

Table S7A and S7B: All differentially expressed genes between OBESE and NASH with a fold change greater than 2log +1 or below 2log -1 were loaded into the STRING 10 software. **A)** Top 10 KEGG pathways identified by the STRING program with corresponding genes. **B)** Top 10 GO-Biological Processes as identified by String program. (For further explanation see <http://string.embl.de/>)

A

KEGG PATHWAY		Number Of Genes	p-value bonferroni	GENES					
1100	<i>Metabolic pathways</i>	25	8.85E-9	ACSS2	SQLE	ACAT2	DHCR7	CYP2C19	LSS
				MSMO1	IDO2	HMGCS1	ACSL4	FDFT1	PLA2G2A
				FDPS	IDI1	P4HA1	CYP51A1	ME1	TYMS
				SDS	ALDOC	CES1	ELOVL6	G6PC	PSPH
				HMGCR					
100	<i>Steroid biosynthesis</i>	6	7.41E-8	FDFT1	MSMO1	DHCR7	CYP51A1	LSS	SQLE
900	<i>Terpenoid backbone biosynthesis</i>	5	9.09E-6	FDPS	ACAT2	HMGCR	HMGCS1	IDI1	
1212	<i>Fatty acid metabolism</i>	6	2.12E-5	FADS2	ACAT2	ACSL4	SCD	ELOVL6	FADS1
3320	<i>PPAR signaling pathway</i>	6	1.76E-4	FADS2	ACSL4	SCD	ME1	ANGPTL4	FABP4
1040	<i>Biosynthesis of unsaturated fatty acids</i>	4	6.2E-4	FADS2	SCD	ELOVL6	FADS1		
1200	<i>Carbon metabolism</i>	6	1.92E-3	ACSS2	ALDOC	ACAT2	ME1	SDS	PSPH
5330	<i>Allograft rejection</i>	4	4.6E-3	HLA-DRB5	HLA-C	HLA-DQA1	HLA-DPB1		
4940	<i>Type I diabetes mellitus</i>	4	8.88E-3	HLA-DRB5	HLA-C	HLA-DQA1	HLA-DPB1		
4672	<i>Intestinal immune network for IgA production</i>	4	1.3E-2	HLA-DRB5	HLA-C	HLA-DQA1	HLA-DPB1		

B

Biological Processes		Number Of Genes	p-value bonferroni	GENES					
6695	<i>cholesterol biosynthetic process</i>	11	8.79E-14	MSMO1	HMGCR	HMGCS1	CYP51A1	SQLE	IDI1
				APOA4	FDFT1	FDPS	DHCR7	LSS	
16126	<i>sterol biosynthetic process</i>	11	4.32E-13	MSMO1	HMGCR	HMGCS1	CYP51A1	SQLE	IDI1
				APOA4	FDFT1	FDPS	DHCR7	LSS	
8203	<i>cholesterol metabolic process</i>	12	7.87E-10	HMGCS1	SQLE	DHCR7	MSMO1	HMGCR	IDI1
				APOA4	FDFT1	CYP51A1	LSS	FDPS	CETP
8202	<i>steroid metabolic process</i>	15	9.78E-10	HMGCS1	DHCR7	HMGCR	CYP2C19	FDFT1	DHRS2
				LSS	FDPS	CETP	SQLE	MSMO1	IDI1
				APOA4	CYP51A1	G6PC			
6629	<i>lipid metabolic process</i>	26	1.37E-9	DHRS2	ABCB4	SQLE	ANGPTL4	CTGF	ACAT2
				CYP51A1	ME1	HMGCR	CETP	APOA4	CYP2C18
				DHCR7	CYP2C19	LSS	SCD	FDPS	IDI1
				FADS2	ACSL4	FADS1	PLA2G2A	FABP4	ELOVL6
				NPAS2	G6PC				
16125	<i>sterol metabolic process</i>	12	2.6E-9	HMGCS1	SQLE	DHCR7	MSMO1	HMGCR	IDI1
				APOA4	FDFT1	CYP51A1	LSS	FDPS	CETP
44283	<i>small molecule biosynthetic process</i>	17	7.82E-9	HMGCS1	FADS2	DHCR7	HMGCR	ACSS2	FADS1
				FDFT1	LSS	SCD	FDPS	SDS	SQLE
				IDI1	APOA4	CYP51A1	ELOVL6	PSPH	

6694	<i>steroid biosynthetic process</i>	11	1.45E-8	HMGCS1	SQLE	DHCR7	MSMO1	HMGCR	IDI1
				APOA4	FDFT1	CYP51A1	LSS	FDPS	
46165	<i>alcohol biosynthetic process</i>	11	2.74E-8	HMGCS1	SQLE	DHCR7	MSMO1	HMGCR	IDI1
				APOA4	FDFT1	CYP51A1	LSS	FDPS	
44255	<i>cellular lipid metabolic process</i>	21	1.77E-7	HMGCR	ACSS2	CETP	ABCB4	APOA4	ANGPTL4
				CTGF	CYP2C18	FADS2	ACSL4	FADS1	CYP2C19
				SCD	PLA2G2A	FDPS	IDI1	FABP4	ELOVL6
				NPAS2	G6PC	ME1			