

Fig S1

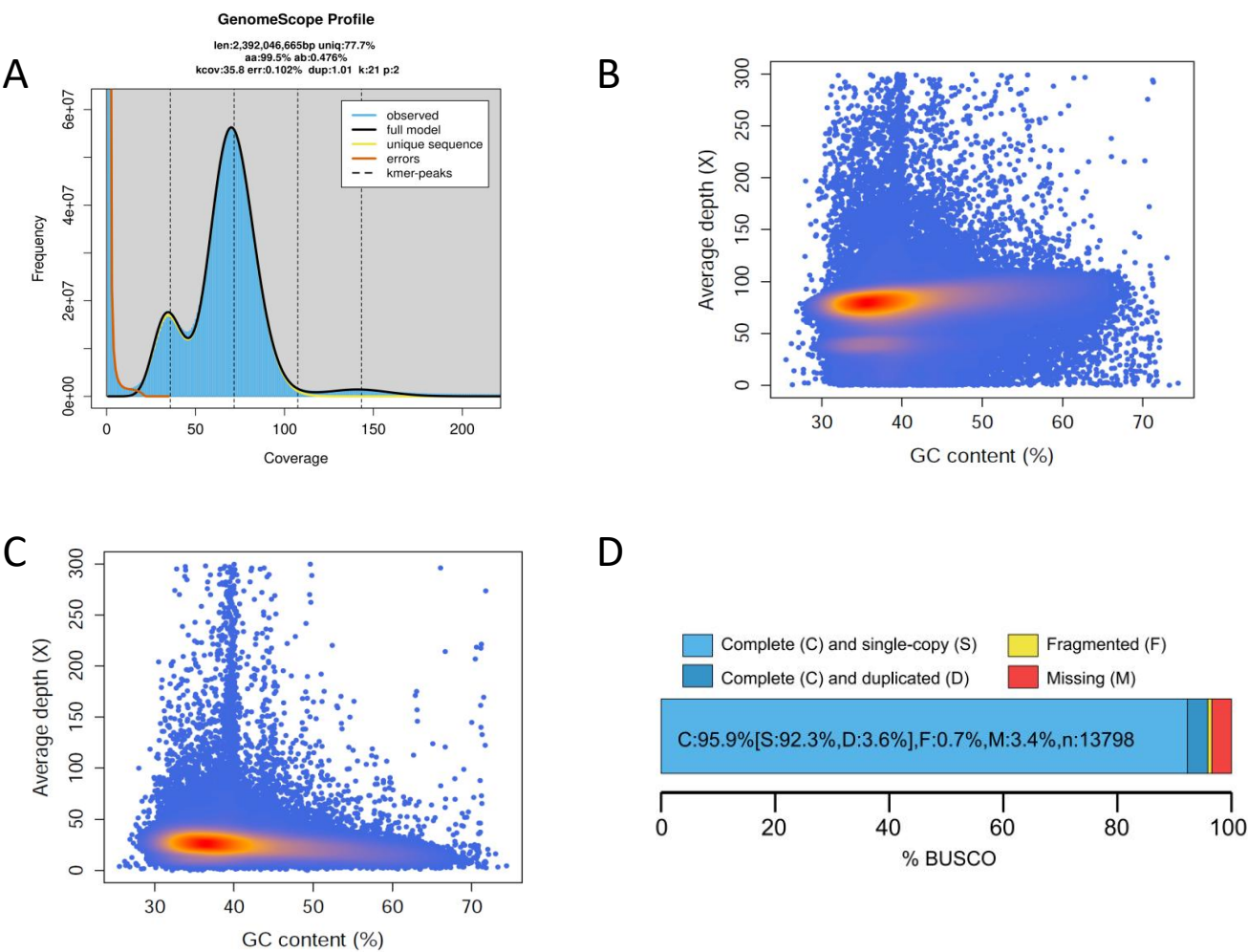


Figure S1. The genomic feature assessment and integrity analysis. (A) The estimation of genome size by K-mer. (B-C) The assessment of sequencing depth versus GC content distribution. Depth of coverage of three-generation (B) and two-generation (C) sequencing data at different GCs. (D) The results of BUSCO assessment of genomic integrity.

Fig S2

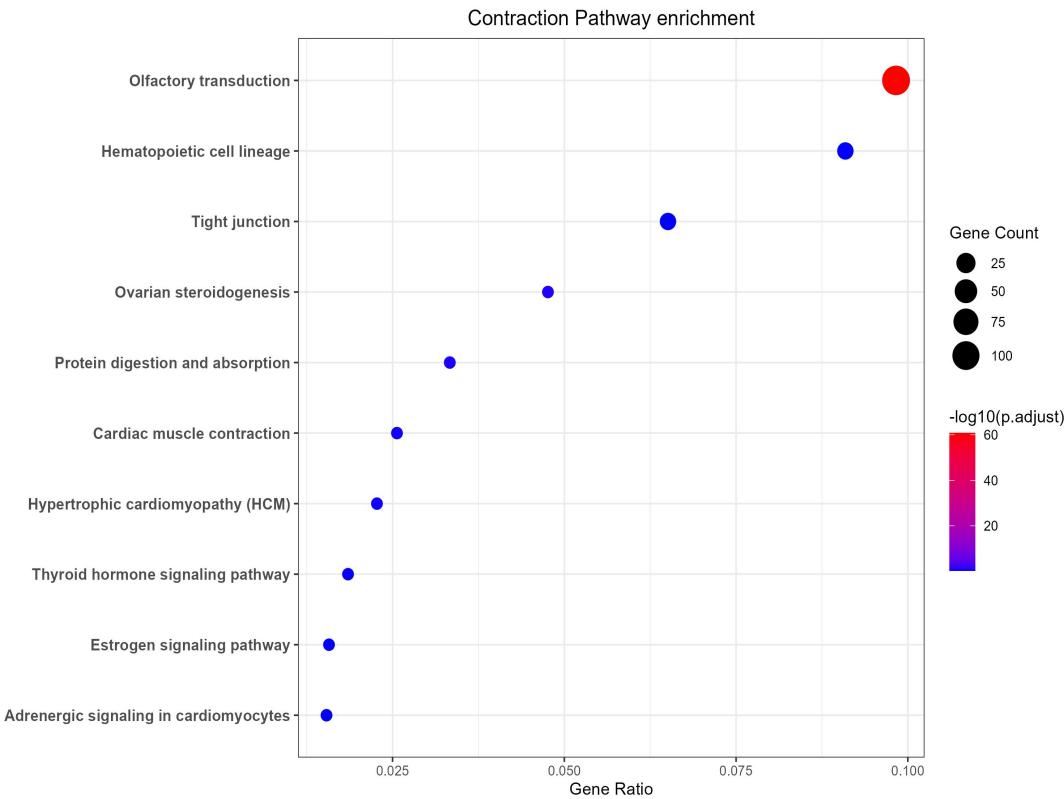


Figure S2. The enrichment analysis of contracted gene families.

Fig S3

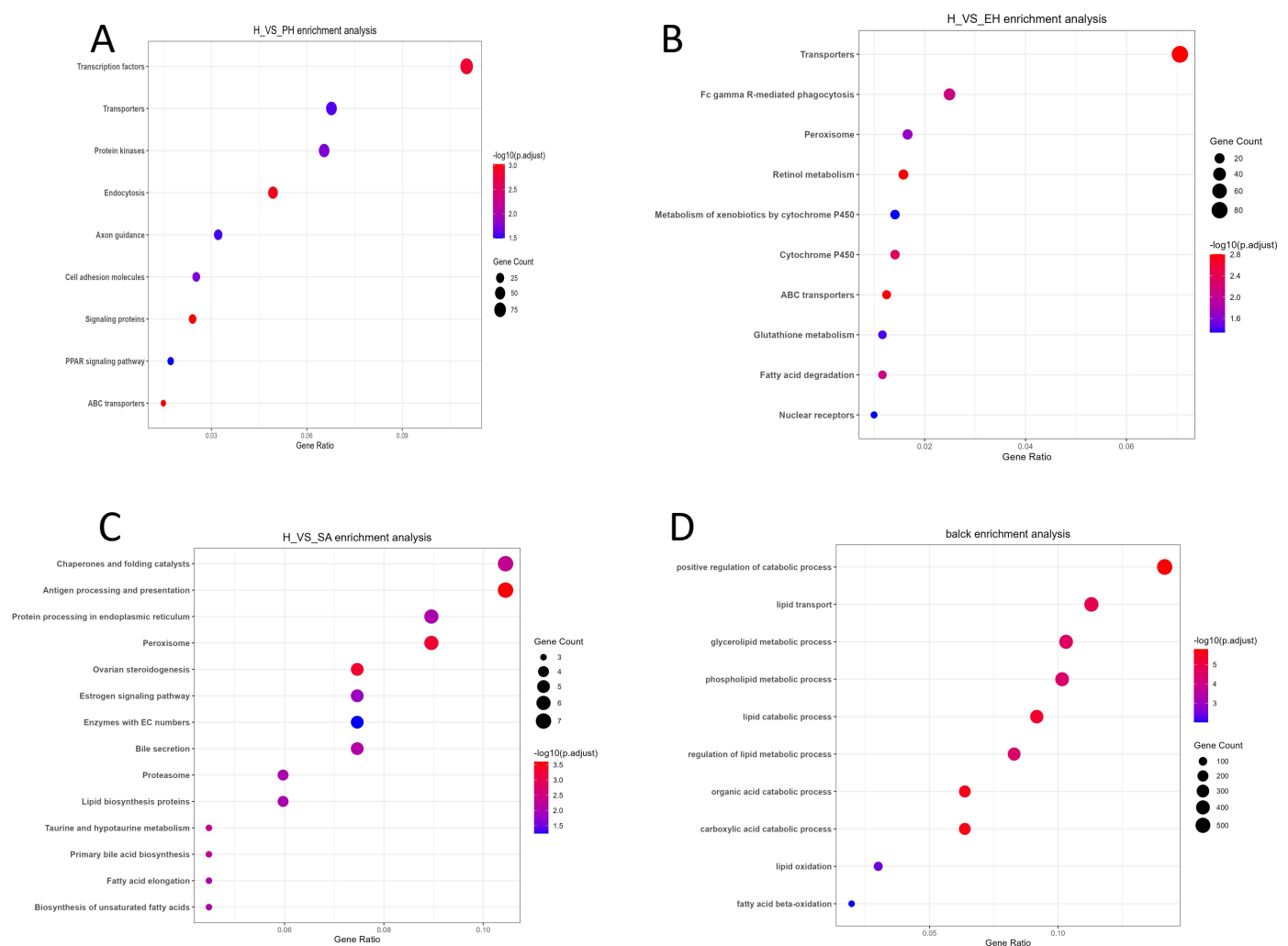


Figure S3. The enrichment analysis of each gene set. (A-C) The differential gene enrichment analysis of H vs PH (A), H vs EH (B), H vs SA (C). (D) The enrichment analysis of MEblack gene set.

Fig S4

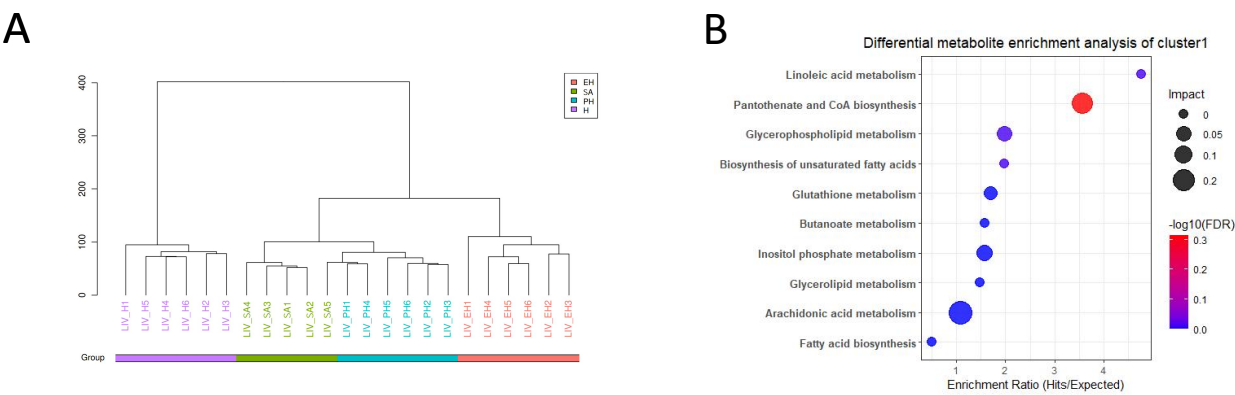


Figure S4. The overall sample cluster analysis and differential metabolite enrichment analysis. (A) The overall sample level clustering tree. The cluster trees that are closer and shorter represent higher similarity between samples, and sample groupings are distinguished by different colors. (B) The enrichment analysis of cluster1 differential metabolites.

Fig S5

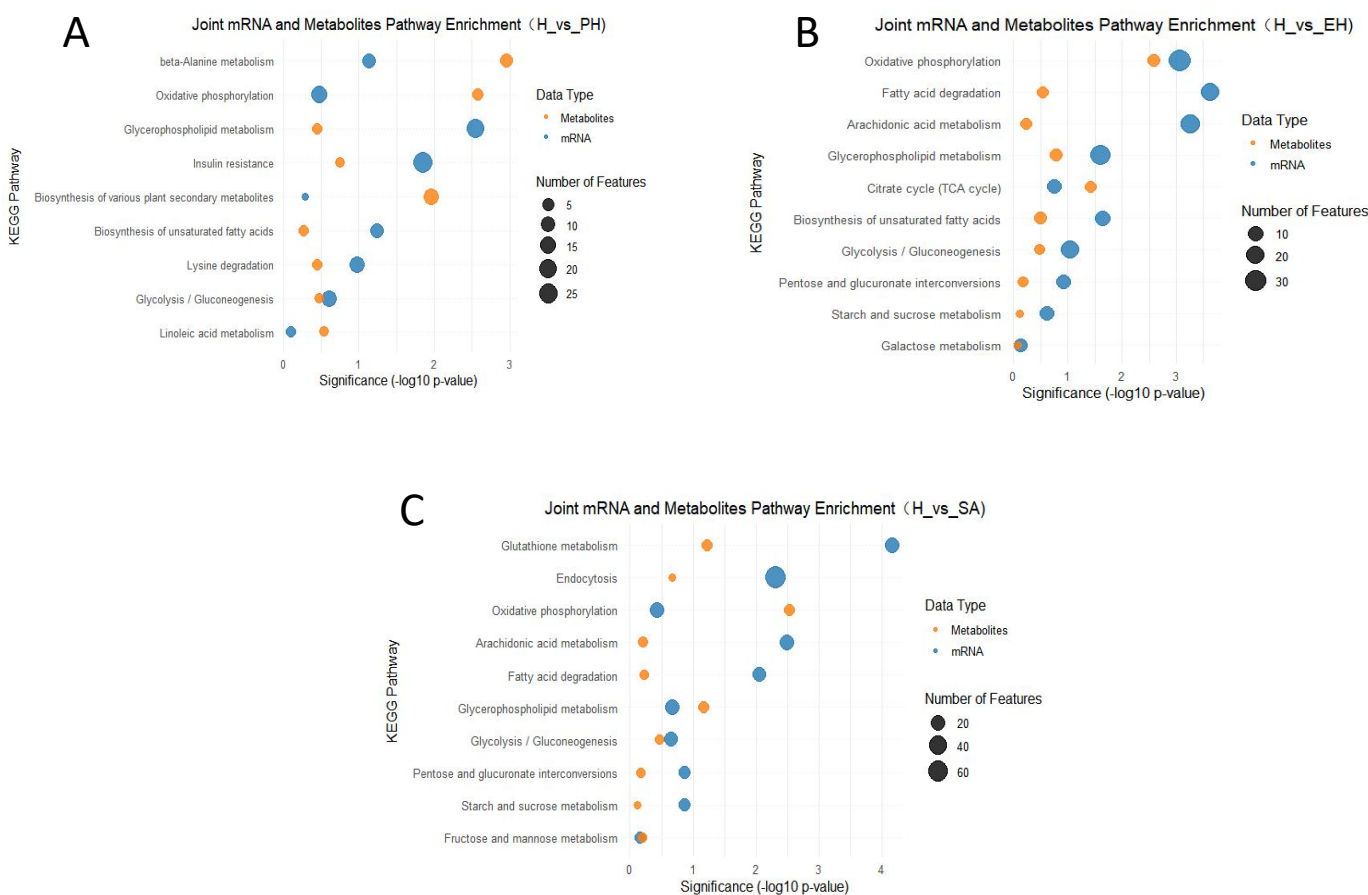


Figure S5. The co-enrichment analysis of differentially expressed genes and metabolites. (A-C) The differential gene and differential metabolite co-enrichment analyses for H vs PH (B), H vs EH (B), and H vs SA (C).

Table S1 The oligonucleotide primers used for RT-qPCR		
Gene	Primer sequence	Product size (bp)
<i>Ppara</i>	F: GGTAACCCTAGGCCAGATAGA	155
	R: AGGGCCTTTAATTCAACTGCG	
<i>Cpt1a</i>	F: GGAGGAGATCAAGCCGATCC	80
	R: CAGTGTTGAACAAGCGCTCC	
<i>Hadh</i>	F: AGTGCCCCTGATGAAACTCG	130
	R: AAACCCAGGAGTGTCTTGC	
<i>Fads2</i>	F: GTCGACCGCAAGGTCTACAA	109
	R: AGGCATTGAAGGCATCCGTA	
<i>Fads1</i>	F: CGGAAAAAGTGGGTGGACCT	255
	R: CCAGTCGTTGAAGGCAGACT	
<i>Trpv1</i>	F: AATCTCCAGCCAAGCCTCAC	249
	R: GATCGTAGAGCTTGAGGGGC	
<i>Actb</i>	F: CCTCTATGCCAACACAGTGC	206
	R: CCTGCTTGCTGATCCACATC	

Table S2 The statistics of sequencing data							
Platform	Tissue	Reads	Total bases(bp)	Average length (bp)	N50 length (bp)	Mean depth of coverage	GC(%)
HiFi	Liver	4,159,564	83,422,205,994	20,055	21,423	~31×	39.52
ONT	Liver	4,946,906	127,848,522,700	25,844	63,581	~48×	40.30
Hi-C	Liver	1,821,081,428	273,160,000,000	150	-	~102×	42.12
RNA-seq	Liver	47,206,470	7,073,335,190	150	-	-	49.62
	Liver	44,852,350	6,719,670,742	150	-	-	49.97
	Liver	35,782,632	5,362,031,295	150	-	-	50.47
	Liver	40,338,160	6,044,344,000	150	-	-	50.16
	Liver	45,775,396	6,855,017,098	150	-	-	48.36
	Liver	42,700,964	6,398,742,900	150	-	-	48.75
	Liver	43,980,064	6,590,334,907	150	-	-	49.43
	Liver	49,177,974	7,368,814,538	150	-	-	49.51
	Liver	29,982,696	4,492,021,799	150	-	-	46.82
	Liver	40,735,708	6,102,101,830	150	-	-	49.3
Illumina	Liver	1,887,058,694	283,060,000,000	150	-	~106×	40.39

Table S3 The chromosome information statistics		
Chromosome	Length (bp)	Gaps
Chr1	272,400,195	6
Chr2	240,072,120	0
Chr3	214,075,258	8
Chr4	211,431,769	10
Chr5	206,823,456	0
Chr6	178,685,825	7
Chr7	160,270,197	7
Chr8	152,472,981	13
Chr9	146,472,771	0
Chr10	142,286,051	0
Chr11	129,319,401	0
Chr12	103,611,480	0
Chr13	80,736,199	9
Chr14	77,345,349	0
Chr15	66,286,584	0
Chr16	56,397,410	7
Chr17	52,709,880	0
ChrX	135,896,491	10
ChrY	4,878,000	3
Scaffold1	30,270,314	-
Scaffold2	12,957,865	-
Scaffold3	6,513,986	-
Scaffold4	5,963,000	-
total	-	80

Table S4 The preliminary prediction of centromere position and length			
Chromosome	Start (bp)	End (bp)	Size (bp)
Chr01	98,931,974	99,086,481	154,508
Chr02	137,424,854	138,032,793	607,940
Chr03	97,066,449	97,247,010	180,562
Chr04	139,799,888	139,915,854	115,967
Chr05	199,216,242	206,836,402	7,620,161
Chr06	176,691,166	177,037,173	346,008
Chr07	160,070,646	160,265,694	195,049
Chr08	1	4,056,154	4,056,154
Chr09	80,208,169	80,622,321	414,153
Chr10	140,206,407	140,368,129	161,723
Chr11	128,824,016	129,137,285	313,270
Chr12	79,877,127	80,767,029	889,903
Chr13	78,172,173	79,992,608	1,820,436
Chr14	6,127,853	6,262,809	134,957
Chr15	858,563	1,115,496	256,934
Chr16	37,182,718	37,287,518	104,801
Chr17	27,068,076	27,209,081	141,006
ChrX	50,598,767	50,706,432	107,666
ChrY	-	-	-

Table S5 The statistics on the coverage of the genome by sequencing data							
Data set	Reads mapped	Properly paired	Bases mapped	$\geq 1\times$	$\geq 5\times$	$\geq 10\times$	$\geq 20\times$
HiFi	99.97%	-	99.97%	99.99%	99.83%	97.88%	77.17%
ONT	96.31%	-	99.85%	99.99%	99.99%	99.81%	95.50%
Illumina	99.69%	96.67%	99.69%	99.94%	99.84%	99.69%	99.19%
HiC	99.78%	47.43%	99.78%	95.89%	81.72%	75.48%	69.50%
RNA-seq	97.47%	-	98.94%	29.10%	9.35%	4.81%	2.60%

Table S6 The statistics of repetitive elements					
Order	Superfamily	Number	Length(bp)	Percent(%)	Mean length(bp)
LTR		572536	192349394	7.31	336
	ERVL	82613	32482494	1.23	393
	ERVL-MaLRs	296716	88150476	3.35	297
	ERV_classI	106563	28385476	1.08	266
	ERV_classII	74747	40380144	1.53	540
SINEs:		1349048	173000512	6.57	128
	Alu/B1	80399	6241023	0.24	78
	B2-B4	83630	4992840	0.19	60
	IDs	553791	68555069	2.6	124
	MIRs	153808	21174915	0.8	138
LINEs:		607759	430180702	16.34	708
	LINE1	515349	405954238	15.42	788
	LINE2	76989	20813640	0.79	270
	L3/CR1	9777	2067261	0.08	211
DNA elements:		224255	46614250	1.77	208
	hAT-Charlie	124459	23904553	0.91	192
	TcMar-Tigger	46798	11780723	0.45	252
Unclassified:		11425	1225638	0.05	107
Small RNA:		44827	3272854	0.12	73
Satellites:		14196	1074454	0.04	76
Simple repeats:		841333	38257805	1.47	46
Low complexity:		118299	7254557	0.28	61
Total		3783678	893376950	33.94	236

Table S7 The integration of annotation statistics					
Feature	Number	Min	Max	Mean	Median
Gene	21585	123	2085031	34958	9021
Transcript	28773	9	22191	1751	1236
CDS	28773	9	22191	1751	1236
Exon	175904	1	11922	180	126

Table S8 The functional gene annotation statistics			
Type		Gene number	Percentage
Total		21,585	100.00%
Nr		19,420	89.97%
Swissprot		14207	65.82%
KEGG		14841	68.76%
KOG		18996	88.01%
Trembl		19420	89.97%
Interpro	All	19854	91.98%
	G	13746	63.68%
Annotated		20062	92.94%
Unannotated		1523	7.06%

Table S9 The summary of comparative statistics for assembled versions of the <i>Spermophilus dauricus</i> genome		
Item	This study	AXRT01
Size of assembly (Gb)	2.69	3.1
Number of scaffolds	23	360,804
N50 (Mb)	160.3	1.8
L50	7	493
GC content	39.92%	40%
Genome complete BUSCOs	95.90%	-
Quality value	51.364	-
Assembly level	Chromosome	Scaffold

Table S10 The species information			
	Species	Abbr	Family
1	<i>Erinaceus europaeus</i>	Eeuropaeus	Erinaceidae
2	<i>Ursus thibetanus thibetanus</i>	Uthibetanus	Ursidae
3	<i>Ursus maritimus</i>	Umaritimus	Ursidae
4	<i>Tremarctos ornatus</i>	Tornatus	Ursidae
5	<i>Ailuropoda melanoleuca</i>	Amelanoleuca	Ursidae
6	<i>Rhinolophus ferrumequinum</i>	Rferrumequinum	Rhinolophidae
7	<i>Myotis lucifugus</i>	Mlucifugus	Vespertilionidae
8	<i>Meriones unguiculatus</i>	Munguiculatus	Muridae
9	<i>Sciurus vulgaris</i>	Svulgaris	Sciuridae
10	<i>Sciurus carolinensis</i>	Scarolinensis	Sciuridae
11	<i>Xerus rutilus</i>	Xrutilus	Sciuridae
12	<i>Tamias sibiricus</i>	Tsibiricus	Sciuridae
13	<i>Urocitellus parryi</i>	Uparryi	Sciuridae
14	<i>Ictidomys tridecemlineatus</i>	Itridecemlineatus	Sciuridae
15	<i>Spermophilus dauricus</i>	Sdauricus	Sciuridae
16	<i>Marmota himalayana</i>	Mmarmota	Sciuridae
17	<i>Mus musculus</i>	Mmusculus	Muridae
18	<i>Homo sapiens</i>	Hsapiens	Hominidae

Table S11 The genome download address	
Species	URL
Europaesus	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/950/295/315/GCF_950295315.1_mEriEur2.1/
Uthibetanus	https://ftp.ensembl.org/pub/release-112/gtf/ursus_thibetanus_thibetanus/
Umaritimus	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/017/311/325/GCF_017311325.1_ASM1731132v1/
Tornatus	https://dnazoo.s3.wasabisys.com/index.html?prefix=Tremarctos_ornatus/
Amelanoleuca	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/007/445/GCF_002007445.2_ASM200744v3/
Rferrumequinum	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/004/115/265/GCF_004115265.2_mRhiFer1_v1.p/
Mlucifugus	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/147/115/GCF_000147115.1_Myoluc2.0/
Munguiculatus	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/030/254/825/GCF_030254825.1_Bangor_MerUng_6.1/
Svulgaris	https://ftp.ensembl.org/pub/release-112/fasta/sciurus_vulgaris/
Scarolinensis	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/902/686/445/GCF_902686445.1_mSciCar1.2/
Xrutilus	https://dnazoo.s3.wasabisys.com/index.html?prefix=Xerus_rutilus/
Tsibiricus	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/025/594/165/GCA_025594165.1_ASM2559416v1/
Uparryii	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/003/426/925/GCF_003426925.1_ASM342692v1/
Itridecemlineatus	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/016/881/025/GCF_016881025.1_HiC_Itri_2/
Mmarmota	https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/001/458/135/GCF_001458135.2_marMar/
Mmusculus	https://www.gencodegenes.org/mouse/release_M33.html
Hsapiens	https://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_44/

Table S12 The annotation of the <i>S. dauricus</i> expansion gene ID in the arachidonic acid metabolic pathway							
Gene ID	Reference Gene Name	Description	Duplication Type	ORF Integrity	Key Motif	Functional Status	Notes
SD02G0847	CBR1	15-hydroxyprostaglandin dehydrogenase (NADP+) activity	Tandem / Segmental	Complete	Intact	Functional	Full-length ORF; no premature stop codons.
SD02G0846	CBR1	15-hydroxyprostaglandin dehydrogenase (NADP+) activity	Tandem / Segmental	Complete	Intact	Functional	Full-length ORF; no premature stop codons.
SD02G0848	CBR3	Carbonyl reductase	Proximal / Tandem	Complete	Intact	Functional	Full-length ORF; no premature stop codons.
SD11G0189	ALOX12	Arachidonate 12-lipoxygenase	WGD / Segmental	Complete	Intact	Functional	Full-length ORF; no premature stop codons.

Table S13 The list of abbreviations

CCS	Circular Consensus Sequencing
CPT1A	Carnitine Palmitoyltransferase 1A
CTAB	Cetyl-trimethyl Ammonium Bromide
DEGs	Differentially Expressed Genes
DEMs	Differentially Expressed Metabolites
eggNOG	Evolutionary Genealogy of Genes: Non-supervised Orthologous Groups
EH	Emergence from Hibernation
ELOVL5	Fatty Acid Elongase 5
FADS1	Fatty Acid Desaturase 1
FADS2	Fatty Acid Desaturase 2
FPKM	Fragments Per Kilobase Million
GC	Guanine-Cytosine
GO	Gene Ontology
H	Hibernation Period
HADH	Hydroxyacyl-CoA Dehydrogenase
Hi-C	High-throughput Chromosome Conformation Capture
IHC	Immunohistochemistry
KAT	Kmer Analysis Toolkit
KEGG	Kyoto Encyclopedia of Genes and Genomes
LC-MS	Liquid Chromatography-Mass Spectrometry
LINEs	Long Interspersed Nuclear Elements
LLMs	lipids and lipid-like molecules
LTR	Long Terminal Repeat
MS	Mass Spectrometry
ncRNA	Non-coding RNA
NR	Non-Redundant
ONT	Oxford Nanopore Technologies
PacBio HiFi	Pacific Biosciences High-Fidelity
PH	Pre-hibernation Period
PPAR	Peroxisome Proliferator-activated Receptor
PPARA	Peroxisome Proliferator-Activated Receptor Alpha
ppm	Parts per Million
RT q-PCR	Real-Time Quantitative Polymerase Chain Reaction
QV	Quality Value
SA	Summer Active Period
SEM	standard error of the mean
SINE	Short Interspersed Nuclear Element
T2T	Telomere-to-telomere
TRPV	Transient Receptor Potential Vanilloid
VIP	Variable Importance in Projection
WGCNA	Weighted Gene Co-expression Network Analysis