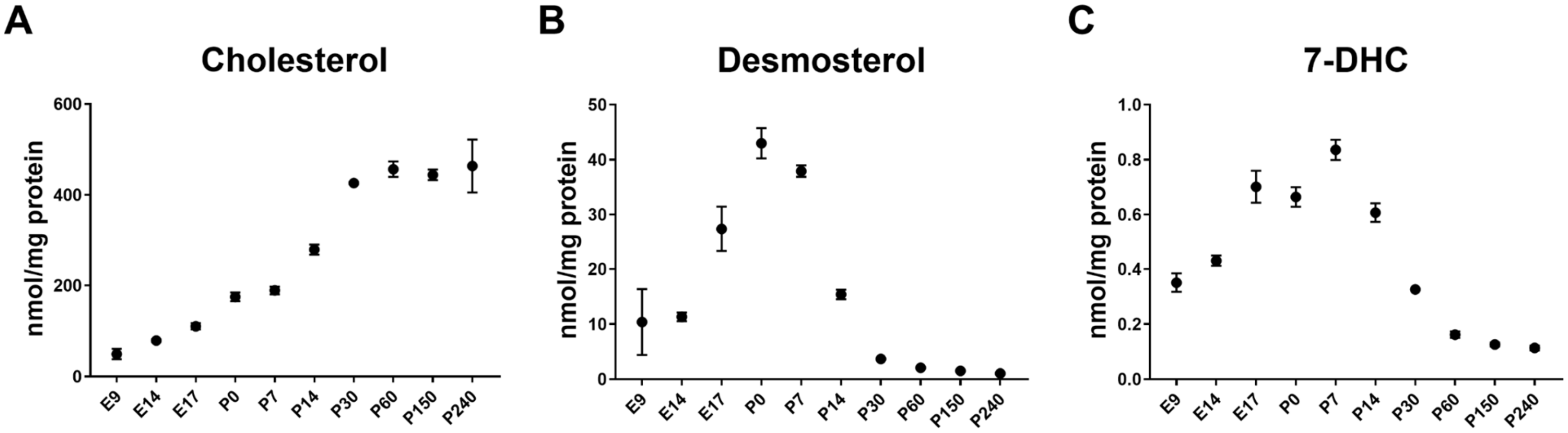
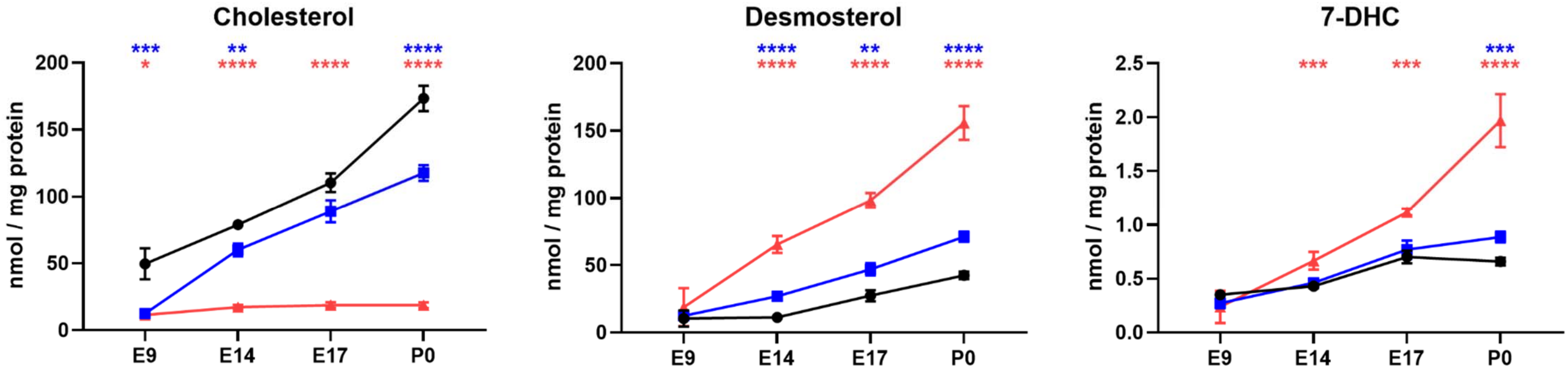


Supplemental Figure 1.



	Cholesterol			
	E9	E14	E17	P0
WT vs. Het	0.0008	0.0037	0.0660	<0.0001
WT vs. KO	0.0310	<0.0001	<0.0001	<0.0001
Het vs. KO	0.8559	0.0003	<0.0001	<0.0001

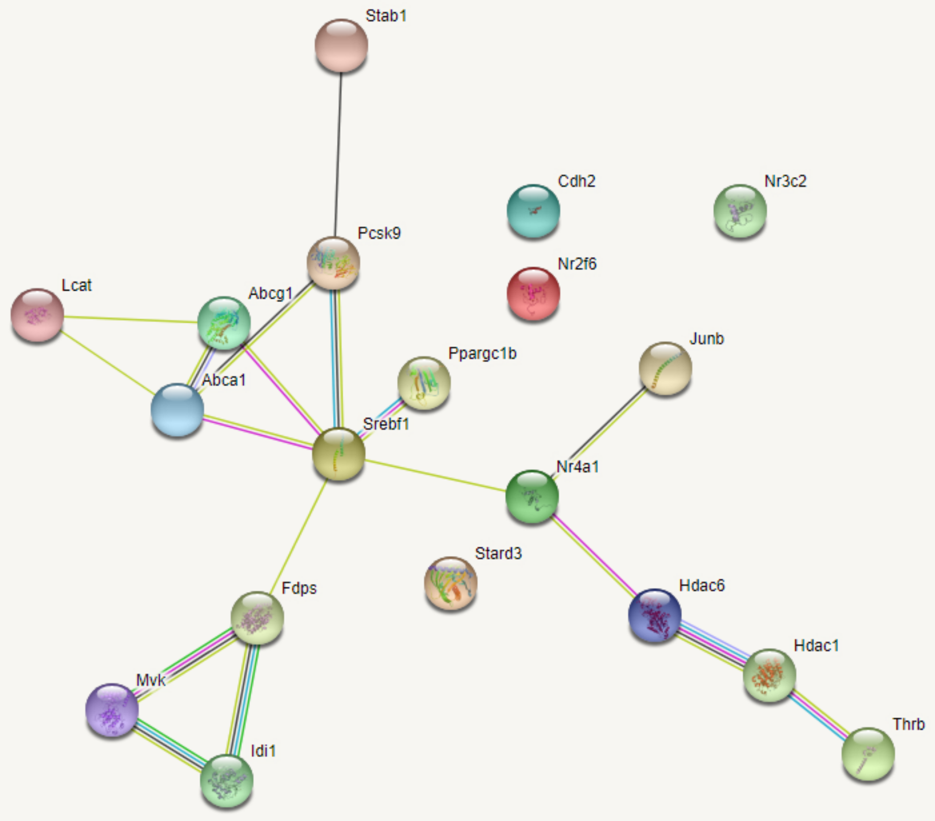
	Desmosterol			
	E9	E14	E17	P0
WT vs. Het	0.7464	<0.0001	0.0063	<0.0001
WT vs. KO	0.6118	<0.0001	<0.0001	<0.0001
Het vs. KO	0.4853	<0.0001	<0.0001	<0.0001

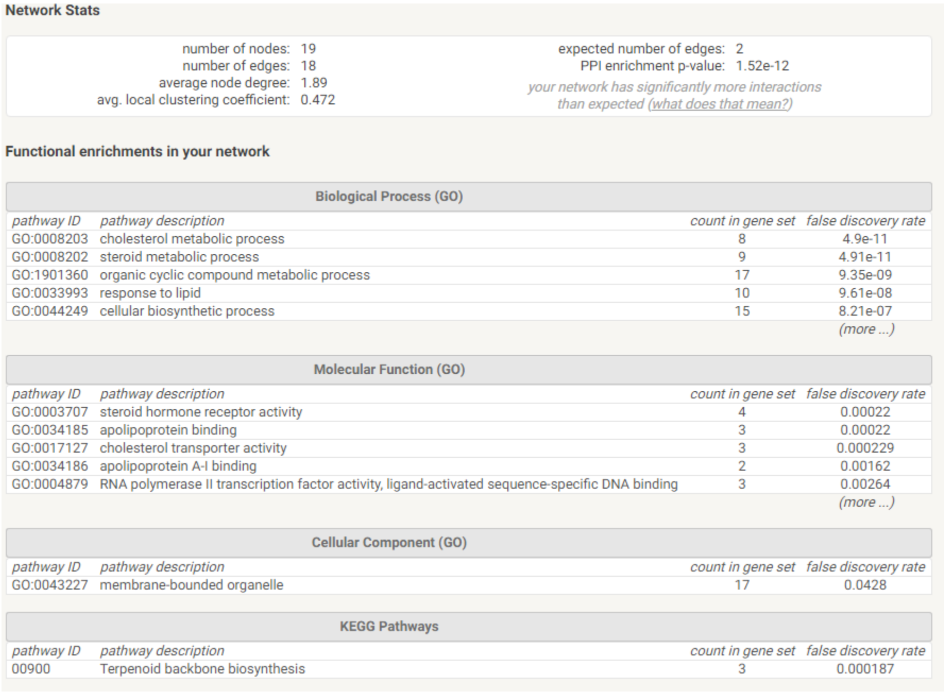
	7-DHC			
	E9	E14	E17	P0
WT vs. Het	0.3447	0.4284	0.5150	0.0005
WT vs. KO	0.5005	0.0006	0.0002	<0.0001
Het vs. KO	0.7715	0.0152	0.0091	<0.0001

	N			
	E9	**E14**	**E17**	**P0**
WT	3	13	8	24
Het	9	15	8	26
KO	2	4	5	7

Supplemental Figure 2.

DESMOSTEROLOSIS





Network Stats

number of nodes: 19
number of edges: 18
average node degree: 1.89
avg. local clustering coefficient: 0.472

expected number of edges: 2
PPI enrichment p-value: 1.52e-12
your network has significantly more interactions than expected (what does that mean?)

Functional enrichments in your network

Biological Process (GO)

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0008203	cholesterol metabolic process	8	4.9e-11
GO:0008202	steroid metabolic process	9	4.91e-11
GO:1901360	organic cyclic compound metabolic process	17	9.35e-09
GO:0033993	response to lipid	10	9.61e-08
GO:0044249	cellular biosynthetic process	15	8.21e-07

(more ...)

Molecular Function (GO)

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0003707	steroid hormone receptor activity	4	0.00022
GO:0034185	apolipoprotein binding	3	0.00022
GO:0017127	cholesterol transporter activity	3	0.000229
GO:0034186	apolipoprotein A-I binding	2	0.00162
GO:0004879	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	3	0.00264

(more ...)

Cellular Component (GO)

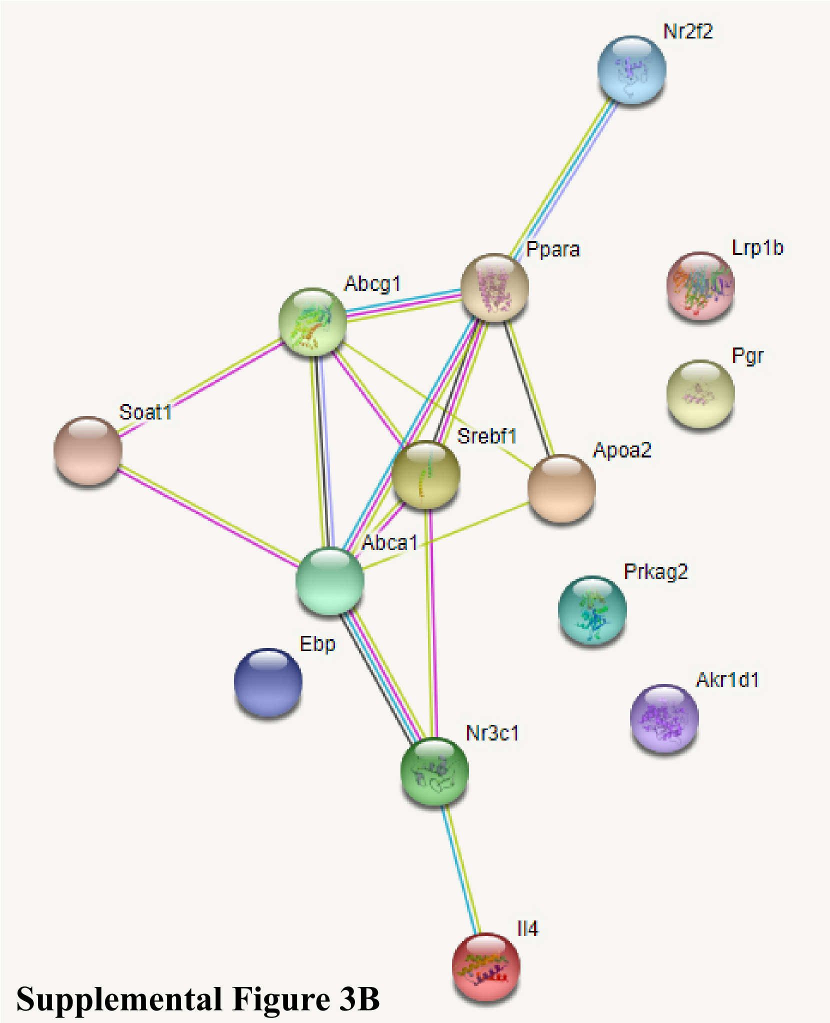
pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0043227	membrane-bounded organelle	17	0.0428

KEGG Pathways

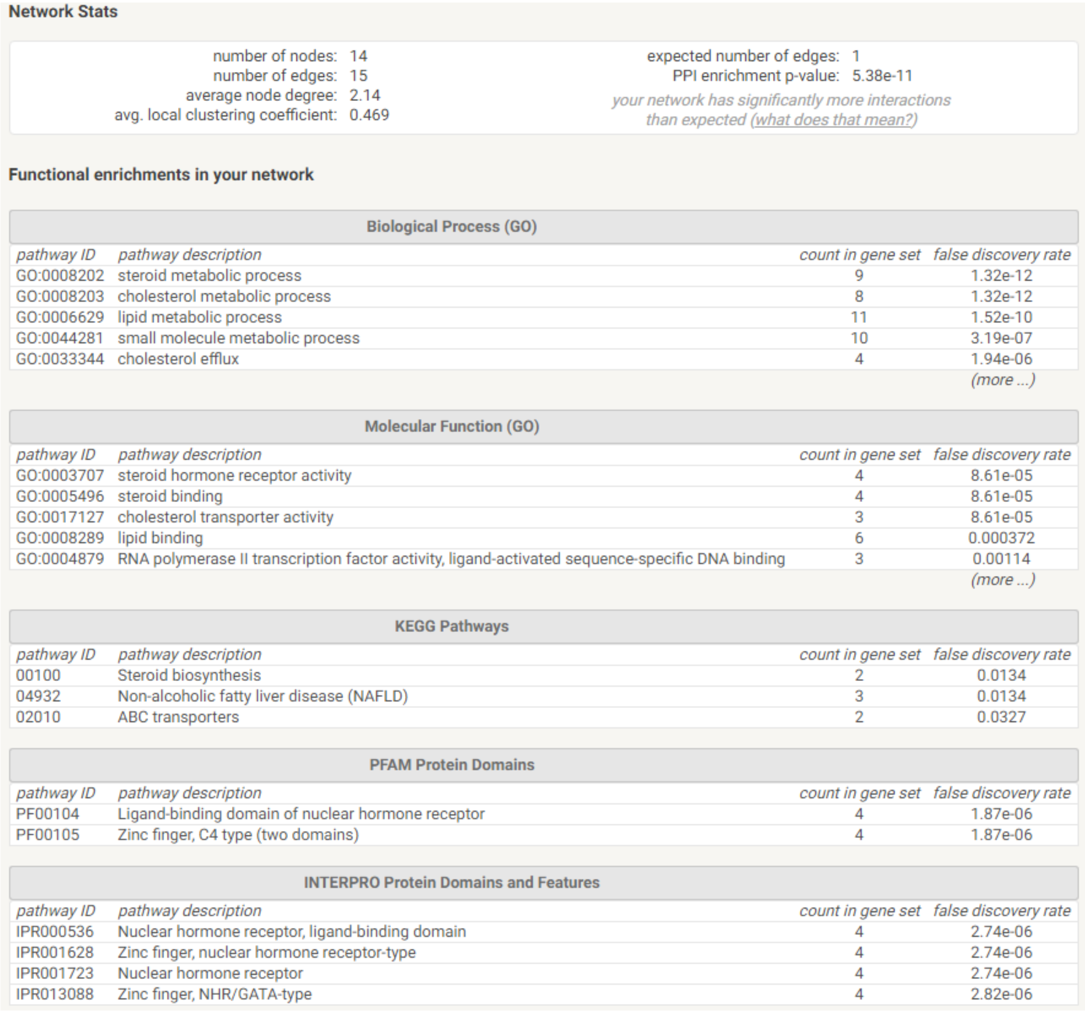
pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
00900	Terpenoid backbone biosynthesis	3	0.000187

Supplemental Figure 3A

SLOS



Supplemental Figure 3B



Network Stats

number of nodes: 14
number of edges: 15
average node degree: 2.14
avg. local clustering coefficient: 0.469

expected number of edges: 1
PPI enrichment p-value: 5.38e-11
your network has significantly more interactions than expected (what does that mean?)

Functional enrichments in your network

Biological Process (GO)

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0008202	steroid metabolic process	9	1.32e-12
GO:0008203	cholesterol metabolic process	8	1.32e-12
GO:0006629	lipid metabolic process	11	1.52e-10
GO:0044281	small molecule metabolic process	10	3.19e-07
GO:0033344	cholesterol efflux	4	1.94e-06

(more ...)

Molecular Function (GO)

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0003707	steroid hormone receptor activity	4	8.61e-05
GO:0005496	steroid binding	4	8.61e-05
GO:0017127	cholesterol transporter activity	3	8.61e-05
GO:0008289	lipid binding	6	0.000372
GO:0004879	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	3	0.00114

(more ...)

KEGG Pathways

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
00100	Steroid biosynthesis	2	0.0134
04932	Non-alcoholic fatty liver disease (NAFLD)	3	0.0134
02010	ABC transporters	2	0.0327

PFAM Protein Domains

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
PF00104	Ligand-binding domain of nuclear hormone receptor	4	1.87e-06
PF00105	Zinc finger, C4 type (two domains)	4	1.87e-06

INTERPRO Protein Domains and Features

pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
IPR000536	Nuclear hormone receptor, ligand-binding domain	4	2.74e-06
IPR001628	Zinc finger, nuclear hormone receptor-type	4	2.74e-06
IPR001723	Nuclear hormone receptor	4	2.74e-06
IPR013088	Zinc finger, NHR/GATA-type	4	2.82e-06