Supplementary File

Table S1. Ingredients and nutrition levels of the basal ration

| Items	% of Dry Matter
Ingredients	
Corn	11.5
Wheat bran	17.85
Soybean meal	3.2
Rapeseed meal	2.8
Calcium hydrophosphate	0.25
Calcium carbonate	0.8
Sodium chloride	0.35
Sodium bicarbonate	0.4
Premix (trace minerals and vitamins)[a]	0.35
Straw	24
Distillers' grains	38.5
In total	100
Nutrition levels	
Dry matter	57.22
Net energy for maintain, NEm (MJ/kg)[b]	5.37
Crude protein, CP	11.98
Ether extract, EE	2.75
Crude fiber, CF	17.30
Neutral detergent fiber, NDF	55.91
Acid detergent fiber, ADF	36.03
Calcium, Ca	0.36
Phosphorus, P	0.30

[a] The premix provided trace minerals and vitamins to the basal ration containing per kilogram of 4500 IU VA, 600 IU VD, 120 IU VE, 0.10 mg Co, 10 mg Cu, 0.50 mg I, 50 mg Mn, 0.25 mg Se, 70 mg Zn, 120 mg Fe. [b] NEm were calculated values, while the others were measured values.

**Table S2 Primer sequences used in the real-time PCR**

Gene	Sequence (5′–3′)	GenBank accession number	Product length(bp)
SCARB1	F: CATCAAGCAGCAGGTCCTCA R: CTTGTGCCTGAACTCCCTGT	XM_014481097.1	196
SCARB2	F: TCATTGAGGCCCTGCTGAAG R: GGGAGAGACGTCGTGTTTGA	XM_005899156.2	128
LDLR	F: TGCAAGTCTGTCACCTGCAA R: AACAGCCTTCTTCGTCCGAG	XM_005890784.2	127
SREBF2	F: ATGTCCTTCTGATGTCGCCT R: TCCGGCTCATCTTTGACCTT	XM_014481975.1	124
HMGCR	F: CTTTTCCGAATGCATGGCCT R: TGTCGCTGCTCAAAACATCC	XM_014476480.1	172
HMGCL	F: TGACCCCAAACTTCAAAGGC R: TCAAACCGCTGCAAACTCTC	XM_005905159.1	136
LSS	F: CGGTATTTGGAACTGCGCTT R: ACAGCCAACCAAAACTTCCC	XM_005902333.2	148
SQLE	F: GTTGGGCTGCTTTCCGTATT R: TACTGAAAATGGCTCGGGGT	XM_005909911.1	133
STAR	F: CCCGAGACTTTGTGAGCGTA R: CTGAGCAGCCAGGTGAGTTT	XM_014481563.1	190
CYP11A1	F: CCGAGGCCCAGAAGTTCATT R: AATTGTGTCCCATGCGGCTA	XM_005905795.2	137
CYP19A1	F: GGTGTCCGAAGTTGTGCCTA R: ACCTGCAGTGGGAAATGAGG	XM_005900467.1	146
HSD17B1	F: CCGTCCCAGAGCTTCAAAGT R: AATCTGCATCCCTCACGTCC	XM_005899199.1	136
HSD17B8	F: AACTTGGACGACACGGGATC R: GCCAAGAATGCGACGACATC	XM_005891389.1	166
ESR1	F: CAAGAACGTGGTGCCTCTCT R: GCTGGGGAAATTCTCTGCCT	XM_014476936.1	190
ESR2	F: TCCTATGTAGAGAGCCGCCA R: AACTGATGGCTGGCAATGGA	XM_014478950.1	180
VEGFA	F: GGGGCTGCTGTAATGACGA R: GCTGGCTTTGGTGAGGTTTG	XM_014479536.1	96
NOS2	F: AGAGCTGTGTTCTTCGCCTC R: TTTCCGATCTCCCCGTCTCT	XM_014478521.1	97
GAPDH	F: TGTTGTGGATCTGACCTGCC R: AAAGTGGTCGTTGAGGGCAA	XM_014482068.1	199
β-actin	F: TGGCGCTTGACTCAGGATTT	XM_005893519.1	80

R: CAATCAAGTCCTCGGCCACA

Abbreviations: SCARB1, scavenger receptor class B member 1; SCARB2, scavenger receptor class B mmber 2; LDLR, lowdensity lipoprotein receptor; SREBF2, sterol regulatory element binding transcription factor 2; HMGCR, 3-Hydroxy-3-Methylglutaryl-CoA Reductase; HMGCL, 3-Hydroxy-3-Methylglutaryl-CoA Lyase; LSS, lanosterol synthase; SQLE, squalene epoxidase; STAR, steroidogenic acute regulatory protein; CYP11A1, cytochrome P450 family 11 subfamily a member 1; CYP19A1, cytochrome P450 family 19 subfamily a member 1; HSD17B1, hydroxysteroid 17-beta dehydrogenase 1; HSD17B8, hydroxysteroid 17-beta dehydrogenase 8; ESR1, Estrogen Receptor 1; ESR2, Estrogen Receptor 2; VEGFA, vascular endothelial growth factor A; NOS2, nitric oxide synthase 2; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.
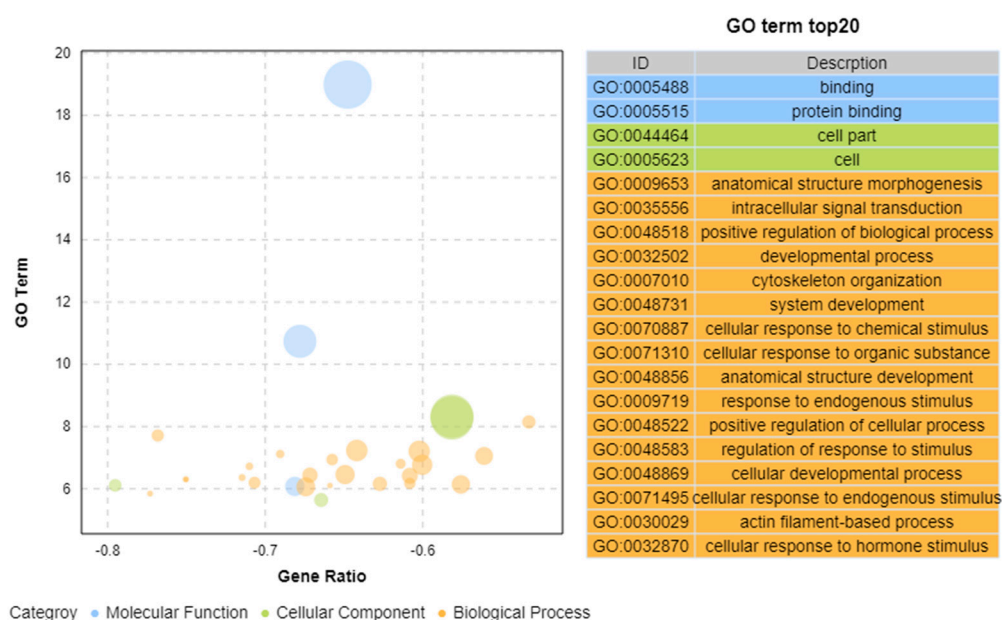
Figure S1. The top-20 enriched GO terms between Control and NCG female yaks, including cellular component, biological process, as well as molecular function.
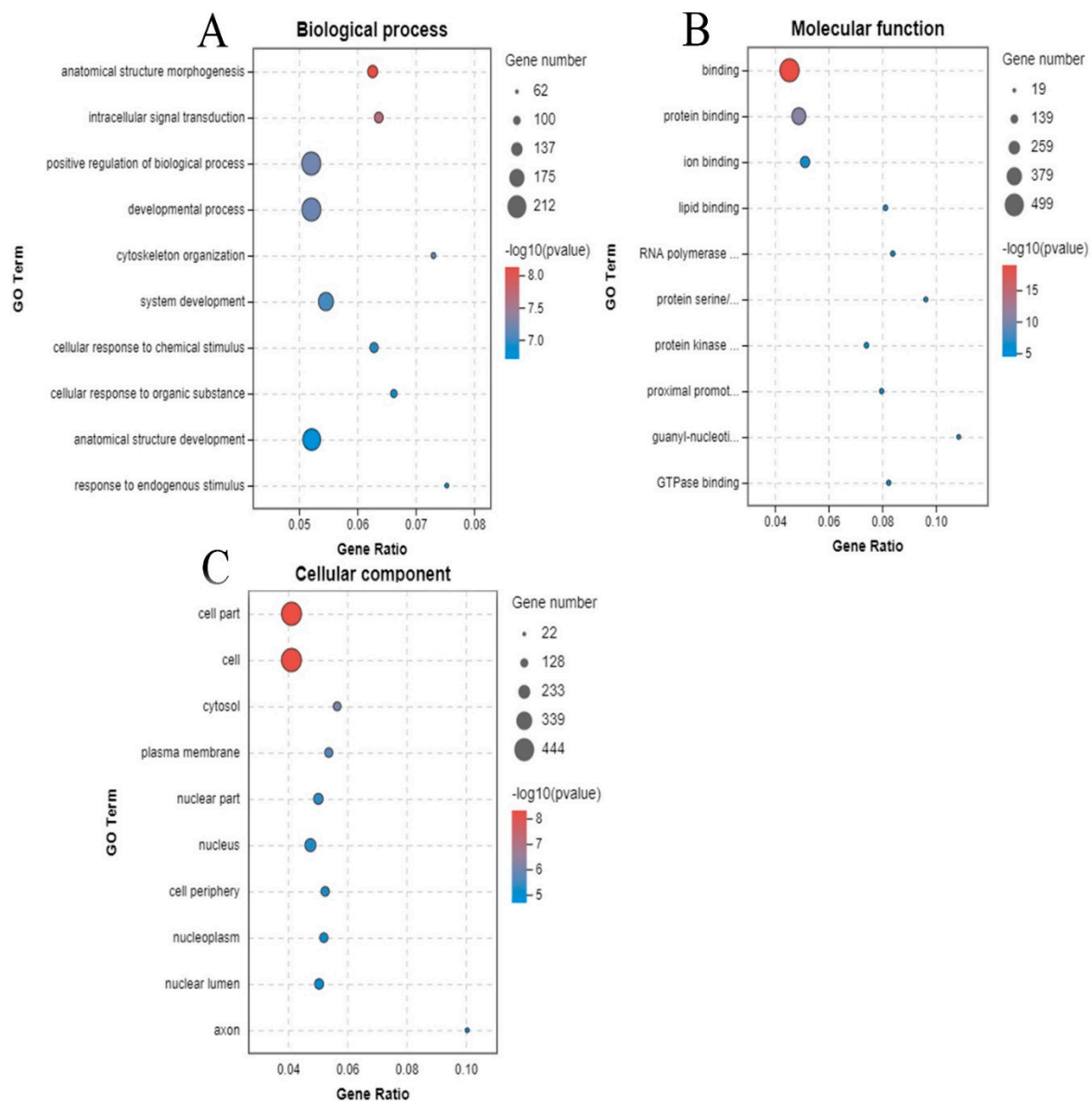
Figure S2. Functional classifications of differentially expressed genes (DEGs) in ovarian tissues of Control (n = 3) and NCG group (n = 3). The gene ontology (GO) domains of: (**A**) Molecular functions, (**B**) Biological processes, and (**C**) Cellular components are shown.