**Supplementary File 1**

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Forward** | **T7 + Reverse** | **Product Size** |
| Cdh1 | CCCAGAGACTGGTGCCATTT | TAATACGACTCACTATAGGGTTTCGAGTCACTTCCGGTCG | 747 |
| Cdh2 | ACAGCGCAGTCTTACCGAAG | TAATACGACTCACTATAGGGGGCCATAAGTGGGATTGCCT | 963 |
| Cdh3 | CAACGAAGCCCCTGTGTTTG | TAATACGACTCACTATAGGGCGTTTCGGAGAACCACCTCA | 899 |
| Cdh4 | ACACAAGAAAGGGCAGACAG | TAATACGACTCACTATAGGGCTGTTGCTACAGTGCCTGCT | 609 |
| Cdh5 | TTGGACCGAGAGAAACAGGC | TAATACGACTCACTATAGGGAGGGTTACCCCGAGAATCCA | 729 |
| Cdh6 | CCAGCCCTACCCAACTTTCT | TAATACGACTCACTATAGGGCCTTCCTGGGTTTCCTGGTC | 939 |
| Cdh7 | GGGAAGCTCCACTCTGATGT | TAATACGACTCACTATAGGGTGTGTCGCTTCTGACACCTC | 968 |
| Cdh8 | AGGTTTTCCATTGACCGCCA | TAATACGACTCACTATAGGGAATCCCCACCGGGGTAAAAA | 824 |
| Cdh9 | ATGTAGATGAGCCCCCTGTG | TAATACGACTCACTATAGGGCCTCTTCAATGCAGCAAACA | 788 |
| Cdh10 | TGACCCTTCCTATGGAAACA | TAATACGACTCACTATAGGGCCACCTAAGGGGTCATCTTT | 999 |
| Cdh11 | CTATACCACAGCCAGGCGTT | TAATACGACTCACTATAGGGATCTGGTACACGCTCTGTGG | 776 |
| Cdh12 | AGCCCCAACAGACTTTAGCC | TAATACGACTCACTATAGGGGAGCCAACAGGGGAAGACTC | 781 |
| Cdh13 | CCGAGAACTCCGCTCACC | TAATACGACTCACTATAGGGCAAACGCTGTCATCCGCATC | 805 |
| Cdh15 | AGCCAGATTAACGTGAGCCA | TAATACGACTCACTATAGGGTGAGAGCTGTGTCGTAGGGA | 610 |
| Cdh16 | TTACCTCTCTGTTATTCAGCTACCA | TAATACGACTCACTATAGGGCTGGTAGTGCACGTCTCCTC | 703 |
| Cdh17 | GAAGGCCAAGAACCGAGTCA | TAATACGACTCACTATAGGGAGACATGTCGGTGGGTTGTC | 905 |
| Cdh18 | ATCCACCTGAACTTGCCAGG | TAATACGACTCACTATAGGGTACGTGAACTCCTCTGCTGC | 601 |
| Cdh19 | ACAAGCTACTGGGGATTGGC | TAATACGACTCACTATAGGGGTGGAAGCGTTAACATGGGC | 823 |
| Cdh20 | ACTGTGAAGAAGCCCCTGAG | TAATACGACTCACTATAGGGCTTGAATGGTAAGCGTGCCG | 775 |
| Cdh22 | AGGAGTACACGGGGACAGAA | TAATACGACTCACTATAGGGACTCAAAGTCCAGGTGCTTC | 831 |
| Cdh23 | TGCGCAGACAGAACTGCTTA | TAATACGACTCACTATAGGGTTCAGCAGCGAGCCCTTAAT | 636 |
| Edil3 | AAATGGTGGCATCTGTCTGT | TAATACGACTCACTATAGGGCATTTCCACGAAAGACCATC | 721 |
| Ptprt | CACCACCTCTTTGTGGGTCT | TAATACGACTCACTATAGGGCACTCTGGGTCTCCTTCTGC | 700 |
| Lsamp | ACTCAAAAGTGGCCTGGTTG | TAATACGACTCACTATAGGGGGATCCGTTGATTCCTCTCA | 776 |
| Negr1 | AGCGGTGCTCAGGTGTTACT | TAATACGACTCACTATAGGGTTGGTCACTGTGAGGATGGA | 693 |

**Supplementary Table 1.** PCR primers for *in situ* hybridization

**Supplementary Table 2.** Specificity of *in situ* probes for PMC cadherins

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Name** | **Product Size** | **% of probe in**  **extracellular**  **domain** | **On target BLAST max score** | **Off target BLAST max score #1** | **Off target BLAST max score #2** | **Off target BLAST max score #3** |
| Cdh2 | 963 | 100 | 1737 | 312 (cdh4) |  |  |
| Cdh6 | 939 | 100 | 1694 | 570 (cdh9) | 568 (cdh10) | 374 (cdh20) |
| Cdh9 | 788 | 91 | 1422 | 279 (cdh6) | 265 (cdh10) |  |
| Cdh10 | 999 | 100 | 1802 | 428 (cdh6) | 376 (cdh9) | 333 (cdh12) |
| Cdh11 | 776 | 100 | 1400 | 408 (cdh20) | 347 (cdh24) | 331 (cdh8) |
| Cdh22 | 831 | 100 | 1499 | 232 (cdh24) | 229 (cdh20) | 226 (cdh12) |

To ascertain the specificity for the designed *in situ* probes to its intended target (given the degree of similarity between members of the cadherin family), we ran each full length probe through BLAST (<https://blast.ncbi.nlm.nih.gov/>) against the refseq\_rna database for *M. Musculus* and checked for cross-reactivity with other cadherins. BLAST outputs a ‘max alignment score’ parameter, which awards points for base matches while penalizing base mismatches, gaps, etc. While all on target alignment scores are high (>1400, dependent on probe length), off target scores are low (<35% of the max alignment score of the intended target).