What is claimed is:

1. Use of a CNP variant in the preparation of a medicament for treating a CNP-responsive bone-related disorder, skeletal dysplasia or short stature disorder in a subject, wherein the CNP variant is to be administered according to a weight-band dosing regimen, wherein

i) a subject between 10–11 kg receives between about 22–24 µg/kg CNP variant;

ii) a subject between 12–16 kg receives between about 18–23 µg/kg CNP variant;

iii) a subject between 17–21 kg receives between about 15–19 µg/kg CNP variant;

iv) a subject between 22–32 kg receives between about 13–18 µg/kg CNP variant;

v) a subject between 33–43 kg receives between about 12–15 µg/kg CNP variant;

vi) a subject between 44–59 kg receives between about 10–14 µg/kg CNP variant;

vii) a subject between 60–89 kg receives between about 8–12 µg/kg CNP variant; or

viii) a subject of weight of ≥ 90 kg receives about ≤ 9 µg/kg CNP variant.

2. The use of claim 1 wherein

i) a subject between 10–11 kg receives about 0.24 mg CNP variant;

ii) a subject between 12–16 kg receives about 0.28 mg CNP variant;

iii) a subject between 17–21 kg receives about 0.32 mg CNP variant;

iv) a subject between 22–32 kg receives about 0.40 mg CNP variant;

v) a subject between 33–43 kg receives about 0.50 mg CNP variant;

vi) a subject between 44–59 kg receives about 0.60 mg CNP variant;

vii) a subject between 60–89 kg receives about 0.7 mg CNP variant; or

viii) a subject of weight of ≥ 90 kg receives about 0.80 mg CNP variant.

3. The use of claim 1 or 2, wherein the short stature disorder is selected from the group consisting of achondroplasia, hypochondroplasia, short stature, idiopathic short stature, dwarfism, osteochondrodysplasias, thanatophoric dysplasia, osteogenesis

congenita, achondrogenesis, chondrodysplasia congenita, homozygous achondroplasia, chondrodysplasia congenita, campomelic dysplasia, congenital lethal hypophosphatasia, perinatal lethal type of osteogenesis congenita, short-rib polydactyly syndromes, rhizomelic type of chondrodysplasia congenita, Jansen-type metaphyseal dysplasia, spondyloepiphyseal dysplasia congenital, atelosteogenesis, diastrophic dysplasia, congenital short femur, Langer-type mesomelic dysplasia, Nievergelt-type mesomelic dysplasia, Robinow syndrome, Reinhardt syndrome, acrodysostosis, peripheral dysostosis, Kniest dysplasia, fibrochondrogenesis, Roberts syndrome, acromesomelic dysplasia, micromelia, Morquio syndrome, Kniest syndrome, metatrophic dysplasia, and spondyloepimetaphyseal dysplasia, disorders related to NPR2 mutation, SHOX mutations, Turner's syndrome/Leri Weill, PTPN11 mutations, Noonan's syndrome, and IGF1R mutation.

4. The use of any one of claims 1-3 wherein the CNP variant is selected from the group consisting of

PGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-Gly-CNP37) (SEQ ID NO: 1); GQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Gly-CNP-37) (SEQ ID NO: 2);
GDLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Gly-CNP53) (SEQ ID NO: 3);
PDLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-CNP53) (SEQ ID NO: 4);
MDLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Met-CNP53) (SEQ ID NO: 5);
DLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSNSGLGC [CNP-53(M48N)] (SEQ ID NO: 6);
LRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-52) (SEQ ID NO: 7);
RVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-51) (SEQ ID NO: 8);
VDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP- 50) (SEQ ID NO: 9);
DTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-49) (SEQ ID NO: 10);
TKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-48) (SEQ ID NO: 11);

KSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-47) (SEQ ID NO: 12);
SRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-46) (SEQ ID NO: 13);
RAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-45) (SEQ ID NO: 14);
AAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-44) (SEQ ID NO: 15);
AWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-43) (SEQ ID NO: 16); WARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-42) (SEQ ID NO: 17); ARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-41) (SEQ ID NO: 18); RLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-40) (SEQ ID NO: 19); LLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-39) (SEQ ID NO: 20); LQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-38) (SEQ ID NO: 21); QEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-37) (SEQ ID NO: 22); EHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-36) (SEQ ID NO: 23); HPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-35) (SEQ ID NO: 24); PNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-34) (SEQ ID NO: 25); NARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-33) (SEQ ID NO: 26); ARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-32) (SEQ ID NO: 27); RKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-31) (SEQ ID NO: 28); KYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-30) (SEQ ID NO: 29); YKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-29) (SEQ ID NO: 30); KGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-28) (SEQ ID NO: 31); GANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-27) (SEQ ID NO: 32); ANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-26) (SEQ ID NO: 33); NKKGLSKGCFGLKLDRIGSMSGLGC (CNP-25) (SEQ ID NO: 34); KKGLSKGCFGLKLDRIGSMSGLGC (CNP-24) (SEQ ID NO: 35); KGLSKGCFGLKLDRIGSMSGLGC (CNP-23) (SEQ ID NO: 36); LSKGCFGLKLDRIGSMSGLGC (CNP-21) (SEQ ID NO: 37); SKGCFGLKLDRIGSMSGLGC (CNP-20) (SEQ ID NO: 38); KGCFGLKLDRIGSMSGLGC (CNP-19) (SEQ ID NO: 39); GCFGLKLDRIGSMSGLGC (CNP-18) (SEQ ID NO: 40); QEHPNARKYKGANKKGLSKGCFGLKLDRIGSNSGLGC [CNP-37(M32N)] (SEQ ID NO: 41); PQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-CNP-37) (SEQ ID NO: 42); MQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Met-CNP-37) (SEQ ID NO: 43);

GQEHPNARKYKGANKKGLSKGCFGLKLDRIGSNSGLGC [Gly-CNP-37(M32N)] (SEQ ID NO: 44);
MGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Met-Gly-CNP-37) (SEQ ID NO: 45);
PGQEHPQARRYRGAQRRGLSRGCFGLKLDRIGSMSGLGC (SEQ ID NO: 46);
PGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 47);
PGQEHPNARRYRGANRRGLSRGCFGLKLDRIGSMSGLGC (SEQ ID NO: 48);
PGQEHPQARKYKGAQKKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 49);
GQEHPNARKYKGANPKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 50);
GQEHPNARKYKGANQKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 51);
GQEHPNARKYKGANQQGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 52); and
GQEHPNARKYKGANKPGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 53).

5. The use of any one of claims 1 to 4, wherein the CNP variant is PGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-Gly-CNP37) (SEQ ID NO: 1); GQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Gly-CNP-37) (SEQ ID NO: 2); or LQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-38) (SEQ ID NO: 21).

6. A method of identifying a variant gene associated with short stature that is a gain of function (GoF) or loss of function (LoF) variant comprising:

-contacting cells comprising a cGMP-reporter expression construct and a lentiviral vector expressing a polynucleotide encoding a variant protein associated with short stature operably linked to one or more unique barcode sequences in culture with c-type natriuretic peptide (CNP) or a variant thereof having CNP activity;

-sorting the cells from the culture based on the level of expression of reporter produced by the cell; and

-identifying the variant protein associated with short stature as a GoF variant or a LoF variant, wherein a GoF variant has a higher level of cGMP production compared to a control, and wherein a LoF variant has a lower level of cGMP production compared to a control.

7. The method of claim 6, wherein the variant gene associated with short stature is selected from the group consisting of natriuretic peptide receptor 2 (NPR2), Natriuretic peptide precursor C (NPPC), fibroblast growth factor receptor 3 (FGFR3) or combinations thereof.

8. The method of claims 6 or 7, wherein the cells are a mammalian cell line.

9. The method of any one of claims 6 to 8, wherein the lentiviral vector comprises a polynucleotide encoding a variant gene associated with short stature, a polynucleotide encoding a puromycin resistance gene and a polynucleotide encoding T2A-BFP promoter.

10. The method of any one of claims 6 to 9, wherein the lentiviral vector further comprising between 20 and 60 barcode sequences, optionally wherein the barcode sequences are from 15 to 30 basepairs.

11. The method of any one of claims 6 to 10, wherein the expression construct comprises a polynucleotide encoding a GFP protein operably linked to a cGMP binding domain, optionally wherein the cGMP binding domain is from mouse phosphodiesterase 5α.

12. The method of any one of claims 6-11, wherein the CNP variant is selected from the group consisting of

PGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-Gly-CNP37) (SEQ ID NO: 1); GQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Gly-CNP-37) (SEQ ID NO: 2);
GDLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Gly-CNP53) (SEQ ID NO: 3);
PDLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-CNP53) (SEQ ID NO: 4);
MDLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Met-CNP53) (SEQ ID NO: 5);
DLRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSNSGLGC [CNP-53(M48N)] (SEQ ID NO: 6);
LRVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-52) (SEQ ID NO: 7);
RVDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-51) (SEQ ID NO: 8);
VDTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP- 50) (SEQ ID NO: 9);
DTKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-49) (SEQ ID NO: 10);
TKSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-48) (SEQ ID NO: 11);

KSRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-47) (SEQ ID NO: 12);
SRAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-46) (SEQ ID NO: 13);
RAAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-45) (SEQ ID NO: 14);
AAWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-44) (SEQ ID NO: 15);
AWARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-43) (SEQ ID NO: 16); WARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-42) (SEQ ID NO: 17); ARLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-41) (SEQ ID NO: 18); RLLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-40) (SEQ ID NO: 19); LLQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-39) (SEQ ID NO: 20); LQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-38) (SEQ ID NO: 21); QEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-37) (SEQ ID NO: 22); EHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-36) (SEQ ID NO: 23); HPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-35) (SEQ ID NO: 24); PNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-34) (SEQ ID NO: 25); NARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-33) (SEQ ID NO: 26); ARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-32) (SEQ ID NO: 27); RKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-31) (SEQ ID NO: 28); KYKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-30) (SEQ ID NO: 29); YKGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-29) (SEQ ID NO: 30); KGANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-28) (SEQ ID NO: 31); GANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-27) (SEQ ID NO: 32); ANKKGLSKGCFGLKLDRIGSMSGLGC (CNP-26) (SEQ ID NO: 33); NKKGLSKGCFGLKLDRIGSMSGLGC (CNP-25) (SEQ ID NO: 34); KKGLSKGCFGLKLDRIGSMSGLGC (CNP-24) (SEQ ID NO: 35); KGLSKGCFGLKLDRIGSMSGLGC (CNP-23) (SEQ ID NO: 36); LSKGCFGLKLDRIGSMSGLGC (CNP-21) (SEQ ID NO: 37); SKGCFGLKLDRIGSMSGLGC (CNP-20) (SEQ ID NO: 38); KGCFGLKLDRIGSMSGLGC (CNP-19) (SEQ ID NO: 39); GCFGLKLDRIGSMSGLGC (CNP-18) (SEQ ID NO: 40); QEHPNARKYKGANKKGLSKGCFGLKLDRIGSNSGLGC [CNP-37(M32N)] (SEQ ID NO: 41); PQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Pro-CNP-37) (SEQ ID NO: 42); MQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Met-CNP-37) (SEQ ID NO: 43);

GQEHPNARKYKGANKKGLSKGCFGLKLDRIGSNSGLGC [Gly-CNP-37(M32N)] (SEQ ID NO: 44);
MGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (Met-Gly-CNP-37) (SEQ ID NO: 45);
PGQEHPQARRYRGAQRRGLSRGCFGLKLDRIGSMSGLGC (SEQ ID NO: 46);
PGQEHPNARKYKGANKKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 47);
PGQEHPNARRYRGANRRGLSRGCFGLKLDRIGSMSGLGC (SEQ ID NO: 48);
PGQEHPQARKYKGAQKKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 49);
GQEHPNARKYKGANPKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 50);
GQEHPNARKYKGANQKGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 51);
GQEHPNARKYKGANQQGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 52); and
GQEHPNARKYKGANKPGLSKGCFGLKLDRIGSMSGLGC (SEQ ID NO: 53).

13. A lentiviral vector comprising

i) a polynucleotide encoding a variant gene associated with short stature, a polynucleotide encoding a puromycin resistance gene and a polynucleotide encoding T2A-BFP promoter; optionally wherein the variant gene associated with short stature is selected from the group consisting of natriuretic peptide receptor 2 (NPR2), Natriuretic peptide precursor C (NPPC), fibroblast growth factor receptor 3 (FGFR3) or combinations thereof; or

ii) a NPR2 variant, a polynucleotide encoding a puromycin resistance gene and a polynucleotide encoding T2A-BFP promoter.

14. A method of making a lentiviral library comprising a variant gene associated with short stature, optionally wherein the variant gene associated with short stature is selected from the group consisting of NPR2, NPPC, FGFR3 or combinations thereof, the method comprising

-amplifying variant genes associated with short stature from a mammalian genome or genomic DNA database;

-cloning the amplified variants into a lentivial vector, wherein the lentiviral vector comprises between 20-60 unique barcodes per vector;

-sequencing the variant associated with the barcodes in the vector;

-aligning the variant sequences with a control gene sequence to generate a read structure;

-extracting the barcodes from the variant read structure;

-identifying the barcodes for each variant;

-isolating the lentiviral vectors expressing variant genes.

15. Use of a CNP variant in the preparation of a medicament for treating a subject with a short stature disorder and identified as having a loss of function variant of a gene associated with short stature identified using a method of any one of claims 6-12,

optionally wherein the short stature disorder is selected from the group consisting of achondroplasia, hypochondroplasia, short stature, idiopathic short stature, dwarfism, osteochondrodysplasias, thanatophoric dysplasia, osteogenesis congenita, achondrogenesis, chondrodysplasia congenita, homozygous achondroplasia, chondrodysplasia congenita, campomelic dysplasia, congenital lethal hypophosphatasia, perinatal lethal type of osteogenesis congenita, short-rib polydactyly syndromes, rhizomelic type of chondrodysplasia congenita, Jansen-type metaphyseal dysplasia, spondyloepiphyseal dysplasia congenital, atelosteogenesis, diastrophic dysplasia, congenital short femur, Langer-type mesomelic dysplasia, Nievergelt-type mesomelic dysplasia, Robinow syndrome, Reinhardt syndrome, acrodysostosis, peripheral dysostosis, Kniest dysplasia, fibrochondrogenesis, Roberts syndrome, acromesomelic dysplasia, micromelia, Morquio syndrome, Kniest syndrome, metatrophic dysplasia, and spondyloepimetaphyseal dysplasia, disorders related to NPR2 mutation, SHOX mutations, Turner’s syndrome/Leri Weill, PTPN11 mutations, Noonan’s syndrome, and IGF1R mutation.