

Supplementary Table 1. Reserve Zone (RZ) 134 Enriched Pathways after Differential Expression Analysis of 259 Genes in Gene List.

GO Parent Category	Go Parent Term	GO (Child) Term	GO ID	% of Array	% of list	Fold Enrichment	P-Value	Total Probe Sets On Array	Probe Sets in Your List	
Biological Process	Biological adhesion/Biological regulation/Cellular process	regulation of cell-matrix adhesion	1952	0.08%	0.77%	9.58	0.017224	25	2	
		negative regulation of cell-matrix adhesion	1953	0.04%	0.77%	21.78	0.003848	11	2	
		regulation of hemostatic process	32844	0.17%	1.16%	6.78	0.008918	5	3	
		erythrocyte homeostasis	34101	0.21%	1.54%	7.48	0.001842	64	4	
		homeostasis of number of cells	48872	0.34%	1.89%	5.85	0.001727	106	5	
		Biological regulation/Biological adhesion/Cellular process	positive regulation of cell adhesion	7162	0.18%	1.54%	8.40	0.002113	57	4
		positive regulation of mesenchymal cell proliferation	2053	0.07%	0.77%	10.41	0.014770	23	2	
		transforming growth factor beta receptor signaling pathway	7179	0.21%	1.16%	5.44	0.015637	66	3	
		integrin-mediated signaling pathway	7229	0.14%	0.77%	5.57	0.044623	43	2	
		regulation of mesenchymal cell proliferation	10464	0.07%	0.77%	10.41	0.014770	23	2	
	Biological regulation/Cellular process	regulation of transforming growth factor beta receptor signaling pathway	17015	0.10%	0.77%	7.72	0.025396	31	2	
		negative regulation of Wnt1 receptor signaling pathway	30178	0.10%	0.77%	7.98	0.023956	30	2	
		regulation of cell redox homeostasis	39053	0.03%	0.77%	29.92	0.001852	8	2	
		cell redox homeostasis	45454	0.20%	1.54%	7.60	0.001741	63	4	
		positive regulation of Ras protein signal transduction	46579	0.09%	0.77%	8.25	0.022546	29	2	
		positive regulation of small GTPase mediated signal transduction	51057	0.10%	0.77%	7.72	0.025396	31	2	
		positive regulation of muscle cell differentiation	51149	0.02%	0.77%	39.90	0.001009	6	2	
		Biological regulation/Cellular process/Developmental process	erythrocyte development	48821	0.04%	0.77%	18.41	0.004949	13	2
		Biological regulation/Cellular process/Developmental process/Immune system process	negative regulation of cell growth	30306	0.23%	1.16%	5.13	0.018094	70	3
		Biological regulation/Cellular process/Growth	cell structure disassembly during apoptosis	6921	0.07%	0.77%	11.40	0.012466	21	2
	Biological regulation/Developmental process/Cellular process	apoptotic nuclear changes	30262	0.07%	1.16%	15.61	0.000865	23	3	
		negative regulation of neuron apoptosis	43524	0.19%	1.16%	6.19	0.011269	58	3	
		positive regulation of anti-apoptosis	45768	0.14%	0.77%	5.44	0.043600	44	2	
		regulation of muscle cell differentiation	51147	0.07%	0.77%	11.40	0.012466	21	2	
		Biological regulation/Immune system process	negative regulation of immune system process	2983	0.26%	1.54%	5.84	0.004969	82	4
		Biological regulation/Multicellular organismal process	negative regulation of cytokine production	1618	0.05%	0.77%	17.10	0.005726	14	2
		Biological regulation/Multicellular organismal process/Developmental process/Cellular process/Immune system process	erythrocyte differentiation	30216	0.20%	1.54%	7.85	0.001551	61	4
		Biological regulation/Response to stimulus	negative regulation of response to stimulus	46566	0.22%	1.16%	6.38	0.016635	67	3
		Biological regulation/Response to stimulus/Immune system process	negative regulation of immune response	50777	0.08%	0.77%	14.96	0.003890	24	3
		Cellular process	nuclear organization and biogenesis	6997	0.14%	1.54%	11.13	0.000426	43	4
	cytoplasm organization and biogenesis		7028	0.05%	0.77%	14.96	0.007426	16	2	
	mesenchymal cell proliferation		10463	0.07%	0.77%	10.41	0.014770	23	2	
	cellular component disassembly		22411	0.07%	0.77%	11.40	0.012466	21	2	
	extracellular matrix organization and biogenesis		30198	0.23%	1.93%	6.31	0.000316	72	5	
	collagen fibril organization		30199	0.06%	1.16%	19.95	0.000415	18	3	
	cell-matrix adhesion		7160	0.30%	1.93%	6.44	0.000986	93	5	
	cell-substrate adhesion		11590	0.33%	1.93%	6.77	0.001467	102	6	
	Cellular process/Biological adhesion/Multicellular organismal process/Developmental process		cartilage condensation	1502	0.05%	0.77%	15.86	0.006552	15	2
	Cellular process/Metabolic process		monosaccharide metabolic process	5996	0.80%	3.09%	5.12	0.000158	187	8
		glucose metabolic process	6006	0.48%	2.70%	5.59	0.000239	150	7	
		DNA catabolic process	6308	0.10%	0.77%	7.72	0.025396	31	2	
		glutathione metabolic process	6749	0.10%	0.77%	7.72	0.025396	31	2	
		cellular carbohydrate catabolic process	44275	0.33%	2.32%	7.04	0.000197	102	6	
		alcohol catabolic process	46164	0.26%	1.93%	7.30	0.000567	82	5	
		axon regeneration	31103	0.08%	0.77%	9.58	0.017224	25	2	
		Developmental process/Cellular process/Developmental process	uretic bud development	1657	0.12%	0.77%	7.82	0.048113	45	2
		Developmental process	regeneration	31099	0.37%	2.32%	6.19	0.000896	116	6
		Developmental process/Biological regulation/Cellular process	anti-apoptosis	6916	0.68%	3.86%	5.10	0.000010	210	10
	Developmental process/Biological regulation/Cellular process/Metabolic process	apoptotic program	9630	0.34%	1.93%	8.75	0.001593	104	5	
		DNA fragmentation during apoptosis	5309	0.05%	0.77%	14.96	0.007426	16	2	
neuron apoptosis		51602	0.45%	2.32%	5.09	0.001038	141	6		
Developmental process/Growth		developmental growth	49599	0.45%	2.32%	5.17	0.000967	139	6	
Developmental process/Multicellular organismal process		blood vessel remodeling	1974	0.08%	0.77%	9.58	0.017224	25	2	
Developmental process/Multicellular organismal process/Biological regulation		regulation of bone mineralization	39556	0.06%	0.77%	12.60	0.000401	18	2	
Localization		phosphate transport	6917	0.39%	2.70%	6.92	0.000005	121	7	
Localization/Cellular process		blood vessel endothelial cell migration	43534	0.04%	0.77%	19.95	0.004223	12	2	
endothelial cell migration		43542	0.08%	0.77%	9.97	0.015979	24	3		
Metabolic process		carbohydrate catabolic process	16052	0.34%	2.32%	6.84	0.000229	105	6	
	collagen metabolic process	32963	0.05%	0.77%	14.96	0.007426	16	2		
	glucose catabolic process	6007	0.24%	1.93%	8.20	0.000336	73	3		
	glycolysis	6096	0.18%	1.93%	10.50	0.000107	57	5		
	RNA elongation	6354	0.05%	0.77%	17.10	0.005726	14	2		
	translational elongation	6414	0.07%	0.77%	10.88	0.013598	22	2		
	oxygen and reactive oxygen species metabolic process	6800	0.14%	0.77%	5.44	0.043600	44	2		
	proteasomal protein catabolic process	10498	0.15%	0.77%	5.32	0.048113	45	2		
	protein sumoylation	16525	0.02%	0.77%	34.20	0.001401	7	2		
	hexose metabolic process	19318	0.59%	3.09%	5.20	0.000142	184	8		
Metabolic process/Cellular process	hexose catabolic process	19320	0.24%	1.93%	8.09	0.000357	74	5		
	lipoprotein metabolic process	42157	0.22%	1.16%	5.20	0.017463	69	3		
	proteasomal ubiquitin-dependent protein catabolic process	43161	0.15%	0.77%	5.32	0.048113	45	2		
	monosaccharide catabolic process	45395	0.24%	1.93%	8.09	0.000357	74	5		
	regulation of tissue remodeling	34103	0.20%	1.16%	5.79	0.013461	62	3		
	bone resorption	45453	0.14%	0.77%	5.44	0.043600	44	2		
	regulation of bone remodeling	49599	0.45%	2.32%	5.17	0.000967	139	6		
	determination of left/right symmetry	7368	0.09%	0.77%	8.55	0.021167	28	2		
	determination of symmetry	9799	0.09%	0.77%	8.25	0.022546	29	2		
	determination of bilateral symmetry	8655	0.09%	0.77%	8.25	0.022546	29	2		
Multicellular organismal process/Developmental process	limbic system development	21543	0.13%	0.77%	6.14	0.037659	39	2		
	hippocampus development	21761	0.06%	0.77%	11.97	0.011373	20	2		
	bone mineralization	21766	0.06%	0.77%	13.70	0.000112	18	2		
	cartilage development	30282	0.12%	1.16%	9.70	0.003378	37	3		
	bone mineralization	51216	0.24%	1.93%	8.09	0.000357	74	5		
	Multicellular organismal process/Developmental process/Cellular process	neuron maturation	42551	0.05%	0.77%	8.07	0.019819	27	2	
	Multicellular organismal process/Developmental process/Growth/Response to stimulus	issue regeneration	42246	0.29%	2.32%	7.89	0.000107	81	6	
	Reproduction/Multicellular organismal process/Developmental process/Rhythmic process	ovarian follicle development	1541	0.13%	0.77%	5.84	0.041203	41	2	
	acute-phase response	9593	0.13%	0.77%	6.14	0.037659	39	2		
	response to toxin	9636	0.12%	0.77%	6.65	0.033003	36	2		
Response to stimulus	response to carbohydrate stimulus	9743	0.16%	1.16%	6.30	0.010775	57	3		
	response to hexose stimulus	9746	0.16%	1.16%	7.04	0.008061	51	3		
	response to glucose stimulus	9749	0.16%	1.16%	7.33	0.007251	49	3		
	response to amine stimulus	14075	0.11%	0.77%	6.84	0.031430	35	2		
	response to cytokine stimulus	34097	0.06%	0.77%	11.97	0.011373	20	2		
	response to monosaccharide stimulus	34284	0.16%	1.16%	7.04	0.008061	51	3		
	wound healing	42060	0.75%	3.86%	5.12	0.000025	234	10		
	response to hydrogen peroxide	42542	0.19%	1.16%	5.98	0.012292	30	3		
	response to copper ion	46688	0.09%	0.77%	15.96	0.006552	15	2		
	response to axon injury	49678	0.09%	0.77%	8.25	0.022546	29	2		
Response to stimulus/Multicellular organismal process/Developmental process/Growth	neutrite regeneration	51102	0.08%	0.77%	8.55	0.021167	28	2		
	Cell	ER-Golgi intermediate compartment	3173	0.12%	0.77%	12.28	0.002593	39	4	
	peroxisomal membrane	5178	0.14%	0.77%	5.44	0.043600	44	2		
	centriole	5814	0.04%	0.77%	21.76	0.003548	11	2		
	late endosome membrane	31902	0.09%	0.77%	8.67	0.019819	27	2		
	microbody membrane	31903	0.14%	0.77%	5.44	0.043600	44	2		
	melanosome	42470	0.31%	1.54%	5.04	0.007140	95	4		
	microtubule organizing center part	44450	0.07%	0.77%	10.88	0.013598	22	2		
	segment granule	48700	0.31%	1.54%	5.04	0.007140	95	4		
	mitochondrial respiratory chain	5746	0.14%	0.77%	5.57	0.044623	43	2		
Cellular Component	Cell/Organelle/Envelope	mitochondrial membrane part	44455	0.21%	1.16%	5.52	0.015051	65	3	
	Cell/Organelle/Macromolecular complex	cytosolic ribosome	22526	0.14%	0.77%	5.57	0.044623	43	2	
	proteinaceous extracellular matrix	5578	0.96%	5.41%	5.62	0.000000	298	14		
	collagen	5581	0.25%	1.54%	6.22	0.003523	77	4		
	barrier collagen	5583	0.11%	0.77%	7.04	0.026862	34	2		
	basement membrane	5604	0.26%	1.93%	7.48	0.000008	80	5		
	extracellular matrix	31012	1.02%	5.41%	5.30	0.000000	316	14		
	extracellular matrix part	44450	0.07%	0.77%	10.88	0.000000	156	9		
	Macromolecular complex/Cell	eukaryotic translation elongation factor 1 complex	5853	0.03%	0.77%	29.92	0.001852	8	2	
	Organelle/Cell	transport vesicle	61313	0.24%	1.54%	6.38	0.002171	75	4	
Organelle/Cell/Macromolecular complex	intrinsinc to Golgi membrane	31228	0.12%	0.77%	8.47	0.034599	37	2		
	cytosolic small ribosomal subunit	22627	0.11%	0.77%	6.84	0.031430	35	2		
	Antioxidant activity	16209	0.16%	1.16%	7.18	0.007659	50	3		
	integrin binding	5178	0.12%	0.77%	6.47	0.034599	37	2		
	selenium binding	8430	0.08%	0.77%	9.97	0.015979	24	2		
	rRNA binding	19843	0.07%	1.16%	17.10	0.000860	21	3		
	calcium-dependent protein binding	48306	0.07%	0.77%	10.41	0.014770	23	2		
	NAD binding	51287	0.17%	1.16%	6.91	0.008484	52	3		
	Binding/Translation regulator activity	translation elongation factor activity	5746	0.09%	1.16%	12.38	0.001088	29	3	
	heme-copper terminal oxidase activity	15002	0.06%	0.77%	11.97	0.011373	20	2		
Catalytic activity	steroid dehydrogenase activity	16229	0.09%	0.77%	8.25	0.022546	29	2		
	oxidoreductase activity, acting on heme group of donors	16675	0.06%	0.77%	11.97	0.011373	20	2		
	oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	16676	0.06%	0.77%	11.97	0.011373	20	2		
	oxidoreductase activity, oxidizing metal ions	16677	0.06%	0.77%	11.97	0.011373	20	2		
	oxidoreductase activity, oxidizing metal ions	16678	0.06%	0.77%	11.97	0.011373	20	2		
	intracellular protein transferase activity, phosphotransferases	16688	0.05%	0.77%	17.10	0.005726	14	2		
	Structural molecule activity	transmembrane protein channel component	6100	0.33%	1.93%	6.92	0.000007	101	6	
	Transporter activity/Catalytic activity	cytochrome c oxidase activity	4129	0.08%	0.77%	11.97	0.011373	20	2	

**Supplementary Table 2.** Reserve Zone (RZ) 16 enriched pathways from the differential expression analysis showing hypergeometric p values less than 0.05 and probe sets in your list greater than 4. These pathways were derived from the entire RZ gene list showing differential upregulation at 16 days. Gray indicated pathways associated with BCMSD.

GO Parent Category	Go Parent Term	GO (Child) Term	GO ID	% of Array	% of list	Fold Enrichment	P-Value	Total Probe Sets On Array	Probe Sets in Your List
Biological Process	Cellular process/Metabolic process	cellular carbohydrate catabolic process	44275	0.33%	2.32%	7.04	0.000197	102	6
		glucose metabolic process	6006	0.48%	2.70%	5.59	0.000239	150	7
		monosaccharide metabolic process	5996	0.60%	3.09%	5.12	0.000158	187	8
	Developmental process	regeneration	31089	0.37%	2.32%	6.19	0.000386	116	6
		anti-apoptosis	6916	0.68%	3.86%	5.70	0.000010	210	10
	Developmental process/Biological regulation/Cellular process	neuron apoptosis	51402	0.45%	2.32%	5.09	0.001038	141	6
		developmental growth	48589	0.45%	2.32%	5.17	0.000967	139	6
	Developmental process/Cellular process	phosphate transport	6817	0.39%	2.70%	6.92	0.000065	121	7
		localization	16052	0.34%	2.32%	6.84	0.000229	105	6
	Metabolic process	carbohydrate catabolic process	19318	0.59%	3.09%	5.20	0.000142	184	8
		hexose metabolic process	42246	0.29%	2.32%	7.89	0.000107	91	6
	Multicellular organismal process/Developmental process/Growth/Response to stimulus	tissue regeneration	42060	0.75%	3.86%	5.12	0.000025	234	10
		wound healing	31012	1.02%	5.41%	5.30	0.000000	316	14
	Response to stimulus	extracellular matrix	44420	0.50%	3.47%	6.91	0.000006	156	9
		proteinaceous extracellular matrix	5578	0.96%	5.41%	5.62	0.000000	298	14
Cellular Component	Extracellular region	extracellular matrix structural constituent	5201	0.33%	2.32%	7.11	0.000187	101	6

**Supplementary Table 3.** PZ 35 enriched pathways from the cluster analysis showing hypergeometric p values less than 0.05. These pathways were derived from the entire PZ gene list showing differential upregulation at 16 days (compared to non-irradiated chondrocytes). Gray indicates a pathways association with BCMSD.

GO Category	GO ID	GO Term	% of Array	% of List	Fold Enrichment	P Value	Total Probe Sets On Array	Probe Sets in Our List
Biological	7229	integrin-mediated signaling pathway	0.14%	22.22%	160.21	0.000067	43	2
	9612	response to mechanical stimulus	0.35%	22.22%	63.79	0.000423	108	2
	6817	phosphate transport	0.39%	22.22%	56.93	0.000529	121	2
	1503	ossification	0.73%	33.33%	45.93	0.000030	225	3
	31214	biomineral formation	0.73%	33.33%	45.52	0.000031	227	3
	46849	bone remodeling	0.82%	33.33%	40.68	0.000043	254	3
	48771	tissue remodeling	0.98%	33.33%	33.88	0.000075	305	3
	1501	skeletal development	1.05%	33.33%	31.79	0.000090	325	3
	48545	response to steroid hormone stimulus	0.71%	22.22%	31.31	0.001718	220	2
	15698	inorganic anion transport	0.75%	22.22%	29.82	0.001890	231	2
	6820	anion transport	0.85%	22.22%	26.19	0.002433	263	2
	9725	response to hormone stimulus	1.09%	22.22%	20.38	0.003954	338	2
	9888	tissue development	1.67%	33.33%	19.95	0.000352	518	3
	9719	response to endogenous stimulus	1.24%	22.22%	17.89	0.005077	385	2
	9628	response to abiotic stimulus	1.42%	22.22%	15.62	0.006578	441	2
	6508	proteolysis	2.24%	22.22%	9.93	0.015383	694	2
	48513	organ development	5.83%	55.56%	9.54	0.000066	1806	5
	9605	response to external stimulus	2.87%	22.22%	7.75	0.024135	889	2
	48731	system development	7.51%	55.56%	7.40	0.000219	2327	5
	6811	ion transport	3.13%	22.22%	7.09	0.028250	971	2
	48856	anatomical structure development	8.36%	55.56%	6.64	0.000363	2593	5
	42221	response to chemical stimulus	3.44%	22.22%	6.47	0.033250	1065	2
	7275	multicellular organismal development	8.77%	55.56%	6.33	0.000452	2719	5
Cellular	5581	collagen	0.25%	33.33%	134.20	0.000001	77	3
	44420	extracellular matrix part	0.50%	44.44%	88.32	0.000000	156	4
	5578	proteinaceous extracellular matrix	0.96%	66.67%	69.35	0.000000	298	6
	31012	extracellular matrix	1.02%	66.67%	65.40	0.000000	316	6
	44421	extracellular region part	2.26%	66.67%	29.48	0.000000	701	6
	5576	extracellular region	4.30%	66.67%	15.49	0.000000	1334	6
Molecular	4222	metalloendopeptidase activity	0.26%	22.22%	85.05	0.000238	81	2
	5201	extracellular matrix structural constituent	0.33%	22.22%	68.21	0.000370	101	2
	8237	metallopeptidase activity	0.51%	22.22%	43.33	0.000908	159	2
	4175	endopeptidase activity	1.25%	22.22%	17.75	0.005153	388	2
	8233	peptidase activity	1.91%	22.22%	11.66	0.011421	591	2
	5198	structural molecule activity	2.02%	22.22%	11.02	0.012674	625	2

\* Gray shading includes GO Terms involved in BCMSD

**Supplementary Table 4.** PC 53 enriched pathways from cluster analysis of cluster (1,1) and 5 enriched pathways from cluster (1,2) showing hypergeometric p values less than 0.05. These pathways were derived from the entire PC gene list showing differential upregulation at 16 days (compared to non-irradiated chondrocytes). Gray indicates a pathways association with BCMSD.

GP Zone	GO Category	GO ID	GO Term	% of Array	% of List	Fold Enrichment	P-Value	Total Probe Sets	Probe Sets in Our List
PC Cluster (1,1)	Biological	51924	regulation of calcium ion transport	0.13%	10.00%	75.61	0.000317	41	2
		1569	patterning of blood vessels	0.15%	10.00%	68.89	0.000382	45	2
		43269	regulation of ion transport	0.19%	10.00%	52.54	0.000655	59	2
		48754	branching morphogenesis of a tube	0.30%	15.00%	50.54	0.000027	92	3
		1763	morphogenesis of a branching structure	0.33%	15.00%	45.59	0.000037	102	3
		9880	embryonic pattern specification	0.24%	10.00%	42.47	0.000997	73	2
		50678	regulation of epithelial cell proliferation	0.26%	10.00%	37.80	0.001254	82	2
		50673	epithelial cell proliferation	0.29%	10.00%	34.07	0.001538	91	2
		32101	regulation of response to external stimulus	0.35%	10.00%	28.97	0.002110	107	2
		1666	response to hypoxia	0.62%	15.00%	24.35	0.000237	191	3
		30334	regulation of cell migration	0.43%	10.00%	23.31	0.003216	133	2
		14070	response to organic cyclic substance	0.44%	10.00%	22.79	0.003358	136	2
		51270	regulation of cell motility	0.48%	10.00%	20.81	0.004002	149	2
		1525	angiogenesis	0.74%	15.00%	20.22	0.000406	230	3
		35239	tube morphogenesis	0.86%	15.00%	17.42	0.000623	267	3
		6816	calcium ion transport	0.64%	10.00%	15.58	0.006946	199	2
		48514	blood vessel morphogenesis	0.99%	15.00%	15.10	0.000936	308	3
		55074	calcium ion homeostasis	0.69%	10.00%	14.49	0.007965	214	2
		48646	anatomical structure formation	1.07%	15.00%	13.96	0.001167	333	3
		55065	metal ion homeostasis	0.74%	10.00%	13.60	0.008970	228	2
		15674	di-, tri-valent inorganic cation transport	0.75%	10.00%	13.36	0.009266	232	2
		1568	blood vessel development	1.13%	15.00%	13.32	0.001333	349	3
		1944	vasculature development	1.14%	15.00%	13.14	0.001387	354	3
		35295	tube development	1.17%	15.00%	12.85	0.001477	362	3
		55066	di-, tri-valent inorganic cation homeostasis	0.84%	10.00%	11.97	0.011373	259	2
		7389	pattern specification process	0.89%	10.00%	11.19	0.012875	277	2
		8015	blood circulation	0.92%	10.00%	10.92	0.013480	284	2
		3013	circulatory system process	0.92%	10.00%	10.92	0.013480	284	2
		48583	regulation of response to stimulus	0.92%	10.00%	10.84	0.013655	286	2
		55080	cation homeostasis	0.96%	10.00%	10.37	0.014813	299	2
		10033	response to organic substance	1.05%	10.00%	9.57	0.017145	324	2
		16477	cell migration	1.60%	15.00%	9.39	0.003515	495	3
		51049	regulation of transport	1.10%	10.00%	9.12	0.018706	340	2
		32879	regulation of localization	1.12%	10.00%	8.96	0.019305	346	2
		6928	cell motility	1.77%	15.00%	8.45	0.004678	550	3
		51674	localization of cell	1.77%	15.00%	8.45	0.004678	550	3
		9887	organ morphogenesis	2.26%	15.00%	6.62	0.008945	702	3
		50801	ion homeostasis	1.58%	10.00%	6.34	0.035477	489	2
		42221	response to chemical stimulus	3.44%	20.00%	5.82	0.003844	1065	4
		2376	immune system process	2.66%	15.00%	5.64	0.013515	824	3
		48878	chemical homeostasis	1.80%	10.00%	5.56	0.044361	558	2
		9790	embryonic development	1.85%	10.00%	5.41	0.046367	573	2
		8283	cell proliferation	2.78%	15.00%	5.39	0.015147	862	3
		9605	response to external stimulus	2.87%	15.00%	5.23	0.016366	889	3
		51094	positive regulation of developmental process	1.92%	10.00%	5.20	0.049489	596	2
		31965	nuclear membrane	0.42%	10.00%	24.03	0.003032	129	2
		5635	nuclear envelope	0.65%	10.00%	15.35	0.007145	202	2
		8528	peptide receptor activity, G-protein coupled	0.42%	10.00%	23.66	0.003124	131	2
		1653	peptide receptor activity	0.42%	10.00%	23.66	0.003124	131	2
		42277	peptide binding	0.76%	10.00%	13.19	0.009491	235	2
		1584	rhodopsin-like receptor activity	1.25%	10.00%	7.97	0.023801	389	2
		4930	G-protein coupled receptor activity	1.57%	10.00%	6.35	0.035353	488	2
		4888	transmembrane receptor activity	2.93%	15.00%	5.12	0.017253	908	3
PC Cluster (1,2)	Molecular	5543	phospholipid binding	0.51%	13.33%	26.16	0.002538	158	2
		8289	lipid binding	1.45%	13.33%	9.21	0.018196	449	2
		16462	pyrophosphatase activity	1.96%	13.33%	6.79	0.031284	609	2
		16818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	1.97%	13.33%	6.75	0.031553	612	2
		16817	hydrolase activity, acting on acid anhydrides	1.99%	13.33%	6.70	0.032003	617	2

**Supplementary Table 5.** HZ 18 enriched pathways from cluster analysis of cluster (2,2) showing hypergeometric p values less than 0.05. These pathways were derived from the entire HZ gene list showing differential upregulation at 16 days (compared to non-irradiated chondrocytes). Gray indicates a pathways association with BCMSD.

GO Category	GO ID	GO Term	% of Array	% of List	Fold Enrichment	P value	Total Probe Sets	Probe Sets in Our List
Biological	6783	heme biosynthetic process	0.05%	11.76%	260.50	0.000026	14	2
	42168	heme metabolic process	0.06%	11.76%	202.61	0.000043	18	2
	6779	porphyrin biosynthetic process	0.09%	11.76%	125.76	0.000113	29	2
	33014	tetrapyrrole biosynthetic process	0.09%	11.76%	125.76	0.000113	29	2
	46148	pigment biosynthetic process	0.10%	11.76%	113.97	0.000138	32	2
	6778	porphyrin metabolic process	0.12%	11.76%	101.31	0.000175	36	2
	33013	tetrapyrrole metabolic process	0.12%	11.76%	101.31	0.000175	36	2
	42440	pigment metabolic process	0.12%	11.76%	95.98	0.000196	38	2
	19748	secondary metabolic process	0.20%	11.76%	58.82	0.000520	62	2
	6935	chemotaxis	0.35%	17.65%	51.13	0.000026	107	3
	42330	taxis	0.35%	17.65%	51.13	0.000026	107	3
	51188	cofactor biosynthetic process	0.34%	11.76%	35.07	0.001443	104	2
	46483	heterocycle metabolic process	0.42%	11.76%	28.27	0.002197	129	2
	7626	locomotory behavior	0.76%	17.65%	23.08	0.000270	237	3
	6952	defense response	1.49%	17.65%	11.87	0.001804	461	3
	7610	behavior	1.60%	17.65%	11.05	0.002200	495	3
	9605	response to external stimulus	2.87%	23.53%	8.20	0.001097	889	4
	42221	response to chemical stimulus	3.44%	23.53%	6.85	0.002096	1065	4