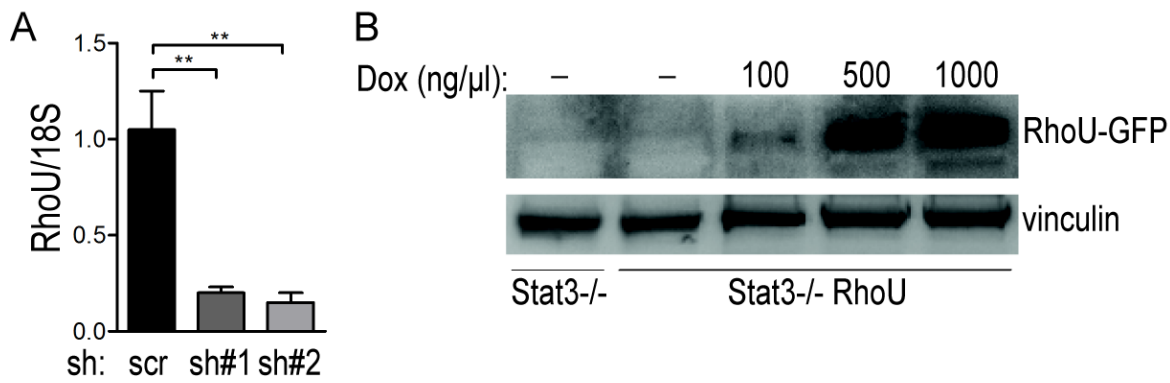
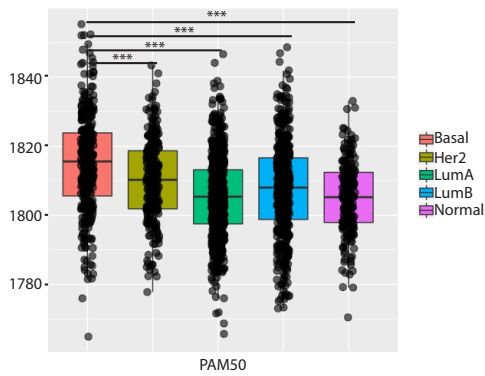


SI Figure 1. RhoU promoter analysis in MEF cells. (A) Cells were transiently transfected with the indicated RhoU promoter constructs or with the TOP-flash and FOP-flash positive and negative control plasmids (TOP, FOP). A SEAP-expressing vector was included as an internal control for transfection efficiency. Transfected cells were co-cultured for 24 h with wild type or WNT1-expressing HEK-293 cells. Luciferase activity was normalized to SEAP activity. Data are shown as mean \pm SEM of 4 independent experiments. **= $P < 0.01$, ***= $P < 0.001$. (B) The indicated linker scanning (Lscanning) constructs based on the -756 RhoU-promoter fragment, along with the wild type -756 construct and the TOP and FOPflash controls were transiently transfected as above and tested for WNT1-responsiveness. Induction was always significant ($P < 0.001$), with the exception of the -167 and FOP negative controls (ns, non significant). A.U., arbitrary units. Data are shown as mean \pm SEM of 4 independent experiments.

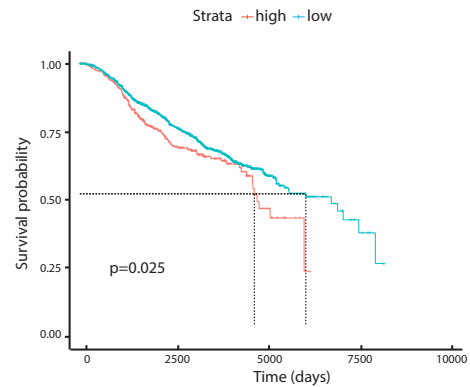


SI Figure 2. Manipulation of RhoU levels in MEF and MDA-MB-231 cells. (A) Lentiviral-mediated shRNA silencing of RhoU mRNA in MDA-MB-231 cells, measured by qRT-PCR upon infection with two distinct shRNA sequences (sh1, sh2) or with a control scrambled vector (scr). **= $P < 0.01$; $n = 4$. (B) RhoU-GFP expression levels in Stat3^{-/-} MEF cells either untransfected or stably transfected with a RhoU-GFP TetON construct (Stat3^{-/-} RhoU) and stimulated with the indicated doses of doxycycline (Dox), measured by Western blot with an anti-GFP monoclonal antibody.

A



B



SI Figure 3

SP1 and STAT3 can functionally cooperate to enhance tumor aggressiveness independently of the tumor subtype. (A) Boxplot showing the distribution of the SP1-S3 score in the 5 breast cancer subtypes, significantly higher in basal-like tumors. $*=P<0.05$, $**=P<0.01$, $***=P<0.001$ between the indicated groups.

(B) Kaplan-Meier plot of overall survival for breast tumor patients, as a function of time in days. Patient samples from the METABRIC database, excluding basal-like tumors, were subdivided according to low or high SP1-S3 score (median value). Even A high SP1-S3 score is predictive of poor prognosis.

SI Table 1. Primers used to generate the RhoU promoter fusions

-1756 forward	5'- ACTAGGTACCGAATTCAGGTGGCCCAAGGGC -3'
-1316 forward	5'- GGCCGGTACCGCATCTCTGTA CTT CAGGTTGTCC -3'
-756 forward	5'- GGCCGGTACCCGCTAACAAAGGGTGGTATCCTGC -3'
-506 forward	5'- GGCCGGTACCCCATGATCACCCCTGCTTCTTCC -3'
-366 forward	5'- ACTAGGTACCCTGCCCTGCCCCCTCC -3'
-234 forward	5'- ACTAGGTACCGCTGGCTCCACCACG -3'
-167 forward	5'- GGCCGGTACCACAGCGCCCCCGTCTGC -3'
reverse	5'- TATCTCGAGGCCGCGAGACCAGCTGCC -3'

SI Table 2. Primers used to generate the Linker Scanning constructs.

Linker	Forward primer 5'-3'	Reverse primer 5'-3'
LSc -605	CCGAATTCAACTCTCCCCCTCC	TTGAATTCGGTGCCTGCTTTTGCAAG
LSc-595	CCGAATTCAACTCCAAACCAAGACAC	TTGAATTCGGCTGTGGGGCCTG
LSc -585	CCGAATTCAAAGACTTGTGTGGAG	TTGAATTCGGGGGAGAGTGCTG
LSc-575	CCGAATTCAAGTGGAGGAGCAAGG	TTGAATTCGGTGGTTTGAGGGGG
LSc -565	CCGAATTCAAAGGGCAGCTGGAGG	TTGAATTCGGACAAGTGTCTTGTTGG
LSc-555	CCGAATTCAAGGAGGAACAGGAAGAG	TTGAATTCGGGCTCCTCCACACAAG
LSc -545	CCGAATTCAAGAAGAGTGGAAGAAGC	TTGAATTCGGAGCTGCCCTTGC
LSc-535	CCGAATTCAAAGAAGCAGGGTGATCATGG	TTGAATTCGGCTGTTCCCTCAGCTGC
LSc -525	CCGAATTCAATGATCATGGTGAGAGG	TTGAATTCGGTCCACTTCTCTGTTG
LSc-515	CCGAATTCAAGAGAGGGAGACCG	TTGAATTCGGCCCTGCTTCTTCCAC
LSc-505	CCGAATTCAACCGCGAAAGGAG	TTGAATTCGGACCATGATCACCTG
LSc -495	CCGAATTCAAGAGGTTGTGGAGTAG	TTGAATTCGGTCTCCCTCTCACC
LSc-484	CCGAATTCAAGTAGAAAGAGAATAGGGGG	TTGAATTCGGCCTTTCCGCGGTCTC
LSc -474	CCGAATTCAAATAGGGGGCGACC	TTGAATTCGGTCCACAACCTCCTTCC
LSc-465	CCGAATTCAACGACCTAAGGAGGG	TTGAATTCGGTCTTTCTACTCCACAACC
LSc -455	CCGAATTCAAAGGGAGAAGGAGGAG	TTGAATTCGGCCCCCTATTCTCTTTC
LSc-445	CCGAATTCAAAGGAGAGGGAAGAG	TTGAATTCGGCCTTAGGTCGCC
LSc -435	CCGAATTCAAAGAGAAAGAGCCGGG	TTGAATTCGGCCTTCTCCCTCCTTAG
LSc-424	CCGAATTCAACGGGAGGGAAGG	TTGAATTCGGTCCCTCTCCTCC
LSc -414	CCGAATTCAAGGGGGAACAGAAGG	TTGAATTCGGGCTCTTCTCTTCCCTC
LSc-405	CCGAATTCAAGAAGGATGGGGAGG	TTGAATTCGGTCCCTCCCGGC
LSc -395	CCGAATTCAAGAGGAGGGGGC	TTGAATTCGGTGTTCCTCCCTTCC
LSc-385	CCGAATTCAACAGGGCAGGAGG	TTGAATTCGGCCCATCCTTCTGTTC
LSc -375	CCGAATTCAAGGAAGTGGAGAGC	TTGAATTCGGCCCCCTCCTCC
LSc-364	CCGAATTCAAGCAAGAGGAGGAAAG	TTGAATTCGGCTCCTGCCCTGC
LSc -354	CCGAATTCAAGAAAGGAAGCTTGGG	TTGAATTCGGTCTCCAGTCTCCTCC
LSc-345	CCGAATTCAACTTGGGAAGGAGCC	TTGAATTCGGTCTCTTGCTCTCC
LSc -335	CCGAATTCAAAGCCGGGAAAGG	TTGAATTCGGCTTCTTCTCCTCCTC
LSc-325	CCGAATTCAAGGGGGGTGGG	TTGAATTCGGCCTTCCCAAGCTTCC
LSc -315	CCGAATTCAAGGATGAGAAGCC	TTGAATTCGGTTTCCGGCTCC
LSc-309	CCGAATTCAAAGAAGCCACAGCAGG	TTGAATTCGGCCCCCTTCCCG
LSc -299	CCGAATTCAAAGCAGGGGCCAG	TTGAATTCGGCATCCCCCACC
LSc-289	CCGAATTCAAAGGGGTAGCTCGG	TTGAATTCGGGTGGGCTTCTCATCC
LSc -278	CCGAATTCAAGGGGTCCGCG	TTGAATTCGGTGGCCCCTGCTG
LSc-268	CCGAATTCAAGGTTGGCGTGG	TTGAATTCGGGAGCTACCCCTGG
LSc-256	CCGAATTCAAGAGCCAGCTAGTCC	TTGAATTCGGCACGCGACCCCCG
LSc-242	CCGAATTCAAGTCCAGCCGCAC	TTGAATTCGGCACCACGCCAACC
LSc-233	CCGAATTCAAACGTTTCGAGGCG	TTGAATTCGGTAGCTGGCTCCACC

SI Table 3. Primers used for qRT- PCR.

Gene	Forward primer 5'-3'	Reverse primer 5'-3'	Probe
<i>Mus musculus</i> RhoU	ACGGCCTTCGACAACCTTCT	ACTCATCCTGTCCTGCAGTGT	78
<i>Homo sapiens</i> RhoU	GACTCCAACCTCTGTGACACTGC	ATGAGGGGGCTCACGACACT	4
<i>Homo sapiens</i> WNT5a	AGGGCTCCTACGAGAGTGCT	GACACCCCATGGCACTTG	/
<i>Homo sapiens</i> WNT5b	AGAAGAACCTTTGCCAAAGGA	CTACGTCTGCCATCTTATACAC	/
<i>Homo sapiens</i> Ror2	GTGACCTTTGTAGACTTTCC	ATTCTGTACATCTTGGTCCC	/
<i>Homo sapiens</i> Ror1	GATTAGAAACCTCGACACCAC	GCAAAGACTCCATAGACGG	/

SI Table 4. List of genes included in the SP1-STAT3 signature.TF.x, SP1; TF.y, STAT3. The chromosome, genomic coordinates of the peaks (Start.x, y; End x,y) and of the genes, and the distance between the peak and the gene (AbsDist. X, y), as well as the signature each gene belongs to, are indicated.

Gene	TF.x	chr.x	Start.x	End.x	GeneChr	GeneStart	GeneEnd	AbsDi	TF.y	chr.y	Start.y	End.y	AbsDist.y	Signature
ACADM	SP1	chr1	76190222	76190574	1	76190031	76229364	191	STAT3	chr1	76187964	76188280	2067	Wnt non canonical
ALAS1	SP1	chr3	52231817	52232137	16	52232098	52248343	281	STAT3	chr3	52227120	52227444	2111	Wnt non canonical
ANGPTL4	SP1	chr19	8426835	8427171	11	8429010	8439259	2175	STAT3	chr19	8426994	8427293	2016	Wnt non canonical
ANPEP	SP1	chr15	90328748	90329084	7	90328125	90358072	623	STAT3	chr15	90325724	90326040	2401	Wnt non canonical
AP2A1	SP1	chr19	50268801	50269125	11	50270179	50310369	553	STAT3	chr19	50268695	50269159	766	Wnt non canonical
AP2B1	SP1	chr17	33914130	33914579	9	33914281	34053436	151	STAT3	chr17	33915581	33915936	1300	Wnt non canonical
AP2M1	SP1	chr3	183892287	183892641	16	183892633	183901879	346	STAT3	chr3	183892117	183892619	516	Wnt non canonical
ARRB2	SP1	chr17	4611768	4612164	9	4613788	4624795	310	STAT3	chr17	4613000	4613280	788	Wnt non canonical
BAK1	SP1	chr6	33538602	33539357	19	33540322	33548070	1720	STAT3	chr6	33538587	33538997	1735	IL6
BHLHE40	SP1	chr3	5020792	5021128	16	5021096	5026866	304	STAT3	chr3	5021923	5022306	827	Wnt non canonical
BTRC	SP1	chr10	103113462	103113853	2	103113789	103317078	327	STAT3	chr10	103113422	103113867	367	Wnt non canonical
CALD1	SP1	chr7	134464178	134464502	20	134464163	134655480	15	STAT3	chr7	134463033	134463349	246	Wnt non canonical
CD14	SP1	chr5	140012649	140012885	18	140011312	140013035	1337	STAT3	chr5	140009809	140010305	511	IL6
CD38	SP1	chr4	15779766	15780086	17	15779887	15854866	121	STAT3	chr4	15775760	15776040	1181	IL6
CD9	SP1	chr12	6304999	6305335	4	6308872	6347437	3873	STAT3	chr12	6305028	6305322	3844	IL6
CDC42	SP1	chr1	22375088	22375408	1	22379119	22417296	153	STAT3	chr1	22380948	22381224	1829	Wnt non canonical
CPT2	SP1	chr1	53661813	53662149	1	53662100	53679869	125	STAT3	chr1	53662284	53662580	184	Wnt non canonical
CFEB1	SP1	chr2	208394233	208394553	12	208394615	208441649	382	STAT3	chr2	208393141	208393421	666	Wnt non canonical
CRY2	SP1	chr11	45864687	45865007	3	45868668	45904799	67	STAT3	chr11	45868357	45868767	311	Wnt non canonical
CSF1	SP1	chr1	110448739	110449059	1	110453232	110467824	4493	STAT3	chr1	110453257	110453573	25	IL6
CSF2	SP1	chr5	131409292	131409628	18	131409484	131411863	192	STAT3	chr5	131409272	131409552	212	IL6
CTGF	SP1	chr6	132272453	132272777	19	132269315	132272518	3138	STAT3	chr6	132270745	132271089	1430	Wnt non canonical
CUL1	SP1	chr7	148395402	148395702	20	148395932	148498202	530	STAT3	chr7	148392769	148393049	3163	Wnt non canonical
DGKA	SP1	chr12	56323778	56324114	4	56324945	56347807	510	STAT3	chr12	56324666	56324952	279	Wnt non canonical
DGKD	SP1	chr2	234262270	234262606	12	234263152	234380743	212	STAT3	chr2	234259396	234259795	3756	Wnt non canonical
DGKH	SP1	chr13	42614570	42614890	5	42614171	42817033	399	STAT3	chr13	42712017	42712340	160	Wnt non canonical
DGKZ	SP1	chr11	46368687	46368995	3	46366816	46402104	268	STAT3	chr11	46358362	46358638	3908	Wnt non canonical
EBI3	SP1	chr19	4229161	4229481	11	4229539	4237525	378	STAT3	chr19	4229185	4229465	354	IL6
ESRRA	SP1	chr11	64072566	64072920	3	64072999	64084215	349	STAT3	chr11	64078640	64078969	4942	Wnt non canonical
FAS	SP1	chr10	90750994	90751314	2	90750315	90776818	50	STAT3	chr10	90750132	90750542	15	IL6
FURIN	SP1	chr15	91417453	91417645	7	91414768	91426688	1346	STAT3	chr15	91412821	91413261	1000	Wnt non canonical
GLI3P1	SP1	chr12	75874448	75874768	4	75874512	75895716	64	STAT3	chr12	75874294	75874610	218	Wnt non canonical
GNAI2	SP1	chr3	50263526	50263846	16	50264119	50296786	347	STAT3	chr3	50288622	50288963	4297	Wnt non canonical
GNB2	SP1	chr7	100270977	100271477	20	100271362	100276792	385	STAT3	chr7	100270927	100271193	435	Wnt non canonical
GNG7	SP1	chr19	2507150	2507486	11	2511217	2702746	4067	STAT3	chr19	2507181	2507525	4036	Wnt non canonical
GNGT2	SP1	chr17	47287833	47288153	9	47283595	47287936	4238	STAT3	chr17	47287699	47288109	4104	Wnt non canonical
GRB2	SP1	chr17	73310035	73310355	9	73314156	73401789	2077	STAT3	chr17	73316161	73316571	2005	IL6
H2AFX	SP1	chr11	118966140	118966512	3	118964583	118966177	1557	STAT3	chr11	118966349	118966670	1766	Wnt non canonical
H2AFZ	SP1	chr4	100871345	100871695	17	100869243	100871512	2102	STAT3	chr4	100871342	100871653	2099	Wnt non canonical
H3F3B	SP1	chr17	73775788	73776223	9	73772514	73776016	3274	STAT3	chr17	73775389	73775702	2875	Wnt non canonical
HAX1	SP1	chr1	154244817	154245137	1	154245038	154248351	221	STAT3	chr1	154244769	154245179	269	IL6
HIST1H2AB	SP1	chr6	26033770	26034046	19	26033319	26033796	451	STAT3	chr6	26033736	26034266	417	Wnt non canonical
HIST1H2AC	SP1	chr6	26124090	26124483	19	26124372	26124918	282	STAT3	chr6	26123950	26124540	422	Wnt non canonical
HIST1H2AD	SP1	chr6	26199420	26199762	19	26199011	26199521	409	STAT3	chr6	26199425	26199769	414	Wnt non canonical
HIST1H2BB	SP1	chr6	26043914	26044266	19	26043454	26043885	460	STAT3	chr6	26043860	26044270	406	Wnt non canonical
HIST1H2BC	SP1	chr6	26121268	26121604	19	26123694	26124132	396	STAT3	chr6	26119272	26119552	256	Wnt non canonical
HIST1H2BD	SP1	chr6	26158017	26158409	19	26158348	26158835	331	STAT3	chr6	26157955	26158610	393	Wnt non canonical
HIST1H2BJ	SP1	chr6	27099571	27099940	19	27100094	27100575	431	STAT3	chr6	27100455	27100963	361	Wnt non canonical
HIST1H2BK	SP1	chr6	27106829	27107185	19	27106071	27114637	439	STAT3	chr6	27106803	27107213	435	Wnt non canonical
HIST1H2BN	SP1	chr6	27807616	27807762	19	27806439	27806888	1177	STAT3	chr6	27806051	27806465	388	Wnt non canonical
HIST1H2BO	SP1	chr6	27860812	27861256	19	27861202	27861669	390	STAT3	chr6	27860924	27861268	278	Wnt non canonical
HIST1H3H	SP1	chr6	27777602	27777938	19	27777841	27778314	239	STAT3	chr6	27777626	27777970	215	Wnt non canonical
HIST2H2AA3	SP1	chr1	149817075	149817399	1	149813784	149814318	3291	STAT3	chr1	149815753	149816071	1969	Wnt non canonical
HIST2H2BE	SP1	chr1	149858165	149858525	1	149856009	149858232	2156	STAT3	chr1	149856474	149856884	465	Wnt non canonical
HIST3H2BB	SP1	chr1	228645515	228645839	1	228645807	228646259	292	STAT3	chr1	228645546	228645890	261	Wnt non canonical
HMOX1	SP1	chr22	35772957	35773304	15	35777059	35790207	1896	STAT3	chr22	35772907	35773453	4152	IL6
HRAS	SP1	chr11	535499	535835	3	532241	535567	3258	STAT3	chr11	534581	534897	2340	Wnt non canonical
IFNGR2	SP1	chr21	34777757	34778093	14	34775201	34809828	2556	STAT3	chr21	34774005	34774324	593	IL6
IL10RB	SP1	chr21	34639186	34639506	14	34638664	34669539	522	STAT3	chr21	34638577	34638837	87	IL6
IL13RA1	SP1	chrX	117860833	117861169	23	117861558	117928496	725	STAT3	chrX	117857419	117857695	211	IL6
IL17RB	SP1	chr3	53880379	53880715	16	53880576	53899827	197	STAT3	chr3	53880382	53880658	194	IL6
IL1R1	SP1	chr2	102682265	102682601	12	102686835	102781830	209	STAT3	chr2	102682283	102682627	197	IL6
IL1R2	SP1	chr2	102615963	102616299	12	102615423	102644885	540	STAT3	chr2	102618318	102618594	2895	IL6
IL4R	SP1	chr16	27324567	27324903	8	27325229	27376099	662	STAT3	chr16	27324694	27325034	420	IL6
IRF9	SP1	chr14	24630211	24630620	6	24630421	24635774	210	STAT3	chr14	24630199	24630609	222	IL6
ITGA4	SP1	chr2	182321361	182321681	12	182321618	182340945	257	STAT3	chr2	182321334	182321744	284	IL6
ITGB3	SP1	chr17	45329657	45329993	9	45331207	45390077	1550	STAT3	chr17	45334941	45335620	3734	IL6/Wnt non canoni

SI Table 5.

Total Binding Affinity of JASPAR Transcription Factors (TF) with the mouse RhoU promoter. The table shows a list of the 130 transcription factors described in the JASPAR Core Vertebrata database (downloaded November 2009), ranked according to their total binding affinity with the WNT-responsive region of the RhoU promoter (-756 to -235). A rank of 0.99 means that the affinity value with the RhoU promoter is higher compared to that shown by 99% of all gene promoters.

TF	rank
MZF1_5-13	0.995208285029755
ZNF354C	0.99408764201252031
ETS1	0.98334492619213232
MZF1_1-4	0.95969549424221345
Mycn	0.95749285107040727
Myc	0.95617899373985626
PPARG::RXRA	0.95204420743488682
Nr2e3	0.94292449184635596
Myf	0.94010356287193753
znf143	0.93426849060978434
INSM1	0.92453048921864134
EWSR1-FLI1	0.91869541695648815
ELK1	0.90644562949223273
SP1	0.89539377077053872
Arnt::Ahr	0.87727026818146692
Spz1	0.8758791251255893
RREB1	0.87421748203106886
ELF5	0.87309683901383417
PLAG1	0.86865290980755849
SPI1	0.85632583661797668
Esrrb	0.85168869309838469
BRCA1	0.83766133395161912

Sox17	0.83731354818764969
PBX1	0.83553597650513955
TLX1::NFIC	0.82943040420434344
Zfx	0.82417497488213931
REST	0.81621454517350644
ESR1	0.80983847283406751
RUNX1	0.80879511554215933
Egr1	0.80411932915990414
ESR2	0.80033232861890413
Klf4	0.79449725635675095
USF1	0.79306747043821002
GATA3	0.77548496792642396
Pax5	0.76779503825643403
NR3C1	0.76601746657392378
Pax4	0.76439446634206665
CTCF	0.76358296622613808
Gfi	0.7626941803848829
Sox2	0.75589303655614803
GABPA	0.75496560785222966
SPIB	0.74611639230234172
MYC::MAX	0.74244532034933153
Foxd3	0.73232089033155578
TFAP2A	0.71002395857485123
SOX9	0.70299095757013674
Stat3	0.69924259989179993
NHLH1	0.69456681350954474
Myb	0.68958188422598343
SRF	0.68757245536749367
Tal1::Gata1	0.68223974031996293

HNF4A	0.67640466805780974
HIF1A::ARNT	0.65801066543009501
E2F1	0.63888244841177833
Hand1::Tcfe2a	0.6313857330551047
IRF2	0.62976273282324757
RXR::RAR_DR5	0.62856480408068627
GATA2	0.62728958961279857
Zfp423	0.62543473220496171
NFATC2	0.61187108741015539
MAX	0.61183244454749208
FEV	0.5974959424994204
SRY	0.59479094211299177
NFKB1	0.58733286961898135
NFIC	0.58273436896205266
Arnt	0.58227065461009353
TAL1::TCF3	0.58049308292758328
TEAD1	0.57527629646804235
Nkx3-2	0.5626014375144911
REL	0.53759950537135792
ARID3A	0.5313393616199088
SOX10	0.5263930751990108
Lhx3	0.52055800293685761
NF-kappaB	0.51823943117706162
Hltf	0.51584357369193912
Nkx2-5	0.4831130690161527
Gata1	0.48017621145374451
Ddit3::Cebpa	0.47078599582657082
MIZF	0.44914599273514183
NR1H2::RXRA	0.44377463482494783

ELK4	0.44137877733982533
EBF1	0.44033542004791715
Pou5f1	0.43175670453667209
NFE2L1::MafG	0.42881984697426384
STAT1	0.42093670299095759
IRF1	0.41888863126980447
En1	0.41884998840714122
RELA	0.41684055954865135
Sox5	0.41363320194760028
TP53	0.41119870159981453
Mafb	0.40710255815750829
YY1	0.39280469897209985
RXRA::VDR	0.39210912744416104
Pax6	0.38774248396321198
Tcfcp2l1	0.38720148388592629
NR2F1	0.36532962361851767
NKX3-1	0.36053790864827268
PPARG	0.33855011979287425
NR4A2	0.32552747507535357
ZEB1	0.31265940180848595
HNF1B	0.28560939794419971
RORA_1	0.28460468351495477
Prrx2	0.27471211067315865
Pax2	0.26791096684442384
MEF2A	0.26586289512327071
T	0.25512017930288278
FOXC1	0.21535667362238195
HNF1A	0.21354045907720845
Evi1	0.18467424066774868

Foxq1	0.18254888322126903
FOXI1	0.17779581111368731
HOXA5	0.17327459618208516
FOXO3	0.15248473606924801
Nobox	0.15202102171728882
Pdx1	0.14823402117628873
CREB1	0.13181080454440064
NFYA	0.12400494628642089
FOXD1	0.12280701754385964
CEBPA	0.1195610170801453
FOXL1	0.096877656696808104
FOXF2	0.09571837081691012
Ar	0.091660870237267184
NFE2L2	0.091081227297318185
FOXA1	0.082966226138032312
HLF	0.079372439910348563
RORA_2	0.064842723548960507
TBP	0.052322436046062293
Foxa2	0.049385578483654068
NFIL3	0.046989720998531569
AP1	0.038449648349949767

Supporting Information Table 6.

Results of the GO analysis performed on the genes of the SP1-S3 signature. Same colors indicate related biological processes mentioned in the text.

PANTHER GO-Slim Biological Process	Homo sapiens-Background	Genes in Anr	expected	over/under	fold Enrichm	raw P-value
chromatin assembly (GO:0031497)	40	10	0,28	+	36,28	1,34E-12
chromatin organization (GO:0006325)	273	17	1,88	+	9,04	1,58E-11
cellular process (GO:0009987)	8247	93	56,83	+	1,64	1,90E-09
metabolic process (GO:0008152)	5878	69	40,51	+	1,7	6,03E-07
intracellular signal transduction (GO:0035556)	1071	23	7,38	+	3,12	1,50E-06
proteolysis (GO:0006508)	448	14	3,09	+	4,53	3,65E-06
signal transduction (GO:0007165)	2318	35	15,97	+	2,19	7,42E-06
regulation of gene expression, epigenetic (GO:0040029)	71	6	0,49	+	12,26	1,47E-05
DNA metabolic process (GO:0006259)	391	12	2,69	+	4,45	2,21E-05
organelle organization (GO:0006996)	1212	22	8,35	+	2,63	3,44E-05
primary metabolic process (GO:0044238)	4753	54	32,75	+	1,65	8,59E-05
cell communication (GO:0007154)	2686	36	18,51	+	1,94	8,38E-05
response to stimulus (GO:0050896)	2677	36	18,45	+	1,95	8,08E-05
transcription, DNA-dependent (GO:0006351)	1020	18	7,03	+	2,56	2,66E-04
cellular component biogenesis (GO:0044085)	776	15	5,35	+	2,81	3,52E-04
MAPK cascade (GO:0000165)	340	9	2,34	+	3,84	6,86E-04
nitrogen compound metabolic process (GO:0006807)	2524	31	17,39	+	1,78	1,26E-03
cellular component organization (GO:0016043)	1964	25	13,53	+	1,85	2,50E-03
cellular component organization or biogenesis (GO:0071840)	2099	26	14,46	+	1,8	3,22E-03