**Supplementary Table 1:** Definition of primers used for C11ORF8, CHI3L1, FN1, PROS1, SDC4, TIMP1 and 18S transcript assays by real-time PCR.

Indication of sequence of primers (F for forward and R for reverse primers), size of the amplicons and hybridization temperature for annealing step in PCR cycle. Column “residues” corresponds to the position of primers on the transcript sequence (GeneBank access number).

| Gene Symbol       | GenBank Access Number | Primers Sequence (5' - 3')                          | Residues | Fragment length (bp) | Hybridization temperature (C) |
|-------------------|-----------------------|------------------------------------------------------|----------|----------------------|------------------------------|
| C11ORF8 (MPPED)   | NM_001584             | F: ACA TCA ACC AGA GCA GAT TCC R: GTC CCA GCT CCG TGA AAT CG | 209 - 229 | 375 - 394            | 188 64                       |
| CHI3L1            | NM_001276             | F: AAA GCA GCT CCT GCT CAG CG R: GTG TTG CTG AAT CTG TCA GG | 633 - 652 | 817 - 836            | 206 57                       |
| FN1               | NM_212482             | F: GTT GCC TGT GCA GAT GCA CTG GAG C R: CTG CAA GCC CAT AGC TGA GAA GTG | 800 - 823 | 1031 - 1055          | 258 65                       |
| PROS1             | NM_000313             | F: ACA GGC TTC ACA AGT CCT GG R: TTA GTT GAC TGA CGT GCA GC | 236 - 255 | 441 - 460            | 227 60                       |
| SDC4              | NM_002999             | F: AGA CGA TGA GGA TGT AGT GG R: ATC CTC ACT TTC TCC AAC GG | 169 - 188 | 393 - 412            | 246 55                       |
| TIMP1             | NM_003254             | F: ATT CCG ACC TCG TCA TCA GG R: TGG GAC CTG TGG AAG TAT CC | 172 - 191 | 342 - 361            | 192 57                       |
| 18S               | X03205                | F: TAG AGG GAC AAG TGG CGT TC R: CGC TGA GCC AGT CAG TGT AG | 1445 - 1464| 1529 - 1548          | 104 64                       |
**Supplementary Table 2:** List of genes either up-regulated (above the dashed line) or down-regulated (below the dashed line) in both PTC-ga(+) and PTC-ga(-).

| Gene Symbol | Gene Name                                      | Gene ID | Biological Process                              | Ref.   | Fold Change | p value (t test) |
|-------------|------------------------------------------------|---------|------------------------------------------------|--------|-------------|-----------------|
|            |                                                 |         |                                                |        | ga(+) / ga(-) | ga(+) / ga(-)   | ga(+) vs NT | ga(-) vs NT | ga(+) vs ga(-) |
| P4HA2      | Procollagen-proline, 2-oxoglutarate 4-dioxygenase | 8974    | Cell adhesion & ECM                             | A, E, F, I | 5.5         | 3.9            | 1.4           | <0.001      | <0.001      | n.s.           |
| CITED1     | Cbp/p300-interacting transactivator 1           | 4435    | Transcription factor activity                   | A, E, F, G, I | 27.3        | 5.6            | 4.9           | <0.001      | <0.001      | <0.01          |
| SERPINA1   | Serine (or cysteine) proteinase inhibitor 1     | 5265    | Proteolysis & peptidolysis                      | A, D, F, G, I | 25.3        | 2.6            | 9.7           | <0.001      | <0.05       | <0.01          |
| NPC2       | Niemann-Pick disease, type C2                    | 10577   | Unknown                                        | F, I    | 6.1         | 2.4            | 2.5           | <0.001      | <0.001      | <0.01          |
| CCL21      | Chemokine (C-C motif) ligand 21                  | 6366    | Chemokine activity                             | A, I    | 116.6       | 143.8          | 1.2           | <0.001      | <0.001      | n.s.           |
| DPT        | Dermatopontin                                   | 1805    | Cell adhesion & ECM                             | A, I    | 20.6        | 24.5           | 1.2           | <0.001      | <0.001      | n.s.           |
| APOD       | Apolipoprotein D                                | 347     | Lipid metabolism                               | A, I    | 16.4        | 20.7           | 1.3           | <0.001      | <0.001      | n.s.           |
| FGL2       | Fibrinogen-like 2                               | 10875   | Cell adhesion & ECM                             | A, I    | 2.8         | 3.8            | 1.4           | <0.001      | <0.001      | n.s.           |
| RGS16      | Regulator of G-protein signalling 16 WW domain containing oxidoreductase | 6048    | Signal transduction                            | A, I    | 9.5         | 5.4            | 0.6           | <0.001      | <0.001      | n.s.           |
| WWOX       | Matrilin 2                                      | 51741   | Lipid metabolism                               | H, I    | 5.0         | 2.7            | 0.5           | <0.001      | <0.001      | n.s.           |
| CRYAB      | Crystallin, alpha B                             | 1410    | Protein folding                                | H, I    | 4.2         | 3.8            | 0.9           | <0.001      | <0.001      | n.s.           |
| FGFR2      | Fibroblast growth factor receptor 2             | 2263    | Growth factors & receptors                      | D, H, I | 2.9         | 3.1            | 1.1           | <0.001      | <0.001      | n.s.           |
| DUSP1      | Dual specificity phosphatase 1                  | 1843    | Cell cycle & apoptosis                          | A, I    | 2.6         | 3.2            | 1.2           | <0.01       | <0.05       | n.s.           |
| TFF3       | Trefoil factor 3 (intestinal)                   | 7033    | Defense response                               | A, D, G, H, I | 57.6  | 13.7           | 0.2           | <0.001      | <0.001      | <0.01          |
| MATN2      | Matrilin 2                                      | 4147    | Cell adhesion & ECM                             | D, G, H, I | 8.7         | 2.9            | 0.3           | <0.001      | <0.001      | <0.01          |
| ChGn       | Chondroitin beta1,4 N-acetylgalactosaminyl transferase | 55790  | Chondroitin sulfate biosynthesis                | H, I    | 6.8         | 2.4            | 0.4           | <0.001      | <0.001      | <0.001         |
| AKR1C2     | Aldo-keto reductase family 1, member C2         | 1646    | Lipid metabolism                               | A, I    | 11.7        | 3.2            | 0.3           | <0.001      | <0.05       | <0.01          |
| CRABP1     | Cellular retinoic acid binding protein 1        | 1381    | Signal transduction                            | A, D, H, I | 12.1        | 3.1            | 0.3           | <0.001      | <0.001      | <0.001         |
| FABP4      | Fatty acid binding protein 4                    | 2167    | Fatty-acid binding                             | A, H, I | 13.5        | 4.3            | 0.3           | <0.01       | <0.001      | <0.01          |
| PGCP       | Plasma glutamate carboxypeptidase               | 10404   | Proteolysis & peptidolysis                      | D, I    | 4.8         | 2.1            | 0.4           | <0.001      | <0.001      | <0.01          |