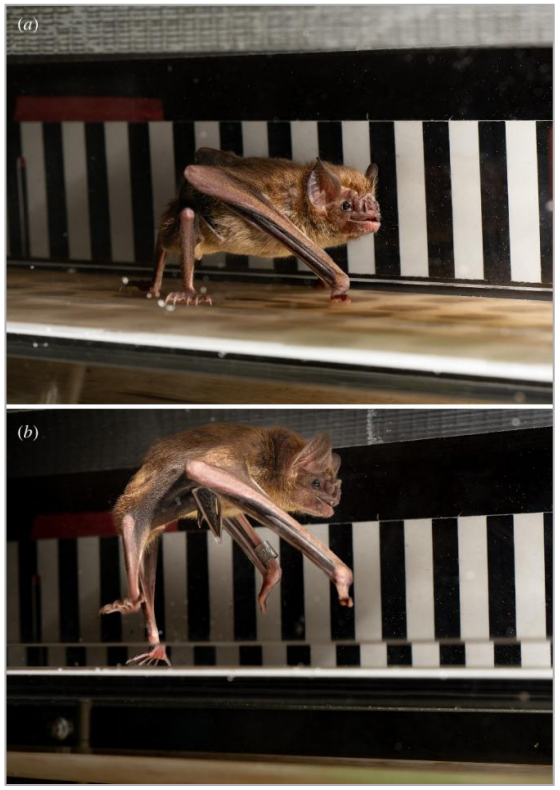
JOURNAL CLUB

Integrated genomics and transcriptomics reveal mechanisms of extreme dietary adaptation in vampire bats

Stomach remodeling / Metabolism / Iron & erythropoiesis

Liu et al. · bioRxiv · 24 July 2026

Anguo Liu | Zhang Lab | 2026/10/16



Price Sewell, Rossi & Welch 2024

Obligate blood feeding (sanguivory) in mammals is restricted to three bat species



Arthropods · Mosquitoes

Dependence on blood varies by taxon



Annelids · Leeches

Independent feeding and anticoagulation adaptations

Mammals · Desmodontinae



Desmodus

Common vampire bat



Diaemus

White-winged vampire bat



Diphylla

Hairy-legged vampire bat

共同挑战：取得血液 → 处理水盐与氮 → 补足糖脂 → 管理铁

Among more than 30,000 tetrapod species, obligate sanguivory has evolved only once and is restricted to three species of vampire bats

Riskin & Carter 2023; Liu et al. 2026

Previous studies explain parts of the adaptation

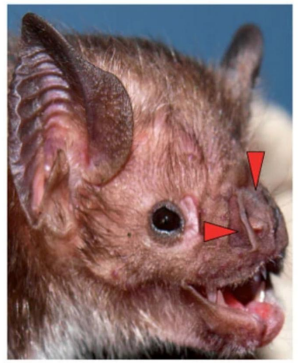
2011

Infrared sensing

Ganglion-specific TRPV1 splicing

Gracheva et al. · *Nature*

Vampire bat (*D. rotundus*)

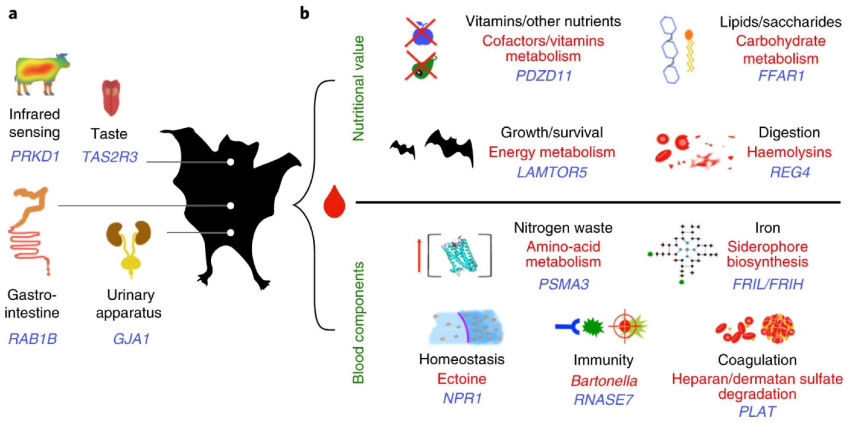


2018

Host & microbiome

Host genome + gut metagenome

Zepeda Mendoza et al. · *Nat. Ecol. Evol.*



2022

Gene loss

13 inactivated genes

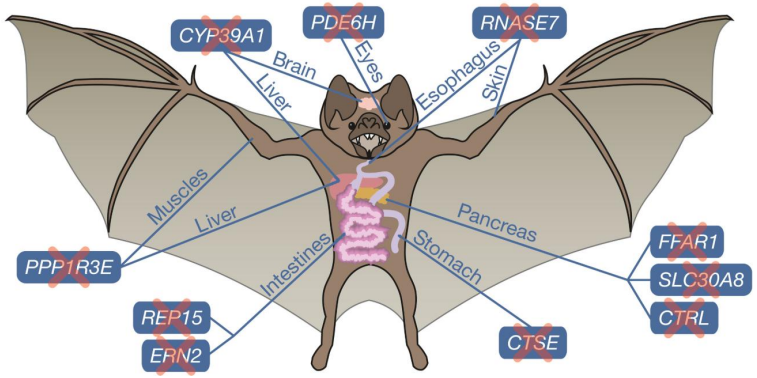
Blumer et al. · *Sci. Adv.*

2024

Amino acids as fuel

Isotope tracing during exercise

Rossi & Welch · *Biol. Lett.*



Do sequence and expression changes converge on physiological needs?

Three challenges of a blood-only diet

High fluid & salt load

Stomach expansion, absorption and rapid excretion

High protein; low sugar/fat

Amino acid catabolism and endogenous lipid synthesis

High heme-iron load

Coordinated uptake, recycling and erythropoiesis

Sequence changes + **Organ expression** → **Pathways & traits**

2026: 3 species × *de novo* assembly × expression data from six organs

High-quality genomes establish the comparative foundation

Haplotype-resolved chromosome-level assemblies for three targeted species

3 backgound species from the same phyllostomid subfamilies

(Taxonomic coverage is key to understand which changes truly occurred in vampire bats)

~ 40X coverage of PacBio HiFi reads
~60X Arima Hi-C data

↓

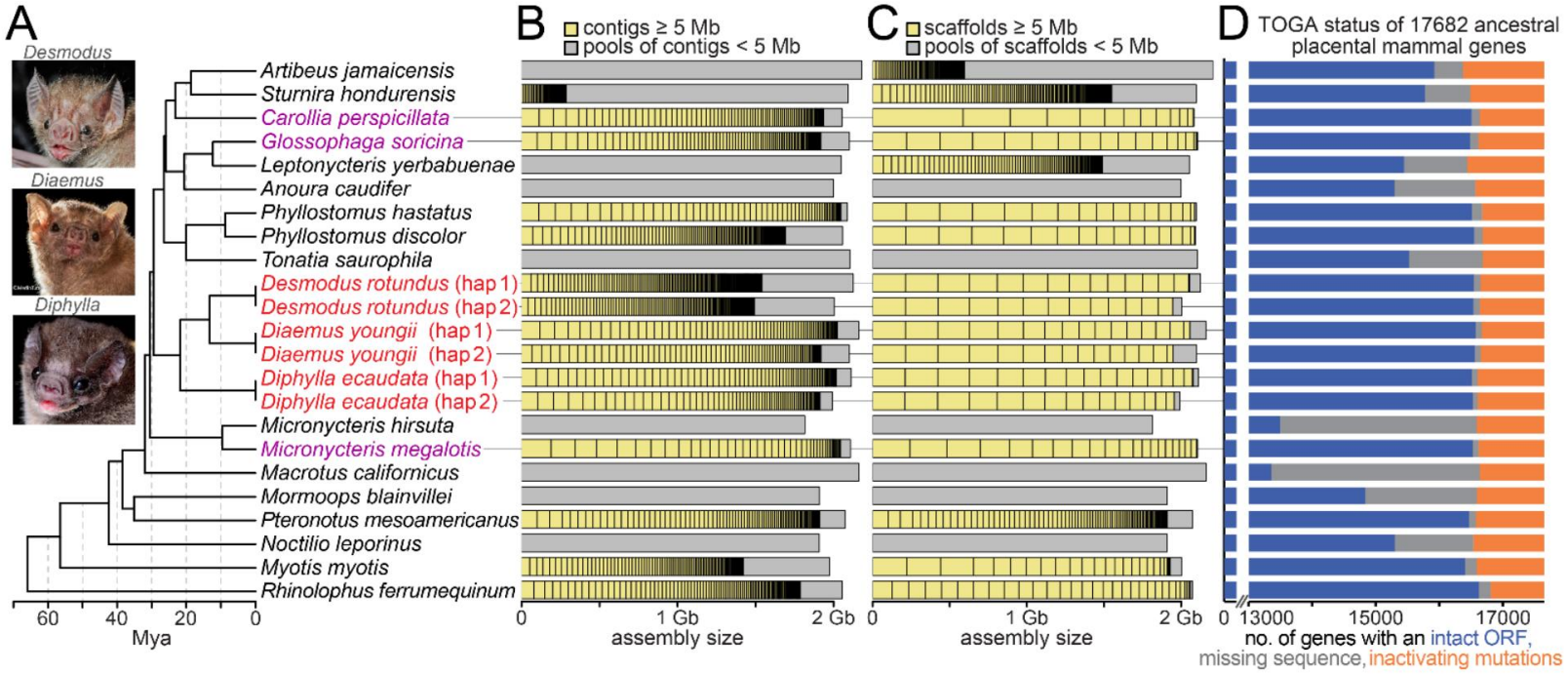
Hifiasm in Hi-C mode + YaHS curation

↓

Polish by HiFi reads

↓

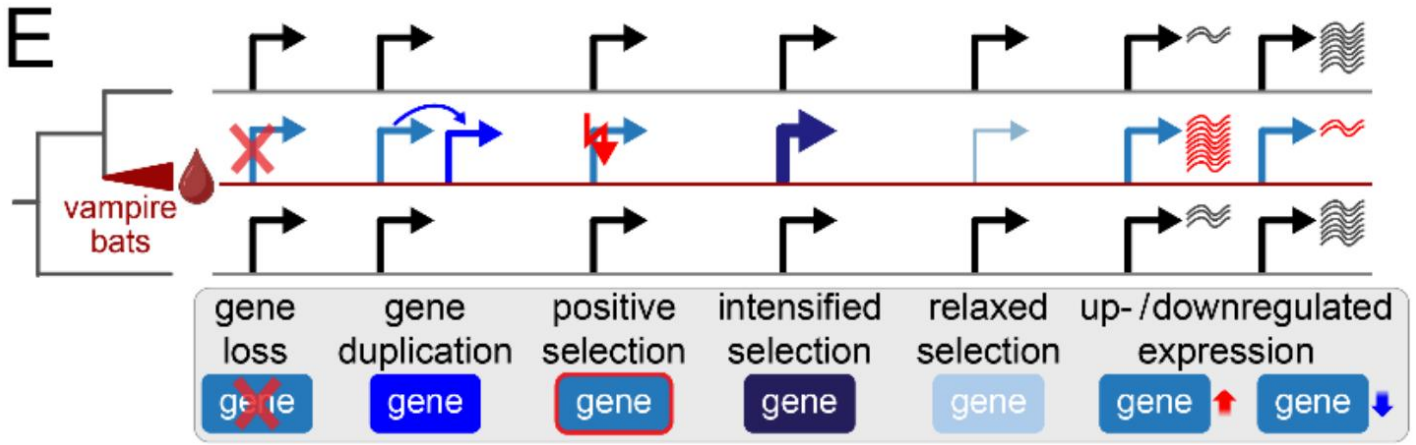
QV values 69 vs. 64 for both haplotypes



Long contig/scaffold; High base accuracy; High gene completeness

Sequence evolution and organ expression provide complementary evidence

15,481 1:1 orthologous genes



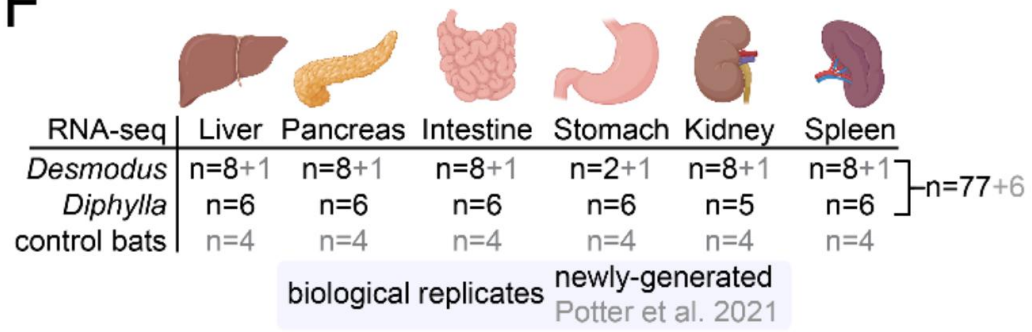
TOGA **aBSREL** **RELAX** **77 RNA-seq + DESeq2**

Transcriptomic coverage

Desmodus (8) + Diphylla (6)
Matched organ data for two species

tissue-matched transcriptomes:
Desmodus (1)
non-vampire phyllostomid species (4)

F

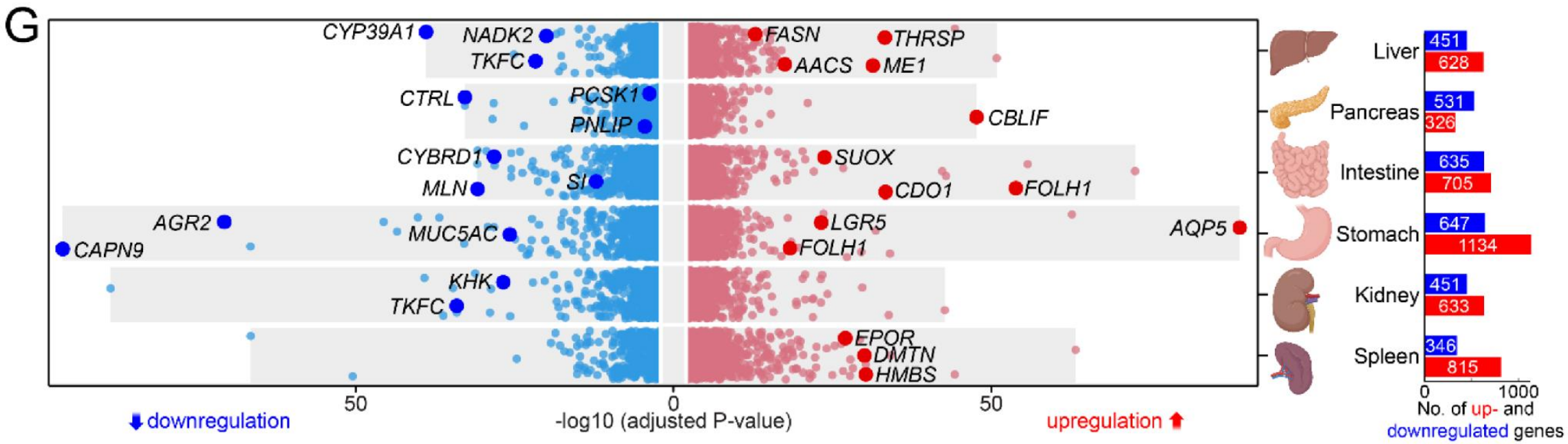


RNA-seq	Liver	Pancreas	Intestine	Stomach	Kidney	Spleen	
Desmodus	n=8+1	n=8+1	n=8+1	n=2+1	n=8+1	n=8+1	n=77+6
Diphylla	n=6	n=6	n=6	n=6	n=5	n=6	
control bats	n=4	n=4	n=4	n=4	n=4	n=4	

biological replicates newly-generated Potter et al. 2021

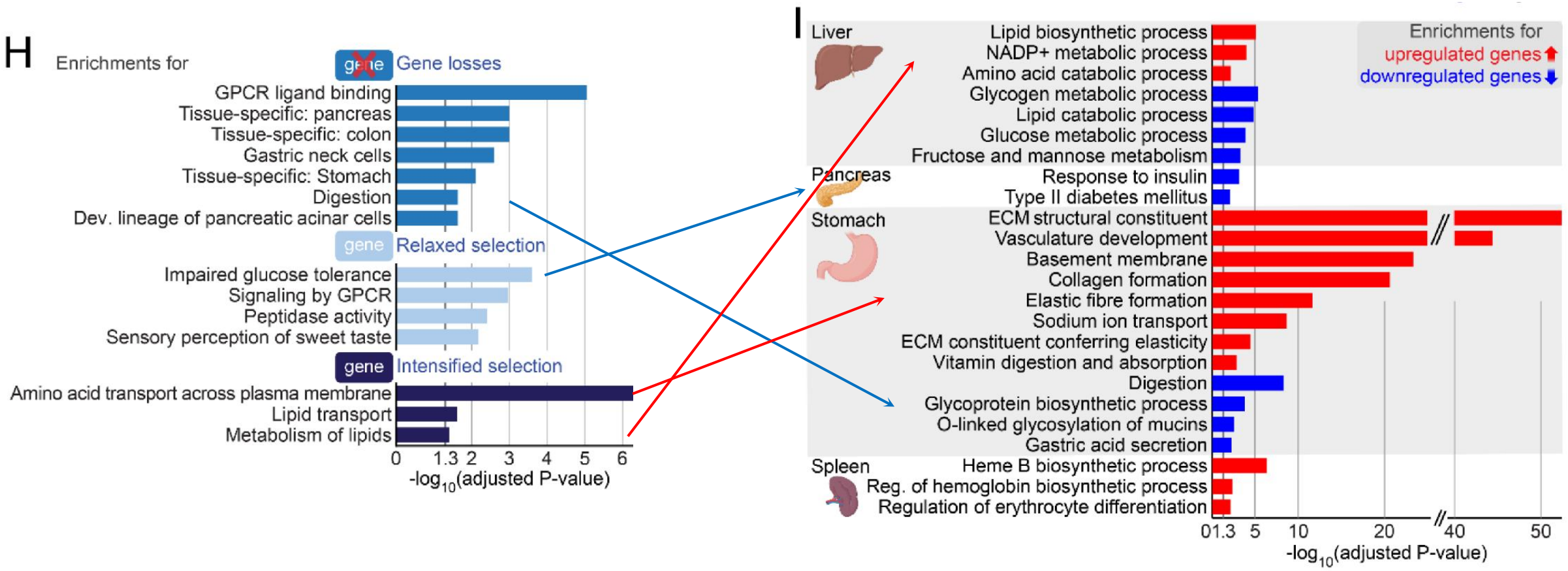
Expression shifts are organ specific

Significantly up- or downregulated orthologous genes in one or both vampire bats



Many of these genes showed coherent expression shifts across both species

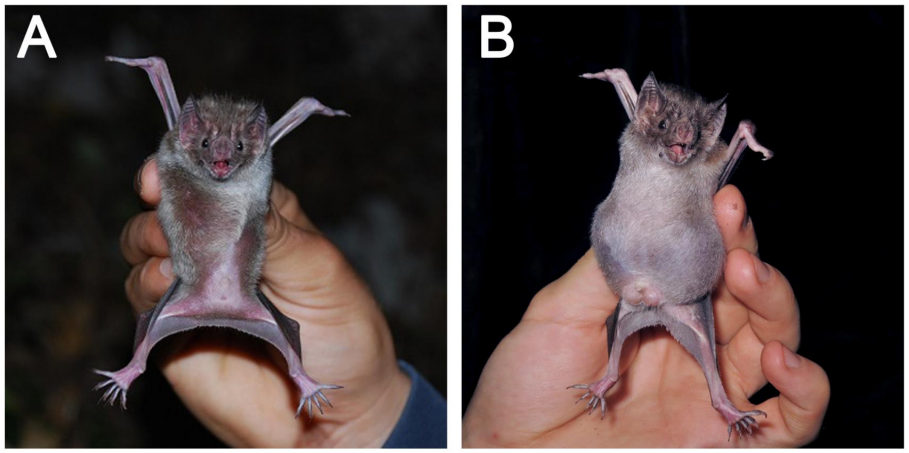
Integrated signals highlight stomach, metabolic and erythropoietic programs

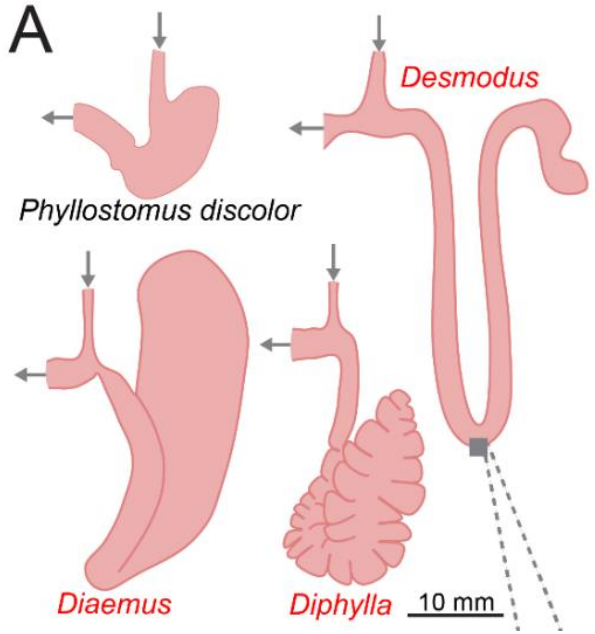


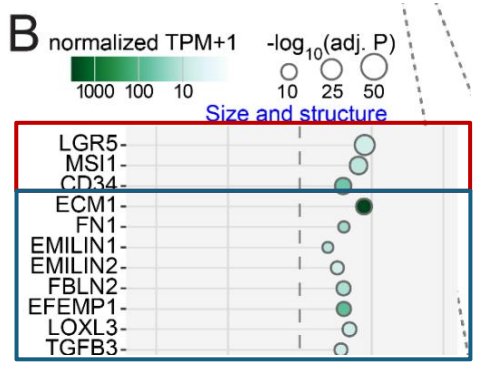
Matched functional enrichments highlight many metabolic and physiological processes

Structural and size adaptations in the stomach

Markedly enlarged stomach

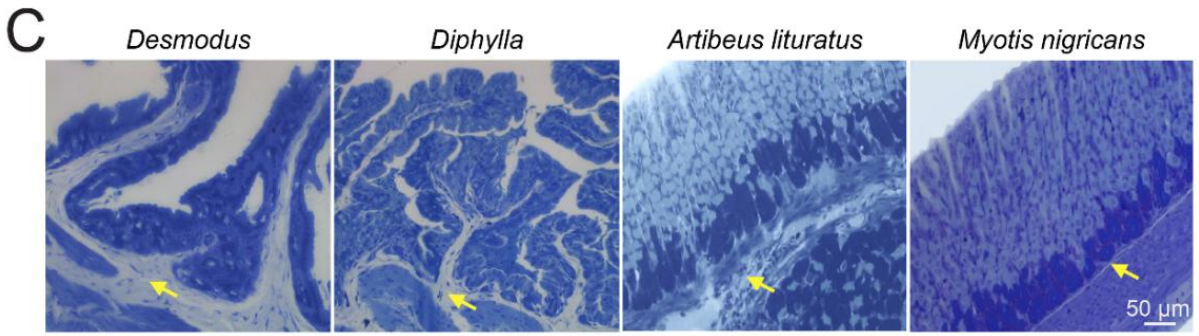


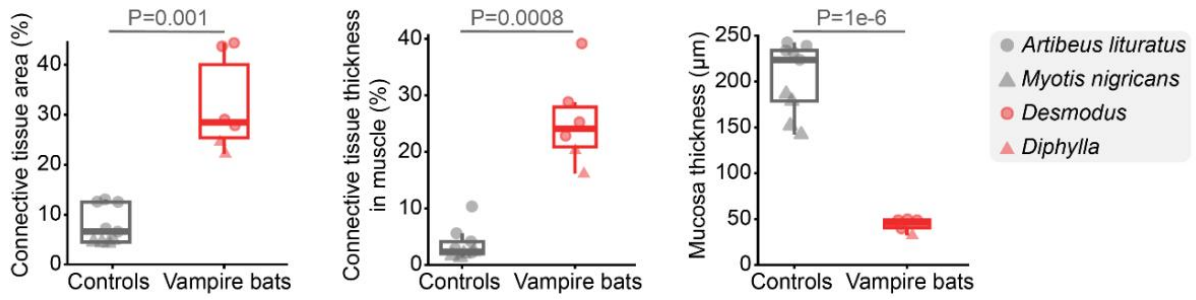




Structure ↑

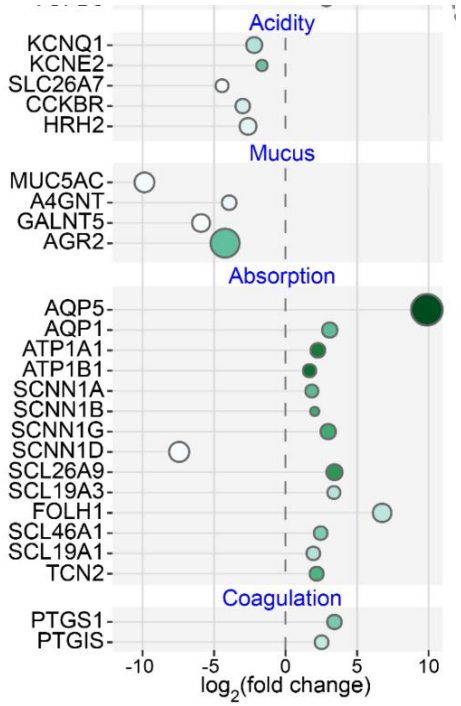
Stem-cell markers
&
extracellular matrix genes





Stomach expansion is associated with more connective tissue

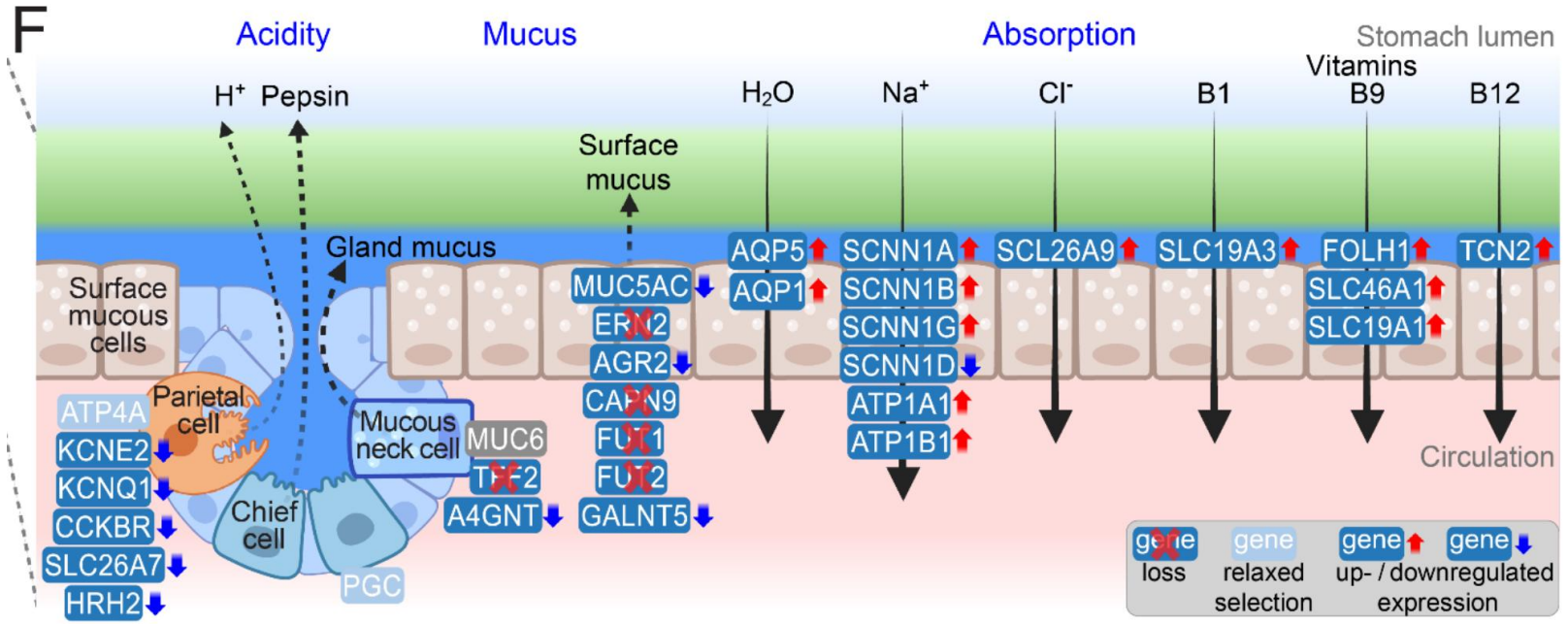
Stomach expression shifts span secretion and absorption



1 near-neutral stomach

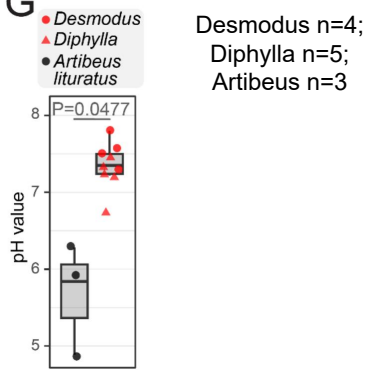
2 reduced mucus production

3 Functional shift of the stomach from digestion to absorption

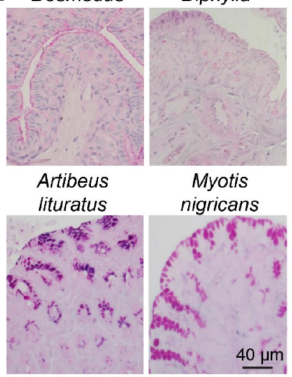


Acid & mucus ↓

Potentially reduced demand for secretion



Desmodus n=4;
Diphylla n=5;
Artibeus n=3

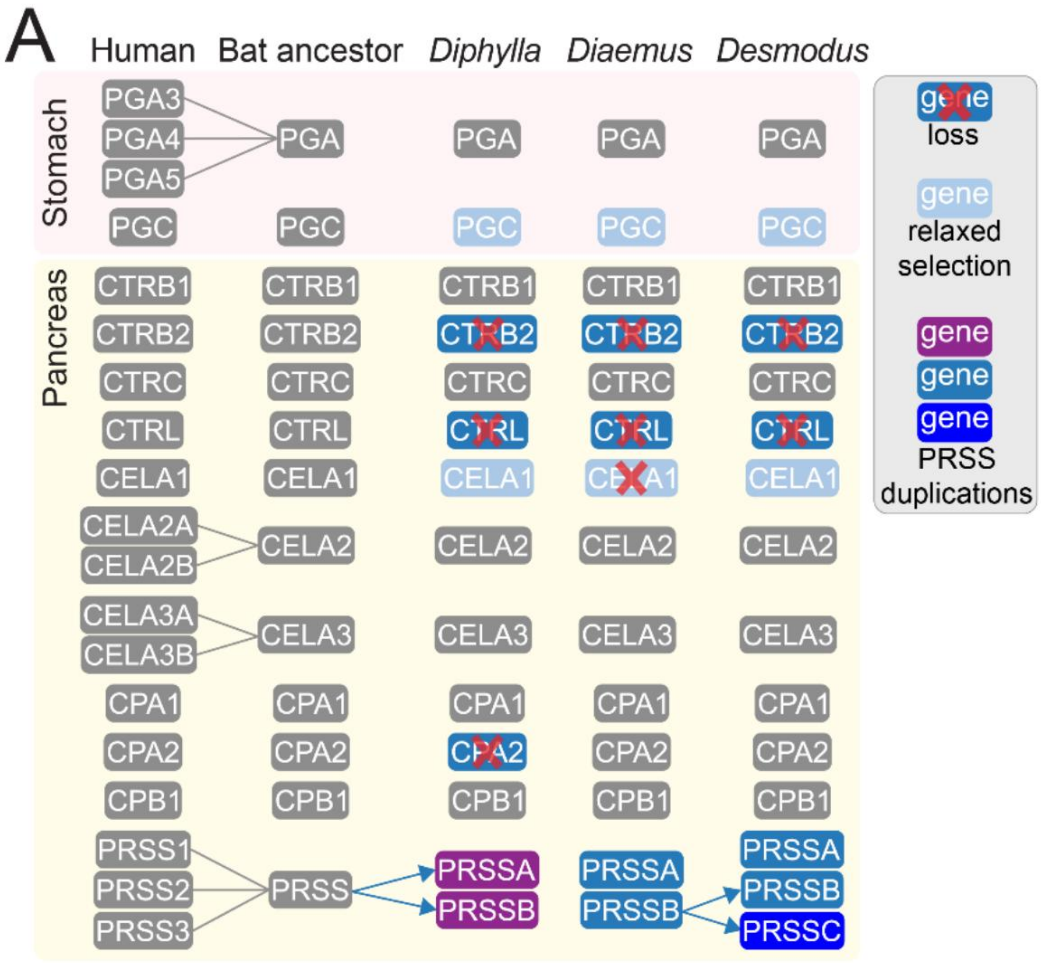


pH: 7.36 ± 0.29 vs 5.67 ± 0.71

Absorption ↑

AQP5, ENaC and vitamin transport programs

A protein-rich diet does not require every digestive protease



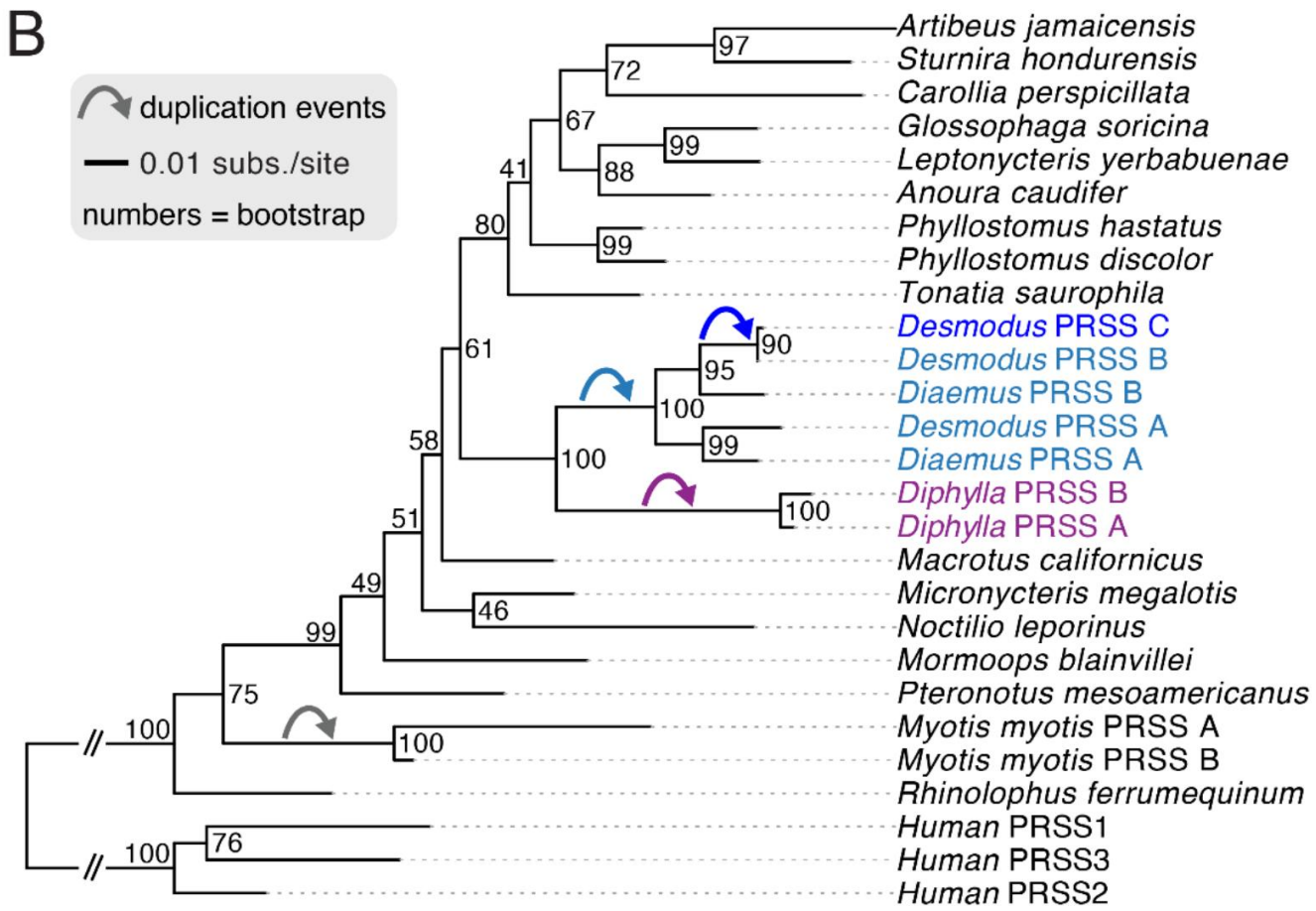
Reduced protease diversity

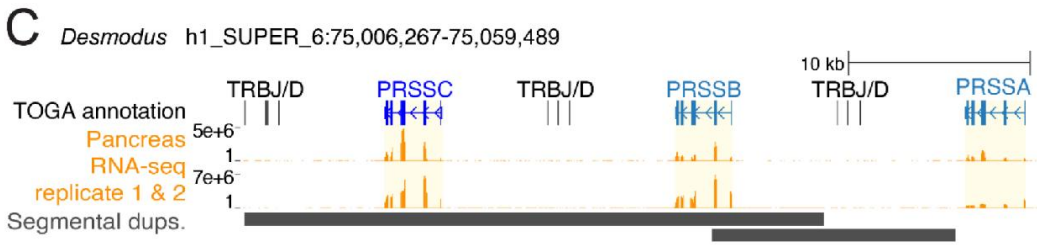
PGC relaxed; CTRB2 / CTRL lost

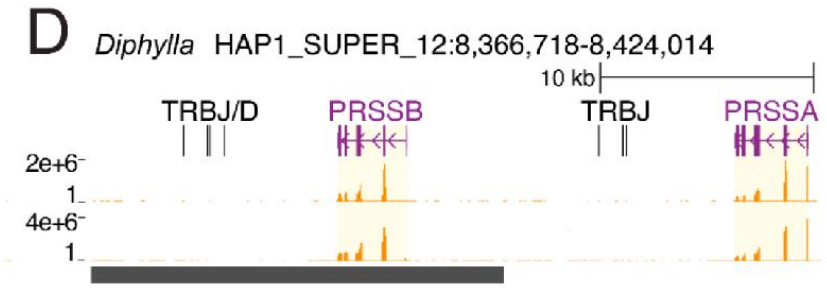
More copies of a key enzyme

PRSS trypsin expansion

Trypsin expands independently and is expressed in the pancreas

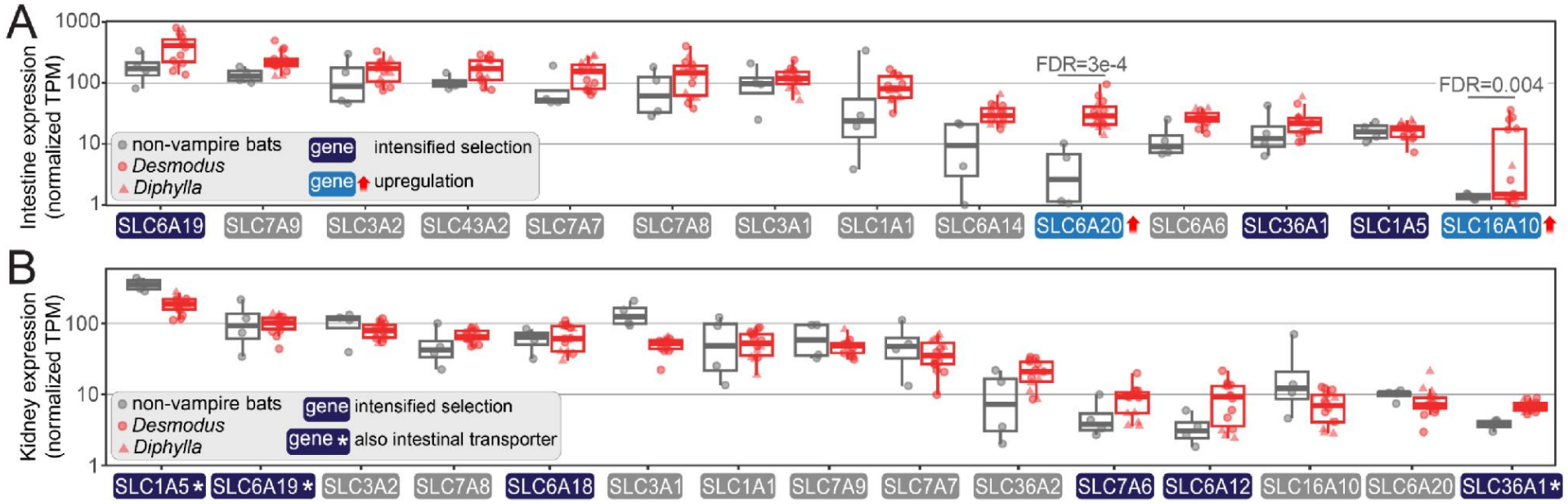






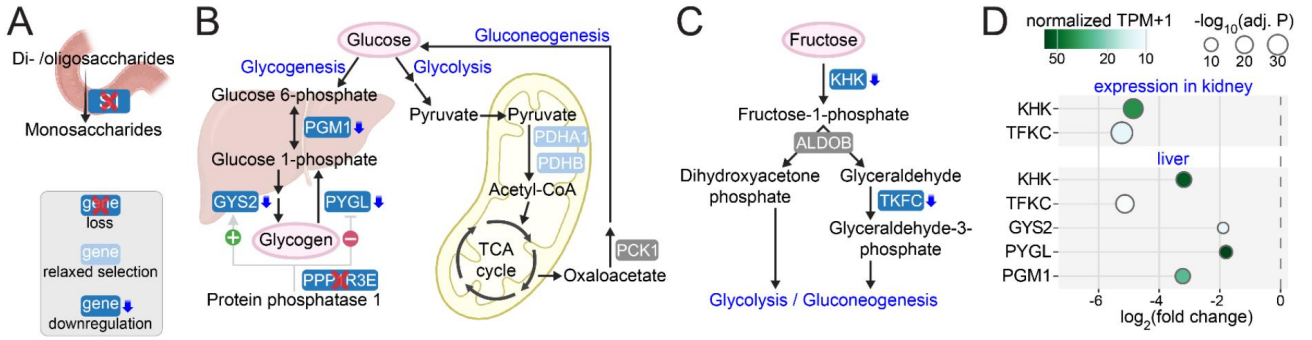
Amino acid uptake and retention match a biased substrate supply

enhanced absorption in the small intestine & kidney reabsoption

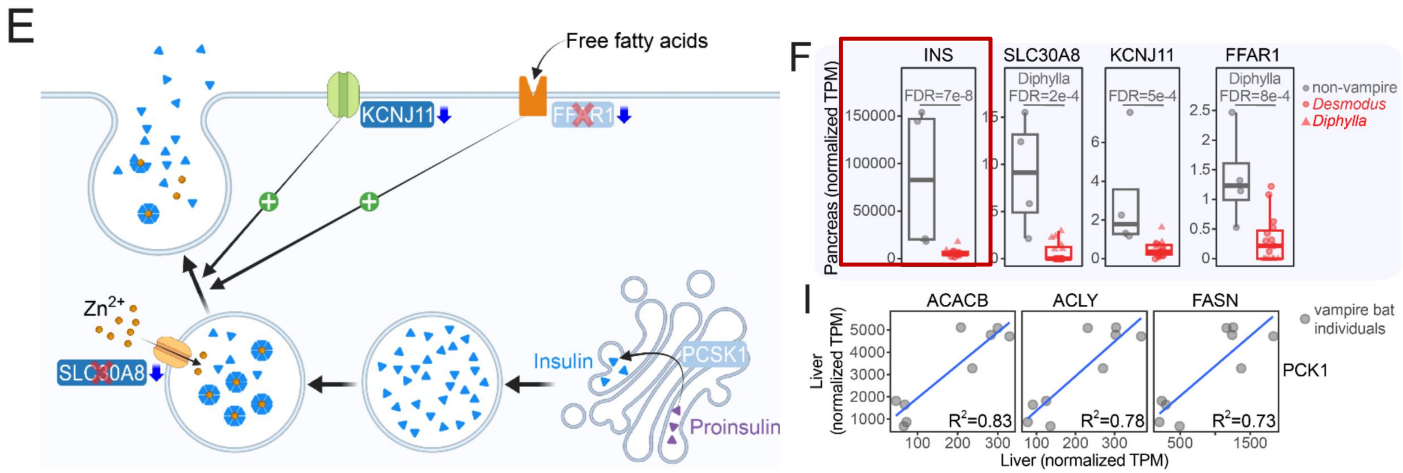


A sugar-poor diet accompanies reduced carbohydrate programs

1 A sugar-poor diet accompanies reduced carbohydrate programs

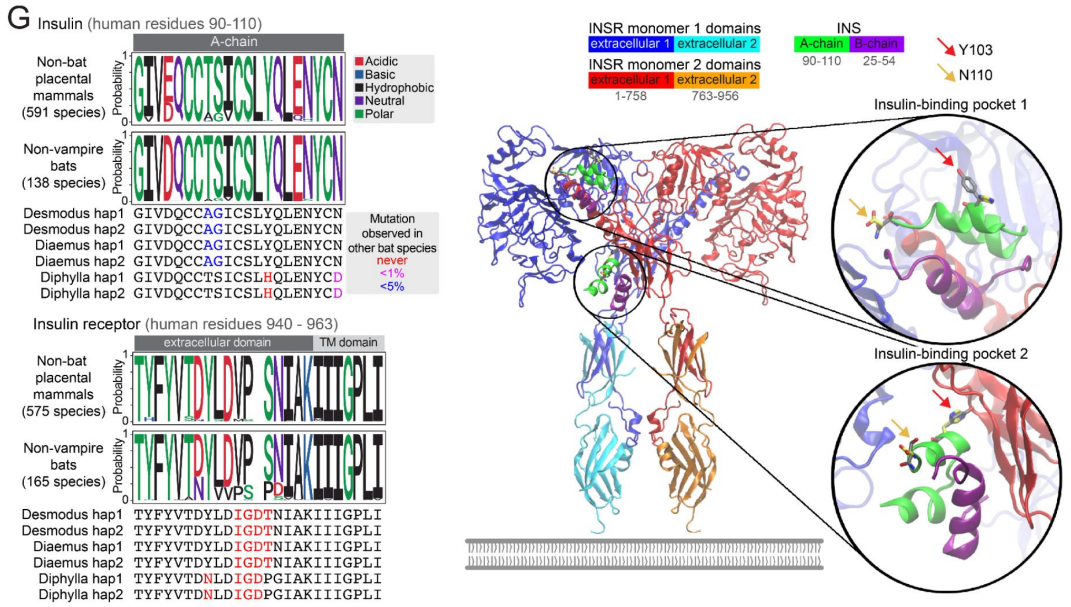


2 Reduced insulin programs accompany correlated metabolic expression

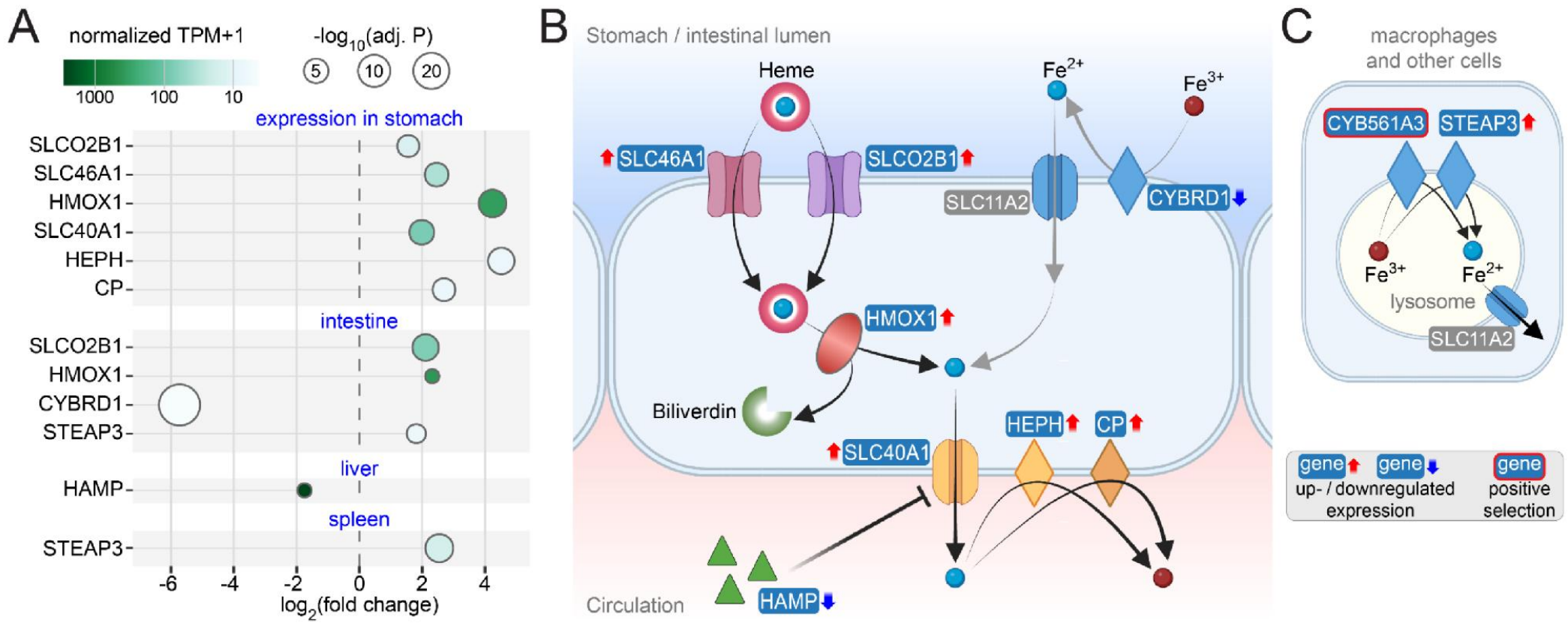


INS expression decreases;
PCK1 is positively correlated with lipid synthesis genes

3 INS and INSR changes suggest testable structural hypotheses



Iron-handling changes favor heme uptake and intracellular recycling



An integrated model of coordinated organ responses

Stomach

Expansion · Neutral pH · Absorptive programs

Pancreas / intestine

Trypsin specialization · Amino acid uptake

Protein / fluid & salts / heme in a blood meal

Liver / kidney

Substrate conversion · Nitrogen & acid–base balance

Spleen / bone marrow

Iron recycling · Species-specific erythropoiesis

Summary & Take-home messages

- **High-quality genomes** of six phyllostomid bats, including new haplotype-resolved assemblies of all three vampire bat species;

- **Changes in gene sequence and expression**, inferred from transcriptomics data of six major organs

- A comprehensive view of the **8 points of molecular adaptations underlying sanguivory** in vampire bats.
    - enlarged, non-acidic, absorptive stomach;
    - altered gastrointestinal motility;
    - trypsin-dependent protein digestion;
    - upregulated amino acid catabolism;
    - increased *de novo* synthesis of fatty acids;
    - defective sugar metabolism and natural insulin deficiency;
    - enhanced heme iron absorption;
    - adult splenic erythropoiesis

Pathways converge; mechanisms remain testable

Thanks



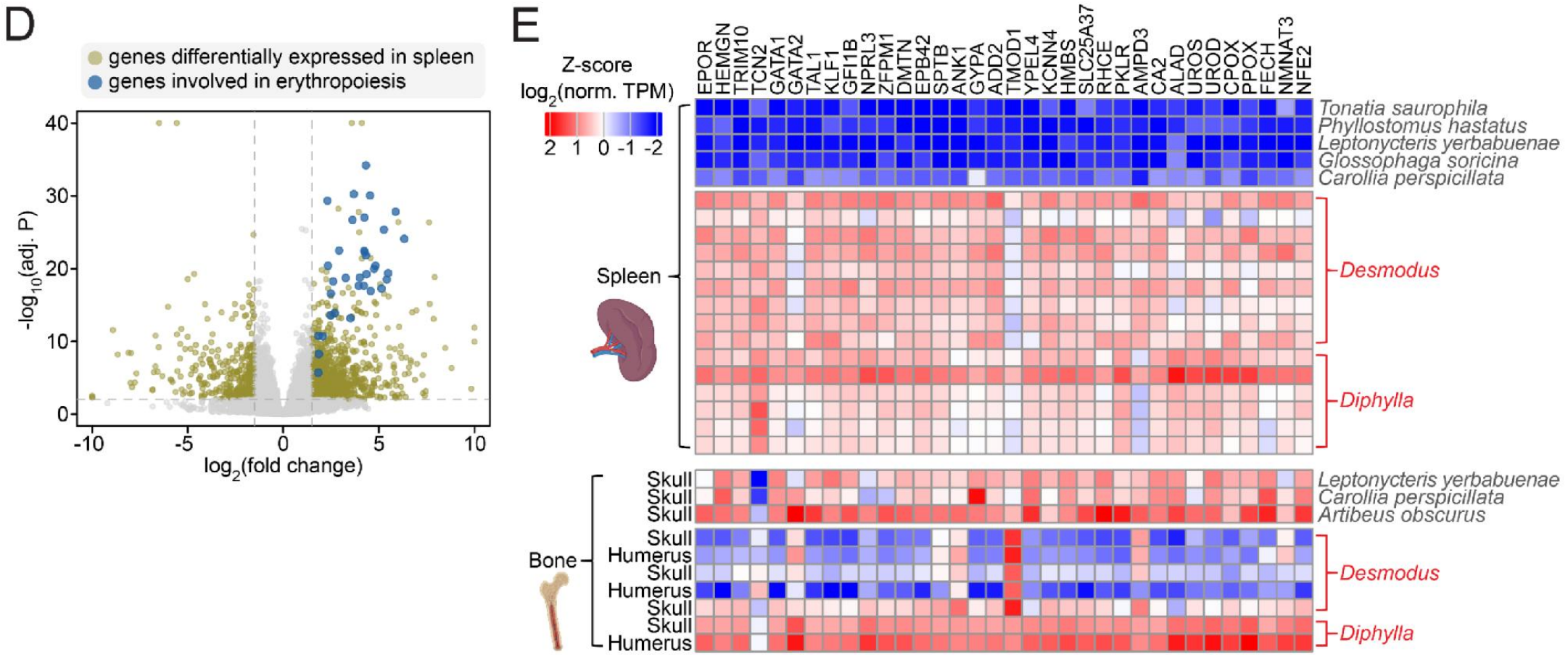
浙江大学
ZHEJIANG UNIVERSITY





浙江大学
生命演化研究中心

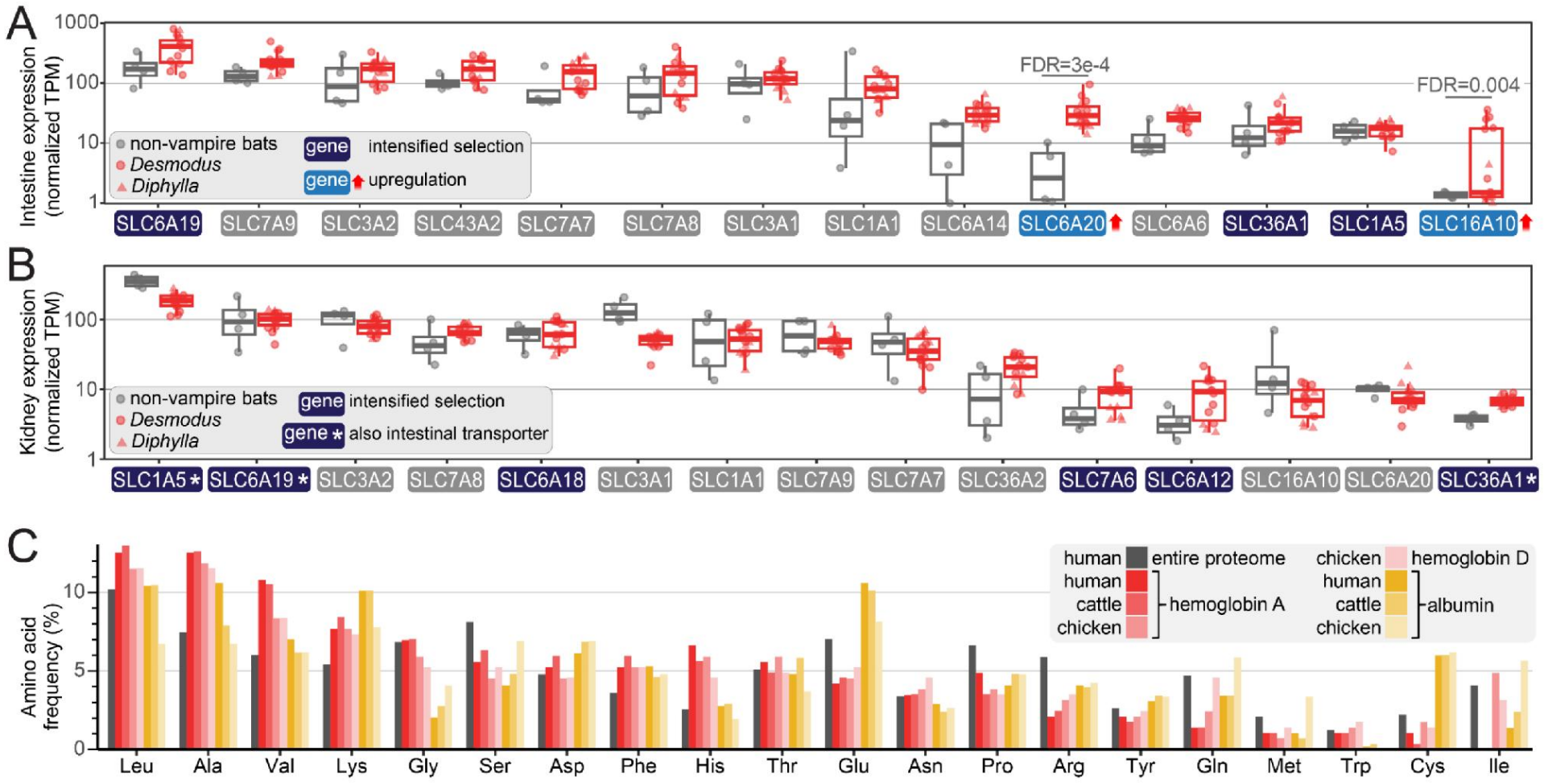
Adult splenic erythropoiesis: bone contributions differ between species



Desmodus：骨中信号低　　Diphylla：脾与骨均有信号

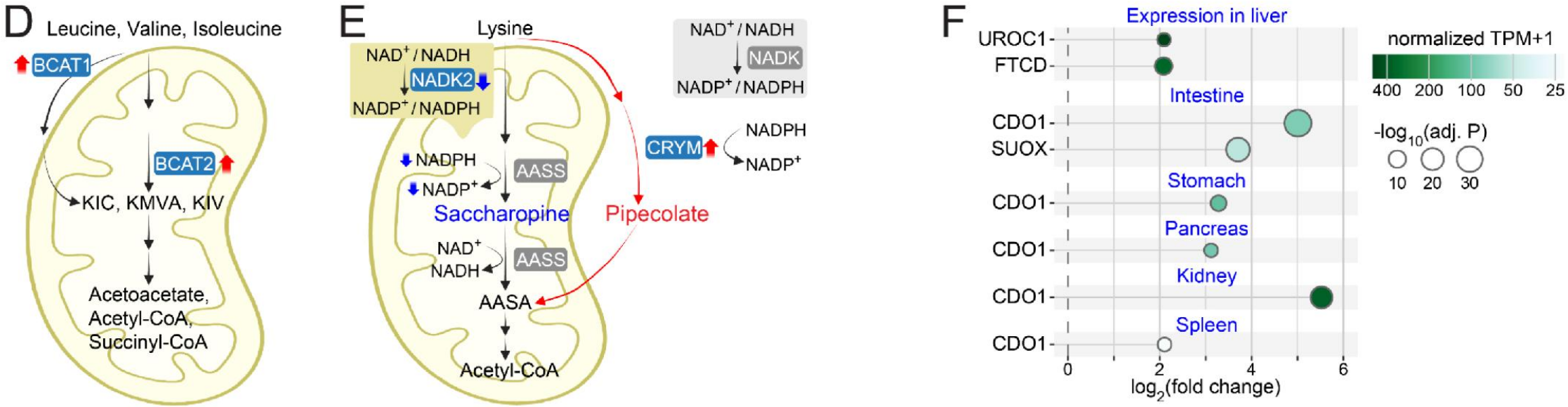
Amino acid uptake and retention match a biased substrate supply

enhanced absorption in the small intestine & kidney reabsoption



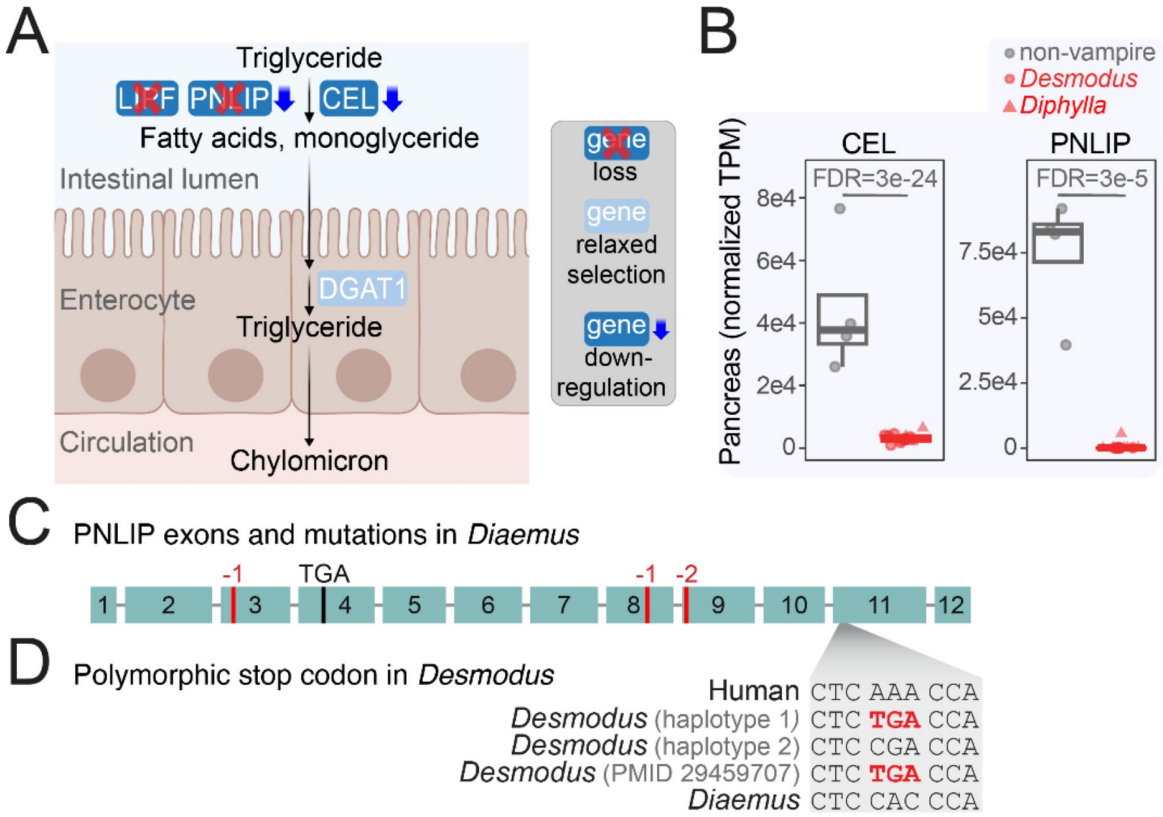
肠道摄取与肾脏保留共同适应偏斜的氨基酸组成

Amino acid catabolism is redistributed across organs and pathways



Different paralogs can serve similar metabolic demands

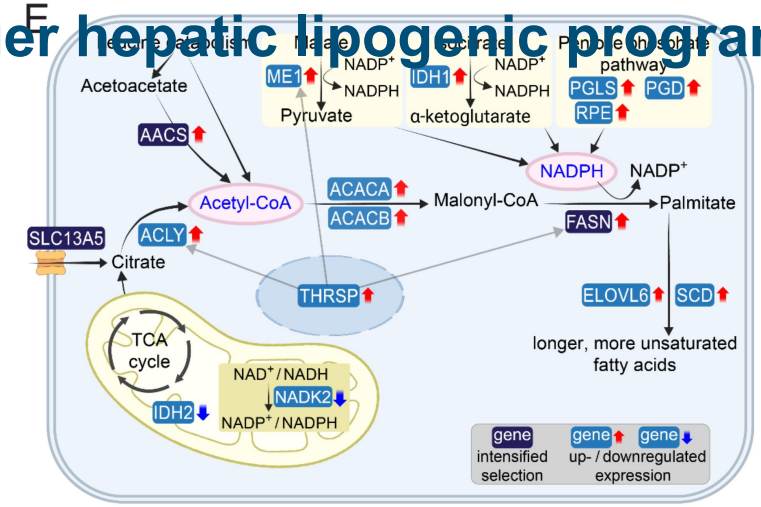
Dietary fat digestion declines through different lineage-specific routes

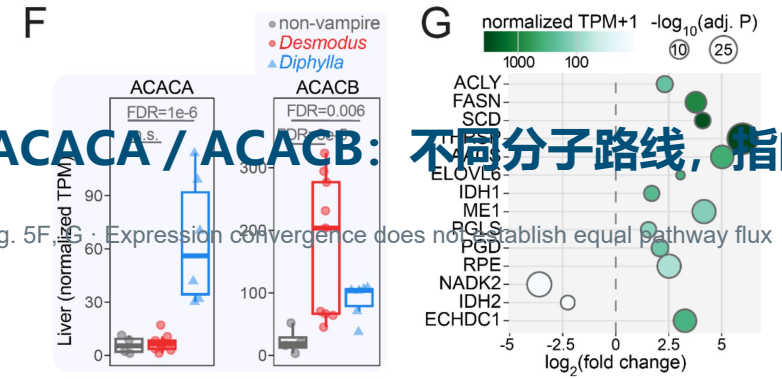


脂肪消化减弱，但固定丢失、表达缺失与多态失活需区分

Fig. 5A, B, C, D · Loss, absent expression and polymorphic inactivation are distinct observations

Reduced fat digestion accompanies a stronger hepatic lipogenic program





ACACA / ACACB：不同分子路线，指向相近生理需求

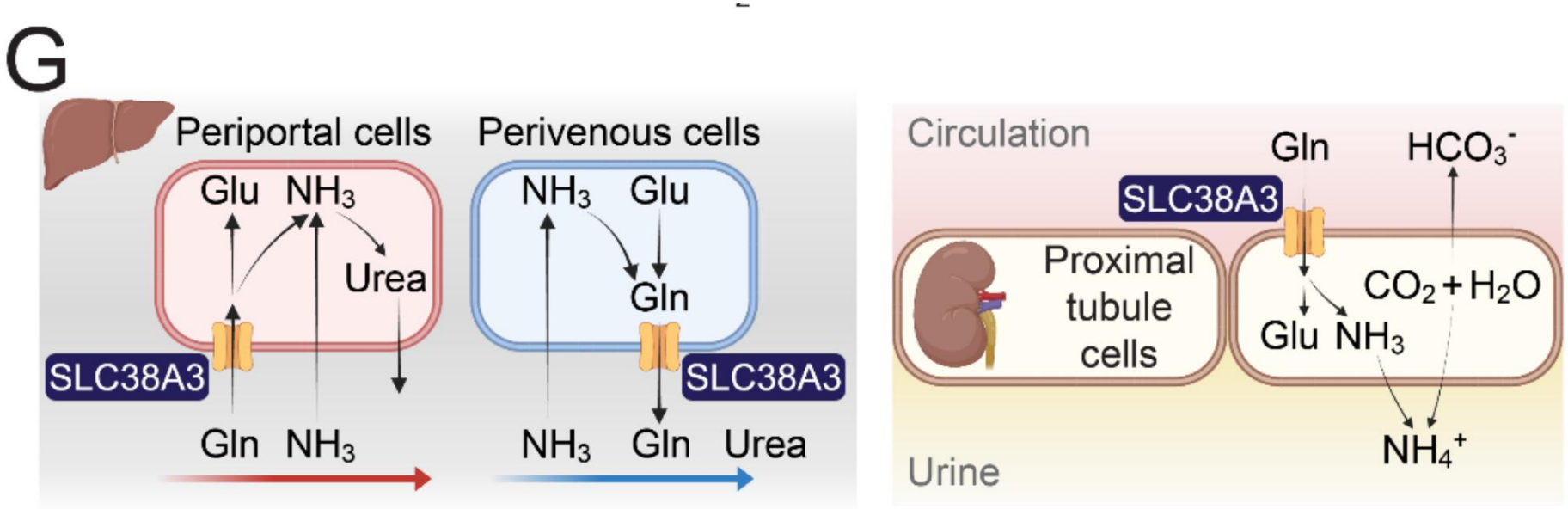
Fig. 5F, G · Expression convergence does not establish equal pathway flux

脂质合成程序增强；实际合成通量仍待测定

Fig. 5E · Acetyl-CoA + NADPH → fatty acid synthesis · Model supported by expression/selection

Different genes contribute to a similar lipogenic program

Liver and kidney coordinate nitrogen and acid–base handling



高蛋白摄入 → 氨处理 + 尿素生成 + 肾脏铵排泄

Pathway model supported by sequence/expression changes; flux not measured