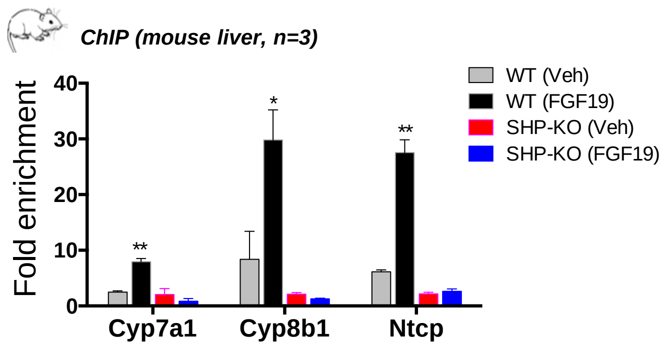
Figure. S1

a



b

Treatment	Group	Unique Mapped Reads	Total Reads
Veh	Input	*16,743,814*	*22,029,930*
FGF19	Input	*17,849,172*	*23,247,293*
Veh	Shp	*17,968,561*	*32,763,382*
FGF19	Shp	*16,301,598*	*25,068,418*

Figure. S2

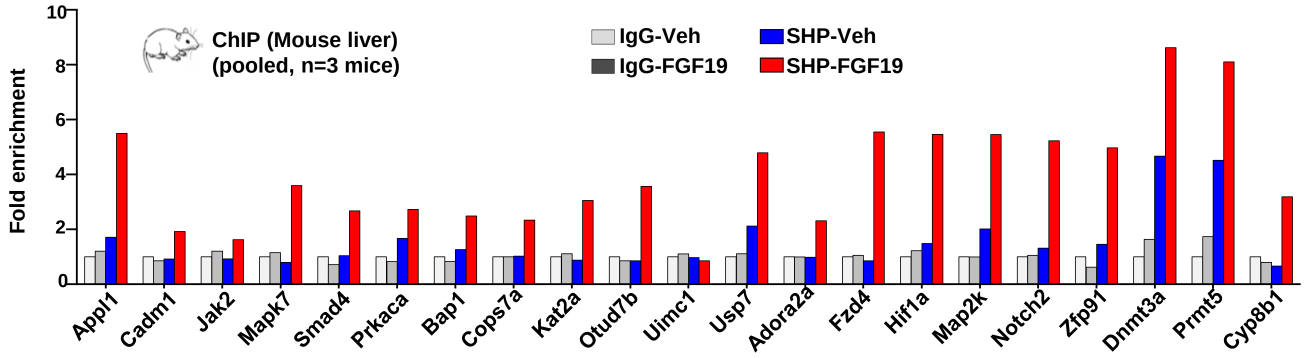


Figure. S3

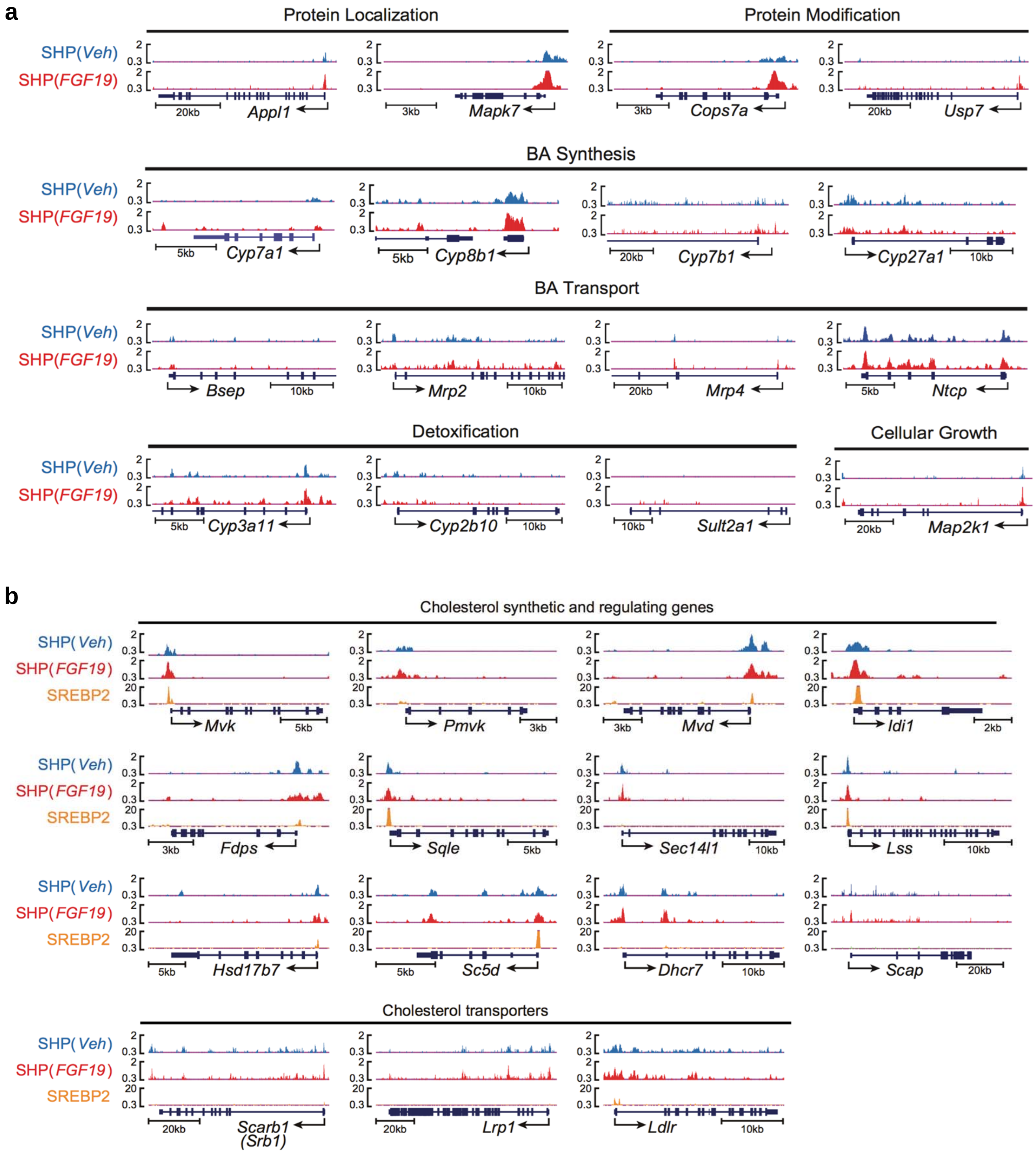

a
Protein Localization
Protein Modification
SHP(Veh)
SHP(FGF19)
2
0.3
Appl1
20kb
Mapk7
3kb
Cops7a
3kb
Usp7
20kb
BA Synthesis
Cyp7a1
5kb
Cyp8b1
5kb
Cyp7b1
20kb
Cyp27a1
10kb
BA Transport
Bsep
10kb
Mrp2
10kb
Mrp4
20kb
Ntcp
5kb
Detoxification
Cellular Growth
Cyp3a11
5kb
Cyp2b10
10kb
Sult2a1
10kb
Map2k1
20kb
b
Cholesterol synthetic and regulating genes
SHP(Veh)
SHP(FGF19)
SREBP2
20
Mvk
5kb
Pmvk
3kb
Mvd
3kb
Idi1
2kb
Fdps
3kb
Sqle
5kb
Sec14l1
10kb
Lss
10kb
Hsd17b7
5kb
Sc5d
5kb
Dhcr7
10kb
Scap
20kb
Cholesterol transporters
Scarb1
(Srb1)
20kb
Lrp1
20kb
Ldlr
10kb

Figure. S4

GO analysis of SREBP2 and SHP (Veh / FGF19) shared binding

Gene Ontology Term	Gene count (Total)	P-value
cellular metabolic process	380 (6562)	5.15E-143
cellular macromolecule metabolic process	299 (4787)	4.40E-113
nitrogen compound metabolic process	222 (3803)	2.41E-78
regulation of cellular metabolic process	224 (3874)	2.63E-68
cellular biosynthetic process	186 (3016)	1.40E-65
RNA metabolic process	156 (2328)	4.83E-60
transcription, DNA-dependent	124 (1738)	4.74E-48
macromolecule modification	116 (1794)	4.83E-38
response to stimulus	220 (6440)	3.01E-34
developmental process	157 (3511)	1.27E-28
organelle organization	89 (1522)	1.35E-28
localization	141 (3226)	2.03E-26
multicellular organismal development	145 (3197)	3.23E-26
negative regulation of biological process	116 (2315)	8.17E-26
transport	119 (2638)	6.79E-24
cell cycle	55 (815)	8.65E-21

Figure. S5

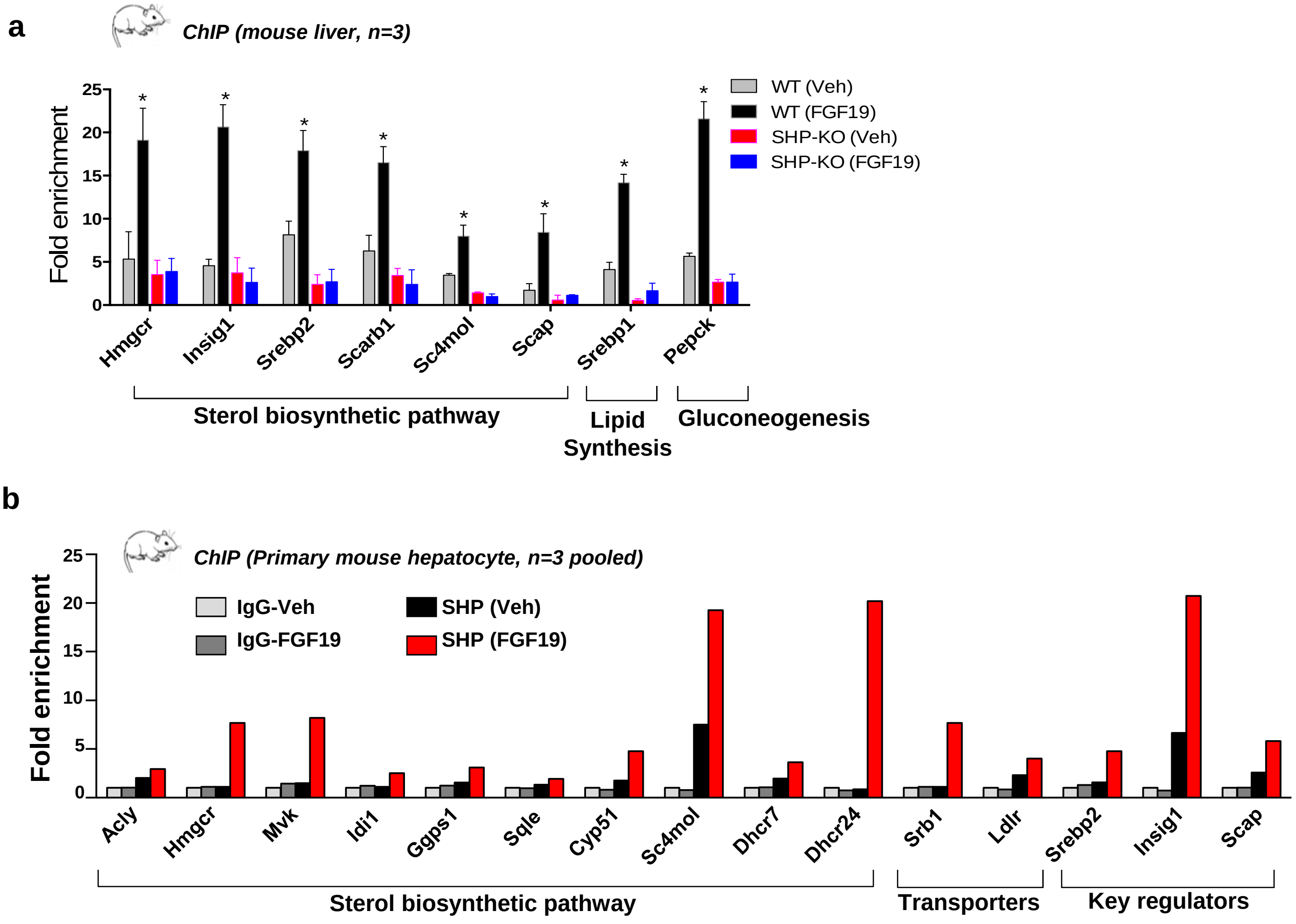
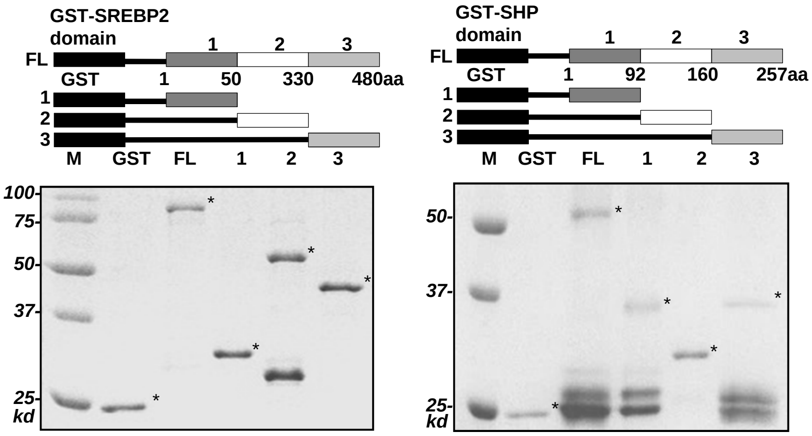


Figure. S6


GST-SREBP2
domain
FL
1
2
3
GST
1
50
330
480aa
1
2
3
M
GST
FL
1
2
3
100-
75-
50-
37-
25-
kd
*
GST-SHP
domain
FL
1
2
3
GST
1
92
160
257aa
1
2
3
M
GST
FL
1
2
3
50-
37-
25-
kd
*