

**Supplementary table 3.** GO term analysis of the 929 differentially methylated CpG sites in knee articular cartilage from normal and osteoarthritis patients.

GO term	Number of DMG	% enrichment	Corrected P-value
fibroblast growth factor-activated receptor activity	4	80%	1.15E-02
somatic stem cell maintenance	9	19%	4.38E-03
integrin-mediated signaling pathway	11	10%	6.26E-02
heparin binding	15	10%	2.89E-02
homophilic cell adhesion via plasma membrane adhesion molecules	14	10%	1.69E-02
positive regulation of Rho GTPase activity	14	9%	2.47E-02
regulation of Rho GTPase activity	16	9%	1.31E-02
regulation of canonical Wnt signaling pathway	14	9%	3.70E-02
regulation of Wnt signaling pathway	19	9%	6.34E-03
skeletal muscle organ development	16	9%	2.32E-02
regulation of Rho protein signal transduction	17	8%	1.79E-02
canonical Wnt signaling pathway	18	8%	1.33E-02
fat cell differentiation	15	8%	5.21E-02
regulation of Ras protein signal transduction	33	8%	8.23E-05
actin cytoskeleton organization	40	8%	1.37E-05
regulation of Ras GTPase activity	26	8%	2.01E-03
Wnt signaling pathway	27	8%	1.59E-03
stem cell development	20	8%	1.46E-02
actin filament organization	21	8%	1.10E-02
regulation of small GTPase mediated signal transduction	36	7%	8.98E-05
actin filament-based process	44	7%	1.37E-05
GTPase regulator activity	22	7%	3.62E-02
ossification	27	7%	3.33E-03
regulation of GTPase activity	36	7%	2.39E-04
positive regulation of Ras GTPase activity	20	7%	3.49E-02
regulation of GTP catabolic process	36	7%	2.42E-04
positive regulation of GTPase activity	32	7%	1.62E-03
regulation of purine nucleotide catabolic process	37	7%	5.92E-04
regulation of nucleotide catabolic process	37	7%	5.92E-04
actin binding	26	7%	3.62E-02
regulation of nucleoside metabolic process	37	7%	7.23E-04
negative regulation of intracellular signal transduction	23	7%	3.34E-02
Ras protein signal transduction	33	6%	4.28E-03
skeletal system development	29	6%	1.19E-02
embryonic morphogenesis	35	6%	4.43E-03
negative regulation of signal transduction	56	6%	7.48E-05
regulation of purine nucleotide metabolic process	41	6%	2.25E-03
regulation of nucleotide metabolic process	41	6%	2.40E-03
regulation of catabolic process	54	6%	1.27E-04
negative regulation of signaling	57	6%	8.23E-05
negative regulation of cell communication	57	6%	8.23E-05
cytoskeleton organization	57	6%	8.92E-05
regulation of cellular catabolic process	47	6%	1.62E-03
GTP catabolic process	41	6%	4.96E-03
cytoskeletal protein binding	44	6%	1.15E-02
guanosine-containing compound catabolic process	41	6%	5.61E-03
GTP metabolic process	41	5%	6.62E-03
organ morphogenesis	50	5%	1.62E-03
guanosine-containing compound metabolic process	41	5%	8.79E-03

negative regulation of response to stimulus	60	5%	3.27E-04
positive regulation of hydrolase activity	44	5%	6.70E-03
regulation of cell development	38	5%	2.95E-02
embryo development	56	5%	1.59E-03
regulation of anatomical structure morphogenesis	39	5%	3.62E-02
regulation of intracellular signal transduction	77	5%	8.23E-05
cell adhesion	54	5%	3.59E-03
biological adhesion	54	5%	4.31E-03
cell morphogenesis involved in differentiation	42	5%	3.34E-02
cell motility	58	5%	3.14E-03
localization of cell	58	5%	3.14E-03
cell migration	53	5%	6.34E-03
cell morphogenesis	57	5%	4.43E-03
enzyme linked receptor protein signaling pathway	50	5%	1.37E-02
cellular component morphogenesis	60	5%	4.11E-03
cell projection organization	58	5%	4.96E-03
neuron development	47	5%	5.27E-02
locomotion	70	5%	3.49E-03
regulation of hydrolase activity	55	5%	3.14E-02
movement of cell or subcellular component	77	5%	2.33E-03
regulation of cell differentiation	63	4%	1.37E-02
generation of neurons	61	4%	1.79E-02
cell development	87	4%	1.59E-03
regulation of multicellular organismal development	64	4%	2.47E-02
positive regulation of molecular function	70	4%	1.38E-02
organonitrogen compound catabolic process	61	4%	5.08E-02
regulation of developmental process	82	4%	4.96E-03
regulation of phosphate metabolic process	81	4%	5.84E-03
regulation of phosphorus metabolic process	81	4%	6.74E-03
tissue development	76	4%	1.33E-02

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