

Supplementary Table 1. The Primer design of PCR.

Primer Name	Sequence	Size
CLCNKB-1-F	GGCAGTTCTGATCGGTTTTTC	355
CLCNKB-1-R	CTCCCTGTCCACCTATGAGCA	
CLCNKB-2-F	TCCCTCCCTCTATCCGCTTCT	360
CLCNKB-2-R	GCTGTATCTCCCGAAAGGCA	
CLCNKB-3-F	CGGGACTACCCCAGAGTATAC	500
CLCNKB-3-R	AGCTCTTGGAACATTCAGGC	
CLCNKB-4-F	CCCAAGGTCACTCAGCTAGGC	364
CLCNKB-4-R	GACTGGCGTAGCGACTGTG	
CLCNKB-5-F	CTTCAGAGGGTTCTGCTGATC	381
CLCNKB-5-R	GTGAGGGCAGCAGAGACGGT	
CLCNKB-6-7F	GCAGGCCAGGTCCCCGGAGT	762

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CLCNKB-6-7R	TGCCCAGAGACCCGTCCAGC	
CLCNKB_8-F	5'GCAGGAGAGCAGGACAGATG3'	389
CLCNKB_8-R	5'CCTCCATCCTCCCAGAAG3'	
CLCNKB-9-10F	GGGCTGACCTGTGTTGAGCA	586
CLCNKB-9-10R	ACATAAGGTTGGGAGTACGG	
CLCNKB-11-12F	TGCCTTGCTAGGCCCTGCTT	697
CLCNKB-11-12R	ATGCCACCAGCTGCGATGAG	
CLCNKB-13-14F	TCCTGTCCTCCCTTGTCCAC	536
CLCNKB-13-14R	GGGGTAGGGGGTTC ACTGGA	
CLCNKB-15-F	TTAGCCCCTGGTCGCAGCCG	571
CLCNKB-15-R	CCGGTTTCCTCAATCTGTAC	
CLCNKB-16-F	CCCTCATTCAGGAACCTCT	400
CLCNKB-16-R	GTCACACGGTTGGTTGCTAAG	

CLCNKB-17-18F	AGCCCCATAGGAACACCAGA	759
CLCNKB-17-18R	CACAGGGAGAATGCGGTGGA	
CLCNKB_19-F	5'TCTTCCTGGCTCAGAGGCGT3'	239
CLCNKB_19-R	5'CCACCTCCCCAGTCTTCTC3'	
CLCNKB_20-F	5'GGTGGCACAGGCTCTACTAT3'	317
CLCNKB_20-R	5'TCTGGGCTAGGTAAAGTTG3'	
KCNJ1-1-F	GCCCAGAGACCTTAGCTG	436
KCNJ1-1-R	AGAAGTACCCCTGATTGATC	
KCNJ1-2-F	GTCAGCTTGCCAAATGATTAG	1300
KCNJ1-2-R	GCTTTACTCCCGTTGA	
SLC12A1-1-F	ATATCCCACCCTTACCTAAAT	837
SLC12A1-1-R	CTTTTCTGGGAACTAGGGAC	
SLC12A1-2-3-F	GAAAAGTTTCATGGAACCCTT	648

SLC12A1-2-3-R	ATTACCTGTTTGGCAAGC	
SLC12A1-4-F	TAGTTTGCAGCAATAGGGAA	379
SLC12A1-4-R	CAATGTGCCAGAGAGATCCAT	
SLC12A1-5-F	ACCAAGAAGGGCTAAGTTATT	496
SLC12A1-5-R	TTGGCTGGTAAGTGCGAGAA	
SLC12A1-6-F	CCCAGGTGTAATTGTATAGTA	420
SLC12A1-6-R	GCAGTCATGTGACTCGTGAG	
SLC12A1-7-F	TTGCATGCCATTCTAATAAGG	407
SLC12A1-7-R	TCCGCATCCACAAGTAAC	
SLC12A1-8-F	ACTAGGGAAGCCAATGGTAA	466
SLC12A1-8-R	TTTGGGGAAATATGACACAC	
SLC12A1-9-F	TTGCCTCAGGAAGGGTAGCC	540
SLC12A1-9-R	TCTCTCCTGCCTCCTAGAAC	

SLC12A1-10-F	GAAATGGCAGCCTGTTACA	451
SLC12A1-10-R	TCAGCCAATAATCAATCAGTT	
SLC12A1-11-F	AGCGAGGCGTGGTAGCAGGT	474
SLC12A1-11-R	ATGATTGCCAGTGAGAACGA	
SLC12A1-12-F	TCGTTCTCACTGGCAATCAT	542
SLC12A1-12-R	CCTCAAAGGCCCTCTACACA	
SLC12A1-13-F	ACAGATGCTCGCTATGTTTTC	354
SLC12A1-13-R	AAGTGGATTACGCTTCCCACT	
SLC12A1-14-F	AGGGACCCAAGACCATAGGAA	415
SLC12A1-14-R	CCTCACCTAAGCCCATAGAA	
SLC12A1-15-F	AAGGGAATGACTTGTAATAAT	448
SLC12A1-15-R	CTAGTCCACCTTGCTATCTC	
SLC12A1-16-F	GACAGGCAGGATGATTCAAG	598

SLC12A1-16-R	TCTGTAGACAGTTATCACCC	
SLC12A1-17-F	TCTTTCCCATTTCTTAACTC	626
SLC12A1-17-R	CCTGACTTGAGCATTGCTAT	
SLC12A1-18-F	ATAGCTGGGATGATTAGAA	483
SLC12A1-18-R	CCCTCAAACCTCTATTATTGGT	
SLC12A1-19-F	AGGTGGATTTTAATAGTTTC	618
SLC12A1-19-R	AGGCTCATTTCCATGTTAGC	
SLC12A1_20-F	5'GAGCTACCTCACCCAACCAA3'	423
SLC12A1_20-R	5'CTTAGATGCTGACTTCGGAC3'	
SLC12A1-21-22-F	CGCTATTTATTTTAGGTATA	626
SLC12A1-21-22-R	GTGAGTGGCAAACCTACTTACA	
SLC12A1-23-F	CTGAAATAAGACGTGATTGCT	615
SLC12A1-23-R	TGCCAAGAAGATACAAGCTAT	

SLC12A1-24-F	CAGTCACACCTGGAGTATCTG	472
SLC12A1-24-R	GAAAGGAGACTTCACAATATG	
SLC12A1-25-F	AAGATGAGATTTTCTGCTTGT	493
SLC12A1-25-R	CGCTGACTTGTGGCTGTTAGG	
SLC12A1-26-F	ATTAAGGCTGCCAGTTATTA	662
SLC12A1-26-R	CAGCCTGTCAATAAGCATTT	
SLC12A3-1-F	GCAGACGCAGCCTATAAAAC	557
SLC12A3-1-R	GTTGCTAGTGATTGGCTAAT	
SLC12A3-2-F	CAGAGACGCCGTCCCTAGCA	374
SLC12A3-2-R	CCCGGCAGGCTTTAATCTAT	
SLC12A3-3-F	GGGCCTAGGTGCTCGATACC	520
SLC12A3-3-R	ACAGCCTCCCAAAGCGTGAG	
SLC12A3-4-F	GAGATGAACGTAGGTCGCAT	239

SLC12A3-4-R	GGATTAGGAGCCCACGAGAG	
SLC12A3-5-F	CTCTCGTGGGCTCCTAATCC	565
SLC12A3-5-R	GGA CT TGTGGGAAAGCAATG	
SLC12A3-6-F	GGGGACTCGATGGCAGGGGT	696
SLC12A3-6-R	CTGGGCCATGTGGACCTAGG	
SLC12A3-7-F	GATCCTGCTGCATAATGGGT	504
SLC12A3-7-R	AAGAAGGTGCCATCTGGACC	
SLC12A3-8-F	TGGCCCATTTGTGTGGACACT	746
SLC12A3-8-R	GGGCAAAGCAGTAGAGCCTC	
SLC12A3_9-F	5'CCAGCCTCAGCCTTAGACAA3'	335
SLC12A3_9-R	5'CCAGCTCTCCCTGTTGTTAG3'	
SLC12A3-10-F	TATCATGGCTCCGGGCACACC	574
SLC12A3-10-R	TGTGGCACTTCATTCCCTACT	

SLC12A3-11-F	GGGGTGGGTTGTGGACTCA	361
SLC12A3-11-R	GCTAGAGACCCCAGTCTAATG	
SLC12A3-12-F	ACCAGGACCCAGGTTGGGGA	548
SLC12A3-12-R	AGGACATGTGAACGCAGACC	
SLC12A3-13-F	CTGGGCGCTTACAGTTTACA	418
SLC12A3-13-R	TGCCAACCTCCACCCATGCC	
SLC12A3-14-F	CTCATGGCTGGTGGGTACAG	494
SLC12A3-14-R	TTAGAGGTCGAGACATAGGC	
SLC12A3-15-F	GGGTGCCCCGGTGCCTAGAGA	513
SLC12A3-15-R	ATTGGCTCCGGCGATACTGT	
SLC12A3-16-F	GCCCTCTGCTACCTCTCGAC	649
SLC12A3-16-R	CATCACACCCAGGCGACTCC	
SLC12A3_17-F	5'CTCCTTGTGTTTTCCCTTAT3'	411

SLC12A3_17-R	5'AAAGTTGGGGCTCCTTCT3'	
SLC12A3-18-F	ACCAAGCGAGAACTAGAAATC	673
SLC12A3-18-R	CTTCAGCCTCAGCGTGTTTC	
SLC12A3-19-F	CAGAAAGGGCGTGGTAGGAA	378
SLC12A3-19-R	CATGACCTTGAATGCGTTGC	
SLC12A3-20-F	CGGGACTTTCTTCCTAGCAT	456
SLC12A3-20-R	GTCACCCAGGCTGGCAATGT	
SLC12A3_21-F	5'TGTTCCACCTGCCAGAGAA3'	321
SLC12A3_21-R	5'CCTGTCCCCTTTGAGAGCA3'	
SLC12A3-22-F	GAGAGGAAGGGGTTTGCTAAT	480
SLC12A3-22-R	TAACTCCCCTCCCTGTCGTAG	
SLC12A3-23-F	GGATCACCCGAGGCCAACAT	446
SLC12A3-23-R	GGCTTGGAGGAGAGACCCTT	

SLC12A3-24-F	AAATGGCAGTGTCCGATGGG	451
SLC12A3-24-R	TGAGTTCCACAGCCGGGTTA	
SLC12A3-25-F	TCTGAGGGTCCCCTTCTTCCT	613
SLC12A3-25-R	CCAAGGAGGGCCAAGTAATTC	
SLC12A3-26-F	CTTTGTTTAGAAACGCTTCA	417
SLC12A3-26-R	TGTGGACTAGAGGCAATCAAG	

Supplementary Table 2. Genetic identifications of the 37 monogenic hypertension causative genes sequencing among the six patients with

BS or GS variants.

<u>Case</u> <u>ID</u>	<u>Disease</u>	<u>Mutation</u> <u>gene</u>	<u>Sequence</u> <u>change</u>	<u>Amino acid</u> <u>change</u>	<u>SIFT</u>	<u>PolyPhen-2</u>	<u>Mutation</u> <u>Taster</u>	<u>CADD-</u> <u>phred</u>	<u>Hom/Het</u>
<u>1</u>	<u>No monogenic hypertension variant identified.</u>								
<u>2</u>	<u>No monogenic hypertension variant identified.</u>								

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<u>3</u>	<u>No monogenic hypertension variant identified.</u>								
<u>4</u>	<u>Primary</u> <u>aldosteronism</u>	<u>CACNA1D</u>	<u>c.5279A>G</u>	<u>p.H1760R</u>	<u>Tolerated</u>	<u>Probably</u> <u>damaging</u>	<u>Disease</u> <u>causing</u>	<u>9.001</u>	<u>Het</u>
	<u>Paragangliomas</u>	<u>SDHA</u>	<u>c.1661G>A</u>	<u>p.R554Q</u>	<u>Deleterious</u>	<u>Probably</u> <u>damaging</u>	<u>Disease</u> <u>causing</u>	<u>13.51</u>	<u>Het</u>
<u>5</u>	<u>No monogenic hypertension variant identified.</u>								
<u>6</u>	<u>Multiple endocrine</u> <u>neoplasia IIA</u>	<u>RET</u>	<u>c.2297C>T</u>	<u>p.P766L</u>	<u>Tolerated</u>	<u>Probably</u> <u>damaging</u>	<u>Disease</u> <u>causing</u>	<u>17.33</u>	<u>Het</u>

Supplementary Table 3. The results of captopril test and saline infusion test for case 4.

	<u>Captopril test</u>		<u>Saline infusion test</u>	
	<u>Aldosterone (ng/dL)</u>	<u>Renin</u> <u>(uIU/ml)</u>	<u>Aldosterone (ng/dL)</u>	<u>Renin</u> <u>(uIU/ml)</u>

带格式的：行距： 双线

带格式表格

带格式的：行距： 双线

<u>Before</u>	<u>20.1</u>	<u>7.9</u>	<u>18.5</u>	<u>5.7</u>
<u>After</u>	<u>11.6</u>	<u>9.2</u>	<u>5.3</u>	<u>4.6</u>

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Supplementary Table 4. Prediction results of BEAGLE software.

<u>CHROM</u>	<u>POS</u>	<u>REF</u>	<u>ALT</u>	<u>FILTER</u>	<u>FORMAT</u>	<u>CIS/TRANS*</u>
<u>16</u>	<u>56899203</u>	<u>G</u>	<u>A</u>	<u>PASS</u>	<u>GT</u>	<u>1 0</u>
<u>16</u>	<u>56904097</u>	<u>G</u>	<u>A</u>	<u>PASS</u>	<u>GT</u>	<u>0 1</u>

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带格式的: 行距: 双线

带格式的: 上标

CHROM, chromosome; POS, position; REF, reference sequence; ALT, altered sequence; “1”, altered sequence; “0”, reference sequence.

*“1” of the two variants located on both sides of the vertical line indicates that the variants were located in trans.

Supplementary Table 5. Prediction results of EAGLE software.

<u>CHROM</u>	<u>POS</u>	<u>REF</u>	<u>ALT</u>	<u>FILTER</u>	<u>FORMAT</u>	<u>CIS/TRANS*</u>
<u>16</u>	<u>56899203</u>	<u>G</u>	<u>A</u>	<u>PASS</u>	<u>GT</u>	<u>0 1</u>

带格式的: 字体: 小四

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带格式的: 行距: 双线

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<u>16</u>	<u>56904097</u>	<u>G</u>	<u>A</u>	<u>PASS</u>	<u>GT</u>	<u>10</u>
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CHROM, chromosome; POS, position; REF, reference sequence; ALT, altered sequence; “1”, altered sequence; “0”, reference sequence.

*“1” of the two variants located on both sides of the vertical line indicates that the variants were located in trans.

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- 带格式的: 字体:小四, 粗体

- 带格式的: 两端对齐, 图案: 清除
- 带格式的: 字体:(中文) Times New Roman, 粗体