Supplementary Table 1. Top 15 enriched gene ontology clusters (following DAVID [20]), based on the set of consistently induced genes affected by β-TCP after 12 hours and 2 days (FDR<0.2).

AC	Biological process terms	FDR
1	***Enrichment Score: 2.685719998661978***	
	GO:0040012~regulation of locomotion	0.0394
	GO:0051270~regulation of cell motion	0.0394
	GO:0030334~regulation of cell migration	0.0592
2	***Enrichment Score: 2.275123253708776***	
	GO:0001503~ossification	0.0394
	GO:0060348~bone development	0.0485
	GO:0001501~skeletal system development	0.1911
3	***Enrichment Score: 2.0956568177368617***	
	GO:0019318~hexose metabolic process	0.0742
	GO:0006006~glucose metabolic process	0.0742
	GO:0005996~monosaccharide metabolic process	0.1163
4	***Enrichment Score: 2.0238683006394806***	
	GO:0001837~epithelial to mesenchymal transition	0.0091
	GO:0014031~mesenchymal cell development	0.0933
	GO:0048762~mesenchymal cell differentiation	0.0933
	GO:0060485~mesenchyme development	0.0962
5	***Enrichment Score: 1.6955918540101629***	
	GO:0042981~regulation of apoptosis	0.1824
	GO:0043067~regulation of programmed cell death	0.1911
	GO:0010941~regulation of cell death	0.1911
6	***Enrichment Score: 1.54702314416345***	
	GO:0030324~lung development	0.1400
	GO:0030323~respiratory tube development	0.1537
	GO:0060541~respiratory system development	0.1637
7	***Enrichment Score: 1.428679148158992***	
	GO:0030968~endoplasmic reticulum unfolded protein response	0.0742
	GO:0034620~cellular response to unfolded protein	0.0742

	GO:0034976~response to endoplasmic reticulum stress	0.1593
	GO:0006984~ER-nuclear signaling pathway	0.1637
8	***Enrichment Score: 1.4263408694560697***	
	GO:0045892~negative regulation of transcription, DNA-dependent	0.2416
	GO:0051253~negative regulation of RNA metabolic process	0.0983
	GO:0016481~negative regulation of transcription	0.2416
	GO:0010558~negative regulation of macromolecule biosynthetic process	0.2937
	GO:0031327~negative regulation of cellular biosynthetic process	0.3333
	GO:0010629~negative regulation of gene expression	0.3604
	GO:0009890~negative regulation of biosynthetic process	0.3699
	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.3887
	GO:0051172~negative regulation of nitrogen compound metabolic process	0.4127
	GO:0010605~negative regulation of macromolecule metabolic process	0.4500
9	***Enrichment Score: 1.4110746405832497***	
	GO:0008643~carbohydrate transport	0.1316
	GO:0015758~glucose transport	0.1267
	GO:0008645~hexose transport	0.1316
	GO:0015749~monosaccharide transport	0.1385
10	***Enrichment Score: 1.3702596975346126***	
	GO:0048609~reproductive process in a multicellular organism	0.1657
	GO:0032504~multicellular organism reproduction	0.1657
	GO:0007276~gamete generation	0.3794
11	***Enrichment Score: 1.2994263317739354***	
	GO:0006351~transcription, DNA-dependent	0.2716
	GO:0006366~transcription from RNA polymerase II promoter	0.2620
	GO:0032774~RNA biosynthetic process	0.2761
12	***Enrichment Score: 1.284820586026303***	
	GO:0043255~regulation of carbohydrate biosynthetic process	0.0742
	GO:0010906~regulation of glucose metabolic process	0.1637
	GO:0010675~regulation of cellular carbohydrate metabolic process	0.1808

	GO:0006109~regulation of carbohydrate metabolic process	0.1857
13	***Enrichment Score: 1.2705300327366442***	
	GO:0001569~patterning of blood vessels	0.0742
	GO:0048754~branching morphogenesis of a tube	0.1593
	GO:0001763~morphogenesis of a branching structure	0.1857
	GO:0035239~tube morphogenesis	0.1958
14	***Enrichment Score: 1.2532056572273087***	
	GO:0055066~di-, tri-valent inorganic cation homeostasis	0.1456
	GO:0055080~cation homeostasis	0.2352
	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	0.2217
	GO:0006874~cellular calcium ion homeostasis	0.2620
	GO:0006873~cellular ion homeostasis	0.3333
	GO:0055074~calcium ion homeostasis	0.2761
	GO:0055082~cellular chemical homeostasis	0.3534
	GO:0030003~cellular cation homeostasis	0.3257
	GO:0006875~cellular metal ion homeostasis	0.3152
	GO:0019725~cellular homeostasis	0.4416
	GO:0055065~metal ion homeostasis	0.3604
	GO:0050801~ion homeostasis	0.4697
15	***Enrichment Score: 1.1859181002242314***	
	GO:0051674~localization of cell	0.2937
	GO:0048870~cell motility	0.2937
	GO:0016477~cell migration	0.4214

AC: annotation cluster number

FDR: false discovery rate

N.B.: the multiple testing correction is too conservative, as it does not take into account the similarity between many GO terms.