Supplementary Table SV Enriched GO terms for up-regulated differentially expressed genes in KS fibroblasts (f-KS1, f-KS2) versus HM fibroblasts (f-HM1, f-HM2). (See also Fig. 2 and Supplementary Table SII) Fertility related GO terms related to Figure 2D in green.

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
macrophage proliferation (GO:0061517)	2	2	0.02	+	97.42	0.000608	0.0499
microglial cell proliferation (GO:0061518)	2	2	0.02	+	97.42	0.000608	0.0502
negative regulation of planar cell polarity pathway involved in axis elongation (GO:2000041)	2	2	0.02	+	97.42	0.000608	0.0507
regulation of planar cell polarity pathway involved in axis elongation (GO:2000040)	2	2	0.02	+	97.42	0.000608	0.0504
lateral sprouting from an epithelium (GO:0060601)	9	3	0.09	+	32.47	0.000213	0.0241
glial cell proliferation (GO:0014009)	11	3	0.11	+	26.57	0.000347	0.0338
regulation of type B pancreatic cell proliferation (GO:0061469)	11	3	0.11	+	26.57	0.000347	0.0336
prostate gland morphogenesis (GO:0060512)	24	6	0.25	+	24.35	0.000000497	0.000234
embryonic skeletal joint morphogenesis (GO:0060272)	12	3	0.12	+	24.35	0.00043	0.0392
regulation of timing of cell differentiation (GO:0048505)	12	3	0.12	+	24.35	0.00043	0.039
maternal behavior (GO:0042711)	13	3	0.13	+	22.48	0.000525	0.0458
regulation of development, heterochronic (GO:0040034)	13	3	0.13	+	22.48	0.000525	0.046
prostate gland epithelium morphogenesis (GO:0060740)	22	5	0.23	+	22.14	0.00000696	0.00174
negative regulation of smooth muscle cell migration (GO:0014912)	20	4	0.21	+	19.48	0.0000939	0.0126
negative regulation of epithelial to mesenchymal transition (GO:0010719)	27	5	0.28	+	18.04	0.0000167	0.00359
positive regulation of morphogenesis of an epithelium (GO:1905332)	33	5	0.34	+	14.76	0.0000395	0.00652
prostate gland development (GO:0030850)	42	6	0.43	+	13.92	0.00000882	0.00211
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage (GO:1902230)	29	4	0.3	+	13.44	0.000337	0.0337
positive regulation of mesenchymal cell proliferation (GO:0002053)	29	4	0.3	+	13.44	0.000337	0.0335
reproductive behavior (GO:0019098)	30	4	0.31	+	12.99	0.000379	0.0358
mammary gland duct morphogenesis (GO:0060603)	30	4	0.31	+	12.99	0.000379	0.0356
regulation of morphogenesis of a branching structure (GO:0060688)	55	7	0.56	+	12.4	0.00000311	0.000876
mammary gland epithelium development (GO:0061180)	58	7	0.6	+	11.76	0.00000428	0.00113
mammary gland morphogenesis (GO:0060443)	42	5	0.43	+	11.6	0.000112	0.0144
negative regulation of peptidyl-tyrosine phosphorylation (GO:0050732)	47	5	0.48	+	10.36	0.000182	0.0212

Continued

Supplementary Table SV **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
negative regulation of BMP signaling pathway (GO:0030514)	49	5	0.5	+	9.94	0.000218	0.0243
gland morphogenesis (GO:0022612)	97	9	1	+	9.04	0.00000137	0.000493
positive regulation of epithelial cell proliferation (GO:0050679)	171	15	1.76	+	8.55	7.99E-10	1.77E-06
negative regulation of cell morphogenesis involved in differentiation (GO:0010771)	81	7	0.83	+	8.42	0.0000321	0.00565
negative regulation of developmental growth (GO:0048640)	83	7	0.85	+	8.22	0.0000371	0.00632
negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090101)	108	9	1.11	+	8.12	0.00000312	0.000865
glycosaminoglycan biosynthetic process (GO:0006024)	101	8	1.04	+	7.72	0.0000157	0.00344
digestive tract development (GO:0048565)	127	10	1.3	+	7.67	0.00000142	0.000501
aminoglycan biosynthetic process (GO:0006023)	102	8	1.05	+	7.64	0.0000168	0.00357
negative regulation of cellular response to growth factor stimulus (GO:0090288)	131	10	1.34	+	7.44	0.00000185	0.000609
response to cAMP (GO:0051591)	97	7	1	+	7.03	0.0000936	0.0126
digestive system development (GO:0055123)	139	10	1.43	+	7.01	0.00000304	0.000874
mammary gland development (GO:0030879)	129	9	1.32	+	6.8	0.0000121	0.00279
regulation of blood coagulation (GO:0030193)	89	6	0.91	+	6.57	0.000421	0.0386
regulation of hemostasis (GO:1900046)	89	6	0.91	+	6.57	0.000421	0.0388
osteoblast differentiation (GO:0001649)	121	8	1.24	+	6.44	0.0000531	0.00807
cardiac chamber development (GO:0003205)	156	10	1.6	+	6.24	0.00000797	0.00193
regulation of coagulation (GO:0050818)	94	6	0.96	+	6.22	0.000553	0.0477
regulation of osteoblast differentiation (GO:0045667)	110	7	1.13	+	6.2	0.000196	0.0225
regulation of epithelial cell proliferation (GO:0050678)	306	19	3.14	+	6.05	1.02E-09	1.76E-06
cellular response to fibroblast growth factor stimulus (GO:0044344)	114	7	1.17	+	5.98	0.000241	0.0263
connective tissue development (GO:0061448)	202	12	2.07	+	5.79	0.00000208	0.000671
lung development (GO:0030324)	169	10	1.73	+	5.76	0.0000154	0.00342
cartilage development (GO:0051216)	153	9	1.57	+	5.73	0.0000431	0.00675
glycosaminoglycan metabolic process (GO:0030203)	153	9	1.57	+	5.73	0.0000431	0.00669
regulation of wound healing (GO:0061041)	137	8	1.41	+	5.69	0.000121	0.0152
negative regulation of peptide secretion (GO:0002792)	120	7	1.23	+	5.68	0.000323	0.033
cardiac chamber morphogenesis (GO:0003206)	121	7	1.24	+	5.64	0.000339	0.0333

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Supplementary Table SV **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
response to fibroblast growth factor (GO:0071774)	121	7	1.24	+	5.64	0.000339	0.0335
respiratory tube development (GO:0030323)	173	10	1.78	+	5.63	0.0000187	0.00386
negative regulation of epithelial cell proliferation (GO:0050680)	123	7	1.26	+	5.54	0.000373	0.0355
respiratory system development (GO:0060541)	195	11	2	+	5.5	0.00000887	0.00208
aminoglycan metabolic process (GO:0006022)	160	9	1.64	+	5.48	0.0000599	0.00902
negative regulation of cell growth (GO:0030308)	161	9	1.65	+	5.45	0.0000627	0.00935
negative regulation of growth (GO:0045926)	236	13	2.42	+	5.37	0.00000173	0.000582
regulation of muscle tissue development (GO:1901861)	127	7	1.3	+	5.37	0.000448	0.0401
response to organophosphorus (GO:0046683)	133	7	1.37	+	5.13	0.000582	0.0496
urogenital system development (GO:0001655)	306	16	3.14	+	5.09	0.00000021	0.00013
regulation of cellular response to growth factor stimulus (GO:0090287)	249	13	2.56	+	5.09	0.00000303	0.000903
regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090092)	215	11	2.21	+	4.98	0.0000211	0.0042
regulation of response to wounding (GO:1903034)	160	8	1.64	+	4.87	0.00033	0.0333
regulation of ossification (GO:0030278)	182	9	1.87	+	4.82	0.000153	0.0183
ossification (GO:0001503)	248	12	2.55	+	4.71	0.0000151	0.0034
negative regulation of cell migration (GO:0030336)	230	11	2.36	+	4.66	0.0000381	0.00642
renal system development (GO:0072001)	272	13	2.79	+	4.66	0.00000755	0.00186
central nervous system neuron differentiation (GO:0021953)	169	8	1.73	+	4.61	0.000468	0.0413
mesenchyme development (GO:0060485)	190	9	1.95	+	4.61	0.000208	0.0237
kidney development (GO:0001822)	254	12	2.61	+	4.6	0.000019	0.00387
negative regulation of cellular component movement (GO:0051271)	261	12	2.68	+	4.48	0.0000245	0.00464
negative regulation of cell motility (GO:2000146)	245	11	2.51	+	4.37	0.0000657	0.00952
positive regulation of growth (GO:0045927)	249	11	2.56	+	4.3	0.0000755	0.0105
negative regulation of locomotion (GO:0040013)	277	12	2.84	+	4.22	0.0000427	0.00683
regulation of developmental growth (GO:0048638)	303	13	3.11	+	4.18	0.0000226	0.00443
negative regulation of apoptotic signaling pathway (GO:2001234)	211	9	2.17	+	4.16	0.000434	0.0391
reproductive structure development (GO:0048608)	423	18	4.34	+	4.15	0.000000656	0.000275
tube development (GO:0035295)	563	24	5.78	+	4.15	7.84E-09	8.1E-06
multi-multicellular organism process (GO:0044706)	212	9	2.18	+	4.14	0.000449	0.04

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Supplementary Table SV **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
reproductive system development (GO:0061458)	427	18	4.38	+	4.11	0.000000748	0.000297
negative regulation of cell development (GO:0010721)	277	11	2.84	+	3.87	0.000186	0.0215
epithelial tube morphogenesis (GO:0060562)	303	12	3.11	+	3.86	0.0000973	0.0129
regulation of organ morphogenesis (GO:2000027)	255	10	2.62	+	3.82	0.000399	0.0373
tube morphogenesis (GO:0035239)	341	13	3.5	+	3.71	0.0000724	0.0102
negative regulation of response to external stimulus (GO:0032102)	269	10	2.76	+	3.62	0.000596	0.0502
angiogenesis (GO:0001525)	297	11	3.05	+	3.61	0.00033	0.0334
developmental growth (GO:0048589)	352	13	3.61	+	3.6	0.0000985	0.0129
gland development (GO:0048732)	409	15	4.2	+	3.57	0.000031	0.00566
blood vessel morphogenesis (GO:0048514)	386	14	3.96	+	3.53	0.0000641	0.00947
negative regulation of cell differentiation (GO:0045596)	639	23	6.56	+	3.51	0.000000307	0.00017
positive regulation of cell proliferation (GO:0008284)	871	31	8.94	+	3.47	2.84E-09	3.67E-06
cell proliferation (GO:0008283)	678	24	6.96	+	3.45	0.000000224	0.000134
blood vessel development (GO:0001568)	466	16	4.78	+	3.34	0.0000363	0.00633
regulation of cell migration (GO:0030334)	733	25	7.52	+	3.32	0.000000242	0.000139
regulation of growth (GO:0040008)	649	22	6.66	+	3.3	0.00000147	0.000508
morphogenesis of an epithelium (GO:0002009)	419	14	4.3	+	3.25	0.000148	0.0179
heart development (GO:0007507)	481	16	4.94	+	3.24	0.0000523	0.00803
growth (GO:0040007)	395	13	4.05	+	3.21	0.000293	0.0303
vasculature development (GO:0001944)	490	16	5.03	+	3.18	0.0000646	0.00945
cardiovascular system development (GO:0072358)	500	16	5.13	+	3.12	0.0000812	0.0112
skeletal system development (GO:0001501)	469	15	4.81	+	3.12	0.000137	0.0169
cellular response to growth factor stimulus (GO:0071363)	470	15	4.82	+	3.11	0.00014	0.0172
regulation of cell motility (GO:2000145)	784	25	8.05	+	3.11	0.000000803	0.000311
response to toxic substance (GO:0009636)	501	16	5.14	+	3.11	0.0000831	0.0114
negative regulation of response to stimulus (GO:0048585)	1477	47	15.16	+	3.1	4.88E-12	1.89E-08
animal organ morphogenesis (GO:0009887)	881	28	9.04	+	3.1	0.000000176	0.000119
post-translational protein modification (GO:0043687)	440	14	4.52	+	3.1	0.00024	0.0264
positive regulation of cell motility (GO:2000147)	445	14	4.57	+	3.06	0.000268	0.0281
head development (GO:0060322)	734	23	7.53	+	3.05	0.00000303	0.000886
developmental process involved in reproduction (GO:0003006)	649	20	6.66	+	3	0.0000174	0.00365
negative regulation of signal transduction (GO:0009968)	1176	36	12.07	+	2.98	6.26E-09	6.94E-06

Continued

Supplementary Table SV **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
negative regulation of signaling (GO:0023057)	1277	39	13.11	+	2.98	1.4E-09	2.17E-06
positive regulation of cellular component movement (GO:0051272)	457	14	4.69	+	2.98	0.000348	0.0335
tissue morphogenesis (GO:0048729)	526	16	5.4	+	2.96	0.000143	0.0175
regulation of cellular component movement (GO:0051270)	858	26	8.81	+	2.95	0.0000012	0.000443
brain development (GO:0007420)	697	21	7.15	+	2.94	0.0000148	0.00337
response to growth factor (GO:0070848)	497	15	5.1	+	2.94	0.00025	0.0268
negative regulation of cell communication (GO:0010648)	1273	38	13.07	+	2.91	4.32E-09	5.15E-06
circulatory system development (GO:0072359)	808	24	8.29	+	2.89	0.00000443	0.00114
positive regulation of locomotion (GO:0040017)	477	14	4.9	+	2.86	0.000526	0.0456
regulation of locomotion (GO:0040012)	855	25	8.78	+	2.85	0.00000361	0.000982
regulation of receptor activity (GO:0010469)	547	16	5.62	+	2.85	0.00022	0.0243
negative regulation of developmental process (GO:0051093)	862	25	8.85	+	2.83	0.00000415	0.00111
positive regulation of developmental process (GO:0051094)	1241	36	12.74	+	2.83	0.000000024	2.07E-05
negative regulation of multicellular organismal process (GO:0051241)	1044	30	10.72	+	2.8	0.000000497	0.000241
embryonic morphogenesis (GO:0048598)	563	16	5.78	+	2.77	0.0003	0.0308
positive regulation of multicellular organismal process (GO:0051240)	1493	41	15.33	+	2.68	9.84E-09	9.53E-06
anatomical structure formation involved in morphogenesis (GO:0048646)	840	23	8.62	+	2.67	0.000025	0.00462
central nervous system development (GO:0007417)	899	24	9.23	+	2.6	0.0000246	0.00459
regulation of neurogenesis (GO:0050767)	675	18	6.93	+	2.6	0.000269	0.028
positive regulation of cell differentiation (GO:0045597)	862	23	8.85	+	2.6	0.0000369	0.00636
regulation of cell proliferation (GO:0042127)	1588	42	16.3	+	2.58	0.000000018	1.64E-05
neuron differentiation (GO:0030182)	925	24	9.5	+	2.53	0.0000383	0.00638
regulation of nervous system development (GO:0051960)	770	20	7.9	+	2.53	0.000172	0.0202
negative regulation of apoptotic process (GO:0043066)	853	22	8.76	+	2.51	0.0000891	0.0121
negative regulation of cell proliferation (GO:0008285)	661	17	6.79	+	2.51	0.000592	0.0502
negative regulation of programmed cell death (GO:0043069)	867	22	8.9	+	2.47	0.000112	0.0145
anatomical structure morphogenesis (GO:0009653)	2021	51	20.75	+	2.46	1.93E-09	2.72E-06
neurogenesis (GO:0022008)	1471	37	15.1	+	2.45	0.00000061	0.00027

Continued

Supplementary Table SV **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
regulation of cell development (GO:0060284)	794	20	8.15	+	2.45	0.000254	0.027
cell adhesion (GO:0007155)	873	22	8.96	+	2.45	0.000123	0.0154
biological adhesion (GO:0022610)	878	22	9.01	+	2.44	0.000217	0.0244
embryo development (GO:0009790)	924	23	9.49	+	2.42	0.000153	0.0183
tissue development (GO:0009888)	1658	41	17.02	+	2.41	0.000000179	0.000116
response to organonitrogen compound (GO:0010243)	884	21	9.07	+	2.31	0.000461	0.0408
regulation of anatomical structure morphogenesis (GO:0022603)	980	23	10.06	+	2.29	0.000265	0.0279
generation of neurons (GO:0048699)	1374	32	14.1	+	2.27	0.0000209	0.00422
regulation of multicellular organismal development (GO:2000026)	1805	42	18.53	+	2.27	0.00000062	0.000267
negative regulation of cell death (GO:0060548)	946	22	9.71	+	2.27	0.000408	0.0379
cellular response to oxygen-containing compound (GO:1901701)	905	21	9.29	+	2.26	0.000578	0.0495
regulation of cell differentiation (GO:0045595)	1643	38	16.87	+	2.25	0.00000282	0.000857
nervous system development (GO:0007399)	2206	50	22.64	+	2.21	8.81E-08	0.000065
reproduction (GO:0000003)	1372	31	14.08	+	2.2	0.0000428	0.00677
reproductive process (GO:0022414)	1371	31	14.07	+	2.2	0.0000424	0.00684
animal organ development (GO:0048513)	2988	66	30.67	+	2.15	9.67E-10	1.87E-06
regulation of developmental process (GO:0050793)	2379	51	24.42	+	2.09	0.000000417	0.000209
regulation of multicellular organismal process (GO:0051239)	2777	59	28.51	+	2.07	4.81E-08	3.92E-05
system development (GO:0048731)	4173	88	42.84	+	2.05	3.87E-12	3E-08
response to oxygen-containing compound (GO:1901700)	1445	30	14.83	+	2.02	0.000358	0.0343
intracellular signal transduction (GO:0035556)	1605	33	16.48	+	2	0.000153	0.0181
multicellular organism development (GO:0007275)	4769	97	48.95	+	1.98	7.12E-13	1.1E-08
cellular response to organic substance (GO:0071310)	2150	43	22.07	+	1.95	0.0000235	0.00455
regulation of signal transduction (GO:0009966)	3083	61	31.65	+	1.93	0.000000335	0.000179
anatomical structure development (GO:0048856)	5137	100	52.73	+	1.9	4.81E-12	2.49E-08
cellular response to chemical stimulus (GO:0070887)	2624	51	26.94	+	1.89	0.00000686	0.00174
regulation of cell communication (GO:0010646)	3374	64	34.63	+	1.85	0.000000604	0.000276
developmental process (GO:0032502)	5497	104	56.43	+	1.84	5.54E-12	1.72E-08
regulation of signaling (GO:0023051)	3423	64	35.14	+	1.82	0.0000011	0.000416
cell surface receptor signaling pathway (GO:0007166)	2278	42	23.38	+	1.8	0.000245	0.0264

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Supplementary Table SV **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (216)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
cell differentiation (GO:0030154)	3491	64	35.84	+	1.79	0.00000218	0.000689
cellular developmental process (GO:0048869)	3565	65	36.6	+	1.78	0.00000258	0.000801
regulation of response to stimulus (GO:0048583)	4078	74	41.86	+	1.77	0.00000038	0.000196
response to organic substance (GO:0010033)	2765	50	28.38	+	1.76	0.0000679	0.00975
negative regulation of cellular process (GO:0048523)	4454	80	45.72	+	1.75	0.000000103	7.25E-05
regulation of localization (GO:0032879)	2595	46	26.64	+	1.73	0.000242	0.0263
negative regulation of biological process (GO:0048519)	4952	87	50.83	+	1.71	7.21E-08	5.59E-05
multicellular organismal process (GO:0032501)	6688	113	68.65	+	1.65	6.33E-10	1.64E-06
response to chemical (GO:0042221)	4164	69	42.74	+	1.61	0.0000241	0.00461
signal transduction (GO:0007165)	4956	77	50.87	+	1.51	0.0000719	0.0102
signaling (GO:0023052)	5349	81	54.91	+	1.48	0.000109	0.0143
cell communication (GO:0007154)	5447	82	55.91	+	1.47	0.00012	0.0153
cellular response to stimulus (GO:0051716)	6423	95	65.93	+	1.44	0.00004	0.00652
response to stimulus (GO:0050896)	8142	120	83.58	+	1.44	0.000000725	0.000296
regulation of cellular process (GO:0050794)	10764	136	110.49	+	1.23	0.000597	0.05
biological_process (GO:0008150)	17500	201	179.64	+	1.12	0.0000312	0.00562

GO: gene ontology