



The HTIRDB:

A resource containing a transcriptional atlas for 105 different tissues from each of seven species of domestic herbivore



Luoyang Ding^{1,5#}, Yifan Wang^{1,2,4#}, Linna Zhang^{2,3#}, Chengfang Luo^{3#}, Feifan Wu^{1#}, Yiming Huang^{2,3#}, Yongkang Zhen^{1,2}, Ning Chen², Limin Wang², Li Song⁴, Kelsey Pool⁵, Dominique Blache^{1,5}, Shane K Maloney⁵, Dongxu Liu³, Zhiquan Yang³, Xiaoyan Huang³, Chuang Li¹, Xiang Yu¹, Zhenbin Zhang¹, Yifei Chen¹, Chun Xue¹, Yalan Gu¹, Weidong Huang¹, Lu Yan¹, Wenjun Wei¹, Yusu Wang¹, Jinying Zhang¹, Yifan Zhang¹, Yiquan Sun¹, Rui Dai³, Shengbo Wang³, Xinle Zhao³, Haodong Wang³, Ping Zhou^{2*}, Qing-Yong Yang^{2,3*}, Mengzhi Wang^{1,2*}

¹ Laboratory of Metabolic Manipulation of Herbivorous Animal Nutrition, College of Animal Science and Technology, Yangzhou University, Yangzhou 225009, China

² State Key Laboratory of Sheep Genetic Improvement and Healthy Production, Xinjiang Academy of Agricultural Reclamation Sciences, Shihezi 832000, China

³ Key Laboratory of Smart Farming for Agricultural Animals, Engineering Technology Research Center of Agricultural Big Data, College of Informatics, Huazhong Agricultural University, Wuhan 430070, China

⁴ College of Life Science, Guizhou University, Guiyang 550025, China

⁵ UWA Institute of Agriculture, The University of Western Australia, Perth WA 6009, Australia

#These authors contributed equally: Luoyang Ding, Yifan Wang, Linna Zhang, Chengfang Luo, Feifan Wu, and Yiming Huang. *Correspondence: Ping Zhou, Qing-Yong Yang, Mengzhi Wang

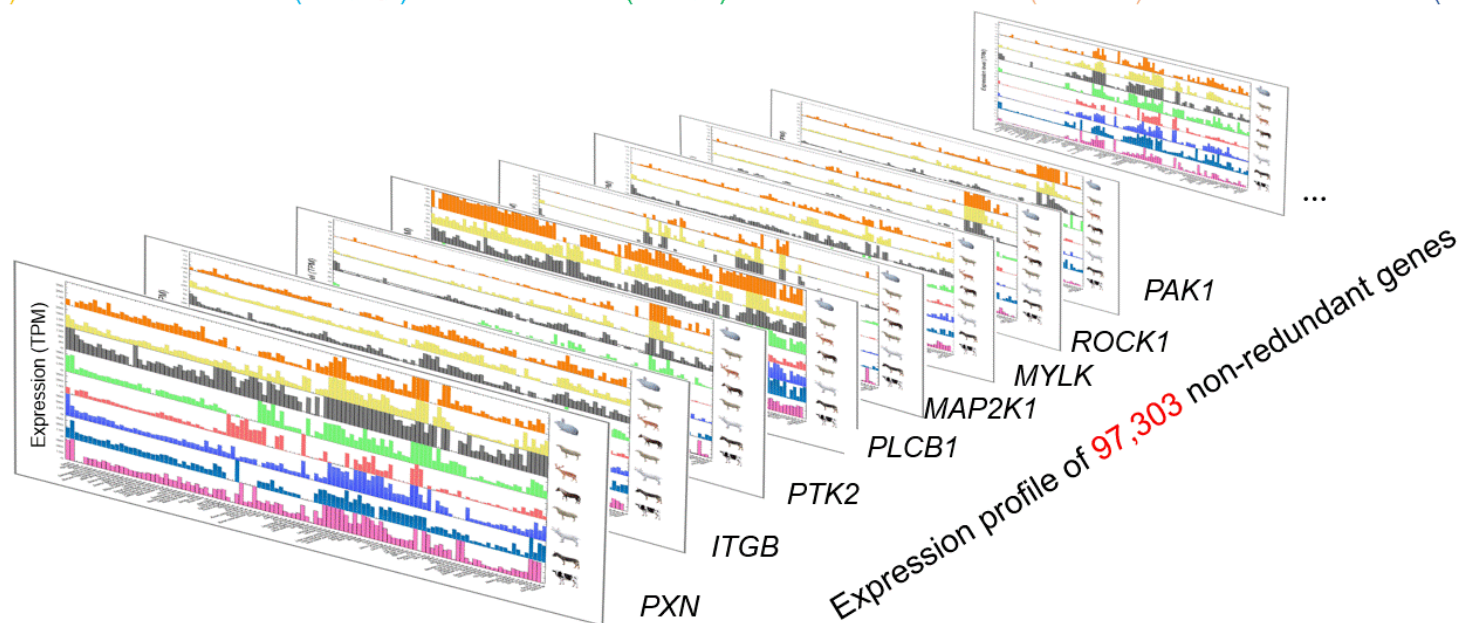
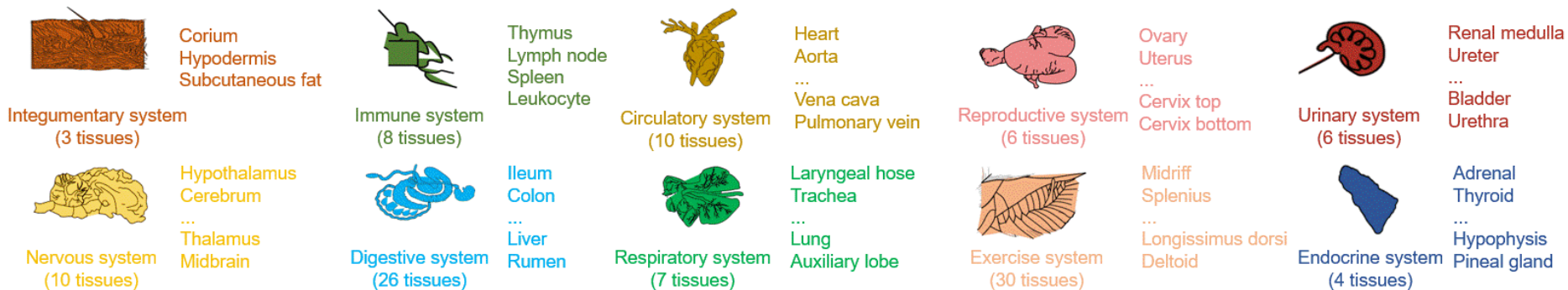
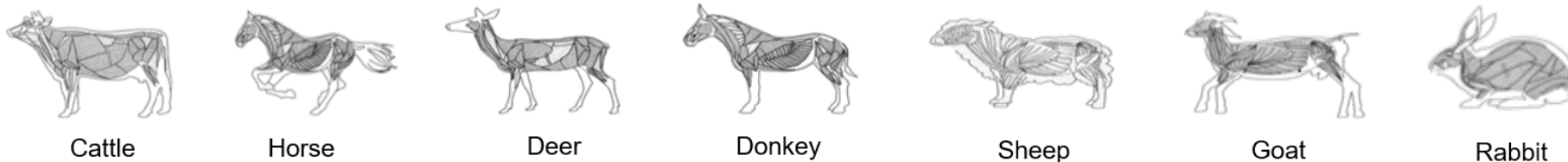
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Graphical abstract

105 different tissues from each of 7 species of domestic herbivore





Data collection and database construction

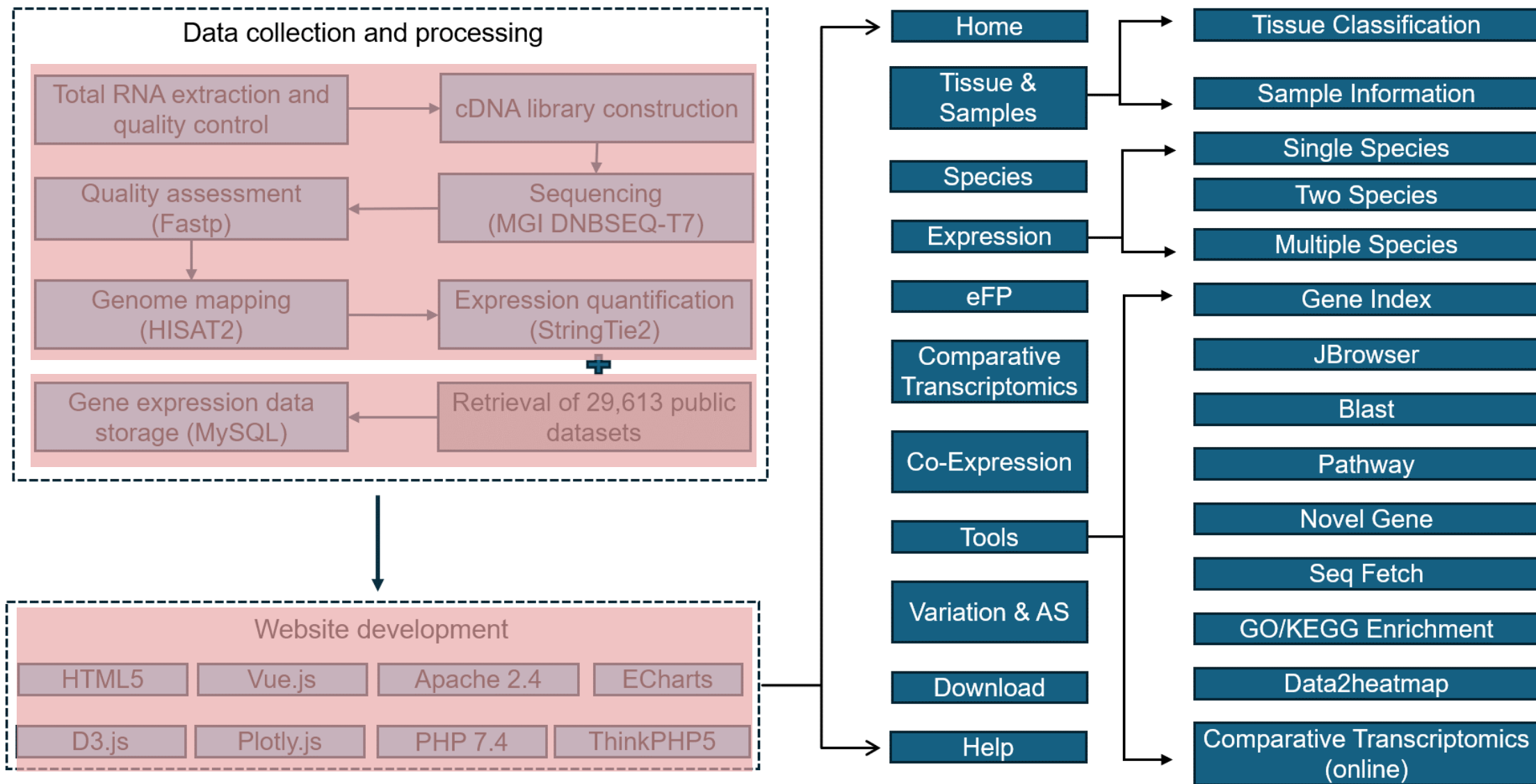


Figure 1B. A schematic overview of the data collection and construction of the HTIRDB



Electronic Fluorescent Pictograph (eFP)

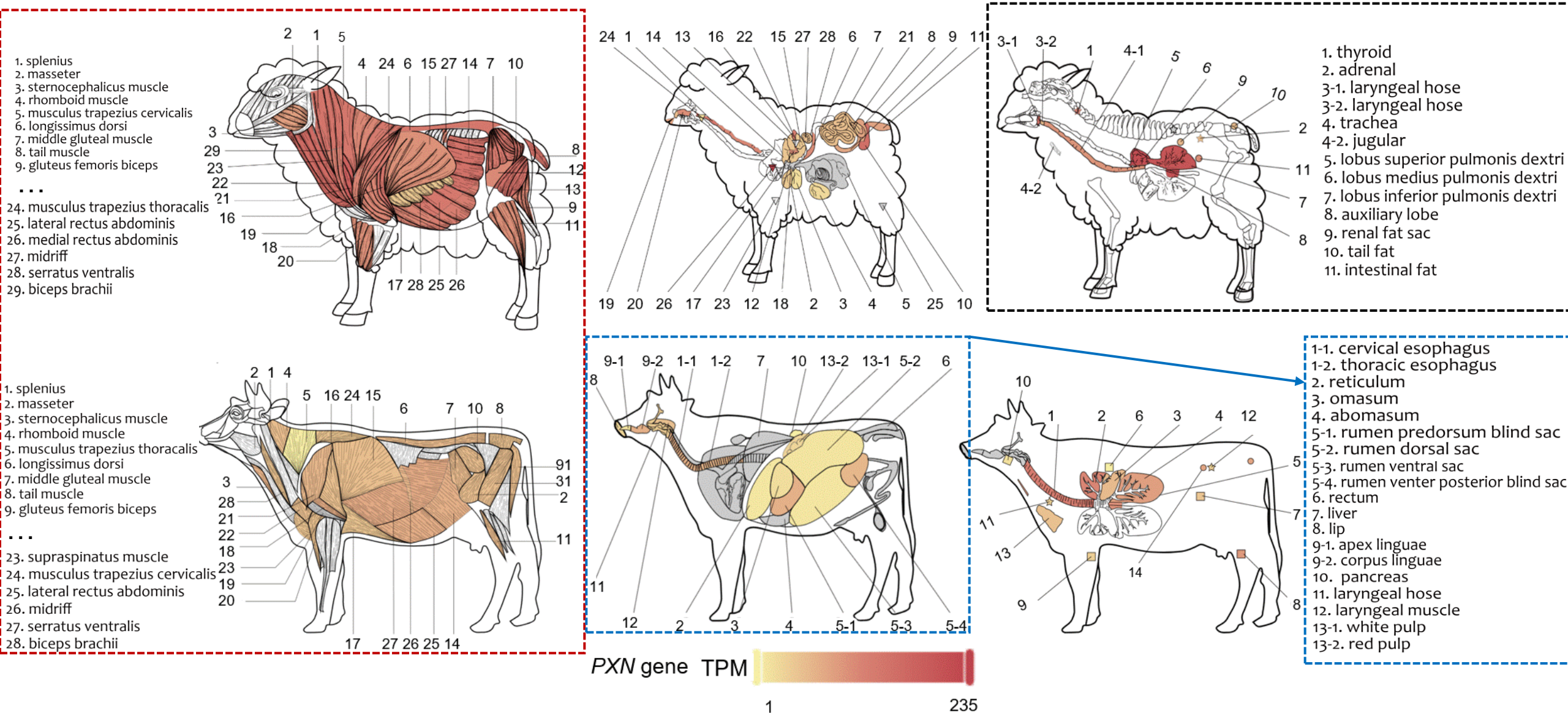
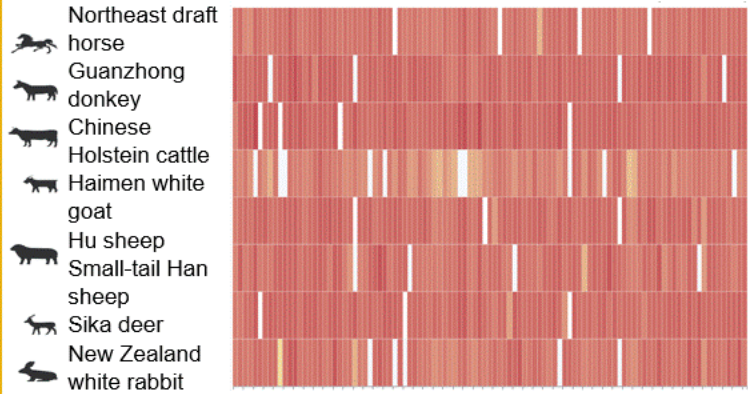


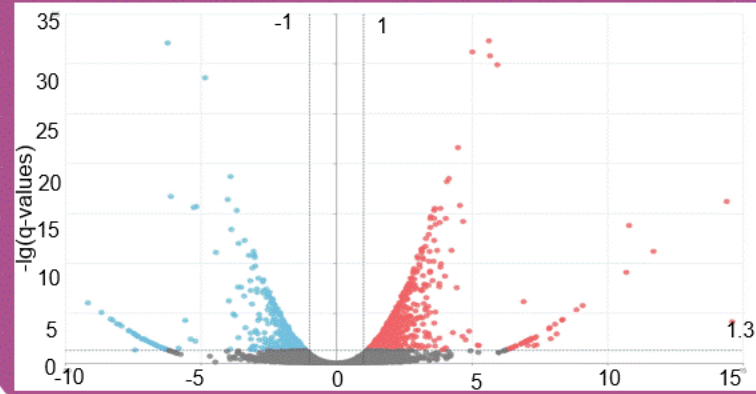
Figure 2A. Examples of Electronic Fluorescent Pictograph (eFP) output for the expression of *paxillin* gene in sheep and cattle

The other widely used functions and bioinformatic tools

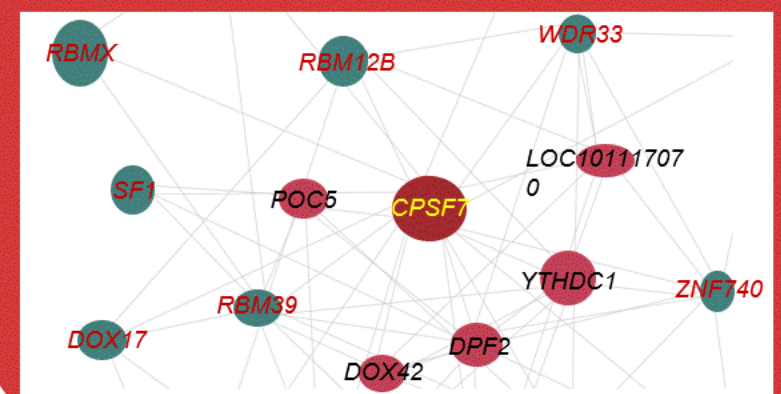
Gene expression



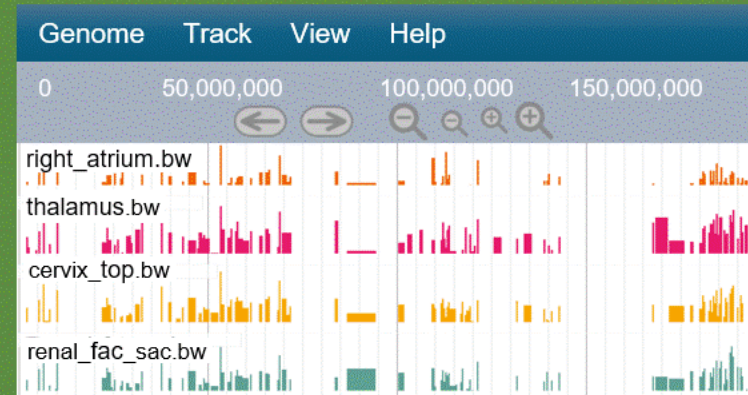
Comparative transcriptomics



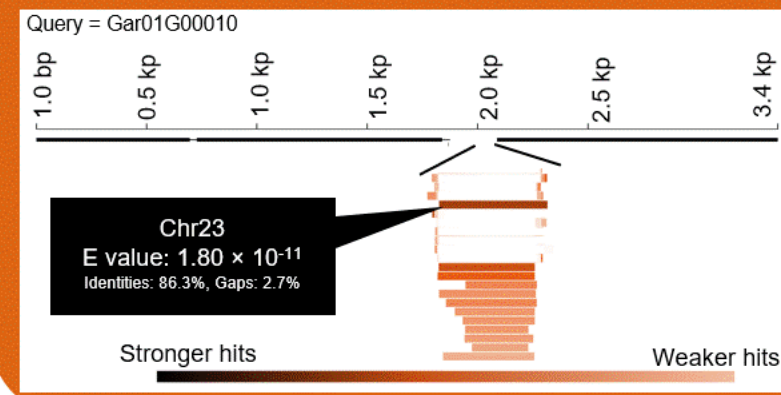
Gene co-expression



JBrowse



Blast



Functional enrichment

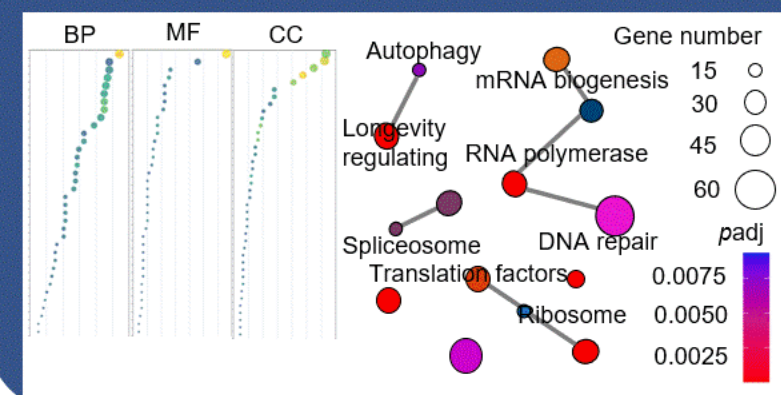


Figure 2B-2G. The functions and tools that are available for the database



Summary

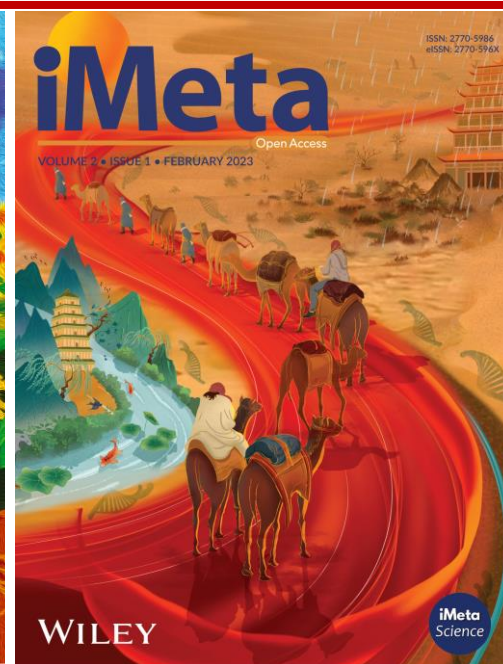
- ❑ The HTIRDB is the most robust (7 species of herbivore) and comprehensive (105 different tissues), and biggest (638 billion raw sequencing reads) transcriptome atlas for herbivores to date;
- ❑ The HTIRDB provides quality assurance by optimizing the sample collection, data processing, and database construction;
- ❑ A diverse range of functional tools will suit users from multiple disciplines and backgrounds;
- ❑ Linkage of the HTIRDB: <https://yanglab.hzau.edu.cn/HTIRDB#/>

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