Supplemental Figure Legends

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SUPPL. FIG. 1. Effect of β -arrestin2 expression on bone metabolic pathways under homeostatic conditions. A, The complete set of 1623 calvarial transcripts with significantly different expression between vehicle treated wild type (wt NS) and β-arrestin2 null (βarr2-/- NS) mice was analyzed by parametric geneset enrichment of classical signaling pathways. Common pathways from two distinct databases were used: Molecular Signatures Database (www.broadinstitute.org/gsea) and Ingenuity Pathway analysis (www.ingenuity.com/). Selected functional signaling pathways corresponding to signal transduction, growth factor signaling, nuclear receptor signaling and cell cycle control are shown with their associated hybrid score ($-\log_{10}(p)$ x pathway enrichment ratio). All pathways shown were significantly populated (p≤0.05) by at least two individual genes. **B**, The wt NS vs βarr2-/- NS geneset was used to query the GObp database (www.geneontology.org). GObp terms falling into the general categories of intermediary metabolism, DNA/RNA/protein synthesis/modification, cell cycle, apoptosis/survival, cytoskeletal rearrangement, and vesicle transport are shown. Hybrid GO term populations scores $(-\log_{10}(p))$ x GO term enrichment factor) shown for each GO term group were calculated using WebGestalt (http://bioinfo.vanderbilt.edu/webgestalt/) from groups populated with at least 2 individual genes and p \leq 0.05. **SUPPL. FIG. 2.** Effect of bPTH(7-34) and hPTH(1-34) treatment on biological processes in wild type and β -arrestin2 null mice. A, The wt bPTH(7-34) vs wt NS geneset was used to query the GO term biological process database. GObp terms falling into the categories of intermediary metabolism, ion transport, cell cycle, apoptosis/survival, and cell adhesion/migration are shown. Hybrid scores for each significantly populated GO term groups were calculated by the product of $-\log_{10}(p)$ x GO term enrichment factor (WebGestalt: http://bioinfo.vanderbilt.edu/webgestalt/). B, Identical analysis performed using the wt hPTH(1-34) vs wt NS geneset. GObp terms falling into the general categories of intermediary metabolism, ion transport, DNA/RNA/protein synthesis and modification, cell adhesion/migration, bone matrix biosynthesis, and skeletal development/ differentiation are shown.

- Hybrid score reflects the probability that the observed differences in gene expression in a given gene
 cluster did not occur by chance. All GObp shown exceed a minimal threshold significance of *p*≤0.05.







