

**Table S1: Reverse transcription qPCR primers.**

| Gene                        | Fragment size (bp) | Annealing temperature (°C) | Primer sequences (5'-3')                          |
|-----------------------------|--------------------|----------------------------|---|
| <i>AFM</i> <sup>1</sup>     | 194                | 60                         | ATGTCTGTGGGGCACTTTTG<br>GTTTCATAACCTTGCTCGTGTC    |
| <i>AFP</i> <sup>1</sup>     | 173                | 56                         | GAAGAAGACAGGGGAGACATTC<br>ACTGTTGCTGCCTTTGTTTGG   |
| <i>ALB</i> <sup>1</sup>     | 134                | 58                         | GAAAGTACCCCAAGTGTCAAC<br>TCAGGACCACGGATAGATAG     |
| <i>AREG</i> <sup>1</sup>    | 91                 | 58                         | GGAGCCGACTATGACTACTC<br>CTACCTGTTCAACTCTGACTG     |
| <i>B2M</i> <sup>2,3</sup>   | 246                | 60                         | GGCTATCCAGCGTACTCCAAA<br>CGGCAGGCATACTCATCTTTTT   |
| <i>CXCL1</i> <sup>1</sup>   | 67                 | 58                         | GATGCTGAACAGTGACAAATC<br>TCAGGAACAGCCACCAGTG      |
| <i>CXCL2</i> <sup>1</sup>   | 279                | 58                         | CGAAAAGATGCTGAAAAATGGC<br>GGAGAGTGTGCAAGTAGATTC   |
| <i>CXCL3</i> <sup>1</sup>   | 74                 | 58                         | GATACTGAACAAGGGGAGCACG<br>CAGGAAGTGTCAATGATACG    |
| <i>CXCL4</i> <sup>1</sup>   | 313                | 56                         | CGAGGCTCAGGAGTCATTG<br>GTGGCTATCAGTTGGGCAG        |
| <i>CXCL4.1</i> <sup>1</sup> | 141                | 56                         | CTGCCCAACTCATAGCCAC<br>TCACAGTTAGATTGAAAGTGC      |
| <i>CXCL5</i> <sup>1</sup>   | 203                | 56                         | CGTTGCGTTTGTTTACAGAC<br>CAGTTTTCTTGTTTCCACC       |
| <i>CXCL6</i> <sup>1</sup>   | 146                | 58                         | CGAACCTCTCTTGACCAC<br>AGCAGAGACAGGACCAGCG         |
| <i>CXCL7</i> <sup>1</sup>   | 207                | 63                         | GCGAAAAGGCAAAGAGGAAAG<br>CTTGATTCTGGGAGCATCTG     |
| <i>CXCL8</i> <sup>1</sup>   | 168                | 58                         | CAGAGACAGCAGAGCACAC<br>AGCACTCCTTGGCAAAACTG       |
| <i>EPGN</i> <sup>1</sup>    | 109/136            | 62                         | GACAGCACTGACCGAAGAG<br>CAGGCAAAGGTGTGAGAAC        |
| <i>EREG</i> <sup>1</sup>    | 77                 | 58                         | GAGGAGGATGGAGATGCTC<br>CTGCCTGTAGAAGATGGAAAC      |
| <i>GAPDH</i> <sup>2,3</sup> | 113                | 60                         | CATGAGAAGTATGACAACAGCCT<br>AGTCCTTCCACGATACCAAAGT |
| <i>HPRT1</i> <sup>2,4</sup> | 94                 | 60                         | TGACACTGGCAAAACAATGCA<br>GGTCCTTTTCACCAGCAAGCT    |
| <i>MTHFD2L</i> <sup>1</sup> | 136                | 62                         | CTCTGCTGTAGGTATTTGTAG<br>GTCTGGTAGTGGTAACTGAAC    |
| <i>RASSF6</i> <sup>1</sup>  | 168                | 60                         | GCAAAGGAATGACACGCTGG<br>GCACTGGGGAGTCTGGTTC       |
| <i>RPLP0</i> <sup>1,2</sup> | 319                | 58-63                      | AGATGCAGCAGATCCGCAT<br>GTGGTGATACCTAAAGCCTG       |

<sup>1</sup> designed with Oligo 4.0 software (National Biosciences, Plymouth, MN, USA)

<sup>2</sup> reference gene

<sup>3</sup> Sequence obtained from PrimerBank (<http://pga.mgh.harvard.edu/primerbank>)

<sup>4</sup> see [59]