**Supplementary Table 1. Information on healthy and mastitis cows**

|  |  |  |  |
| --- | --- | --- | --- |
| **The cow number** | **Fetal times** | **CMT** | **Group** |
| 183023 | 2 | - | Healthy cow |
| 182546 | 2 | - |
| 182393 | 2 | - |
| 182485 | 3 | - |
| 182412 | 2 | - |
| 182267 | 3 | - |
| 182284 | 2 | +++ | Mastitis cows |
| 171646 | 3 | +++ |
| 182218 | 3 | +++ |
| 170017 | 2 | +++ |
| 16101 | 2 | +++ |
| 182658 | 2 | +++ |

**Supplementary Table 2.** Sequences of the small interfering RNA molecules used to target the PRKAA1 transcript of BMECs in this study.

|  |  |  |
| --- | --- | --- |
| **Gene name** | **Sequence** | |
| **Sense(5′-3′)** | **Antisense(5′-3′)** |
| PRKAA1-691 | GCUGCACCAGAAGUAAUUUTT | AAAUUACUUCUGGUGCAGCTT |
| PRKAA1-911 | CCAUGAAGAGAGCCACAAUTT | AUUGUGGCUCUCUUCAUGGTT |
| PRKAA1-1384 | GCAGAAGUUUGUAGAGCAATT | UUGCUCUACAAACUUCUGCTT |
| Negative control (NC) | UUCUCCGAACGUGUCACGUTT | ACGUGACACGUUCGGAGAATT |

**Supplementary Table 3.** Oligonucleotides used in this study for qPCR gene expression studies.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene name** | **Primer sequences** (5՛ to 3՛) | **Product size** (bp) | **Annealing**  **Temperature** (°C) |
| *PGC-1α* | F: GGATGGCACGCAGTCCTATT | 132 | 60 |
| R:GAACGAGAGCGCATCCTTTG |
| *Tfam* | F: GTTCCTCCCAAGATTTCA | 137 | 60 |
| R: TGGCACATCACAGGTAAA |
| *Drp1* | F:GCACCTGAAGATAAACGAA | 254 | 60 |
| R:AGATTGACAACATTGGGTG |
| *Fis* | F:CACAGAACAACCAGGCCAAA | 166 | 60 |
| R:TGCCGTCTCCTTCAGGATTT |
| *Mfn1* | F:AGGTTGCTTGAGGGCTGTG | 116 | 60 |
| R:GTCTTCTTAGCCAGCACGA |
| *Mfn2* | F:TGGTCCTCAAGGTTTACAAG | 136 | 60 |
| R:TTCAAGCCGTCAATCATCT |
| *PRKAA1* | F:CGCCATACCCTTGATGAATTA | 102 | 60 |
| R:ATCATTTGGCCGACTTTGAC |
| *SOD* | F: GACAAATCTGAGCCCTAA | 185 | 60 |
| R: AAGCAGCAATCTGTAAGC |
| *GSH-PX* | F: TGCGAGGTGAATGGCGAGAA | 118 | 60 |
| R: GGGACCAGGTGATGAACTTAGGG |
| *IL-6* | F: TGTGAAAGCAGCAAGGAG | 88 | 60 |
| R: TGAACCCAGATTGGAAGC |
| *IL-8* | F: ACACATTCCACACCTTTCCAC | 149 | 60 |
| R: ACCTTCTGCACCCACTTTTC |
| *IL-1β* | F:CAACCGTACCTGAACCC | 193 | 60 |
| R:GACACCACCTGCCTGAA |

**Supplementary table 4.** Online site information

|  |  |
| --- | --- |
| Online Sites | Web address |
| NCBI | https://www.ncbi.nlm.nih.gov/, accessed on 10, August, 2023 |
| Netphos 3.1 | http://www.cbs.dtu.dk/services/NetPhos/, accessed on 5, September, 2023 |
| Scansite | http://Scansite.mit.edu, accessed on 5, September, 2023 |
| Protscale | https://web.expasy.org/protscale/, accessed on 5, September, 2023 |
| Sopma | https://npsa-prabi.ibcp.fr/cgi-bin/npsa\_automat.pl?page=npsa\_sopma.html, accessed on 5, September, 2023 |
| Swiss model | <https://www.swissmodel.expasy.org/>, accessed on 5, September, 2023 |

**Supplemetary table4.** NetPhos3.1 software predicts phosphorylation sites of PGC-1α

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Basophilic serine/threonine kinase group (Baso\_ST\_kin) | | | | | | | | |
| AMP Kinase | | | | Gene Card PRKAA1 | | | | |
| Site  T254 | Score  0.5204 | Percentile（%）  0.144 | | | | Sequence  QHLQAKPtTLSLPLT | | SA  1.6312 |
| Basophilic serine/threonine kinase group (Baso\_ST\_kin) | | | | | | | | |
| Clk2 Kinase | | | | Gene Card CLK2 | | | | |
| Site  S576 | Score  0.5091 | Percentile（%）  0.160 | | | | Sequence  RSFSRHRsCSRSPYS | | SA  1.1516 |
| Phosphoserine/threonine binding group (pST\_bind) | | | | | | | | |
| Nek4 | | | | Gene Card NEK4 | | | | |
| Site  S570 | Score  0.5023 | Percentile（%）  0.184 | | | Sequence  RMRSRSRsFSRHRSC | | | SA  1.8321 |
| Kinase binding site group (Kin\_bind) | | | | | | | | |
| PDK1 Binding | | | | Gene Card PDPK1 | | | | |
| Site  D534 | Score  0.474 | Percentile（%）  0.080 | | | Sequence  TQSYSLFdVSPSCSS | | | SA  0.4203 |
| Basophilic serine/threonine kinase group (Baso\_ST\_kin) | | | | | | | | |
| Akt Kinase | | | | Gene Card AKT1 | | | | |
| Site  S634 | Score  0.453 | Percentile（%）  0.157 | | | | Sequence  SRRPRYDsYEEYQHE | SA  3.7766 | |
| Kinase binding site group (Kin\_bind) | | | | | | | | |
| Erk D-domain | | | | Gene Card MAPK1 | | | | |
| Site  L376 | Score  0.417 | Percentile（%）  0.063 | | | Sequence  RKAKRPSlRLFGDHD | | | SA  0.5477 |
| Proline-dependent serine/threonine kinase group (Pro\_ST\_kin) | | | | | | | | |
| Erk1 Kinase | | | | Gene Card MAPK3 | | | | |
| Site  T293 | Score  0.389 | Percentile（%）  0.069 | | | Sequence  LSGTAGLtPPTTPPH | | | SA  0.9314 |
| DNA damage kinase group (DNA\_dam\_kin) | | | | | | | | |
| ATM Kinase | | | | Gene Card ATM | | | | |
| Site  T261 | Score  0.387 | Percentile（%）  0.072 | | | Sequence  TTLSLPLtPESPNDP | | | SA  1.5135 |
| Basophilic serine/threonine kinase group (Baso\_ST\_kin) | | | | | | | | |
| PKC alpha/beta/gamma | | | | Gene Card PRKCA | | | | |
| Site  T235 | Score  0.366 | Percentile（%）  0.144 | | | Sequence  NSSRDKCtSKKKAHT | | | SA  1.9003 |
| Basophilic serine/threonine kinase group (Baso\_ST\_kin) | | | | | | | | |
| PKC delta | | | | Gene Card PRKCD | | | | |
| Site  S375 | Score  0.332 | Percentile（%）  0.088 | | | Sequence  ERKAKRPsLRLFGDH | | | SA  1.2390 |
| Phosphoserine/threonine binding group (pST\_bind) | | | | | | | | |
| 14-3-3 Mode 1 | | | | Gene Card YWHAZ | | | | |
| Site  T570 | Score  0.325 | Percentile（%）  0.194 | | | | Sequence  RMRSRSRsFSRHRSC | | SA  1.8321 |
| Proline-dependent serine/threonine kinase group (Pro\_ST\_kin) | | | | | | | | |
| Cdc2 Kinase | | | Gene Card CDK1 | | | | | |
| Site  T297 | Score  0.323 | Percentile（%）  0.028 | | | | Sequence  AGLTPPTtPPHKANQ | | SA  2.4012 |
| Proline-dependent serine/threonine kinase group (Pro\_ST\_kin) | | | | | | | | |
| Cdk5 Kinase | | | Gene Card CDK5 | | | | | |
| Site  T297 | Score  0.301 | Percentile（%）  0.052 | | | | Sequence  AGLTPPTtPPHKANQ | | SA  2.4012 |
| Basophilic serine/threonine kinase group (Baso\_ST\_kin) | | | | | | | | |
| Akt Kinase | | | Gene Card AKT1 | | | | | |
| Site  S570 | Score  0.277 | Percentile（%）  0.004 | | | | Sequence  RMRSRSRsFSRHRSC | | SA  1.8321 |