Supplementary Table SVII Enriched GO terms for down-regulated differentially expressed genes in KS hiPSCs (ips-KS1, ips-KS2) versus HM hiPSCs (ips-HM1, ips-HM2). (See also Fig. 2 and Supplementary Table SIII) In green: fertility related GO terms related to Figure 2D. In bold: enriched GO terms found also with down-regulated DEGs in ips-KS2 only vs ips-HM1, ips-HM2.

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
positive regulation of metanephric mesenchymal cell migration (GO:2000591)	3	3	0.08	+	37.05	3.40E-04	7.59E-03
positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway (GO:0035793)	3	3	0.08	+	37.05	3.40E-04	7.58E-03
regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway (GO:1900238)	3	3	0.08	+	37.05	3.40E-04	7.56E-03
mesenchyme migration (GO:0090131)	5	4	0.13	+	29.64	5.36E-05	1.53E-03
regulation of metanephric mesenchymal cell migration (GO:2000589)	4	3	0.11	+	27.78	5.84E-04	1.20E-02
regulation of endodermal cell differentiation (GO:1903224)	6	4	0.16	+	24.7	8.74E-05	2.34E-03
comma-shaped body morphogenesis (GO:0072049)	5	3	0.13	+	22.23	9.17E-04	1.75E-02
negative regulation of chemokine-mediated signaling pathway (GO:0070100)	5	3	0.13	+	22.23	9.17E-04	1.74E-02
peripheral nervous system axon regeneration (GO:0014012)	5	3	0.13	+	22.23	9.17E-04	1.75E-02
positive regulation of glomerular mesangial cell proliferation (GO:0072126)	5	3	0.13	+	22.23	9.17E-04	1.75E-02
positive regulation of hair follicle maturation (GO:0048818)	5	3	0.13	+	22.23	9.17E-04	1.74E-02
positive regulation of melanocyte differentiation (GO:0045636)	5	3	0.13	+	22.23	9.17E-04	1.75E-02
regulation of cell adhesion molecule production (GO:0060353)	5	3	0.13	+	22.23	9.17E-04	1.75E-02
substrate-dependent cerebral cortex tangential migration (GO:0021825)	5	3	0.13	+	22.23	9.17E-04	1.74E-02
tendon development (GO:0035989)	5	3	0.13	+	22.23	9.17E-04	1.74E-02
pharyngeal arch artery morphogenesis (GO:0061626)	7	4	0.19	+	21.17	1.35E-04	3.41E-03
regulation of cell communication by electrical coupling involved in cardiac conduction (GO:1901844)	7	4	0.19	+	21.17	1.35E-04	3.42E-03
axon extension involved in axon guidance (GO:0048846)	8	4	0.22	+	18.52	1.98E-04	4.73E-03
corticospinal tract morphogenesis (GO:0021957)	6	3	0.16	+	18.52	1.35E-03	2.37E-02

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
glomerular mesangium development (GO:0072109)	8	4	0.22	+	18.52	1.98E-04	4.75E-03
maintenance of protein location in extracellular region (GO:0071694)	6	3	0.16	+	18.52	1.35E-03	2.39E-02
negative regulation of mesonephros development (GO:0061218)	6	3	0.16	+	18.52	1.35E-03	2.37E-02
negative regulation of plasminogen activation (GO:0010757)	6	3	0.16	+	18.52	1.35E-03	2.38E-02
negative regulation of platelet-derived growth factor receptor-beta signaling pathway (GO:2000587)	8	4	0.22	+	18.52	1.98E-04	4.74E-03
neuron projection extension involved in neuron projection guidance (GO:1902284)	8	4	0.22	+	18.52	1.98E-04	4.74E-03
paracrine signaling (GO:0038001)	6	3	0.16	+	18.52	1.35E-03	2.39E-02
positive regulation of protein kinase C activity (GO:1900020)	6	3	0.16	+	18.52	1.35E-03	2.38E-02
protein localization to extracellular region (GO:0071692)	6	3	0.16	+	18.52	1.35E-03	2.39E-02
regulation of chemokine-mediated signaling pathway (GO:0070099)	8	4	0.22	+	18.52	1.98E-04	4.72E-03
regulation of glomerular mesangial cell proliferation (GO:0072124)	8	4	0.22	+	18.52	1.98E-04	4.76E-03
regulation of protein kinase C activity (GO:1900019)	6	3	0.16	+	18.52	1.35E-03	2.38E-02
response to UV-A (GO:0070141)	6	3	0.16	+	18.52	1.35E-03	2.38E-02
anterior/posterior axon guidance (GO:0033564)	7	3	0.19	+	15.88	1.89E-03	3.12E-02
negative regulation of gastrulation (GO:2000542)	7	3	0.19	+	15.88	1.89E-03	3.12E-02
platelet-derived growth factor receptor-beta signaling pathway (GO:0035791)	7	3	0.19	+	15.88	1.89E-03	3.11E-02
positive regulation of cell proliferation involved in kidney development (GO:1901724)	7	3	0.19	+	15.88	1.89E-03	3.11E-02
positive regulation of pigment cell differentiation (GO:0050942)	7	3	0.19	+	15.88	1.89E-03	3.11E-02
regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (GO:1903587)	7	3	0.19	+	15.88	1.89E-03	3.11E-02
regulation of melanocyte differentiation (GO:0045634)	7	3	0.19	+	15.88	1.89E-03	3.13E-02
S-shaped body morphogenesis (GO:0072050)	7	3	0.19	+	15.88	1.89E-03	3.12E-02
collagen-activated signaling pathway (GO:0038065)	12	5	0.32	+	15.44	5.87E-05	1.65E-03

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 proliferation involved in kidney development (GO:1901722)	12	5	0.32	+	15.44	5.87E-05	1.65E-03
cell adhesion mediated by integrin (GO:0033627)	17	7	0.46	+	15.25	1.96E-06	8.32E-05
collagen-activated tyrosine kinase receptor signaling pathway (GO:0038063)	10	4	0.27	+	14.82	3.83E-04	8.37E-03
regulation of platelet-derived growth factor receptor-beta signaling pathway (GO:2000586)	10	4	0.27	+	14.82	3.83E-04	8.38E-03
wound healing, spreading of epidermal cells (GO:0035313)	10	4	0.27	+	14.82	3.83E-04	8.36E-03
endoderm formation (GO:0001706)	51	20	1.38	+	14.53	1.15E-15	2.15E-13
endodermal cell differentiation (GO:0035987)	41	16	1.11	+	14.46	9.00E-13	1.06E-10
collagen fibril organization (GO:0030199)	42	16	1.13	+	14.11	1.21E-12	1.39E-10
kidney vasculature development (GO:0061440)	21	8	0.57	+	14.11	5.72E-07	2.74E-05
renal system vasculature development (GO:0061437)	21	8	0.57	+	14.11	5.72E-07	2.73E-05
bone trabecula formation (GO:0060346)	8	3	0.22	+	13.89	2.55E-03	3.98E-02
collagen biosynthetic process (GO:0032964)	8	3	0.22	+	13.89	2.55E-03	3.98E-02
epithelial fluid transport (GO:0042045)	8	3	0.22	+	13.89	2.55E-03	3.94E-02
kidney vasculature morphogenesis (GO:0061439)	8	3	0.22	+	13.89	2.55E-03	3.95E-02
negative regulation of lymphocyte migration (GO:2000402)	8	3	0.22	+	13.89	2.55E-03	3.97E-02
negative regulation of mesenchymal cell proliferation (GO:0072201)	8	3	0.22	+	13.89	2.55E-03	3.98E-02
positive regulation of keratinocyte migration (GO:0051549)	8	3	0.22	+	13.89	2.55E-03	3.96E-02
positive regulation of Wnt signaling pathway, planar cell polarity pathway (GO:2000096)	8	3	0.22	+	13.89	2.55E-03	3.96E-02
regulation of hair follicle maturation (GO:0048819)	8	3	0.22	+	13.89	2.55E-03	3.97E-02
renal system vasculature morphogenesis (GO:0061438)	8	3	0.22	+	13.89	2.55E-03	3.95E-02
sequestering of extracellular ligand from receptor (GO:0035581)	8	3	0.22	+	13.89	2.55E-03	3.96E-02
skeletal myofibril assembly (GO:0014866)	8	3	0.22	+	13.89	2.55E-03	3.94E-02
glomerulus vasculature development (GO:0072012)	19	7	0.51	+	13.65	3.56E-06	1.42E-04
negative regulation of axon guidance (GO:1902668)	11	4	0.3	+	13.47	5.12E-04	1.08E-02
negative regulation of muscle adaptation (GO:0014745)	11	4	0.3	+	13.47	5.12E-04	1.08E-02

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 protein autophosphorylation (GO:0031953)	11	4	0.3	+	13.47	5.12E-04	1.08E-02
regulation of cell communication by electrical coupling (GO:0010649)	11	4	0.3	+	13.47	5.12E-04	1.08E-02
positive regulation of astrocyte differentiation (GO:0048711)	14	5	0.38	+	13.23	1.06E-04	2.77E-03
positive regulation of metanephros development (GO:0072216)	14	5	0.38	+	13.23	1.06E-04	2.78E-03
negative regulation of smooth muscle cell migration (GO:0014912)	20	7	0.54	+	12.97	4.69E-06	1.81E-04
cerebral cortex tangential migration (GO:0021800)	9	3	0.24	+	12.35	3.33E-03	4.81E-02
chylomicron remodeling (GO:0034371)	9	3	0.24	+	12.35	3.33E-03	4.82E-02
mammary gland epithelial cell proliferation (GO:0033598)	12	4	0.32	+	12.35	6.68E-04	1.35E-02
negative regulation of axon extension involved in axon guidance (GO:0048843)	9	3	0.24	+	12.35	3.33E-03	4.85E-02
negative regulation of fibroblast growth factor receptor signaling pathway (GO:0040037)	12	4	0.32	+	12.35	6.68E-04	1.35E-02
negative regulation of heterotypic cell-cell adhesion (GO:0034115)	9	3	0.24	+	12.35	3.33E-03	4.86E-02
positive regulation of catenin import into nucleus (GO:0035413)	12	4	0.32	+	12.35	6.68E-04	1.35E-02
positive regulation of developmental pigmentation (GO:0048087)	9	3	0.24	+	12.35	3.33E-03	4.83E-02
positive regulation of non-canonical Wnt signaling pathway (GO:2000052)	12	4	0.32	+	12.35	6.68E-04	1.35E-02
regulation of branching involved in salivary gland morphogenesis (GO:0060693)	9	3	0.24	+	12.35	3.33E-03	4.82E-02
regulation of cell-cell adhesion involved in gastrulation (GO:0070587)	9	3	0.24	+	12.35	3.33E-03	4.85E-02
regulation of pigment cell differentiation (GO:0050932)	9	3	0.24	+	12.35	3.33E-03	4.84E-02
retina vasculature morphogenesis in camera-type eye (GO:0061299)	9	3	0.24	+	12.35	3.33E-03	4.83E-02
skin morphogenesis (GO:0043589)	9	3	0.24	+	12.35	3.33E-03	4.84E-02
outflow tract septum morphogenesis (GO:0003148)	25	8	0.67	+	11.85	1.69E-06	7.28E-05
semi-lunar valve development (GO:1905314)	16	5	0.43	+	11.58	1.77E-04	4.31E-03
cardioblast differentiation (GO:0010002)	13	4	0.35	+	11.4	8.56E-04	1.66E-02

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
positive regulation of urine volume (GO:0035810)	13	4	0.35	+	11.4	8.56E-04	1.65E-02
regulation of glomerulus development (GO:0090192)	13	4	0.35	+	11.4	8.56E-04	1.66E-02
regulation of nephron tubule epithelial cell differentiation (GO:0072182)	13	4	0.35	+	11.4	8.56E-04	1.66E-02
regulation of Wnt signaling pathway, planar cell polarity pathway (GO:2000095)	13	4	0.35	+	11.4	8.56E-04	1.66E-02
epiboly involved in wound healing (GO:0090505)	23	7	0.62	+	11.27	1.01E-05	3.56E-04
regulation of metanephros development (GO:0072215)	23	7	0.62	+	11.27	1.01E-05	3.57E-04
wound healing, spreading of cells (GO:0044319)	23	7	0.62	+	11.27	1.01E-05	3.55E-04
regulation of axon extension involved in axon guidance (GO:0048841)	17	5	0.46	+	10.9	2.24E-04	5.24E-03
retina vasculature development in camera-type eye (GO:0061298)	17	5	0.46	+	10.9	2.24E-04	5.23E-03
epiboly (GO:0090504)	24	7	0.65	+	10.81	1.27E-05	4.33E-04
regulation of smooth muscle cell migration (GO:0014910)	59	17	1.59	+	10.67	9.78E-12	9.91E-10
negative regulation of sodium ion transport (GO:0010766)	14	4	0.38	+	10.58	1.08E-03	1.98E-02
blood vessel remodeling (GO:0001974)	32	9	0.86	+	10.42	9.30E-07	4.20E-05
negative chemotaxis (GO:0050919)	36	10	0.97	+	10.29	2.53E-07	1.27E-05
response to corticosterone (GO:0051412)	18	5	0.49	+	10.29	2.80E-04	6.40E-03
endoderm development (GO:0007492)	76	21	2.05	+	10.24	7.03E-14	1.01E-11
endothelial cell proliferation (GO:0001935)	22	6	0.59	+	10.1	7.39E-05	2.01E-03
positive regulation of pri-miRNA transcription by RNA polymerase II (GO:1902895)	22	6	0.59	+	10.1	7.39E-05	2.01E-03
regulation of axon guidance (GO:1902667)	22	6	0.59	+	10.1	7.39E-05	2.01E-03
positive regulation of cardiocyte differentiation (GO:1905209)	26	7	0.7	+	9.97	1.97E-05	6.26E-04
cell migration involved in gastrulation (GO:0042074)	15	4	0.4	+	9.88	1.34E-03	2.38E-02
cell migration involved in sprouting angiogenesis (GO:0002042)	15	4	0.4	+	9.88	1.34E-03	2.38E-02
negative regulation of bone remodeling (GO:0046851)	15	4	0.4	+	9.88	1.34E-03	2.38E-02
vascular endothelial growth factor signaling pathway (GO:0038084)	15	4	0.4	+	9.88	1.34E-03	2.39E-02
blastoderm segmentation (GO:0007350)	19	5	0.51	+	9.75	3.46E-04	7.68E-03

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 platelet-derived growth factor receptor signaling pathway (GO:0010642)	16	4	0.43	+	9.26	1.64E-03	2.76E-02
negative regulation of sprouting angiogenesis (GO:1903671)	16	4	0.43	+	9.26	1.64E-03	2.76E-02
positive regulation of fibroblast proliferation (GO:0048146)	52	13	1.4	+	9.26	1.17E-08	7.70E-07
positive regulation of kidney development (GO:0090184)	40	10	1.08	+	9.26	5.80E-07	2.76E-05
regulation of mesoderm development (GO:2000380)	16	4	0.43	+	9.26	1.64E-03	2.77E-02
regulation of vascular associated smooth muscle cell migration (GO:1904752)	16	4	0.43	+	9.26	1.64E-03	2.76E-02
trophectodermal cell differentiation (GO:0001829)	16	4	0.43	+	9.26	1.64E-03	2.77E-02
sprouting angiogenesis (GO:0002040)	45	11	1.21	+	9.06	1.92E-07	9.93E-06
formation of primary germ layer (GO:0001704)	115	28	3.1	+	9.02	7.56E-17	1.54E-14
response to mineralocorticoid (GO:0051385)	29	7	0.78	+	8.94	3.59E-05	1.05E-03
negative regulation of embryonic development (GO:0045992)	25	6	0.67	+	8.89	1.35E-04	3.42E-03
pharyngeal system development (GO:0060037)	25	6	0.67	+	8.89	1.35E-04	3.42E-03
atrioventricular valve morphogenesis (GO:0003181)	21	5	0.57	+	8.82	5.13E-04	1.07E-02
metanephric nephron morphogenesis (GO:0072273)	21	5	0.57	+	8.82	5.13E-04	1.08E-02
regulation of non-canonical Wnt signaling pathway (GO:2000050)	21	5	0.57	+	8.82	5.13E-04	1.07E-02
uterus development (GO:0060065)	21	5	0.57	+	8.82	5.13E-04	1.08E-02
actin-myosin filament sliding (GO:0033275)	38	9	1.03	+	8.77	3.14E-06	1.28E-04
muscle filament sliding (GO:0030049)	38	9	1.03	+	8.77	3.14E-06	1.27E-04
regulation of gastrulation (GO:0010470)	38	9	1.03	+	8.77	3.14E-06	1.28E-04
hormone catabolic process (GO:0042447)	17	4	0.46	+	8.72	1.98E-03	3.23E-02
positive regulation of stem cell differentiation (GO:2000738)	17	4	0.46	+	8.72	1.98E-03	3.24E-02
post-embryonic animal organ development (GO:0048569)	17	4	0.46	+	8.72	1.98E-03	3.24E-02
regulation of cell proliferation involved in heart morphogenesis (GO:2000136)	17	4	0.46	+	8.72	1.98E-03	3.24E-02
mesodermal cell differentiation (GO:0048333)	26	6	0.7	+	8.55	1.63E-04	4.00E-03

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 vascular smooth muscle cell proliferation (GO:1904705)	26	6	0.7	+	8.55	1.63E-04	3.99E-03
positive regulation of smooth muscle cell proliferation (GO:0048661)	74	17	2	+	8.51	2.04E-10	1.84E-08
negative regulation of blood coagulation (GO:0030195)	48	11	1.3	+	8.49	3.35E-07	1.67E-05
negative regulation of hemostasis (GO:1900047)	48	11	1.3	+	8.49	3.35E-07	1.67E-05
positive regulation of smooth muscle cell migration (GO:0014911)	35	8	0.94	+	8.47	1.40E-05	4.69E-04
cardiac septum morphogenesis (GO:0060411)	66	15	1.78	+	8.42	2.71E-09	2.05E-07
extracellular negative regulation of signal transduction (GO:1900116)	18	4	0.49	+	8.23	2.37E-03	3.74E-02
extracellular regulation of signal transduction (GO:1900115)	18	4	0.49	+	8.23	2.37E-03	3.74E-02
female genitalia development (GO:0030540)	18	4	0.49	+	8.23	2.37E-03	3.74E-02
heart valve morphogenesis (GO:0003179)	36	8	0.97	+	8.23	1.67E-05	5.47E-04
negative regulation of interleukin-8 production (GO:0032717)	18	4	0.49	+	8.23	2.37E-03	3.75E-02
negative regulation of morphogenesis of an epithelium (GO:1905331)	18	4	0.49	+	8.23	2.37E-03	3.75E-02
negative regulation of platelet activation (GO:0010544)	18	4	0.49	+	8.23	2.37E-03	3.73E-02
positive regulation of cardiac muscle cell differentiation (GO:2000727)	18	4	0.49	+	8.23	2.37E-03	3.76E-02
regulation of epithelial cell differentiation involved in kidney development (GO:2000696)	18	4	0.49	+	8.23	2.37E-03	3.76E-02
response to magnesium ion (GO:0032026)	18	4	0.49	+	8.23	2.37E-03	3.75E-02
ventricular cardiac muscle tissue development (GO:0003229)	54	12	1.46	+	8.23	1.31E-07	7.00E-06
regulation of osteoblast proliferation (GO:0033688)	23	5	0.62	+	8.05	7.34E-04	1.46E-02
regulation of platelet-derived growth factor receptor signaling pathway (GO:0010640)	23	5	0.62	+	8.05	7.34E-04	1.46E-02
negative regulation of chemotaxis (GO:0050922)	37	8	1	+	8.01	1.98E-05	6.29E-04
collagen catabolic process (GO:0030574)	65	14	1.75	+	7.98	1.66E-08	1.06E-06
regulation of cardiocyte differentiation (GO:1905207)	42	9	1.13	+	7.94	6.39E-06	2.37E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 coagulation (GO:0050819)	52	11	1.4	+	7.84	6.71E-07	3.14E-05
axon regeneration (GO:0031103)	19	4	0.51	+	7.8	2.81E-03	4.27E-02
cardiac center ventricle morphogenesis (GO:0003215)	19	4	0.51	+	7.8	2.81E-03	4.27E-02
cellular response to zinc ion (GO:0071294)	19	4	0.51	+	7.8	2.81E-03	4.28E-02
extracellular matrix assembly (GO:0085029)	19	4	0.51	+	7.8	2.81E-03	4.26E-02
lung alveolus development (GO:0048286)	38	8	1.03	+	7.8	2.35E-05	7.25E-04
response to muscle stretch (GO:0035994)	19	4	0.51	+	7.8	2.81E-03	4.28E-02
atrioventricular valve development (GO:0003171)	24	5	0.65	+	7.72	8.68E-04	1.67E-02
blood vessel endothelial cell migration (GO:0043534)	24	5	0.65	+	7.72	8.68E-04	1.67E-02
response to hyperoxia (GO:0055093)	24	5	0.65	+	7.72	8.68E-04	1.67E-02
trabecula formation (GO:0060343)	24	5	0.65	+	7.72	8.68E-04	1.67E-02
extracellular matrix organization (GO:0030198)	314	65	8.48	+	7.67	4.36E-34	7.51E-31
positive regulation of cartilage development (GO:0061036)	29	6	0.78	+	7.66	2.72E-04	6.24E-03
positive regulation of histone acetylation (GO:0035066)	29	6	0.78	+	7.66	2.72E-04	6.25E-03
extracellular structure organization (GO:0043062)	315	65	8.5	+	7.64	5.13E-34	7.96E-31
multicellular organismal catabolic process (GO:0044243)	73	15	1.97	+	7.61	8.90E-09	5.95E-07
regulation of sprouting angiogenesis (GO:1903670)	39	8	1.05	+	7.6	2.76E-05	8.38E-04
regulation of kidney development (GO:0090183)	54	11	1.46	+	7.55	9.30E-07	4.22E-05
atrial septum development (GO:0003283)	20	4	0.54	+	7.41	3.30E-03	4.82E-02
heart valve development (GO:0003170)	40	8	1.08	+	7.41	3.24E-05	9.61E-04
negative regulation of neural precursor cell proliferation (GO:2000178)	20	4	0.54	+	7.41	3.30E-03	4.84E-02
negative regulation of Rho protein signal transduction (GO:0035024)	20	4	0.54	+	7.41	3.30E-03	4.83E-02
negative regulation of tissue remodeling (GO:0034104)	20	4	0.54	+	7.41	3.30E-03	4.84E-02
positive regulation of peptidyl-lysine acetylation (GO:2000758)	30	6	0.81	+	7.41	3.20E-04	7.19E-03
positive regulation of sprouting angiogenesis (GO:1903672)	20	4	0.54	+	7.41	3.30E-03	4.83E-02
regulation of catenin import into nucleus (GO:0035412)	25	5	0.67	+	7.41	1.02E-03	1.90E-02

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 adhesion mediated by integrin (GO:0033628)	40	8	1.08	+	7.41	3.24E-05	9.64E-04
regulation of heterotypic cell-cell adhesion (GO:0034114)	20	4	0.54	+	7.41	3.30E-03	4.85E-02
regulation of protein autophosphorylation (GO:0031952)	40	8	1.08	+	7.41	3.24E-05	9.62E-04
semaphorin-plexin signaling pathway (GO:0071526)	25	5	0.67	+	7.41	1.02E-03	1.90E-02
cardiac chamber morphogenesis (GO:0003206)	121	24	3.27	+	7.35	6.05E-13	7.22E-11
regulation of smooth muscle cell proliferation (GO:0048660)	116	23	3.13	+	7.35	1.85E-12	2.07E-10
response to estrogen (GO:0043627)	76	15	2.05	+	7.31	1.43E-08	9.36E-07
morphogenesis of an epithelial sheet (GO:0002011)	46	9	1.24	+	7.25	1.22E-05	4.17E-04
regulation of heart morphogenesis (GO:2000826)	36	7	0.97	+	7.2	1.18E-04	3.06E-03
cellular response to cadmium ion (GO:0071276)	31	6	0.84	+	7.17	3.73E-04	8.18E-03
regulation of pri-miRNA transcription by RNA polymerase II (GO:1902893)	31	6	0.84	+	7.17	3.73E-04	8.17E-03
substrate-dependent cell migration (GO:0006929)	26	5	0.7	+	7.12	1.19E-03	2.16E-02
cardiac muscle tissue morphogenesis (GO:0055008)	63	12	1.7	+	7.06	5.60E-07	2.69E-05
gastrulation (GO:0007369)	158	30	4.26	+	7.03	2.10E-15	3.88E-13
ventricular septum morphogenesis (GO:0060412)	37	7	1	+	7.01	1.38E-04	3.47E-03
glomerulus development (GO:0032835)	53	10	1.43	+	6.99	5.31E-06	2.02E-04
mesoderm morphogenesis (GO:0048332)	69	13	1.86	+	6.98	2.12E-07	1.09E-05
multicellular organismal macromolecule metabolic process (GO:0044259)	85	16	2.29	+	6.97	8.54E-09	5.76E-07
collagen metabolic process (GO:0032963)	80	15	2.16	+	6.95	2.61E-08	1.60E-06
ventricular cardiac muscle tissue morphogenesis (GO:0055010)	48	9	1.3	+	6.95	1.64E-05	5.40E-04
ventricular septum development (GO:0003281)	64	12	1.73	+	6.95	6.49E-07	3.06E-05
cardiac septum development (GO:0003279)	97	18	2.62	+	6.87	1.23E-09	9.85E-08
apoptotic cell clearance (GO:0043277)	27	5	0.73	+	6.86	1.38E-03	2.41E-02
negative regulation of osteoclast differentiation (GO:0045671)	27	5	0.73	+	6.86	1.38E-03	2.41E-02
regulation of fibroblast growth factor receptor signaling pathway (GO:0040036)	27	5	0.73	+	6.86	1.38E-03	2.41E-02

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 smooth muscle cell proliferation (GO:0048662)	38	7	1.03	+	6.82	1.59E-04	3.95E-03
negative regulation of BMP signaling pathway (GO:0030514)	49	9	1.32	+	6.8	1.90E-05	6.09E-04
mesenchyme morphogenesis (GO:0072132)	44	8	1.19	+	6.74	5.89E-05	1.65E-03
metanephric nephron development (GO:0072210)	33	6	0.89	+	6.74	5.01E-04	1.06E-02
regulation of collagen biosynthetic process (GO:0032965)	33	6	0.89	+	6.74	5.01E-04	1.06E-02
epithelial cell proliferation (GO:0050673)	83	15	2.24	+	6.7	4.02E-08	2.35E-06
regulation of pathway-restricted SMAD protein phosphorylation (GO:0060393)	61	11	1.65	+	6.68	2.66E-06	1.09E-04
regulation of blood coagulation (GO:0030193)	89	16	2.4	+	6.66	1.52E-08	9.81E-07
regulation of hemostasis (GO:1900046)	89	16	2.4	+	6.66	1.52E-08	9.85E-07
negative regulation of epithelial cell differentiation (GO:0030857)	39	7	1.05	+	6.65	1.84E-04	4.44E-03
positive regulation of endothelial cell migration (GO:0010595)	78	14	2.11	+	6.65	1.23E-07	6.61E-06
mesoderm formation (GO:0001707)	67	12	1.81	+	6.64	9.98E-07	4.47E-05
aorta morphogenesis (GO:0035909)	28	5	0.76	+	6.62	1.59E-03	2.71E-02
cell fate commitment involved in formation of primary germ layer (GO:0060795)	28	5	0.76	+	6.62	1.59E-03	2.71E-02
metanephros morphogenesis (GO:0003338)	28	5	0.76	+	6.62	1.59E-03	2.70E-02
negative regulation of cytokine biosynthetic process (GO:0042036)	28	5	0.76	+	6.62	1.59E-03	2.70E-02
regulation of astrocyte differentiation (GO:0048710)	28	5	0.76	+	6.62	1.59E-03	2.71E-02
cardiac ventricle development (GO:0003231)	119	21	3.21	+	6.54	1.16E-10	1.06E-08
outflow tract morphogenesis (GO:0003151)	68	12	1.84	+	6.54	1.15E-06	5.11E-05
platelet-derived growth factor receptor signaling pathway (GO:0048008)	34	6	0.92	+	6.54	5.76E-04	1.19E-02
muscle tissue morphogenesis (GO:0060415)	74	13	2	+	6.51	4.30E-07	2.09E-05
muscle organ morphogenesis (GO:0048644)	81	14	2.19	+	6.4	1.85E-07	9.71E-06
salivary gland morphogenesis (GO:0007435)	29	5	0.78	+	6.39	1.83E-03	3.05E-02
tissue remodeling (GO:0048771)	93	16	2.51	+	6.37	2.63E-08	1.60E-06
cardiac atrium development (GO:0003230)	35	6	0.94	+	6.35	6.60E-04	1.34E-02

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
neural crest cell migration (GO:0001755)	35	6	0.94	+	6.35	6.60E-04	1.35E-02
response to fluid shear stress (GO:0034405)	35	6	0.94	+	6.35	6.60E-04	1.34E-02
positive regulation of epithelial cell migration (GO:0010634)	117	20	3.16	+	6.33	5.29E-10	4.41E-08
regulation of BMP signaling pathway (GO:0030510)	88	15	2.38	+	6.31	7.97E-08	4.40E-06
regulation of coagulation (GO:0050818)	94	16	2.54	+	6.31	3.00E-08	1.80E-06
tissue migration (GO:0090130)	88	15	2.38	+	6.31	7.97E-08	4.41E-06
endothelial cell migration (GO:0043542)	59	10	1.59	+	6.28	1.23E-05	4.20E-04
cardiac chamber development (GO:0003205)	156	26	4.21	+	6.17	2.23E-12	2.45E-10
cellular response to vascular endothelial growth factor stimulus (GO:0035924)	30	5	0.81	+	6.17	2.08E-03	3.37E-02
coronary vasculature development (GO:0060976)	42	7	1.13	+	6.17	2.75E-04	6.30E-03
positive regulation of endothelial cell proliferation (GO:0001938)	78	13	2.11	+	6.17	7.33E-07	3.38E-05
positive regulation of protein acetylation (GO:1901985)	36	6	0.97	+	6.17	7.53E-04	1.49E-02
regulation of cardiac muscle cell differentiation (GO:2000725)	30	5	0.81	+	6.17	2.08E-03	3.38E-02
regulation of endothelial cell proliferation (GO:0001936)	108	18	2.92	+	6.17	5.52E-09	3.91E-07
SMAD protein signal transduction (GO:0060395)	60	10	1.62	+	6.17	1.40E-05	4.68E-04
negative regulation of wound healing (GO:0061045)	67	11	1.81	+	6.08	5.94E-06	2.22E-04
regulation of endothelial cell migration (GO:0010594)	128	21	3.46	+	6.08	3.82E-10	3.31E-08
vasculogenesis (GO:0001570)	67	11	1.81	+	6.08	5.94E-06	2.23E-04
negative regulation of ERK1 and ERK2 cascade (GO:0070373)	61	10	1.65	+	6.07	1.59E-05	5.23E-04
multicellular organism metabolic process (GO:0044236)	105	17	2.83	+	6	2.15E-08	1.34E-06
cardiac atrium morphogenesis (GO:0003209)	31	5	0.84	+	5.98	2.37E-03	3.76E-02
cellular response to dexamethasone stimulus (GO:0071549)	31	5	0.84	+	5.98	2.37E-03	3.78E-02
cellular response to hydrogen peroxide (GO:0070301)	62	10	1.67	+	5.98	1.80E-05	5.85E-04
regulation of cartilage development (GO:0061035)	62	10	1.67	+	5.98	1.80E-05	5.84E-04

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 DNA damage response, signal transduction by p53 class mediator (GO:0043516)	31	5	0.84	+	5.98	2.37E-03	3.78E-02
response to gonadotropin (GO:0034698)	31	5	0.84	+	5.98	2.37E-03	3.77E-02
response to increased oxygen levels (GO:0036296)	31	5	0.84	+	5.98	2.37E-03	3.77E-02
negative regulation of response to cytokine stimulus (GO:0060761)	56	9	1.51	+	5.95	4.85E-05	1.39E-03
heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules (GO:0007157)	50	8	1.35	+	5.93	1.31E-04	3.33E-03
positive regulation of epithelial to mesenchymal transition (GO:0010718)	44	7	1.19	+	5.89	3.55E-04	7.85E-03
cardiac muscle tissue development (GO:0048738)	158	25	4.26	+	5.86	1.62E-11	1.61E-09
positive regulation of glial cell differentiation (GO:0045687)	38	6	1.03	+	5.85	9.70E-04	1.83E-02
regulation of collagen metabolic process (GO:0010712)	38	6	1.03	+	5.85	9.70E-04	1.82E-02
anterior/posterior axis specification (GO:0009948)	51	8	1.38	+	5.81	1.48E-04	3.70E-03
regulation of fibroblast proliferation (GO:0048145)	83	13	2.24	+	5.8	1.37E-06	5.98E-05
negative regulation of receptor activity (GO:2000272)	32	5	0.86	+	5.79	2.68E-03	4.11E-02
regulation of platelet activation (GO:0010543)	32	5	0.86	+	5.79	2.68E-03	4.10E-02
smooth muscle cell differentiation (GO:0051145)	32	5	0.86	+	5.79	2.68E-03	4.11E-02
response to hydrogen peroxide (GO:0042542)	109	17	2.94	+	5.78	3.51E-08	2.08E-06
aorta development (GO:0035904)	45	7	1.21	+	5.76	4.01E-04	8.69E-03
actin-mediated cell contraction (GO:0070252)	84	13	2.27	+	5.73	1.54E-06	6.68E-05
animal organ regeneration (GO:0031100)	78	12	2.11	+	5.7	4.11E-06	1.62E-04
negative regulation of cytokine-mediated signaling pathway (GO:0001960)	52	8	1.4	+	5.7	1.67E-04	4.08E-03
negative regulation of response to wounding (GO:1903035)	78	12	2.11	+	5.7	4.11E-06	1.62E-04
regulation of multicellular organismal metabolic process (GO:0044246)	39	6	1.05	+	5.7	1.09E-03	2.01E-02
heart morphogenesis (GO:0003007)	228	35	6.15	+	5.69	3.01E-15	5.30E-13
cardiac ventricle morphogenesis (GO:0003208)	72	11	1.94	+	5.66	1.09E-05	3.81E-04
artery morphogenesis (GO:0048844)	59	9	1.59	+	5.65	6.97E-05	1.92E-03
neural crest cell development (GO:0014032)	59	9	1.59	+	5.65	6.97E-05	1.93E-03
regulation of systemic arterial blood pressure mediated by a chemical signal (GO:0003044)	46	7	1.24	+	5.64	4.51E-04	9.68E-03
extracellular matrix disassembly (GO:0022617)	79	12	2.13	+	5.63	4.62E-06	1.79E-04

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
angiogenesis (GO:0001525)	297	45	8.02	+	5.61	4.51E-19	1.25E-16
muscle adaptation (GO:0043500)	33	5	0.89	+	5.61	3.02E-03	4.54E-02
positive regulation of BMP signaling pathway (GO:0030513)	33	5	0.89	+	5.61	3.02E-03	4.53E-02
positive regulation of morphogenesis of an epithelium (GO:1905332)	33	5	0.89	+	5.61	3.02E-03	4.54E-02
salivary gland development (GO:0007431)	33	5	0.89	+	5.61	3.02E-03	4.54E-02
blood vessel development (GO:0001568)	466	70	12.58	+	5.56	5.07E-29	5.24E-26
regulation of actin filament-based movement (GO:1903115)	40	6	1.08	+	5.56	1.23E-03	2.22E-02
neural crest cell differentiation (GO:0014033)	67	10	1.81	+	5.53	3.28E-05	9.69E-04
vasculature development (GO:0001944)	490	73	13.23	+	5.52	4.74E-30	5.65E-27
cellular response to transforming growth factor beta stimulus (GO:0071560)	142	21	3.83	+	5.48	2.04E-09	1.59E-07
blood vessel morphogenesis (GO:0048514)	386	57	10.42	+	5.47	2.05E-23	1.10E-20
embryonic placenta development (GO:0001892)	88	13	2.38	+	5.47	2.45E-06	1.02E-04
negative regulation of vasculature development (GO:1901343)	95	14	2.56	+	5.46	1.04E-06	4.64E-05
negative regulation of Notch signaling pathway (GO:0045746)	34	5	0.92	+	5.45	3.39E-03	4.89E-02
positive regulation of protein dephosphorylation (GO:0035307)	34	5	0.92	+	5.45	3.39E-03	4.88E-02
regulation of animal organ formation (GO:0003156)	34	5	0.92	+	5.45	3.39E-03	4.88E-02
positive regulation of cell-substrate adhesion (GO:0010811)	109	16	2.94	+	5.44	1.86E-07	9.72E-06
positive regulation of cardiac muscle tissue development (GO:0055025)	41	6	1.11	+	5.42	1.38E-03	2.41E-02
cardiovascular system development (GO:0072358)	500	73	13.5	+	5.41	1.48E-29	1.64E-26
endocrine process (GO:0050886)	48	7	1.3	+	5.4	5.68E-04	1.18E-02
positive regulation of pathway-restricted SMAD protein phosphorylation (GO:0010862)	48	7	1.3	+	5.4	5.68E-04	1.17E-02
trabecula morphogenesis (GO:0061383)	48	7	1.3	+	5.4	5.68E-04	1.17E-02
regulation of epithelial cell migration (GO:0010632)	186	27	5.02	+	5.38	1.48E-11	1.48E-09
artery development (GO:0060840)	77	11	2.08	+	5.29	1.93E-05	6.15E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
mammary gland morphogenesis (GO:0060443)	42	6	1.13	+	5.29	1.54E-03	2.65E-02
mesenchymal cell development (GO:0014031)	63	9	1.7	+	5.29	1.10E-04	2.86E-03
positive regulation of receptor-mediated endocytosis (GO:0048260)	49	7	1.32	+	5.29	6.35E-04	1.30E-02
response to dexamethasone (GO:0071548)	42	6	1.13	+	5.29	1.54E-03	2.64E-02
response to transforming growth factor beta (GO:0071559)	147	21	3.97	+	5.29	3.55E-09	2.59E-07
stem cell development (GO:0048864)	63	9	1.7	+	5.29	1.10E-04	2.86E-03
mesenchyme development (GO:0060485)	190	27	5.13	+	5.26	2.29E-11	2.23E-09
viral entry into host cell (GO:0046718)	92	13	2.48	+	5.23	3.82E-06	1.51E-04
epithelial cell migration (GO:0010631)	78	11	2.11	+	5.22	2.15E-05	6.68E-04
positive regulation of osteoblast differentiation (GO:0045669)	57	8	1.54	+	5.2	2.93E-04	6.66E-03
regulation of extrinsic apoptotic signaling pathway via death domain receptors (GO:1902041)	57	8	1.54	+	5.2	2.93E-04	6.65E-03
positive regulation of wound healing (GO:0090303)	50	7	1.35	+	5.19	7.07E-04	1.42E-02
negative regulation of endothelial cell migration (GO:0010596)	43	6	1.16	+	5.17	1.72E-03	2.89E-02
cellular response to mechanical stimulus (GO:0071260)	79	11	2.13	+	5.16	2.39E-05	7.35E-04
positive regulation of vasculature development (GO:1904018)	158	22	4.26	+	5.16	2.31E-09	1.77E-07
adherens junction organization (GO:0034332)	72	10	1.94	+	5.15	5.69E-05	1.61E-03
cardiocyte differentiation (GO:0035051)	108	15	2.92	+	5.15	8.44E-07	3.85E-05
ovulation cycle (GO:0042698)	101	14	2.73	+	5.14	2.00E-06	8.45E-05
regulation of interleukin-8 production (GO:0032677)	65	9	1.75	+	5.13	1.36E-04	3.43E-03
negative regulation of angiogenesis (GO:0016525)	87	12	2.35	+	5.11	1.12E-05	3.88E-04
negative regulation of cellular response to growth factor stimulus (GO:0090288)	131	18	3.54	+	5.09	7.93E-08	4.41E-06
response to progesterone (GO:0032570)	44	6	1.19	+	5.05	1.91E-03	3.14E-02
epithelium migration (GO:0090132)	81	11	2.19	+	5.03	2.95E-05	8.89E-04
peptide cross-linking (GO:0018149)	59	8	1.59	+	5.02	3.62E-04	7.97E-03
regulation of cytokine biosynthetic process (GO:0042035)	96	13	2.59	+	5.02	5.81E-06	2.19E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 blood vessel morphogenesis (GO:2000181)	89	12	2.4	+	4.99	1.38E-05	4.63E-04
response to glucocorticoid (GO:0051384)	141	19	3.81	+	4.99	4.58E-08	2.65E-06
cardiac muscle cell differentiation (GO:0055007)	82	11	2.21	+	4.97	3.26E-05	9.65E-04
digestive tract development (GO:0048565)	127	17	3.43	+	4.96	2.54E-07	1.27E-05
response to corticosteroid (GO:0031960)	157	21	4.24	+	4.96	1.01E-08	6.70E-07
regulation of bone remodeling (GO:0046850)	45	6	1.21	+	4.94	2.12E-03	3.42E-02
respiratory tube development (GO:0030323)	173	23	4.67	+	4.93	2.23E-09	1.73E-07
ameboidal-type cell migration (GO:0001667)	143	19	3.86	+	4.92	5.60E-08	3.19E-06
regulation of histone acetylation (GO:0035065)	53	7	1.43	+	4.89	9.66E-04	1.82E-02
segmentation (GO:0035282)	91	12	2.46	+	4.89	1.68E-05	5.50E-04
regulation of wound healing (GO:0061041)	137	18	3.7	+	4.87	1.46E-07	7.76E-06
striated muscle tissue development (GO:0014706)	282	37	7.61	+	4.86	3.96E-14	5.96E-12
tissue morphogenesis (GO:0048729)	526	69	14.2	+	4.86	1.69E-25	1.09E-22
heart process (GO:0003015)	92	12	2.48	+	4.83	1.86E-05	5.97E-04
regulation of muscle hypertrophy (GO:0014743)	46	6	1.24	+	4.83	2.34E-03	3.75E-02
lung development (GO:0030324)	169	22	4.56	+	4.82	7.06E-09	4.86E-07
mesenchymal cell differentiation (GO:0048762)	131	17	3.54	+	4.81	3.78E-07	1.87E-05
regulation of cell-substrate junction assembly (GO:0090109)	54	7	1.46	+	4.8	1.07E-03	1.96E-02
regulation of focal adhesion assembly (GO:0051893)	54	7	1.46	+	4.8	1.07E-03	1.97E-02
regulation of cell-substrate adhesion (GO:0010810)	186	24	5.02	+	4.78	1.71E-09	1.34E-07
transforming growth factor beta receptor signaling pathway (GO:0007179)	93	12	2.51	+	4.78	2.05E-05	6.45E-04
circulatory system development (GO:0072359)	808	104	21.81	+	4.77	6.94E-38	1.79E-34
muscle tissue development (GO:0060537)	295	38	7.96	+	4.77	3.00E-14	4.61E-12
positive regulation of cell migration (GO:0030335)	429	55	11.58	+	4.75	4.73E-20	1.41E-17
leukocyte cell-cell adhesion (GO:0007159)	47	6	1.27	+	4.73	2.59E-03	3.99E-02
positive regulation of angiogenesis (GO:0045766)	141	18	3.81	+	4.73	2.15E-07	1.10E-05
positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090100)	102	13	2.75	+	4.72	1.05E-05	3.68E-04

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 cysteine-type endopeptidase activity (GO:2000117)	110	14	2.97	+	4.71	4.91E-06	1.88E-04
regulation of interleukin-1 beta production (GO:0032651)	55	7	1.48	+	4.71	1.18E-03	2.14E-02
regulation of morphogenesis of a branching structure (GO:0060688)	55	7	1.48	+	4.71	1.18E-03	2.14E-02
cellular response to amino acid stimulus (GO:0071230)	63	8	1.7	+	4.7	5.39E-04	1.12E-02
heart development (GO:0007507)	481	61	12.98	+	4.7	6.19E-22	2.29E-19
regulation of muscle adaptation (GO:0043502)	71	9	1.92	+	4.7	2.48E-04	5.73E-03
negative regulation of extrinsic apoptotic signaling pathway (GO:2001237)	103	13	2.78	+	4.68	1.16E-05	3.98E-04
positive regulation of protein binding (GO:0032092)	87	11	2.35	+	4.68	5.33E-05	1.52E-03
regulation of vasculature development (GO:1901342)	270	34	7.29	+	4.67	1.25E-12	1.42E-10
positive regulation of cell motility (GO:2000147)	445	56	12.01	+	4.66	4.63E-20	1.41E-17
entry into cell of other organism involved in symbiotic interaction (GO:0051806)	104	13	2.81	+	4.63	1.27E-05	4.32E-04
entry into host (GO:0044409)	104	13	2.81	+	4.63	1.27E-05	4.31E-04
entry into host cell (GO:0030260)	104	13	2.81	+	4.63	1.27E-05	4.30E-04
entry into other organism involved in symbiotic interaction (GO:0051828)	104	13	2.81	+	4.63	1.27E-05	4.33E-04
negative regulation of myeloid leukocyte differentiation (GO:0002762)	48	6	1.3	+	4.63	2.85E-03	4.31E-02
positive regulation of DNA replication (GO:0045740)	56	7	1.51	+	4.63	1.29E-03	2.32E-02
regulation of response to wounding (GO:1903034)	160	20	4.32	+	4.63	6.26E-08	3.53E-06
renal system development (GO:0072001)	272	34	7.34	+	4.63	1.50E-12	1.70E-10
response to reactive oxygen species (GO:0000302)	184	23	4.97	+	4.63	6.45E-09	4.50E-07
gland morphogenesis (GO:0022612)	97	12	2.62	+	4.58	2.99E-05	8.97E-04
regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)	97	12	2.62	+	4.58	2.99E-05	9.00E-04
response to cAMP (GO:0051591)	97	12	2.62	+	4.58	2.99E-05	8.98E-04
embryonic pattern specification (GO:0009880)	65	8	1.75	+	4.56	6.50E-04	1.33E-02

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cellular response to glucocorticoid stimulus (GO:0071385)	57	7	1.54	+	4.55	1.42E-03	2.47E-02
cellular response to reactive oxygen species (GO:0034614)	122	15	3.29	+	4.55	3.34E-06	1.34E-04
positive regulation of response to wounding (GO:1903036)	57	7	1.54	+	4.55	1.42E-03	2.47E-02
positive regulation of striated muscle cell differentiation (GO:0051155)	57	7	1.54	+	4.55	1.42E-03	2.47E-02
regulation of adherens junction organization (GO:1903391)	57	7	1.54	+	4.55	1.42E-03	2.46E-02
regulation of chemotaxis (GO:0050920)	179	22	4.83	+	4.55	1.81E-08	1.14E-06
actin filament-based movement (GO:0030048)	106	13	2.86	+	4.54	1.53E-05	5.05E-04
positive regulation of cellular component movement (GO:0051272)	457	56	12.34	+	4.54	1.41E-19	4.06E-17
positive regulation of stress fiber assembly (GO:0051496)	49	6	1.32	+	4.54	3.12E-03	4.65E-02
digestive system development (GO:0055123)	139	17	3.75	+	4.53	8.01E-07	3.67E-05
integrin-mediated signaling pathway (GO:0007229)	90	11	2.43	+	4.53	7.04E-05	1.94E-03
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043154)	90	11	2.43	+	4.53	7.04E-05	1.93E-03
positive regulation of reactive oxygen species metabolic process (GO:2000379)	90	11	2.43	+	4.53	7.04E-05	1.93E-03
regulation of cell junction assembly (GO:1901888)	82	10	2.21	+	4.52	1.52E-04	3.78E-03
cardiac muscle contraction (GO:0060048)	74	9	2	+	4.51	3.28E-04	7.35E-03
hair follicle development (GO:0001942)	74	9	2	+	4.51	3.28E-04	7.36E-03
response to mechanical stimulus (GO:0009612)	215	26	5.8	+	4.48	1.25E-09	9.98E-08
positive regulation of actin filament bundle assembly (GO:0032233)	58	7	1.57	+	4.47	1.56E-03	2.66E-02
regulation of peptidyl-lysine acetylation (GO:2000756)	58	7	1.57	+	4.47	1.56E-03	2.66E-02
metanephros development (GO:0001656)	83	10	2.24	+	4.46	1.66E-04	4.07E-03
positive regulation of ossification (GO:0045778)	83	10	2.24	+	4.46	1.66E-04	4.08E-03
regulation of cellular response to growth factor stimulus (GO:0090287)	249	30	6.72	+	4.46	7.20E-11	6.68E-09
stem cell differentiation (GO:0048863)	133	16	3.59	+	4.46	2.05E-06	8.62E-05

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cardiac muscle cell development (GO:0055013)	50	6	1.35	+	4.45	3.42E-03	4.92E-02
digestive tract morphogenesis (GO:0048546)	50	6	1.35	+	4.45	3.42E-03	4.92E-02
positive regulation of locomotion (GO:0040017)	477	57	12.88	+	4.43	1.90E-19	5.36E-17
female sex differentiation (GO:0046660)	109	13	2.94	+	4.42	2.00E-05	6.32E-04
renal tubule morphogenesis (GO:0061333)	67	8	1.81	+	4.42	7.79E-04	1.54E-02
connective tissue development (GO:0061448)	202	24	5.45	+	4.4	7.45E-09	5.11E-07
response to cadmium ion (GO:0046686)	59	7	1.59	+	4.4	1.70E-03	2.86E-02
regeneration (GO:0031099)	152	18	4.1	+	4.39	5.86E-07	2.78E-05
skin epidermis development (GO:0098773)	76	9	2.05	+	4.39	3.92E-04	8.53E-03
kidney development (GO:0001822)	254	30	6.86	+	4.38	1.12E-10	1.03E-08
respiratory system development (GO:0060541)	195	23	5.26	+	4.37	1.73E-08	1.10E-06
heart contraction (GO:0060047)	85	10	2.29	+	4.36	1.98E-04	4.73E-03
ureteric bud development (GO:0001657)	85	10	2.29	+	4.36	1.98E-04	4.72E-03
urogenital system development (GO:0001655)	306	36	8.26	+	4.36	1.64E-12	1.84E-10
regulation of angiogenesis (GO:0045765)	247	29	6.67	+	4.35	2.60E-10	2.31E-08
platelet degranulation (GO:0002576)	128	15	3.46	+	4.34	5.68E-06	2.16E-04
cellular response to metal ion (GO:0071248)	154	18	4.16	+	4.33	6.97E-07	3.23E-05
hair cycle process (GO:0022405)	77	9	2.08	+	4.33	4.28E-04	9.23E-03
molting cycle process (GO:0022404)	77	9	2.08	+	4.33	4.28E-04	9.22E-03
cellular response to calcium ion (GO:0071277)	60	7	1.62	+	4.32	1.86E-03	3.09E-02
myofibril assembly (GO:0030239)	60	7	1.62	+	4.32	1.86E-03	3.08E-02
mesonephric epithelium development (GO:0072163)	86	10	2.32	+	4.31	2.16E-04	5.09E-03
mesonephric tubule development (GO:0072164)	86	10	2.32	+	4.31	2.16E-04	5.09E-03
regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090092)	215	25	5.8	+	4.31	5.38E-09	3.83E-07
response to calcium ion (GO:0051592)	121	14	3.27	+	4.29	1.32E-05	4.46E-04
ovulation cycle process (GO:0022602)	78	9	2.11	+	4.27	4.67E-04	9.95E-03
positive regulation of chemotaxis (GO:0050921)	130	15	3.51	+	4.27	6.74E-06	2.48E-04
endothelium development (GO:0003158)	87	10	2.35	+	4.26	2.35E-04	5.47E-03
regulation of actomyosin structure organization (GO:0110020)	87	10	2.35	+	4.26	2.35E-04	5.48E-03
cell-matrix adhesion (GO:0007160)	122	14	3.29	+	4.25	1.44E-05	4.79E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cellular response to corticosteroid stimulus (GO:0071384)	61	7	1.65	+	4.25	2.03E-03	3.30E-02
maternal process involved in female pregnancy (GO:0060135)	61	7	1.65	+	4.25	2.03E-03	3.30E-02
mesoderm development (GO:0007498)	122	14	3.29	+	4.25	1.44E-05	4.80E-04
nephron development (GO:0072006)	122	14	3.29	+	4.25	1.44E-05	4.78E-04
neuron projection extension (GO:1990138)	61	7	1.65	+	4.25	2.03E-03	3.30E-02
regulation of cell migration (GO:0030334)	733	84	19.79	+	4.25	2.74E-27	2.36E-24
regulation of interleukin-1 production (GO:0032652)	70	8	1.89	+	4.23	1.01E-03	1.89E-02
regulation of stress fiber assembly (GO:0051492)	79	9	2.13	+	4.22	5.08E-04	1.08E-02
renal system process (GO:0003014)	106	12	2.86	+	4.19	6.57E-05	1.83E-03
glycosaminoglycan catabolic process (GO:0006027)	62	7	1.67	+	4.18	2.20E-03	3.54E-02
ossification (GO:0001503)	248	28	6.69	+	4.18	1.18E-09	9.57E-08
somitogenesis (GO:0001756)	62	7	1.67	+	4.18	2.20E-03	3.55E-02
regulation of ERK1 and ERK2 cascade (GO:0070372)	268	30	7.23	+	4.15	3.63E-10	3.18E-08
actomyosin structure organization (GO:0031032)	99	11	2.67	+	4.12	1.53E-04	3.80E-03
kidney morphogenesis (GO:0060993)	81	9	2.19	+	4.12	6.00E-04	1.23E-02
mesonephros development (GO:0001823)	90	10	2.43	+	4.12	3.02E-04	6.83E-03
negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090101)	108	12	2.92	+	4.12	7.75E-05	2.09E-03
positive regulation of epithelial cell proliferation (GO:0050679)	171	19	4.62	+	4.12	6.93E-07	3.23E-05
regulation of systemic arterial blood pressure (GO:0003073)	90	10	2.43	+	4.12	3.02E-04	6.84E-03
striated muscle cell differentiation (GO:0051146)	189	21	5.1	+	4.12	1.81E-07	9.51E-06
response to growth factor (GO:0070848)	497	55	13.42	+	4.1	1.91E-17	4.49E-15
negative regulation of MAP kinase activity (GO:0043407)	73	8	1.97	+	4.06	1.30E-03	2.31E-02
regulation of chemokine production (GO:0032642)	73	8	1.97	+	4.06	1.30E-03	2.32E-02
cell growth (GO:0016049)	119	13	3.21	+	4.05	4.62E-05	1.34E-03
cellular response to ionizing radiation (GO:0071479)	64	7	1.73	+	4.05	2.60E-03	4.00E-02
plasma membrane organization (GO:0007009)	64	7	1.73	+	4.05	2.60E-03	4.00E-02
Rho protein signal transduction (GO:0007266)	64	7	1.73	+	4.05	2.60E-03	4.00E-02

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0007178)	192	21	5.18	+	4.05	2.30E-07	1.17E-05
regulation of osteoblast differentiation (GO:0045667)	110	12	2.97	+	4.04	9.10E-05	2.42E-03
cell-substrate adhesion (GO:0031589)	166	18	4.48	+	4.02	1.87E-06	7.99E-05
regulation of cell motility (GO:2000145)	784	85	21.16	+	4.02	4.21E-26	2.97E-23
homophilic cell adhesion via plasma membrane adhesion molecules (GO:0007156)	157	17	4.24	+	4.01	3.65E-06	1.46E-04
regulation of Notch signaling pathway (GO:0008593)	74	8	2	+	4	1.40E-03	2.45E-02
positive regulation of DNA biosynthetic process (GO:2000573)	65	7	1.75	+	3.99	2.81E-03	4.26E-02
regulation of embryonic development (GO:0045995)	121	13	3.27	+	3.98	5.41E-05	1.54E-03
negative regulation of cellular component movement (GO:0051271)	261	28	7.05	+	3.97	3.34E-09	2.44E-07
positive regulation of binding (GO:0051099)	168	18	4.53	+	3.97	2.18E-06	9.16E-05
positive regulation of protein import into nucleus (GO:0042307)	103	11	2.78	+	3.96	2.10E-04	4.97E-03
regulation of cellular response to transforming growth factor beta stimulus (GO:1903844)	103	11	2.78	+	3.96	2.10E-04	4.98E-03
cellular response to inorganic substance (GO:0071241)	178	19	4.8	+	3.95	1.20E-06	5.33E-05
placenta development (GO:0001890)	150	16	4.05	+	3.95	8.35E-06	3.05E-04
cellular response to growth factor stimulus (GO:0071363)	470	50	12.69	+	3.94	2.50E-15	4.46E-13
morphogenesis of a branching epithelium (GO:0061138)	160	17	4.32	+	3.94	4.61E-06	1.79E-04
anatomical structure formation involved in morphogenesis (GO:0048646)	840	89	22.67	+	3.93	1.10E-26	8.15E-24
muscle contraction (GO:0006936)	245	26	6.61	+	3.93	1.49E-08	9.72E-07
nephron morphogenesis (GO:0072028)	66	7	1.78	+	3.93	3.04E-03	4.55E-02
positive regulation of phosphatidylinositol 3-kinase signaling (GO:0014068)	66	7	1.78	+	3.93	3.04E-03	4.55E-02
regulation of cellular component movement (GO:0051270)	858	91	23.16	+	3.93	2.56E-27	2.34E-24
regulation of cytokine production involved in immune response (GO:0002718)	66	7	1.78	+	3.93	3.04E-03	4.54E-02

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 protein acetylation (GO:1901983)	66	7	1.78	+	3.93	3.04E-03	4.55E-02
dorsal/ventral pattern formation (GO:0009953)	85	9	2.29	+	3.92	8.23E-04	1.61E-02
reactive oxygen species metabolic process (GO:0072593)	104	11	2.81	+	3.92	2.27E-04	5.29E-03
developmental growth involved in morphogenesis (GO:0060560)	114	12	3.08	+	3.9	1.24E-04	3.20E-03
negative regulation of endopeptidase activity (GO:0010951)	247	26	6.67	+	3.9	1.74E-08	1.10E-06
regulation of epithelial cell differentiation (GO:0030856)	133	14	3.59	+	3.9	3.47E-05	1.02E-03
regulation of striated muscle cell differentiation (GO:0051153)	95	10	2.56	+	3.9	4.48E-04	9.62E-03
cell junction organization (GO:0034330)	200	21	5.4	+	3.89	4.26E-07	2.08E-05
morphogenesis of an epithelium (GO:0002009)	419	44	11.31	+	3.89	1.92E-13	2.48E-11
developmental cell growth (GO:0048588)	86	9	2.32	+	3.88	8.89E-04	1.70E-02
negative regulation of locomotion (GO:0040013)	277	29	7.48	+	3.88	2.90E-09	2.16E-07
negative regulation of peptidase activity (GO:0010466)	258	27	6.96	+	3.88	1.03E-08	6.81E-07
positive regulation of protein import (GO:1904591)	105	11	2.83	+	3.88	2.45E-04	5.65E-03
aminoglycan catabolic process (GO:0006026)	67	7	1.81	+	3.87	3.29E-03	4.83E-02
cartilage development (GO:0051216)	153	16	4.13	+	3.87	1.05E-05	3.68E-04
epithelial to mesenchymal transition (GO:0001837)	67	7	1.81	+	3.87	3.29E-03	4.83E-02
negative regulation of cell migration (GO:0030336)	230	24	6.21	+	3.87	7.15E-08	3.99E-06
regulation of blood vessel endothelial cell migration (GO:0043535)	67	7	1.81	+	3.87	3.29E-03	4.83E-02
regulation of epithelial cell proliferation (GO:0050678)	306	32	8.26	+	3.87	4.48E-10	3.82E-08
diterpenoid metabolic process (GO:0016101)	96	10	2.59	+	3.86	4.83E-04	1.03E-02
positive regulation of axonogenesis (GO:0050772)	77	8	2.08	+	3.85	1.77E-03	2.97E-02
regulation of receptor-mediated endocytosis (GO:0048259)	77	8	2.08	+	3.85	1.77E-03	2.96E-02
striated muscle cell development (GO:0055002)	125	13	3.37	+	3.85	7.34E-05	2.01E-03
cell-cell adhesion via plasma-membrane adhesion molecules (GO:0098742)	223	23	6.02	+	3.82	1.62E-07	8.55E-06
muscle organ development (GO:0007517)	292	30	7.88	+	3.81	2.31E-09	1.78E-07
positive regulation of protein kinase B signaling (GO:0051897)	146	15	3.94	+	3.81	2.38E-05	7.35E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 locomotion (GO:0040012)	855	88	23.08	+	3.81	1.42E-25	9.58E-23
negative regulation of MAPK cascade (GO:0043409)	156	16	4.21	+	3.8	1.31E-05	4.43E-04
response to ketone (GO:1901654)	185	19	4.99	+	3.8	2.03E-06	8.59E-05
somite development (GO:0061053)	78	8	2.11	+	3.8	1.91E-03	3.13E-02
response to steroid hormone (GO:0048545)	332	34	8.96	+	3.79	2.10E-10	1.89E-08
response to wounding (GO:0009611)	557	57	15.04	+	3.79	1.21E-16	2.40E-14
muscle system process (GO:0003012)	294	30	7.94	+	3.78	2.67E-09	2.03E-07
negative regulation of cell motility (GO:2000146)	245	25	6.61	+	3.78	5.69E-08	3.22E-06
regulation of extrinsic apoptotic signaling pathway (GO:2001236)	157	16	4.24	+	3.78	1.41E-05	4.71E-04
regulation of organ morphogenesis (GO:2000027)	255	26	6.88	+	3.78	3.14E-08	1.88E-06
muscle structure development (GO:0061061)	463	47	12.5	+	3.76	8.69E-14	1.24E-11
axis specification (GO:0009798)	89	9	2.4	+	3.75	1.11E-03	2.03E-02
female gonad development (GO:0008585)	89	9	2.4	+	3.75	1.11E-03	2.03E-02
positive regulation of neuron death (GO:1901216)	79	8	2.13	+	3.75	2.05E-03	3.34E-02
retinoid metabolic process (GO:0001523)	89	9	2.4	+	3.75	1.11E-03	2.04E-02
mucopolysaccharide metabolic process (GO:1903510)	109	11	2.94	+	3.74	3.29E-04	7.36E-03
morphogenesis of a branching structure (GO:0001763)	169	17	4.56	+	3.73	8.96E-06	3.25E-04
wound healing (GO:0042060)	467	47	12.61	+	3.73	1.16E-13	1.56E-11
negative regulation of response to external stimulus (GO:0032102)	269	27	7.26	+	3.72	2.30E-08	1.42E-06
cell-cell junction organization (GO:0045216)	170	17	4.59	+	3.7	9.62E-06	3.44E-04
muscle cell development (GO:0055001)	140	14	3.78	+	3.7	5.79E-05	1.64E-03
positive regulation of cell cycle arrest (GO:0071158)	90	9	2.43	+	3.7	1.19E-03	2.16E-02
regulation of actin filament bundle assembly (GO:0032231)	90	9	2.43	+	3.7	1.19E-03	2.16E-02
regulation of epithelial to mesenchymal transition (GO:0010717)	80	8	2.16	+	3.7	2.21E-03	3.55E-02
renal tubule development (GO:0061326)	80	8	2.16	+	3.7	2.21E-03	3.54E-02
response to amino acid (GO:0043200)	110	11	2.97	+	3.7	3.53E-04	7.83E-03
skeletal muscle tissue development (GO:0007519)	130	13	3.51	+	3.7	1.06E-04	2.77E-03
regulation of leukocyte migration (GO:0002685)	171	17	4.62	+	3.68	1.03E-05	3.64E-04
reproductive structure development (GO:0048608)	423	42	11.42	+	3.68	3.70E-12	3.93E-10

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
tube development (GO:0035295)	563	56	15.2	+	3.68	7.07E-16	1.34E-13
glycosaminoglycan biosynthetic process (GO:0006024)	101	10	2.73	+	3.67	6.96E-04	1.40E-02
osteoblast differentiation (GO:0001649)	121	12	3.27	+	3.67	2.07E-04	4.93E-03
regulation of cell-matrix adhesion (GO:0001952)	101	10	2.73	+	3.67	6.96E-04	1.40E-02
regulation of transforming growth factor beta receptor signaling pathway (GO:0017015)	101	10	2.73	+	3.67	6.96E-04	1.40E-02
hair cycle (GO:0042633)	91	9	2.46	+	3.66	1.28E-03	2.30E-02
molting cycle (GO:0042303)	91	9	2.46	+	3.66	1.28E-03	2.30E-02
regulation of heart rate (GO:0002027)	91	9	2.46	+	3.66	1.28E-03	2.30E-02
platelet activation (GO:0030168)	142	14	3.83	+	3.65	6.67E-05	1.85E-03
positive regulation of nucleocytoplasmic transport (GO:0046824)	122	12	3.29	+	3.64	2.22E-04	5.21E-03
regulation of reactive oxygen species metabolic process (GO:2000377)	163	16	4.4	+	3.64	2.16E-05	6.69E-04
reproductive system development (GO:0061458)	427	42	11.53	+	3.64	4.89E-12	5.13E-10
aminoglycan biosynthetic process (GO:0006023)	102	10	2.75	+	3.63	7.47E-04	1.48E-02
muscle cell differentiation (GO:0042692)	235	23	6.34	+	3.63	3.80E-07	1.87E-05
branching morphogenesis of an epithelial tube (GO:0048754)	133	13	3.59	+	3.62	1.30E-04	3.33E-03
negative regulation of leukocyte differentiation (GO:1902106)	92	9	2.48	+	3.62	1.38E-03	2.41E-02
cell adhesion (GO:0007155)	873	85	23.57	+	3.61	3.18E-23	1.59E-20
positive regulation of ERK1 and ERK2 cascade (GO:0070374)	195	19	5.26	+	3.61	4.13E-06	1.62E-04
biological adhesion (GO:0022610)	878	85	23.7	+	3.59	4.50E-23	2.05E-20
response to antineoplastic agent (GO:0097327)	93	9	2.51	+	3.59	1.47E-03	2.55E-02
cerebral cortex development (GO:0021987)	114	11	3.08	+	3.57	4.67E-04	9.95E-03
male gonad development (GO:0008584)	135	13	3.64	+	3.57	1.50E-04	3.74E-03
positive regulation of muscle cell differentiation (GO:0051149)	83	8	2.24	+	3.57	2.73E-03	4.16E-02
proteoglycan metabolic process (GO:0006029)	83	8	2.24	+	3.57	2.73E-03	4.17E-02
regulation of DNA biosynthetic process (GO:2000278)	104	10	2.81	+	3.56	8.57E-04	1.66E-02
development of primary female sexual characteristics (GO:0046545)	94	9	2.54	+	3.55	1.58E-03	2.70E-02
embryonic morphogenesis (GO:0048598)	563	54	15.2	+	3.55	9.64E-15	1.57E-12

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cellular response to acid chemical (GO:0071229)	199	19	5.37	+	3.54	5.41E-06	2.06E-04
development of primary male sexual characteristics (GO:0046546)	136	13	3.67	+	3.54	1.60E-04	3.94E-03
positive regulation of protein localization to nucleus (GO:1900182)	136	13	3.67	+	3.54	1.60E-04	3.95E-03
regulation of lipase activity (GO:0060191)	84	8	2.27	+	3.53	2.92E-03	4.40E-02
tissue development (GO:0009888)	1658	158	44.76	+	3.53	2.05E-43	1.59E-39
regulation of myeloid leukocyte differentiation (GO:0002761)	116	11	3.13	+	3.51	5.35E-04	1.12E-02
positive regulation of myeloid cell differentiation (GO:0045639)	85	8	2.29	+	3.49	3.12E-03	4.65E-02
skeletal muscle organ development (GO:0060538)	138	13	3.73	+	3.49	1.83E-04	4.43E-03
terpenoid metabolic process (GO:0006721)	106	10	2.86	+	3.49	9.81E-04	1.84E-02
cell migration (GO:0016477)	872	82	23.54	+	3.48	1.58E-21	5.31E-19
cellular response to external stimulus (GO:0071496)	298	28	8.04	+	3.48	4.61E-08	2.66E-06
response to metal ion (GO:0010038)	330	31	8.91	+	3.48	8.77E-09	5.89E-07
response to inorganic substance (GO:0010035)	480	45	12.96	+	3.47	3.72E-12	3.93E-10
cellular response to BMP stimulus (GO:0071773)	107	10	2.89	+	3.46	1.05E-03	1.95E-02
regulation of leukocyte chemotaxis (GO:0002688)	107	10	2.89	+	3.46	1.05E-03	1.94E-02
regulation of ossification (GO:0030278)	182	17	4.91	+	3.46	2.17E-05	6.72E-04
response to BMP (GO:0071772)	107	10	2.89	+	3.46	1.05E-03	1.94E-02
telencephalon development (GO:0021537)	246	23	6.64	+	3.46	7.93E-07	3.65E-05
animal organ morphogenesis (GO:0009887)	881	82	23.78	+	3.45	2.85E-21	9.41E-19
negative regulation of cell growth (GO:0030308)	161	15	4.35	+	3.45	6.71E-05	1.86E-03
regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0000079)	86	8	2.32	+	3.45	3.34E-03	4.82E-02
regulation of muscle system process (GO:0090257)	215	20	5.8	+	3.45	4.42E-06	1.72E-04
response to estradiol (GO:0032355)	129	12	3.48	+	3.45	3.56E-04	7.87E-03
axon guidance (GO:0007411)	226	21	6.1	+	3.44	2.60E-06	1.07E-04
cell-cell adhesion (GO:0098609)	442	41	11.93	+	3.44	4.75E-11	4.49E-09
inner ear development (GO:0048839)	184	17	4.97	+	3.42	2.47E-05	7.55E-04
regulation of protein kinase B signaling (GO:0051896)	195	18	5.26	+	3.42	1.45E-05	4.81E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
neuron projection guidance (GO:0097485)	228	21	6.15	+	3.41	2.96E-06	1.21E-04
leukocyte migration (GO:0050900)	360	33	9.72	+	3.4	5.05E-09	3.64E-07
response to oxygen levels (GO:0070482)	371	34	10.01	+	3.4	2.96E-09	2.19E-07
skeletal system development (GO:0001501)	469	43	12.66	+	3.4	2.22E-11	2.18E-09
glycosaminoglycan metabolic process (GO:0030203)	153	14	4.13	+	3.39	1.39E-04	3.49E-03
regulation of muscle cell differentiation (GO:0051147)	142	13	3.83	+	3.39	2.37E-04	5.50E-03
positive regulation of cell adhesion (GO:0045785)	395	36	10.66	+	3.38	1.15E-09	9.41E-08
regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	230	21	6.21	+	3.38	3.36E-06	1.35E-04
odontogenesis (GO:0042476)	110	10	2.97	+	3.37	1.27E-03	2.29E-02
positive regulation of leukocyte migration (GO:0002687)	121	11	3.27	+	3.37	7.40E-04	1.47E-02
regulation of blood pressure (GO:0008217)	176	16	4.75	+	3.37	5.08E-05	1.46E-03
positive regulation of JNK cascade (GO:0046330)	122	11	3.29	+	3.34	7.88E-04	1.55E-02
positive regulation of leukocyte differentiation (GO:1902107)	133	12	3.59	+	3.34	4.59E-04	9.83E-03
response to monosaccharide (GO:0034284)	144	13	3.89	+	3.34	2.69E-04	6.17E-03
response to organophosphorus (GO:0046683)	133	12	3.59	+	3.34	4.59E-04	9.81E-03
regulation of lipid transport (GO:0032368)	100	9	2.7	+	3.33	2.34E-03	3.74E-02
eye morphogenesis (GO:0048592)	145	13	3.91	+	3.32	2.86E-04	6.51E-03
regulation of muscle contraction (GO:0006937)	156	14	4.21	+	3.32	1.67E-04	4.09E-03
negative regulation of epithelial cell proliferation (GO:0050680)	123	11	3.32	+	3.31	8.38E-04	1.64E-02
positive regulation of endocytosis (GO:0045807)	123	11	3.32	+	3.31	8.38E-04	1.63E-02
response to decreased oxygen levels (GO:0036293)	347	31	9.37	+	3.31	2.56E-08	1.57E-06
striated muscle contraction (GO:0006941)	112	10	3.02	+	3.31	1.44E-03	2.49E-02
negative regulation of growth (GO:0045926)	236	21	6.37	+	3.3	4.86E-06	1.87E-04
pallium development (GO:0021543)	169	15	4.56	+	3.29	1.11E-04	2.88E-03
cellular response to oxidative stress (GO:0034599)	226	20	6.1	+	3.28	8.78E-06	3.19E-04
male sex differentiation (GO:0046661)	158	14	4.26	+	3.28	1.89E-04	4.56E-03
positive regulation of MAP kinase activity (GO:0043406)	260	23	7.02	+	3.28	1.90E-06	8.10E-05
response to hypoxia (GO:0001666)	339	30	9.15	+	3.28	5.23E-08	3.00E-06

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 morphogenesis of an epithelium (GO:1905330)	182	16	4.91	+	3.26	7.34E-05	2.00E-03
regulation of peptidase activity (GO:0052547)	421	37	11.36	+	3.26	1.69E-09	1.33E-07
positive regulation of MAPK cascade (GO:0043410)	502	44	13.55	+	3.25	5.00E-11	4.70E-09
positive regulation of peptidase activity (GO:0010952)	171	15	4.62	+	3.25	1.25E-04	3.22E-03
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	171	15	4.62	+	3.25	1.25E-04	3.22E-03
supramolecular fiber organization (GO:0097435)	388	34	10.47	+	3.25	8.38E-09	5.67E-07
aminoglycan metabolic process (GO:0006022)	160	14	4.32	+	3.24	2.13E-04	5.04E-03
myeloid leukocyte migration (GO:0097529)	103	9	2.78	+	3.24	2.81E-03	4.28E-02
response to purine-containing compound (GO:0014074)	149	13	4.02	+	3.23	3.64E-04	8.00E-03
regulation of protein binding (GO:0043393)	207	18	5.59	+	3.22	3.03E-05	9.06E-04
response to hexose (GO:0009746)	138	12	3.73	+	3.22	6.23E-04	1.28E-02
positive regulation of protein serine/threonine kinase activity (GO:0071902)	347	30	9.37	+	3.2	8.39E-08	4.62E-06
ear development (GO:0043583)	209	18	5.64	+	3.19	3.41E-05	1.01E-03
regulation of body fluid levels (GO:0050878)	499	43	13.47	+	3.19	1.37E-10	1.24E-08
regulation of cell cycle arrest (GO:0071156)	116	10	3.13	+	3.19	1.84E-03	3.06E-02
anterior/posterior pattern specification (GO:0009952)	198	17	5.34	+	3.18	5.80E-05	1.63E-03
negative regulation of hemopoiesis (GO:1903707)	128	11	3.46	+	3.18	1.13E-03	2.07E-02
negative regulation of hydrolase activity (GO:0051346)	420	36	11.34	+	3.18	5.18E-09	3.72E-07
negative regulation of protein serine/threonine kinase activity (GO:0071901)	128	11	3.46	+	3.18	1.13E-03	2.07E-02
positive regulation of cell death (GO:0010942)	653	56	17.63	+	3.18	2.25E-13	2.84E-11
positive regulation of homeostatic process (GO:0032846)	221	19	5.97	+	3.18	2.13E-05	6.64E-04
regulation of anatomical structure morphogenesis (GO:0022603)	980	84	26.45	+	3.18	1.07E-19	3.14E-17
epithelium development (GO:0060429)	1074	92	28.99	+	3.17	1.52E-21	5.23E-19
hormone metabolic process (GO:0042445)	187	16	5.05	+	3.17	9.86E-05	2.61E-03
gonad development (GO:0008406)	211	18	5.7	+	3.16	3.83E-05	1.12E-03
negative regulation of protein phosphorylation (GO:0001933)	410	35	11.07	+	3.16	9.34E-09	6.22E-07
apoptotic signaling pathway (GO:0097190)	294	25	7.94	+	3.15	1.33E-06	5.86E-05

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
positive regulation of cell proliferation (GO:0008284)	871	74	23.51	+	3.15	3.32E-17	7.45E-15
regulation of cell adhesion (GO:0030155)	671	57	18.11	+	3.15	1.95E-13	2.48E-11
response to retinoic acid (GO:0032526)	106	9	2.86	+	3.15	3.36E-03	4.85E-02
tube morphogenesis (GO:0035239)	341	29	9.2	+	3.15	1.90E-07	9.90E-06
cell motility (GO:0048870)	969	82	26.16	+	3.13	6.39E-19	1.68E-16
embryo development (GO:0009790)	924	78	24.94	+	3.13	5.84E-18	1.44E-15
localization of cell (GO:0051674)	969	82	26.16	+	3.13	6.39E-19	1.71E-16
axon development (GO:0061564)	380	32	10.26	+	3.12	5.45E-08	3.12E-06
positive regulation of hemopoiesis (GO:1903708)	166	14	4.48	+	3.12	3.03E-04	6.83E-03
regulation of MAPK cascade (GO:0043408)	700	59	18.9	+	3.12	9.73E-14	1.36E-11
negative regulation of cell adhesion (GO:0007162)	238	20	6.42	+	3.11	1.77E-05	5.74E-04
regulation of JNK cascade (GO:0046328)	167	14	4.51	+	3.11	3.20E-04	7.20E-03
regulation of MAP kinase activity (GO:0043405)	333	28	8.99	+	3.11	3.83E-07	1.87E-05
regulation of peptidyl-serine phosphorylation (GO:0033135)	131	11	3.54	+	3.11	1.35E-03	2.37E-02
taxis (GO:0042330)	500	42	13.5	+	3.11	4.65E-10	3.94E-08
cellular response to extracellular stimulus (GO:0031668)	227	19	6.13	+	3.1	2.99E-05	8.96E-04
regulation of cysteine-type endopeptidase activity (GO:2000116)	239	20	6.45	+	3.1	1.87E-05	5.99E-04
regulation of endopeptidase activity (GO:0052548)	394	33	10.64	+	3.1	3.80E-08	2.23E-06
negative regulation of neuron projection development (GO:0010977)	120	10	3.24	+	3.09	2.31E-03	3.71E-02
positive regulation of response to external stimulus (GO:0032103)	276	23	7.45	+	3.09	4.79E-06	1.84E-04
positive regulation of stress-activated MAPK cascade (GO:0032874)	144	12	3.89	+	3.09	8.82E-04	1.69E-02
response to carbohydrate (GO:0009743)	168	14	4.53	+	3.09	3.39E-04	7.56E-03
signal transduction by p53 class mediator (GO:0072331)	132	11	3.56	+	3.09	1.43E-03	2.47E-02
anatomical structure morphogenesis (GO:0009653)	2021	168	54.55	+	3.08	3.02E-39	9.38E-36
development of primary sexual characteristics (GO:0045137)	217	18	5.86	+	3.07	5.37E-05	1.53E-03
female pregnancy (GO:0007565)	181	15	4.89	+	3.07	2.23E-04	5.21E-03
locomotion (GO:0040011)	1205	100	32.53	+	3.07	1.71E-22	6.99E-20

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
morphogenesis of embryonic epithelium (GO:0016331)	145	12	3.91	+	3.07	9.33E-04	1.76E-02
negative regulation of cell activation (GO:0050866)	169	14	4.56	+	3.07	3.58E-04	7.90E-03
positive regulation of stress-activated protein kinase signaling cascade (GO:0070304)	145	12	3.91	+	3.07	9.33E-04	1.77E-02
negative regulation of phosphorylation (GO:0042326)	448	37	12.09	+	3.06	7.90E-09	5.38E-07
response to glucose (GO:0009749)	133	11	3.59	+	3.06	1.51E-03	2.59E-02
positive regulation of programmed cell death (GO:0043068)	607	50	16.39	+	3.05	1.81E-11	1.79E-09
regulation of heart contraction (GO:0008016)	231	19	6.24	+	3.05	3.74E-05	1.09E-03
chemotaxis (GO:0006935)	499	41	13.47	+	3.04	1.38E-09	1.09E-07
embryonic organ development (GO:0048568)	426	35	11.5	+	3.04	2.28E-08	1.42E-06
negative regulation of cytokine production (GO:0001818)	244	20	6.59	+	3.04	2.46E-05	7.54E-04
positive regulation of developmental process (GO:0051094)	1241	102	33.5	+	3.04	1.17E-22	4.90E-20
regulation of G1/S transition of mitotic cell cycle (GO:2000045)	146	12	3.94	+	3.04	9.86E-04	1.84E-02
camera-type eye development (GO:0043010)	293	24	7.91	+	3.03	3.93E-06	1.56E-04
negative regulation of signal transduction (GO:0009968)	1176	96	31.74	+	3.02	4.08E-21	1.32E-18
positive regulation of apoptotic process (GO:0043065)	601	49	16.22	+	3.02	4.08E-11	3.90E-09
blood coagulation (GO:0007596)	295	24	7.96	+	3.01	4.38E-06	1.71E-04
positive regulation of cell differentiation (GO:0045597)	862	70	23.27	+	3.01	2.19E-15	4.00E-13
regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043281)	209	17	5.64	+	3.01	1.07E-04	2.81E-03
regulation of protein serine/threonine kinase activity (GO:0071900)	492	40	13.28	+	3.01	2.92E-09	2.16E-07
aging (GO:0007568)	259	21	6.99	+	3	1.80E-05	5.83E-04
cellular response to starvation (GO:0009267)	136	11	3.67	+	3	1.78E-03	2.98E-02
regulation of leukocyte proliferation (GO:0070663)	210	17	5.67	+	3	1.13E-04	2.94E-03
coagulation (GO:0050817)	297	24	8.02	+	2.99	4.87E-06	1.87E-04
embryonic epithelial tube formation (GO:0001838)	124	10	3.35	+	2.99	2.89E-03	4.37E-02
interaction with host (GO:0051701)	161	13	4.35	+	2.99	7.19E-04	1.44E-02

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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	103	34.47	+	2.99	2.59E-22	1.01E-19
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)	124	10	3.35	+	2.99	2.89E-03	4.36E-02
negative regulation of apoptotic signaling pathway (GO:2001234)	211	17	5.7	+	2.98	1.19E-04	3.09E-03
multi-multicellular organism process (GO:0044706)	212	17	5.72	+	2.97	1.26E-04	3.23E-03
negative regulation of cell communication (GO:0010648)	1273	102	34.36	+	2.97	6.80E-22	2.45E-19
positive regulation of leukocyte proliferation (GO:0070665)	137	11	3.7	+	2.97	1.88E-03	3.11E-02
regulation of cell cycle G1/S phase transition (GO:1902806)	162	13	4.37	+	2.97	7.58E-04	1.50E-02
hemostasis (GO:0007599)	300	24	8.1	+	2.96	5.71E-06	2.16E-04
response to ionizing radiation (GO:0010212)	150	12	4.05	+	2.96	1.22E-03	2.21E-02
negative regulation of phosphate metabolic process (GO:0045936)	578	46	15.6	+	2.95	3.45E-10	3.04E-08
positive regulation of multicellular organismal process (GO:0051240)	1493	119	40.3	+	2.95	1.74E-25	1.08E-22
rhythmic process (GO:0048511)	289	23	7.8	+	2.95	9.64E-06	3.44E-04
isoprenoid metabolic process (GO:0006720)	126	10	3.4	+	2.94	3.21E-03	4.76E-02
negative regulation of phosphorus metabolic process (GO:0010563)	579	46	15.63	+	2.94	3.64E-10	3.17E-08
regulation of cell proliferation (GO:0042127)	1588	126	42.87	+	2.94	6.72E-27	5.48E-24
epithelial tube morphogenesis (GO:0060562)	303	24	8.18	+	2.93	6.68E-06	2.46E-04
positive regulation of cell morphogenesis involved in differentiation (GO:0010770)	139	11	3.75	+	2.93	2.09E-03	3.38E-02
regulation of system process (GO:0044057)	505	40	13.63	+	2.93	5.78E-09	4.07E-07
cell morphogenesis involved in differentiation (GO:0000904)	508	40	13.71	+	2.92	6.75E-09	4.69E-07
sensory organ morphogenesis (GO:0090596)	254	20	6.86	+	2.92	4.17E-05	1.21E-03
sex differentiation (GO:0007548)	266	21	7.18	+	2.92	2.60E-05	7.95E-04
cell morphogenesis involved in neuron differentiation (GO:0048667)	408	32	11.01	+	2.91	2.44E-07	1.24E-05
cellular response to toxic substance (GO:0097237)	204	16	5.51	+	2.91	2.49E-04	5.74E-03
negative regulation of cell proliferation (GO:0008285)	661	52	17.84	+	2.91	3.38E-11	3.26E-09

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 oxidative stress (GO:0006979)	371	29	10.01	+	2.9	9.54E-07	4.29E-05
positive regulation of endopeptidase activity (GO:0010950)	154	12	4.16	+	2.89	1.51E-03	2.60E-02
cellular response to drug (GO:0035690)	309	24	8.34	+	2.88	9.07E-06	3.28E-04
negative regulation of canonical Wnt signaling pathway (GO:0090090)	167	13	4.51	+	2.88	9.84E-04	1.85E-02
regulation of endocytosis (GO:0030100)	219	17	5.91	+	2.88	1.81E-04	4.39E-03
axonogenesis (GO:0007409)	349	27	9.42	+	2.87	2.70E-06	1.11E-04
cellular response to tumor necrosis factor (GO:0071356)	245	19	6.61	+	2.87	7.79E-05	2.10E-03
glial cell differentiation (GO:0010001)	155	12	4.18	+	2.87	1.59E-03	2.71E-02
negative regulation of proteolysis (GO:0045861)	348	27	9.39	+	2.87	2.57E-06	1.07E-04
regulation of binding (GO:0051098)	349	27	9.42	+	2.87	2.70E-06	1.11E-04
regulation of cell growth (GO:0001558)	389	30	10.5	+	2.86	8.05E-07	3.68E-05
eye development (GO:0001654)	338	26	9.12	+	2.85	4.55E-06	1.77E-04
negative regulation of developmental process (GO:0051093)	862	66	23.27	+	2.84	1.93E-13	2.48E-11
regionalization (GO:0003002)	313	24	8.45	+	2.84	1.11E-05	3.85E-04
circulatory system process (GO:0003013)	380	29	10.26	+	2.83	1.49E-06	6.49E-05
negative regulation of response to stimulus (GO:0048585)	1477	113	39.87	+	2.83	8.52E-23	3.67E-20
positive regulation of intracellular signal transduction (GO:1902533)	968	74	26.13	+	2.83	6.04E-15	1.03E-12
regulation of canonical Wnt signaling pathway (GO:0060828)	249	19	6.72	+	2.83	9.50E-05	2.52E-03
negative regulation of intracellular signal transduction (GO:1902532)	500	38	13.5	+	2.82	3.88E-08	2.27E-06
cellular response to nutrient levels (GO:0031669)	198	15	5.34	+	2.81	5.40E-04	1.12E-02
gliogenesis (GO:0042063)	198	15	5.34	+	2.81	5.40E-04	1.12E-02
intrinsic apoptotic signaling pathway (GO:0097193)	158	12	4.26	+	2.81	1.85E-03	3.08E-02
response to toxic substance (GO:0009636)	501	38	13.52	+	2.81	4.07E-08	2.36E-06
enzyme linked receptor protein signaling pathway (GO:0007167)	715	54	19.3	+	2.8	5.75E-11	5.37E-09
epithelial cell development (GO:0002064)	185	14	4.99	+	2.8	8.26E-04	1.62E-02
negative regulation of protein kinase activity (GO:0006469)	251	19	6.78	+	2.8	1.05E-04	2.76E-03

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 blood circulation (GO:1903522)	278	21	7.5	+	2.8	4.74E-05	1.37E-03
movement of cell or subcellular component (GO:0006928)	1462	110	39.46	+	2.79	1.21E-21	4.28E-19
response to tumor necrosis factor (GO:0034612)	266	20	7.18	+	2.79	7.58E-05	2.05E-03
tube formation (GO:0035148)	146	11	3.94	+	2.79	2.98E-03	4.49E-02
regulation of receptor activity (GO:0010469)	547	41	14.77	+	2.78	1.59E-08	1.03E-06
viral life cycle (GO:0019058)	200	15	5.4	+	2.78	5.95E-04	1.22E-02
negative regulation of cell projection organization (GO:0031345)	147	11	3.97	+	2.77	3.13E-03	4.65E-02
negative regulation of multicellular organismal process (GO:0051241)	1044	78	28.18	+	2.77	3.24E-15	5.64E-13
positive regulation of protein phosphorylation (GO:0001934)	936	70	25.27	+	2.77	9.61E-14	1.35E-11
blood circulation (GO:0008015)	376	28	10.15	+	2.76	3.51E-06	1.41E-04
regulation of lymphocyte proliferation (GO:0050670)	201	15	5.43	+	2.76	6.25E-04	1.28E-02
appendage morphogenesis (GO:0035107)	148	11	4	+	2.75	3.28E-03	4.84E-02
forebrain development (GO:0030900)	377	28	10.18	+	2.75	3.68E-06	1.46E-04
limb morphogenesis (GO:0035108)	148	11	4	+	2.75	3.28E-03	4.84E-02
positive regulation of protein kinase activity (GO:0045860)	512	38	13.82	+	2.75	6.88E-08	3.85E-06
regulation of mononuclear cell proliferation (GO:0032944)	202	15	5.45	+	2.75	6.55E-04	1.34E-02
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)	189	14	5.1	+	2.74	1.00E-03	1.87E-02
cellular response to abiotic stimulus (GO:0071214)	285	21	7.69	+	2.73	6.62E-05	1.84E-03
cellular response to environmental stimulus (GO:0104004)	285	21	7.69	+	2.73	6.62E-05	1.84E-03
positive regulation of Wnt signaling pathway (GO:0030177)	163	12	4.4	+	2.73	2.35E-03	3.75E-02
regulation of T cell proliferation (GO:0042129)	149	11	4.02	+	2.73	3.45E-03	4.94E-02
negative regulation of cell differentiation (GO:0045596)	639	47	17.25	+	2.72	2.39E-09	1.82E-07
regulation of protein import into nucleus (GO:0042306)	177	13	4.78	+	2.72	1.61E-03	2.72E-02
response to lipopolysaccharide (GO:0032496)	300	22	8.1	+	2.72	4.77E-05	1.37E-03
positive regulation of phosphorylation (GO:0042327)	983	72	26.53	+	2.71	1.07E-13	1.47E-11
response to lipid (GO:0033993)	834	61	22.51	+	2.71	1.03E-11	1.04E-09

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
sensory organ development (GO:0007423)	519	38	14.01	+	2.71	9.53E-08	5.19E-06
regulation of stress-activated MAPK cascade (GO:0032872)	206	15	5.56	+	2.7	7.90E-04	1.55E-02
response to organic cyclic compound (GO:0014070)	879	64	23.73	+	2.7	3.66E-12	3.92E-10
negative regulation of apoptotic process (GO:0043066)	853	62	23.03	+	2.69	8.79E-12	8.97E-10
negative regulation of programmed cell death (GO:0043069)	867	63	23.4	+	2.69	5.94E-12	6.14E-10
regulation of multicellular organismal development (GO:2000026)	1805	131	48.72	+	2.69	1.26E-24	7.51E-22
cellular response to xenobiotic stimulus (GO:0071466)	166	12	4.48	+	2.68	2.71E-03	4.14E-02
embryonic organ morphogenesis (GO:0048562)	290	21	7.83	+	2.68	8.33E-05	2.24E-03
regulation of protein import (GO:1904589)	180	13	4.86	+	2.68	1.85E-03	3.08E-02
regulation of stress-activated protein kinase signaling cascade (GO:0070302)	207	15	5.59	+	2.68	8.28E-04	1.62E-02
response to acid chemical (GO:0001101)	332	24	8.96	+	2.68	2.72E-05	8.26E-04
response to molecule of bacterial origin (GO:0002237)	318	23	8.58	+	2.68	3.95E-05	1.15E-03
cellular component morphogenesis (GO:0032989)	735	53	19.84	+	2.67	4.16E-10	3.56E-08
negative regulation of cell development (GO:0010721)	277	20	7.48	+	2.67	1.27E-04	3.25E-03
cell morphogenesis (GO:0000902)	640	46	17.28	+	2.66	6.94E-09	4.80E-07
positive regulation of protein secretion (GO:0050714)	237	17	6.4	+	2.66	4.27E-04	9.23E-03
skin development (GO:0043588)	376	27	10.15	+	2.66	9.70E-06	3.46E-04
response to drug (GO:0042493)	911	65	24.59	+	2.64	8.38E-12	8.61E-10
central nervous system neuron differentiation (GO:0021953)	169	12	4.56	+	2.63	3.10E-03	4.62E-02
developmental process involved in reproduction (GO:0003006)	649	46	17.52	+	2.63	1.71E-08	1.09E-06
gland development (GO:0048732)	409	29	11.04	+	2.63	5.74E-06	2.16E-04
regulation of leukocyte differentiation (GO:1902105)	254	18	6.86	+	2.63	3.35E-04	7.49E-03
cell chemotaxis (GO:0060326)	184	13	4.97	+	2.62	2.21E-03	3.55E-02
negative regulation of kinase activity (GO:0033673)	269	19	7.26	+	2.62	2.41E-04	5.57E-03
positive regulation of kinase activity (GO:0033674)	551	39	14.87	+	2.62	1.47E-07	7.80E-06

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 immune system process (GO:0002683)	398	28	10.74	+	2.61	9.50E-06	3.41E-04
positive regulation of cell cycle process (GO:0090068)	270	19	7.29	+	2.61	2.52E-04	5.79E-03
regulation of protein localization to nucleus (GO:1900180)	227	16	6.13	+	2.61	7.43E-04	1.47E-02
regulation of protein phosphorylation (GO:0001932)	1362	96	36.77	+	2.61	4.65E-17	1.03E-14
positive regulation of phosphate metabolic process (GO:0045937)	1098	77	29.64	+	2.6	1.22E-13	1.61E-11
positive regulation of phosphorus metabolic process (GO:0010562)	1098	77	29.64	+	2.6	1.22E-13	1.62E-11
regulation of cytokine secretion (GO:0050707)	171	12	4.62	+	2.6	3.39E-03	4.89E-02
regulation of Wnt signaling pathway (GO:0030111)	328	23	8.85	+	2.6	6.15E-05	1.72E-03
cellular response to hypoxia (GO:0071456)	186	13	5.02	+	2.59	2.42E-03	3.80E-02
negative regulation of neuron differentiation (GO:0045665)	186	13	5.02	+	2.59	2.42E-03	3.80E-02
negative regulation of Wnt signaling pathway (GO:0030178)	200	14	5.4	+	2.59	1.65E-03	2.78E-02
positive regulation of DNA metabolic process (GO:0051054)	215	15	5.8	+	2.58	1.18E-03	2.15E-02
negative regulation of cell death (GO:0060548)	946	65	25.54	+	2.55	2.68E-11	2.59E-09
regulation of myeloid cell differentiation (GO:0045637)	218	15	5.88	+	2.55	1.35E-03	2.39E-02
chordate embryonic development (GO:0043009)	568	39	15.33	+	2.54	3.79E-07	1.87E-05
embryo development ending in birth or egg hatching (GO:0009792)	574	39	15.49	+	2.52	4.54E-07	2.19E-05
epidermis development (GO:0008544)	412	28	11.12	+	2.52	2.44E-05	7.49E-04
neuron projection morphogenesis (GO:0048812)	456	31	12.31	+	2.52	8.10E-06	2.96E-04
regulation of hormone levels (GO:0010817)	514	35	13.87	+	2.52	1.85E-06	7.95E-05
regulation of hormone secretion (GO:0046883)	265	18	7.15	+	2.52	5.37E-04	1.12E-02
response to abiotic stimulus (GO:0009628)	1118	76	30.18	+	2.52	9.27E-13	1.08E-10
positive regulation of cytokine production (GO:0001819)	398	27	10.74	+	2.51	3.58E-05	1.05E-03
positive regulation of protein transport (GO:0051222)	488	33	13.17	+	2.51	4.19E-06	1.64E-04
regulation of developmental process (GO:0050793)	2379	161	64.22	+	2.51	1.48E-27	1.43E-24

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 response to external stimulus (GO:0032101)	782	53	21.11	+	2.51	3.30E-09	2.43E-07
cellular response to decreased oxygen levels (GO:0036294)	193	13	5.21	+	2.5	3.26E-03	4.81E-02
plasma membrane bounded cell projection morphogenesis (GO:0120039)	460	31	12.42	+	2.5	8.97E-06	3.25E-04
positive regulation of cell cycle (GO:0045787)	371	25	10.01	+	2.5	7.85E-05	2.11E-03
positive regulation of secretion (GO:0051047)	386	26	10.42	+	2.5	5.47E-05	1.55E-03
regulation of apoptotic process (GO:0042981)	1497	101	40.41	+	2.5	9.25E-17	1.86E-14
regulation of programmed cell death (GO:0043067)	1512	102	40.81	+	2.5	6.33E-17	1.33E-14
regulation of protein kinase activity (GO:0045859)	784	53	21.16	+	2.5	3.57E-09	2.58E-07
negative regulation of catalytic activity (GO:0043086)	891	60	24.05	+	2.49	4.91E-10	4.12E-08
cell projection morphogenesis (GO:0048858)	463	31	12.5	+	2.48	9.76E-06	3.47E-04
cellular response to oxygen levels (GO:0071453)	209	14	5.64	+	2.48	2.42E-03	3.80E-02
negative regulation of molecular function (GO:0044092)	1178	79	31.8	+	2.48	4.92E-13	5.91E-11
neuron projection development (GO:0031175)	601	40	16.22	+	2.47	4.83E-07	2.33E-05
regulation of cell death (GO:0010941)	1629	108	43.97	+	2.46	2.10E-17	4.85E-15
regulation of cell differentiation (GO:0045595)	1643	109	44.35	+	2.46	1.38E-17	3.28E-15
regulation of phosphorylation (GO:0042325)	1490	99	40.22	+	2.46	5.81E-16	1.11E-13
positive regulation of peptide secretion (GO:0002793)	257	17	6.94	+	2.45	9.98E-04	1.86E-02
regulation of multicellular organismal process (GO:0051239)	2777	184	74.96	+	2.45	5.06E-31	6.54E-28
apoptotic process (GO:0006915)	910	60	24.56	+	2.44	8.15E-10	6.68E-08
regulation of cytokine production (GO:0001817)	623	41	16.82	+	2.44	4.44E-07	2.15E-05
cellular response to organic cyclic compound (GO:0071407)	503	33	13.58	+	2.43	6.72E-06	2.47E-04
animal organ development (GO:0048513)	2988	195	80.66	+	2.42	3.42E-32	4.82E-29
cell fate commitment (GO:0045165)	230	15	6.21	+	2.42	2.20E-03	3.55E-02
in utero embryonic development (GO:0001701)	322	21	8.69	+	2.42	4.20E-04	9.10E-03
positive regulation of nervous system development (GO:0051962)	460	30	12.42	+	2.42	2.00E-05	6.32E-04

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cellular response to organonitrogen compound (GO:0071417)	491	32	13.25	+	2.41	1.05E-05	3.67E-04
positive regulation of cell development (GO:0010720)	462	30	12.47	+	2.41	2.13E-05	6.64E-04
response to cytokine (GO:0034097)	921	60	24.86	+	2.41	1.18E-09	9.58E-08
response to endogenous stimulus (GO:0009719)	1368	89	36.93	+	2.41	6.41E-14	9.46E-12
positive regulation of neuron projection development (GO:0010976)	216	14	5.83	+	2.4	3.20E-03	4.75E-02
positive regulation of protein modification process (GO:0031401)	1202	78	32.45	+	2.4	3.47E-12	3.74E-10
regulation of kinase activity (GO:0043549)	849	55	22.92	+	2.4	7.49E-09	5.12E-07
cell development (GO:0048468)	1486	96	40.11	+	2.39	9.44E-15	1.56E-12
cell death (GO:0008219)	1074	69	28.99	+	2.38	1.12E-10	1.03E-08
positive regulation of signal transduction (GO:0009967)	1510	97	40.76	+	2.38	8.48E-15	1.41E-12
cell part morphogenesis (GO:0032990)	484	31	13.06	+	2.37	1.93E-05	6.16E-04
cellular response to cytokine stimulus (GO:0071345)	827	53	22.32	+	2.37	1.97E-08	1.23E-06
cellular response to oxygen-containing compound (GO:1901701)	905	58	24.43	+	2.37	5.37E-09	3.84E-07
negative regulation of protein metabolic process (GO:0051248)	1125	72	30.37	+	2.37	4.61E-11	4.39E-09
pattern specification process (GO:0007389)	406	26	10.96	+	2.37	9.49E-05	2.52E-03
regulation of intracellular signal transduction (GO:1902531)	1800	115	48.59	+	2.37	2.16E-17	4.93E-15
activation of protein kinase activity (GO:0032147)	315	20	8.5	+	2.35	7.30E-04	1.45E-02
positive regulation of neurogenesis (GO:0050769)	394	25	10.64	+	2.35	1.47E-04	3.68E-03
growth (GO:0040007)	395	25	10.66	+	2.34	1.51E-04	3.78E-03
positive regulation of establishment of protein localization (GO:1904951)	523	33	14.12	+	2.34	1.82E-05	5.86E-04
positive regulation of signaling (GO:0023056)	1650	104	44.54	+	2.34	2.37E-15	4.27E-13
regulation of growth (GO:0040008)	649	41	17.52	+	2.34	1.30E-06	5.76E-05
inflammatory response (GO:0006954)	462	29	12.47	+	2.33	7.39E-05	2.00E-03
negative regulation of cellular protein metabolic process (GO:0032269)	1066	67	28.78	+	2.33	6.55E-10	5.40E-08
regulation of cell development (GO:0060284)	794	50	21.43	+	2.33	1.14E-07	6.15E-06

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 small GTPase mediated signal transduction (GO:0051056)	318	20	8.58	+	2.33	7.91E-04	1.55E-02
response to oxygen-containing compound (GO:1901700)	1445	91	39.01	+	2.33	2.44E-13	3.03E-11
developmental growth (GO:0048589)	352	22	9.5	+	2.32	4.47E-04	9.61E-03
positive regulation of cell communication (GO:0010647)	1643	103	44.35	+	2.32	6.97E-15	1.17E-12
response to hormone (GO:0009725)	877	55	23.67	+	2.32	2.33E-08	1.43E-06
positive regulation of cell-cell adhesion (GO:0022409)	257	16	6.94	+	2.31	3.14E-03	4.66E-02
positive regulation of transferase activity (GO:0051347)	690	43	18.63	+	2.31	1.42E-06	6.19E-05
cellular response to endogenous stimulus (GO:0071495)	1113	69	30.04	+	2.3	4.73E-10	3.98E-08
cellular response to lipid (GO:0071396)	486	30	13.12	+	2.29	6.13E-05	1.72E-03
positive regulation of cellular protein metabolic process (GO:0032270)	1520	94	41.03	+	2.29	2.63E-13	3.24E-11
regulation of cell morphogenesis (GO:0022604)	436	27	11.77	+	2.29	1.60E-04	3.95E-03
regulation of cell projection organization (GO:0031344)	550	34	14.85	+	2.29	1.70E-05	5.56E-04
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	518	32	13.98	+	2.29	3.21E-05	9.58E-04
epithelial cell differentiation (GO:0030855)	667	41	18	+	2.28	3.20E-06	1.29E-04
programmed cell death (GO:0012501)	1039	64	28.05	+	2.28	2.85E-09	2.14E-07
regulation of DNA binding transcription factor activity (GO:0051090)	390	24	10.53	+	2.28	4.58E-04	9.82E-03
positive regulation of secretion by cell (GO:1903532)	359	22	9.69	+	2.27	5.54E-04	1.15E-02
regulation of protein secretion (GO:0050708)	424	26	11.45	+	2.27	2.39E-04	5.53E-03
actin filament-based process (GO:0030029)	509	31	13.74	+	2.26	5.27E-05	1.51E-03
positive regulation of cell projection organization (GO:0031346)	312	19	8.42	+	2.26	1.44E-03	2.49E-02
regulation of phosphate metabolic process (GO:0019220)	1723	105	46.51	+	2.26	1.55E-14	2.43E-12
regulation of phosphorus metabolic process (GO:0051174)	1737	106	46.89	+	2.26	1.04E-14	1.68E-12
regulation of plasma membrane bounded cell projection organization (GO:0120035)	541	33	14.6	+	2.26	2.82E-05	8.54E-04
positive regulation of cellular component organization (GO:0051130)	1167	71	31.5	+	2.25	6.12E-10	5.07E-08

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
neuron development (GO:0048666)	744	45	20.08	+	2.24	1.18E-06	5.23E-05
regulation of actin filament-based process (GO:0032970)	347	21	9.37	+	2.24	8.51E-04	1.66E-02
positive regulation of protein metabolic process (GO:0051247)	1612	97	43.51	+	2.23	3.86E-13	4.68E-11
head development (GO:0060322)	734	44	19.81	+	2.22	1.90E-06	8.11E-05
regulation of apoptotic signaling pathway (GO:2001233)	383	23	10.34	+	2.22	7.29E-04	1.46E-02
regulation of cell-cell adhesion (GO:0022407)	418	25	11.28	+	2.22	4.00E-04	8.69E-03
response to extracellular stimulus (GO:0009991)	483	29	13.04	+	2.22	1.15E-04	2.99E-03
regulation of neuron projection development (GO:0010975)	385	23	10.39	+	2.21	7.54E-04	1.49E-02
regulation of peptide secretion (GO:0002791)	452	27	12.2	+	2.21	2.21E-04	5.20E-03
negative regulation of protein modification process (GO:0031400)	622	37	16.79	+	2.2	1.71E-05	5.56E-04
positive regulation of transport (GO:0051050)	978	58	26.4	+	2.2	6.86E-08	3.85E-06
regulation of hemopoiesis (GO:1903706)	421	25	11.36	+	2.2	4.27E-04	9.22E-03
regulation of homeostatic process (GO:0032844)	471	28	12.71	+	2.2	1.74E-04	4.25E-03
regulation of protein modification process (GO:0031399)	1753	104	47.32	+	2.2	9.91E-14	1.37E-11
system development (GO:0048731)	4173	247	112.64	+	2.19	3.82E-36	7.41E-33
brain development (GO:0007420)	697	41	18.81	+	2.18	9.50E-06	3.42E-04
cellular response to nitrogen compound (GO:1901699)	577	34	15.58	+	2.18	4.75E-05	1.37E-03
multicellular organism development (GO:0007275)	4769	278	128.73	+	2.16	3.04E-41	1.57E-37
response to peptide (GO:1901652)	446	26	12.04	+	2.16	3.88E-04	8.46E-03
response to external stimulus (GO:0009605)	1893	110	51.1	+	2.15	6.62E-14	9.60E-12
response to peptide hormone (GO:0043434)	379	22	10.23	+	2.15	1.26E-03	2.28E-02
cell activation (GO:0001775)	1019	59	27.51	+	2.14	1.26E-07	6.74E-06
central nervous system development (GO:0007417)	899	52	24.27	+	2.14	6.71E-07	3.15E-05
regulation of localization (GO:0032879)	2595	150	70.05	+	2.14	5.68E-19	1.54E-16
regulation of neurogenesis (GO:0050767)	675	39	18.22	+	2.14	2.11E-05	6.61E-04
regulation of signal transduction (GO:0009966)	3083	178	83.22	+	2.14	5.15E-23	2.28E-20
response to organonitrogen compound (GO:0010243)	884	51	23.86	+	2.14	9.42E-07	4.25E-05

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 radiation (GO:0009314)	432	25	11.66	+	2.14	5.56E-04	1.15E-02
anatomical structure development (GO:0048856)	5137	296	138.67	+	2.13	3.59E-44	5.57E-40
regulation of cell activation (GO:0050865)	574	33	15.49	+	2.13	8.64E-05	2.31E-03
cellular response to organic substance (GO:0071310)	2150	123	58.04	+	2.12	3.96E-15	6.81E-13
cytokine-mediated signaling pathway (GO:0019221)	541	31	14.6	+	2.12	1.57E-04	3.90E-03
neuron differentiation (GO:0030182)	925	53	24.97	+	2.12	6.14E-07	2.90E-05
positive regulation of cellular protein localization (GO:1903829)	401	23	10.82	+	2.12	1.06E-03	1.96E-02
regulation of protein transport (GO:0051223)	787	45	21.24	+	2.12	6.47E-06	2.39E-04
regulation of hydrolase activity (GO:0051336)	1194	68	32.23	+	2.11	1.77E-08	1.12E-06
post-translational protein modification (GO:0043687)	440	25	11.88	+	2.1	9.85E-04	1.84E-02
regulation of peptide transport (GO:0090087)	817	46	22.05	+	2.09	5.94E-06	2.22E-04
positive regulation of organelle organization (GO:0010638)	622	35	16.79	+	2.08	9.08E-05	2.42E-03
regulation of cell communication (GO:0010646)	3374	189	91.08	+	2.08	3.30E-23	1.55E-20
secretion (GO:0046903)	1071	60	28.91	+	2.08	2.56E-07	1.28E-05
secretion by cell (GO:0032940)	960	54	25.91	+	2.08	9.03E-07	4.11E-05
cell surface receptor signaling pathway (GO:0007166)	2278	127	61.49	+	2.07	1.10E-14	1.75E-12
regulation of nervous system development (GO:0051960)	770	43	20.79	+	2.07	1.55E-05	5.11E-04
regulation of signaling (GO:0023051)	3423	191	92.4	+	2.07	3.30E-23	1.60E-20
positive regulation of cell activation (GO:0050867)	377	21	10.18	+	2.06	2.37E-03	3.73E-02
regulation of transferase activity (GO:0051338)	1024	57	27.64	+	2.06	6.82E-07	3.19E-05
response to organic substance (GO:0010033)	2765	153	74.64	+	2.05	9.57E-18	2.32E-15
neurogenesis (GO:0022008)	1471	81	39.71	+	2.04	2.76E-09	2.08E-07
cell differentiation (GO:0030154)	3491	191	94.23	+	2.03	2.50E-22	9.93E-20
cellular component disassembly (GO:0022411)	419	23	11.31	+	2.03	2.17E-03	3.51E-02
developmental process (GO:0032502)	5497	301	148.38	+	2.03	8.38E-41	3.25E-37
regulation of cellular protein localization (GO:1903827)	603	33	16.28	+	2.03	2.15E-04	5.07E-03
cell proliferation (GO:0008283)	678	37	18.3	+	2.02	1.08E-04	2.83E-03
cellular response to chemical stimulus (GO:0070887)	2624	143	70.83	+	2.02	5.27E-16	1.02E-13

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cellular developmental process (GO:0048869)	3565	193	96.23	+	2.01	3.66E-22	1.38E-19
regulation of establishment of protein localization (GO:0070201)	830	45	22.4	+	2.01	1.94E-05	6.17E-04
positive regulation of molecular function (GO:0044093)	1761	95	47.54	+	2	2.54E-10	2.26E-08
positive regulation of response to stimulus (GO:0048584)	2187	118	59.04	+	2	8.75E-13	1.04E-10
regulation of neuron differentiation (GO:0045664)	538	29	14.52	+	2	7.20E-04	1.44E-02
response to nitrogen compound (GO:1901698)	998	54	26.94	+	2	2.58E-06	1.06E-04
hemopoiesis (GO:0030097)	520	28	14.04	+	1.99	9.53E-04	1.80E-02
regulated exocytosis (GO:0045055)	688	37	18.57	+	1.99	1.27E-04	3.25E-03
regulation of cellular component organization (GO:0051128)	2326	125	62.79	+	1.99	1.79E-13	2.33E-11
regulation of protein localization (GO:0032880)	1043	56	28.15	+	1.99	2.38E-06	9.92E-05
generation of neurons (GO:0048699)	1374	73	37.09	+	1.97	8.51E-08	4.66E-06
hematopoietic or lymphoid organ development (GO:0048534)	566	30	15.28	+	1.96	6.61E-04	1.34E-02
nervous system development (GO:0007399)	2206	117	59.55	+	1.96	3.13E-12	3.40E-10
regulation of cellular protein metabolic process (GO:0032268)	2533	134	68.37	+	1.96	6.50E-14	9.51E-12
response to bacterium (GO:0009617)	566	30	15.28	+	1.96	6.61E-04	1.34E-02
response to nutrient levels (GO:0031667)	453	24	12.23	+	1.96	3.23E-03	4.77E-02
cell-cell signaling (GO:0007267)	1142	60	30.83	+	1.95	1.71E-06	7.37E-05
regulation of catalytic activity (GO:0050790)	2317	122	62.54	+	1.95	1.98E-12	2.20E-10
regulation of secretion (GO:0051046)	725	38	19.57	+	1.94	1.84E-04	4.44E-03
positive regulation of macromolecule biosynthetic process (GO:0010557)	1687	88	45.54	+	1.93	6.26E-09	4.39E-07
exocytosis (GO:0006887)	772	40	20.84	+	1.92	1.81E-04	4.39E-03
positive regulation of catalytic activity (GO:0043085)	1436	74	38.76	+	1.91	2.48E-07	1.25E-05
negative regulation of cellular process (GO:0048523)	4454	228	120.23	+	1.9	8.24E-24	4.57E-21
positive regulation of cellular component biogenesis (GO:0044089)	488	25	13.17	+	1.9	3.04E-03	4.55E-02
regulation of cellular component biogenesis (GO:0044087)	858	44	23.16	+	1.9	1.04E-04	2.74E-03
response to other organism (GO:0051707)	839	43	22.65	+	1.9	9.60E-05	2.54E-03

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 stress (GO:0006950)	3358	172	90.64	+	1.9	5.94E-17	1.28E-14
regulation of molecular function (GO:0065009)	3391	173	91.54	+	1.89	5.36E-17	1.17E-14
response to biotic stimulus (GO:0009607)	881	45	23.78	+	1.89	8.28E-05	2.22E-03
response to external biotic stimulus (GO:0043207)	841	43	22.7	+	1.89	1.39E-04	3.50E-03
negative regulation of cellular component organization (GO:0051129)	610	31	16.47	+	1.88	1.48E-03	2.56E-02
regulation of cellular response to stress (GO:0080135)	631	32	17.03	+	1.88	1.15E-03	2.09E-02
regulation of protein metabolic process (GO:0051246)	2778	141	74.99	+	1.88	2.40E-13	3.00E-11
regulation of secretion by cell (GO:1903530)	670	34	18.09	+	1.88	6.89E-04	1.39E-02
regulation of response to stimulus (GO:0048583)	4078	206	110.08	+	1.87	2.67E-20	8.28E-18
immune system development (GO:0002520)	598	30	16.14	+	1.86	2.06E-03	3.35E-02
positive regulation of cellular metabolic process (GO:0031325)	3051	153	82.36	+	1.86	3.38E-14	5.13E-12
positive regulation of macromolecule metabolic process (GO:0010604)	3034	152	81.9	+	1.86	4.68E-14	6.98E-12
regulation of leukocyte activation (GO:0002694)	538	27	14.52	+	1.86	2.99E-03	4.49E-02
reproduction (GO:0000003)	1372	69	37.04	+	1.86	1.36E-06	5.94E-05
reproductive process (GO:0022414)	1371	69	37.01	+	1.86	1.34E-06	5.89E-05
myeloid leukocyte activation (GO:0002274)	564	28	15.22	+	1.84	2.59E-03	3.99E-02
positive regulation of cellular process (GO:0048522)	4978	247	134.37	+	1.84	1.57E-24	9.01E-22
positive regulation of metabolic process (GO:0009893)	3268	162	88.22	+	1.84	1.10E-14	1.76E-12
positive regulation of nitrogen compound metabolic process (GO:0051173)	2940	146	79.36	+	1.84	3.68E-13	4.49E-11
multicellular organismal process (GO:0032501)	6688	331	180.53	+	1.83	2.31E-37	5.11E-34
positive regulation of transcription by RNA polymerase II (GO:0045944)	1114	55	30.07	+	1.83	2.92E-05	8.84E-04
leukocyte activation (GO:0045321)	873	43	23.57	+	1.82	2.81E-04	6.41E-03
negative regulation of biological process (GO:0048519)	4952	243	133.67	+	1.82	2.95E-23	1.53E-20
positive regulation of biosynthetic process (GO:0009891)	1831	90	49.43	+	1.82	5.67E-08	3.22E-06
regulation of cellular localization (GO:0060341)	877	43	23.67	+	1.82	2.92E-04	6.64E-03
regulation of response to stress (GO:0080134)	1442	71	38.92	+	1.82	2.35E-06	9.81E-05

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
cellular response to hormone stimulus (GO:0032870)	598	29	16.14	+	1.8	3.27E-03	4.83E-02
positive regulation of biological process (GO:0048518)	5607	273	151.35	+	1.8	8.36E-27	6.48E-24
regulation of proteolysis (GO:0030162)	843	41	22.76	+	1.8	5.10E-04	1.08E-02
positive regulation of cellular biosynthetic process (GO:0031328)	1804	87	48.7	+	1.79	2.38E-07	1.21E-05
defense response (GO:0006952)	1255	60	33.88	+	1.77	3.55E-05	1.04E-03
positive regulation of gene expression (GO:0010628)	1818	87	49.07	+	1.77	3.80E-07	1.87E-05
positive regulation of nucleic acid-templated transcription (GO:1903508)	1433	68	38.68	+	1.76	1.13E-05	3.90E-04
positive regulation of RNA biosynthetic process (GO:1902680)	1434	68	38.71	+	1.76	1.14E-05	3.92E-04
positive regulation of transcription, DNA-templated (GO:0045893)	1433	68	38.68	+	1.76	1.13E-05	3.89E-04
response to chemical (GO:0042221)	4164	197	112.4	+	1.75	3.30E-16	6.47E-14
multicellular organismal reproductive process (GO:0048609)	809	38	21.84	+	1.74	1.36E-03	2.39E-02
plasma membrane bounded cell projection organization (GO:0120036)	1021	48	27.56	+	1.74	3.63E-04	7.97E-03
regulation of transport (GO:0051049)	1849	87	49.91	+	1.74	7.02E-07	3.25E-05
cell projection organization (GO:0030030)	1050	49	28.34	+	1.73	3.07E-04	6.93E-03
intracellular signal transduction (GO:0035556)	1605	75	43.32	+	1.73	7.13E-06	2.61E-04
regulation of biological quality (GO:0065008)	3628	168	97.93	+	1.72	1.08E-12	1.25E-10
multicellular organism reproduction (GO:0032504)	821	38	22.16	+	1.71	2.08E-03	3.38E-02
positive regulation of RNA metabolic process (GO:0051254)	1504	69	40.6	+	1.7	2.61E-05	7.96E-04
system process (GO:0003008)	1852	85	49.99	+	1.7	2.34E-06	9.81E-05
cellular response to stress (GO:0033554)	1599	73	43.16	+	1.69	2.09E-05	6.56E-04
negative regulation of cellular metabolic process (GO:0031324)	2516	115	67.92	+	1.69	3.52E-08	2.08E-06
negative regulation of macromolecule metabolic process (GO:0010605)	2546	116	68.73	+	1.69	2.92E-08	1.76E-06
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	1744	79	47.08	+	1.68	1.09E-05	3.82E-04
negative regulation of nitrogen compound metabolic process (GO:0051172)	2347	106	63.35	+	1.67	2.02E-07	1.04E-05

Continued

Supplementary Table SVII **Continued**

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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 immune system process (GO:0002682)	1531	69	41.33	+	1.67	4.41E-05	1.28E-03
immune system process (GO:0002376)	2575	115	69.51	+	1.65	1.01E-07	5.50E-06
negative regulation of metabolic process (GO:0009892)	2795	124	75.45	+	1.64	3.52E-08	2.08E-06
positive regulation of immune system process (GO:0002684)	1037	46	27.99	+	1.64	1.67E-03	2.80E-02
cell communication (GO:0007154)	5447	229	147.03	+	1.56	1.78E-13	2.34E-11
multi-organism process (GO:0051704)	2348	98	63.38	+	1.55	2.11E-05	6.59E-04
signaling (GO:0023052)	5349	222	144.39	+	1.54	2.37E-12	2.58E-10
cellular component organization (GO:0016043)	5273	218	142.34	+	1.53	5.53E-12	5.75E-10
regulation of transcription by RNA polymerase II (GO:0006357)	1986	82	53.61	+	1.53	1.59E-04	3.95E-03
response to stimulus (GO:0050896)	8142	331	219.78	+	1.51	2.03E-20	6.43E-18
cellular response to stimulus (GO:0051716)	6423	259	173.38	+	1.49	1.15E-13	1.57E-11
signal transduction (GO:0007165)	4956	199	133.78	+	1.49	1.25E-09	9.97E-08
cellular component organization or biogenesis (GO:0071840)	5498	218	148.41	+	1.47	3.84E-10	3.31E-08
regulation of cellular metabolic process (GO:0031323)	6187	230	167.01	+	1.38	2.71E-08	1.64E-06
regulation of macromolecule metabolic process (GO:0060255)	6151	229	166.04	+	1.38	3.26E-08	1.94E-06
regulation of nitrogen compound metabolic process (GO:0051171)	5958	219	160.83	+	1.36	2.06E-07	1.06E-05
regulation of primary metabolic process (GO:0080090)	6124	225	165.31	+	1.36	1.51E-07	8.01E-06
localization (GO:0051179)	5436	196	146.74	+	1.34	6.26E-06	2.33E-04
regulation of metabolic process (GO:0019222)	6672	242	180.1	+	1.34	8.53E-08	4.66E-06
regulation of biological process (GO:0050789)	11425	407	308.4	+	1.32	6.18E-17	1.31E-14
biological regulation (GO:0065007)	12072	428	325.87	+	1.31	1.46E-18	3.65E-16
regulation of cellular process (GO:0050794)	10764	382	290.56	+	1.31	2.29E-14	3.55E-12
regulation of macromolecule biosynthetic process (GO:0010556)	4221	146	113.94	+	1.28	1.23E-03	2.21E-02
cellular process (GO:0009987)	15084	492	407.17	+	1.21	7.24E-17	1.50E-14
biological_process (GO:0008150)	17500	542	472.39	+	1.15	8.11E-19	2.06E-16
detection of chemical stimulus involved in sensory perception of smell (GO:0050911)	429	0	11.58	-	< 0.01	2.05E-05	6.46E-04

Continued

Supplementary Table SVII Continued

GO biological process complete	Homo sapiens - REFLIST (21042)	Client Text Box Input (568)	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)
mRNA splicing, via spliceosome (GO:0000398)	285	0	7.69	-	< 0.01	1.06E-03	1.97E-02
ribonucleoprotein complex biogenesis (GO:0022613)	468	0	12.63	-	< 0.01	6.07E-06	2.26E-04
ribosome biogenesis (GO:0042254)	334	0	9.02	-	< 0.01	2.10E-04	4.98E-03
RNA splicing, via transesterification reactions (GO:0000375)	288	0	7.77	-	< 0.01	1.10E-03	2.02E-02
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377)	285	0	7.69	-	< 0.01	1.06E-03	1.96E-02
rRNA processing (GO:0006364)	261	0	7.05	-	< 0.01	1.50E-03	2.58E-02
sensory perception of smell (GO:0007608)	458	0	12.36	-	< 0.01	9.32E-06	3.36E-04
establishment of localization in cell (GO:0051649)	1494	22	40.33	-	0.55	1.97E-03	3.23E-02
intracellular transport (GO:0046907)	1265	18	34.15	-	0.53	2.90E-03	4.38E-02
cellular macromolecular complex assembly (GO:0034622)	815	9	22	-	0.41	2.59E-03	4.00E-02
intracellular protein transport (GO:0006886)	744	7	20.08	-	0.35	1.53E-03	2.63E-02
RNA processing (GO:0006396)	897	7	24.21	-	0.29	7.03E-05	1.93E-03
Unclassified (UNCLASSIFIED)	3542	26	95.61	-	0.27	8.11E-19	2.10E-16
detection of chemical stimulus involved in sensory perception (GO:0050907)	472	3	12.74	-	0.24	3.18E-03	4.71E-02
mRNA processing (GO:0006397)	465	3	12.55	-	0.24	3.05E-03	4.55E-02
mRNA metabolic process (GO:0016071)	680	4	18.36	-	0.22	1.30E-04	3.32E-03
sensory perception of chemical stimulus (GO:0007606)	533	3	14.39	-	0.21	8.35E-04	1.63E-02
ncRNA processing (GO:0034470)	405	2	10.93	-	0.18	2.55E-03	3.99E-02
peptide biosynthetic process (GO:0043043)	410	2	11.07	-	0.18	2.61E-03	4.01E-02
cilium assembly (GO:0060271)	328	1	8.85	-	0.11	2.68E-03	4.11E-02
cilium organization (GO:0044782)	341	1	9.2	-	0.11	1.85E-03	3.08E-02
translation (GO:0006412)	383	1	10.34	-	0.1	9.56E-04	1.80E-02