1. The exact sample size (n) for each experimental group/condition (as a number, not a range). Include details of a power analysis if done, or any other relevant considerations that determined the choice of sample size. For n < 6, individual data values should be shown rather than summary statistics alone.

**Methods, paragraph 1.** Eight rabbits (four rabbits with high wool production, four rabbits with low wool production) were used in histology and RNA-seq experiment, respectively. The average wool production of the each rabbit was showed in Table 1.

**Table 1 The average****wool production of the rabbits.** “L” and “H” represent low wool production and high wool production groups, respectively.

|  |  |  |
| --- | --- | --- |
| Samples | Wool production (g) | Average wool production (g) |
| H1 | 435.5  | 430.1  |
| H2 | 449.3  |
| H3 | 410.2  |
| H4 | 425.4  |
| L1 | 305.8  | 291.6  |
| L2 | 298.0  |
| L3 | 287.3  |
| L4 | 275.2  |

1. A description of sample collection that enables the reader to understand whether the samples represent technical or biological replicates, and an explanation of inclusion/exclusion criteria if samples or organisms were excluded from the analysis.

**Methods, paragraph 2.** The eight rabbits selected (four rabbits with high wool production, four rabbits with low wool production) were given anesthesia through an ear vein injection of 0.7% pentobarbital sodium (6 ml/kg) before sampling. Skin tissue samples (1 cm2) from the backs, abdomens, sides and hips were collected at the fourth week after plucking for histological analysis.

**Methods, paragraph 3.** Under anesthesia, skin samples from the back of the eight rabbits selected (four rabbits with high wool production and four rabbits with low wool production; 430.1 ± 16.5 g vs 291.6 ± 13.3 g, *P* < 0.0001) were collected at the fourth week after plucking for RNA-seq. The skin samples were firstly frozen in liquid nitrogen immediatelly after cutting and then stored at -80℃ before RNA extration.

1. How samples/ organisms were allocated to experimental groups and processed, and full details of the randomisation procedure used (if relevant).

**Methods, paragraph 1.** The samples were allocated to high and low wool production groups according to the average wool weight (430.1 ± 16.5 g vs 291.6 ± 13.3 g, *P* < 0.0001) .

1. For sample assessment by human investigators, a statement on whether the investigator was blinded to group assignment and outcome assessment, and how this blinding was achieved and evaluated (if relevant).

**N/A**

1. How many times each experiment shown was replicated and an indication of the extent of variation from experiment to experiment.

**Methods, paragraph 6.** Histology and RNA-seq experiments were conducted one time. q-RCR experiment were conducted with four biological replicates and three technical replicates.

1. Information on the statistical methods and measures used. It should be clear whether the tests are one-sided or two-sided, whether there are adjustments for multiple comparisons, whether medians or means are being shown, whether error bars are standard deviations (SD), standard error of mean (SEM) or confidence intervals.

**Methods, paragraph 7.** Student’s *t*-test with two-sided was used in statistical comparisons in wool weight between HWP and LWP groups and RNA expression. Error bars represent the mean ± standard deviation (SD) as determined using GraphPad Prism 5.

1. A justification for the appropriateness of statistical tests used to assess significance. Do the data meet the assumptions of the tests? Is there an estimate of variation within each group of data, and is the variance similar between groups that are being statistically compared?

**Methods, paragraph 7.** Student’s *t*-test with two-sided was used to assess significance, and *P* value < 0.05 were considered to be statistically significant.

**Methods, paragraph 5.** Significance of differential expression between HWP and LWP groups in RNA-seq was analyzed by using cuffdiff (https://www.genepattern.org/modules/docs/Cuffdiff/7), and the threshold was set as |log2 (Fold Change)| ≥ 1 and *P* value < 0.05.