

Supplementary information, Table S3 Functional Annotation Terms (FATs) enriched in genes up- or down-regulated by sFGF2. Analysis was conducted using the DAVID Functional Annotation Clustering (DFAC) web tool. FATs common to both sets were shaded as light blue.

Set T1. Terms enriched for gene set G1 (732 genes up-regulated by sFGF2 in mSSCs)			
No.	FAT	p-Value	Number of Genes
1	GO:0032502~developmental process	1.19E-08	138
2	GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.12E-08	153
3	GO:0043283~biopolymer metabolic process	4.03E-08	192
4	dna-binding	7.15E-08	75
5	GO:0044428~nuclear part	1.15E-07	65
6	GO:0007275~multicellular organismal development	1.21E-07	108
7	nucleus	1.51E-07	142
8	GO:0003677~DNA binding	2.43E-07	101
9	GO:0005634~nucleus	5.37E-07	170
10	GO:0065007~biological regulation	7.80E-07	182
11	GO:0050789~regulation of biological process	1.49E-06	168
12	GO:0016070~RNA metabolic process	1.53E-06	118
13	Transcription	3.52E-06	68
14	GO:0031981~nuclear lumen	3.75E-06	46
15	GO:0003676~nucleic acid binding	3.88E-06	141
16	GO:0030528~transcription regulator activity	4.59E-06	68
17	GO:0044238~primary metabolic process	5.12E-06	256
18	GO:0050794~regulation of cellular process	5.39E-06	153
19	GO:0006351~transcription, DNA-dependent	6.67E-06	100
20	GO:0032774~RNA biosynthetic process	7.37E-06	100
21	PIRSF001950:small inducible chemokine, C/CC types	7.79E-06	7
22	GO:0030154~cell differentiation	9.03E-06	86
23	GO:0048869~cellular developmental process	9.03E-06	86
24	GO:0006350~transcription	9.76E-06	105

25	IPR001356:Homeobox	1.01E-05	20
26	GO:0044451~nucleoplasm part	1.40E-05	37
27	GO:0043170~macromolecule metabolic process	1.55E-05	227
28	GO:0005667~transcription factor complex	1.60E-05	31
29	GO:0002376~immune system process	2.12E-05	48
30	GO:0006355~regulation of transcription, DNA-dependent	2.14E-05	97
31	IPR000827:Small chemokine, C-C	2.24E-05	7
32	GO:0005654~nucleoplasm	2.37E-05	38
33	Transcription regulation	2.70E-05	64
34	GO:0003700~transcription factor activity	3.22E-05	51
35	GO:0045449~regulation of transcription	3.36E-05	100
36	GO:0010468~regulation of gene expression	3.89E-05	105
37	GO:0048731~system development	3.95E-05	80
38	GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.30E-05	101
39	GO:0044237~cellular metabolic process	4.43E-05	251
40	GO:0048856~anatomical structure development	5.73E-05	90
41	GO:0031974~membrane-enclosed lumen	8.05E-05	46
42	GO:0043233~organelle lumen	8.05E-05	46
43	Homeobox	8.73E-05	21
44	GO:0008152~metabolic process	9.16E-05	273
45	GO:0031323~regulation of cellular metabolic process	0.0001124	106
46	GO:0010467~gene expression	0.000116153	127
47	IPR012287:Homeodomain-related	0.000157162	17
48	GO:0019222~regulation of metabolic process	0.000196643	108
49	GO:0046578~regulation of Ras protein signal transduction	0.000221271	14
50	GO:0051056~regulation of small GTPase mediated signal transduction	0.000279479	16
51	GO:0006954~inflammatory response	0.000349765	18
52	GO:0006955~immune response	0.000384717	32
53	GO:0048513~organ development	0.000397138	64
54	GO:0042330~taxis	0.000444422	12
55	GO:0006935~chemotaxis	0.000444422	12
56	SM00389:HOX	0.000458126	20

57	IPR001811:Small chemokine, interleukin-8-like	0.000646246	7
58	GO:0009653~anatomical structure morphogenesis	0.000703248	55
59	GO:0043227~membrane-bound organelle	0.000756108	227
60	GO:0048468~cell development	0.000913182	56
61	GO:0008009~chemokine activity	0.000940092	7
62	GO:0043231~intracellular membrane-bound organelle	0.000978103	226
63	GO:0009611~response to wounding	0.00103914	21
64	GO:0005083~small GTPase regulator activity	0.00105089	16
65	GO:0042379~chemokine receptor binding	0.00107868	7
66	GO:0005622~intracellular	0.00119825	307
67	IPR000219:DH	0.00129474	8
68	IPR001849:Pleckstrin-like	0.00144693	16
69	GO:0035023~regulation of Rho protein signal transduction	0.0014605	9
70	GO:0009966~regulation of signal transduction	0.00149185	26
71	GO:0007265~Ras protein signal transduction	0.00162118	15
72	GO:0005085~guanyl-nucleotide exchange factor activity	0.00163847	13
73	GO:0030695~GTPase regulator activity	0.00191729	22
74	SM00199:SCY	0.00193581	7
75	IPR000047:Helix-turn-helix motif, lambda-like repressor	0.00211506	9
76	GO:0009792~embryonic development ending in birth or egg hatching	0.0024379	16
77	GO:0006950~response to stress	0.00255186	40
78	GO:0001664~G-protein-coupled receptor binding	0.00279914	8
79	IPR001331:Guanine-nucleotide dissociation stimulator, CDC24	0.00287039	6
80	GO:0009887~organ morphogenesis	0.00331477	28
81	signal	0.00360303	99
82	GO:0007264~small GTPase mediated signal transduction	0.00385481	23
83	GO:0009790~embryonic development	0.0038818	25
84	inflammatory response	0.00394892	8
85	SM00325:RhoGEF	0.00426803	8

86	GO:0043234~protein complex	0.0042858	73
87	GO:0005089~Rho guanyl-nucleotide exchange factor activity	0.00464166	8
88	GO:0044424~intracellular part	0.00467809	287
89	cytokine	0.00531529	13
90	GO:0043009~chordate embryonic development	0.00547599	15
91	chemotaxis	0.00613015	7
92	GO:0030234~enzyme regulator activity	0.00634434	35
93	GO:0007242~intracellular signaling cascade	0.00698364	51
94	GO:0043229~intracellular organelle	0.00698689	245
95	SM00233:PH	0.0073129	17
96	GO:0043226~organelle	0.0073143	245
97	GO:0044421~extracellular region part	0.00796572	83
98	DNA-binding region:Homeobox	0.00801167	13
99	GO:0007266~Rho protein signal transduction	0.00862147	9
100	Secreted	0.00927875	51
101	GO:0007610~behavior	0.0102384	19
102	GO:0009605~response to external stimulus	0.0103596	25
103	GO:0005615~extracellular space	0.010534	78
104	IPR011993:Pleckstrin homology-type	0.0107027	15
105	GO:0005088~Ras guanyl-nucleotide exchange factor activity	0.0108857	8
106	GO:0005102~receptor binding	0.011495	32
107	GO:0007626~locomotory behavior	0.0117685	14
108	SH3 domain	0.0137261	13
109	GO:0032319~regulation of Rho GTPase activity	0.0160441	3
110	domain:DH	0.0164646	5
111	GO:0009987~cellular process	0.0180404	381
112	GO:0032991~macromolecular complex	0.0182883	83
113	GO:0005576~extracellular region	0.0197542	86
114	guanine-nucleotide releasing factor	0.0198966	7
115	GO:0008219~cell death	0.0201319	32
116	domain:SH3	0.0202933	10
117	GO:0016265~death	0.0214721	32
118	IPR001452:Src homology-3	0.0216037	12
119	GO:0043565~sequence-specific DNA binding	0.0217464	24
120	GO:0030027~lamellipodium	0.0241404	6

121	mmu04060:Cytokine-cytokine receptor interaction	0.0293542	15
122	GO:0005125~cytokine activity	0.0433126	13
Set T2. Terms enriched for gene set G2 (854 genes down-regulated by sFGF2 in mSSCs)			
No.	Annotation	p-Value	Number of Genes
1	signal	2.50E-23	186
2	GO:0032502~developmental process	1.80E-20	194
3	GO:0007275~multicellular organismal development	3.24E-20	160
4	GO:0048856~anatomical structure development	3.97E-20	150
5	glycoprotein	2.60E-19	197
6	GO:0022610~biological adhesion	3.80E-18	73
7	GO:0007155~cell adhesion	3.80E-18	73
8	GO:0005576~extracellular region	2.17E-16	160
9	GO:0009653~anatomical structure morphogenesis	3.42E-16	98
10	GO:0031012~extracellular matrix	3.49E-16	46
11	GO:0005578~proteinaceous extracellular matrix	5.50E-16	45
12	GO:0044421~extracellular region part	1.77E-15	149
13	GO:0048731~system development	3.64E-15	124
14	Secreted	5.72E-15	99
15	GO:0048513~organ development	2.53E-12	101
16	extracellular matrix	7.06E-12	31
17	signal peptide	9.82E-12	154
18	GO:0005615~extracellular space	1.55E-09	125
19	GO:0044420~extracellular matrix part	2.83E-09	20
20	GO:0009887~organ morphogenesis	1.66E-08	46
21	GO:0035295~tube development	2.37E-08	27
22	GO:0035239~tube morphogenesis	2.81E-08	22
23	egf-like domain	4.69E-08	27
24	glycosylation site:N-linked (GlcNAc...)	8.03E-08	153
25	cell adhesion	9.35E-08	35
26	GO:0032989~cellular structure morphogenesis	1.43E-07	44
27	GO:0000902~cell morphogenesis	1.43E-07	44
28	IPR006209:EGF-like	2.20E-07	20
29	IPR001881:EGF-like calcium-binding	4.76E-07	16
30	GO:0005604~basement membrane	5.57E-07	14
31	GO:0001822~kidney development	9.88E-07	14

32	IPR006210:EGF	1.04E-06	23
33	disulfide bond	1.47E-06	117
34	GO:0001655~urogenital system development	2.90E-06	14
35	IPR000152:Aspartic acid and asparagine hydroxylation site	3.09E-06	15
36	GO:0016010~dystrophin-associated glycoprotein complex	7.53E-06	7
37	IPR000742:EGF-like, type 3	1.16E-05	21
38	GO:0022008~neurogenesis	1.32E-05	31
39	SM00179:EGF_CA	1.40E-05	16
40	IPR013032:EGF-like region	1.40E-05	25
41	GO:0016477~cell migration	1.54E-05	27
42	SM00181:EGF	1.58E-05	24
43	GO:0032501~multicellular organismal process	2.20E-05	186
44	GO:0048754~branching morphogenesis of a tube	4.34E-05	11
45	GO:0005605~basal lamina	5.50E-05	8
46	GO:0001763~morphogenesis of a branching structure	8.59E-05	11
47	IPR013091:EGF calcium-binding	8.73E-05	11
48	GO:0001568~blood vessel development	9.40E-05	21
49	GO:0001944~vasculature development	0.000112787	21
50	GO:0048514~blood vessel morphogenesis	0.000121241	19
51	GO:0030182~neuron differentiation	0.000127287	25
52	GO:0031175~neurite development	0.000133507	20
53	GO:0006928~cell motility	0.000139814	28
54	GO:0051674~localization of cell	0.000139814	28
55	GO:0048699~generation of neurons	0.000143717	27
56	GO:0048812~neurite morphogenesis	0.000490235	17
57	GO:0048667~neuron morphogenesis during differentiation	0.000490235	17
58	GO:0032990~cell part morphogenesis	0.000578295	23
59	GO:0030030~cell projection organization and biogenesis	0.000578295	23
60	GO:0048858~cell projection morphogenesis	0.000578295	23
61	GO:0048666~neuron development	0.000606578	20
62	GO:0000904~cellular morphogenesis during differentiation	0.000652186	18
63	GO:0007409~axonogenesis	0.000742025	16

64	GO:0007411~axon guidance	0.000825205	11
65	GO:0001656~metanephros development	0.00114332	8
66	GO:0009880~embryonic pattern specification	0.00146257	8
67	GO:0001569~patterning of blood vessels	0.00166023	6
68	GO:0048646~anatomical structure formation	0.00184639	17
69	IPR013111:EGF, extracellular	0.00413771	9
70	domain:EGF-like 2; calcium-binding	0.00420666	7
71	GO:0016011~dystroglycan complex	0.00446398	4
72	GO:0001525~angiogenesis	0.00600151	13
73	domain:EGF-like 4; calcium-binding	0.0179139	5
74	domain:EGF-like 3; calcium-binding	0.0179139	5
75	GO:0001657~ureteric bud development	0.0278243	5
76	GO:0016012~sarcoglycan complex	0.0307113	3