**SUPPLEMENTARY TABLES**

**Supplementary Table 1. Sequences of the wild-type GREM1 dual reporting vector and the GREM1 mutant sites vector.**

| Name | Sequences |
|------|-----------|
| The wild-type GREM1 dual reporting vector | gccaaatccaggtgcacccagcatgtcctaggaatgcagccccaggaagtcccagacctaaaacaaccagattcttacttggcttaaacctagaggccagaagaacccccagctgcctcctggcaggagcctgcttgtgcgtagttcgtgtgcatgagtgtggatgggtgcctgtgggtgtttttagacaccagagaaaacacagtctctgctagagagcactccctattttgtaaacatatctgttaatggggatgtaccagaaacccacctcaccccggctcacatctaaaggggcggggccgtggtctggttctgactttgtgtttttgtgccctcctggggaccagaatctcctttcggaatgaatgttcatggagaaggctcctctgagggcaagagacctgttttagtgctgcattcgacatggaaaagtccttttaacctgtgcttgcatcctcctttcctcctcctcctcacaatccatctcttcttaagttgatatgtgacatatgtcagtctaatctcttgtttgccaaggttcctaaattaattcacttaaccatgatgcaaatgtttttcattttgtgaagaccctccagactctgggagaggctggtgtgggcaaggacaagcaggatagtggagtgagaaagggagggtggagggtgaggccaaatcaggtccagcaaaagtcagtagggacattgcagaagcttgaaaggccaataccagaacacaggctgatgcttctgagaaagtccttttcctagtatttaacagaacccaagtgaacagaggagaaatgagattgccagaaagtgattaactttggccgttgcaatctgctcaaacctaacaccaaactgaaaacataaatactgaccactcctatgttcggacccaagcaagttagctaaaccaaaccaactcctctgctttgtccctcaggtggaaaagagaggtagtttagaactctctgcataggggtgggaattaat |
| The GREM1 mutant sites vector | gccaaatccaggtgcacccagcatgtcctaggaatgcagccccaggaagtcccagacctaaaacaaccagattcttacttggcttaaacctagaggccagaagaacccccagctgcctcctggcaggagcctgcttgtgcgtagttcgtgtgcatgagtgtggatgggtgcctgtgggtgtttttagacaccagagaaaacacagtctctgctagagagcactccctattttgtaaacatatctgttaatggggatgtaccagaaacccacctcaccccggctcacatctaaaggggcggggccgtggtctggttctgactttgtgtttttgtgccctcctggggaccagaatctcctttcggaatgaatgttcatggagaaggctcctctgagggcaagagacctgttttagtgctgcattcgacatggaaaagtccttttaacctgtgcttgcatcctcctttcctcctcctcctcacaatccatctcttcttaagttgatatgtgacatatgtcagtctaatctcttgtttgccagaaggttcctaaattaattcacttaaccatgatgcaaatgtttttcattttgtgaagaccctccagactctgggagaggctggtgtgggcaaggacaagcaggatagtggagtgagaaagggagggtggagggtgaggccaaatcaggtccagcaaaagtcagtagggacattgcagaagcttgaaaggccaataccagaacacaggctgatgcttctgagaaagtccttttcctagtatttaacagaacccaagtgaacagaggagaaatgagattgccagaaagtgattaactttggcgttgcaatctgctcaaacctaacaccaaactgaaaacataaatactgaccactcctatgttcggacccaagcaagttagctaaaccaaaccaactcctctgctttgtccctcaggtggaaaagagaggtagtttagaactctctgcataggggtgggaattaat |

The yellow area in sequence of the wild-type GREM1 dual reporting vector indicates the rs3743104 site; The sequences within the range of upstream 1000bp to downstream 1000bp of GREM1 rs3743104 are display in the table; The yellow area in sequence of the GREM1 mutant sites vector indicates the area to be mutated.

**Supplementary Table 2. Sequences of miR-182, miR-212, miR-221, miR-3128 mimics.**

| Name | Accession | Sequence |
|------|-----------|----------|
| hsa-miR-182-5p mimics | MIMAT0000259 | UUUGGCAAUUGGUAACUCACACU |
| hsa-miR-212-5p mimics | MIMAT0022695 | ACCUUGGCUCAGACUGUUACU |
| hsa-miR-221-5p mimics | MIMAT0004568 | ACCUGGCAUACAAUGUAU |
| hsa-miR-3128 mimics | MIMAT0014991 | UCUGGCAAGUAAAAACUCUAC |

**Supplementary Table 3. Luciferase activities in HEK293T cells transfected with respective construct, either miR-182, miR-212, miR-221, miR-3128 mimics and correspond MicroRNA inhibitor.**

| mean | blank | NC | mir182 | mir212 | mir221 | mir3128 |
|------|-------|----|--------|--------|--------|--------|
| pSicheck2 | 0.37±0.07 | 0.31±0.01 | 0.33±0.04 | 0.29±0.03 | 0.37±0.07 | 0.35±0.05 |
| 3'UTR GREM1 | 0.82±0.03 | 0.82±0.01 | 0.71±0.02 | 0.85±0.05 | 0.81±0.02 | 0.75±0.03 |
| 3'UTR mutGREM1 | 0.97±0.09 | 0.92±0.18 | 0.80±0.06 | 0.80±0.06 | 0.94±0.02 | 0.91±0.02 |

Data are shown as mean ± SD; NC: Negative control; Comparing each group with the blank group.