**Supplementary Table S1:**

Accession numbers, forward and reverse primer sequences, probe sequences, and exon boundaries for ovine transcripts analyzed with qPCR.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Transcript | Accession number | Primers, forward and reverse | Probe | Exons |
| ov. -actin | NM\_001009784.1 | Forward: GCTCTTCCAGCCGTCCTT  Reverse: TGAAGGTGGTCTCGTGAATGC | CCTGGGTATGGAGTCCTG | 2-3 |
| ov. CAT | GQ421282.1 | Forward: CATCTGAAAGACGCACAGCTT  Reverse: GATGCGGGAGCCATACTCA | AAGCGGTTAAGAACTTC | 12-13 |
| ov. SOD1 | NM\_001145185.1 | Forward: GGGCCGGAGAGCCTTTC  Reverse: GGGCCGTCACCCTTCAG | TCGTCGCCATGACTCG | 1-2 |
| ov. SOD2 | GQ221055.1 | Forward: CGTCGCCGAGGAGAAGTAC  Reverse: GCAGGCTGCAGAGCTATCT | CTGTGACATCACCCTTCTC | 2-3 |
| ov. HbF  (-chain) | UO1378.1 | Forward: GGCTTCTGTCATCTCCCTATTTGC  Reverse: GTGCTCGAAGAACCTCTGAGT | CAACCAGCAGCACCTTG | 1-2 |
| ov. HbA  (-chain | EU938073.1 | Forward: TGCACGCCCACAAGCT  Reverse: AGGGTCACCAGCAGGGT | TCAGAAGCTTGAAGTTGACC | 1-2 |
| ov. PLGF | AY157708.1 | Forward: CCCTGGAGACAGCCAACG  Reverse: GGCTGGTCCAGAGAGTGGTACT | CCATGCAGCTCATG |  |
| ov. s-Flt1 | AF488351 | Forward: GACTGTGGAAAGAAACGTGAACTT  Reverse: CATTTTGTCCAAGCTCACCTGAA | CACAGATGTGCCCCATGGAT | 12-13 |
| ov. VEGF | X89506 | Forward: GGATGTCTACCAGCGCAGC  Reverse: TCTGGGTACTCCTGGAAGATGTC | TCTGCCGTCCCATTGAGACCCTG |  |
| ov. TGF | NM\_001009400 | Forward: AAGCGGAAGGGCATCGA  Reverse: CGAGCCGAAGTTTGGACAAA | CCATCCGCGGTCAGA |  |
| ov. HGF | AF213397.1 | Forward: TCAAATGCCAGCCCTGGAAT  Reverse: GTCTTTACCCCGATAGCTCGAA | CACATGAACACAGCTTTT | 4-5 |
| ov. IL-6 | NM\_001009392 | Forward: AGGAAAAAGATGGATGCTTCCA  Reverse: GACCAGCAGTGGTTTTGATCAA | CTGGGTTCAATCAGGCGA |  |
| ov. IL-10 | NM\_001009327.1 | Forward: CATGCTGTTGACCCAGTCTCT  Reverse: GGTAAAACTGGATCATTTCCGACAAG | CCAGGTAACCCTTAAAGTC | 2-3 |
| bov HMOX1 | NM\_001014912.1 | Bt03218621\_m1 |  |  |
| bov Ambp | NM\_173989.2 | Bt03212235\_m1 |  |  |

**Supplementary Table S2:** Ewe parameters.

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Placebo group** | **A1M group** |
| Ewe age (years) | 3 (2.8-8)a | 3 (2.5-5.5)a |
| Ewe weight (kg) | 75 (68-82)b | 76 (69-84)b |
| Gestation day | 130 (129-130)a | 130 (128-131)a |

a Median (25% percentile-75% percentile)

b Mean (95% confidence interval)

**Supplementary Table S3:** Lamb parameters.

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Placebo group** | **A1M group** |
| Number of off-spring per Ewe | 1.5 (1-2.25)a | 3 (1.5-3)a |
| Total weight of off-spring per Ewe (g) | 4700 (2400-7000)b | 7300 (4200-10400)b |
| Weight per off-spring (g) | 2800 (2200-3400)b | 3000 (2400-3500)b |

a Median (25% percentile-75% percentile)

b Mean (95% confidence interval)

**Supplementary Table S4:** Starvation parameters.

|  |  |  |  |
| --- | --- | --- | --- |
| **Parameter** | **0h** | **15h** | **36h** |
| Blood glucose (mmol/L) | 2.3 (1.5-3)a | 1.8 (1.3-2.2) | 1.6 (1-2.1) |
| Urine-pH | 8.5 (7.9-9.2) | 8.1 (7.3-8.9) | 6.6 (5.8-7.4)  *(p<0.004)b* |
| Plasma-Ca2+ (mmol/L) | 2.16 (2.04-2.28) | 2.13 (1.98-2.28) | 2.05 (1.93-2.17) |
| Urine-ketones (mg/dL) | 55 (21-90) | 62 (29-95) | 102 (66-136) *(p<0.11)* |
| Plasma- heme (µM) | 14.2 (12.7-18.1) | 14.9 (12.9-16.9) | 15.2 (13.4-17.1) |
| Plasma-bilirubin (µM) | 3.2 (2.2-4.3) | 5.1 (3.3-6.8)  *(p<0.06)* | 6.5 (5.0-8.0)  *(p<0.001)* |
| ΔPlasma-free thiolsc (ΔA405nm) | 0 | -11.84 (-18.8- -4.9) | -11.82 (-24.4- 0.75)  *(p<0.04)* |

aMean (95% confidence interval).

bp-values for the change in comparison to the 0h time point were calculated by unpaired t-test and are presented in parentheses in italic.

cThe free thiols are presented in relation to the 0h-value.

**Supplementary Table S5:** Incidence of positive detection in urine.



Positive detection of urine protein, leukocytes and erythrocytes, respectively are shown. Positive detection is defined as: for protein (>25mg/dL), leukocytes (>15cells/µl), erythrocytes (>10cells/µl).