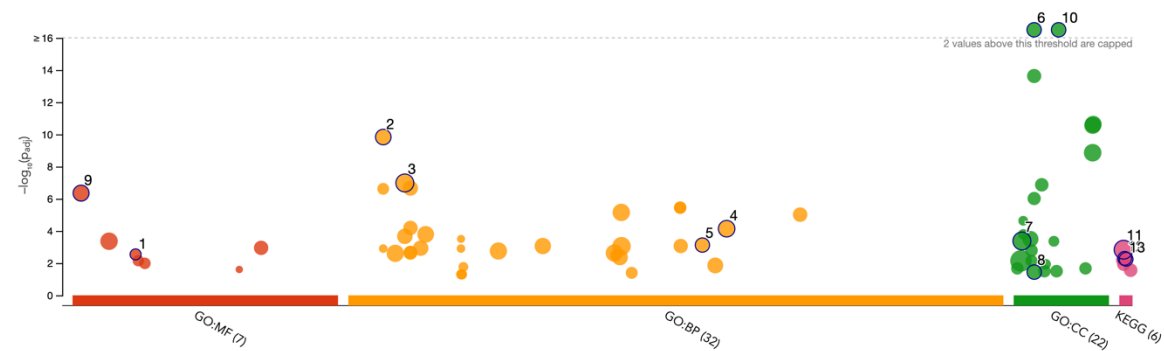


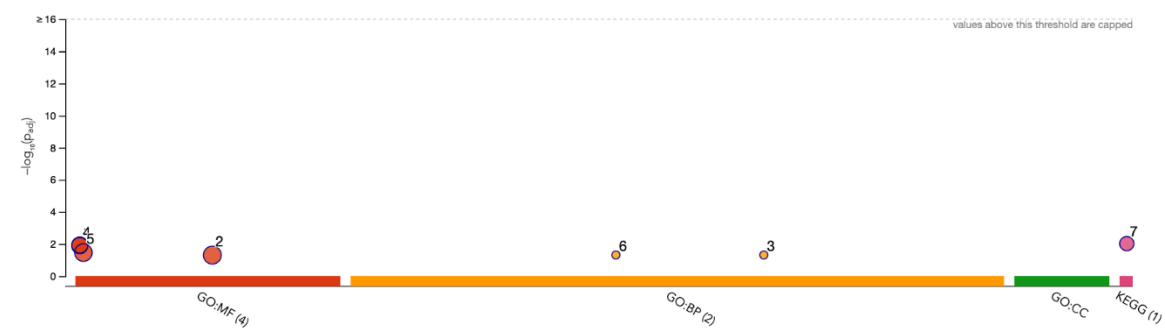
Supplementary Table S1. Details of primers used for qPCR analysis

Gene name	Primer	Sequence (5'-3')	Annealing temperature (°C)
<i>KRTAP8</i>	Forward	GGCTTCGGCTATGGCTACAA	60°
	Reverse	GAAGTCCGCCTCTTGGGTTT	
<i>FOSB</i>	Forward	TCCGCCGAGTCTCAGTATCTGTC	59°
	Reverse	TCCGCCGAGTCTCAGTATCTGTC	
<i>FOS</i>	Forward	TCCAAGCGGAGACAGACCAA	59°
	Reverse	TCAAGGGAAGCCACAGACATC	
<i>FOSL1</i>	Forward	TAGGACCGAGGTAATGGGGG	60°
	Reverse	ATCGCCGGAGTTGAGACAAG	
<i>FGF5</i>	Forward	AAACTCCATGCAAGTGCCAA	59°
	Reverse	TGGAGGTCCTGGCTGGTTGTG	
<i>GAPDH</i>	Forward	GGCGTGAACCACGAGAAGTA	60°
	Reverse	GGCGTGGACAGTGGTCATAA	



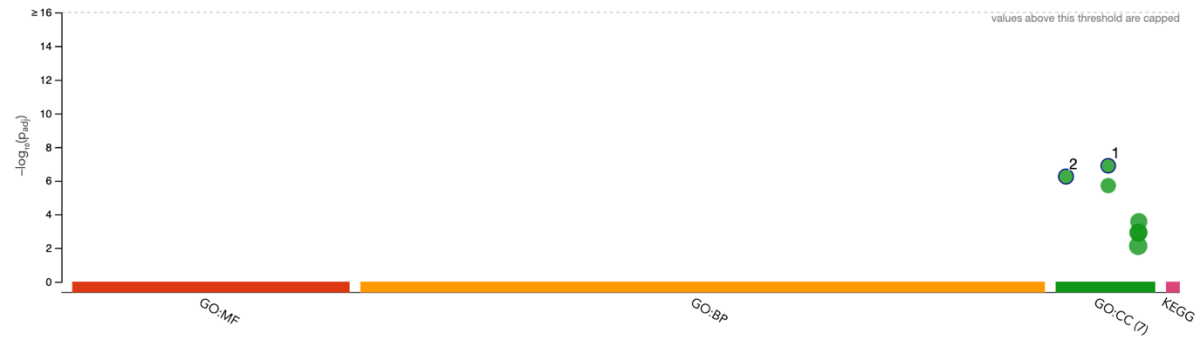
ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0015645	fatty acid ligase activity	2.866×10^{-3}
2	GO:BP	GO:0003012	muscle system process	1.457×10^{-10}
3	GO:BP	GO:0006629	lipid metabolic process	1.041×10^{-7}
4	GO:BP	GO:0061061	muscle structure development	7.242×10^{-5}
5	GO:BP	GO:0055001	muscle cell development	7.541×10^{-4}
6	GO:CC	GO:0030016	myofibril	2.150×10^{-19}
7	GO:CC	GO:0005783	endoplasmic reticulum	4.195×10^{-4}
8	GO:CC	GO:0030055	cell-substrate junction	3.599×10^{-2}
9	GO:MF	GO:0003779	actin binding	4.460×10^{-7}
10	GO:CC	GO:0043292	contractile fiber	4.854×10^{-19}
11	KEGG	KEGG:01100	Metabolic pathways	1.458×10^{-3}
12	KEGG	KEGG:03320	PPAR signaling pathway	5.019×10^{-3}
13	KEGG	KEGG:04260	Cardiac muscle contraction	5.740×10^{-3}

Supplementary Fig. S1. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Anagen Female versus Eskisehir Anagen Male comparison group.



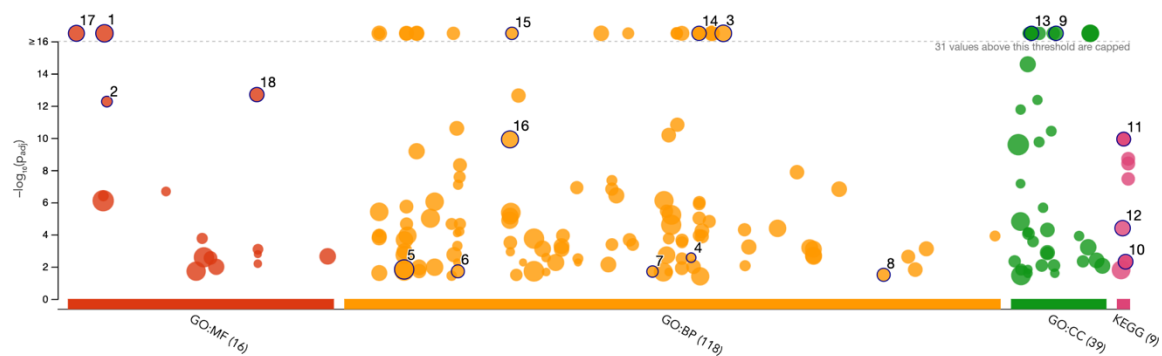
ID	Source	Term ID	Term Name	p _{adj} (query_1)
1	GO:MF	GO:0001228	DNA-binding transcription activator activity, R...	1.163×10^{-2}
2	GO:MF	GO:0043565	sequence-specific DNA binding	4.938×10^{-2}
3	GO:BP	GO:0071376	cellular response to corticotropin-releasing ho...	4.824×10^{-2}
4	GO:MF	GO:0001216	DNA-binding transcription activator activity	1.263×10^{-2}
5	GO:MF	GO:0003700	DNA-binding transcription factor activity	3.440×10^{-2}
6	GO:BP	GO:0043435	response to corticotropin-releasing hormone	4.824×10^{-2}
7	KEGG	KEGG:04380	Osteoclast differentiation	9.484×10^{-3}

Supplementary Fig. S2. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Catagen Female versus Eskisehir Catagen Male comparison group.



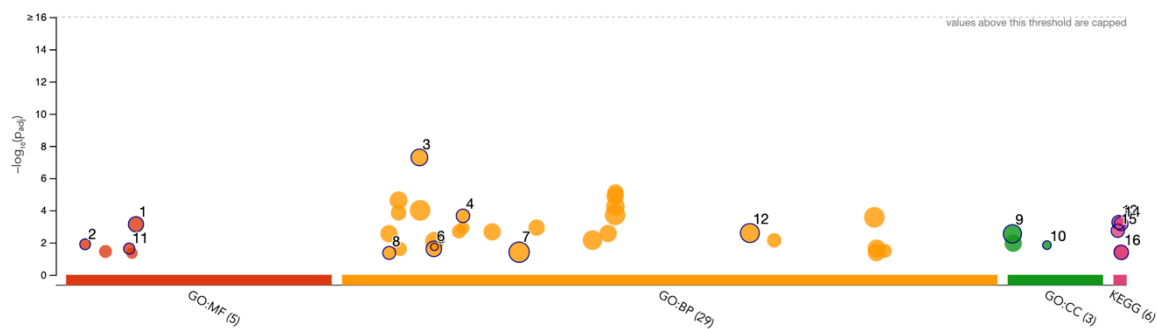
ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:CC	GO:0045095	keratin filament	1.290x10 ⁻⁷
2	GO:CC	GO:0005882	intermediate filament	5.645x10 ⁻⁷

Supplementary Fig. S3. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Telogen Female versus Eskisehir Telogen Male comparison group.



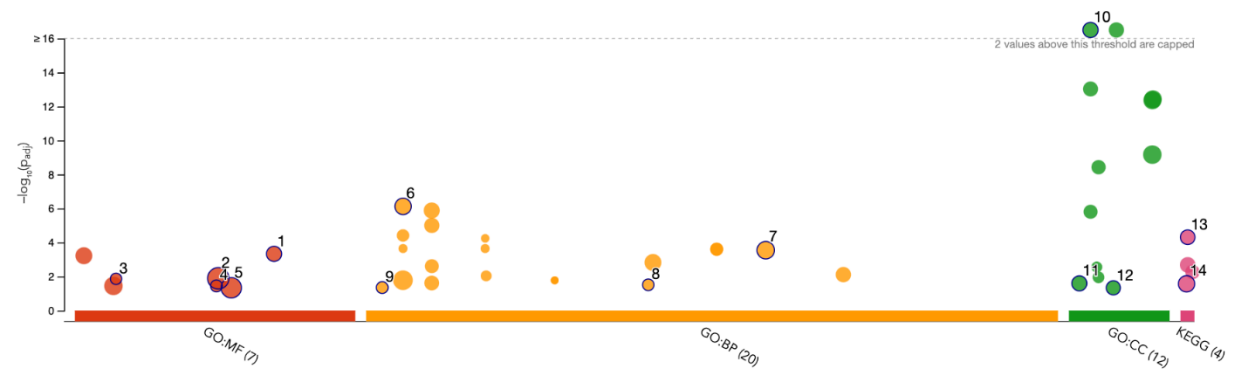
ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0008092	cytoskeletal protein binding	1.303×10 ⁻²¹
2	GO:MF	GO:0008307	structural constituent of muscle	5.491×10 ⁻¹³
3	GO:BP	GO:0061061	muscle structure development	1.858×10 ⁻³⁹
4	GO:BP	GO:0051694	pointed-end actin filament capping	2.714×10 ⁻³
5	GO:BP	GO:0006796	phosphate-containing compound metabolic pr...	1.483×10 ⁻²
6	GO:BP	GO:0014812	muscle cell migration	1.933×10 ⁻²
7	GO:BP	GO:0046716	muscle cell cellular homeostasis	1.987×10 ⁻²
8	GO:BP	GO:1901879	regulation of protein depolymerization	3.183×10 ⁻²
9	GO:CC	GO:0043292	contractile fiber	6.789×10 ⁻⁶²
10	KEGG	KEGG:04921	Oxytocin signaling pathway	4.903×10 ⁻³
11	KEGG	KEGG:04260	Cardiac muscle contraction	1.180×10 ⁻¹⁰
12	KEGG	KEGG:04020	Calcium signaling pathway	4.024×10 ⁻⁵
13	GO:CC	GO:0030016	myofibril	2.752×10 ⁻⁶¹
14	GO:BP	GO:0055001	muscle cell development	7.583×10 ⁻³²
15	GO:BP	GO:0030239	myofibril assembly	3.342×10 ⁻²⁴
16	GO:BP	GO:0030029	actin filament-based process	1.225×10 ⁻¹⁰
17	GO:MF	GO:0003779	actin binding	1.599×10 ⁻¹⁸
18	GO:MF	GO:0051015	actin filament binding	2.028×10 ⁻¹³

Supplementary Fig. S4. The enriched GO terms and KEGG pathway results obtained for the Lalahan Anagen Female versus Lalahan Anagen Male comparison group.



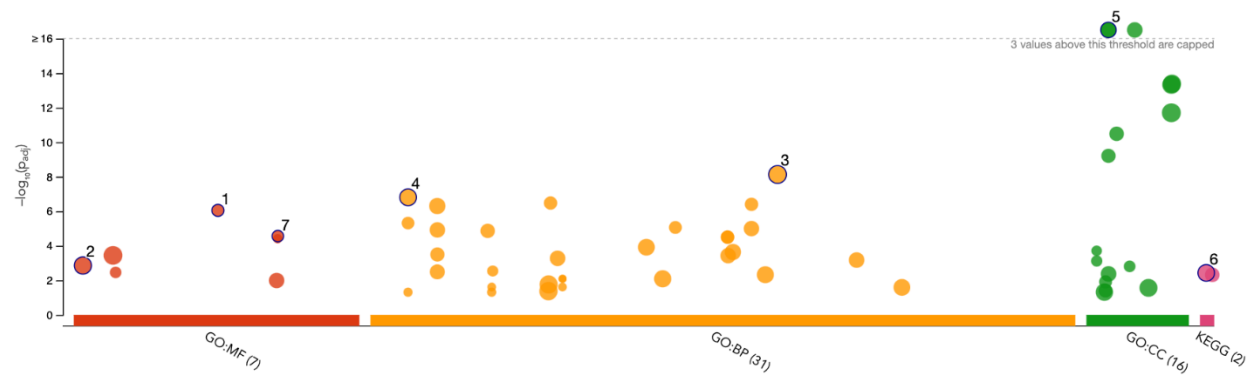
ID	Source	Term ID	Term Name	p _{adj} (query_1)
1	GO:MF	GO:0016747	acyltransferase activity, transferring groups ot...	7.306×10 ⁻⁴
2	GO:MF	GO:0004467	long-chain fatty acid-CoA ligase activity	1.273×10 ⁻²
3	GO:BP	GO:0008610	lipid biosynthetic process	5.120×10 ⁻⁸
4	GO:BP	GO:0015908	fatty acid transport	2.169×10 ⁻⁴
5	GO:BP	GO:0010025	wax biosynthetic process	1.840×10 ⁻²
6	GO:BP	GO:0009991	response to extracellular stimulus	2.444×10 ⁻²
7	GO:BP	GO:0031323	regulation of cellular metabolic process	3.929×10 ⁻²
8	GO:BP	GO:0006094	gluconeogenesis	4.388×10 ⁻²
9	GO:CC	GO:0005576	extracellular region	2.872×10 ⁻³
10	GO:CC	GO:0035976	transcription factor AP-1 complex	1.437×10 ⁻²
11	GO:MF	GO:0015645	fatty acid ligase activity	2.355×10 ⁻²
12	GO:BP	GO:0070887	cellular response to chemical stimulus	2.547×10 ⁻³
13	KEGG	KEGG:03320	PPAR signaling pathway	5.479×10 ⁻⁴
14	KEGG	KEGG:04657	IL-17 signaling pathway	6.736×10 ⁻⁴
15	KEGG	KEGG:01212	Fatty acid metabolism	1.836×10 ⁻³
16	KEGG	KEGG:04668	TNF signaling pathway	4.064×10 ⁻²

Supplementary Fig. S5. The enriched GO terms and KEGG pathway results obtained for the Lalahan Catagen Female versus Lalahan Catagen Male comparison group.



ID	Source	Term ID	Term Name	P _{adj} (query_1)
1	GO:MF	GO:0051015	actin filament binding	4.680×10^{-4}
2	GO:MF	GO:0043167	ion binding	1.282×10^{-2}
3	GO:MF	GO:0008307	structural constituent of muscle	1.371×10^{-2}
4	GO:MF	GO:0042805	actinin binding	3.589×10^{-2}
5	GO:MF	GO:0046872	metal ion binding	4.609×10^{-2}
6	GO:BP	GO:0003012	muscle system process	7.518×10^{-7}
7	GO:BP	GO:0061061	muscle structure development	2.841×10^{-4}
8	GO:BP	GO:0043501	skeletal muscle adaptation	3.091×10^{-2}
9	GO:BP	GO:0002026	regulation of the force of heart contraction	4.482×10^{-2}
10	GO:CC	GO:0030016	myofibril	8.942×10^{-18}
11	GO:CC	GO:0005882	intermediate filament	2.541×10^{-2}
12	GO:CC	GO:0042383	sarcolemma	4.655×10^{-2}
13	KEGG	KEGG:04260	Cardiac muscle contraction	4.905×10^{-5}
14	KEGG	KEGG:04020	Calcium signaling pathway	2.698×10^{-2}

Supplementary Fig. S6. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Female Anagen versus Eskisehir Female Catagen comparison group.

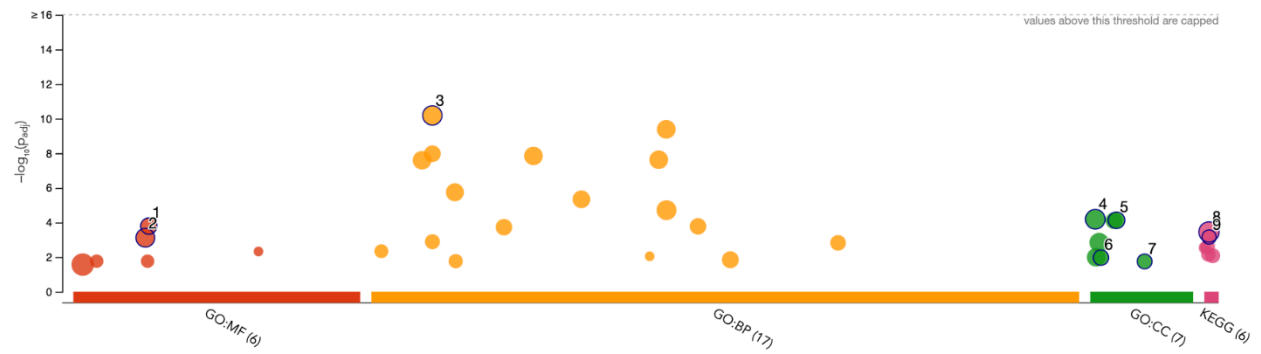


ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0042805	actinin binding	8.903×10^{-7}
2	GO:MF	GO:0003779	actin binding	1.387×10^{-5}
3	GO:BP	GO:0061061	muscle structure development	7.432×10^{-9}
4	GO:BP	GO:0003012	muscle system process	1.558×10^{-7}
5	GO:CC	GO:0030016	myofibril	1.055×10^{-21}
6	KEGG	KEGG:04020	Calcium signaling pathway	3.720×10^{-3}
7	GO:MF	GO:0051393	alpha-actinin binding	2.752×10^{-5}

Supplementary Fig. S7. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Female Anagen versus Eskisehir Female Telogen comparison group.



Supplementary Fig. S8. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Male Anagen versus Eskisehir Male Catagen comparison group.

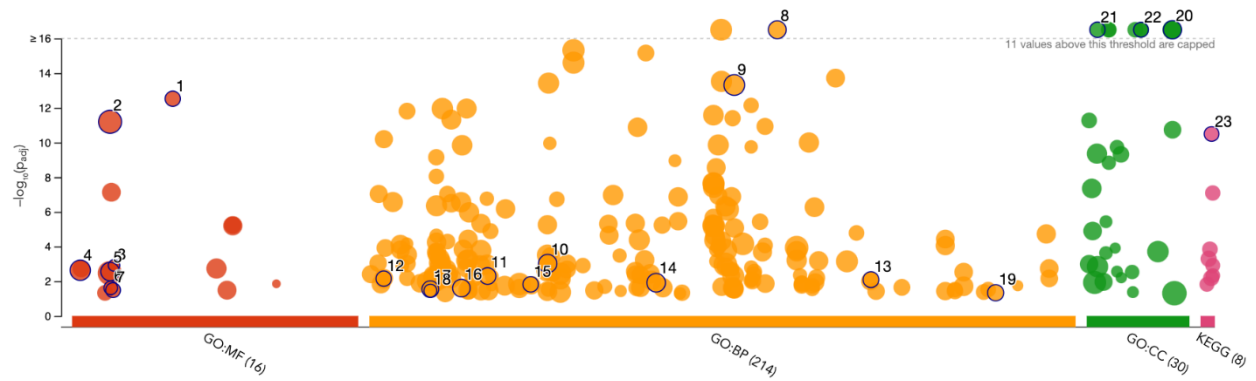


ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0016747	acyltransferase activity, transferring groups ot...	1.625×10 ⁻⁴
2	GO:MF	GO:0016491	oxidoreductase activity	7.640×10 ⁻⁴
3	GO:BP	GO:0006629	lipid metabolic process	6.530×10 ⁻¹¹
4	GO:CC	GO:0005576	extracellular region	6.527×10 ⁻⁵
5	GO:CC	GO:0031012	extracellular matrix	7.477×10 ⁻⁵
6	GO:CC	GO:0005882	intermediate filament	1.077×10 ⁻²
7	GO:CC	GO:0045095	keratin filament	1.784×10 ⁻²
8	KEGG	KEGG:01100	Metabolic pathways	3.534×10 ⁻⁴
9	KEGG	KEGG:01212	Fatty acid metabolism	6.967×10 ⁻⁴

Supplementary Fig. S9. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Male Anagen versus Eskisehir Male Telogen comparison group.



Supplementary Fig. S10. The enriched GO terms and KEGG pathway results obtained for the Eskisehir Male Catagen versus Eskisehir Male Telogen comparison group.



ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0030527	structural constituent of chromatin	2.995×10 ⁻¹³
2	GO:MF	GO:0005515	protein binding	6.415×10 ⁻¹²
3	GO:MF	GO:0008307	structural constituent of muscle	1.224×10 ⁻³
4	GO:MF	GO:0003677	DNA binding	2.327×10 ⁻³
5	GO:MF	GO:0005509	calcium ion binding	2.761×10 ⁻³
6	GO:MF	GO:0008009	chemokine activity	2.421×10 ⁻²
7	GO:MF	GO:0008201	heparin binding	3.253×10 ⁻²
8	GO:BP	GO:0061061	muscle structure development	1.184×10 ⁻¹⁸
9	GO:BP	GO:0051239	regulation of multicellular organismal process	4.852×10 ⁻¹⁴
10	GO:BP	GO:0030029	actin filament-based process	9.580×10 ⁻⁴
11	GO:BP	GO:0010959	regulation of metal ion transport	5.005×10 ⁻³
12	GO:BP	GO:0001935	endothelial cell proliferation	7.098×10 ⁻³
13	GO:BP	GO:0097529	myeloid leukocyte migration	8.072×10 ⁻³
14	GO:BP	GO:0043436	oxoacid metabolic process	1.221×10 ⁻²
15	GO:BP	GO:0019722	calcium-mediated signaling	1.507×10 ⁻²
16	GO:BP	GO:0009617	response to bacterium	2.485×10 ⁻²
17	GO:BP	GO:0006631	fatty acid metabolic process	2.877×10 ⁻²
18	GO:BP	GO:0006636	unsaturated fatty acid biosynthetic process	3.502×10 ⁻²
19	GO:BP	GO:1904062	regulation of monoatomic cation transmembra...	4.634×10 ⁻²
20	GO:CC	GO:0099512	supramolecular fiber	2.705×10 ⁻²⁸
21	GO:CC	GO:0005882	intermediate filament	6.601×10 ⁻²³
22	GO:CC	GO:0045095	keratin filament	1.882×10 ⁻²¹
23	KEGG	KEGG:05150	Staphylococcus aureus infection	3.215×10 ⁻¹¹

Supplementary Fig. S11. The enriched GO terms and KEGG pathway results obtained for the Lalahan Male Anagen versus Lalahan Male Catagen comparison group.



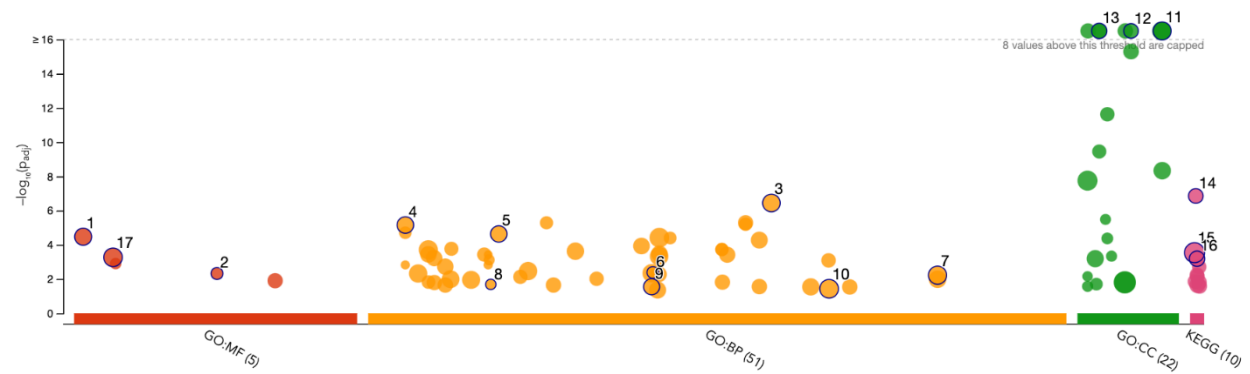
Supplementary Fig. S12. The enriched GO terms and KEGG pathway results obtained for the Lalahan Male Anagen versus Lalahan Male Telogen comparison group.



Supplementary Fig. S13. The enriched GO terms and KEGG pathway results obtained for the Lalahan Male Catagen versus Lalahan Male Telogen comparison group.

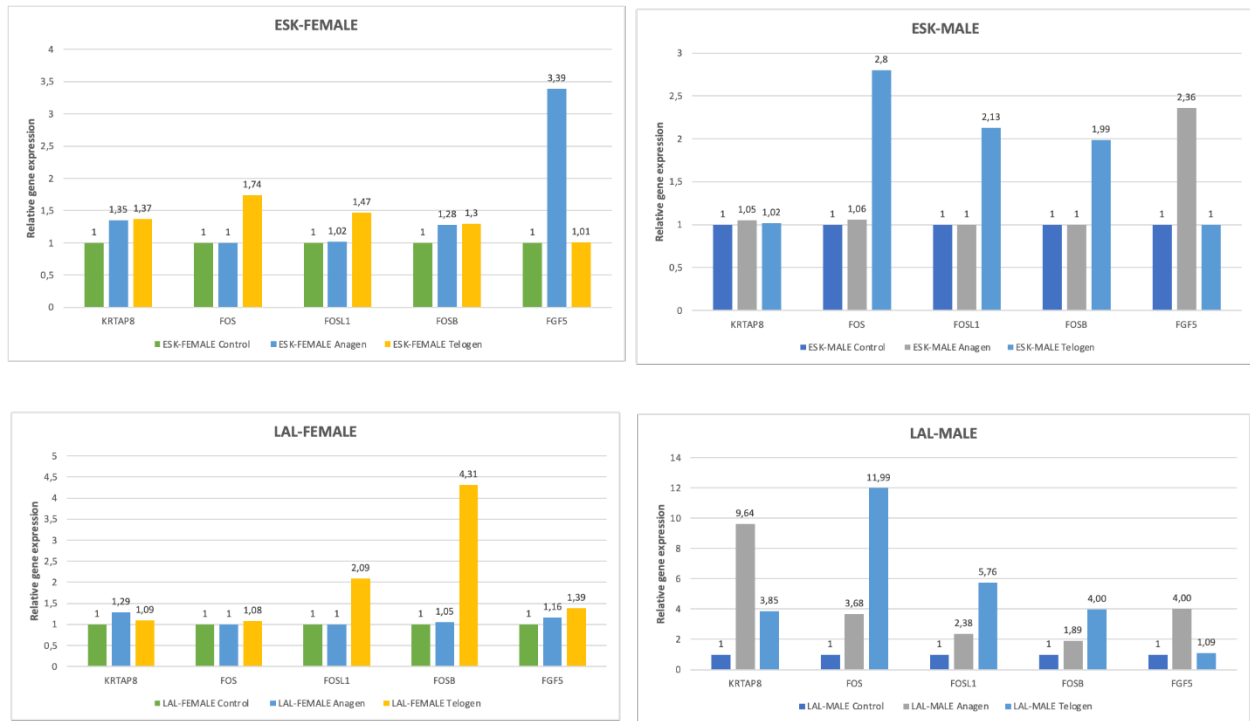


Supplementary Fig. S14. The enriched GO terms and KEGG pathway results obtained for the Catagen Female Eskisehir versus Catagen Female Lalahan comparison group.

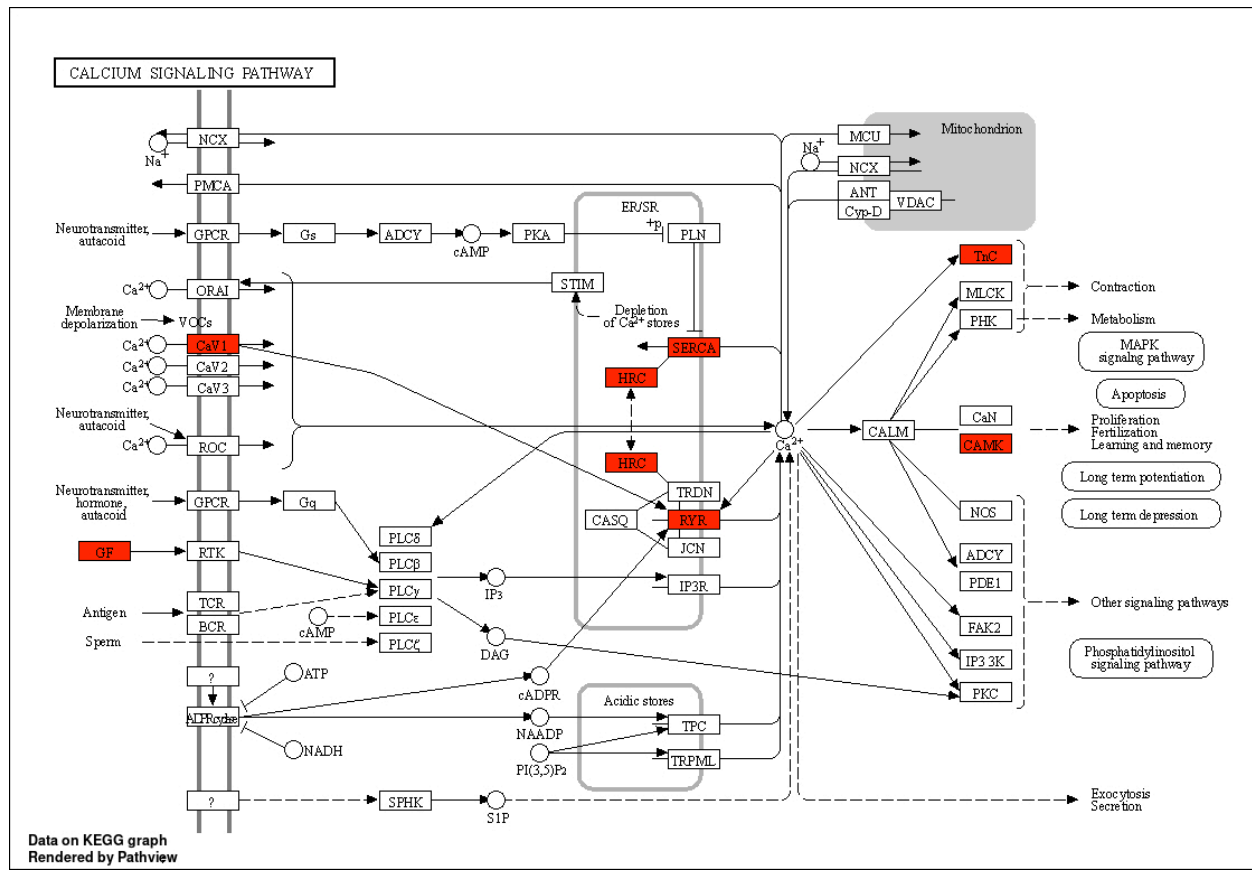


ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0003779	actin binding	3.388×10^{-5}
2	GO:MF	GO:0042805	actinin binding	4.779×10^{-3}
3	GO:BP	GO:0061061	muscle structure development	3.625×10^{-7}
4	GO:BP	GO:0003012	muscle system process	7.018×10^{-6}
5	GO:BP	GO:0016042	lipid catabolic process	2.333×10^{-5}
6	GO:BP	GO:0043501	skeletal muscle adaptation	4.147×10^{-3}
7	GO:BP	GO:1901698	response to nitrogen compound	5.994×10^{-3}
8	GO:BP	GO:0014883	transition between fast and slow fiber	2.076×10^{-2}
9	GO:BP	GO:0043434	response to peptide hormone	2.852×10^{-2}
10	GO:BP	GO:0072359	circulatory system development	3.741×10^{-2}
11	GO:CC	GO:0099512	supramolecular fiber	2.489×10^{-30}
12	GO:CC	GO:0045095	keratin filament	1.042×10^{-20}
13	GO:CC	GO:0030016	myofibril	4.326×10^{-25}
14	KEGG	KEGG:03320	PPAR signaling pathway	1.408×10^{-7}
15	KEGG	KEGG:01100	Metabolic pathways	2.903×10^{-4}
16	KEGG	KEGG:04152	AMPK signaling pathway	6.524×10^{-4}
17	GO:MF	GO:0008092	cytoskeletal protein binding	5.419×10^{-4}

Supplementary Fig. S15. The enriched GO terms and KEGG pathway results obtained for the Catagen Male Eskisehir versus Male Female Lalahan comparison group.



Supplementary Fig. S16. QPCR validation of RNA-Sequencing result. Five mRNAs were selected for validation including *KRTAP8*, *FOS*, *FOSL1*, *FOSB*, and *FGF5*. The x-axis shows the two main cycles of the hair follicles (anagen and telogen) in female and male Ankara goats of the Eskisehir and Lalahan varieties. The y-axis indicates mRNA relative expression level. ESK: Ankara goats of Eskisehir varieties; LAL: Ankara goats of Lalahan varieties.



Supplementary Fig. S17. Involvement of Differentially Expressed Genes in the Calcium Signaling Pathway. Seven differentially expressed genes (*ATP2A1*, *TNNC2*, *FGF21*, *HRC*, *CAMK2A*, *RYR1*, and *CACNA1S*) were identified as components of the calcium signaling pathway (KEGG pathway chx04020).