

Supplementary table 8 - Gene enrichment analysis on overlapping genes with similar direction of effect between the subchondral bone and the articular cartilage (N= 305 genes)

Category	Term	Count	Percentage	FDR	Genes
Cellular Component	GO:0005615~extracellular space	37	12	4,42E-03	WNT16, CRLF1, VCAN, DKK3, CHRDL2, FAP, DLG3, WNT11, IL11, CCN4, OGN, TPI1, FRMD4B, SPP1, TNFSF11, TNFAIP6, OMD, POSTN, CD63, GGH, LUM, MANF, LGI4, SEMA3D, GDF6, SCUBE1, FRZB, COL6A3, FSTL1, HTRA1, GPRC5B, ERF, GPC5, RELN, SPOCK3, S100A4, GPX3
Cellular Component	GO:0005576~extracellular region	36	12	4,56E-03	WNT16, CRLF1, VCAN, DKK3, WNT11, IL11, FGF14, OGN, TNR, SPP1, TNFSF11, CRISPLD1, OMD, CALU, FGF13, SPATA6, PDZD2, NGF, FST, LUM, ADAM12, PAMR1, CRIM1, LGI4, GDF6, FRZB, COL6A3, FSTL1, HTRA1, THBS3, HTRA3, ERF, GPC5, PLAC9, CD55, GPX3
Cellular Component	GO:0005578~proteinaceous extracellular matrix	17	6	7,98E-03	WNT16, VCAN, WNT11, CHADL, COCH, CCN4, OGN, ASPN, TNR, OMD, POSTN, LUM, ADAMTS17, COL6A3, GPC5, RELN, SPOCK3