Fig. 1

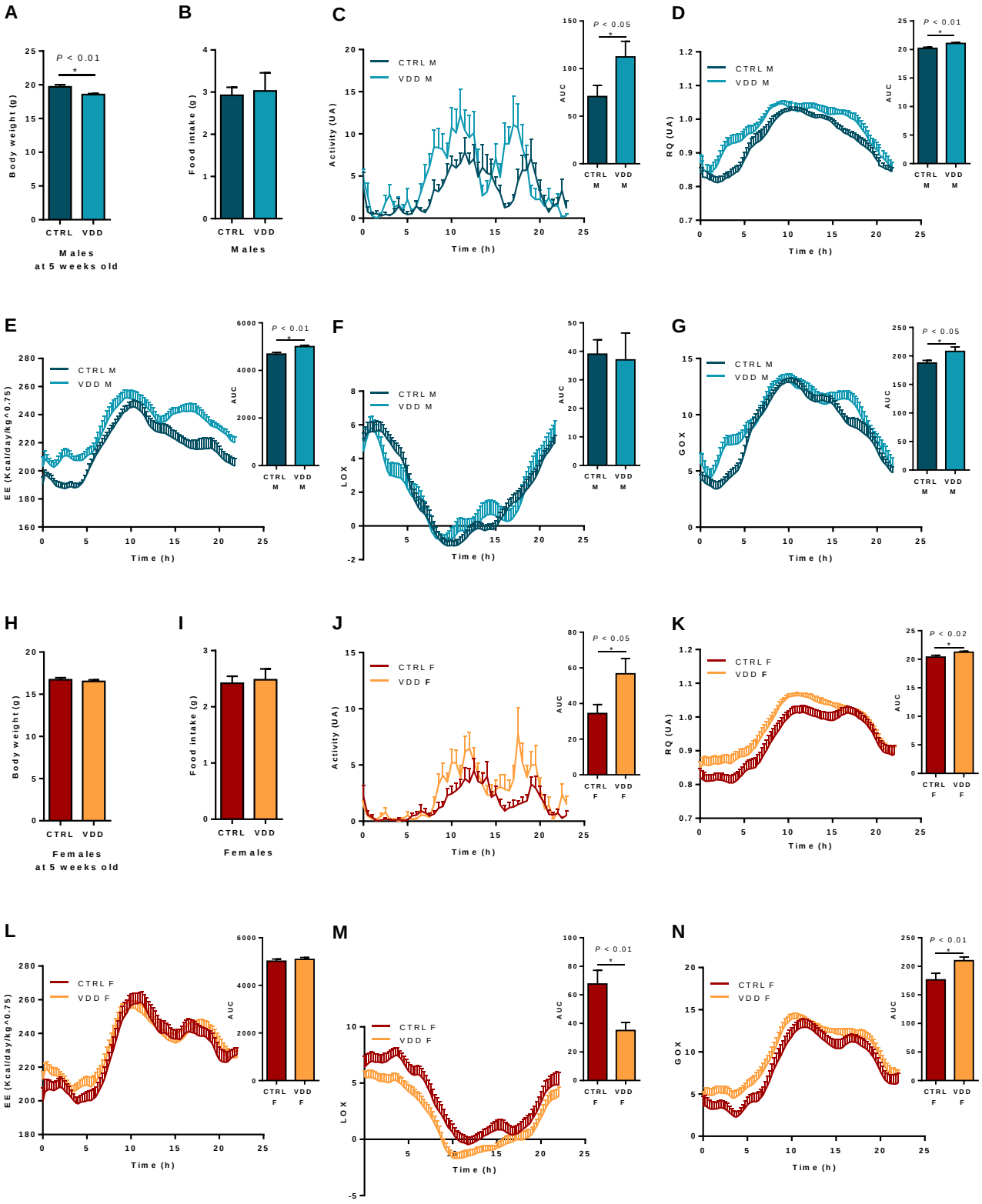

A
Body weight (g)
P < 0.01
CTRL
VDD
Males
at 5 weeks old
B
Food intake (g)
Males
C
Activity (UA)
CTRL M
VDD M
Time (h)
AUC
P < 0.05
D
RQ (UA)
P < 0.01
E
EE (Kcal/day/kg^0.75)
P < 0.01
F
LOX
G
GOX
P < 0.05
H
Females
at 5 weeks old
I
Females
J
CTRL F
VDD F
P < 0.05
K
P < 0.02
L
M
P < 0.01
N
P < 0.01

Fig. 2

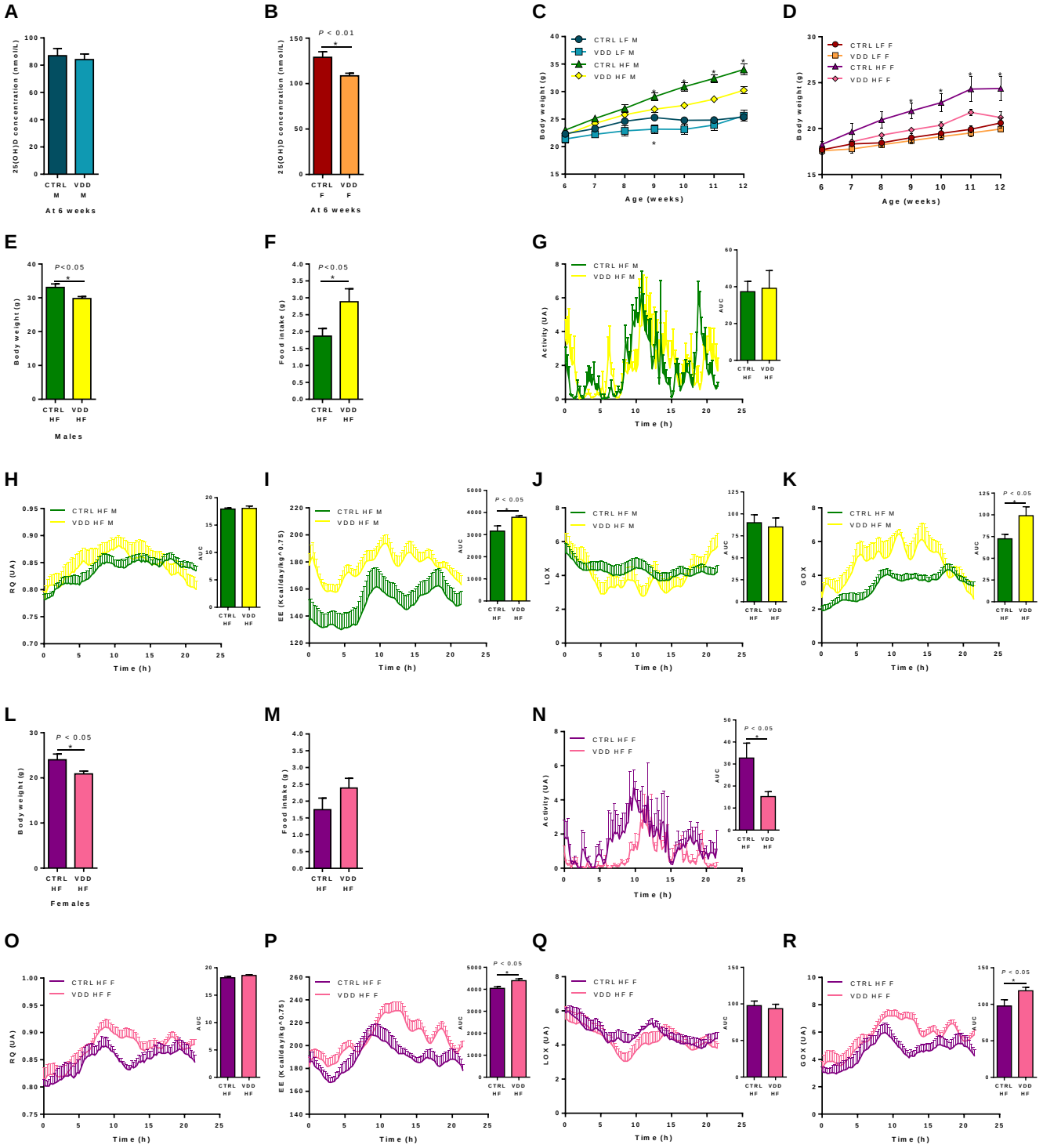

A
25(OH)D concentration (nmol/L)
CTRL M
VDD M
At 6 weeks
B
P < 0.01
25(OH)D concentration (nmol/L)
CTRL F
VDD F
At 6 weeks
C
CTRL LF M
VDD LF M
CTRL HF M
VDD HF M
Body weight (g)
Age (weeks)
D
CTRL LF F
VDD LF F
CTRL HF F
VDD HF F
Body weight (g)
Age (weeks)
E
P<0.05
Body weight (g)
CTRL HF
VDD HF
Males
F
P<0.05
Food intake (g)
CTRL HF
VDD HF
G
CTRL HF M
VDD HF M
Activity (UA)
Time (h)
AUC
H
CTRL HF M
VDD HF M
RQ (UA)
Time (h)
AUC
I
CTRL HF M
VDD HF M
EE (Kcal/day/kg^0.75)
Time (h)
P < 0.05
AUC
J
CTRL HF M
VDD HF M
LOX
Time (h)
AUC
K
CTRL HF M
VDD HF M
GOX
Time (h)
P < 0.05
AUC
L
P < 0.05
Body weight (g)
CTRL HF
VDD HF
Females
M
Food intake (g)
CTRL HF
VDD HF
N
CTRL HF F
VDD HF F
Activity (UA)
Time (h)
P < 0.05
AUC
O
CTRL HF F
VDD HF F
RQ (UA)
Time (h)
AUC
P
CTRL HF F
VDD HF F
EE (Kcal/day/kg^0.75)
Time (h)
P < 0.05
AUC
Q
CTRL HF F
VDD HF F
LOX (UA)
Time (h)
AUC
R
CTRL HF F
VDD HF F
GOX (UA)
Time (h)
P < 0.05
AUC

Fig. 3

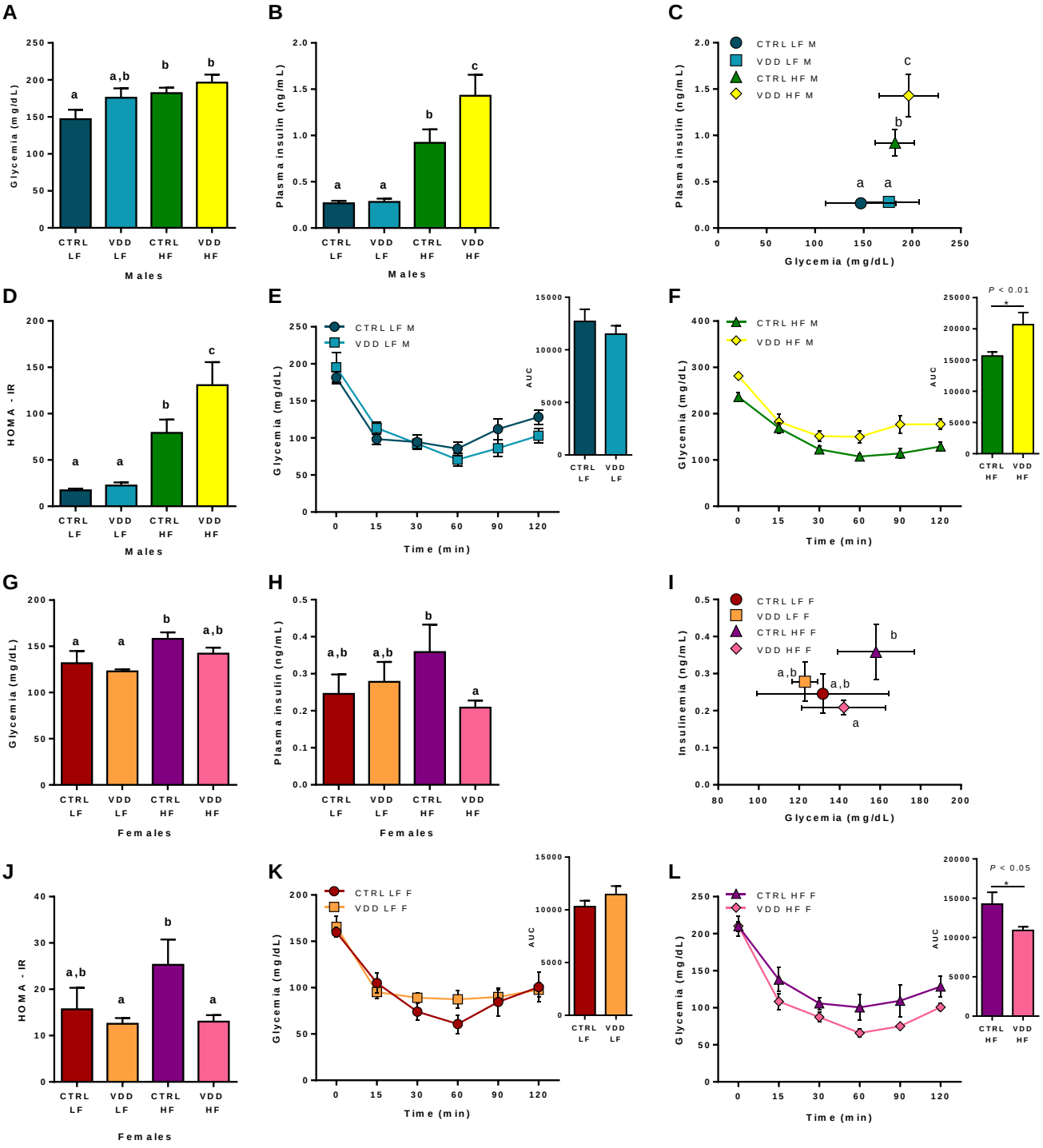

A
Glycemia (mg/dL)
CTRL LF
VDD LF
CTRL HF
VDD HF
Males
B
Plasma insulin (ng/mL)
Males
C
CTRL LF M
VDD LF M
CTRL HF M
VDD HF M
Plasma insulin (ng/mL)
Glycemia (mg/dL)
D
HOMA - IR
Males
E
CTRL LF M
VDD LF M
Glycemia (mg/dL)
Time (min)
AUC
F
CTRL HF M
VDD HF M
Glycemia (mg/dL)
Time (min)
AUC
P < 0.01
G
Glycemia (mg/dL)
Females
H
Plasma insulin (ng/mL)
Females
I
CTRL LF F
VDD LF F
CTRL HF F
VDD HF F
Insulinemia (ng/mL)
Glycemia (mg/dL)
J
HOMA - IR
Females
K
CTRL LF F
VDD LF F
Glycemia (mg/dL)
Time (min)
AUC
L
CTRL HF F
VDD HF F
Glycemia (mg/dL)
Time (min)
AUC
P < 0.05

Fig. 4

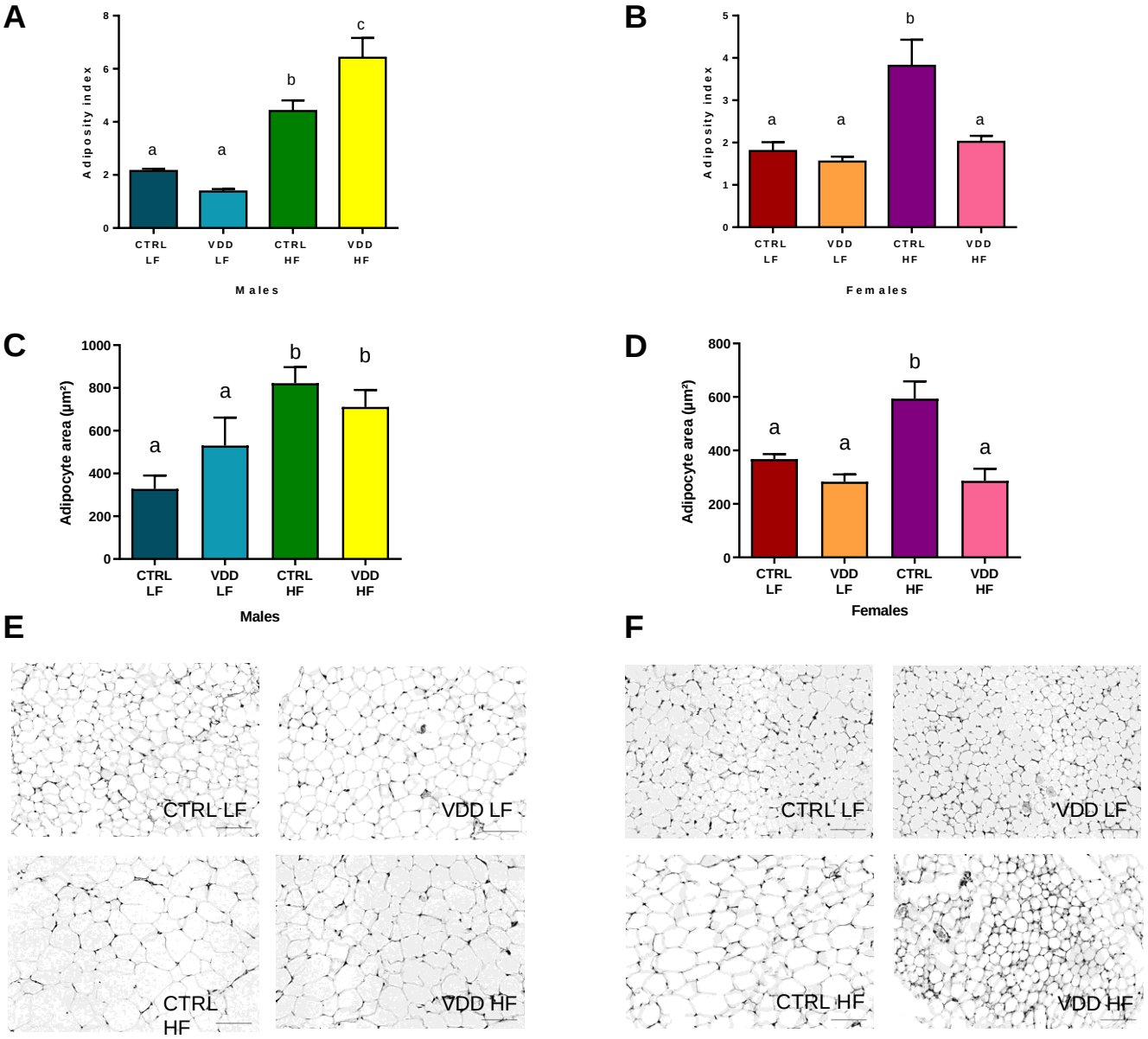
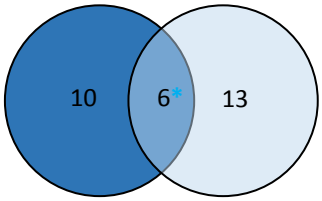

A
Adiposity index
0
2
4
6
8
a
a
b
c
CTRL LF
VDD LF
CTRL HF
VDD HF
Males
B
Adiposity index
0
1
2
3
4
5
a
a
b
a
CTRL LF
VDD LF
CTRL HF
VDD HF
Females
C
Adipocyte area (µm²)
0
200
400
600
800
1000
a
a
b
b
CTRL LF
VDD LF
CTRL HF
VDD HF
Males
D
Adipocyte area (µm²)
0
200
400
600
800
a
a
b
a
CTRL LF
VDD LF
CTRL HF
VDD HF
Females
E
CTRL LF
VDD LF
CTRL HF
VDD HF
F
CTRL LF
VDD LF
CTRL HF
VDD HF

Fig. 5

CTRL LF vs CTRL HF
(Males)
16

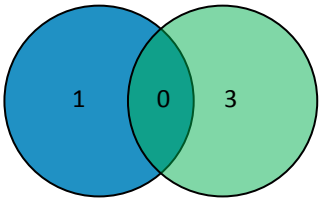


VDD LF vs VDD HF
(Males)
19

Canonical Pathways	-log(p-value)	Z-score
GP6 Signaling Pathway*	6,67E00	2,982
Apelin Liver Signaling Pathway*	4,43E00	2,646
Apelin Cardiomyocyte Signaling Pathway	3,38E00	-0,302
Triacylglycerol Biosynthesis*	2,76E00	-2,646
Stearate Biosynthesis I (Animals) *	2,72E00	-1,890
γ-linolenate Biosynthesis II (Animals)	2,36E00	-2,000
Mitochondrial L-carnitine Shuttle Pathway	2,36E00	-1,000
LPS/IL-1 Mediated Inhibition of RXR Function	2,23E00	1,890
Valine Degradation I*	2,21E00	-2,000
CDP-diacylglycerol Biosynthesis I	2,07E00	-2,000
NRF2-mediated Oxidative Stress Response*	1,98E00	-1,342
Phosphatidylglycerol Biosynthesis II (Non-plastidic)	1,89E00	-2,000
Intrinsic Prothrombin Activation Pathway	1,84E00	2,000
Fatty Acid β-oxidation I	1,72E00	-2,236
Apelin Cardiac Fibroblast Signaling Pathway	1,55E00	1,000
p53 Signaling	1,38E00	-0,378

Canonical Pathways	-log(p-value)	Z-score
Oxidative Phosphorylation	6,92E00	-5,292
GP6 Signaling Pathway*	4,45E00	4,200
Triacylglycerol Biosynthesis*	4,22E00	-1,807
Nicotine Degradation II	2,56E00	-1,667
Valine Degradation I*	2,36E00	-2,449
Sirtuin Signaling Pathway	2,33E00	1,300
Apelin Liver Signaling Pathway*	2,28E00	1,890
NRF2-mediated Oxidative Stress Response*	1,93E00	-1,508
Stearate Biosynthesis I (Animals) *	1,78E00	-1,667
Superpathway of Melatonin Degradation	1,73E00	-0,707
Apelin Adipocyte Signaling Pathway	1,7E00	-1,941
Melatonin Degradation I	1,68E00	-1,134
Ethanol Degradation IV	1,64E00	-1,342
Nicotine Degradation III	1,52E00	-0,816
Isoleucine Degradation I	1,48E00	-2,000
Oxidative Ethanol Degradation III	1,48E00	-1,000
Ethanol Degradation II	1,48E00	-1,342
Glutathione-mediated Detoxification	1,4E00	-0,816
Bupropion Degradation	1,32E00	-2,000

CTRL LF vs VDD LF
(Males)
1



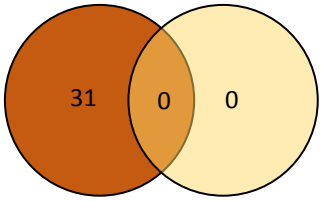
CTRL HF vs VDD HF
(Males)
3

Canonical Pathways	-log(p-value)	Z-score
cAMP-mediated signaling	1,98E00	-1,000

Canonical Pathways	-log(p-value)	Z-score
Protein Kinase A Signaling	4,55E00	-0,447
Actin Cytoskeleton Signaling	4,32E00	2,236
RhoA Signaling	3,74E00	0,447

Fig. 6

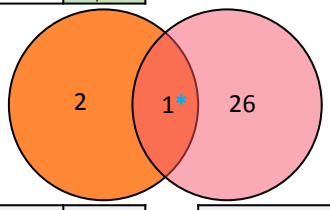
CTRL LF vs CTRL HF (Females) 31



VDD LF vs VDD HF (Females) 0

Canonical Pathways	-log(p-value)	Z-score
Valine Degradation I	6,19E00	-3,162
Fatty Acid β-oxidation I	4,62E00	-3,606
Oxidative Phosphorylation	4,44E00	-5,000
TCA Cycle II (Eukaryotic)	3,53E00	-3,162
Complement System	3,53E00	0,333
Branched-chain α-keto acid Dehydrogenase Complex	3,15E00	-2,000
Acetyl-CoA Biosynthesis I (Pyruvate Dehydrogenase Complex)	3,15E00	-2,000
Isoleucine Degradation I	2,99E00	-2,449
Sirtuin Signaling Pathway	2,75E00	1,372
Triacylglycerol Biosynthesis	2,62E00	-2,496
Apelin Adipocyte Signaling Pathway	2,53E00	-1,500
GP6 Signaling Pathway	2,2E00	2,837
Dendritic Cell Maturation	2,16E00	2,600
EIF2 Signaling	2,07E00	2,294
CDP-diacylglycerol Biosynthesis I	2	-1,414
LPS/IL-1 Mediated Inhibition of RXR Function	1,97E00	2,496
Calcium-induced T Lymphocyte Apoptosis	1,95E00	0,577
Glutaryl-CoA Degradation	1,94E00	-2,449
Salvage Pathways of Pyrimidine Ribonucleotides	1,94E00	-2,840
Glutathione Redox Reactions I	1,76E00	-1,633
Phosphatidylglycerol Biosynthesis II (Non-plastidic)	1,73E00	-1,414
Nicotine Degradation II*	1,73E00	-2,828
Mitochondrial L-carnitine Shuttle Pathway	1,65E00	-1,342
Intrinsic Prothrombin Activation Pathway*	1,6E00	1,342
Gluconeogenesis I*	1,6E00	-1,633
LXR/RXR Activation	1,47E00	-1,897
Ethanol Degradation IV	1,47E00	-2,236
Tryptophan Degradation III (Eukaryotic)	1,46E00	-2,449
Oxidative Ethanol Degradation III	1,35E00	-2,000
Coagulation System*	1,32E00	0,447
Ethanol Degradation II	1,32E00	-2,236

CTRL LF vs VDD LF (Females) 3



CTRL HF vs VDD HF (Females) 27

Canonical Pathways	-log(p-value)	Z-score
EIF2 Signaling	1,65E01	3,464
GP6 Signaling Pathway*	8,59E00	-2,530
Apelin Liver Signaling Pathway	4,8E00	-2,000

Canonical Pathways	-log(p-value)	Z-score
Oxidative Phosphorylation	4,77E01	7,211
Sirtuin Signaling Pathway	1,86E01	-3,212
TCA Cycle II (Eukaryotic)	1,61E01	4,000
Valine Degradation I	1,01E01	3,162
Fatty Acid β-oxidation I	8,11E00	3,464
Isoleucine Degradation I	5,25E00	2,449
Branched-chain α-keto acid Dehydrogenase Complex	4,73E00	2,000
Acetyl-CoA Biosynthesis I (Pyruvate Dehydrogenase Complex)	4,73E00	2,000
Ethanol Degradation II	4,68E00	2,646
Glutaryl-CoA Degradation	4,04E00	2,449
Tryptophan Degradation III (Eukaryotic)	3,44E00	2,449
Leucine Degradation I	3,25E00	2,000
Noradrenaline and Adrenaline Degradation	3,13E00	2,449
Oxidative Ethanol Degradation III	2,74E00	2,000
Intrinsic Prothrombin Activation Pathway	2,68E00	-1,000
Gluconeogenesis I	2,68E00	1,342
Mitochondrial L-carnitine Shuttle Pathway	2,37E00	2,000
LPS/IL-1 Mediated Inhibition of RXR Function	2,27E00	-1,890
Triacylglycerol Biosynthesis	2,23E00	2,646
Ethanol Degradation IV	2,22E00	2,000
Coagulation System	2,08E00	-1,000
Serotonin Degradation	2,06E00	2,449
GP6 Signaling Pathway*	2,06E00	-2,714
Nicotine Degradation II	1,9E00	1,342
Estrogen Biosynthesis	1,65E00	2,000
Stearate Biosynthesis I (Animals)	1,47E00	2,236
Superpathway of Methionine Degradation	1,41E00	2,000