Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
1	20.43	8.64E-22	3.70E-21	SP_PIR_KEYWORDS	Transcription regulation	216	13.4%	1.06E-24	9.18E-22	4.59E-22	1.64E-21	3.80
				GOTERM_BP_ALL	GO:0006355~regulation of transcription, DNA-dependent	308	19.1%	1.76E-23	9.15E-20	1.14E-20	3.37E-20	3.19
				GOTERM_BP_ALL	GO:0006351~transcription, DNA-dependent	308	19.1%	1.12E-22	5.80E-19	5.28E-20	2.14E-19	3.17
				GOTERM_BP_ALL	GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	321	19.9%	1.43E-22	7.42E-19	6.18E-20	2.73E-19	3.05
				SP_PIR_KEYWORDS	Transcription	213	13.2%	1.50E-22	1.30E-19	4.35E-20	2.33E-19	3.63
				GOTERM_BP_ALL	GO:0032774~RNA biosynthetic process	308	19.1%	1.61E-22	8.35E-19	6.42E-20	3.07E-19	3.17
				GOTERM_MF_ALL	GO:0030528~transcription regulator activity	208	12.9%	1.82E-22	4.92E-19	1.64E-19	3.24E-19	3.89
				GOTERM_BP_ALL	GO:0045449~regulation of transcription	314	19.5%	8.64E-22	4.49E-18	2.80E-19	1.65E-18	3.11
				GOTERM_BP_ALL	GO:0006350~transcription	318	19.7%	1.08E-20	5.61E-17	2.95E-18	2.06E-17	3.06
				GOTERM_MF_ALL	GO:0003677~DNA binding	278	17.3%	7.11E-19	1.92E-15	4.81E-16	1.27E-15	3.26
				SP_PIR_KEYWORDS	dna-binding	204	12.7%	8.89E-18	7.70E-15	1.93E-15	1.38E-14	3.75
				GOTERM_MF_ALL	GO:0003700~transcription factor activity	151	9.4%	2.23E-16	6.01E-13	1.20E-13	4.00E-13	4.38
2	16.11	2.87E-14	7.82E-17	GOTERM_BP_ALL	GO:0048856~anatomical structure development	292	18.1%	2.91E-23	1.51E-19	1.68E-20	5.57E-20	3.20
				GOTERM_BP_ALL	GO:0007275~multicellular organismal development	313	19.4%	4.93E-23	2.56E-19	2.56E-20	9.42E-20	3.06
				GOTERM_BP_ALL	GO:0048731~system development	257	15.9%	2.17E-22	1.13E-18	8.06E-20	4.15E-19	3.41
				GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	194	12.0%	1.06E-21	5.48E-18	3.22E-19	2.02E-18	3.92
				GOTERM_BP_ALL	GO:0007399~nervous system development	121	7.5%	8.82E-17	5.76E-13	2.51E-14	2.11E-13	4.76
				GOTERM_BP_ALL	GO:0048869~cellular developmental process	240	14.9%	5.74E-14	2.98E-10	1.03E-11	1.10E-10	3.17
				GOTERM_BP_ALL	GO:0030154~cell differentiation	240	14.9%	5.74E-14	2.98E-10	1.03E-11	1.10E-10	3.32
				GOTERM_BP_ALL	GO:0009887~organ morphogenesis	97	6.0%	5.76E-14	2.99E-10	9.97E-12	1.10E-10	4.77
				GOTERM_BP_ALL	GO:0048513~organ development	194	12.0%	2.25E-13	1.17E-09	3.66E-11	4.31E-10	3.68
				GOTERM_BP_ALL	GO:0048468~cell development	173	10.7%	7.73E-13	4.02E-09	1.15E-10	1.48E-09	3.91
3	9.66	2.94E-10	2.21E-10	GOTERM_BP_ALL	GO:0048522~positive regulation of cellular process	143	8.9%	5.07E-15	2.65E-11	1.02E-12	9.76E-12	4.26
				GOTERM_BP_ALL	GO:0048518~positive regulation of biological process	150	9.3%	1.26E-12	6.55E-09	1.77E-10	2.41E-09	4.11
				GOTERM_BP_ALL	GO:0045941~positive regulation of transcription	68	4.2%	6.39E-12	3.32E-08	8.29E-10	1.22E-08	5.76
				GOTERM_BP_ALL	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	68	4.2%	1.93E-11	1.00E-07	2.39E-09	3.69E-08	5.71
				GOTERM_BP_ALL	GO:0006366~transcription from RNA polymerase II promoter	80	5.0%	2.69E-10	1.40E-06	3.04E-08	5.15E-07	5.30
				GOTERM_BP_ALL	GO:0006357~regulation of transcription from RNA polymerase II promoter	74	4.6%	2.94E-10	1.52E-06	3.18E-08	5.61E-07	5.45
				GOTERM_BP_ALL	GO:0031325~positive regulation of cellular metabolic process	75	4.7%	3.99E-10	2.07E-06	4.23E-08	7.62E-07	5.35
				GOTERM_BP_ALL	GO:0009893~positive regulation of metabolic process	77	4.8%	1.07E-09	5.57E-06	1.07E-07	2.05E-06	5.30
				GOTERM_BP_ALL	GO:0045893~positive regulation of transcription, DNA-dependent	54	3.4%	5.60E-09	2.91E-05	5.19E-07	1.07E-05	6.04
				GOTERM_BP_ALL	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	45	2.8%	1.48E-08	7.69E-05	1.35E-06	2.83E-05	6.40
				GOTERM_MF_ALL	GO:0016563~transcription activator activity	37	2.3%	2.77E-05	0.072	0.005	0.049	6.43
4	7.75	2.84E-07	1.79E-08	GOTERM_BP_ALL	GO:0022008~neurogenesis	76	4.7%	1.86E-13	9.67E-10	3.12E-11	3.56E-10	5.52
				GOTERM_BP_ALL	GO:0048699~generation of neurons	71	4.4%	7.76E-13	4.03E-09	1.12E-10	1.48E-09	5.60
				GOTERM_BP_ALL	GO:0030182~neuron differentiation	65	4.0%	1.37E-12	7.11E-09	1.87E-10	2.62E-09	5.77
				GOTERM_BP_ALL	GO:0032989~cellular structure morphogenesis	89	5.5%	1.07E-10	5.56E-07	1.26E-08	2.05E-07	5.04
				GOTERM_BP_ALL	GO:0000902~cell morphogenesis	89	5.5%	1.07E-10	5.56E-07	1.26E-08	2.05E-07	5.13
				GOTERM_BP_ALL	GO:0048666~neuron development	51	3.2%	5.81E-10	3.02E-06	6.04E-08	1.11E-06	6.21
				GOTERM_BP_ALL	GO:0016477~cell migration	59	3.7%	6.92E-10	3.59E-06	7.05E-08	1.32E-06	5.99
				GOTERM_BP_ALL	GO:0006928~cell motility	65	4.0%	3.81E-09	1.98E-05	3.74E-07	7.29E-06	5.72
				GOTERM_BP_ALL	GO:0051674~localization of cell	65	4.0%	3.81E-09	1.98E-05	3.74E-07	7.29E-06	5.72
				GOTERM_BP_ALL	GO:0031175~neurite development	41	2.5%	5.64E-07	0.003	4.37E-05	0.001	6.53
				GOTERM_BP_ALL	GO:0032990~cell part morphogenesis	51	3.2%	7.54E-07	0.004	5.60E-05	0.001	5.94
				GOTERM_BP_ALL	GO:0048858~cell projection morphogenesis	51	3.2%	7.54E-07	0.004	5.60E-05	0.001	5.98
				GOTERM_BP_ALL	GO:0030030~cell projection organization and biogenesis	51	3.2%	7.54E-07	0.004	5.60E-05	0.001	5.98
				GOTERM_BP_ALL	GO:0007411~axon guidance	22	1.4%	6.27E-06	0.032	3.87E-04	0.012	7.89
				GOTERM_BP_ALL	GO:0007409~axonogenesis	32	2.0%	1.89E-05	0.094	0.001	0.036	6.87
				GOTERM_BP_ALL	GO:0000904~cellular morphogenesis during differentiation	36	2.2%	2.22E-05	0.109	0.001	0.042	6.54
				GOTERM_BP_ALL	GO:0048812~neurite morphogenesis	32	2.0%	6.62E-05	0.291	0.003	0.126	6.77
				GOTERM_BP_ALL	GO:0048667~neuron morphogenesis during differentiation	32	2.0%	6.62E-05	0.291	0.003	0.126	6.77

The DAVID Functional Annotation tool identified 64 functional groups enriched in WT1 bound genes. Geometric means for each functional group were negative log-transformed to generate an enrichment score which ranks each functional group by overall importance (enrichment). The absolute (count) and relative frequency (% of total) of each term within a given functional group is given, together with its associated *P*-Value and information content. Multiple testing correction techniques were applied to control family-wise error rate (Bonferroni) and false discovery rate (FDR) (Benjamini-Hochberg).

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Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
5	7.23	1.14E-06	5.92E-08	GOTERM_BP_ALL	GO:0048519~negative regulation of biological process	160	9.9%	9.78E-16	5.19E-12	2.08E-13	1.91E-12	4.08
				GOTERM_BP_ALL	GO:0048523~negative regulation of cellular process	150	9.3%	7.88E-15	4.09E-11	1.52E-12	1.51E-11	4.20
				GOTERM_BP_ALL	GO:0016481~negative regulation of transcription	49	3.0%	8.14E-07	0.004	5.87E-05	0.002	6.00
				GOTERM_BP_ALL	GO:0031324~negative regulation of cellular metabolic process	57	3.5%	1.00E-06	0.005	7.11E-05	0.002	5.51
				GOTERM_BP_ALL	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	51	3.2%	1.14E-06	0.006	7.99E-05	0.002	5.90
				GOTERM_BP_ALL	GO:0009892~negative regulation of metabolic process	62	3.9%	1.33E-06	0.007	9.21E-05	0.003	5.41
				GOTERM_MF_ALL	GO:0016564~transcription repressor activity	33	2.1%	9.54E-06	0.025	0.003	0.017	6.72
				GOTERM_BP_ALL	GO:0045892~negative regulation of transcription, DNA-dependent	36	2.2%	4.59E-05	0.212	0.002	0.088	6.43
				GOTERM_BP_ALL	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	24	1.5%	0.002	1	0.069	3.999	6.93
6	7.14	1.28E-07	7.17E-08	GOTERM_BP_ALL	GO:0050793~regulation of developmental process	57	3.5%	4.03E-09	2.09E-05	3.81E-07	7.70E-06	4.53
				GOTERM_BP_ALL	GO:0045596~negative regulation of cell differentiation	26	1.6%	8.97E-08	4.65E-04	7.76E-06	1.71E-04	7.35
				GOTERM_BP_ALL	GO:0045595~regulation of cell differentiation	38	2.4%	1.66E-07	8.59E-04	1.36E-05	3.16E-04	6.16
				GOTERM_BP_ALL	GO:0051093~negative regulation of developmental process	28	1.7%	4.42E-07	0.002	3.48E-05	8.44E-04	5.80
7	5.49	1.92E-05	3.25E-06	GOTERM_BP_ALL	GO:0000074~regulation of progression through cell cycle	62	3.9%	1.14E-07	5.91E-04	9.69E-06	2.17E-04	5.64
				GOTERM_BP_ALL	GO:0051726~regulation of cell cycle	62	3.9%	1.49E-07	7.74E-04	1.25E-05	2.85E-04	5.64
				GOTERM_BP_ALL	GO:0007049~cell cycle	94	5.8%	1.92E-05	0.095	0.001	0.037	4.66
				GOTERM_BP_ALL	GO:0022402~cell cycle process	79	4.9%	2.28E-05	0.112	0.001	0.044	5.00
				GOTERM_BP_ALL	GO:0045786~negative regulation of progression through cell cycle	27	1.7%	4.90E-05	0.225	0.003	0.094	7.00
8	4.90	1.77E-05	1.25E-05	SP_PIR_KEYWORDS	zinc	198	12.3%	1.27E-06	0.001	1.00E-04	0.002	3.54
				GOTERM_MF_ALL	GO:0008270~zinc ion binding	227	14.1%	1.68E-06	0.005	5.05E-04	0.003	3.33
				SP_PIR_KEYWORDS	zinc-finger	156	9.7%	2.31E-05	0.020	0.002	0.036	3.96
				SP_PIR_KEYWORDS	metal-binding	243	15.1%	1.39E-04	0.114	0.008	0.216	3.10
9	4.84	1.38E-04	1.46E-05	GOTERM_MF_ALL	GO:0043565~sequence-specific DNA binding	87	5.4%	1.21E-11	3.26E-08	5.44E-09	2.15E-08	5.28
				INTERPRO	IPR012287:Homeodomain-related	34	2.1%	2.68E-05	0.145	0.145	0.052	6.52
				INTERPRO	IPR001356:Homeobox	34	2.1%	1.24E-04	0.516	0.305	0.239	6.51
				SP_PIR_KEYWORDS	Homeobox	41	2.5%	1.52E-04	0.124	0.008	0.236	6.24
				UP_SEQ_FEATURE	DNA-binding region:Homeobox	31	1.9%	5.28E-04	1	0.670	1.113	6.70
				SMART	SM00389:HOX	37	2.3%	0.003	0.842	0.842	4.404	6.39
10	4.53	9.09E-06	2.95E-05	GOTERM_BP_ALL	GO:0030029~actin filament-based process	38	2.4%	4.97E-06	0.025	3.19E-04	0.010	6.50
				GOTERM_BP_ALL	GO:0030036~actin cytoskeleton organization and biogenesis	36	2.2%	9.09E-06	0.046	5.42E-04	0.017	6.57
				GOTERM_BP_ALL	GO:0007010~cytoskeleton organization and biogenesis	67	4.2%	5.70E-04	0.948	0.022	1.083	5.29
11	4.33	8.05E-05	4.64E-05	GOTERM_BP_ALL	GO:0007389~pattern specification process	44	2.7%	7.27E-07	0.004	5.55E-05	0.001	6.31
				GOTERM_BP_ALL	GO:0003002~regionalization	28	1.7%	8.05E-05	0.342	0.004	0.154	6.96
				GOTERM_BP_ALL	GO:0009952~anterior/posterior pattern formation	18	1.1%	0.002	1	0.060	3.213	7.63
12	4.06	7.18E-05	8.66E-05	GOTERM_BP_ALL	GO:0001501~skeletal development	35	2.2%	8.13E-06	0.041	4.91E-04	0.016	6.63
				GOTERM_BP_ALL	GO:0046849~bone remodeling	23	1.4%	2.95E-05	0.142	0.002	0.056	7.40
				GOTERM_BP_ALL	GO:0001503~ossification	21	1.3%	6.14E-05	0.273	0.003	0.117	7.55
				GOTERM_BP_ALL	GO:0031214~biomineral formation	21	1.3%	7.18E-05	0.311	0.004	0.137	7.52
				GOTERM_BP_ALL	GO:0009888~tissue development	45	2.8%	1.30E-04	0.491	0.006	0.248	5.06
				GOTERM_BP_ALL	GO:0048771~tissue remodeling	24	1.5%	1.47E-04	0.534	0.007	0.281	7.16
				GOTERM_BP_ALL	GO:0001649~osteoblast differentiation	9	0.6%	0.002	1	0.061	3.381	9.30
13	3.88	3.90E-05	1.31E-04	GOTERM_BP_ALL	GO:0030324~lung development	19	1.2%	2.99E-06	0.015	1.96E-04	0.006	8.13
				GOTERM_BP_ALL	GO:0030323~respiratory tube development	19	1.2%	3.80E-06	0.020	2.47E-04	0.007	8.11
				GOTERM_BP_ALL	GO:0035295~tube development	35	2.2%	3.90E-05	0.183	0.002	0.075	6.47
				GOTERM_BP_ALL	GO:0001763~morphogenesis of a branching structure	13	0.8%	0.008	1	0.179	13.737	8.02
				GOTERM_BP_ALL	GO:0048754~branching morphogenesis of a tube	12	0.7%	0.011	1	0.234	19.451	8.11
14	3.84	1.14E-04	1.46E-04	GOTERM_BP_ALL	GO:0008283~cell proliferation	71	4.4%	7.12E-05	0.309	0.004	0.136	5.09
				GOTERM_BP_ALL	GO:0042127~regulation of cell proliferation	53	3.3%	1.14E-04	0.446	0.005	0.217	5.63
				GOTERM_BP_ALL	GO:0008284~positive regulation of cell proliferation	32	2.0%	3.86E-04	0.865	0.016	0.734	6.51
15	3.83	8.33E-05	1.48E-04	GOTERM_BP_ALL	GO:0007417~central nervous system development	41	2.5%	6.06E-05	0.270	0.003	0.116	6.26
				GOTERM_BP_ALL	GO:0007420~brain development	34	2.1%	8.33E-05	0.351	0.004	0.159	6.58
				GOTERM_BP_ALL	GO:0030900~forebrain development	20	1.2%	6.40E-04	0.964	0.025	1.217	7.52

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16	3.83	1.07E-04	1.48E-04	GOTERM_BP_ALL	GO:0009790~embryonic development	66	4.1%	7.97E-06	0.041	4.87E-04	0.015	5.40
				GOTERM_BP_ALL	GO:0048598~embryonic morphogenesis	35	2.2%	2.04E-05	0.101	0.001	0.039	6.32
				GOTERM_BP_ALL	GO:0021915~neural tube development	15	0.9%	8.25E-05	0.348	0.004	0.157	8.47
				GOTERM_BP_ALL	GO:0043009~chordate embryonic development	36	2.2%	1.32E-04	0.495	0.006	0.251	6.43
				GOTERM_BP_ALL	GO:0009792~embryonic development ending in birth or egg hatching	36	2.2%	1.73E-04	0.592	0.008	0.329	6.42
				GOTERM_BP_ALL	GO:0001701~in utero embryonic development	18	1.1%	0.035	1	0.463	48.883	7.25
17	3.72	0.002	1.92E-04	GOTERM_BP_ALL	GO:0006464~protein modification process	214	13.3%	2.24E-12	1.16E-08	2.98E-10	4.27E-09	3.50
				GOTERM_BP_ALL	GO:0043412~biopolymer modification	219	13.6%	6.87E-12	3.57E-08	8.70E-10	1.31E-08	3.45
				GOTERM_BP_ALL	GO:0043687~post-translational protein modification	188	11.7%	3.16E-11	1.64E-07	3.82E-09	6.04E-08	3.71
				GOTERM_BP_ALL	GO:0006468~protein amino acid phosphorylation	96	6.0%	3.54E-08	1.84E-04	3.16E-06	6.75E-05	4.83
				GOTERM_BP_ALL	GO:0006793~phosphorus metabolic process	120	7.4%	1.73E-07	8.98E-04	1.38E-05	3.30E-04	4.39
				GOTERM_BP_ALL	GO:0006796~phosphate metabolic process	120	7.4%	1.73E-07	8.98E-04	1.38E-05	3.30E-04	4.39
				GOTERM_BP_ALL	GO:0016310~phosphorylation	101	6.3%	1.71E-06	0.009	1.15E-04	0.003	4.65
				GOTERM_MF_ALL	GO:0016301~kinase activity	113	7.0%	3.36E-05	0.087	0.006	0.060	4.40
				GOTERM_MF_ALL	GO:0016773~phosphotransferase activity, alcohol group as acceptor	92	5.7%	7.24E-05	0.178	0.011	0.129	4.73
				GOTERM_MF_ALL	GO:0004672~protein kinase activity	80	5.0%	1.23E-04	0.283	0.017	0.219	4.97
				INTERPRO	IPR000719:Protein kinase, core	50	3.1%	1.58E-04	0.604	0.265	0.305	5.71
				SP_PIR_KEYWORDS	kinase	90	5.6%	7.23E-04	0.466	0.029	1.115	4.33
				GOTERM_MF_ALL	GO:0016772~transferase activity, transferring phosphorus-containing groups	119	7.4%	0.001	0.943	0.108	1.869	4.21
				GOTERM_MF_ALL	GO:0000166~nucleotide binding	207	12.8%	0.002	0.986	0.138	2.788	3.24
				GOTERM_MF_ALL	GO:0004674~protein serine/threonine kinase activity	62	3.9%	0.002	0.993	0.145	3.240	5.26
				GOTERM_MF_ALL	GO:0016740~transferase activity	191	11.9%	0.002	0.999	0.175	4.225	3.38
				GOTERM_MF_ALL	GO:0004713~protein-tyrosine kinase activity	42	2.6%	0.004	1.000	0.251	6.608	5.87
				UP_SEQ_FEATURE	domain:Protein kinase	54	3.4%	0.004	1	0.982	8.370	5.69
				SP_PIR_KEYWORDS	nucleotide-binding	144	8.9%	0.005	0.980	0.119	6.777	3.76
				GOTERM_MF_ALL	GO:0032553~ribonucleotide binding	173	10.7%	0.007	1	0.355	11.400	3.51
				GOTERM_MF_ALL	GO:0032555~purine ribonucleotide binding	173	10.7%	0.007	1	0.355	11.400	3.51
				UP_SEQ_FEATURE	binding site:ATP	56	3.5%	0.008	1	0.994	15.038	5.61
				SP_PIR_KEYWORDS	Serine/threonine-protein kinase	45	2.8%	0.017	1	0.282	22.923	5.73
				GOTERM_MF_ALL	GO:0032559~adenyl ribonucleotide binding	141	8.8%	0.018	1	0.539	27.459	3.82
				GOTERM_MF_ALL	GO:0017076~purine nucleotide binding	175	10.9%	0.018	1	0.542	28.048	3.45
				UP_SEQ_FEATURE	active site:Proton acceptor	67	4.2%	0.019	1	1.000	33.256	5.26
				SP_PIR_KEYWORDS	transferase	135	8.4%	0.024	1	0.333	31.413	3.69
				UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	80	5.0%	0.028	1	1.000	45.609	4.90
				INTERPRO	IPR002290:Serine/threonine protein kinase	27	1.7%	0.032	1	0.978	46.786	6.48
				INTERPRO	IPR008271:Serine/threonine protein kinase, active site	31	1.9%	0.038	1	0.979	52.671	6.21
				GOTERM_MF_ALL	GO:0005524~ATP binding	135	8.4%	0.046	1	0.766	56.466	3.84
				GOTERM_MF_ALL	GO:0030554~adenyl nucleotide binding	143	8.9%	0.047	1	0.770	57.269	3.75
				SP_PIR_KEYWORDS	atp-binding	105	6.5%	0.081	1	0.632	72.920	4.18
				SMART	SM00220:S_TKc	45	2.8%	0.108	1	0.923	81.616	5.69
18	3.38	5.64E-04	4.13E-04	SP_PIR_KEYWORDS	cytoskeleton	47	2.9%	1.01E-04	0.084	0.006	0.156	5.24
				GOTERM_MF_ALL	GO:0008092~cytoskeletal protein binding	55	3.4%	1.40E-04	0.316	0.018	0.249	5.58
				GOTERM_MF_ALL	GO:0003779~actin binding	39	2.4%	9.88E-04	0.931	0.105	1.745	6.08
				SP_PIR_KEYWORDS	actin-binding	28	1.7%	0.002	0.837	0.067	3.191	6.37
19	2.62	0.003	0.002	GOTERM_BP_ALL	GO:0048646~anatomical structure formation	34	2.1%	1.35E-04	0.505	0.006	0.259	5.99
				GOTERM_BP_ALL	GO:0001944~vasculature development	33	2.1%	0.002	1	0.063	3.568	6.27
				GOTERM_BP_ALL	GO:0001568~blood vessel development	32	2.0%	0.003	1	0.092	5.503	6.29
				GOTERM_BP_ALL	GO:0048514~blood vessel morphogenesis	28	1.7%	0.005	1	0.127	8.472	6.51
				GOTERM_BP_ALL	GO:0001525~angiogenesis	21	1.3%	0.024	1	0.365	36.690	6.85
20	2.55	0.004	0.003	GOTERM_BP_ALL	GO:0021915~neural tube development	15	0.9%	8.25E-05	0.348	0.004	0.157	8.47
				GOTERM_BP_ALL	GO:0035239~tube morphogenesis	25	1.6%	8.60E-04	0.989	0.032	1.630	6.93
				GOTERM_BP_ALL	GO:0001841~neural tube formation	11	0.7%	0.002	1	0.079	4.653	8.81
				GOTERM_BP_ALL	GO:0001839~neural plate morphogenesis	11	0.7%	0.003	1	0.092	5.527	8.77
				GOTERM_BP_ALL	GO:0001840~neural plate development	11	0.7%	0.004	1	0.105	6.521	8.77
				GOTERM_BP_ALL	GO:0001838~embryonic epithelial tube formation	11	0.7%	0.004	1	0.117	7.645	8.70
				GOTERM_BP_ALL	GO:0001843~neural tube closure	9	0.6%	0.005	1	0.137	9.611	9.25
				GOTERM_BP_ALL	GO:0002009~morphogenesis of an epithelium	19	1.2%	0.007	1	0.178	13.349	7.11

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
20	2.55	0.004	0.003	GOTERM_BP_ALL	GO:0014020~primary neural tube formation	9	0.6%	0.008	1	0.180	13.560	9.11
				GOTERM_BP_ALL	GO:0016331~morphogenesis of embryonic epithelium	12	0.7%	0.013	1	0.256	21.603	8.33
21	2.55	0.003	0.003	GOTERM_BP_ALL	GO:0016049~cell growth	24	1.5%	1.89E-04	0.625	0.008	0.360	7.18
				GOTERM_BP_ALL	GO:0008361~regulation of cell size	25	1.6%	3.35E-04	0.824	0.014	0.638	7.00
				GOTERM_BP_ALL	GO:0040007~growth	39	2.4%	0.002	1	0.060	3.261	6.07
				GOTERM_BP_ALL	GO:0001558~regulation of cell growth	18	1.1%	0.005	1	0.126	8.357	7.43
				GOTERM_BP_ALL	GO:0040008~regulation of growth	24	1.5%	0.018	1	0.319	29.928	6.68
				SP_PIR_KEYWORDS	growth regulation	8	0.5%	0.057	1	0.554	59.732	8.73
22	2.54	0.003	0.003	GOTERM_BP_ALL	GO:0014706~striated muscle development	25	1.6%	3.35E-04	0.824	0.014	0.638	7.07
				GOTERM_BP_ALL	GO:0007517~muscle development	29	1.8%	0.001	0.997	0.042	2.155	6.68
				GOTERM_BP_ALL	GO:0048747~muscle fiber development	15	0.9%	0.002	1	0.059	3.101	8.04
				GOTERM_BP_ALL	GO:0048741~skeletal muscle fiber development	15	0.9%	0.002	1	0.059	3.101	8.04
				GOTERM_BP_ALL	GO:0007519~skeletal muscle development	19	1.2%	0.003	1	0.081	4.841	7.43
				GOTERM_BP_ALL	GO:0045662~negative regulation of myoblast differentiation	4	0.3%	0.005	1	0.129	8.865	12.06
				GOTERM_BP_ALL	GO:0042692~muscle cell differentiation	14	0.9%	0.006	1	0.150	10.789	7.93
				GOTERM_BP_ALL	GO:0045661~regulation of myoblast differentiation	5	0.3%	0.009	1	0.203	16.330	11.06
				GOTERM_BP_ALL	GO:0045445~myoblast differentiation	9	0.6%	0.019	1	0.325	30.925	8.81
23	2.43	0.004	0.004	INTERPRO	IPR011700:Basic leucine zipper	8	0.5%	3.26E-04	0.852	0.380	0.629	9.77
				INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	12	0.7%	0.001	1	0.539	2.520	8.39
				UP_SEQ_FEATURE	domain:Leucine-zipper	19	1.2%	0.004	1	0.972	8.889	7.58
				SMART	SM00338:BRLZ	12	0.7%	0.012	1	0.828	15.773	8.31
				INTERPRO	IPR000837:Fos transforming protein	4	0.3%	0.031	1	0.977	45.489	10.77
24	2.39	0.002	0.004	GOTERM_BP_ALL	GO:0016568~chromatin modification	31	1.9%	1.43E-04	0.524	0.006	0.273	6.73
				GOTERM_BP_ALL	GO:0006323~DNA packaging	40	2.5%	8.08E-04	0.985	0.031	1.532	5.89
				SP_PIR_KEYWORDS	Chromatin regulator	20	1.2%	0.001	0.691	0.048	2.082	7.46
				GOTERM_BP_ALL	GO:0006325~establishment and/or maintenance of chromatin architecture	38	2.4%	0.002	1	0.061	3.353	6.04
				GOTERM_BP_ALL	GO:0006259~DNA metabolic process	66	4.1%	0.113	1	0.786	89.812	4.81
				GOTERM_BP_ALL	GO:0051276~chromosome organization and biogenesis	40	2.5%	0.156	1	0.862	96.047	5.69
25	2.28	0.007	0.005	GOTERM_BP_ALL	GO:0012501~programmed cell death	84	5.2%	3.61E-04	0.846	0.015	0.687	4.73
				GOTERM_BP_ALL	GO:0008219~cell death	86	5.3%	4.63E-04	0.910	0.019	0.882	4.68
				GOTERM_BP_ALL	GO:0043068~positive regulation of programmed cell death	33	2.1%	4.66E-04	0.911	0.019	0.887	6.47
				GOTERM_BP_ALL	GO:0016265~death	86	5.3%	5.04E-04	0.927	0.020	0.958	4.68
				GOTERM_BP_ALL	GO:0006915~apoptosis	82	5.1%	5.25E-04	0.935	0.021	0.999	4.76
				GOTERM_BP_ALL	GO:0043065~positive regulation of apoptosis	31	1.9%	0.002	1	0.057	2.954	6.49
				GOTERM_BP_ALL	GO:0006917~induction of apoptosis	24	1.5%	0.007	1	0.175	12.925	6.84
				GOTERM_BP_ALL	GO:0012502~induction of programmed cell death	24	1.5%	0.007	1	0.175	12.925	6.84
				SP_PIR_KEYWORDS	apoptosis	35	2.2%	0.009	1	0.200	13.723	5.76
				GOTERM_BP_ALL	GO:0043067~regulation of programmed cell death	54	3.4%	0.010	1	0.211	17.080	5.32
				GOTERM_BP_ALL	GO:0042981~regulation of apoptosis	53	3.3%	0.011	1	0.236	19.765	5.35
				GOTERM_BP_ALL	GO:0043066~negative regulation of apoptosis	22	1.4%	0.095	1	0.743	85.055	6.57
				GOTERM_BP_ALL	GO:0043069~negative regulation of programmed cell death	22	1.4%	0.107	1	0.776	88.474	6.54
				GOTERM_BP_ALL	GO:0006916~anti-apoptosis	9	0.6%	0.605	1	0.997	100	7.47
				SP_PIR_KEYWORDS	glycosyltransferase	29	1.8%	0.003	0.936	0.088	4.804	6.56
				GOTERM_BP_ALL	GO:0006486~protein amino acid glycosylation	16	1.0%	0.004	1	0.105	6.615	7.68
				GOTERM_BP_ALL	GO:0043413~biopolymer glycosylation	16	1.0%	0.005	1	0.132	9.152	7.63
				GOTERM_BP_ALL	GO:0009100~glycoprotein metabolic process	19	1.2%	0.006	1	0.156	11.295	6.96
				GOTERM_MF_ALL	GO:0016757~transferase activity, transferring glycosyl groups	32	2.0%	0.009	1	0.401	14.669	6.21
				GOTERM_BP_ALL	GO:0009101~glycoprotein biosynthetic process	16	1.0%	0.010	1	0.217	17.792	7.28
26	2.25	0.006	0.006	SP_PIR_KEYWORDS	glycosyltransferase	29	1.8%	0.003	0.936	0.088	4.804	6.5599
				GOTERM_BP_ALL	GO:0006486~protein amino acid glycosylation	16	1.0%	0.004	1	0.105	6.615	7.6846
				GOTERM_BP_ALL	GO:0043413~biopolymer glycosylation	16	1.0%	0.005	1	0.132	9.152	7.6333
				GOTERM_BP_ALL	GO:0009100~glycoprotein metabolic process	19	1.2%	0.006	1	0.156	11.295	6.9616
				GOTERM_MF_ALL	GO:0016757~transferase activity, transferring glycosyl groups	32	2.0%	0.009	1	0.401	14.669	6.2078
				GOTERM_BP_ALL	GO:0009101~glycoprotein biosynthetic process	16	1.0%	0.010	1	0.217	17.792	7.2782
27	2.20	0.005	0.006	GOTERM_BP_ALL	GO:0050673~epithelial cell proliferation	11	0.7%	2.79E-04	0.765	0.012	0.532	8.97
				GOTERM_BP_ALL	GO:0050678~regulation of epithelial cell proliferation	8	0.5%	0.005	1	0.132	9.212	9.30

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
27	2.20	0.005	0.006	GOTERM_BP_ALL	GO:0050679~positive regulation of epithelial cell proliferation	4	0.3%	0.179	1	0.884	97.698	9.81
28	2.15	0.018	0.007									
				SP_PIR_KEYWORDS	golgi apparatus	60	3.7%	1.57E-04	0.127	0.008	0.243	5.36
				GOTERM_MF_ALL	GO:0008194~UDP-glycosyltransferase activity	20	1.2%	5.09E-04	0.748	0.058	0.903	7.49
				SP_PIR_KEYWORDS	glycosyltransferase	29	1.8%	0.003	0.936	0.088	4.804	6.56
				GOTERM_MF_ALL	GO:0016757~transferase activity, transferring glycosyl groups	32	2.0%	0.009	1	0.401	14.669	6.21
				SP_PIR_KEYWORDS	Manganese	19	1.2%	0.018	1	0.299	24.901	7.23
				GOTERM_MF_ALL	GO:0016758~transferase activity, transferring hexosyl groups	22	1.4%	0.020	1	0.559	30.691	6.85
				SP_PIR_KEYWORDS	signal-anchor	42	2.6%	0.028	1	0.366	36.088	5.68
				UP_SEQ_FEATURE	topological domain:Lumenal	37	2.3%	0.035	1	1	53.440	6.09
				KEGG_PATHWAY	mmu01030:Glycan structures - biosynthesis 1	19	1.2%	0.054	1	0.314	50.292	7.40
29	2.14	0.012	0.007	INTERPRO	IPR011598:Helix-loop-helix DNA-binding	16	1.0%	0.001	0.997	0.631	1.952	7.73
				UP_SEQ_FEATURE	DNA-binding region:Basic motif	24	1.5%	0.001	1	0.862	3.087	7.22
				INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	16	1.0%	0.012	1	0.897	21.311	7.39
				SMART	SM00353:HLH	18	1.1%	0.031	1	0.798	37.377	7.31
				UP_SEQ_FEATURE	domain:Helix-loop-helix motif	15	0.9%	0.033	1	1	50.744	7.79
30	3.11	0.011	0.008	GOTERM_BP_ALL	GO:0045926~negative regulation of growth	11	0.7%	0.001	0.997	0.042	2.172	8.74
				GOTERM_BP_ALL	GO:0001558~regulation of cell growth	18	1.1%	0.005	1	0.126	8.357	7.43
				GOTERM_BP_ALL	GO:0030308~negative regulation of cell growth	7	0.4%	0.017	1	0.300	27.374	9.36
				GOTERM_BP_ALL	GO:0045792~negative regulation of cell size	7	0.4%	0.043	1	0.521	56.863	9.02
31	2.05	0.012	0.009	INTERPRO	IPR000504:RNA recognition motif, RNP-1	27	1.7%	0.001	0.998	0.536	2.007	6.87
				INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	27	1.7%	0.001	0.998	0.536	2.007	6.87
				SP_PIR_KEYWORDS	rna-binding	48	3.0%	0.012	1	0.236	17.522	5.58
				SMART	SM00360:RRM	29	1.8%	0.032	1	0.776	37.781	6.71
				GOTERM_MF_ALL	GO:0003723~RNA binding	60	3.7%	0.126	1	0.948	90.907	4.92
32	2.04	0.024	0.009	GOTERM_BP_ALL	GO:0048598~embryonic morphogenesis	35	2.2%	2.04E-05	0.101	0.001	0.039	6.32
				GOTERM_BP_ALL	GO:0030326~embryonic limb morphogenesis	12	0.7%	0.016	1	0.293	26.307	8.18
				GOTERM_BP_ALL	GO:0035113~embryonic appendage morphogenesis	12	0.7%	0.016	1	0.293	26.307	8.18
				GOTERM_BP_ALL	GO:0048736~appendage development	13	0.8%	0.024	1	0.372	37.682	7.99
				GOTERM_BP_ALL	GO:0060173~limb development	13	0.8%	0.024	1	0.372	37.682	7.99
				GOTERM_BP_ALL	GO:0035107~appendage morphogenesis	12	0.7%	0.041	1	0.513	55.386	8.06
				GOTERM_BP_ALL	GO:0035108~limb morphogenesis	12	0.7%	0.041	1	0.513	55.386	8.06
33	2.00	0.003	0.010	GOTERM_BP_ALL	GO:0048332~mesoderm morphogenesis	9	0.6%	0.002	1	0.061	3.381	9.42
				GOTERM_BP_ALL	GO:0001704~formation of primary germ layer	9	0.6%	0.002	1	0.061	3.381	9.42
				GOTERM_BP_ALL	GO:0007498~mesoderm development	12	0.7%	0.002	1	0.067	3.821	8.57
				GOTERM_BP_ALL	GO:0007369~gastrulation	13	0.8%	0.002	1	0.073	4.237	8.36
				GOTERM_BP_ALL	GO:0001707~mesoderm formation	8	0.5%	0.004	1	0.117	7.402	9.54
				GOTERM_BP_ALL	GO:0048729~tissue morphogenesis	13	0.8%	0.038	1	0.485	51.894	6.48
				GOTERM_BP_ALL	GO:0048340~paraxial mesoderm morphogenesis	3	0.2%	0.165	1	0.868	96.790	10.89
				GOTERM_BP_ALL	GO:0048339~paraxial mesoderm development	3	0.2%	0.258	1	0.935	99.664	10.60
34	2.00	0.010	0.010	GOTERM_BP_ALL	GO:0007423~sensory organ development	27	1.7%	0.006	1	0.156	11.316	6.70
				GOTERM_BP_ALL	GO:0042471~ear morphogenesis	12	0.7%	0.009	1	0.199	15.562	8.23
				GOTERM_BP_ALL	GO:0043583~ear development	14	0.9%	0.010	1	0.219	18.144	7.93
				GOTERM_BP_ALL	GO:0042472~inner ear morphogenesis	11	0.7%	0.013	1	0.258	22.038	8.39
				GOTERM_BP_ALL	GO:0048839~inner ear development	13	0.8%	0.014	1	0.265	22.946	8.06
35	2.00	0.003	0.010	GOTERM_BP_ALL	GO:0030334~regulation of cell migration	14	0.9%	0.002	1	0.056	2.918	8.13
				GOTERM_BP_ALL	GO:0051270~regulation of cell motility	15	0.9%	0.002	1	0.063	3.557	7.87
				GOTERM_BP_ALL	GO:0040011~locomotion	16	1.0%	0.003	1	0.097	5.904	5.49
				GOTERM_BP_ALL	GO:0040012~regulation of locomotion	15	0.9%	0.003	1	0.097	5.949	7.72
				GOTERM_BP_ALL	GO:0030335~positive regulation of cell migration	5	0.3%	0.045	1	0.537	58.666	9.89
				GOTERM_BP_ALL	GO:0051272~positive regulation of cell motility	5	0.3%	0.088	1	0.719	82.730	9.60
				GOTERM_BP_ALL	GO:0040017~positive regulation of locomotion	5	0.3%	0.088	1	0.719	82.730	9.20
36	1.95	0.009	0.011	GOTERM_BP_ALL	GO:0048546~digestive tract morphogenesis	7	0.4%	5.07E-04	0.928	0.020	0.964	10.36
				GOTERM_BP_ALL	GO:0048557~embryonic digestive tract morphogenesis	5	0.3%	0.004	1	0.115	7.462	10.74
				GOTERM_BP_ALL	GO:0048565~gut development	7	0.4%	0.004	1	0.120	7.841	9.89
				GOTERM_BP_ALL	GO:0048568~embryonic organ development	10	0.6%	0.004	1	0.121	7.978	8.93

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
36	1.95	0.009	0.011	GOTERM_BP_ALL	GO:0048562~embryonic organ morphogenesis	7	0.4%	0.007	1	0.174	12.773	9.60
				GOTERM_BP_ALL	GO:0048567~ectodermal gut morphogenesis	5	0.3%	0.009	1	0.203	16.330	10.89
				GOTERM_BP_ALL	GO:0007439~ectodermal gut development	5	0.3%	0.009	1	0.203	16.330	10.89
				GOTERM_BP_ALL	GO:0048547~gut morphogenesis	5	0.3%	0.013	1	0.258	22.181	10.60
				GOTERM_BP_ALL	GO:0048566~embryonic gut development	5	0.3%	0.018	1	0.312	28.816	10.36
				GOTERM_BP_ALL	GO:0048558~embryonic gut morphogenesis	4	0.3%	0.023	1	0.358	35.267	10.89
				GOTERM_BP_ALL	GO:0007440~foregut morphogenesis	3	0.2%	0.057	1	0.603	67.308	11.74
				GOTERM_BP_ALL	GO:0048613~embryonic ectodermal gut morphogenesis	3	0.2%	0.081	1	0.704	79.966	11.47
				GOTERM_BP_ALL	GO:0048611~embryonic ectodermal gut development	3	0.2%	0.081	1	0.704	79.966	11.47
37	1.86	0.015	0.014	GOTERM_BP_ALL	GO:0022610~biological adhesion	76	4.7%	0.005	1	0.128	8.626	4.89
				GOTERM_BP_ALL	GO:0007155~cell adhesion	76	4.7%	0.005	1	0.128	8.626	4.89
				GOTERM_BP_ALL	GO:0016337~cell-cell adhesion	32	2.0%	0.026	1	0.385	39.221	6.27
				SP_PIR_KEYWORDS	cell adhesion	39	2.4%	0.064	1	0.573	63.923	5.71
38	1.79	0.013	0.016	INTERPRO	IPR003659:Plexin/semaphorin/integrin	11	0.7%	0.003	1	0.637	5.199	8.88
				INTERPRO	IPR002165:Plexin	8	0.5%	0.009	1	0.886	15.757	9.51
				INTERPRO	IPR001627:Semaphorin/CD100 antigen	8	0.5%	0.011	1	0.893	18.657	9.45
				SMART	SM00423:PSI	11	0.7%	0.013	1	0.726	17.266	8.88
				UP_SEQ_FEATURE	domain:Sema	7	0.4%	0.029	1	1	46.201	9.84
				SMART	SM00630:Sema	8	0.5%	0.032	1	0.755	38.166	9.45
				PIR_SUPERFAMILY	PIRSF005526:semaphorin	4	0.3%	0.104	1	1	86.177	10.63
39	1.78	0.035	0.017	INTERPRO	IPR003619:MAD homology 1, Dwarfin-type	6	0.4%	0.003	1	0.636	4.880	10.39
				SMART	SM00523:DWA	6	0.4%	0.007	0.983	0.871	9.505	10.39
				INTERPRO	IPR000647:CTF/NF-I	3	0.2%	0.035	1	0.978	50.147	11.51
				PIR_SUPERFAMILY	PIRSF018476:nuclear factor 1	3	0.2%	0.037	1	1	49.151	11.51
				UP_SEQ_FEATURE	DNA-binding region:CTF/NF-I	3	0.2%	0.058	1	1	71.818	11.77
40	1.76	0.016	0.017	INTERPRO	IPR000697:EVH1	5	0.3%	0.013	1	0.895	21.721	10.39
				UP_SEQ_FEATURE	domain:WH1	5	0.3%	0.016	1	1	28.187	10.51
				SMART	SM00461:WH1	5	0.3%	0.027	1	0.869	32.789	10.39
41	1.75	0.024	0.018	GOTERM_BP_ALL	GO:0007267~cell-cell signaling	56	3.5%	1.29E-05	0.065	0.001	0.025	5.65
				GOTERM_BP_ALL	GO:0019226~transmission of nerve impulse	34	2.1%	0.006	1	0.143	10.140	6.20
				GOTERM_BP_ALL	GO:0007268~synaptic transmission	27	1.7%	0.024	1	0.366	36.905	6.47
				GOTERM_BP_ALL	GO:0050877~neurological system process	47	2.9%	1	1	1	100	3.61
				GOTERM_BP_ALL	GO:0003008~system process	56	3.5%	1	1	1	100	3.48
42	1.75	0.016	0.018	GOTERM_MF_ALL	GO:0019901~protein kinase binding	13	0.8%	0.015	1	0.506	23.923	8.13
				GOTERM_MF_ALL	GO:0019900~kinase binding	14	0.9%	0.016	1	0.513	24.698	7.95
				GOTERM_MF_ALL	GO:0019899~enzyme binding	28	1.7%	0.023	1	0.580	34.051	6.46
43	1.73	0.037	0.019	GOTERM_BP_ALL	GO:0007369~gastrulation	13	0.8%	0.002	1	0.073	4.237	8.36
				GOTERM_BP_ALL	GO:0010003~gastrulation (sensu Mammalia)	6	0.4%	0.016	1	0.294	26.762	9.47
				GOTERM_BP_ALL	GO:0048276~gastrulation (sensu Vertebrata)	6	0.4%	0.057	1	0.599	67.392	9.47
				GOTERM_BP_ALL	GO:0001702~gastrulation with mouth forming second	6	0.4%	0.057	1	0.599	67.392	9.47
44	1.73	0.017	0.019	GOTERM_MF_ALL	GO:0008194~UDP-glycosyltransferase activity	20	1.2%	5.09E-04	0.748	0.058	0.903	7.49
				GOTERM_MF_ALL	GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity	7	0.4%	0.001	0.959	0.116	2.083	10.25
				GOTERM_MF_ALL	GO:0008376~acetylgalactosaminyltransferase activity	9	0.6%	0.002	0.993	0.147	3.190	9.36
				UP_SEQ_FEATURE	region of interest:Catalytic subdomain A	7	0.4%	0.004	1	0.982	8.814	10.28
				UP_SEQ_FEATURE	region of interest:Catalytic subdomain B	7	0.4%	0.004	1	0.982	8.814	10.28
				INTERPRO	IPR000772:Ricin B lectin	8	0.5%	0.005	1	0.737	8.826	9.63
				GOTERM_MF_ALL	GO:0030145~manganese ion binding	21	1.3%	0.005	1	0.317	9.338	7.13
				UP_SEQ_FEATURE	domain:Ricin B-type lectin	7	0.4%	0.006	1	0.986	12.201	10.18
				SMART	SM00458:RICIN	8	0.5%	0.015	1	0.739	20.487	9.63
				SP_PIR_KEYWORDS	Manganese	19	1.2%	0.018	1	0.299	24.901	7.23
				INTERPRO	IPR001173:Glycosyl transferase, family 2	6	0.4%	0.019	1	0.939	31.446	9.84
				GOTERM_MF_ALL	GO:0016758~transferase activity, transferring hexosyl groups	22	1.4%	0.020	1	0.559	30.691	6.85
				KEGG_PATHWAY	mmu01030:Glycan structures - biosynthesis 1	19	1.2%	0.054	1	0.314	50.292	7.40
				KEGG_PATHWAY	mmu00512:O-Glycan biosynthesis	7	0.4%	0.067	1	0.346	58.054	9.39
				PIR_SUPERFAMILY	PIRSF005670:polypeptide N-acetylgalactosaminyltransferase	3	0.2%	0.198	1	1	98.163	11.09
				GOTERM_BP_ALL	GO:0006493~protein amino acid O-linked glycosylation	3	0.2%	0.441	1	0.986	99.999	9.97

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
44	1.73	0.017	0.019	SP_PIR_KEYWORDS	lectin	13	0.8%	0.783	1	0.999	100	5.94
				GOTERM_MF_ALL	GO:0005529~sugar binding	14	0.9%	0.892	1	1	100	6.49
45	1.72	0.015	0.019	INTERPRO	IPR000832:GPCR, family 2, secretin-like	13	0.8%	0.001	0.998	0.505	2.067	8.63
				INTERPRO	IPR000539:Frizzled protein	5	0.3%	0.009	1	0.879	15.969	10.77
				INTERPRO	IPR015526:Frizzled related	6	0.4%	0.009	1	0.873	16.781	10.18
				INTERPRO	IPR000024:Frizzled CRD region	7	0.4%	0.011	1	0.885	18.685	9.63
				UP_SEQ_FEATURE	domain:FZ	7	0.4%	0.015	1	1	26.702	9.77
				SMART	SM00063:FRI	7	0.4%	0.029	1	0.861	35.138	9.63
				UP_SEQ_FEATURE	short sequence motif:Lys-Thr-X-X-X-Trp motif	4	0.3%	0.061	1	1	73.613	11.09
				UP_SEQ_FEATURE	short sequence motif:PDZ-binding	11	0.7%	0.081	1	1	83.367	8.42
				PIR_SUPERFAMILY	PIRSF006696:fruit fly frizzled protein	3	0.2%	0.167	1	1	96.357	11.09
46	1.71	0.046	0.019	INTERPRO	IPR001202:WW/Rsp5/WWP	12	0.7%	0.002	1	0.633	3.569	8.63
				SMART	SM00456:WW	12	0.7%	0.012	1	0.828	15.773	8.60
				UP_SEQ_FEATURE	domain:WW 1	5	0.3%	0.081	1	1	83.194	10.18
				UP_SEQ_FEATURE	domain:WW 2	5	0.3%	0.081	1	1	83.194	10.18
47	1.71	0.043	0.020	GOTERM_MF_ALL	GO:0003682~chromatin binding	21	1.3%	0.001	0.970	0.122	2.279	7.32
				INTERPRO	IPR000953:Chromo	7	0.4%	0.019	1	0.940	30.996	9.51
				SMART	SM00298:CHROMO	7	0.4%	0.066	1	0.862	63.721	9.51
				UP_SEQ_FEATURE	domain:Chromo 1	3	0.2%	0.090	1	1	86.451	12.09
48	1.68	0.019	0.021	GOTERM_BP_ALL	GO:0045665~negative regulation of neuron differentiation	6	0.4%	0.016	1	0.294	26.762	9.81
				GOTERM_BP_ALL	GO:0045664~regulation of neuron differentiation	8	0.5%	0.019	1	0.318	30.022	7.93
				GOTERM_BP_ALL	GO:0048663~neuron fate commitment	6	0.4%	0.030	1	0.423	43.964	9.60
49	1.67	0.030	0.022	INTERPRO	IPR001965:Zinc finger, PHD-type	16	1.0%	0.003	1	0.631	5.435	8.18
				SMART	SM00249:PHD	16	1.0%	0.030	1	0.839	35.916	8.11
				UP_SEQ_FEATURE	zinc finger region:PHD-type	6	0.4%	0.117	1	1	92.904	8.77
50	1.64	0.081	0.023	GOTERM_BP_ALL	GO:0001649~osteoblast differentiation	9	0.6%	0.002	1	0.061	3.381	9.30
				GOTERM_BP_ALL	GO:0045668~negative regulation of osteoblast differentiation	3	0.2%	0.081	1	0.704	79.966	11.47
				GOTERM_BP_ALL	GO:0045667~regulation of osteoblast differentiation	4	0.3%	0.085	1	0.714	81.531	10.47
51	1.62	0.017	0.024	INTERPRO	IPR011511:Variant SH3	11	0.7%	0.011	1	0.877	18.707	8.51
				SP_PIR_KEYWORDS	SH3 domain	27	1.7%	0.016	1	0.276	21.522	6.59
				INTERPRO	IPR001452:Src homology-3	25	1.6%	0.017	1	0.946	27.916	6.70
				UP_SEQ_FEATURE	domain:SH3	19	1.2%	0.054	1	1	68.887	7.15
				SMART	SM00326:SH3	28	1.7%	0.056	1	0.827	57.561	6.63
52	1.60	0.015	0.025	GOTERM_BP_ALL	GO:0001655~urogenital system development	14	0.9%	0.013	1	0.256	21.831	7.83
				GOTERM_BP_ALL	GO:0001656~metanephros development	10	0.6%	0.015	1	0.281	24.760	8.51
				GOTERM_BP_ALL	GO:0001822~kidney development	13	0.8%	0.015	1	0.285	25.145	7.99
				GOTERM_BP_ALL	GO:0001657~ureteric bud development	8	0.5%	0.019	1	0.318	30.022	8.97
				GOTERM_BP_ALL	GO:0001658~ureteric bud branching	4	0.3%	0.201	1	0.902	98.612	9.74
53	1.55	0.118	0.028	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	29	1.8%	2.05E-04	0.951	0.778	0.433	7.10
				UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	27	1.7%	5.31E-04	1	0.623	1.120	7.18
				UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	27	1.7%	0.001	1	0.805	2.327	7.10
				UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	20	1.2%	0.006	1	0.988	11.415	7.54
				UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	13	0.8%	0.118	1	1	92.969	7.86
				INTERPRO	IPR007087:Zinc finger, C2H2-type	51	3.2%	0.209	1	1	98.939	5.44
				INTERPRO	IPR015880:Zinc finger, C2H2-like	33	2.1%	0.688	1	1	100	5.88
				INTERPRO	IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding	24	1.5%	0.884	1	1	100	6.16
				SMART	SM00355:ZnF_C2H2	35	2.2%	0.983	1	1	100	5.74
54	1.53	0.029	0.029	SP_PIR_KEYWORDS	mitogen	8	0.5%	0.023	1	0.325	30.118	8.11
				SP_PIR_KEYWORDS	growth factor	18	1.1%	0.029	1	0.356	36.144	6.13
				GOTERM_MF_ALL	GO:0008083~growth factor activity	21	1.3%	0.039	1	0.720	50.546	6.77
55	1.53	0.041	0.030	INTERPRO	IPR011333:BTB/POZ fold	23	1.4%	0.005	1	0.750	9.557	7.07
				INTERPRO	IPR000210:BTB/POZ-like	22	1.4%	0.009	1	0.871	16.099	7.10
				SMART	SM00225:BTB	24	1.5%	0.041	1	0.775	46.185	7.06
				INTERPRO	IPR013069:BTB/POZ	15	0.9%	0.054	1	0.979	65.802	7.67
				UP_SEQ_FEATURE	domain:BTB	9	0.6%	0.222	1	1	99.507	8.42

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
56	1.51	0.036	0.031	SP_PIR_KEYWORDS	protein phosphatase	21	1.3%	4.59E-04	0.328	0.020	0.710	6.94
				INTERPRO	IPR008343:MAP kinase phosphatase	5	0.3%	0.004	1	0.701	7.280	10.92
				INTERPRO	IPR014393:Dual specificity protein phosphatase (MAP kinase phosphatase)	4	0.3%	0.005	1	0.749	8.718	11.77
				GOTERM_MF_ALL	GO:0004721~phosphoprotein phosphatase activity	24	1.5%	0.005	1	0.323	9.294	7.00
				GOTERM_MF_ALL	GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase activity	5	0.3%	0.006	1	0.350	10.728	10.89
				GOTERM_MF_ALL	GO:0033549~MAP kinase phosphatase activity	5	0.3%	0.006	1	0.350	10.728	10.89
				GOTERM_MF_ALL	GO:0042578~phosphoric ester hydrolase activity	40	2.5%	0.007	1	0.358	12.044	5.94
				GOTERM_MF_ALL	GO:0016791~phosphoric monoester hydrolase activity	33	2.1%	0.009	1	0.399	14.849	6.31
				GOTERM_MF_ALL	GO:0004725~protein tyrosine phosphatase activity	16	1.0%	0.010	1	0.425	16.932	7.77
				UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	13	0.8%	0.011	1	0.999	20.883	8.51
				UP_SEQ_FEATURE	domain:Rhodanese	5	0.3%	0.031	1	1	48.450	10.28
				GOTERM_BP_ALL	GO:0006470~protein amino acid dephosphorylation	18	1.1%	0.032	1	0.444	46.635	7.25
				BIOCARTA	m_dspPathway:Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases	5	0.3%	0.034	1	0.802	36.418	10.63 10.63
				INTERPRO	IPR000340:Protein-tyrosine phosphatase, dual specificity	7	0.4%	0.036	1	0.977	50.676	9.18
				PIR_SUPERFAMILY	PIRSF000939:dual specificity protein phosphatase (MAP kinase phosphatase)	3	0.2%	0.037	1	1	49.151	12.09
				INTERPRO	IPR000387:Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type	13	0.8%	0.041	1	0.979	55.667	7.90
				GOTERM_BP_ALL	GO:0016311~dephosphorylation	19	1.2%	0.050	1	0.567	62.559	7.11
				INTERPRO	IPR001763:Rhodanese-like	5	0.3%	0.053	1	0.982	64.942	9.92
				UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	9	0.6%	0.088	1	1	85.656	8.54
				SMART	SM00195:DSPc	7	0.4%	0.098	1	0.918	78.243	9.14
				GOTERM_MF_ALL	GO:0008138~protein tyrosine/serine/threonine phosphatase activity	7	0.4%	0.106	1	0.938	86.431	8.85
				SMART	SM00450:RHOD	5	0.3%	0.118	1	0.922	84.483	9.84
				GOTERM_MF_ALL	GO:0016788~hydrolase activity, acting on ester bonds	66	4.1%	0.121	1	0.943	89.915	4.89
				INTERPRO	IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type	6	0.4%	0.284	1	1	99.844	9.05
				SP_PIR_KEYWORDS	phosphoric monoester hydrolase	6	0.4%	0.323	1	0.918	99.763	8.67
				SP_PIR_KEYWORDS	tyrosine-specific phosphatase	4	0.3%	0.362	1	0.941	99.907	9.51
				SMART	SM00194:PTPc	6	0.4%	0.483	1	0.986	99.994	9.05
57	1.49	0.019	0.032	INTERPRO	IPR013088:Zinc finger, NHR/GATA-type	9	0.6%	0.012	1	0.892	20.377	8.77
				INTERPRO	IPR013629:Zinc finger-associated region	3	0.2%	0.019	1	0.946	30.556	12.09
				PIR_SUPERFAMILY	PIRSF500849:orphan nuclear receptor COUP-TF	3	0.2%	0.019	1	1	29.851	12.09
				INTERPRO	IPR003068:Transcription factor COUP	3	0.2%	0.035	1	0.978	50.147	11.77
				PIR_SUPERFAMILY	PIRSF002534:retinoic acid receptor alpha	3	0.2%	0.230	1	1	99.110	10.51
58	1.48	0.100	0.033	INTERPRO	IPR011993:Pleckstrin homology-type	36	2.2%	4.62E-04	0.934	0.419	0.890	6.31
				INTERPRO	IPR001849:Pleckstrin-like	25	1.6%	0.06	1	0.980	70.064	6.57
				SMART	SM00233:PH	29	1.8%	0.14	1	0.908	89.062	6.47
				UP_SEQ_FEATURE	domain:PH	14	0.9%	0.30	1	1	99.954	7.27
59	1.45	0.047	0.036	GOTERM_BP_ALL	GO:0051098~regulation of binding	8	0.5%	0.01	1	0.203	16.386	8.39
				GOTERM_BP_ALL	GO:0051101~regulation of DNA binding	5	0.3%	0.01	1	0.258	22.181	8.85
				GOTERM_BP_ALL	GO:0043388~positive regulation of DNA binding	3	0.2%	0.08	1	0.704	79.966	9.30
				GOTERM_BP_ALL	GO:0051099~positive regulation of binding	3	0.2%	0.16	1	0.868	96.790	9.15
60	1.42	0.042	0.038	SP_PIR_KEYWORDS	mitogen	8	0.5%	0.02	1	0.325	30.118	8.11
				INTERPRO	IPR000072:Platelet-derived growth factor (PDGF)	4	0.3%	0.03	1	0.977	45.489	10.51
				GOTERM_BP_ALL	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	8	0.5%	0.05	1	0.583	64.481	8.93
				SMART	SM00141:PDGF	4	0.3%	0.05	1	0.832	56.266	10.51
61	1.41	0.037	0.039	GOTERM_BP_ALL	GO:0050770~regulation of axonogenesis	9	0.6%	0.008	1	0.180	13.560	8.93
				GOTERM_BP_ALL	GO:0050767~regulation of neurogenesis	10	0.6%	0.027	1	0.400	40.854	7.62
				GOTERM_BP_ALL	GO:0030516~regulation of axon extension	5	0.3%	0.037	1	0.479	51.223	9.81
				GOTERM_BP_ALL	GO:0050772~positive regulation of axonogenesis	5	0.3%	0.037	1	0.479	51.223	10.15
				GOTERM_BP_ALL	GO:0048675~axon extension	6	0.4%	0.049	1	0.564	61.863	9.36
				GOTERM_BP_ALL	GO:0050769~positive regulation of neurogenesis	5	0.3%	0.088	1	0.719	82.730	9.11
				GOTERM_BP_ALL	GO:0045773~positive regulation of axon extension	3	0.2%	0.107	1	0.776	88.493	11.06
62	1.41	0.058	0.039	GOTERM_MF_ALL	GO:0008603~cAMP-dependent protein kinase regulator activity	6	0.4%	0.002	0.992	0.150	3.153	10.47
				INTERPRO	IPR002373:cAMP/cGMP-dependent protein kinase	5	0.3%	0.002	1	0.621	4.384	10.92
				GOTERM_MF_ALL	GO:0019887~protein kinase regulator activity	14	0.9%	0.003	1	0.221	5.580	8.06
				GOTERM_MF_ALL	GO:0016208~AMP binding	6	0.4%	0.008	1	0.365	12.566	10.25

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
62	1.41	0.058	0.039	INTERPRO	IPR003117:cAMP-dependent protein kinase regulator, type II PKA R subunit	4	0.3%	0.022	1	0.951	34.824	11.28
				INTERPRO	IPR012198:cAMP-dependent protein kinase regulatory subunit	3	0.2%	0.035	1	0.978	50.147	12.09
				PIR_SUPERFAMILY	PIRSF000548:cAMP-dependent protein kinase, regulatory subunit	3	0.2%	0.037	1	1.000	49.151	12.09
				SMART	SM00394:RIIa	4	0.3%	0.039	1	0.780	44.590	11.28
				UP_SEQ_FEATURE	binding site:cAMP 2	3	0.2%	0.058	1	1	71.818	12.09
				UP_SEQ_FEATURE	binding site:cAMP 1	3	0.2%	0.058	1	1	71.818	12.09
				UP_SEQ_FEATURE	region of interest:Dimerization and phosphorylation	3	0.2%	0.058	1	1	71.818	12.09
				SP_PIR_KEYWORDS	camp-binding	4	0.3%	0.061	1	0.575	62.468	10.77
				GOTERM_MF_ALL	GO:0030552~cAMP binding	4	0.3%	0.069	1	0.868	72.223	10.74
				GOTERM_MF_ALL	GO:0030551~cyclic nucleotide binding	5	0.3%	0.088	1	0.912	80.687	9.81
				UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP 1	3	0.2%	0.090	1	1	86.451	11.77
				UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP 2	3	0.2%	0.090	1	1	86.451	11.77
				SP_PIR_KEYWORDS	camp	5	0.3%	0.113	1	0.707	84.512	9.05
				INTERPRO	IPR014710:RmlC-like jelly roll fold	5	0.3%	0.156	1	0.999	96.207	9.63
				INTERPRO	IPR000595:Cyclic nucleotide-binding	5	0.3%	0.188	1	0.999	98.235	9.39
				SMART	SM00100:cNMP	5	0.3%	0.360	1	0.972	99.865	9.34
63	1.35	0.032	0.045	GOTERM_BP_ALL	GO:0031016~pancreas development	5	0.3%	0.023	1	0.363	36.036	10.47
				GOTERM_BP_ALL	GO:0031018~endocrine pancreas development	4	0.3%	0.032	1	0.441	45.995	10.89
				GOTERM_BP_ALL	GO:0035270~endocrine system development	8	0.5%	0.121	1	0.804	91.509	8.42
64	1.33	0.056	0.046	GOTERM_MF_ALL	GO:0005262~calcium channel activity	15	0.9%	0.002	0.995	0.146	3.376	8.15
				SP_PIR_KEYWORDS	Calcium channel	12	0.7%	0.002	0.826	0.068	3.081	8.70
				GOTERM_BP_ALL	GO:0006816~calcium ion transport	19	1.2%	0.009	1	0.199	15.658	7.35
				GOTERM_MF_ALL	GO:0046873~metal ion transmembrane transporter activity	38	2.4%	0.010	1	0.414	15.820	5.93
				GOTERM_MF_ALL	GO:0022843~voltage-gated cation channel activity	20	1.2%	0.011	1	0.426	17.278	7.16
				GOTERM_MF_ALL	GO:0005261~cation channel activity	33	2.1%	0.014	1	0.478	21.986	6.17
				SP_PIR_KEYWORDS	calcium transport	12	0.7%	0.019	1	0.303	25.659	8.23
				GOTERM_MF_ALL	GO:0005244~voltage-gated ion channel activity	24	1.5%	0.020	1	0.563	30.192	6.74
				GOTERM_MF_ALL	GO:0022832~voltage-gated channel activity	24	1.5%	0.020	1	0.563	30.192	6.74
				GOTERM_MF_ALL	GO:0022836~gated channel activity	34	2.1%	0.021	1	0.556	30.858	6.09
				SP_PIR_KEYWORDS	Ionic channel	36	2.2%	0.021	1	0.311	27.848	5.98
				GOTERM_MF_ALL	GO:0005216~ion channel activity	42	2.6%	0.022	1	0.573	32.798	5.70
				GOTERM_MF_ALL	GO:0022838~substrate specific channel activity	43	2.7%	0.023	1	0.577	33.445	5.65
				INTERPRO	IPR003131:Potassium channel, voltage dependent, Kv, tetramerisation	9	0.6%	0.024	1	0.956	36.986	8.63
				GOTERM_BP_ALL	GO:0015674~di-, tri-valent inorganic cation transport	21	1.3%	0.028	1	0.415	42.424	6.96
				GOTERM_MF_ALL	GO:0005245~voltage-gated calcium channel activity	6	0.4%	0.036	1	0.700	47.822	9.81
				GOTERM_MF_ALL	GO:0005249~voltage-gated potassium channel activity	14	0.9%	0.050	1	0.790	59.872	7.55
				GOTERM_MF_ALL	GO:0015267~channel activity	44	2.7%	0.054	1	0.808	62.742	5.52
				GOTERM_MF_ALL	GO:0022803~passive transmembrane transporter activity	44	2.7%	0.054	1	0.808	62.742	5.52
				GOTERM_BP_ALL	GO:0006811~ion transport	78	4.8%	0.054	1	0.591	65.566	4.59
				SP_PIR_KEYWORDS	ion transport	51	3.2%	0.056	1	0.553	59.099	5.22
				GOTERM_MF_ALL	GO:0030955~potassium ion binding	15	0.9%	0.062	1	0.843	68.209	7.32
				GOTERM_BP_ALL	GO:0030001~metal ion transport	46	2.9%	0.068	1	0.653	74.119	5.44
				INTERPRO	IPR003968:Potassium channel, voltage dependent, Kv	5	0.3%	0.098	1	0.996	86.339	9.63
				GOTERM_MF_ALL	GO:0022892~substrate-specific transporter activity	96	6.0%	0.107	1	0.938	86.616	4.22
				GOTERM_MF_ALL	GO:0022891~substrate-specific transmembrane transporter activity	77	4.8%	0.114	1	0.942	88.419	4.55
				SP_PIR_KEYWORDS	voltage-gated channel	16	1.0%	0.119	1	0.714	86.084	7.17
				GOTERM_MF_ALL	GO:0008324~cation transmembrane transporter activity	52	3.2%	0.121	1	0.943	89.830	5.06
				GOTERM_BP_ALL	GO:0006812~cation transport	53	3.3%	0.126	1	0.814	92.289	5.15
				INTERPRO	IPR005821:Ion transport	13	0.8%	0.129	1	0.998	93.157	7.57
				GOTERM_MF_ALL	GO:0005267~potassium channel activity	16	1.0%	0.148	1	0.967	94.254	7.09
				GOTERM_MF_ALL	GO:0015075~ion transmembrane transporter activity	66	4.1%	0.154	1	0.971	94.950	4.71
				SP_PIR_KEYWORDS	potassium	13	0.8%	0.161	1	0.795	93.424	7.20
				GOTERM_MF_ALL	GO:0031420~alkali metal ion binding	20	1.2%	0.172	1	0.976	96.539	6.61
				SP_PIR_KEYWORDS	transport	121	7.5%	0.233	1	0.869	98.368	3.66
				PIR_SUPERFAMILY	PIRSF002449:potassium channel protein Drk1	3	0.2%	0.261	1	1	99.585	10.51
				UP_SEQ_FEATURE	short sequence motif:Selectivity filter	7	0.4%	0.282	1	1	99.909	8.70
				GOTERM_MF_ALL	GO:0005215~transporter activity	120	7.4%	0.294	1	0.997	99.796	3.82

Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.

Functional Group	Enrichment Score	Median *P*-Value	Geometric Mean	Category	Term	Count	% of Total	*P*-Value	Bonferroni	Benjamini	FDR	Information Content (bits)
64	1.33	0.056	0.046	INTERPRO	IPR003091:Voltage-dependent potassium channel	5	0.3%	0.315	1	1	99.934	9.09
				GOTERM_BP_ALL	GO:0006813~potassium ion transport	17	1.1%	0.328	1	0.962	99.949	6.77
				SP_PIR_KEYWORDS	Potassium channel	7	0.4%	0.377	1	0.944	99.935	7.26
				SP_PIR_KEYWORDS	potassium transport	10	0.6%	0.401	1	0.953	99.964	7.51
				GOTERM_MF_ALL	GO:0022857~transmembrane transporter activity	80	5.0%	0.405	1	1	100	4.35
				GOTERM_BP_ALL	GO:0015672~monovalent inorganic cation transport	25	1.6%	0.808	1	1	100	5.84