Supplementary Information

Fibroblasts' secretome from calcified and non-calcified dermis in Pseudoxanthoma elasticum differently contributes to elastin calcification.

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Supplementary Table 1 List of a) candidates for reference genes and of b) target genes.

Supplementary Figure 1 Uncropped immunoblot images in CUS and CAS secretome for decorin, perlecan and HMGB1.

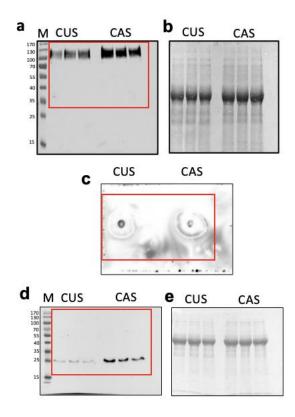
Supplementary Figure 2 Representative light microscopy image of insoluble elastin coacervated in presence of 200 μg heparan sulphate.

Supplementary Figure 3 Flow chart for the identification of reference genes.

Supplementary Figure 4 Gene stability rankings derived from four computational programs.

Supplementary Table 1. List of a) candidates for reference genes and of b) target genes.

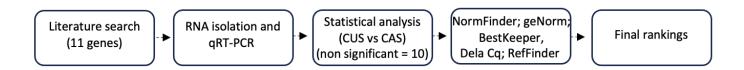
| Gene acronymous | Gene name | Gene function | Gene ID | Code HS (ThermoFisher Scientific) | |
|--------------------|---|---|---------------|-----------------------------------|--|
| | a) c | andidates for reference genes | | | |
| 185 | RNA, 18S ribosomal 1 | Essential component of 18S ribosomal subunit. | Hs99999901_s1 | | |
| АСТВ | β-actin | Major constituent of the contractile apparatus. | 60 | Hs01060665_g1 | |
| B2M | β-2-microglobulin | Serum protein associated to heavy chain of histocompatibility complex. | 567 | Hs00187842_m1 | |
| GAPDH | Glyceraldehyde-phosphate dehydrogenase | Enzyme in glycolysis and gluconeogenesis. | 138400 | Hs02786624_g1 | |
| HMBS | Hydroxymethylbilane synthase | Enzyme involved in heme biosynthetic pathway. | 3145 | Hs00609297_m1 | |
| HPRT1 | Hypoxanthine phosphoribosyltransferase 1 | Enzyme involved in purine synthesis. | 3251 | Hs02800695_m1 | |
| RPL13A | Ribosomal protein L13a | Structural component of 60S ribosomal subunit. | 40687 | Hs 04194366_g1 | |
| SDHA | Succinate dehydrogenase complex flavoprotein subunit A | Major catalytic subunit of succinate- ubiquinone oxidoreductase, essential complex of the mitochondrial respiratory chain. | 6389 | Hs07291714_mH | |
| ТВР | TATA-box binding protein | Component of transcription factor IID (TFIID) is able to bind TATA box. | 600075 | Hs00427620_m1 | |
| UBC | Ubiquitin C | Polyubiquitin precursor. | 7316 | Hs00824723_m1 | |
| YWHAZ | Tyrosine3- monooxygenase/tryptophan 5- monooxygenase activation protein zeta | Signal transduction | 7534 | Hs03044281_g1 | |
| | | b) target genes | | | |
| ВМР2 | Bone morphogenetic protein 2 | Growth factor of the TGF-beta superfamily involved in essential processes as cartilage and bone formation. | Hs00154192_m1 | | |
| PXN | Paxillin | Cytoskeletal protein that is part of the focal adhesion components. | 5829 | Hs01104424_m1 | |



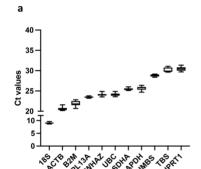
Supplementary Figure 1. Uncropped immunoblot images for decorin, perlecan and HMGB1 in CUS and CAS secretome. Uncropped immunoblot images for decorin protein content (a) normalized against the amount the total protein content revealed by Ponceau S (b); for perlecan quantification (c); for HMGB1 protein content (d) normalized against the amount the total protein content revealed by Ponceau S (e). The area blot chosen for publication (Figure 5 a, 5b and 6a) is delimited by a red rectangle and the size ladder is aligned with them.



Supplementary Figure 2. Representative light microscopy image of insoluble elastin coacervated in the presence of 200 μ g heparan sulphate. Scale bar: 10 μ m.

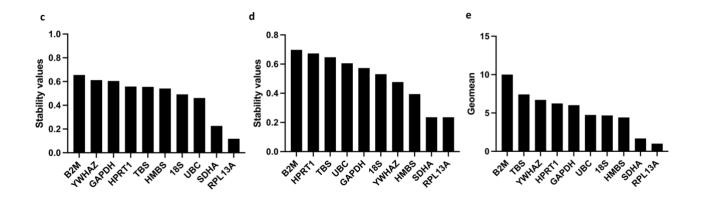


Supplementary Figure 3. Flow chart for the identification of reference genes.



b

| BestKeeper | RPL13A | SDHA | GAPDH | HPRT1 | HMBS | 185 | YWHAZ | UBC | TBS | B2M |
|----------------|--------|-------|-------|-------|-------|------|-------|-------|-------|-------|
| n | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 |
| geo Mean [CP] | 23.00 | 25.05 | 24.99 | 29.88 | 28.33 | 8.60 | 23.61 | 23.55 | 29.49 | 21.27 |
| AR Mean [CP] | 23.00 | 25.06 | 25.00 | 29.89 | 28.33 | 8.61 | 23.61 | 23.56 | 29.50 | 21.28 |
| min [CP] | 23.00 | 25.00 | 24.00 | 29.00 | 28.00 | 8.00 | 23.00 | 23.00 | 29.00 | 20.00 |
| max [CP] | 23.00 | 26.00 | 26.00 | 31.00 | 29.00 | 9.00 | 24.00 | 24.00 | 31.00 | 22.00 |
| std dev [± CP] | 0.00 | 0.10 | 0.33 | 0.40 | 0.44 | 0.48 | 0.48 | 0.49 | 0.56 | 0.56 |



Supplementary Figure 4. a Mean Ct values of each candidate reference gene are shown in a box-and-whisker plot and sorted from the lowest (left) to the highest (right). **b** Bestkeeper candidate reference gene ranking sorted according to their SD and CV% values and their crossing point (CP). **c** NormFinder ranking based on stability value. Candidate reference genes are plotted based on their stability value from the least (left) to the most stable (right). **d** geNorm ranking of stability M value. Candidate reference genes are plotted based on their stability M value from the least (left) to the most stable (right). **e** According to the gene stability rankings derived from four computational programs, RefFinder calculates the geometric mean of weights for the final ranking.