

Table S1 Primers for qPCR

Genes	Accession	Primer sequence (5'-3')	Product size (bp)	T _m (°C)
<i>FGF5-1</i>	NM_001246263.2	Forward: TGTGTCTCAGGGGATTGTAGG Reverse: GGCGGAGGCATAGGTATTATAG	157	60
<i>FGF5-2</i>	NM_001246263.2	Forward: CACGTCTCTACCCACTTTCTG Reverse: TTAGGACTTCTCCGAGGTGC	143	60
<i>FGFR1</i>	XM_015104616.1	Forward: CAAACCAAACCGTATGCCCCG Reverse: ACCTTGTAGCCTCCGATCCT	192	60
<i>GR</i>	>NM_001114186.1	Forward: CCACCTCCCAAACCTCTGCCTAG Reverse: TGCTGTCCTTCCACTGCTCTT	113	60
<i>Ki67</i>	>XM_042238739.1	Forward: GAGGCCAATTTGATCGTGGC Reverse: AGTGTGGCTCTTCTCTGCC	129	60
<i>HGF</i>	>XM_004007806.5	Forward: AGGTACGCTACGAAGTCTGTGA Reverse: CGGTGTGGTGTCTGATGATCC	142	60
<i>Bcl2</i>	>XM_012103831.4	Forward: CCTGTGGATGACCGAGTACCTG Reverse: CCAGACTGAGCAGTGCCTTCA	149	60
<i>Bax</i>	>XM_027978592.2	Forward: TCATGGGCTGGACATTGGACTT Reverse: CAGATGGTGAGTGAGGCAGTGA	157	60
<i>RSPO1</i>	>XM_042245742.1	Forward: GAGGAACGACATCCGCCAAG Reverse: GCCTCGCAGTGCTCAATCTT	117	60
<i>RSPO2</i>	>XM_015097839.3	Forward: GTGTGGAAGGATGTGAGGTTGG Reverse: TGGATTGAGCAATGGTTGGACA	159	60
<i>RSPO3</i>	>XM_004011136.4	Forward: CCAGTGAGGCGAGGAAGTGTA Reverse: GGGCTCCAGACCTTTGTTGTC	143	60
<i>RSPO4</i>	>XM_004014778.4	Forward: CACTCTGCCTGTTGCTGCTTG Reverse: GGATACCTTCCCACGGATGAA	180	60
<i>LRP5</i>	>XM_027959820.2	Forward: CGACGGCTCTGACGAACTCA Reverse: CGCTGGCACACGAAGTAGAC	141	60
<i>LRP6</i>	>XM_042247517.1	Forward: ATCCGCCGCTCCTTCATAGAT Reverse: TATCCGATCAGTGCCAGTGTCT	132	60
<i>Axin2</i>	>XM_042256527.1	Forward: CAACAGCATCGTCTCCAAGCA Reverse: GGTAGGCGTTCTCCTCCATCA	140	60
<i>LEF1</i>	>XM_042251151.1	Forward: AAGGAACAGCAGCAGACTCAGT Reverse: CAACGACGCAGTCAGCAACA	106	60
<i>Notum</i>	>XM_042256238.1	Forward: TGGAATGCCAACATGGTCTTCA Reverse: TCGCACAACCTCCTGGATGA	123	60
<i>DKK2</i>	>XM_004009640.5	Forward: TTGCTGTGCTCGTCACTTCTG Reverse: TTGGAGGAGTAGGTGGCATCTT	171	60
<i>CCND1</i>	>XM_027959928.2	Forward: GCCGAGGAGAACAAGCAGATC Reverse: TGATAGGAGAGGAAGCCGTTGG	170	60
<i>c-Myc</i>	>XM_042253807.1	Forward: GGACACGGAGGAGAATGACAAG Reverse: TGGACCGACAGGATGTATGCT	177	60

Figure S1 Proportion statistics of non-medullated wool, heterotypical wool, and medullated wool during anagen phase: (A) Proportion statistics of non-medullar wool in the three parts; (B) Proportion statistics of heterotypical wool in the three parts; (C) Proportion statistics of medullated wool in the three parts.

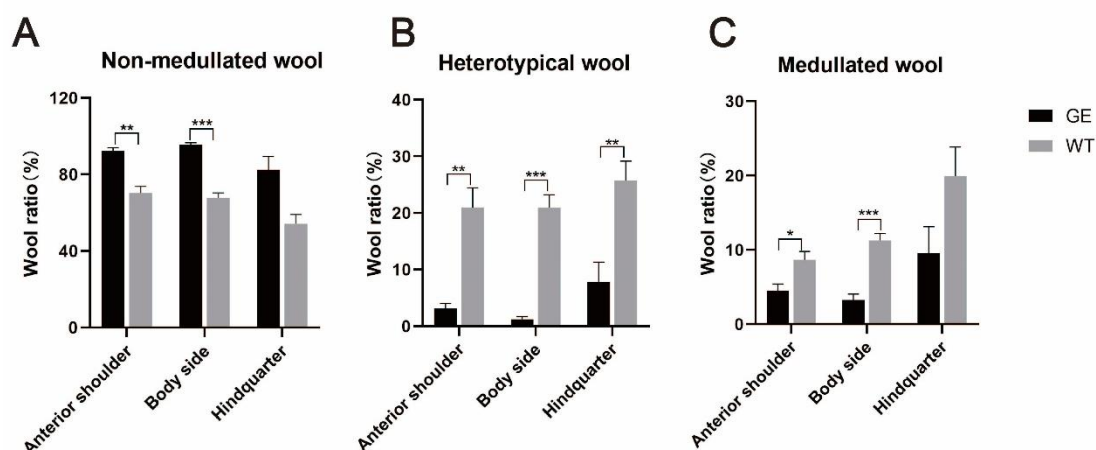


Figure S2 Detection of wool density during telogen: (A) Photograph of skin follicles 48 h after shaving. The actual area shown in the picture is 9 mm². (B) Changes in coarse and fine wool density in different parts of GE and control group. The statistical results in figure B are from figure A.

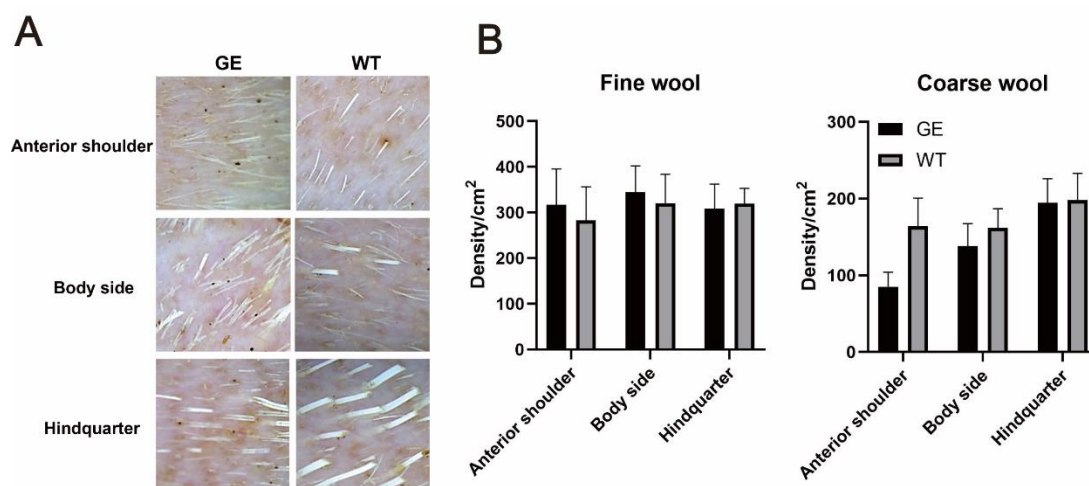


Figure S3 One-month wool stretched length of GE sheep and WT sheep: (A) The stretched length of fine wool; (B) The stretched length of coarse wool.

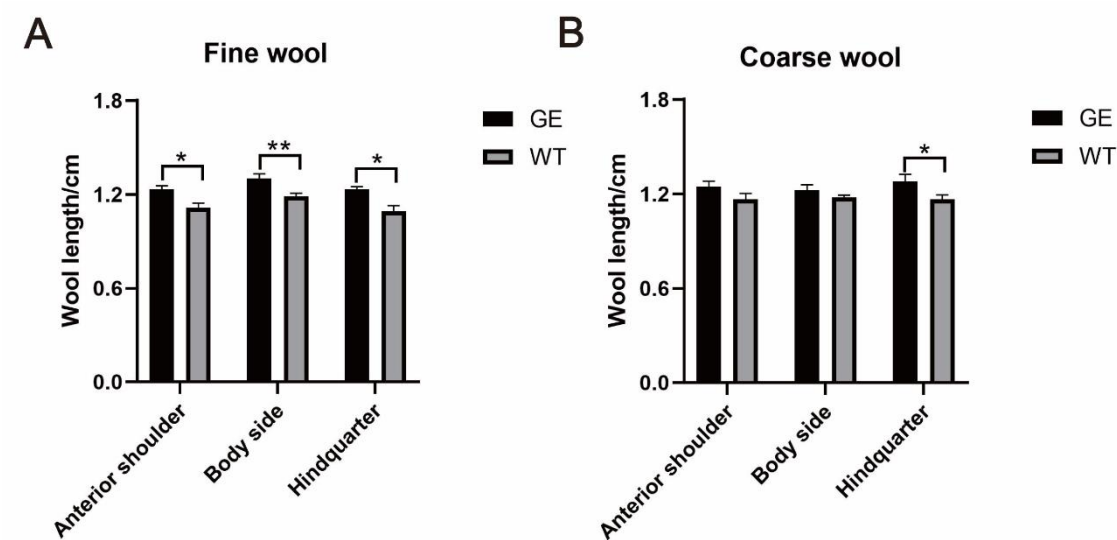


Figure S4 The wool yield of GE and WT sheep.

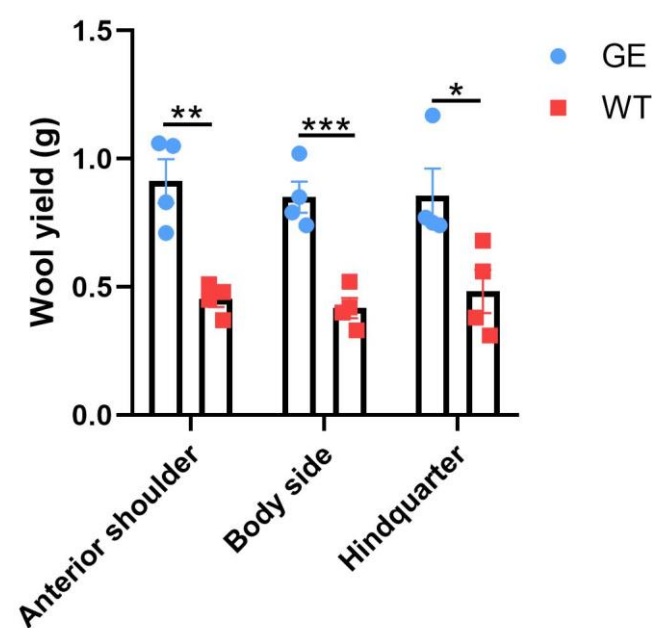


Figure S5 The clean wool yield and wool grease rate in GE and WT sheep: (A) The clean wool yield of GE and WT sheep; (B) The wool grease rate of GE and WT sheep.

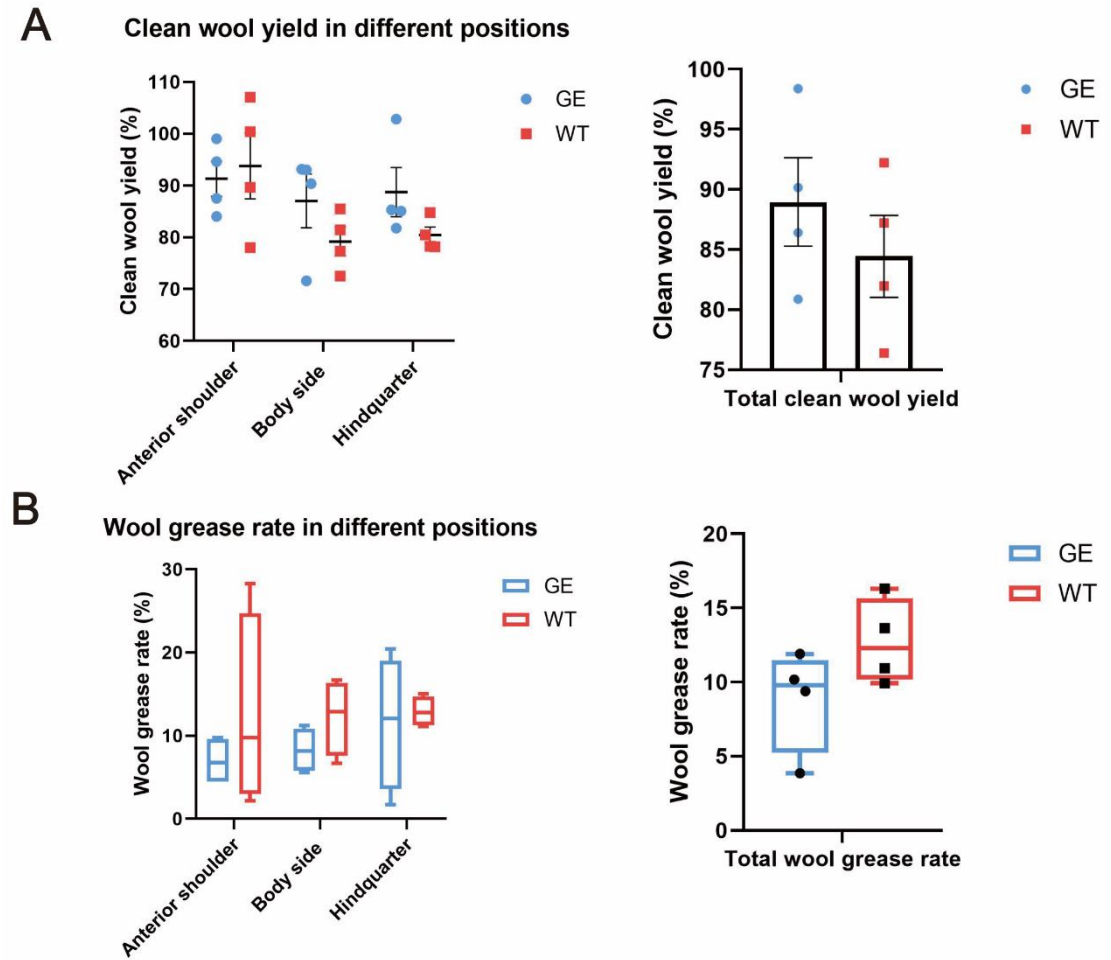


Figure S6 Skin tissue structural parameters in the GE and WT groups: (A) Primary hair follicle diameter statistics of GE and WT; (B) The depth of primary hair follicle in GE and WT groups; (C) The depth of secondary follicle in GE and WT groups.

