

The nutritional metabolic process of the dung beetle *Phelotrupes auratus* depends on the host animal

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Supplementary Figure 1.

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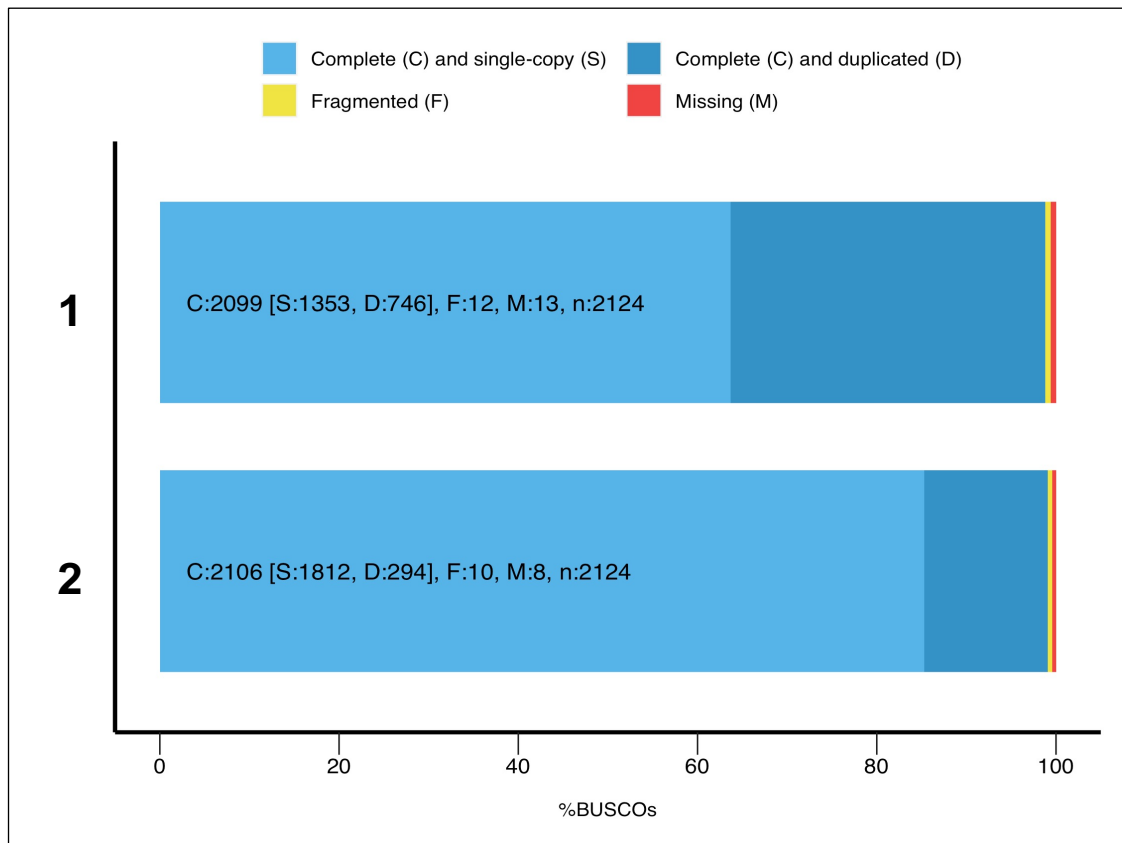
Supplementary Figure 6.

Supplementary Table 1.

Supplementary Table 2.

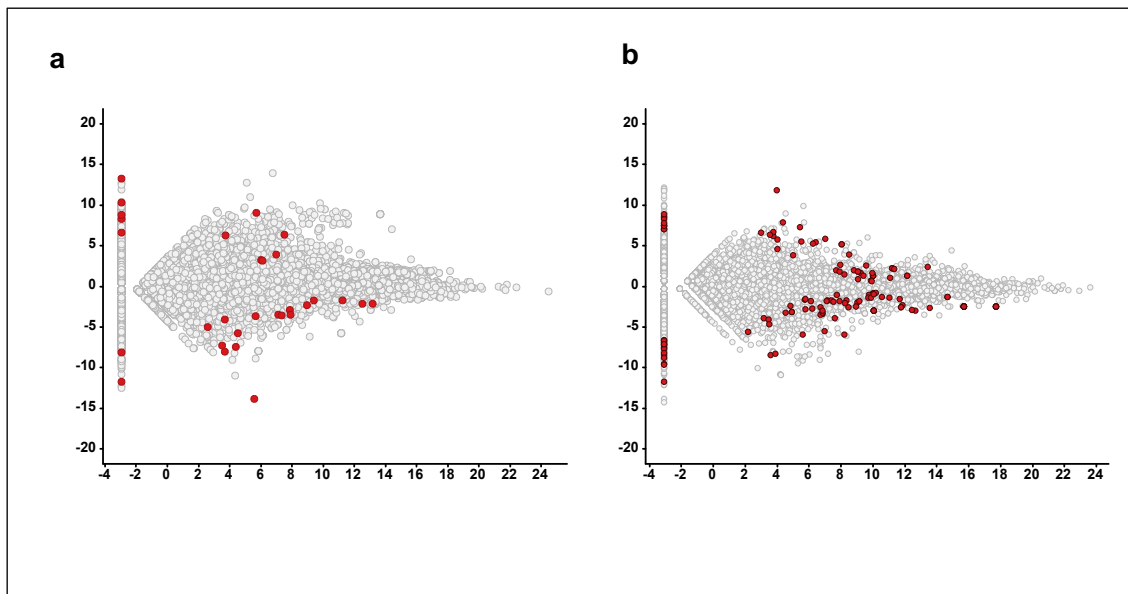
Supplementary Table 3.

Supplementary Table 4.

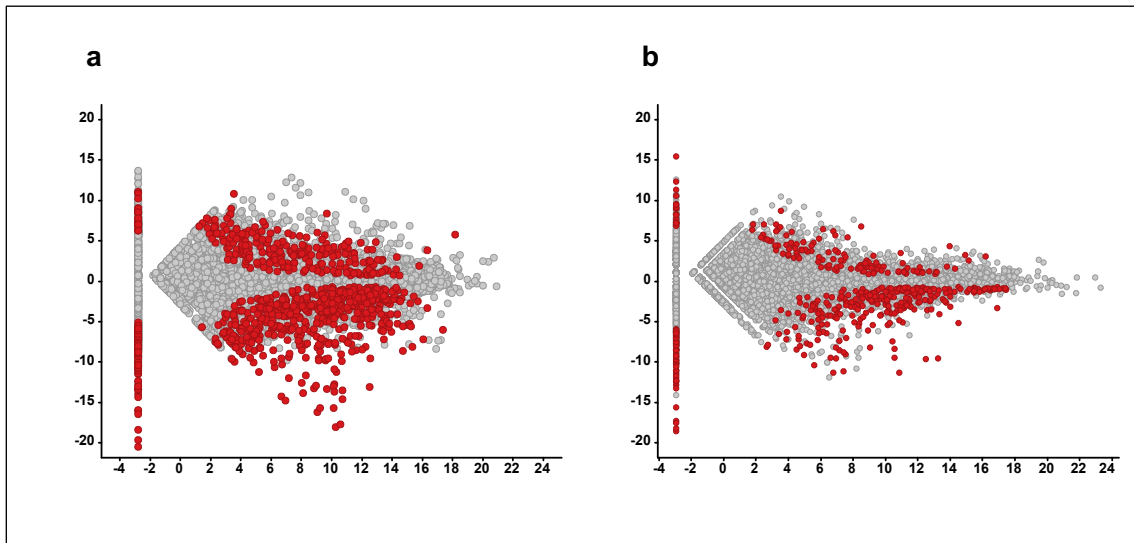


Supplementary figure 1. Assessment for assembled *P.auratus* genome sequences.

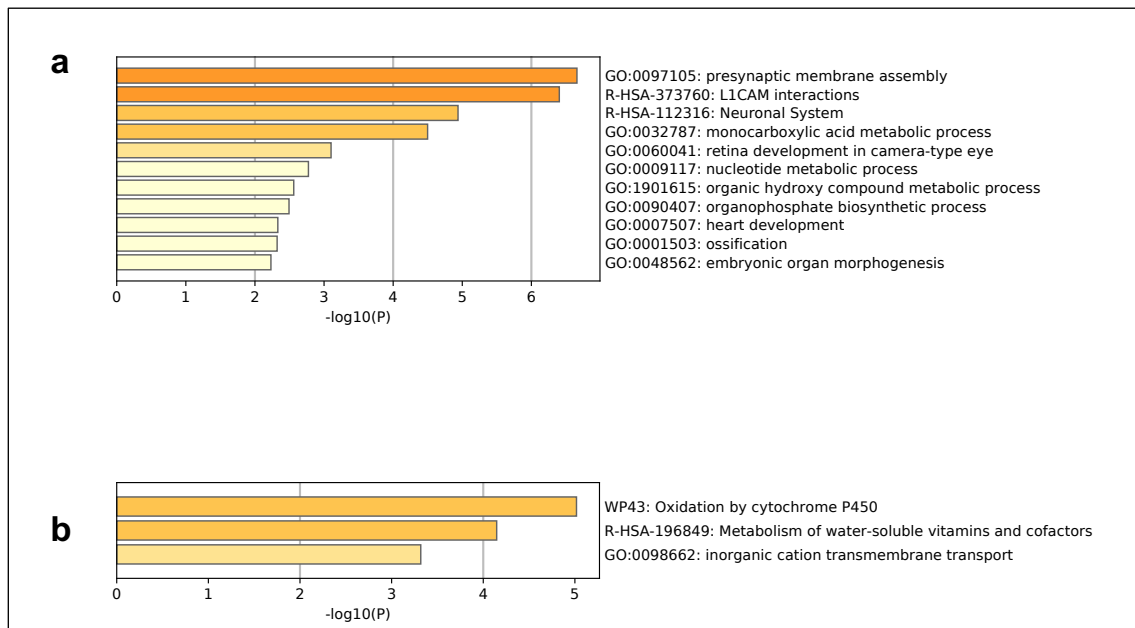
Busco used for evaluation of genome assemble. 1: Genome sample from Cape Toi, individual1;
2: Genome sample from Cape Toi, individual 2. Each color indicates core gene sets in the graph.



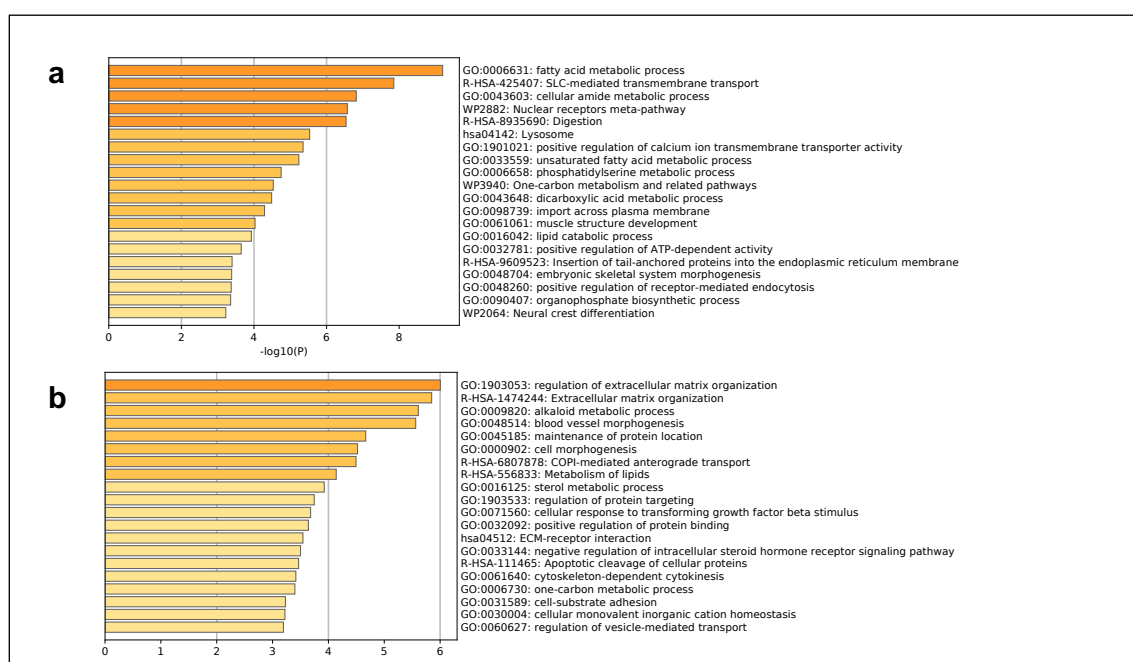
Supplementary figure 2. The extraction of fluctuated transcripts in the Cape-Toi group. Fluctuated transcripts were extracted and plotted on the graph. Red dots, transcripts that fluctuated more than two times in the Cape-Toi group. (a) : midgut, (b) : fat body.



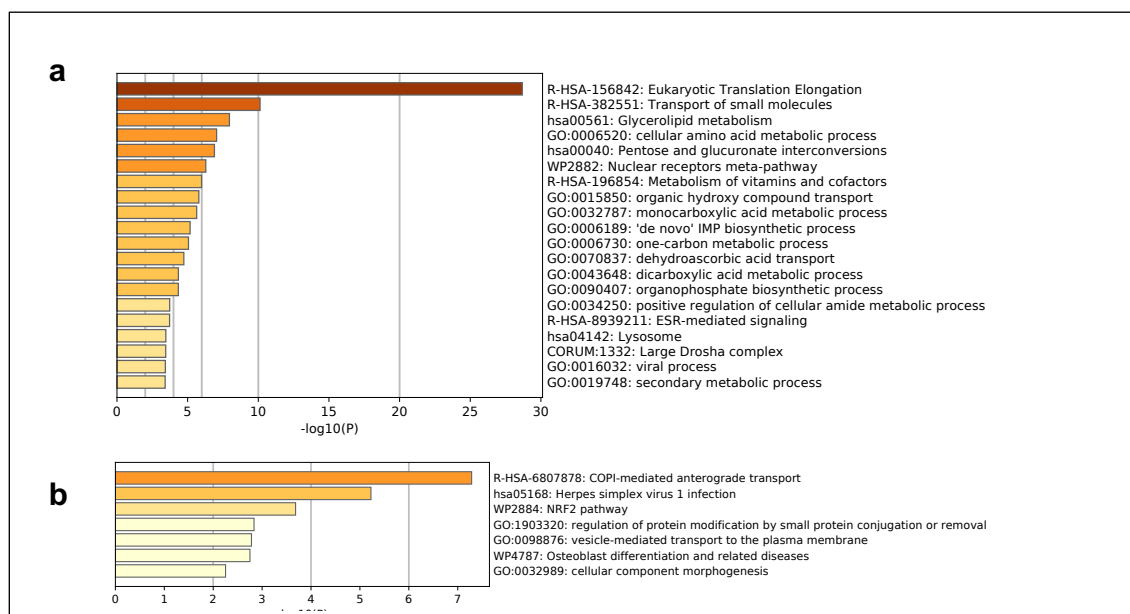
Supplementary figure 3. The extraction of fluctuated transcripts in the Nara-Park group. Fluctuated transcripts were extracted and plotted on the graph. Red dots, transcripts that fluctuated more than two times in the Nara-Park group. (a) : midgut, (b) : fat body.



Supplementary figure 4. The gene enrichment analysis of fluctuated fat body transcripts in the Cape-Toi group using Metascape. A heatmap of enriched terms across the input transcripts lists; different colored bars, P values. (a) Upregulated genes in the group a (n=3); (b) Upregulated genes in the group b (n=3).



Supplementary figure 5. The gene enrichment analysis of fluctuated fat body transcripts in the Nara-Park group using Metascape. A heatmap of enriched terms across the input transcripts lists; different colored bars, P values. (a) Upregulated genes in the group a (n=3); (b) Upregulated genes in the group b (n=3)



Supplementary figure 6. The gene enrichment analysis of fluctuated midgut transcripts in the Nara-Park group using Metascape. A heatmap of enriched terms across the input transcripts lists; different colored bars, P values. (a) Upregulated genes in the group a (n=3); (b) Upregulated genes in the group b (n=3)

Supplementary Table 1. Assembled genome sequence in *P. auratus*

individual	Number of contig	Sum of contig length	Average of contig length	Maximum of contig length
1	36,291	1,577,576,937	43,470	1,908,500
2	19,932	1,066,449,501	53,504	7,365,120

Supplementary Table 2. Mapping rate for each transcriptome data.

Mapping rate (%) in Nara Park		Mapping rate (%) in Cape Toi	
Fat body	Midgut	Fat body	Midgut
92.2 $\pm$ 0.004	91.1 $\pm$ 0.024	94.9 $\pm$ 0.017	92.0 $\pm$ 0.079

Mapping rate show as mean $\pm$ SD

Supplementary Table 3. The count data in the midgut for the up-regulated genes in the biological oxidations.

Transcript_IDs	Nara-Park_MG1	Nara-Park_MG2	Nara-Park_MG3	Cape-Toi_MG1	Cape-Toi_MG2	Cape-Toi_MG3	NCBI_IDs
MSTRG.24054	322.30	1730.15	2021.70	30.93	149.84	68.15	NP_997235.3
MSTRG.22735	1326.78	187.12	8620.11	532.95	187.93	147.45	NP_001189784.1
MSTRG.10820	3090.97	4975.40	8222.66	555.55	480.75	915.70	XP_005262992.1
MSTRG.9769	559.79	781.29	819.22	1351.40	1864.32	1413.83	NP_000766.2
MSTRG.18860	222.95	151.51	285.92	418.74	633.72	862.42	NP_000756.3
MSTRG.17887	164.79	413.34	478.56	1004.03	1055.78	1146.18	NP_997235.3
MSTRG.21976	285.95	215.74	792.86	9294.43	348.39	2276.25	NP_001189784.1
MSTRG.13809	490.73	336.53	1101.09	49686.49	1603.34	4707.39	NP_001189784.1
MSTRG.10814	0.00	3.49	0.00	27.36	54.32	24.78	NP_997235.3

Supplementary Table 4. The count data in the fat body for the up-regulated genes in the biological oxidations.

Transcript_IDs	Nara-Park_FB1	Nara-Park_FB2	Nara-Park_FB3	Cape-Toi_FB1	Cape-Toi_FB2	Cape-Toi_FB3	NCBI_IDs
MSTRG.23098	33046.3	22977.4	16514.8	0.0	12.8	223.4	NP_997235.3
MSTRG.2486	1323.2	2277.9	126.8	208.5	41.9	22.5	NP_997235.3
MSTRG.20708	7190.7	16398.8	16060.0	511.4	1677.0	811.7	NP_000756.3
MSTRG.23108	414.2	326.3	305.9	781.5	658.0	723.4	NP_997235.3
MSTRG.11616	117.8	474.9	479.2	2689.3	3527.6	982.8	NP_997235.3
MSTRG.17892	382.5	566.0	823.5	8348.6	2990.7	941.4	XP_016863526.1
MSTRG.10804	820.2	1115.2	2563.6	33718.1	10273.0	2810.7	XP_005262992.1
MSTRG.11621	74.3	176.2	280.3	1486.9	3690.6	528.8	NP_001073.3
MSTRG.23101	511.2	2267.2	1903.0	27365.3	22946.3	5035.9	NP_997235.3
MSTRG.17887	1345.9	6031.0	1547.0	60155.1	40230.3	5176.4	NP_997235.3
MSTRG.28440	5343.7	4567.3	16024.0	136489.3	200573.7	17060.7	NP_997235.3
MSTRG.16692	33.5	106.5	48.9	1258.8	1211.2	282.9	NP_001265850.1
MSTRG.21974	841.1	3930.8	5914.8	101277.7	46073.1	12289.7	NP_001189784.1
MSTRG.13809	6.3	19.1	31.4	617.6	245.7	32.4	NP_001278758.1
MSTRG.11623	68.9	324.0	886.3	3642.6	21867.9	1694.5	NP_997235.3
MSTRG.16689	20.8	46.0	15.1	3696.3	614.9	273.9	NP_001265850.1
MSTRG.3748	172.2	0.0	438.5	18724.3	21973.8	2685.5	NP_059488.2
MSTRG.10814	3.6	0.0	0.0	393.4	659.2	138.7	NP_997235.3
MSTRG.14420	2393.592045	2316.969641	4343.315458	21590.62571	12880.57788	7119.57676	NP_000844.2