

## Supplementary Tables

**Table S1.** Forward and reverse primer sequences for genes analysed in the fetal and postnatal hepatic samples using qPCR and qRT-PCR.

Gene	Forward Sequence	Reverse Sequence
<i>MT-ND1</i>	CAACGTTCTAACACTCATCATTCC	GGGTCGTAGGGGTTCTTTGA
<i>MT-ND2</i>	AATTGCCACATAGGCTGAA	GGGGGAAGTCCTCCTATTGA
<i>MT-ND6</i>	GGGGGTATGATGGTAGTTTTTG	AACCCAGAATCCCCCGTAT
<i>RPS11</i>	ATCCGCCGAGACTACCTTCA	CCTGAAGCAGGGAGAAAGGT
<i>RPS25</i>	CCTCACCCCAGGACAGTTTC	CAGCATGGGGAAAGTGGGAT
<i>NDUFA7</i>	CGCCCTCGATTGTCATGTCT	CCCCCAGCCAAAGTCATAGG
<i>NDUFA12</i>	TCTGGGATGTGGATGGAAGC	TACGTACTGTTGTGGAGTGCC
<i>NDUFB4</i>	GAAGATCCTGCCTTGATTCTG	CAATTCCGAACAGAGCTCCTA
<i>CYCS</i>	GGTGATGTTGAGAAAGGCAAG	TTGTTTTTGTGGCATCTGTG
<i>UQCRB</i>	AACGCTTCTGTGTCAGGTCA	AACCCGGCAGCGTTGTAATA
<i>UQCRC1</i>	AAAACCTCCTCCGAAACGCT	CCGTATGTCAGGAGACTGCG
<i>COX5A</i>	CGCTGGGTGACATACTTCAA	GATGCGAACTGCACTAGCAA
<i>COX6B1</i>	CCAGACTGCTCCTTTTGACA	GATATGGGGCAAAGGGACTT
<i>COX7B</i>	AGATTGGCATAACAGTGGGGC	TGAGCAGCAGAGTGCTTAAAGA
<i>ATP5IF1</i>	CTCGGAATCGGGAGATAGTG	GGAAGTATCGCTCCTCTTCG
<i>ATP5MC3</i>	GCTGTCCCGAAGAGTGCAAG	CGCAGTGGTCTGAAACTCCC
<i>ATP5PO</i>	GACTCGGGTTTGACCTACAG	AAGAGCTGAGGCATAGCGAC

**Table S2.** Differentially expressed hepatic genes and proteins relevant to TCA cycle and OXPHOS in adolescent prenatally androgenized males as compared with adolescent male controls.

Gene ID	Template	Detection technique	Fold change	P Value	Q Value
<b>TCA cycle</b>					
CS	mRNA	RNAseq	-1.43	0.00	0.00
CS	protein	Proteomics	-1.12	0.06	0.35
ACO2	protein	Proteomics	-1.37	0.01	0.14
IDH2	mRNA	RNAseq	-1.29	0.01	0.07
IDH2	protein	Proteomics	-1.13	0.14	0.49
IDH3A	mRNA	RNAseq	-1.15	0.04	0.20
OGDH	mRNA	RNAseq	-1.16	0.00	0.05
OGDH	protein	Proteomics	-1.24	0.00	0.14
SUCLG1	mRNA	RNAseq	-1.13	0.00	0.04
SUCLA2	mRNA	RNAseq	-1.14	0.03	0.17
SUCLA2	protein	Proteomics	-1.51	0.18	0.53
SDHA	mRNA	RNAseq	-1.03	0.59	0.80
SDHA	protein	Proteomics	-1.62	0.02	0.22
SDHB	mRNA	RNAseq	-1.12	0.33	0.61
SDHB	protein	Proteomics	-1.17	0.02	0.24
SDHC	mRNA	RNAseq	-1.09	0.08	0.28
SDHC	protein	Proteomics	-1.31	0.38	0.72
SDHD	mRNA	RNAseq	-1.11	0.01	0.10
MDH2	mRNA	RNAseq	-1.09	0.04	0.19
MDH2	protein	Proteomics	-1.15	0.04	0.32

<b>OXPHOS Complex I</b>					
<i>NDUFA1</i>	mRNA	RNAseq	-1.11	0.03	0.17
<i>NDUFA12</i>	mRNA	RNAseq	-1.19	0.00	0.01
<i>NDUFA2</i>	mRNA	RNAseq	-1.13	0.02	0.14
<i>NDUFA2</i>	protein	Proteomics	-1.18	0.22	0.58
<i>NDUFA4</i>	mRNA	RNAseq	-1.20	0.00	0.03
<i>NDUFA4</i>	protein	Proteomics	-1.14	0.08	0.42
<i>NDUFA5</i>	mRNA	RNAseq	-1.27	0.00	0.02
<i>NDUFA7</i>	mRNA	RNAseq	-1.25	0.00	0.03
<i>NDUFA7</i>	protein	Proteomics	-1.81	0.03	0.28
<i>NDUFA9</i>	mRNA	RNAseq	-1.10	0.01	0.07
<i>NDUFA9</i>	protein	Proteomics	-1.20	0.02	0.22
<i>NDUFAB1</i>	mRNA	RNAseq	-1.19	0.00	0.01
<i>NDUFB1</i>	mRNA	RNAseq	-1.14	0.01	0.09
<i>NDUFB10</i>	mRNA	RNAseq	-1.12	0.02	0.14
<i>NDUFB11</i>	mRNA	RNAseq	-1.13	0.01	0.09
<i>NDUFB3</i>	mRNA	RNAseq	-1.22	0.00	0.01
<i>NDUFB4</i>	mRNA	RNAseq	-1.21	0.00	0.00
<i>NDUFB5</i>	mRNA	RNAseq	-1.16	0.00	0.02
<i>NDUFB6</i>	mRNA	RNAseq	-1.14	0.01	0.08
<i>NDUFB8</i>	mRNA	RNAseq	-1.11	0.01	0.07
<i>NDUFB9</i>	mRNA	RNAseq	-1.15	0.00	0.04
<i>NDUFB9</i>	protein	Proteomics	-1.15	0.05	0.34
<i>NDUFC1</i>	mRNA	RNAseq	-1.11	0.01	0.10
<i>NDUFC2</i>	mRNA	RNAseq	-1.13	0.02	0.12
<i>NDUFS3</i>	mRNA	RNAseq	-1.17	0.00	0.01
<i>NDUFS4</i>	mRNA	RNAseq	-1.16	0.00	0.03
<i>NDUFS7</i>	mRNA	RNAseq	-1.13	0.03	0.16
<i>NDUFS8</i>	mRNA	RNAseq	-1.15	0.00	0.03
<i>NDUFS8</i>	protein	Proteomics	-1.15	0.03	0.28
<i>NDUFV2</i>	mRNA	RNAseq	-1.24	0.00	0.00
<b>OXPHOS Complex III</b>					
<i>CYC1</i>	mRNA	RNAseq	-1.16	0.01	0.07
<i>CYC1</i>	protein	Proteomics	-1.25	0.01	0.14
<i>CYCS</i>	mRNA	RNAseq	-1.23	0.00	0.05
<i>UQCRB</i>	mRNA	RNAseq	-1.26	0.00	0.00
<i>UQCRC1</i>	mRNA	RNAseq	-1.15	0.01	0.07
<i>UQCRC2</i>	mRNA	RNAseq	-1.12	0.01	0.10
<i>UQCRC2</i>	protein	Proteomics	-1.14	0.05	0.33
<i>UQCRFS1</i>	mRNA	RNAseq	-1.12	0.02	0.13
<i>UQCRH</i>	mRNA	RNAseq	-1.20	0.00	0.01
<b>OXPHOS Complex IV</b>					
<i>MT-CO1</i>	mRNA	RNAseq	-1.15	0.03	0.17
<i>MT-CO2</i>	mRNA	RNAseq	-1.20	0.01	0.09
<i>MT-CO2</i>	protein	Proteomics	-1.38	0.10	0.44
<i>COX4I1</i>	mRNA	RNAseq	-1.08	0.03	0.17
<i>COX5A</i>	mRNA	RNAseq	-1.30	0.00	0.00
<i>COX5B</i>	mRNA	RNAseq	-1.14	0.00	0.06
<i>COX6B1</i>	mRNA	RNAseq	-1.12	0.00	0.05
<i>COX6C</i>	mRNA	RNAseq	-1.15	0.00	0.03
<i>COX7A1</i>	mRNA	RNAseq	-1.64	0.02	0.13
<i>COX7A2</i>	mRNA	RNAseq	-1.12	0.02	0.14
<i>COX7B</i>	mRNA	RNAseq	-1.19	0.00	0.03

OXPHOS Complex V					
<i>MT-ATP8</i>	mRNA	RNAseq	-1.18	0.03	0.16
<i>MT-ATP8</i>	protein	Proteomics	-1.23	0.57	0.83
<i>ATP5F1A</i>	mRNA	RNAseq	-1.11	0.03	0.17
<i>ATP5F1A</i>	protein	Proteomics	-1.10	0.11	0.45
<i>ATP5F1B</i>	mRNA	RNAseq	-1.12	0.01	0.07
<i>ATP5F1C</i>	mRNA	RNAseq	-1.15	0.00	0.04
<i>ATP5F1E</i>	mRNA	RNAseq	-1.12	0.02	0.13
<i>ATP5F1E</i>	protein	Proteomics	-1.14	0.37	0.71
<i>ATP5IF1</i>	mRNA	RNAseq	-1.17	0.00	0.01
<i>ATP5MC1</i>	mRNA	RNAseq	-1.17	0.01	0.09
<i>ATP5MC3</i>	mRNA	RNAseq	-1.19	0.00	0.02
<i>ATP5MD</i>	mRNA	RNAseq	-1.18	0.00	0.03
<i>ATP5MF</i>	mRNA	RNAseq	-1.11	0.03	0.17
<i>ATP5MF</i>	protein	Proteomics	-1.41	0.13	0.48
<i>ATP5MG</i>	mRNA	RNAseq	-1.11	0.00	0.05
<i>ATP5PB</i>	mRNA	RNAseq	-1.10	0.03	0.17
<i>ATP5PD</i>	mRNA	RNAseq	-1.09	0.04	0.18
<i>ATP5PD</i>	protein	Proteomics	-1.10	0.28	0.64
<i>ATP5PF</i>	mRNA	RNAseq	-1.11	0.03	0.17
<i>ATP5PF</i>	protein	Proteomics	-1.12	0.41	0.73
<i>ATP5PO</i>	mRNA	RNAseq	-1.13	0.01	0.09
<i>ATP5PO</i>	protein	Proteomics	-1.14	0.09	0.43

Fold change is PA compared to control animals. P values cited are nominal values, false discovery rate adjusted Q values were calculated by Benjamini and Hochberg method.

**Table S3.** Correlation between hepatic ATP levels and OXPHOS genes in adolescent control and prenatally androgenized males.

OXPHOS	Correlation with hepatic ATP	
Gene ID	Pearson r	P value
<i>NDUFA1</i>	0.31	0.06
<i>NDUFA4</i>	0.38	0.03
<i>NDUFA12</i>	0.27	0.09
<i>NDUFAB1</i>	0.46	0.01
<i>NDUFB3</i>	0.31	0.06
<i>NDUFB4</i>	0.37	0.03
<i>NDUFB10</i>	0.31	0.06
<i>NDUFA9</i>	0.56	0.00
<i>NDUFB5</i>	0.36	0.04
<i>NDUFB11</i>	0.31	0.06
<i>NDUFC1</i>	0.28	0.08
<i>NDUFS4</i>	0.39	0.02
<i>NDUFS7</i>	0.42	0.02
<i>NDUFV2</i>	0.30	0.07
<i>UQCRB</i>	0.27	0.09
<i>UQCRC2</i>	0.37	0.03
<i>UQCRFS1</i>	0.35	0.04
<i>COX5A</i>	0.27	0.09
<i>COX5B</i>	0.33	0.05
<i>COX7B</i>	0.35	0.04
<i>ATP5F1B</i>	0.27	0.09
<i>ATP5MC1</i>	0.32	0.05
<i>ATP5MD</i>	0.32	0.06

<i>ATP5MG</i>	0.36	0.04
<i>ATP5PD</i>	0.39	0.02
<i>ATP5PF</i>	0.30	0.07
<i>ATP5PO</i>	0.40	0.02

**Table S4.** Differentially expressed genes and proteins relevant to hepatic fatty acid and cholesterol metabolism in adolescent prenatally androgenized males as compared with adolescent male controls.

Gene ID	Template	Detection technique	Fold change	P value	Q Value
<b>Hepatic FA uptake and trafficking</b>					
<i>CD36</i>	mRNA	RNAseq	1.26	0.11	0.34
<i>SLC27A5</i>	mRNA	RNAseq	1.11	0.06	0.23
<i>SLC27A5</i>	protein	Proteomics	1.29	0.00	0.12
<i>FABP5</i>	mRNA	RNAseq	1.40	0.04	0.19
<b>Mitochondrial uptake of FA</b>					
<i>CPT1A</i>	mRNA	RNAseq	1.33	0.00	0.01
<i>CPT1A</i>	protein	Proteomics	1.22	0.01	0.14
<i>CPT1B</i>	mRNA	RNAseq	1.42	0.00	0.01
<i>SLC25A20</i>	mRNA	RNAseq	1.16	0.09	0.30
<i>CPT2</i>	mRNA	RNAseq	1.15	0.01	0.09
<i>CPT2</i>	protein	Proteomics	1.76	0.10	0.44
<i>CRAT</i>	mRNA	RNAseq	1.17	0.01	0.09
<b>Fatty acid activation</b>					
<i>ACSS2</i>	mRNA	RNAseq	-2.03	0.00	0.02
<i>ACSS2</i>	protein	Proteomics	-1.32	0.48	0.79
<i>ACSL3</i>	mRNA	RNAseq	-1.44	0.00	0.01
<i>ACSL5</i>	mRNA	RNAseq	-1.19	0.02	0.11
<i>ACSL5</i>	protein	Proteomics	-1.23	0.00	0.13
<b>Mitochondrial beta oxidation</b>					
<i>ACADSB</i>	mRNA	RNAseq	-1.25	0.00	0.05
<i>ACADSB</i>	protein	Proteomics	-1.19	0.02	0.25
<i>ECHS1</i>	mRNA	RNAseq	-1.17	0.01	0.09
<i>ECHS1</i>	protein	Proteomics	-1.16	0.02	0.24
<i>DECR1</i>	mRNA	RNAseq	-1.22	0.00	0.06
<i>DECR1</i>	protein	Proteomics	-1.14	0.07	0.39
<b>Peroxisomal beta oxidation</b>					
<i>ACOX2</i>	protein	Proteomics	5.02	0.00	0.08
<i>EHHADH</i>	protein	Proteomics	3.53	0.00	0.10
<i>ACAA1</i>	protein	Proteomics	1.57	0.00	0.07
<i>CROT</i>	mRNA	RNAseq	1.19	0.02	0.11
<b>Hepatic FA lipogenesis, elongation and desaturation</b>					
<i>MLYCD</i>	mRNA	RNAseq	1.2	0.00	0.06
<i>ACLY</i>	mRNA	RNAseq	-1.9	0.00	0.00
<i>ACLY</i>	protein	Proteomics	-2.0	0.03	0.29
<i>ACACA</i>	mRNA	RNAseq	-1.8	0.00	0.01
<i>FASN</i>	mRNA	RNAseq	-2.5	0.00	0.03
<i>FASN</i>	protein	Proteomics	-2.5	0.04	0.32
<i>ELOVL6</i>	mRNA	RNAseq	-2.5	0.00	0.00
<i>SCD</i>	mRNA	RNAseq	-4.3	0.00	0.00
<b>Cholesterol trafficking and metabolism</b>					
<i>NPC1</i>	mRNA	RNAseq	-1.34	0.00	0.06
<i>NPC2</i>	mRNA	RNAseq	-1.02	0.60	0.81
<i>SOAT2</i>	mRNA	RNAseq	1.2	0.00	0.03
<b>Lipid droplet accumulation</b>					
<i>PLIN2</i>	mRNA	RNAseq	1.95	0.01	0.07
<i>PLIN5</i>	mRNA	RNAseq	1.27	0.00	0.03

Fold change is PA compared to control animals. P values cited are nominal values, false discovery rate adjusted Q values were calculated by Benjamini and Hochberg method.

**Table S5.** Differentially expressed genes and proteins relevant to hepatic glucose metabolism in adolescent prenatally androgenized males as compared with adolescent male controls.

Gene ID	Template	Detection technique	Fold change	P value	Q Value
<b>Glycolysis</b>					
<i>HK1</i>	mRNA	RNAseq	1.01	0.87	0.95
<i>HK2</i>	mRNA	RNAseq	-1.09	0.11	0.34
<i>HK3</i>	mRNA	RNAseq	-1.04	0.73	0.88
<i>PFKL</i>	mRNA	RNAseq	-1.09	0.37	0.65
<i>PFKL</i>	protein	Proteomics	-1.28	0.01	0.14
<i>PKLR</i>	mRNA	RNAseq	-1.05	0.43	0.69
<i>PKLR</i>	protein	Proteomics	-1.33	0.03	0.28
<b>Pyruvate transport</b>					
<i>MPC1</i>	mRNA	RNAseq	1.26	0.01	0.06
<i>MPC2</i>	mRNA	RNAseq	-1.05	0.34	0.62
<b>Pyruvate dehydrogenase complex</b>					
<i>PDHA1</i>	mRNA	RNAseq	-1.09	0.15	0.40
<i>PDHA1</i>	protein	Proteomics	-1.42	0.00	0.08
<i>PDHB</i>	mRNA	RNAseq	-1.10	0.04	0.19
<i>DLAT</i>	mRNA	RNAseq	-1.14	0.00	0.03
<i>DLAT</i>	protein	Proteomics	-1.33	0.03	0.29
<b>PDHC kinases</b>					
<i>PDK1</i>	mRNA	RNAseq	1.01	0.88	0.95
<i>PDK2</i>	mRNA	RNAseq	1.04	0.37	0.65
<i>PDK3</i>	mRNA	RNAseq	-1.10	0.17	0.42
<i>PDK4</i>	mRNA	RNAseq	1.55	0.00	0.01
<b>Gluconeogenesis</b>					
<i>PC</i>	mRNA	RNAseq	1.82	0.00	0.01
<i>PC</i>	protein	Proteomics	1.17	0.16	0.52
<i>PCK1</i>	mRNA	RNAseq	1.12	0.18	0.44
<i>FBP1</i>	mRNA	RNAseq	1.03	0.73	0.88
<i>FBP1</i>	protein	Proteomics	1.13	0.07	0.38
<i>FBP2</i>	mRNA	RNAseq	1.54	0.01	0.09
<i>G6PC2</i>	mRNA	RNAseq	1.21	0.08	0.28
<b>Glycogen synthesis</b>					
<i>GYS2</i>	mRNA	RNAseq	1.21	0.01	0.11

Fold change is PA compared to control animals. P values cited are nominal values, false discovery rate adjusted Q values were calculated by Benjamini and Hochberg method.

**Table S6.** Correlation between hepatic free cholesterol levels and OXPHOS genes in adolescent control and prenatally androgenized males.

OXPHOS	Correlation with hepatic free cholesterol	
	Pearson r	P value
<b>Complex I</b>		
<i>NDUFA1</i>	-0.27	0.16
<i>NDUFA2</i>	-0.16	0.41
<i>NDUFA4</i>	-0.32	0.09
<i>NDUFA5</i>	-0.48	0.01
<i>NDUFA7</i>	-0.28	0.14
<i>NDUFA9</i>	-0.44	0.01
<i>NDUFA12</i>	-0.39	0.03
<i>NDUFAB1</i>	-0.49	0.00
<i>NDUFB1</i>	-0.14	0.47

<i>NDUFB3</i>	-0.42	0.02
<i>NDUFB4</i>	-0.33	0.08
<i>NDUFB5</i>	-0.39	0.04
<i>NDUFB6</i>	-0.39	0.04
<i>NDUFB8</i>	-0.30	0.12
<i>NDUFB9</i>	-0.41	0.03
<i>NDUFB10</i>	-0.42	0.02
<i>NDUFB11</i>	-0.24	0.22
<i>NDUFC1</i>	-0.25	0.20
<i>NDUFC2</i>	-0.29	0.13
<i>NDUFS3</i>	-0.44	0.01
<i>NDUFS4</i>	-0.41	0.02
<i>NDUFS7</i>	-0.15	0.45
<i>NDUFS8</i>	-0.26	0.17
<i>NDUFV2</i>	-0.46	0.01
<b>Complex III</b>		
<i>CYC1</i>	-0.31	0.10
<i>CYCS</i>	-0.31	0.10
<i>UQCRB</i>	-0.44	0.02
<i>UQCRC1</i>	-0.30	0.11
<i>UQCRC2</i>	-0.21	0.27
<i>UQCRFS1</i>	-0.33	0.08
<i>UQCRH</i>	-0.32	0.09
<b>Complex IV</b>		
<i>MT-CO2</i>	-0.13	0.5
<i>COX5A</i>	-0.39	0.03
<i>COX5B</i>	-0.25	0.21
<i>COX6B1</i>	-0.35	0.07
<i>COX6C</i>	-0.35	0.06
<i>COX7B</i>	-0.42	0.02
<b>Complex V</b>		
<i>MT-ATP8</i>	-0.33	0.08
<i>ATP5F1A</i>	-0.29	0.13
<i>ATP5F1B</i>	-0.18	0.34
<i>ATP5F1E</i>	-0.29	0.13
<i>ATP5F1C</i>	-0.35	0.06
<i>ATP5IF1</i>	-0.44	0.01
<i>ATP5MC1</i>	-0.20	0.29
<i>ATP5MC3</i>	-0.28	0.10
<i>ATP5MD</i>	-0.36	0.05
<i>ATP5MF</i>	-0.39	0.03
<i>ATP5MG</i>	-0.45	0.01
<i>ATP5PF</i>	-0.38	0.04
<i>ATP5PD</i>	-0.37	0.05
<i>ATP5PO</i>	-0.39	0.04

**Table S7.** Differentially expressed genes and proteins relevant to hepatic mitochondrial transporters, translocases and channels in adolescent prenatally androgenized males as compared with adolescent male controls.

Gene ID	Template	Detection technique	Fold change	P value	Q Value
Mitochondrial transporters, translocases and channels					
<i>CLIC2</i>	mRNA	RNAseq	-1.33	0.00	0.05
<i>SFXN3</i>	mRNA	RNAseq	-1.34	0.02	0.12
<i>SLC25A3</i>	mRNA	RNAseq	-1.13	0.00	0.01
<i>SLC25A5</i>	mRNA	RNAseq	-1.28	0.00	0.03

<i>SLC25A11</i>	mRNA	RNAseq	-1.11	0.02	0.13
<i>SLC25A12</i>	mRNA	RNAseq	-1.24	0.01	0.06
<i>SLC25A17</i>	mRNA	RNAseq	-1.10	0.03	0.15
<i>SLC25A25</i>	mRNA	RNAseq	1.31	0.02	0.13
<i>SLC25A29</i>	mRNA	RNAseq	1.39	0.00	0.02
<i>SLC25A30</i>	mRNA	RNAseq	1.95	0.00	0.02
<i>SLC25A32</i>	mRNA	RNAseq	1.11	0.02	0.14
<i>SLC25A34</i>	mRNA	RNAseq	1.52	0.00	0.00
<i>SLC25A35</i>	mRNA	RNAseq	-1.40	0.00	0.01
<i>SLC25A42</i>	mRNA	RNAseq	1.36	0.00	0.01
<i>SLC25A44</i>	mRNA	RNAseq	1.12	0.01	0.10
<i>SLC25A45</i>	mRNA	RNAseq	1.89	0.00	0.02
<i>SLC25A47</i>	mRNA	RNAseq	1.77	0.00	0.03
<i>SLC25A48</i>	mRNA	RNAseq	1.25	0.00	0.02
<i>TIMM8B</i>	mRNA	RNAseq	1.13	0.01	0.10
<i>TIMM9</i>	mRNA	RNAseq	-1.23	0.00	0.01
<i>TIMM21</i>	mRNA	RNAseq	-1.11	0.00	0.05
<i>TIMM23</i>	mRNA	RNAseq	-1.23	0.00	0.01
<i>TIMM50</i>	mRNA	RNAseq	-1.19	0.00	0.01
<i>TIMMDC1</i>	mRNA	RNAseq	-1.15	0.00	0.02
<i>TOMM5</i>	mRNA	RNAseq	-1.15	0.01	0.09
<i>TOMM22</i>	mRNA	RNAseq	-1.16	0.02	0.13
<i>TOMM34</i>	mRNA	RNAseq	-1.21	0.02	0.14
<i>TOMM40</i>	mRNA	RNAseq	-1.21	0.00	0.05
<i>TOMM40</i>	protein	Proteomics	-1.30	0.18	0.54
<i>TOMM70A</i>	mRNA	RNAseq	-1.08	0.02	0.12
<i>VDAC2</i>	mRNA	RNAseq	-1.10	0.01	0.06
<i>VDAC3</i>	mRNA	RNAseq	-1.10	0.01	0.10

Fold change is PA compared to control animals. P values cited are nominal values, false discovery rate adjusted Q values were calculated by Benjamini and Hochberg method.

**Table S8.** Differentially expressed genes and proteins relevant to hepatic mitochondrial quality control in adolescent prenatally androgenized males as compared with adolescent male controls.

Gene ID	Template	Detection technique	Fold change	P value	Q Value
<b>Mitochondrial Fusion</b>					
<i>MFN1</i>	mRNA	RNAseq	1.0	0.57	0.79
<i>MFN2</i>	mRNA	RNAseq	1.1	0.08	0.28
<i>OPA1</i>	mRNA	RNAseq	-1.1	0.03	0.17
<i>OPA1</i>	protein	Proteomics	-1.1	0.50	0.80
<b>Mitochondrial Fission</b>					
<i>DNM1L</i>	mRNA	RNAseq	-1.2	0.00	0.03
<i>MTFP1</i>	mRNA	RNAseq	-1.4	0.00	0.05
<i>MTFR1</i>	mRNA	RNAseq	-1.1	0.01	0.07
<b>Mitophagy</b>					
<i>CALCOCO2</i>	mRNA	RNAseq	-1.3	0.00	0.00
<i>FUNDC1</i>	mRNA	RNAseq	-1.1	0.00	0.04
<i>GABARAPL2</i>	mRNA	RNAseq	-1.1	0.00	0.01
<i>OPTN</i>	mRNA	RNAseq	-1.1	0.01	0.09
<i>PARK2</i>	mRNA	RNAseq	1.17	0.01	0.07
<i>PARK7</i>	mRNA	RNAseq	-1.16	0.00	0.01
<i>PHB1</i>	mRNA	RNAseq	-1.2	0.00	0.03
<i>PINK1</i>	mRNA	RNAseq	-1.1	0.04	0.19
<i>PGAM5</i>	mRNA	RNAseq	-1.1	0.01	0.07
<i>RHOT1</i>	mRNA	RNAseq	-1.1	0.00	0.03

<i>USP30</i>	mRNA	RNAseq	1.1	0.00	0.01
<i>ZNF746</i>	mRNA	RNAseq	1.1	0.01	0.08

Fold change is PA compared to control animals. P values cited are nominal values, false discovery rate adjusted Q values were calculated by Benjamini and Hochberg method.

**Table S9.** Correlation between ROS levels and hepatic lipid metabolism, detoxification potential and fibrosis effectors in adolescent control and prenatally androgenized males.

Correlation with hepatic ROS levels	Pearson r	P value
<b>Hepatic cholesterol metabolism</b>		
Hepatic <i>CYP7A1</i> expression	-0.42	0.03
Hepatic <i>NPC1</i> expression	-0.41	0.04
Hepatic free cholesterol	0.36	0.06
<b>Mitochondrial FA uptake</b>		
Hepatic <i>CPT1A</i> expression	0.54	0.00
Hepatic <i>CPT1B</i> expression	0.64	0.00
<b>Regulation of lipid metabolism</b>		
Hepatic <i>PPARA</i> expression	0.40	0.04
Hepatic <i>NR1I2</i> expression	0.69	0.00
<b>Liver detoxification potential</b>		
Hepatic <i>GSS</i> expression	-0.38	0.05
Hepatic <i>GSTM1</i> expression	-0.36	0.07
Hepatic <i>GSTO1</i> expression	-0.51	0.01
Hepatic <i>GPX4</i> expression	-0.43	0.02
Hepatic <i>GPX7</i> expression	0.36	0.06
<b>Fibrosis effectors</b>		
Hepatic <i>FGFR2</i> expression	0.47	0.01
Hepatic <i>FGFR3</i> expression	0.42	0.03
Hepatic <i>COL4A1</i> expression	0.51	0.01
Hepatic <i>COL4A2</i> expression	0.52	0.01
Hepatic <i>COL4A4</i> expression	0.33	0.09
Hepatic <i>COL18A1</i> expression	0.66	0.00
Hepatic <i>COL27A1</i> expression	0.47	0.01