

Table S1. Chromosomal loci amplified in ChIP-PCR for WT1 gene targets

Probe chromosomal locus	Gene	RefSeq accession number	Fold-enrichment
chr12:81360406-81360451	<i>Actn1</i>	NM_134156	1.885162211
chr12:81360886-81360931	<i>Actn1</i>	NM_134156	2.123701916
chr12:81361062-81361108	<i>Actn1</i>	NM_134156	2.929542597
chr12:81361329-81361374	<i>Actn1</i>	NM_134156	3.524859728
chr12:81361473-81361518	<i>Actn1</i>	NM_134156	24.31048345
chr12:81361601-81361646	<i>Actn1</i>	NM_134156	4.263625077
chr12:81361795-81361845	<i>Actn1</i>	NM_134156	4.348359654
chr12:81361940-81361985	<i>Actn1</i>	NM_134156	1.767946788
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chr7:91557697-91557757	<i>Arnt2</i>	NM_007488	3.129574932
chr7:91557860-91557917	<i>Arnt2</i>	NM_007488	6.569380768
chr7:91557985-91558039	<i>Arnt2</i>	NM_007488	10.89387706
chr7:91558101-91558146	<i>Arnt2</i>	NM_007488	10.08329549
chr7:91558231-91558276	<i>Arnt2</i>	NM_007488	7.597717035
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chr14:47007581-47007626	<i>Bmp4</i>	NM_007554	3.685465809
chr14:47007693-47007740	<i>Bmp4</i>	NM_007554	5.67119259
chr14:47007907-47007967	<i>Bmp4</i>	NM_007554	4.403054679
chr14:47008137-47008187	<i>Bmp4</i>	NM_007554	7.004617637
chr14:47008246-47008291	<i>Bmp4</i>	NM_007554	8.822840486
chr14:47008451-47008501	<i>Bmp4</i>	NM_007554	5.68974169
chr14:47009773-47009827	<i>Bmp4</i>	NM_007554	2.787582852
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chr2:172764762-172764807	<i>Bmp7</i>	NM_007557	3.322869114
chr2:172764969-172765019	<i>Bmp7</i>	NM_007557	3.406469008
chr2:172765155-172765200	<i>Bmp7</i>	NM_007557	2.779228295
chr2:172765859-172765904	<i>Bmp7</i>	NM_007557	4.831320846
chr2:172765976-172766021	<i>Bmp7</i>	NM_007557	12.87208012
chr2:172766162-172766207	<i>Bmp7</i>	NM_007557	3.583262283
chr2:172766584-172766638	<i>Bmp7</i>	NM_007557	3.844485195
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chr9:23027189-23027234	<i>Bmper</i>	NM_028472	2.526008917
chr9:23027603-23027648	<i>Bmper</i>	NM_028472	2.809731786
chr9:23027727-23027772	<i>Bmper</i>	NM_028472	4.98164993
chr9:23027848-23027893	<i>Bmper</i>	NM_028472	5.139692259
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chr14:70474926-70474971	<i>Egr3</i>	NM_018781	3.888523381
chr14:70475028-70475073	<i>Egr3</i>	NM_018781	19.40777108
chr14:70475219-70475264	<i>Egr3</i>	NM_018781	24.51984838
chr14:70475325-70475370	<i>Egr3</i>	NM_018781	7.660779059
chr14:70475524-70475569	<i>Egr3</i>	NM_018781	1.413367113
chr14:70475637-70475682	<i>Egr3</i>	NM_018781	8.821325541
chr14:70475820-70475880	<i>Egr3</i>	NM_018781	8.517142461
chr14:70476003-70476048	<i>Egr3</i>	NM_018781	2.7308202
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chr11:98273670-98273715	<i>Erbb2</i>	NM_001003817	1.957810511
chr11:98273790-98273835	<i>Erbb2</i>	NM_001003817	10.86298349
chr11:98273966-98274011	<i>Erbb2</i>	NM_001003817	1.889541533
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chr7:137409139-137409185	<i>Fgfr2</i>	NM_010207	5.53030562
chr7:137409274-137409319	<i>Fgfr2</i>	NM_010207	3.280239815
chr7:137409376-137409424	<i>Fgfr2</i>	NM_010207	5.924066939
chr7:137409536-137409581	<i>Fgfr2</i>	NM_010207	2.87008429
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chr5:34064468-34064513	<i>Fgfr3</i>	NM_008010	2.484248062
chr5:34064586-34064631	<i>Fgfr3</i>	NM_008010	4.936873665
chr5:34064725-34064770	<i>Fgfr3</i>	NM_008010	3.615329019

chr5:34064927-34064972	<i>Fgfr3</i>	NM_008010	2.549270022
chr10:39089847-39089892	<i>Fyn</i>	NM_008054	1.564046674
chr10:39090282-39090342	<i>Fyn</i>	NM_008054	18.71706365
chr4:122910233-122910278	<i>Heyl</i>	NM_013905	3.692497849
chr4:122910601-122910652	<i>Heyl</i>	NM_013905	3.311598782
chr4:122910756-122910801	<i>Heyl</i>	NM_013905	4.55858851
chr4:122910859-122910904	<i>Heyl</i>	NM_013905	2.541881335
chr4:122911146-122911193	<i>Heyl</i>	NM_013905	25.1419019
chr4:122911325-122911373	<i>Heyl</i>	NM_013905	13.20722708
chr4:122911495-122911555	<i>Heyl</i>	NM_013905	2.981349965
chr1:194596332-194596386	<i>Hhat</i>	NM_144881	2.568933819
chr1:194596508-194596555	<i>Hhat</i>	NM_144881	4.514940719
chr1:194596616-194596672	<i>Hhat</i>	NM_144881	5.349621816
chr1:194596819-194596864	<i>Hhat</i>	NM_144881	4.681517195
chr1:194596974-194597019	<i>Hhat</i>	NM_144881	11.44601784
chr1:194597148-194597193	<i>Hhat</i>	NM_144881	5.40315551
chr1:194597336-194597382	<i>Hhat</i>	NM_144881	3.652075846
chr1:194597502-194597562	<i>Hhat</i>	NM_144881	3.593429155
chr2:74565721-74565766	<i>Hoxd4</i>	NM_010469	8.614434632
chr2:74565868-74565918	<i>Hoxd4</i>	NM_010469	6.643002341
chr2:74566023-74566070	<i>Hoxd4</i>	NM_010469	16.55598521
chr2:74566185-74566230	<i>Hoxd4</i>	NM_010469	3.883200335
chr2:74566364-74566423	<i>Hoxd4</i>	NM_010469	4.996171293
chr3:130812572-130812629	<i>Lef1</i>	NM_010703	1.934877536
chr3:130812839-130812897	<i>Lef1</i>	NM_010703	4.938118888
chr3:130813037-130813083	<i>Lef1</i>	NM_010703	3.263052169
chr3:130813309-130813354	<i>Lef1</i>	NM_010703	2.031235399
chr3:130813444-130813489	<i>Lef1</i>	NM_010703	4.673422167
chr3:130813627-130813682	<i>Lef1</i>	NM_010703	3.477142506
chr3:130813795-130813855	<i>Lef1</i>	NM_010703	2.936702235
chr3:130814332-130814377	<i>Lef1</i>	NM_010703	1.916384879
chr3:130814529-130814579	<i>Lef1</i>	NM_010703	5.96324733
chr3:130814762-130814813	<i>Lef1</i>	NM_010703	4.701323172
chr3:130814942-130814987	<i>Lef1</i>	NM_010703	5.116507061
chr3:130815358-130815403	<i>Lef1</i>	NM_010703	2.883503056
chr1:52556594-52556640	<i>Nab1</i>	NM_008667	2.461156585
chr1:52556859-52556904	<i>Nab1</i>	NM_008667	7.732770253
chr1:52557045-52557090	<i>Nab1</i>	NM_008667	3.888633984
chr1:52557631-52557676	<i>Nab1</i>	NM_008667	2.229038673
chr10:127102470-127102530	<i>Nab2</i>	NM_008668	3.213688433
chr10:127102967-127103012	<i>Nab2</i>	NM_008668	4.267911483
chr10:127103213-127103263	<i>Nab2</i>	NM_008668	13.39061571
chr10:127103344-127103389	<i>Nab2</i>	NM_008668	10.67535378
chr10:127103495-127103540	<i>Nab2</i>	NM_008668	20.11941172
chr10:127103623-127103668	<i>Nab2</i>	NM_008668	8.006574663
chr19:44827636-44827681	<i>Pax2</i>	NM_011037	5.126745443
chr19:44827794-44827848	<i>Pax2</i>	NM_011037	6.475285785
chr19:44827957-44828002	<i>Pax2</i>	NM_011037	6.608847117
chr19:44828127-44828181	<i>Pax2</i>	NM_011037	9.296241051
chr19:44828244-44828304	<i>Pax2</i>	NM_011037	8.11138572

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chr5:028122197-028122241	<i>Paxip1</i>	NM_018878	1.961888607
chr1:170361694-170361749	<i>Pbx1</i>	NM_183355	2.176399275
chr1:170362020-170362076	<i>Pbx1</i>	NM_183355	10.31159147
chr1:170362145-170362190	<i>Pbx1</i>	NM_008783	3.587618032
chr17:34729644-34729690	<i>Pbx2</i>	NM_017463	12.8134639
chr17:34729790-34729849	<i>Pbx2</i>	NM_017463	4.579223142
chr17:34729960-34730009	<i>Pbx2</i>	NM_017463	4.178332977
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chr9:108998328-108998373	<i>Plxnb1</i>	NM_172775	2.802128647
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chr13:63665972-63666017	<i>Ptch1</i>	NM_008957	1.843057247
chr13:63666138-63666193	<i>Ptch1</i>	NM_008957	5.76945033
chr13:63666273-63666320	<i>Ptch1</i>	NM_008957	7.033637766
chr13:63666384-63666429	<i>Ptch1</i>	NM_008957	1.520197045
chr5:77694648-77694693	<i>Rest</i>	NM_011263	6.797812781
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chr5:77695406-77695451	<i>Rest</i>	NM_011263	9.463158347
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chr8:91567009-91567059	<i>Sall1</i>	NM_021390	9.233639151
chr8:91567167-91567212	<i>Sall1</i>	NM_021390	5.311786495
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chr15:76286655-76286702	<i>Scx</i>	NM_198885	2.203542688
chr15:76287234-76287279	<i>Scx</i>	NM_198885	3.911941305
chr15:76287601-76287657	<i>Scx</i>	NM_198885	12.18619789
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chr15:76288981-76289026	<i>Scx</i>	NM_198885	2.768685593
chr2:124435389-124435449	<i>Sema6d</i>	NM_172537	3.215933752
chr2:124435597-124435642	<i>Sema6d</i>	NM_172537	3.833153329
chr2:124435760-124435806	<i>Sema6d</i>	NM_172537	14.05544767
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chr2:124436107-124436152	<i>Sema6d</i>	NM_172537	4.945232261

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chr17:085597280-085597324	<i>Six2</i>	NM_011380	2.567491338
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chr12:74213667-74213712	<i>Six4</i>	NM_011382	2.013468101
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chr11:34935290-34935335	<i>Slit3</i>	NM_011412	2.828986313
chr11:34935458-34935505	<i>Slit3</i>	NM_011412	6.671547335
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chr11:34935754-34935808	<i>Slit3</i>	NM_011412	2.971228032
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chr9:63605810-63605855	<i>Smad3</i>	NM_016769	4.682243478
chr9:63605972-63606017	<i>Smad3</i>	NM_016769	7.111903005
chr9:63606199-63606249	<i>Smad3</i>	NM_016769	8.248561033
chr9:63606311-63606356	<i>Smad3</i>	NM_016769	6.160097609
chr9:63606469-63606524	<i>Smad3</i>	NM_016769	6.875655551
chr18:73863445-73863490	<i>Smad4</i>	NM_008540	8.673345952
chr18:73863654-73863699	<i>Smad4</i>	NM_008540	2.795492204
chr9:63870056-63870101	<i>Smad6</i>	NM_008542	2.111988835
chr9:63870208-63870254	<i>Smad6</i>	NM_008542	4.353732665
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chr18:75527141-75527186	<i>Smad7</i>	NM_001042660	2.478944837
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chr18:75527381-75527426	<i>Smad7</i>	NM_001042660	3.016364783
chr18:75528879-75528924	<i>Smad7</i>	NM_001042660	2.630810343
chr18:75529419-75529479	<i>Smad7</i>	NM_001042660	2.362047322
chr6:29685666-29685711	<i>Smo</i>	NM_176996	2.797807879
chr6:29685802-29685847	<i>Smo</i>	NM_176996	4.020960332
chr6:29685976-29686021	<i>Smo</i>	NM_176996	3.096481046
chr6:29686120-29686165	<i>Smo</i>	NM_176996	3.08131583
chr12:28027842-28027887	<i>Sox11</i>	NM_009234	2.539585452
chr12:28028010-28028055	<i>Sox11</i>	NM_009234	2.09473395
chr12:28028212-28028257	<i>Sox11</i>	NM_009234	15.57544715
chr12:28028338-28028383	<i>Sox11</i>	NM_009234	2.929086121
chr12:28028439-28028499	<i>Sox11</i>	NM_009234	10.37509824
chr12:28028589-28028642	<i>Sox11</i>	NM_009234	4.998722019
chr14:106294461-106294506	<i>Spry2</i>	NM_011897	3.112268827
chr14:106294617-106294677	<i>Spry2</i>	NM_011897	3.743660349
chr14:106296835-106296880	<i>Spry2</i>	NM_011897	1.411173652
chr14:106296947-106297000	<i>Spry2</i>	NM_011897	6.615629183
chr14:106297132-106297186	<i>Spry2</i>	NM_011897	3.490559634
chr2:166820990-166821050	<i>Stau1</i>	NM_011490	3.089740778
chr2:166821163-166821213	<i>Stau1</i>	NM_011490	4.516269924
chr2:166821400-166821445	<i>Stau1</i>	NM_011490	3.405898012
chr2:165980866-165980921	<i>Sulf2</i>	NM_028072	5.263198268
chr2:165981030-165981075	<i>Sulf2</i>	NM_028072	1.892322462

chr17:46165927-46165972	<i>Vegfa</i>	NM_001025250	4.799762458
chr17:46166092-46166137	<i>Vegfa</i>	NM_001025250	4.441552756
chr17:46166198-46166243	<i>Vegfa</i>	NM_001025250	2.381367448
mm chr17:46167233-46167286	<i>Vegfa</i>	NM_001025250	3.255572239
chr17:46167362-46167407	<i>Vegfa</i>	NM_001025250	3.935303472
chr17:46167511-46167556	<i>Vegfa</i>	NM_001025250	2.392782464
chr17:46167696-46167741	<i>Vegfa</i>	NM_001025250	8.130999176
chr17:46167808-46167853	<i>Vegfa</i>	NM_001025250	7.265683176
chr17:46167969-46168014	<i>Vegfa</i>	NM_001025250	7.108455984
chr17:46168084-46168129	<i>Vegfa</i>	NM_001025250	3.087414303
chr17:46168261-46168306	<i>Vegfa</i>	NM_001025250	3.711736562

chr15:12047157-12047214	<i>Zfr</i>	NM_011767	8.028833219
chr15:12047388-12047433	<i>Zfr</i>	NM_011767	12.01663356
chr15:12047514-12047559	<i>Zfr</i>	NM_011767	6.05037632
chr15:12047663-12047717	<i>Zfr</i>	NM_011767	10.6784367
chr15:12047808-12047853	<i>Zfr</i>	NM_011767	2.182854239

chr6:42299668-42299713	<i>Zyx</i>	NM_011777	2.497418422
chr6:42299887-42299932	<i>Zyx</i>	NM_011777	5.103425692
chr6:42300024-42300069	<i>Zyx</i>	NM_011777	2.888080344
chr6:42300192-42300237	<i>Zyx</i>	NM_011777	11.54813576
chr6:42300447-42300492	<i>Zyx</i>	NM_011777	2.382498451
chr6:42300594-42300639	<i>Zyx</i>	NM_011777	2.010529457
chr6:42300727-42300772	<i>Zyx</i>	NM_011777	3.411675383

For ChIP-PCR validation of selected WT1 target genes identified by ChIP-chip, primers were designed to amplify a 150-300 bp region around the genomic location of probes that showed peak levels of immunoenrichment by WT1 ChIP-chip (highlighted in red).