a FAIR open-source resource for life-science research. *Nucleic Acids Res* 2022;**50**:D1541–D1552. https://doi.org/10.1093/nar/gkab1026
15. Groza T, Gomez FL, Mashhadi HH *et al.* The international mouse phenotyping consortium: comprehensive knockout phenotyping underpinning the study of human disease. *Nucleic Acids Res* 2023;**51**:D1038–D1045. https://doi.org/10.1093/nar/gkac972
16. Morel J-D, Sauzéat L, Goeminne LJE *et al.* The mouse metallomic landscape of aging and metabolism. *Nat Commun* 2022;**13**:607. https://doi.org/10.1038/s41467-022-28060-x
17. Ma S, Lee S-G, Kim EB *et al.* Organization of the mammalian ionome according to organ origin, lineage specialization, and longevity. *Cell Rep* 2015;**13**:1319–26. https://doi.org/10.1016/j.celrep.2015.10.014
18. Keen CL, Lönnerdal B, Clegg M *et al.* Developmental changes in composition of rat milk: trace elements, minerals, protein, carbohydrate and fat. *J Nutr* 1981;**111**:226–36. https://doi.org/10.1093/jn/111.2.226
19. Aron AT, Petras D, Schmid R *et al.* Native mass spectrometry-based metabolomics identifies metal-binding compounds. *Nat Chem* 2022;**14**:100–9. https://doi.org/10.1038/s41557-021-00803-1
20. Zhang B, Podolskiy DI, Mariotti M *et al.* Systematic age-, organ-, and diet-associated ionome remodeling and the development of ionomic aging clocks. *Aging Cell* 2020;**19**:e13119. https://doi.org/10.1111/acel.13119
21. Okashita N, Maeda R, Kuroki S *et al.* Maternal iron deficiency causes male-to-female sex reversal in mouse embryos. *Nature* 2025;**643**:262–70. https://doi.org/10.1038/s41586-025-09063-2
22. Zhang X, Wei H, Guan Q *et al.* Maternal exposure to trace elements, toxic metals, and longitudinal changes in infancy anthropometry and growth trajectories: a prospective cohort study. *Environ Sci Technol* 2023;**57**:11779–91. https://doi.org/10.1021/acs.est.3c02535
23. Zeng H, Zhang W, Lin Q *et al.* PigBiobank: a valuable resource for understanding genetic and biological mechanisms of diverse complex traits in pigs. *Nucleic Acids Res* 2024;**52**:D980–D989. https://doi.org/10.1093/nar/gkad1080
24. Zhou T, Pu S-Y, Zhang S-J *et al.* Dog10K: an integrated Dog10K database summarizing canine multi-omics. *Nucleic Acids Res* 2025;**53**:D939–D947. https://doi.org/10.1093/nar/gkae928
25. Yang Z, Wang J, Huang Y *et al.* CottonMD: a multi-omics database for cotton biological study. *Nucleic Acids Res* 2023;**51**:D1446–1D1456. https://doi.org/10.1093/nar/gkac863
26. Li X, Meng B, Zhang Z *et al.* qPrimerDB 2.0: an updated comprehensive gene-specific qPCR primer database for 1172 organisms. *Nucleic Acids Res* 2025;**53**:D205–D210. https://doi.org/10.1093/nar/gkae684
27. Blum M, Andreeva A, Florentino LC *et al.* InterPro: the protein sequence classification resource in 2025. *Nucleic Acids Res* 2025;**53**:D444–D456. https://doi.org/10.1093/nar/gkae1082
28. Buchfink B, Reuter K, Drost H-G. Sensitive protein alignments at tree-of-life scale using DIAMOND. *Nat Methods* 2021;**18**:366–8. https://doi.org/10.1038/s41592-021-01101-x
29. Cantalapiedra CP, Hernandez-Plaza A, Letunic I *et al.* eggNOG-mapper v2: functional annotation, orthology assignments, and domain prediction at the metagenomic scale. *Mol Biol Evol* 2021;**38**:5825–9. https://doi.org/10.1093/molbev/msab293
30. Aleksander SA, Balhoff J, Carbon S *et al.* The gene ontology knowledgebase in 2023. *Genetics* 2023;**224**:iyad031.
31. Caspi R, Billington R, Keseler IM *et al.* The MetaCyc database of metabolic pathways and enzymes - a 2019 update. *Nucleic Acids Res* 2020;**48**:D445–D453. https://doi.org/10.1093/nar/gkz862
32. Milacic M, Beavers D, Conley P *et al.* The reactome pathway knowledgebase 2024. *Nucleic Acids Res* 2024;**52**:D672–D678. https://doi.org/10.1093/nar/gkad1025
33. Wang Y, Tang H, DeBarry JD *et al.* MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. *Nucleic Acids Res* 2012;**40**:e49. https://doi.org/10.1093/nar/gkr1293
34. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 2014;**15**:550. https://doi.org/10.1186/s13059-014-0550-8
35. Raivo K. pheatmap: pretty Heatmaps. *R Package Version 1.0.12*. 2025;**2019**. https://CRAN.R-project.org/package=pheatmap (Accessed 2 Aug 2025).
36. Ginestet C. ggplot2: elegant graphics for data analysis. *J R Stat Soc Ser A-Stat Soc* 2011;**174**:245–6. https://doi.org/10.1111/j.1467-985X.2010.00676_9.x
37. Slowikowski K. ggrepel: automatically position non-overlapping text labels with 'ggplot2'. R Package Version 0.9.6. 2024. 2025. https://CRAN.R-project.org/package=ggrepel (Accessed 3 Mar 2025).
38. Li H, Handsaker B, Wysoker A *et al.* The sequence alignment/map format and SAMtools. *Bioinformatics* 2009;**25**:2078–9. https://doi.org/10.1093/bioinformatics/btp352
39. Diesh C, Stevens GJ, Xie P *et al.* JBrowse 2: a modular genome browser with views of synteny and structural variation. *Genome Biol* 2023;**24**:74. https://doi.org/10.1186/s13059-023-02914-z

40. Qiu L, Frazer DM, Hu M *et al*. Mechanism and regulation of iron absorption throughout the life cycle. *J Adv Res* 2025;**S2090-1232**: 00002–5. https://doi.org/10.1016/j.jare.2025.01.002

41. Liziczai M, Fuchs A, Manatschal C *et al*. Structural basis for metal ion transport by the human SLC11 proteins DMT1 and NRAMP1. *Nat Commun* 2025;**16**:761. https://doi.org/10.1038/s41467-024-54705-0

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