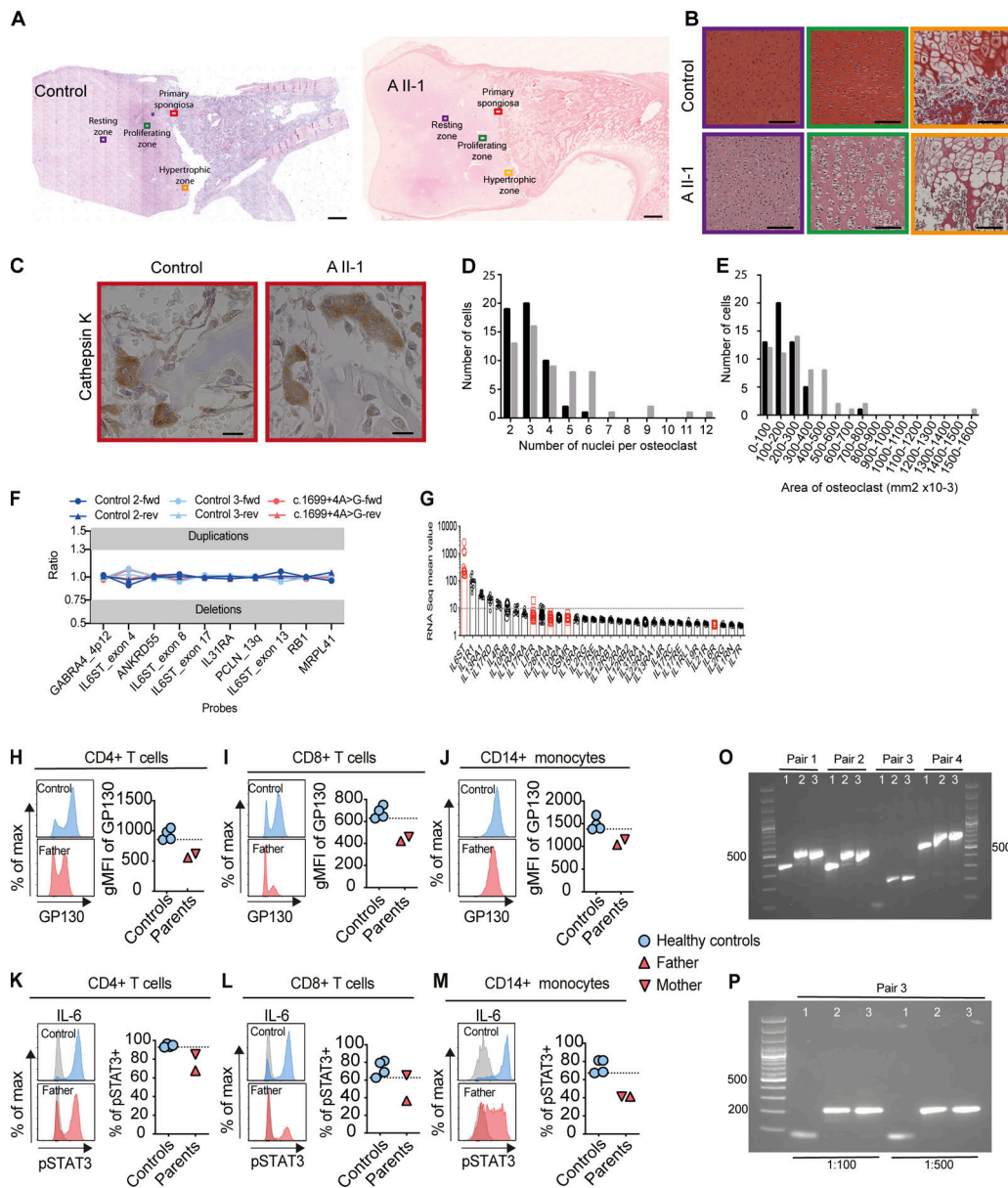


**Supplemental material**



**Figure S1. Bone phenotype, MLPA analysis of the *IL6ST* gene, RNA-seq expression data of multiple cytokine receptor units in control amniocytes, the parental analysis of GP130 and pSTAT3 response, and PCR analysis.** (A) H&E staining of femur bones from affected patient A-II-1 and an age-matched control. Several anatomic regions are labeled and color-coordinated, for guidance in the other panels. Scale bar indicates 1 mm. (B) Growth plate zones following safranin O/fast green (SOFG) staining show resting (left), proliferative (middle), and hypertrophic (right) zones. Scale bar indicates 50  $\mu$ m. (C) Multinuclear osteoclasts in the primary spongiosa were visualized by immunostaining for Cathepsin K and counterstaining with hematoxylin. Scale bar indicates 20  $\mu$ m. (D) Quantification of the number of nuclei in cathepsin K-positive cells, with only cells containing two or more nuclei counted. (E) Quantification of the size of cathepsin K-positive cells containing two or more nuclei. (C-E) Six visual fields analyzed with three images from each side of the bone; black bars indicate control; gray bars indicate patient A-II-1. Note that colored boxes surrounding images in B and C correspond to regions indicated in A. (F) Ratio for each probe (deletions would cause a ratio of <0.75 and duplications of >1.3). Exons 4, 8, 13, and 17 in *IL6ST* and genes upstream and downstream of *IL6ST* (*ANKRD55* and *IL31RA*) were investigated. (G) RNA-seq expression of multiple cytokine receptor units in control amniocytes. In case of multiple RNA-Seq Probe Set IDs of each receptor, the one with highest expression was shown. Blue lines represent the median of  $n = 11$  individual amniocyte samples. GP130-dependent cytokine receptors are shown in red. Each dot represents one individual sample, data taken from Kang et al. (2015). (H-J) GP130 surface expression in ex vivo CD3<sup>+</sup>CD4<sup>+</sup>, CD3<sup>+</sup>CD8<sup>+</sup>, and CD14<sup>+</sup> cells gated from peripheral blood mononuclear cells of heterozygous parents compared with four healthy donors. Representative histograms of one control and the father (left) and geometric mean fluorescence intensity (gMFI; right) are shown. (K-M) Response of pSTAT3 in heterozygous parents after stimulation with IL-6 (100 ng/ml for 15 min) compared with four healthy controls (gray, unstimulated; blue and red, stimulated). Representative histograms are shown on the left. (H-M) Blue, controls; red, father (upper triangle) and mother (lower triangle). Dashed line indicates the lowest value from the healthy controls. (O-P) Agarose gels for RT-PCR and nested PCR using four primer pairs (pair 1, exon 11 and boundary of exons 14–15; pair 2, exons 12–16; pair 3, exons 12–14; pair 4 exons 11–16). 1, amplicon from cDNA from EBV-LCLs of patient C-II-3 with c.1699+4A>G variant; 2–3, control EBV-LCLs, 100-bp ladder on the side of each gel. (P) Nested PCR using amplicons from exons 12–14 with primer pair 3. Amplicon of expected 218-bp size in control samples versus amplicon of ~70-bp in patient sample confirming skipping of exon 13. 1:100 and 1:500 indicate dilution ratio for the RT-PCR products.

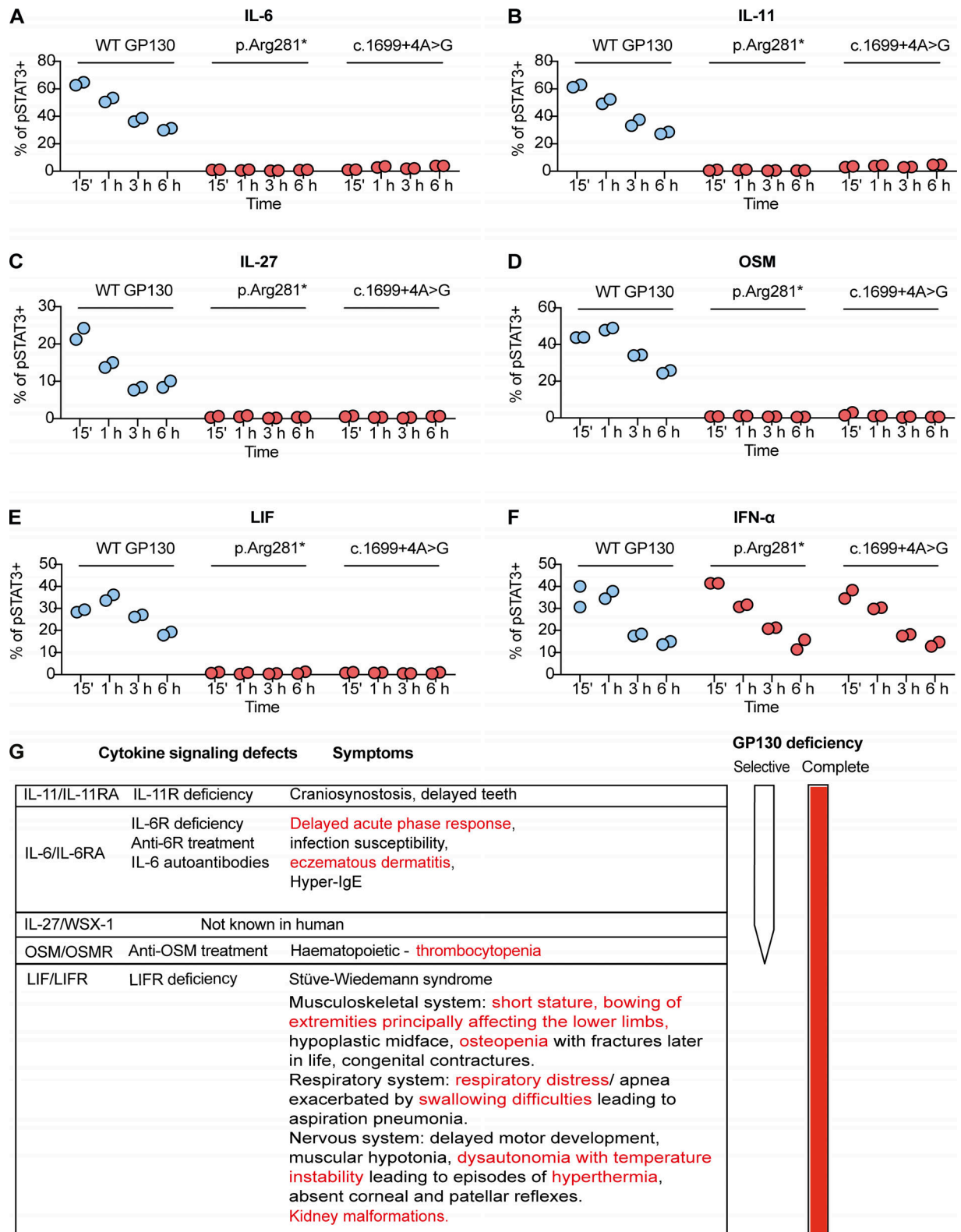


Figure S2. The complete loss of GP130-dependent IL-6, IL-11, IL-27, OSM, and LIF signaling in p.Arg281\* and c.1699+4A>G variant is not due to delayed kinetics; and a schematic summary of GP130 deficiency, the relationship between loss of cytokine signaling and clinical symptoms. (A-F) Response of pSTAT3 in c.1699+4A>G transfected GP130-deficient HEK293 after stimulations with IL-6, IL-11, IL-27, OSM, LIF, and IFN-α stimulation (all 100 ng/ml) over a time course covering 15 min, 1 h, 3 h, and 6 h. For assessment of IL-6 and IL-11 signaling, cells were cotransfected with plasmids encoding IL-6Rα and IL-11Rα, respectively. Successfully transfected cells were gated based on GFP expression. Quantification is based on individual independent experiments per cytokine, with duplicates per experiment. (G) A schematic summary of GP130 deficiency and the relationship between loss of cytokine signaling and clinical symptoms. The symptoms described in red were noticed in our patients.

**Table S1 is provided online as a separate Word file and lists rare sequence variants identified using whole-genome variant analysis in family A (quadro) and whole exome variant analysis in families B and C (trios).**