

## Supplemental Tables and Figure

**Supplemental Table1.** The composition of experimental diets

Ingredient of diet (%)	HS	BGP	TP
	g/ 100g diet		
Corn starch	12.95	10.22	12.95
Casein	20	19.78	20
Cellulose	5	3.09	5
Sucrose	50	50	50
Soybean oil	7	6.89	7
AIN 93G mineral mix	3.5	3.5	3.5
AIN 93 vitamin mix	1	1	1
L-cystine	0.3	0.3	0.3
Choline	0.25	0.25	0.25
Bitter gourd powder	-	5	-
Testosterone propionate	-	-	0.007
kcal/g	3.948	3.948	3.948
CHO calorie/ total calories (%)	63.78	63.78	63.78
Fat calorie/ total calories (%)	15.96	15.96	15.96
Protein calorie/ total calories (%)	20.26	20.26	20.26

**Supplemental Table2.** The list of Taqman<sup>®</sup> primers used in the qPCR analysis

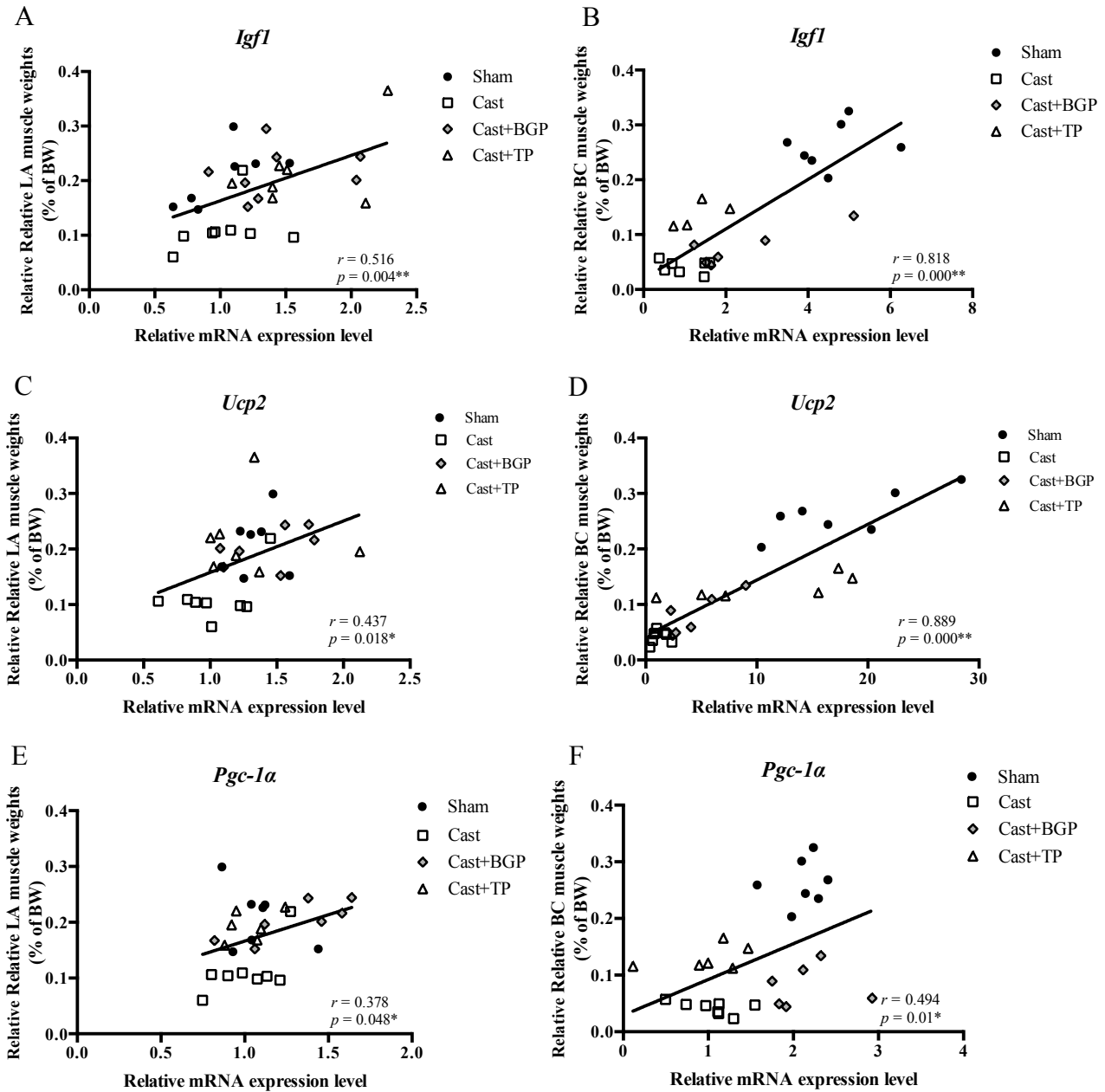
<b>Gene symbol</b>	<b>ID</b>	<b>Gene name</b>
PGC1 $\alpha$	Mm01208835_m1	Peroxisome proliferator activated receptor, gamma, coactivator 1 $\alpha$
Tfam	Mm00447485_m1	transcription factor A, mitochondrial
Nrf1	Mm01135606_m1	nuclear respiratory factor 1
Fis1	Mm00481580_m1	fission 1 (mitochondrial outer membrane) homolog (yeast)
Opa1	Mm01349707_g1	optic atrophy 1
Mfn1	Mm00612599_m1	mitofusin 1
Mfn2	Mm00500120_m1	mitofusin 2
Cox7a1	Mm00438296_m1	cytochrome c oxidase subunit VIIa 1
Cox8b	Mm00432648_m1	cytochrome c oxidase subunit VIIIb
UCP2	Mm00627599_m1	uncoupling protein 2 (mitochondrial, proton carrier)
UCP3	Mm00494077_m1	uncoupling protein 3 (mitochondrial, proton carrier)
Pax7	Mm01354484_m1	paired box 7
MyoD1	Mm00440387_m1	myogenic differentiation 1
Myog	Mm00446194_m1	Myogenin
Myf5	Mm00435125_m1	myogenic factor 5
Myf6	Mm00435126_m1	myogenic factor 6
Igf1	Mm00439560_m1	insulin like growth factor 1
Igf1r	Mm00802831_m1	insulin like growth factor 1 receptor
Eif3f	Mm00517953_m1	eukaryotic translation initiation factor 3, subunit F
Mstn	Mm01254559_m1	Myostatin
Gapdh	Mm99999915_g1	Glyceraldehyde 3-phosphate dehydrogenase

**Supplemental Table3.** The potential androgen receptor binding sites upstream of Ucp2 genes.

Strand	Start	End	p-value	q-value	Matched Sequence
+	-4861	-4845	0.000186	0.37	TAGCAGATGATGTCCTT
-	-4861	-4845	0.000218	0.37	AAGGACATCATCTGCTA
+	-4565	-4549	0.000224	0.37	TTGAAGACTCTGTTCCC
-	-4565	-4549	0.000116	0.37	GGGAACAGAGTCTTCAA
-	-4379	-4363	8.27E-05	0.37	GAGCACTGCGTGTCTG
+	-4379	-4363	8.45E-05	0.37	CAGGACACGCAGTGCTC
+	-4377	-4361	0.000355	0.461	GGACACGCAGTGCTCCT
-	-4377	-4361	0.000372	0.461	AGGAGCACTGCGTGTCC
-	-2475	-2459	0.000943	0.718	GGGTCACCGGTGTGCTT
+	-1511	-1495	0.000878	0.718	AAGAGCAATCAGTGCTC
-	-1511	-1495	0.000905	0.718	GAGCACTGATTGCTCTT
-	-1365	-1349	0.00078	0.718	GGGTGGATAGTGATCCC
+	-772	-756	0.000735	0.718	AAGCAAAAAGGGTTCCA

Eight potentials ARE in the mice UCP2 promoter were predicted by using the FIMO-MEME suite software. The Ucp2 (*Mus musculus*) promoter region sequences and ARE motif (Martix ID: MA0007.3) were accessed from eukaryotic promoter database (EPD) and JASPAR database, respectively.

**Supplemental Figure 1.**



**Supplemental Figure 1. Correlation between the relative weight of androgen responsive muscle and the level of muscle mRNA expression.** The expression of *Igf1*(A), *Ucp2* (C)and *Pgc1a* (E) show positive correlation with relative levator ani (LA) muscle weight (n=7-8/group). The expression of *Igf1*(B), *Ucp2* (D)and *Pgc1a* (F) show positive correlation with relative bulbocavernosus (BC) muscle weight(n=7-8/group). Data were analyzed by Pearson’s Correlation. \* denotes significant correlation,  $p < 0.05$ . \*\* denotes significant correlation,  $p < 0.01$ .