**Supplementary figures**



Figure S1. Whole mount in situ hybridization of Fgf4 in the 2-day in vitro organ cultivated tooth germs (A-B, E-F). The expression of Fgf4 is almost similar in both group. 3D- reconstruction showing similar size of enamel knots in control and 4PBA group (C-D, G-H). Dotted lines indicate section views (A, E) and epithelial boundary (B, F). Scale bars: 50 μm (B, F).

**Table S1. List of primers used in the study**

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | Accession | Primer sequence | Product size |
| **Ambn** | NM\_001303431.1 | Forward: TTCTTGCTTTCCCCAATGAC | 234 |
| Reverse: GGTGCACTTTGTTTCCAGGT |
| **Amelx** | XM\_017348358,1 | Forward: GCAGCCGTATCCTTCCTATGGTT | 120 |
| Reverse: GGAAGGTGGTGATGAGGCTGAA |
| **Atf6** | NM\_001081304.1 | Forward: GCAGATTGACTGTCAGGTGA | 206 |
| Reverse: TCTTCAGTCTCTCGTGTCCA |
| **Bmp2** | NM\_007553.3 | Forward: AAGTGGCCCATTTAGAGGAG | 104 |
| Reverse: CAATGGCCTTATCTGTGACC |
| **Bmp4** | NM\_007554.2 | Forward: ACCTCAAGGGAGTGGAGATT | 113 |
| Reverse: GATGCTTGGGACTACGTTTG |
| **Dmp1** | NM\_001359013.1 | Forward: CAGAGGGACAGGCAAATAGTGAC | 168 |
| Reverse: CATCGCCAAAGGTATCATCTCC |
| **Dspp** | NM\_010080.3 | Forward: GGCTCCGAGTCAATACATGTAReverse: CTCCTTGGTGTCCATTGCTAT | 933 |
| **Enam** | NM\_017468.3 | Forward: GCCCCACCAATGATGCCTAT | 200 |
| Reverse: TGTGGATTGGTCTGGTTGGG |
| **Fgf4** | NM\_010202.5 | Forward: TCGCCTACCATGAAGGTAAC | 114 |
| Reverse: TCTCCATCGAGAGAAAGTGC |
| **lre1** | NM\_012016.3 | Forward: TTTAGCTTTGCCGACCGTGA | 123 |
| Reverse: TGCACACAGCTCGATAGCAA |
| **Perk** | NM\_010121.3 | Forward: CACGCAGATCACAGTCAGGT | 166 |
| Reverse: GGGCTGAGGATGGAAAAGCC |
| **Shh** | NM\_009170.3 | Forward: CAGCGCGTGTACGTGGTGGC | 335 |
| Reverse: GGAGCGTCGGCAGCACCTG |
| **Hprt** | NM\_013556.1 | Forward: CCTAAGATGATCGCAAGTTG | 86 |
| Reverse: CCACAGGGACTAGAACACCTGCTAA |

**Table S2**. Statistical evaluation of immunohistochemical staining against GRP78 and HRD1

|  |  |  |
| --- | --- | --- |
| **Group** | **Control** | **4PBA** |
| GRP78 | ++ | +++ |
| HRD1 | + | ++ |

-:none, +: exist, ++: strong, +++: strongest