

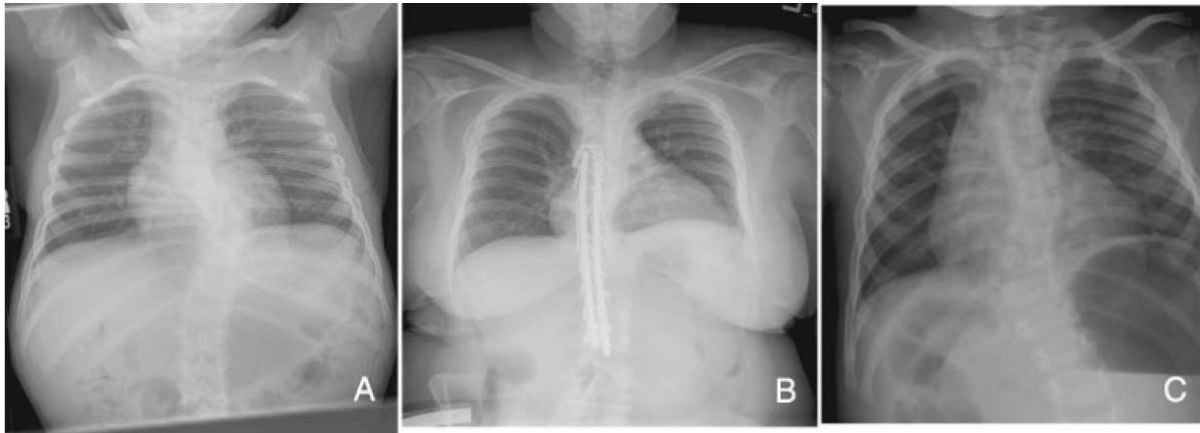
Supplemental Data

**Mutations in Fibronectin Cause a Subtype of
Spondylometaphyseal Dysplasia with “Corner Fractures”**

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Figure S1. Radiographs of all individuals with FN1 mutations.

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AP thoracic spine radiographs of the older boy (A), mother (B), and younger boy (C) showing severe scoliosis.



Lateral views of the lumbar spine. **A:** Younger boy at 3 years of age; L4 vertebral body is almost completely aplastic with only posterior elements present and L5 is hypoplastic. **B:** Older boy at 5 years of age showing hypoplasia of T12 and ovoid vertebral bodies. S1 has a triangular configuration.

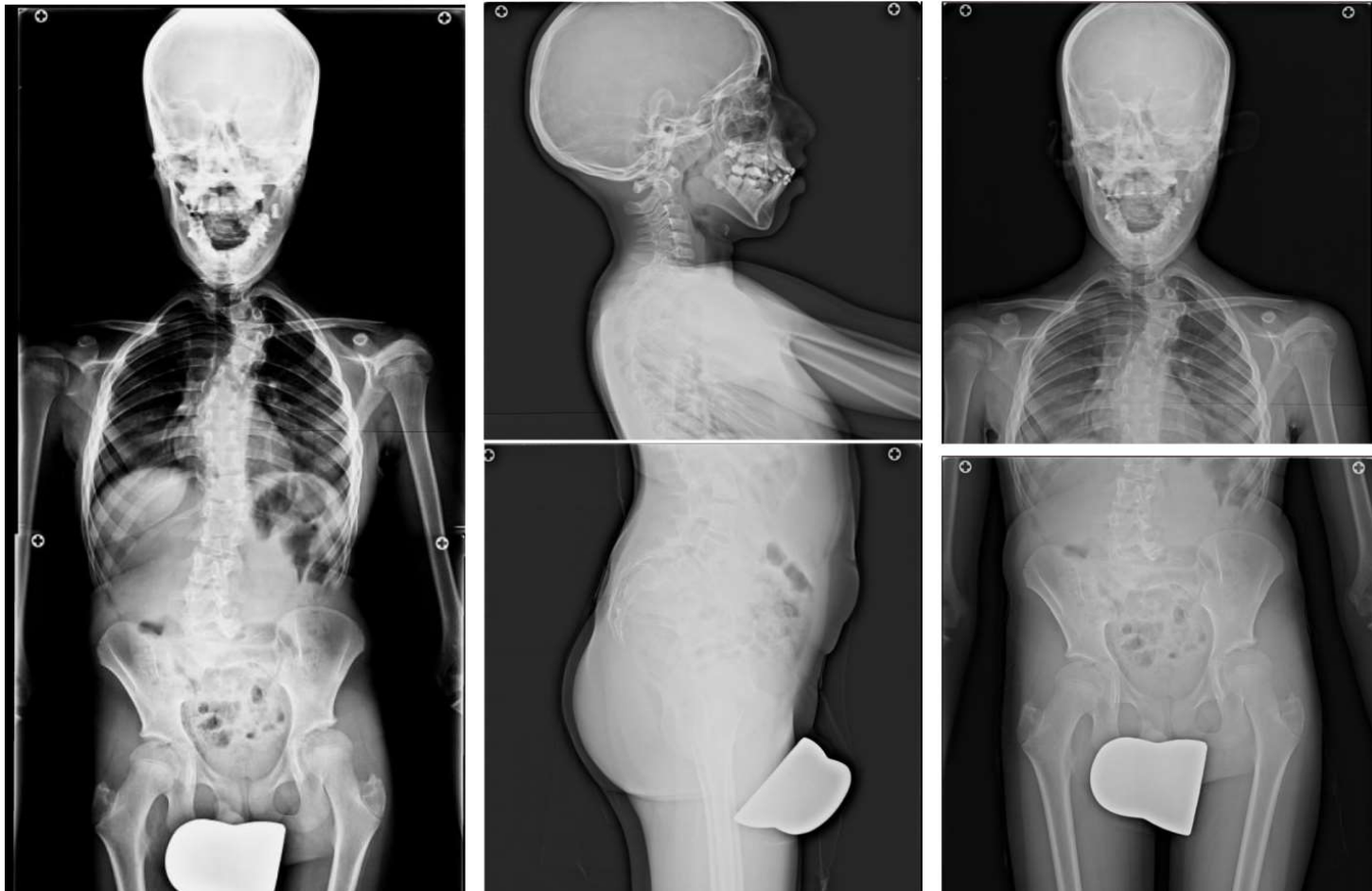


A: AP pelvis and hips demonstrating absence of coxa vara in older boy. **B:** Hand image of mother demonstrating absence of brachydactyly.



Arrows in the following panels point to metaphyseal fragmentation or "corner fractures". **A:** Right knee and leg radiograph of younger boy at 3 years of age showing metaphyseal dysplasia. **B:** Proximal humerus of younger boy at 3 years of age. **C:** Right knee of older boy at 5 years of age. **D:** Right shoulder radiograph of older boy at 5 years of age showing fragmented ossification and metaphyseal dysplasia.

Family 2







Family 3







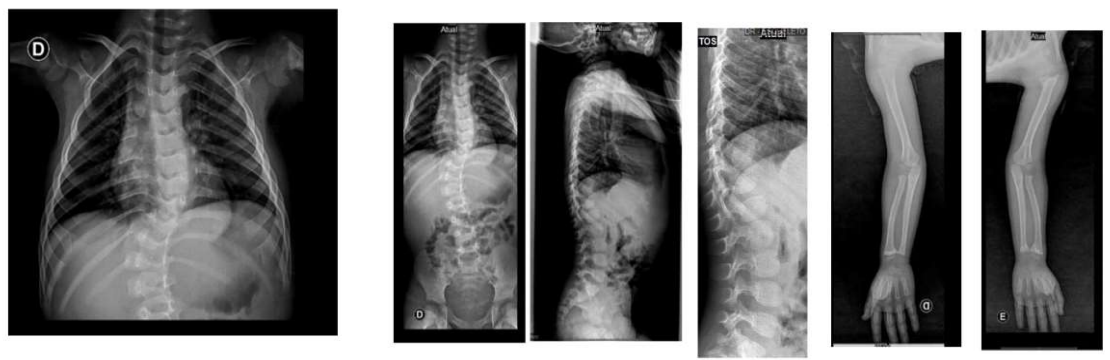
Family 4







Family 5



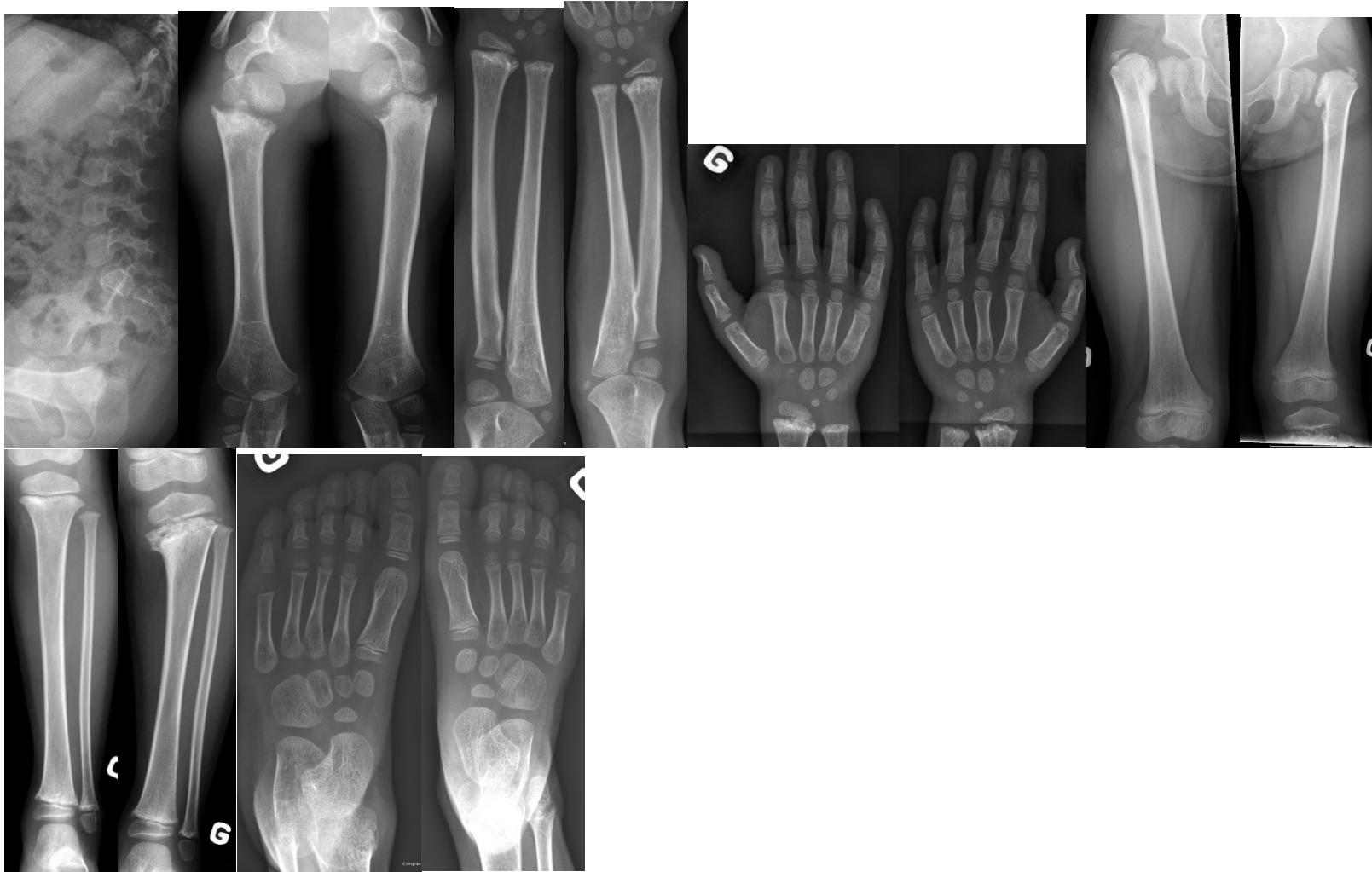


Family 6



Family 7





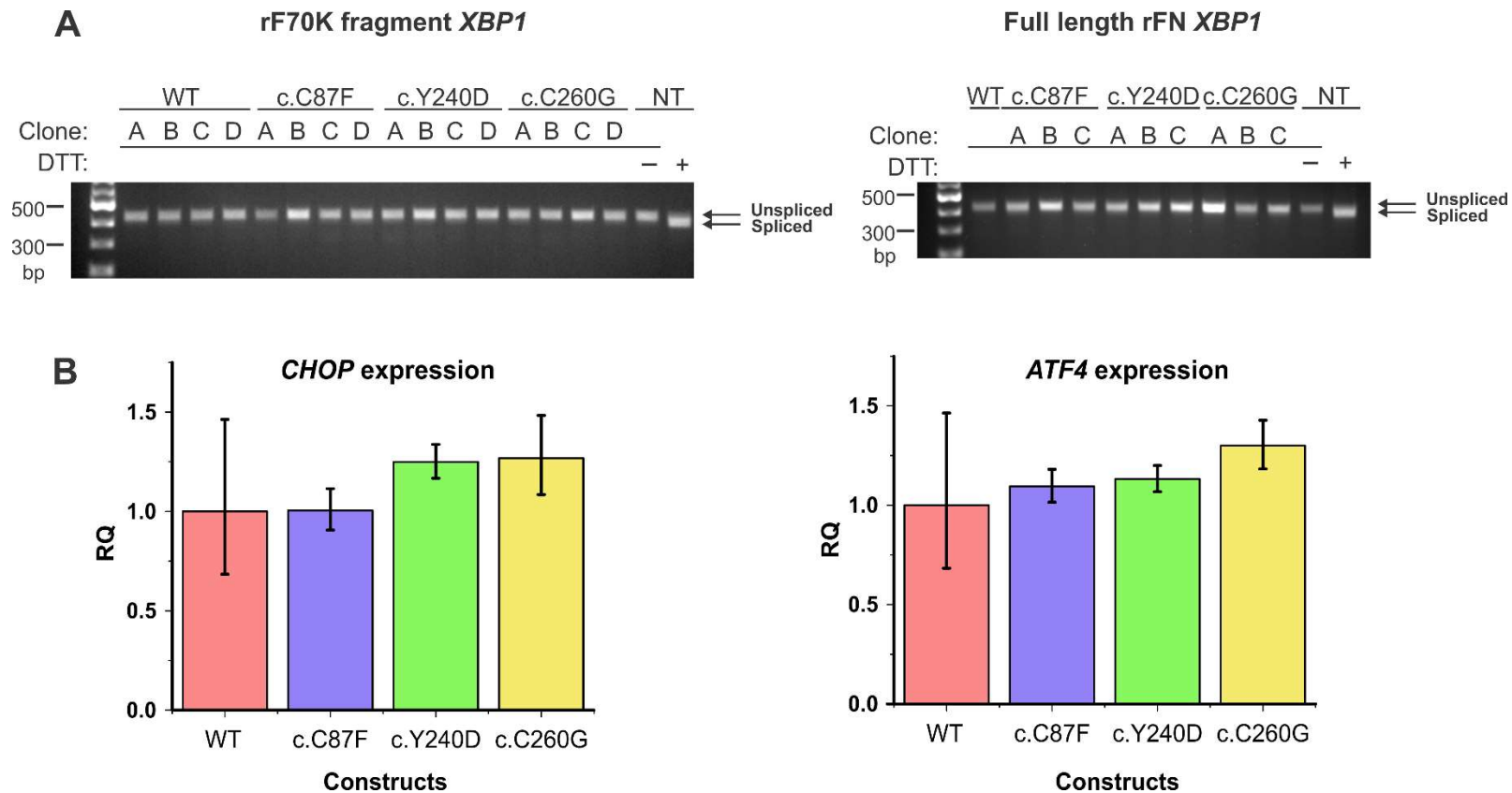


Figure S2. Analysis of the unfolded protein response of the recombinant rF70K and rFN wild-type and mutant proteins.

A) *XBP1* mRNA analysis. Mutations do not induce *XBP1*-mediated unfolded protein response. rF70K wild-type (WT) and mutants were analyzed in the left panel, and full length rFN WT and mutants in the right panel. NT represents non-transfected HEK293 cells as controls. Addition of dithiothreitol (DTT) for 1 h induces the unfolded protein response and causes *XBP1* splicing and is included as a positive control. The unspliced amplification product is 424 bp, the spliced product is 398 bp. Note that all analyzed mutations, both in rF70K and in full length rFN, do not induce the *XBP1*-mediated unfolded protein response (absence of the 398 bp band). **B)** qPCR mRNA expression analysis of *CHOP* and *ATF4* from full length rFN WT and rFN mutant cells. Both analyses showed no significant changes between rFN WT and the rFN mutants. RQ represents relative quantification of mRNA levels normalized to *GAPDH* levels. The rFN mutants were compared to the rFN WT, set to 1. Quantitative real time PCR was performed in a StepOne Real-Time PCR System (Applied Biosystems) using SYBR Select Master Mix (ThermoFisher Scientific), according to the manufacturer's protocol. Melt-curve analysis was performed after each run to determine the specificity of the detected product. Relative quantification of mRNA levels (fold change) was calculated using the $2^{-\Delta\Delta C_t}$ method. Error bars represent standard deviation. The values of all mutants were not statistically different from the wild-type ($p \geq 0.05$; Student's t-test).

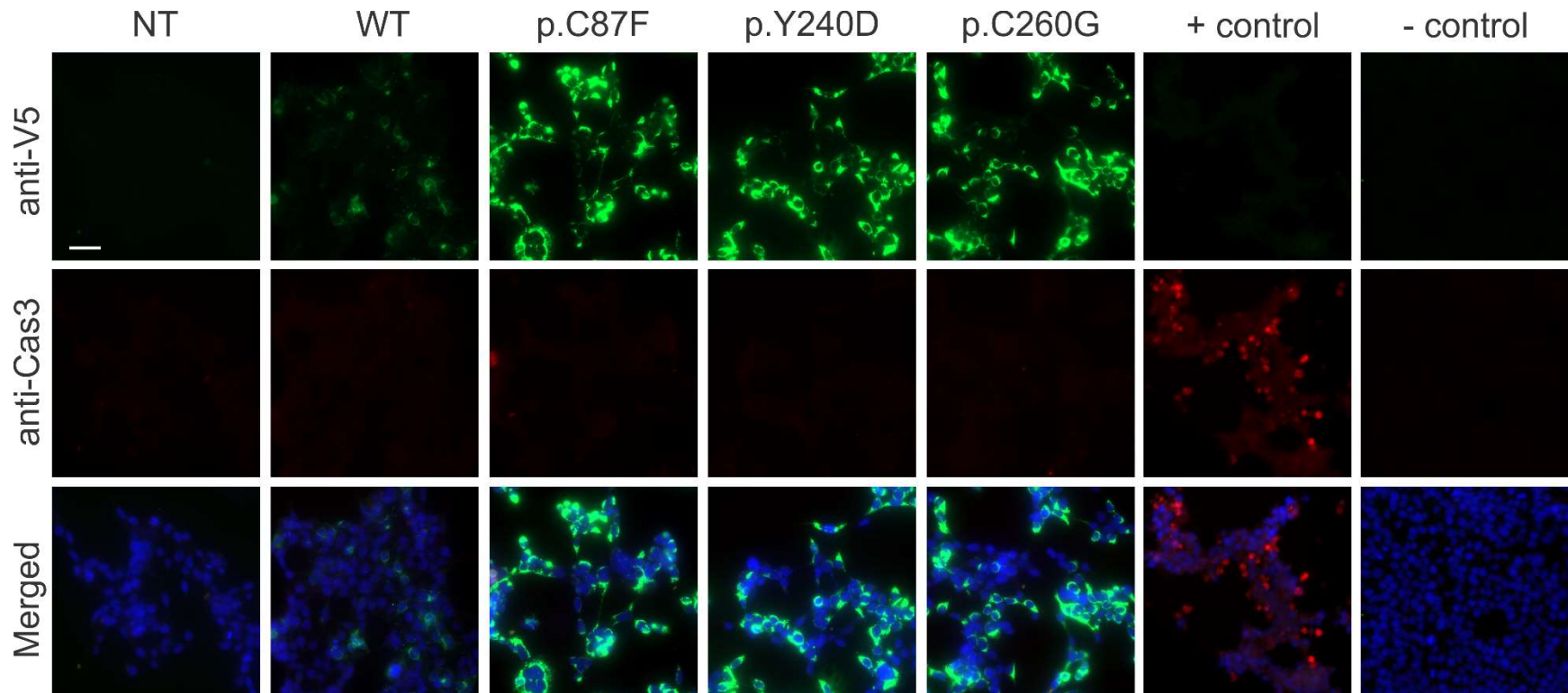


Figure S3. Analysis of caspase-3 mediated apoptosis of the recombinant rFN wild-type and mutant proteins.

Immunofluorescence of full length rFN WT and mutant cell clones with antibodies against cleaved caspase-3. Cleavage of caspase-3 is an indication of unfolded protein response mediated apoptosis. Cells were analyzed 3 days post-seeding. Note that both non-transfected HEK293 cells (NT) and transfected cells showed no staining of cleaved caspase-3 (Cas3; no red signal, primary antibody Cell Signaling; 9661S, secondary Alexa-488 conjugated antibody Thermo Fisher Scientific; A-11008), indicating the absence of detectable apoptosis. Non-transfected HEK293 cells treated for 12 h with 2 μ M staurosporine (Abcam; ab120056) in DMSO (0.2% DMSO final concentration) served as a positive control for apoptosis (+ control; red signal). Non-transfected HEK293 cells treated with 0.2% DMSO alone (- control) did not induce apoptosis. The rFN constructs were stained with an anti-V5 antibody (green signal). Cell nuclei were counterstained with DAPI (blue signal in the merged images). The scale bar indicates 50 μ m. Images were recorded at 400 \times magnification.

Table S1. Phenotypes of cases without a *FN1* mutation.

| Family | 8 ^a | 9 ^a | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
|--|-------------------|----------------|--------------------------------------|----------------------------|--|--------------------------|------------|--------------------|---------------------------------------|
| Age at last assessment | 12 yrs | 13 yrs | 4 yrs 6 mos | NA | 6 yrs 6 mos | 3 yrs 11 mos | 1 y 4 m | 5yrs 7 mos | 7 yrs, 2 mos |
| Gender | M | M | M | F | F | F | M | F | F |
| Height in cm (and SD) | 75.7 cm (-3 S.D.) | | 95.2 cm | NA | 94.0 cm (ca. -4 S.D.) | 99.5 cm (25th centile) | NA | unknown | 101 cm (<5 th centile) |
| Ovoid vertebral bodies | Some | Some | NA | NA | + | + | + | + | - |
| Other vertebral Changes (e.g. platyspondyly) | platyspondyly | platyspondyly | NA | NA | Platyspondyly ; disproportionate decreased height dorsally | - | - | Anterior wedging | End plate sclerosis; anterior wedging |
| Scoliosis | Mild | Mild | - | - (but excessive lordosis) | + (progressive, requiring casting) | - (mild lumbar lordosis) | + | unknown | + (mild S-shaped) |
| Odontoid hypoplasia | + | - | NA | NA | -; but craniocervical stenosis requiring decompression | - | NA | - | - |
| Developmental coxa vara | - | + | -, slipped capital femoral epiphyses | + | - | + | + | + | + |
| Irregular metaphyses | + | + | NA | + | + | + | + | + | + |
| "Corner fractures" | + | + | + | + | + | + | + | +/- | +/- |
| Knee anomalies | Vara then valga | - | - | NA | Abnormal patellar tracking | Left varum | Genu varum | Dislocated patella | - |

| | | | | | | | | | |
|--|---|---|--|----|--|-----------------------------|---|---|---|
| Short trunk | - | + | + | NA | - | - | - | + | unknown |
| Short long bones (rhizo, meso or micromelia) | | | - | NA | Mesomelic disproportion | - | + | (rhizo, meso | |
| Chest or rib anomaly (e.g. pectus) | - | - | broad | NA | AP flattening | - | NA | Short sternum | Mild anterior rib cupping |
| Hand and feet anomalies | - | - | - | | Profound brachydactyly ; short metacarpals and phalanges | - | - | - | Cupped metacarpal and phalangeal metaphyses |
| Other | | | Pes planus, hypospadias, speech delay, | | Dentinogenesis imperfecta; multiple fractures; hip uncoverage; tibia varus and internal tibial torsion | mild leg length discrepancy | relative macrocephaly , high forehead, hypertelorism , shawl scrotum, slightly bowed forearms | Unossified CFE, other epiphyses nl; metaphyseal irregularities throughout | |

^a Published (Machol K et al.¹)

Table S2. Details on targeted enrichment, sequencing and WES data analysis

| Family | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|-------------------------------|---|--|-----------------------------|------------------------------------|--|---|
| Connection for enrollment in project | Texas Children's bone program | Genematcher | SkelDys listserv | ISDR | Genematcher | Collaboration | Shriners Canada Skeletal Dysplasia Clinic |
| Site for sequencing | BCM-HGSC | OPBG | Radboud | BCM-HGSC | CEGH-CEL-Universidade de São Paulo | BGI | Calgary |
| Exome library capture | Roche SeqCap EZ HGSC VCRome | Illumina Nextera v1.2 | No exome done, FN1 Sanger sequencing only. | Roche SeqCap EZ HGSC VCRome | Illumina TrueSeq kit | Agilent SureSelect Human All Exon v4 | Illumina TruSight One Sequencing Panel |
| Sequencing | Illumina HiSeq | Illumina HiSeq | | Illumina HiSeq | Illumina HiSeq | Illumina HiSeq | Illumina HiSeq |
| Alignment | Mercury pipeline | In-house pipeline (GATK) | | Mercury pipeline | Burrows-Wheeler Aligner (BWA) | Novoalign software | In-house pipeline (GATK) |
| Variant calling, filtering and annotation | Mercury pipeline | In-house pipeline (GATK, SnpEff, CADD/dbNSFP_SVM) | | Mercury pipeline | GATK/ ANNOVAR | In-house pipeline (GATK, ANNOVAR, Perl and Bash scripts) | In-house pipeline |

Supplemental References

1. Machol, K., Jain, M., Almannai, M., Orand, T., Lu, J.T., Tran, A., Chen, Y., Schlesinger, A., Gibbs, R., Bonafe, L., et al. (2017). Corner fracture type spondylometaphyseal dysplasia: Overlap with type II collagenopathies. *Am J Med Genet A* 173, 733-739.
2. Sutton, V.R., Hyland, J.C., Phillips, W.A., Schlesinger, A.E., and Brill, P.W. (2005). A dominantly inherited spondylometaphyseal dysplasia with "corner fractures" and congenital scoliosis. *Am J Med Genet A* 133A, 209-212.