

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 <i>GREM1</i> dual reporting vector	<p>gccaaatccaggtgcaccagcatgctcctaggaatgcagcccaggaagtcaccagactaaacaaccagattcttacttgcttaaacctagaggccagaagaacccccagctgcctctggcaggagcctgctgctgtagtctgtgcatgagtgatgggtgcctgtgggtgttttagacaccagagaaaacacagctctctgtagagagcactccctattttgaaacatatctgctttaatgggatgtaccagaaccacctcaccggctcacatctaagggggccgggctggtctgacttggtttttggccctctgggaccagaatctcttccggaatgaatgttcaggaagaggctcctctgagggcaagagacctgttttagtgcctcattgcacatggaaaagtcctttaacctgtgcttgcacctctctcctcctcctcacaatccatctctttaaagttagatgtgatgtcagctaatctctgtttgccatgggttcctaaataatcactaacatgatgcaaatgttttcaatttggagaccctccagactctgggagaggctgggtggcaagacagcagcagatgtggagtgagaaaggaggggtgagggcgaatcaggtccagcaaaaagcagtagggacattgcagaagcttgaaggccaataccagaacacagcctgatcctctgagaaagtctttcctagtatttaacagaaccgaagtgaaacagaggagaaatgagattgccagaaaagtgattaaccttggccgtgcaactgctcaaacctaacaccaactgaaacataatactgaccactctatgttcggaccaagcaagttagtaaaccaaacactcctctccttgcctcaggtggaaaagagagtagtttagaactctcctgataggggtgggaattaat</p> <p>Gccaaatccaggtgcaccagcatgctcctaggaatgcagcccaggaagtcaccagactaaacaaccagattcttacttgcttaaacctagaggccagaagaacccccagctgcctctggcaggagcctgctgctgtagtctgtgcatgagtgatgggtgcctgtgggtgttttagacaccagagaaaacacagctctctgtagagagcactccctattttgaaacatatctgctttaatgggatgtaccagaaccacctcaccggctcacatctaagggggccgggctggtctgacttggtttttggccctctgggaccagaatctcttccggaatgaatgttcaggaagaggctcctctgagggcaagagacctgttttagtgcctcattgcacatggaaaagtcctttaacctgtgcttgcacctctctcctcctcctcacaatccatctctttaaagttagatgtgatgtcagctaatctctgtttgccatgggttcctaaataatcactaacatgatgcaaatgttttcaatttggagaccctccagactctgggagaggctgggtggcaagacagcagcagatgtggagtgagaaaggaggggtgagggcgaatcaggtccagcaaaaagcagtagggacattgcagaagcttgaaggccaataccagaacacagcctgatcctctgagaaagtctttcctagtatttaacagaaccgaagtgaaacagaggagaaatgagattgccagaaaagtgattaaccttggccgtgcaactgctcaaacctaacaccaactgaaacataatactgaccactctatgttcggaccaagcaagttagtaaaccaaacactcctctccttgcctcaggtggaaaagagagtagtttagaactctcctgataggggtgggaattaat</p>
The <i>GREM1</i> mutant sites vector	<p>WT: a MT: g</p> <p>agaccctccagactctgggagagctggtgtgggcaaggacaagcagatagtgagtagaagagggggtggagggtgaggccaatcaggtccagcaaaaagcagtagggacattgcagaagcttgaaggccaataccagaacacagcctgatgctctgagaaagtctttcctagtatttaacagaaccgaagtgaaacagaggagaaatgagattgccagaaaagtgattaaccttggccgtgcaactgctcaaacctaacaccaactgaaacataatactgaccactctatgttcggaccaagcaagttagctaaacaaacactcctctccttgcctcctcaggtggaaaagagagtagtitttagaactctcctgataggggtgggaattaat</p>
<i>GREM1</i>-WT-XhoI	5'ccgctcgagGCCAAATCCAGGTGCACCCAGCATGTCCTA 3'
<i>GREM1</i>-WT-NotI	5'ataagaatcgggccgcATTAATTCCCACCCTATGCAGAGAGT 3'
<i>GREM1</i>-mutF	5'CTAATCTCTGTTTGCCAGGGTTCCTAAATTAATTCACCTTAACCATGATGCAAAATG 3'
<i>GREM1</i>-mutR:	5'TTAATTTAGGAACCCTGGCAAACAAGAGATTAGACTGACATAGTCACTATCAACTT 3'

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	UUUGGCAAUGGUAGAACUCACACU
hsa-miR-212-5p mimics	MIMAT0022695	ACCUUGGCUCUAGACUGCUUACU
hsa-miR-221-5p mimics	MIMAT0004568	ACCUGGCAUACAAUGUAGAUUU
hsa-miR-3128 mimics	MIMAT0014991	UCUGGCAAGUAAAAAACUCUCAU

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 <i>GREM1</i>	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 mut <i>GREM1</i>	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.