
**Supplementary Figure S9.** Sequence alignment of mouse and human PDGFB proteins and the PDGF1 and PDGF2 peptides. The sequence alignment was carried out using the MUSCLE program.[S1]

**Supplementary Table S1.** *High-performance liquid chromatography analysis of compounds*

| *Compound* | *Retention Time (min)* | *Purity (%)* |
|---|---|---|
| PDGF1 | 4.47 | 97.8 |
| PDGF2 | 4.76 | 98.2 |
| PDGF2-HTT | 5.57 | 98.6 |

The purity of the peptides was verified by analytical UPLC with Nexera X2 (Schimadzu) on the C8 Kinetex 2.6 $\mu$m 100 Å column (2.1 × 100 mm; Phenomenex). The following eluents were used: A = 0.1% TFA in water and B = 0.1% TFA and 80% ACN in $H_2O$. The flow rate was 0.5 mL/min, and UV detection at $\lambda = 223$ nm was performed. A linear gradient of 5 → 100% B over 15 min was used. The percentage purity of peptides was determined as the % of area under the peak.

ACN, acetonitrile; HTT, head-to-tail cyclization methodology; PDGF, platelet-derived growth factor; TFA, trifluoroacetic acid.

**Supplementary Table S2.** *Quantitative PCR primers*

| *Gene* | *Forward/Reverse* | *Sequence* |
|---|---|---|
| *ACTB* | Forward | CATGGGTCAGAAGGATTCCT |
| *ACTB* | Reverse | ACACGCAGCTCATTGTAGAA |
| *CDKN1A* | Forward | CTGGCACCTCACCTGCTCTG |
| *CDKN1A* | Reverse | CGGATTAGGGCTTCCTCTTGG |
| *MYC* | Forward | ATAGCAGCGGGCGGGCA |
| *MYC* | Reverse | CGAGGTCATAGTTCCTGTTGGTG |
| *POU5F1* | Forward | TCAGCCACATCGCCCA |
| *POU5F1* | Reverse | AGACCCAGCAGCCTCAA |
| *TBP* | Forward | TCCACAGTGAATCTTGGTTGTA |
| *TBP* | Reverse | CACCATTTTCCCAGAACTGA |
| *TGFB3* | Forward | CGTGAGTGGCTGTTGAGAAG |
| *TGFB3* | Reverse | GATTAGATGAGGGTTGTGGTGA |
| *TP53* | Forward | GCTTTGAGGTGCGTGTTTGTG |
| *TP53* | Reverse | AGTGGTTTCTTCTTTGGCTGGG |
| *KIT* | Forward | CTGCGTTCTGCTCCTACTGCTT |
| *KIT* | Reverse | CCTGGATGGATGGATGGT |