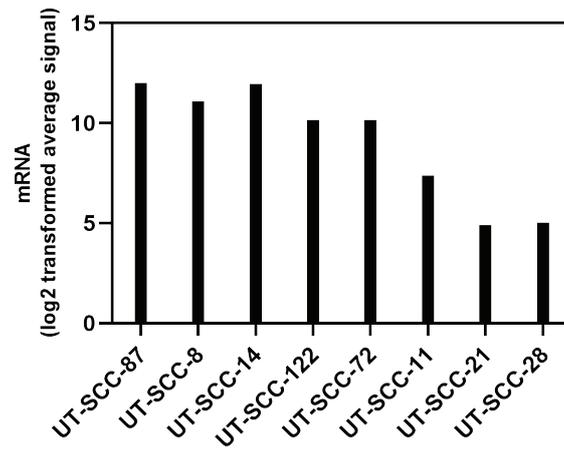


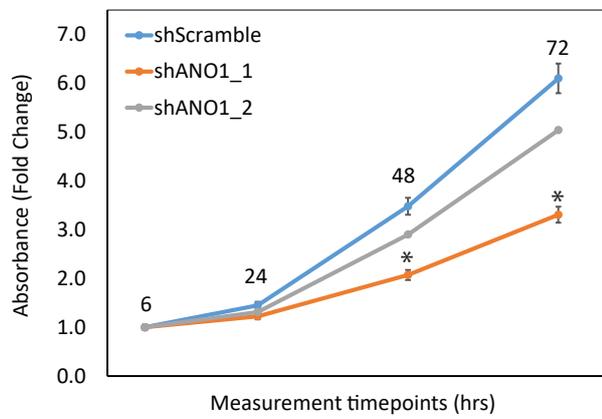
Figure S1

A ANO1 mRNA expression

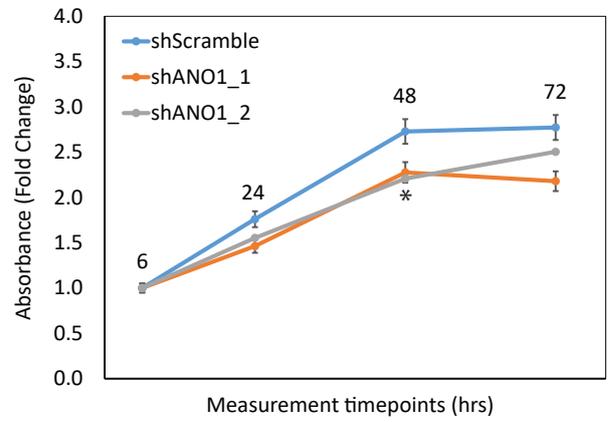


B

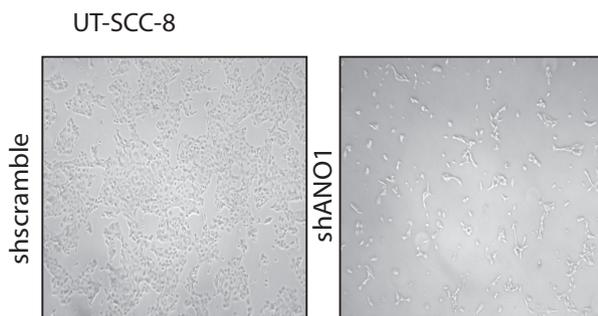
Proliferation curves of UT-SCC-8



Proliferation curves of UT-SCC-14



C



D

Caspase activity of UT-SCC-8 cell line

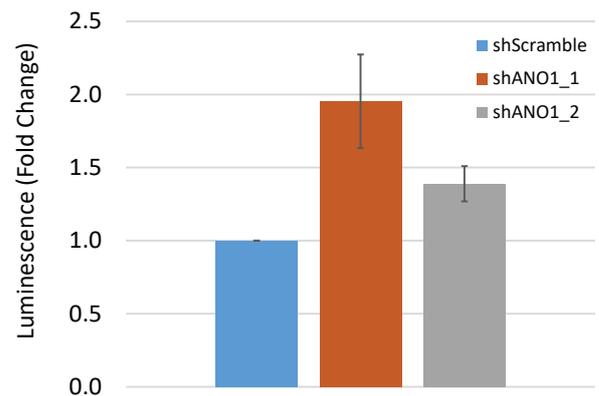
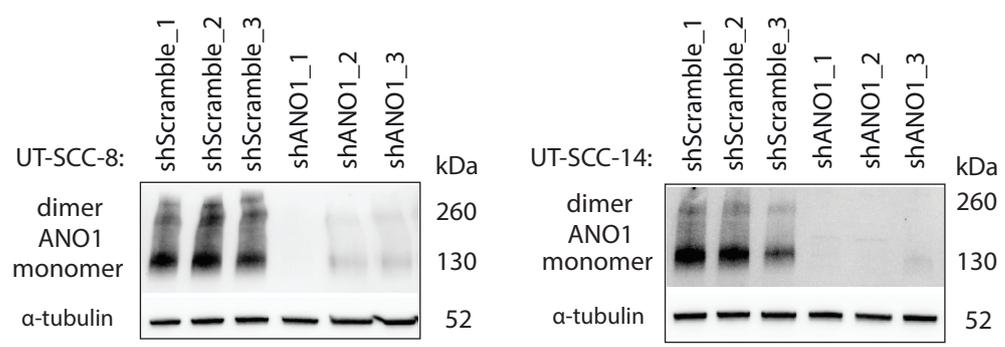


Figure S2

A



B

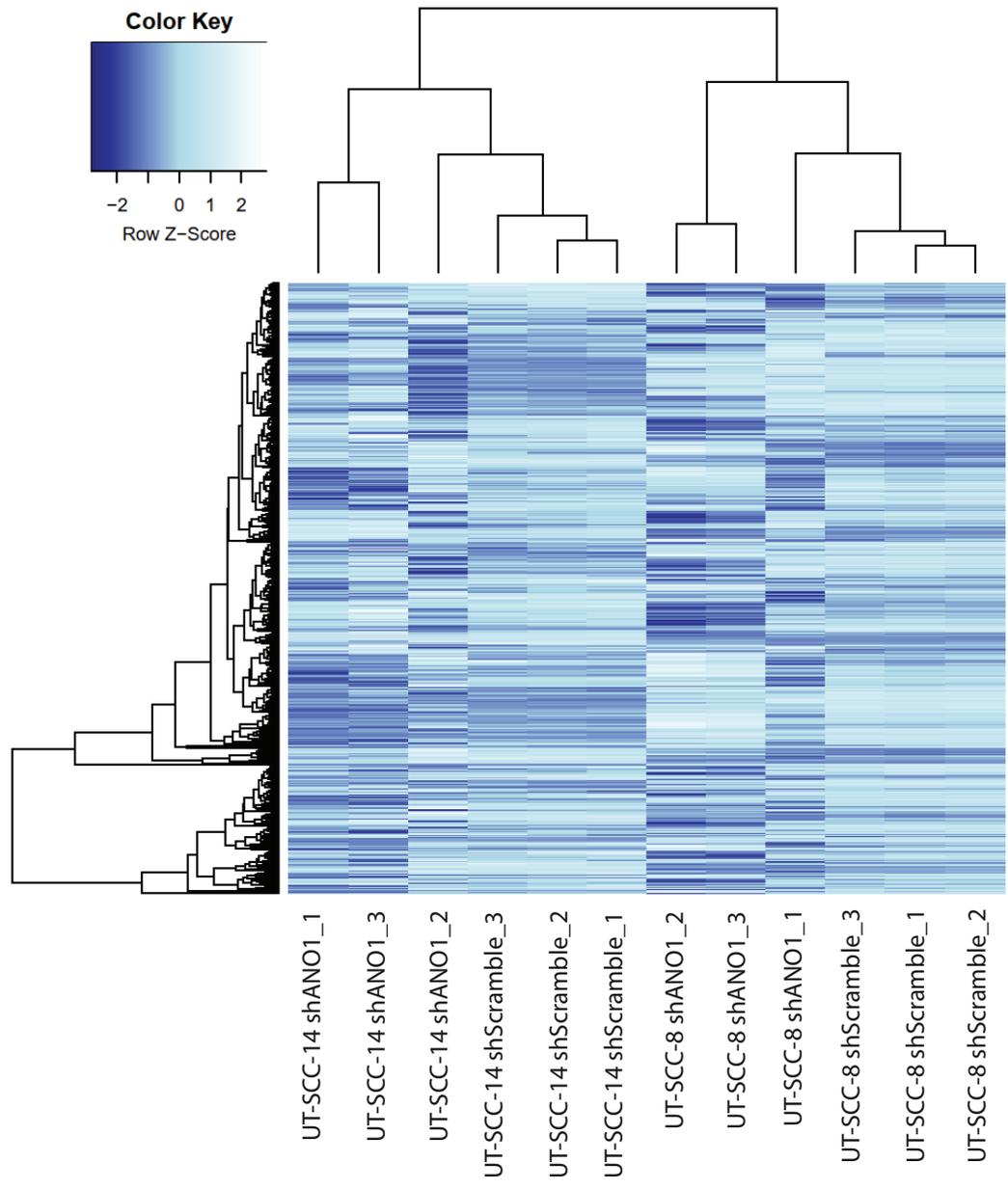
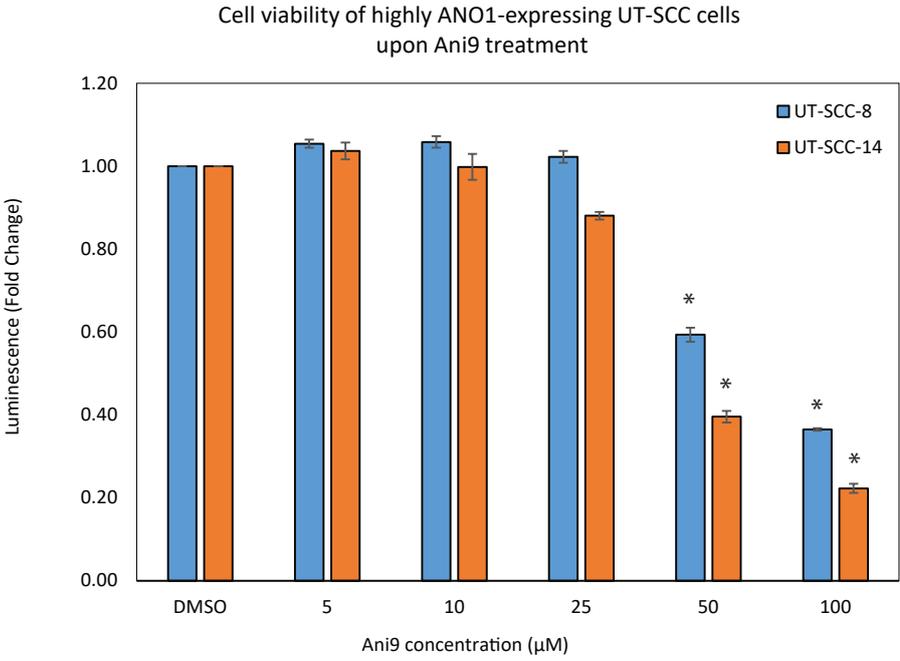


Figure S4

A



B

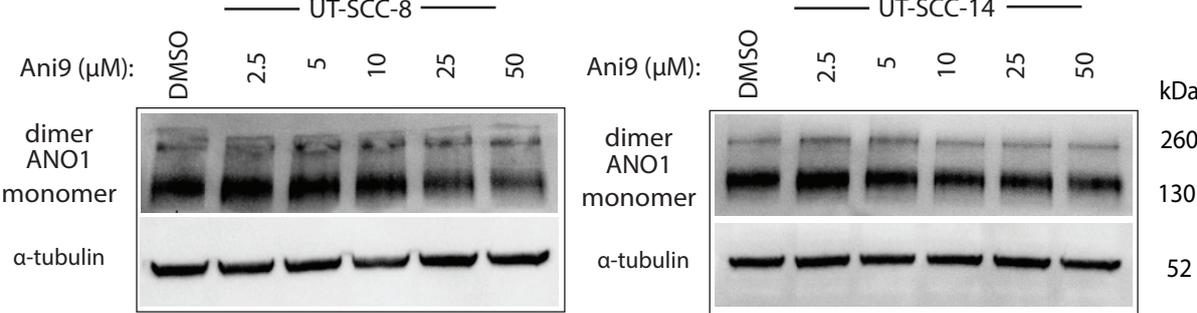
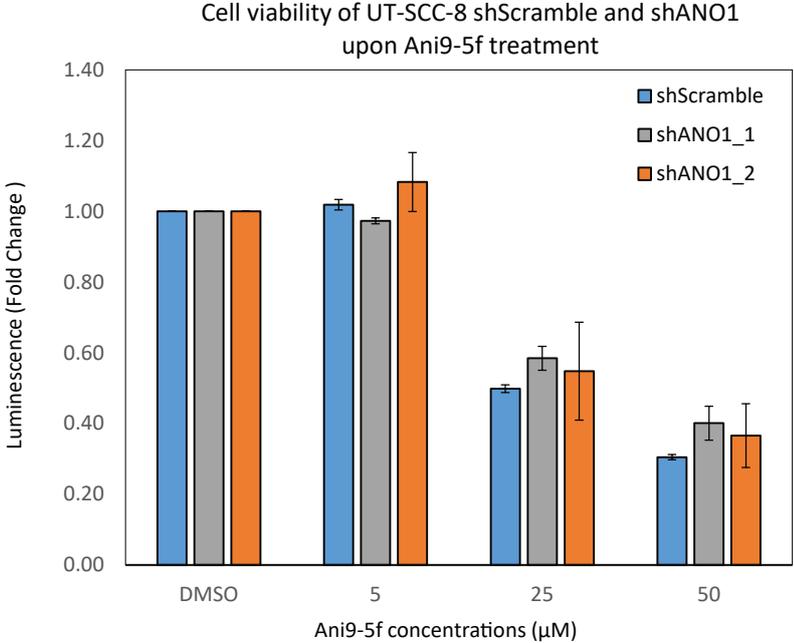


Figure S5

A



B

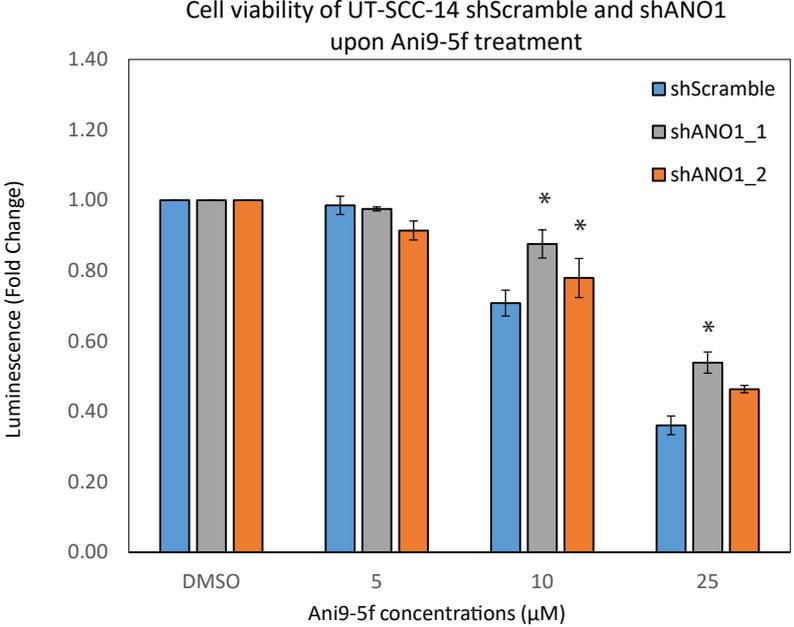
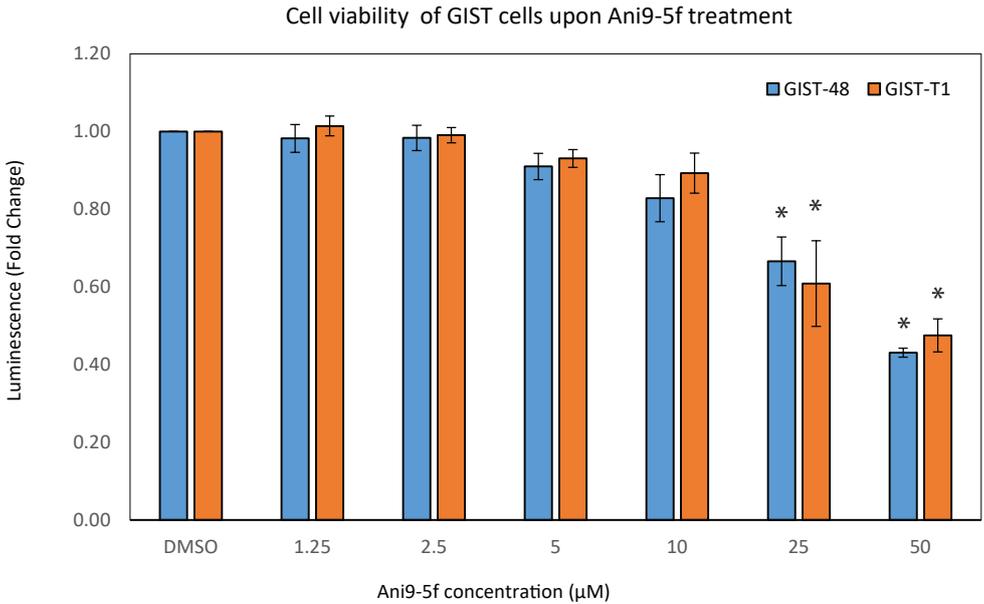


Figure S6

A



B

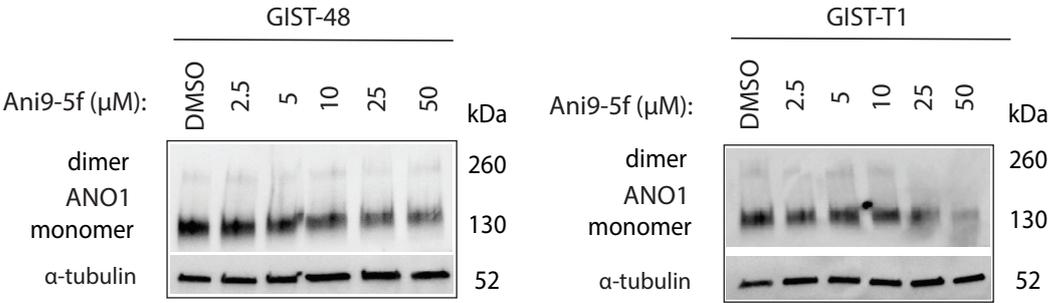
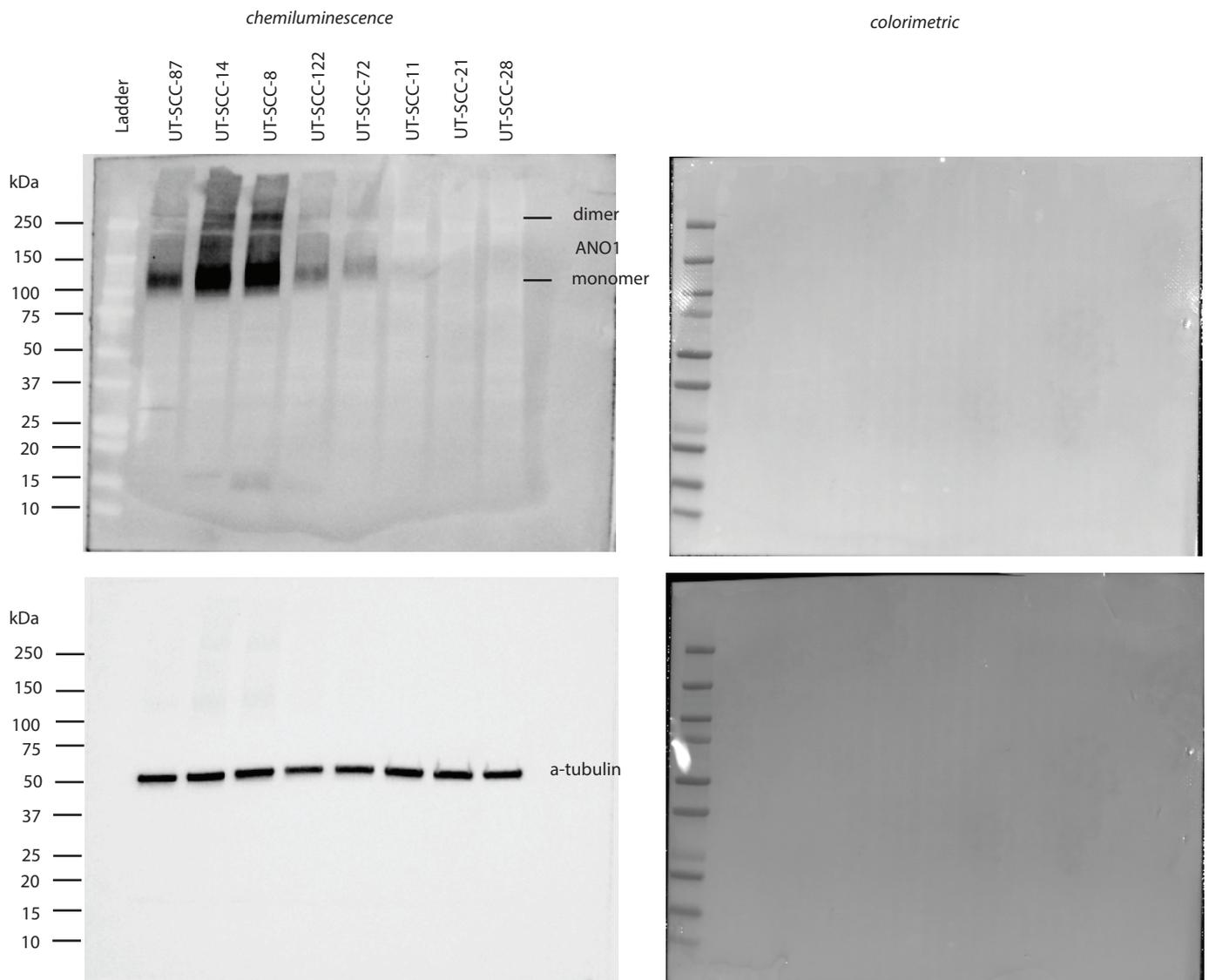


Figure S7 Uncropped blots of Figure 1A.

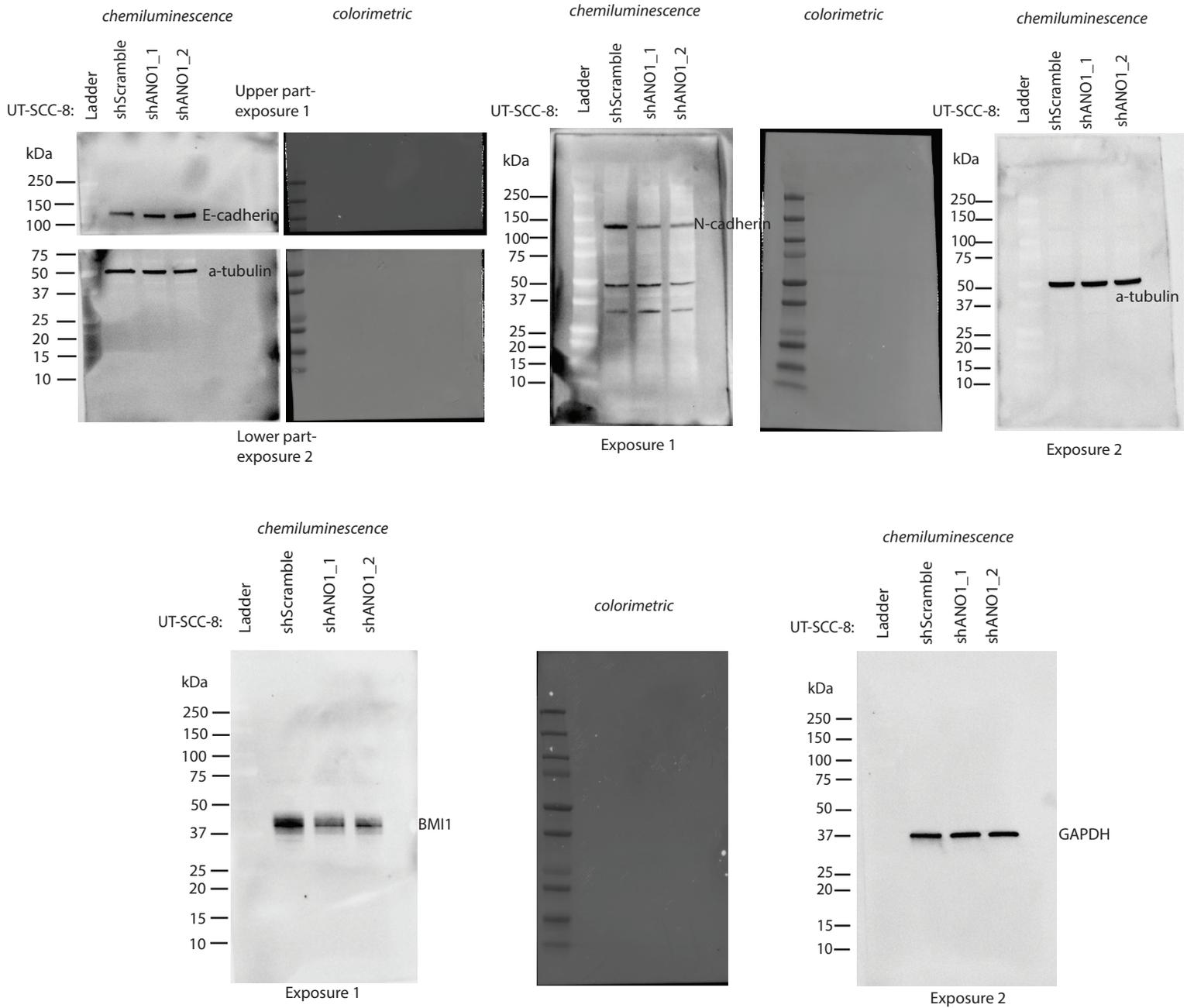
Immunoblot analysis of the proteins ANO1 and α -tubulin from a panel of ANO1-high/-low UT-SCC cell lines. Cell lines were selected based on their varying ANO1 mRNA expression (see Figure S1 and Lepikhova et al., 2018). Alpha-tubulin was used as the loading control to normalize the quantities of the proteins. Immunoblot figures, densitometry readings and normalized values are presented in the table below.



	Intensity of each band (background adjusted)							
	UT-SCC-87	UT-SCC-14	UT-SCC-8	UT-SCC-122	UT-SCC-72	UT-SCC-11	UT-SCC-21	UT-SCC-28
ANO1	2122120	4222667	4081735	1125580	719798	92608	25521	16267
α -tubulin	2167346	2171457	2001814	1308144	1489957	1881457	1921531	1677118
Intensity ratio	0.98	1.94	2.04	0.86	0.48	0.05	0.01	0.01

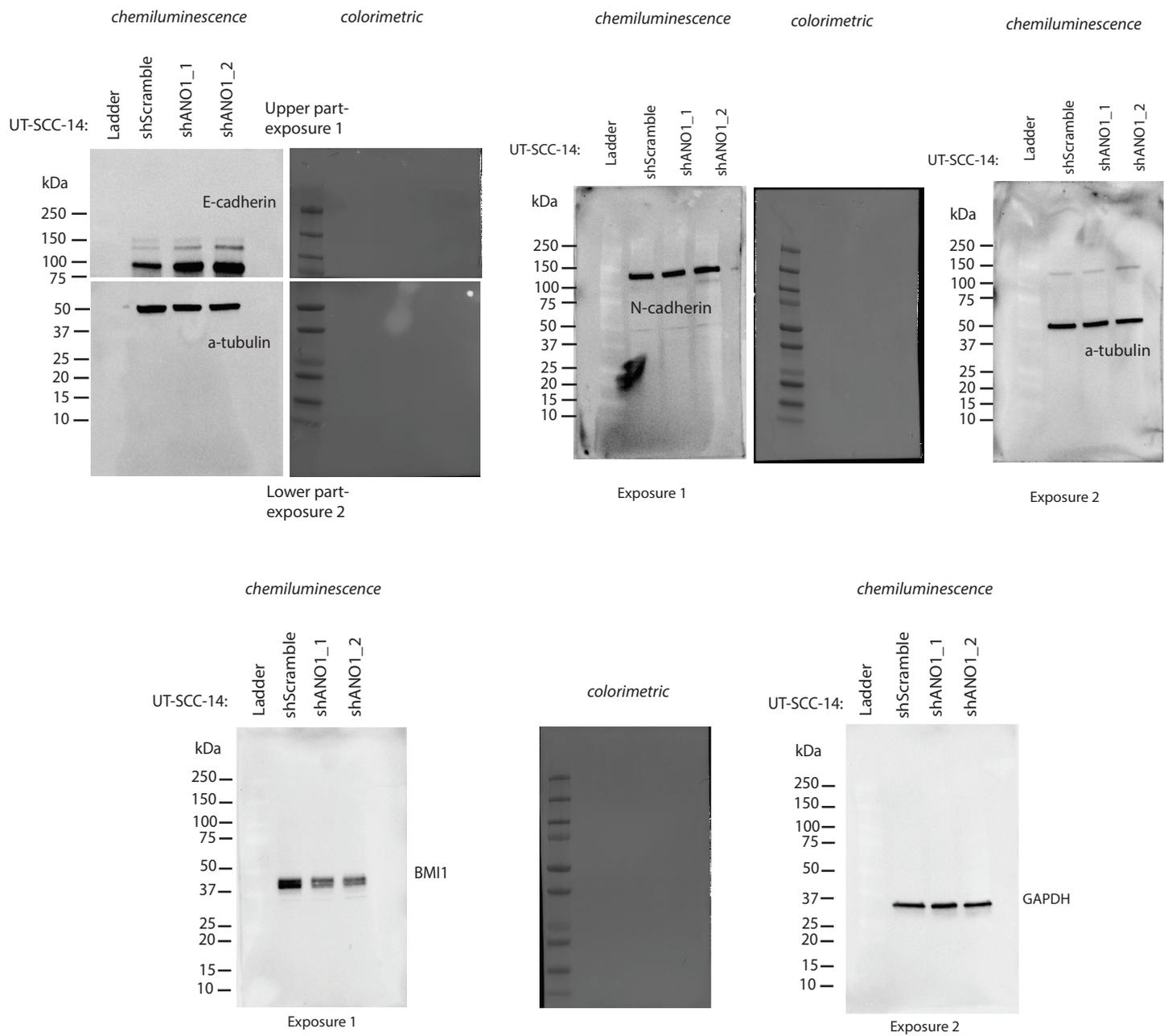
Figure S7 Uncropped blots of Figure 1C.

Immunoblot analysis of the proteins E-cadherin, N-cadherin, BMI1 in cell lines UT-SCC-8 shScramble and shANO1_1, shANO1_2, as well as UT-SCC-14 shScramble and shANO1_1, shANO1_2. Alpha-tubulin or GAPDH were used as the loading controls to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the table under the whole blots.



	Intensity of each band (background adjusted)		
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2
E-cadherin	754248	1019701	1559675
α -tubulin	1196417	1497757	1369201
Intensity ratio	0.63	0.68	1.14
N-cadherin	722962	16034	3697
α -tubulin	1517226	1558147	1609075
Intensity ratio	0.477	0.010	0.002
BMI1	4807371	2355650	2474908
α -tubulin	1587335	1742467	1626584
Intensity ratio	3.03	1.35	1.52

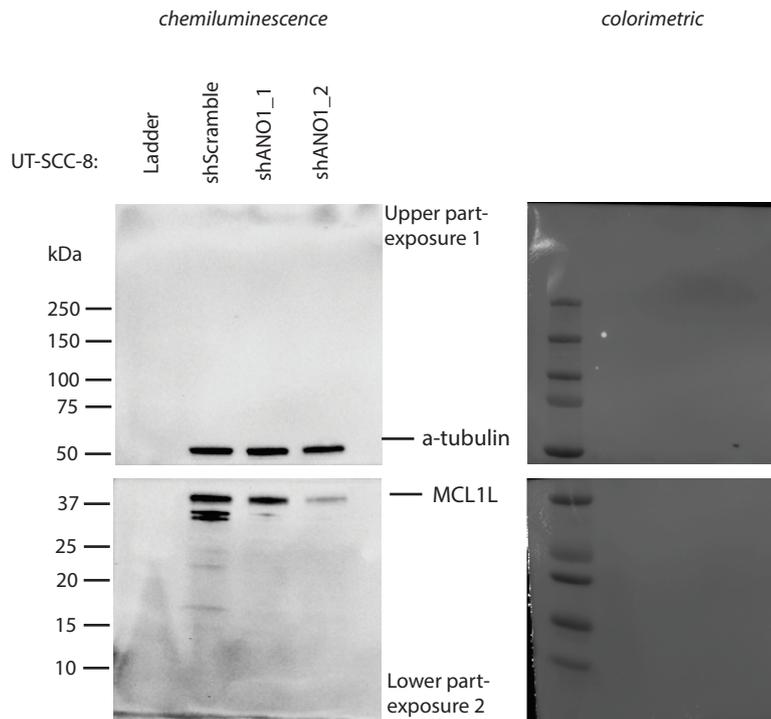
Figure S7 Uncropped blots of Figure 1C.



	Intensity of each band (background adjusted)		
	UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
E-cadherin	1123628	2484411	3173673
α -tubulin	2054479	1696848	1854173
Intensity ratio	0.55	1.46	1.71
N-cadherin	1129594	835372	1641356
α -tubulin	1819949	1381151	1466748
Intensity ratio	0.62	0.60	1.12
BMI1	4752423	2702459	2518232
GAPDH	1926586	1840563	1691702
Intensity ratio	2.47	1.47	1.49

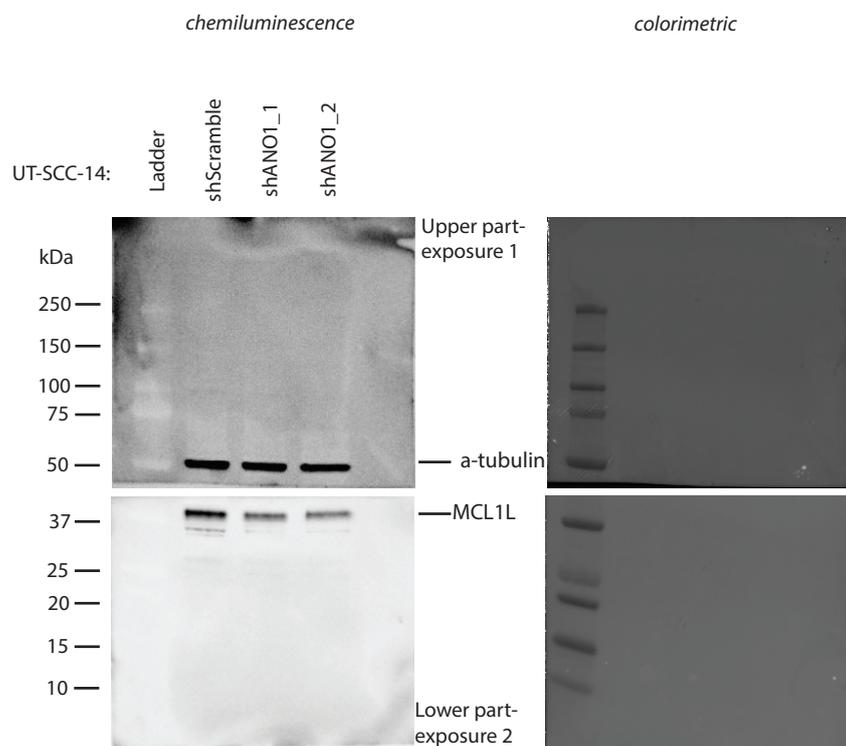
Figure S7 Uncropped blots of Figure 2B.

Immunoblot analysis of the proteins MCL-1, BCL-2, BCL-XL and BIM in cell lines UT-SCC-8 shScramble and shANO1_1, shANO1_2, as well as UT-SCC-14 shScramble and shANO1_1, shANO1_2. Alpha-tubulin was used as the loading control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the respective figures.



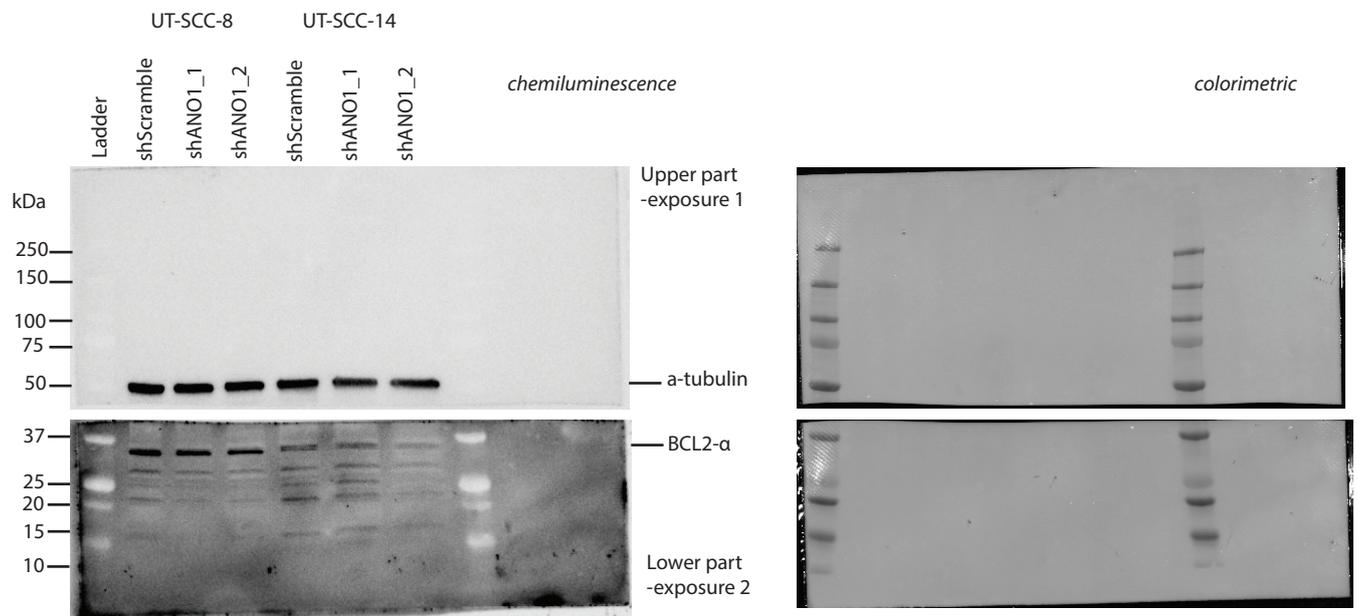
	Intensity of each band (background adjusted)		
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2
MCL1L	1379494	1043672	315049
α -tubulin	2163007	2363063	1671994
Intensity ratio	0.64	0.44	0.19

Figure S7 Uncropped blots of Figure 2B.

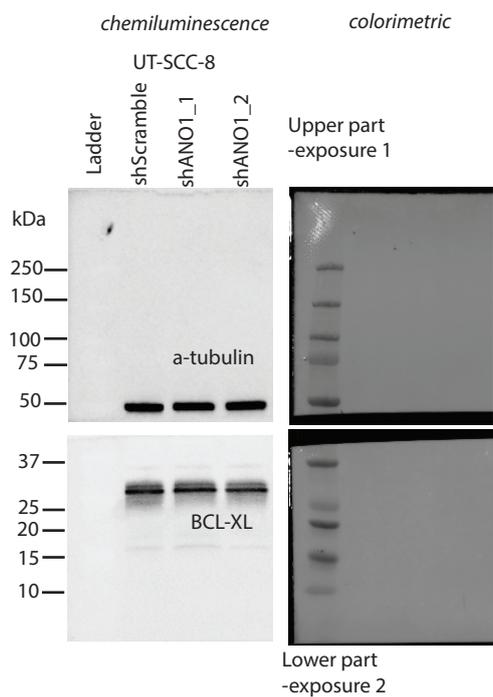


	Intensity of each band (background adjusted)		
	UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
MCL1L	1748141	747115	617846
α -tubulin	1783245	1259613	996603
Intensity ratio	0.98	0.59	0.62

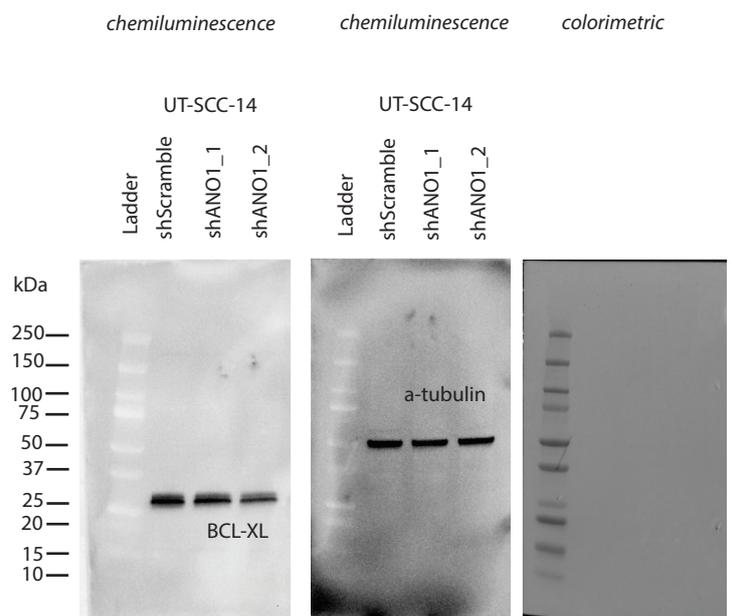
Figure S7 Uncropped blots of Figure 2B.



	Intensity of each band (background adjusted)					
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2	UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
BCL2-α	770898	547671	495145	178472	136895	90218
α-tubulin	2302198	2155391	2034745	1694849	1371401	1413635
Intensity ratio	0.33	0.25	0.24	0.11	0.10	0.06

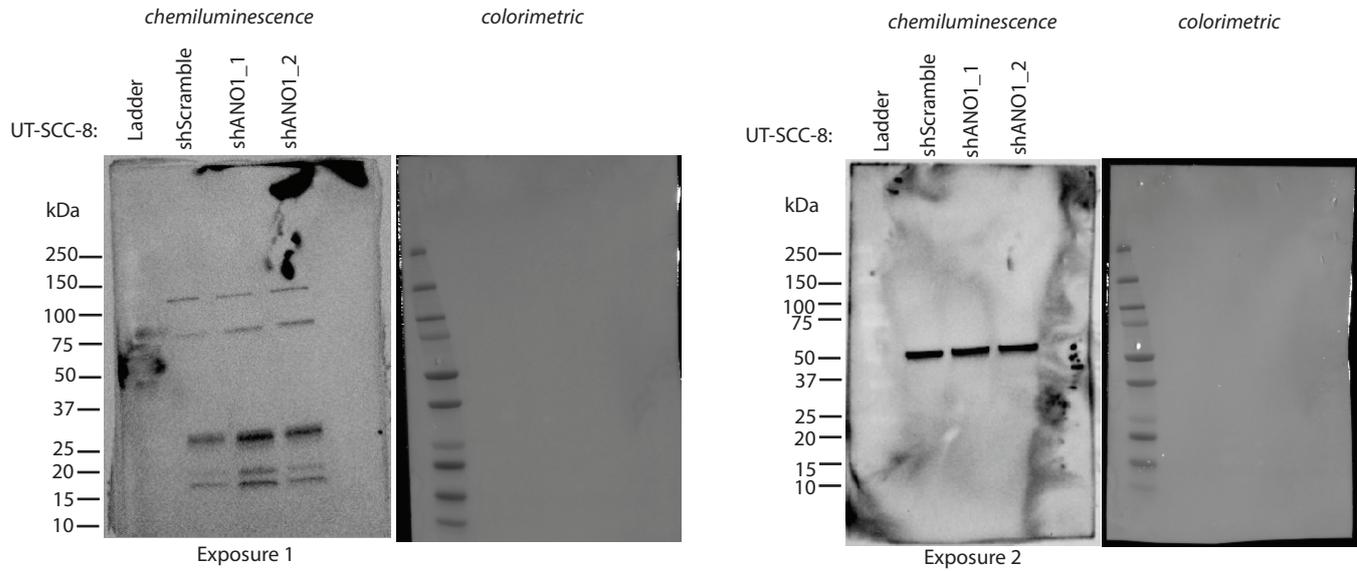


	Intensity of each band (background adjusted)		
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2
BCL-XL	3255706	2582922	2712684
α-tubulin	2068165	1959181	1760224
Intensity ratio	1.57	1.32	1.54

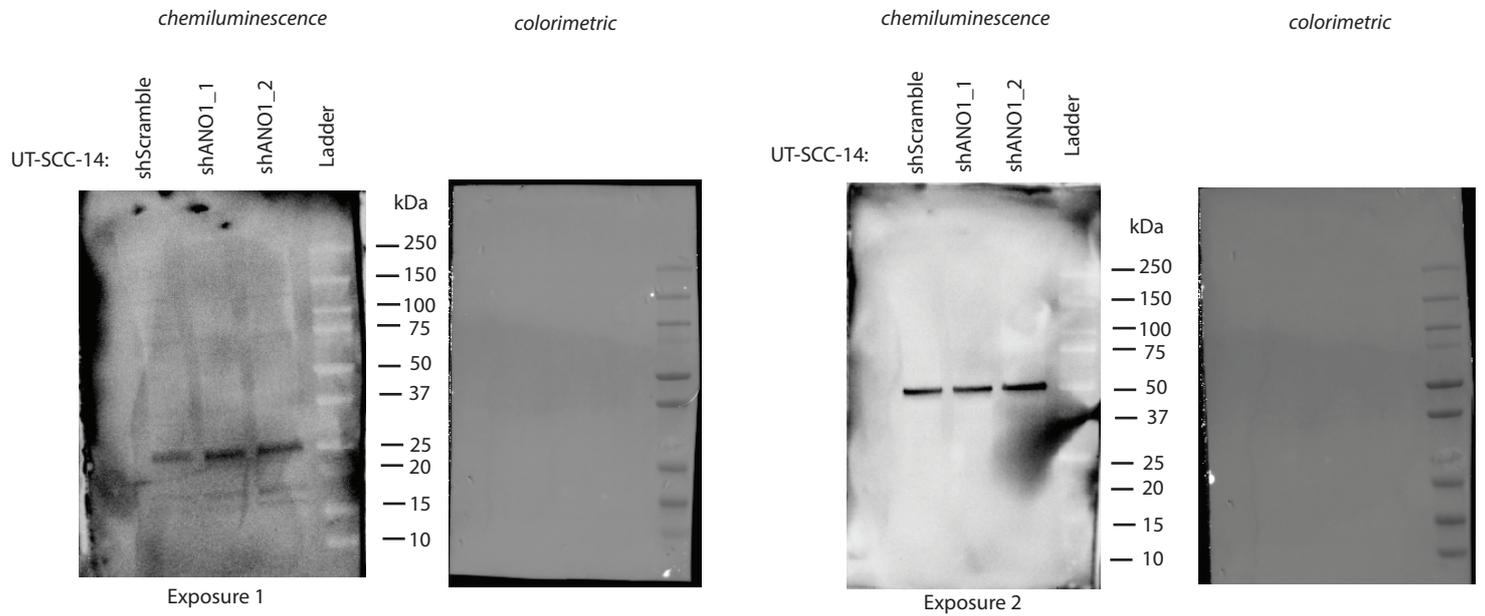


	Intensity of each band (background adjusted)		
	UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
BCL-XL	2977950	2804066	2099190
α-tubulin	1371232	984975	1248328
Intensity ratio	2.17	2.85	1.68

Figure S7 Uncropped blots of Figure 2B.



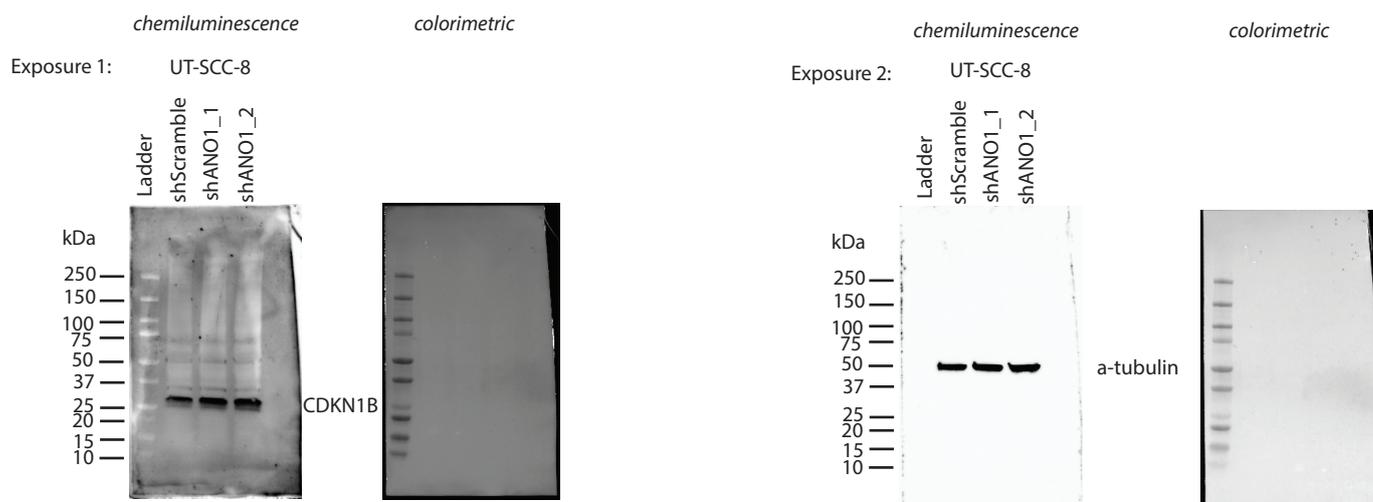
	Intensity of each band (background adjusted)		
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2
BIM	129874	261924	221288
α-tubulin	1281083	1182915	1069172
Intensity ratio	0.10	0.22	0.21



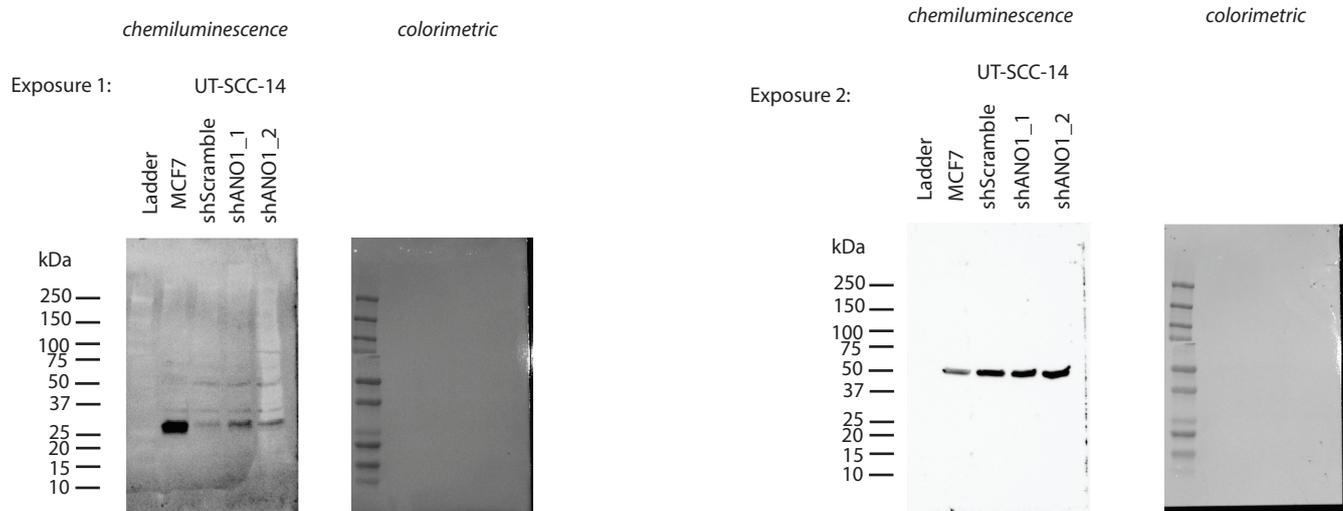
	Intensity of each band (background adjusted)		
	UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
BIM	152245	285054	326040
α-tubulin	1238184	1198241	1410510
Intensity ratio	0.12	0.24	0.23

Figure S7 Uncropped blots from Figure 4A.

Immunoblot analysis of the protein CDKN1B (p27kip1) in cell lines UT-SCC-8 shScramble and shANO1_1, shANO1_2, as well as UT-SCC-14 shScramble and shANO1_1, shANO1_2. Alpha-tubulin was used as the control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the respective whole blots.



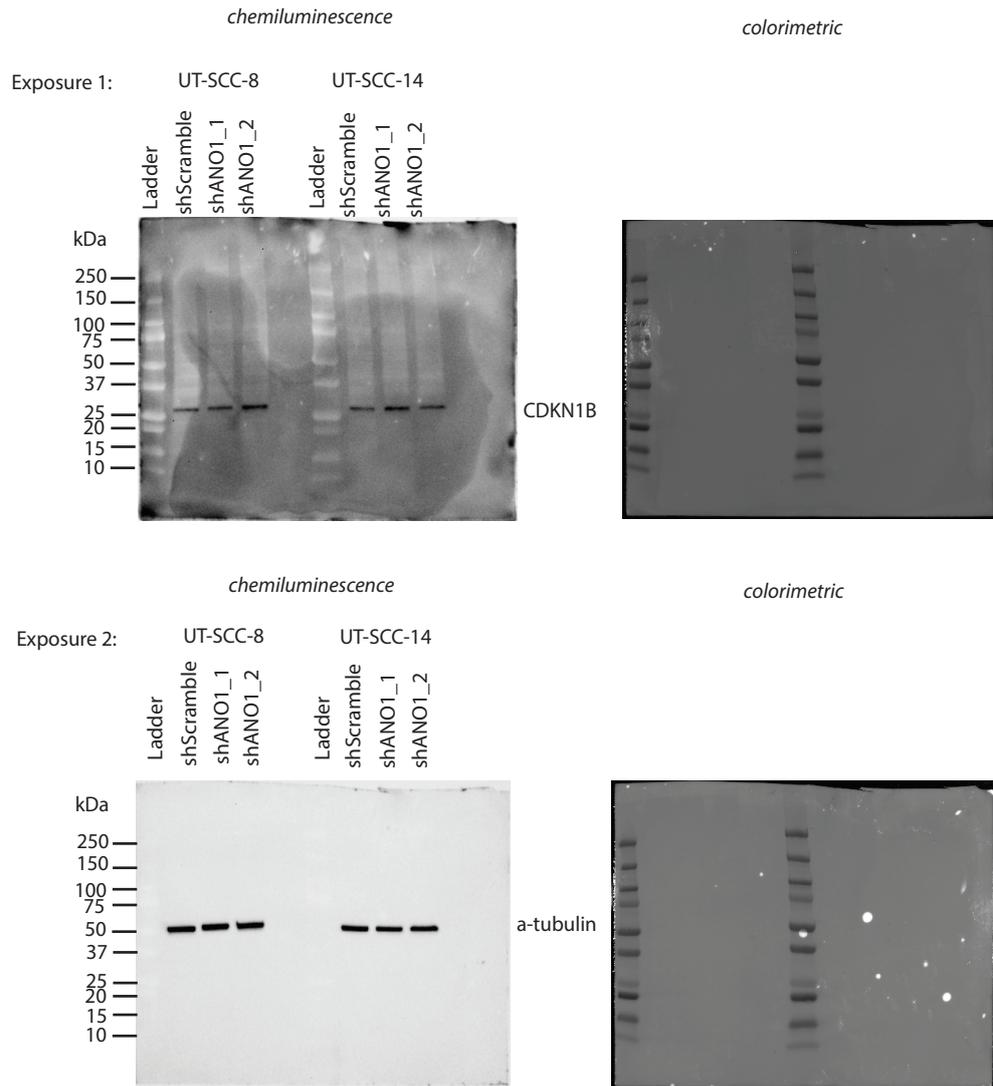
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2
CDKN1B	6954665	9387748	10598253
α -tubulin	14466840	16481549	17634530
Intensity ratio	0.48	0.57	0.60



	MCF7	Intensity of each band (background adjusted)		
		UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
CDKN1B	1465825	129064	330047	198153
α -tubulin	2625200	5544654	5449901	7602643
Intensity ratio	0.56	0.02	0.06	0.03

*MCF7 was used as positive control for the antibody

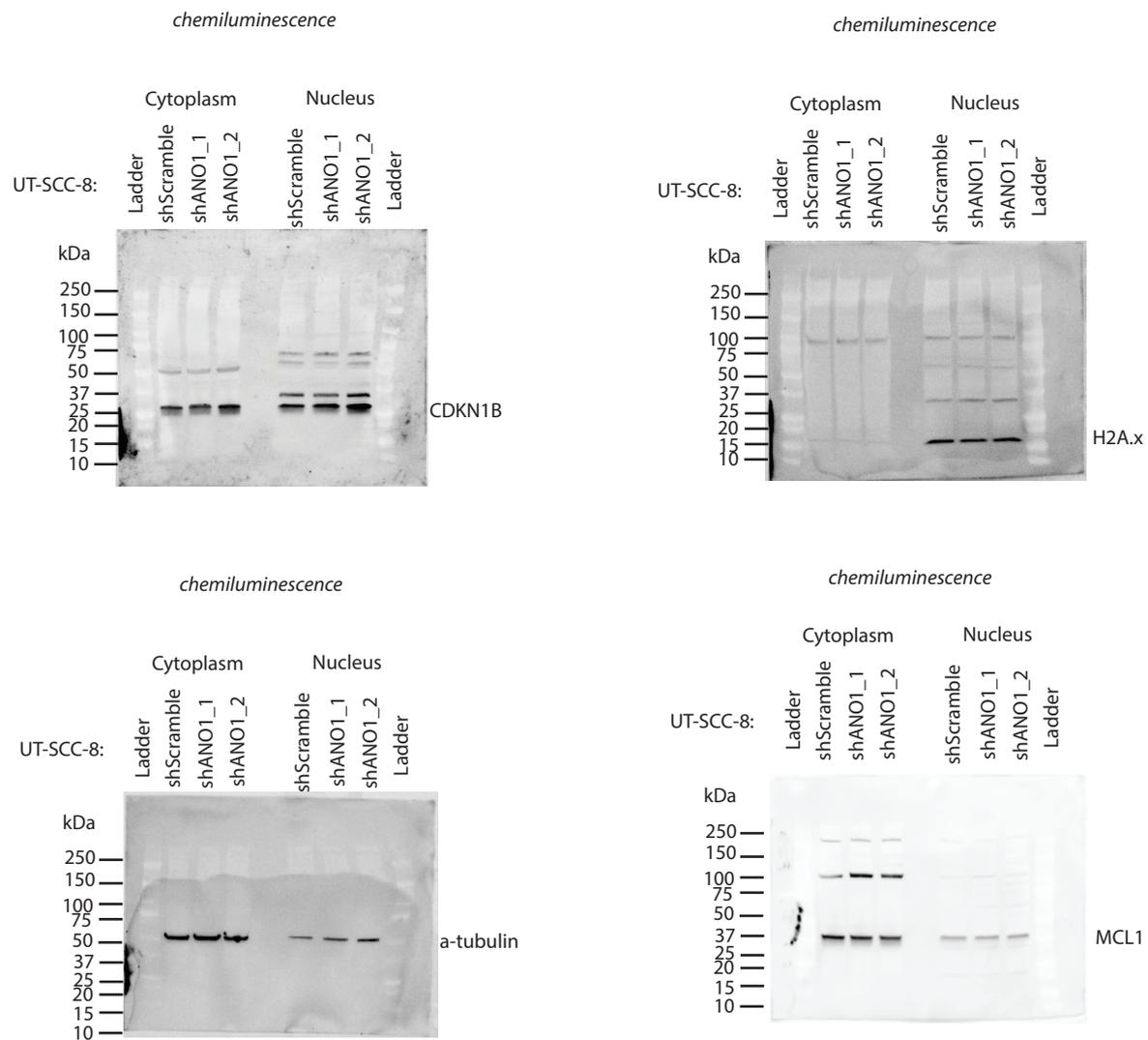
Figure S7 Addition uncropped blots (not included in Main Figure), showing the same result as Figure 4A. Immunoblot analysis of the protein CDKN1B (p27kip1) in cell lines UT-SCC-8 shScramble and shANO1_1, shANO1_2, as well as UT-SCC-14 shScramble and shANO1_1, shANO1_2. Alpha-tubulin was used as the control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the whole blots.



	Intensity of each band (background adjusted)					
	UT-SCC-8 shScramble	UT-SCC-8 shANO1_1	UT-SCC-8 shANO1_2	UT-SCC-14 shScramble	UT-SCC-14 shANO1_1	UT-SCC-14 shANO1_2
CDKN1B	126132	289606	613225	320905	657558	466882
α -tubulin	2317065	1972136	1882290	1681519	1461723	1454817
Intensity ratio	0.05	0.15	0.33	0.19	0.45	0.32

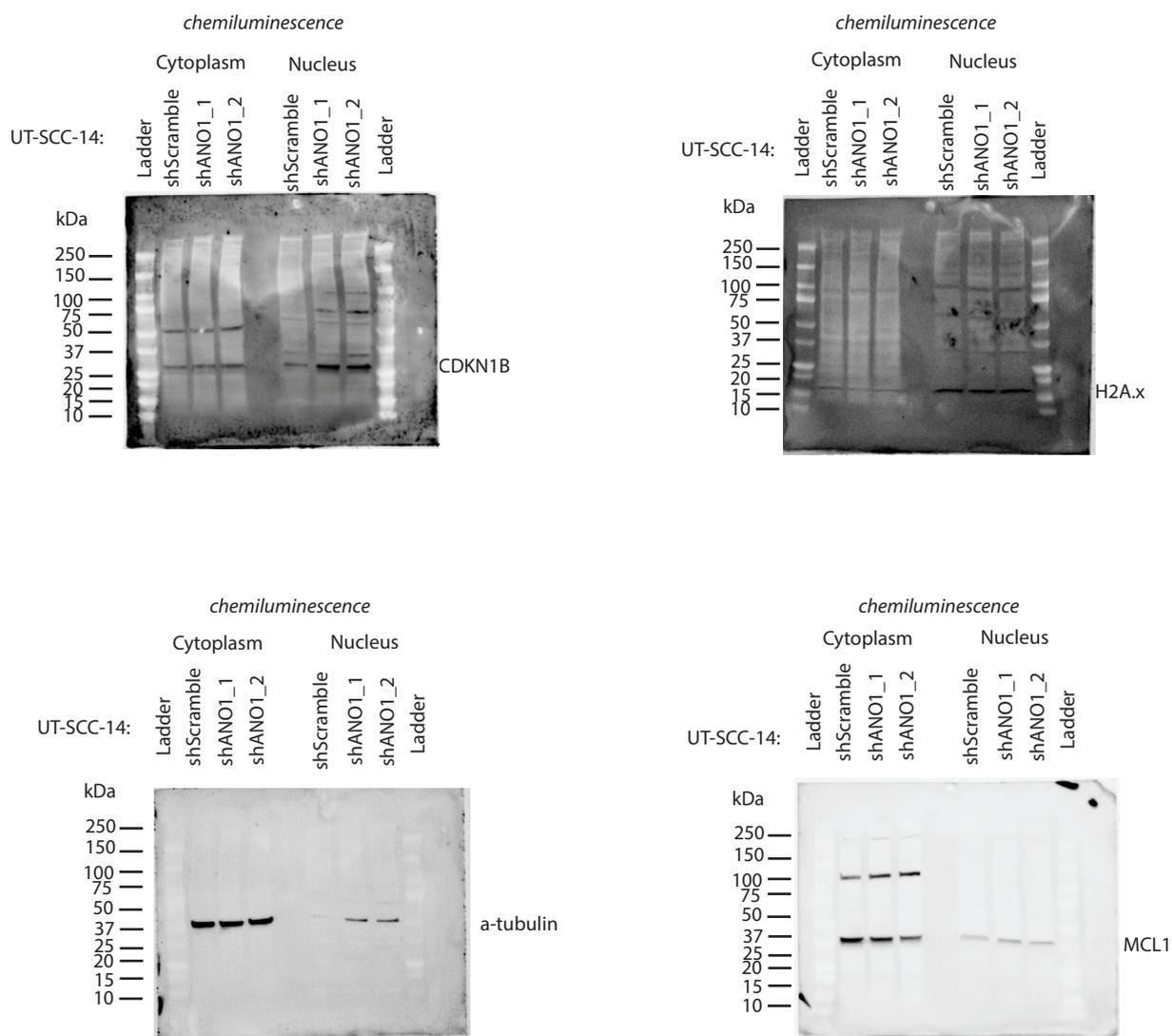
Figure S7 Uncropped blots of Figure 4B.

Immunoblot analysis of the proteins CDKN1B, H2A.x, α -tubulin, MCL1 in the cytoplasmic and nuclear fraction of the cell lines UT-SCC-8 shScramble and shANO1_1, shANO1_2, as well as UT-SCC-14 shScramble and shANO1_1, shANO1_2. Densitometry readings and normalized values are presented in the tables under the respective whole blots.



	Intensity of each band (background adjusted)					
	UT-SCC-8 shScramble cytoplasmic	UT-SCC-8 shANO1_1 cytoplasmic	UT-SCC-8 shANO1_2 cytoplasmic	UT-SCC-8 shScramble nuclear	UT-SCC-8 shANO1_1 nuclear	UT-SCC-8 shANO1_2 nuclear
CDKN1B	1613620	1726694	2195320	1775510	2390283	3665279
α -tubulin	1246482	1382003	1150454	289300	417286	468484
H2Ax	17221	25344	1668	605133	414028	562209
Intensity ratio (to α -tubulin)	1.29	1.25	1.91	6.14	5.73	7.82
Intensity ratio (to H2Ax)	93.70	68.13	1316.39	2.93	5.77	6.52
MCL1	881311	854091	636320	142116	63535	115539
Intensity ratio (to α -tubulin)	0.71	0.62	0.55	0.49	0.15	0.25
Intensity ratio (to H2Ax)	51.18	33.70	381.56	0.23	0.15	0.21

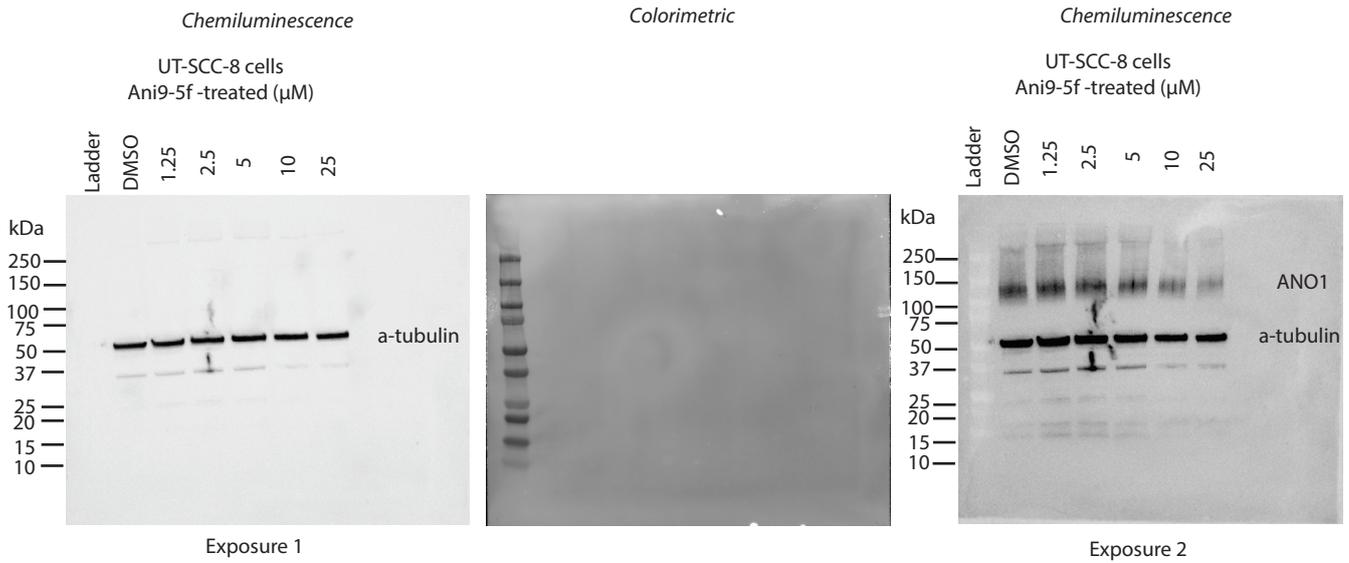
Figure S7 Uncropped blots of Figure 4B.



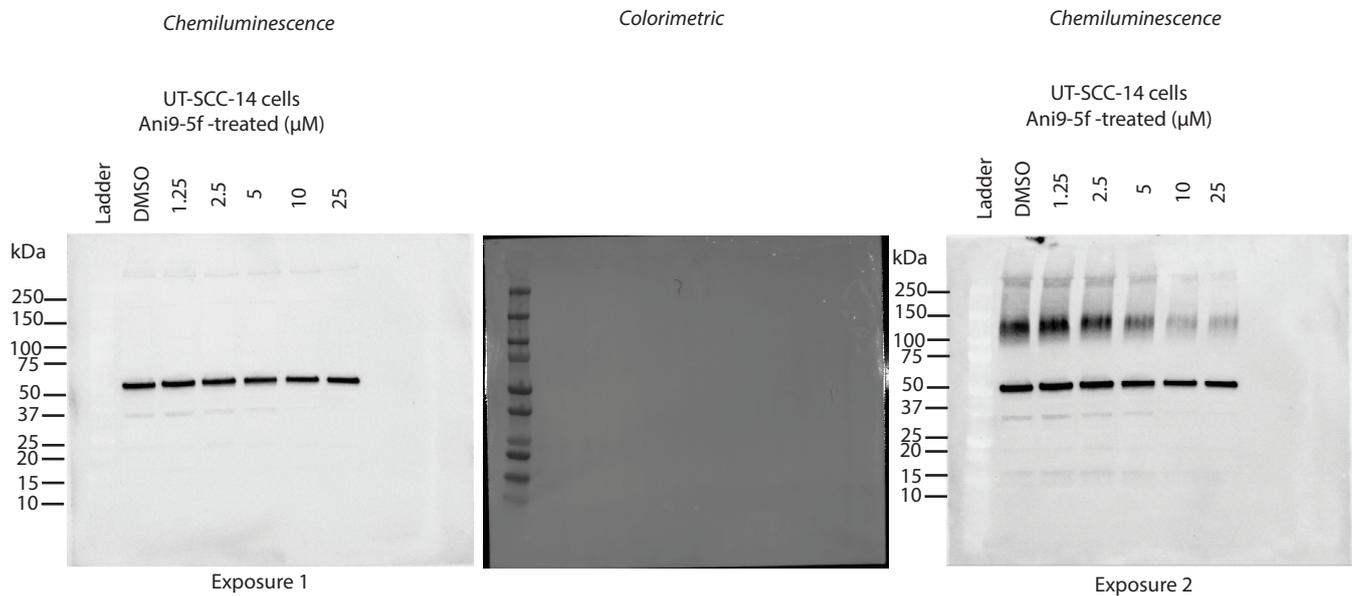
	Intensity of each band (background adjusted)					
	UT-SCC-14 shScramble cytoplasmic	UT-SCC-14 shANO1_1 cytoplasmic	UT-SCC-14 shANO1_2 cytoplasmic	UT-SCC-14 shScramble nuclear	UT-SCC-14 shANO1_1 nuclear	UT-SCC-14 shANO1_2 nuclear
CDKN1B	251426	426953	620078	358407	1449579	1448372
α -tubulin	2060382	1483864	1791450	1430	300191	348997
H2Ax	7683	11107	241691	2962334	945262	1820972
Intensity ratio (to α -tubulin)	0.12	0.29	0.35	250.71	4.83	4.15
Intensity ratio (to H2Ax)	32.72	38.44	2.57	0.12	1.53	0.80
MCL1	574987	547793	318055	28143	90272	105174
Intensity ratio (to α -tubulin)	0.28	0.37	0.18	19.69	0.30	0.30
Intensity ratio (to H2Ax)	74.84	49.32	1.32	0.01	0.10	0.06

Figure S7 Uncropped blots of Figure 5A.

Immunoblot analysis of ANO1 and a-tubulin upon treatment with a range of concentrations of Ani9-5f inhibitor. Cell lines used were UT-SCC-8 and UT-SCC-14. Densitometry readings and normalized values are presented in the tables under the respective figures.



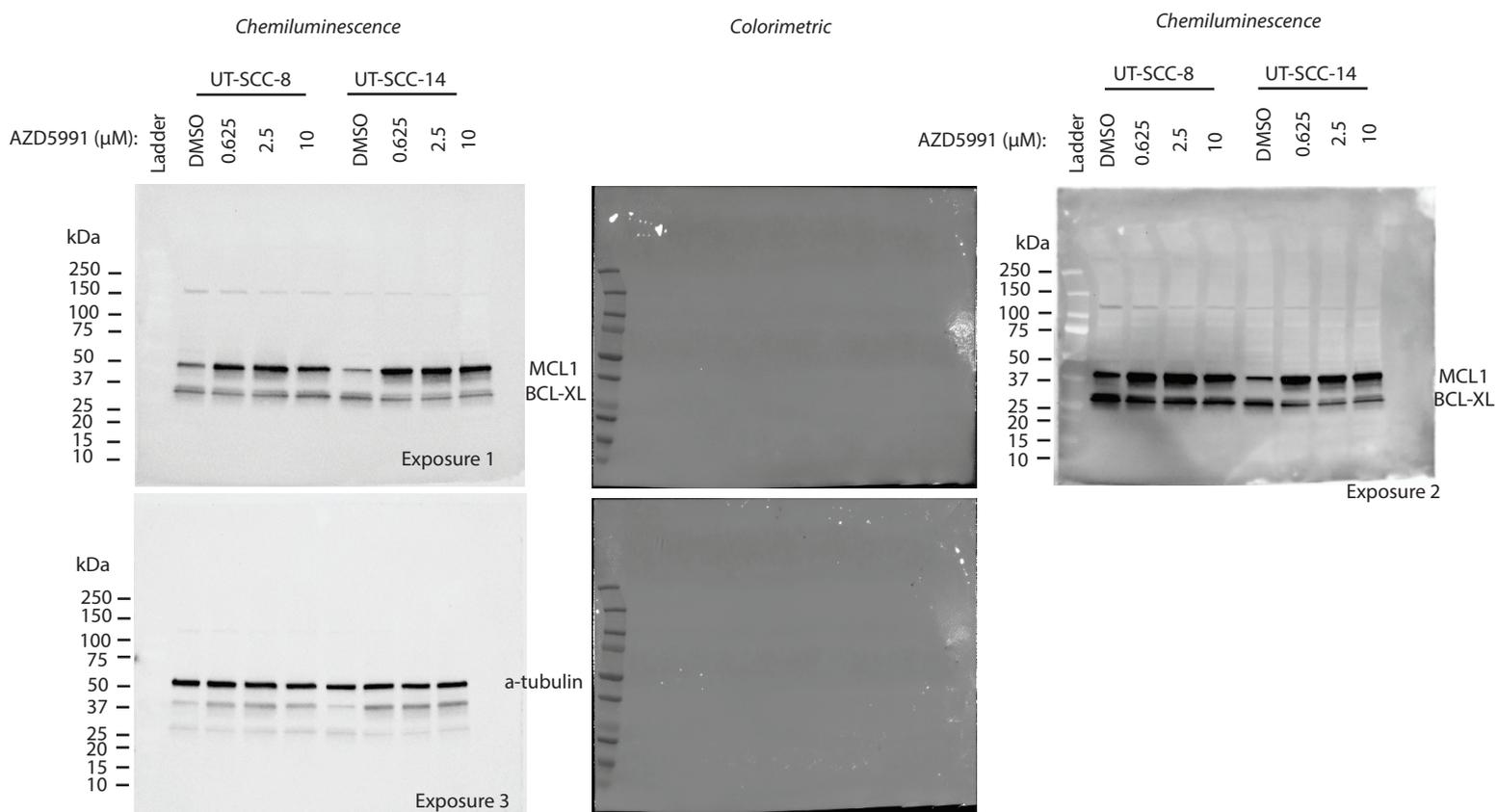
	Intensity of each band (background adjusted)					
	UT-SCC-8 DMSO	UT-SCC-8 1.25 μM	UT-SCC-8 2.5 μM	UT-SCC-8 5 μM	UT-SCC-8 10 μM	UT-SCC-8 25 μM
ANO1 (monomer)	1413815	1505826	1255117	1224846	857044	597264
a-tubulin	2036621	2279962	2613640	2682535	2508756	2262548
Intensity ratio (to a-tubulin)	0.69	0.66	0.48	0.46	0.34	0.26



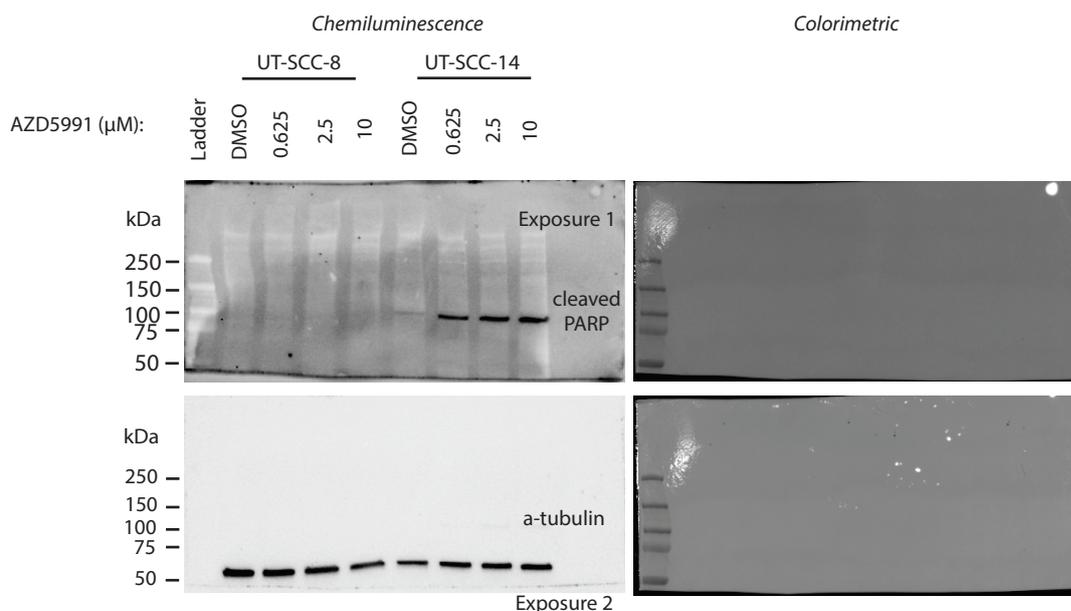
	Intensity of each band (background adjusted)					
	UT-SCC-14 DMSO	UT-SCC-14 1.25 μM	UT-SCC-14 2.5 μM	UT-SCC-14 5 μM	UT-SCC-14 10 μM	UT-SCC-14 25 μM
ANO1 (monomer)	6109486	6747155	5586846	3730226	1799467	1720249
a-tubulin	3502227	3223582	2766304	2624671	2579560	2943333
Intensity ratio (to a-tubulin)	1.74	2.09	2.02	1.42	0.70	0.58

Figure S7 Uncropped blots of Figure 6B.

Immunoblot analysis of the proteins MCL-1, BCL-XL and α -tubulin from cell lysates of UT-SCC-8 and UT-SCC-14 treated with a range of concentrations of AZD-5991 inhibitor. Alpha-tubulin was used as the control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the respective figures.



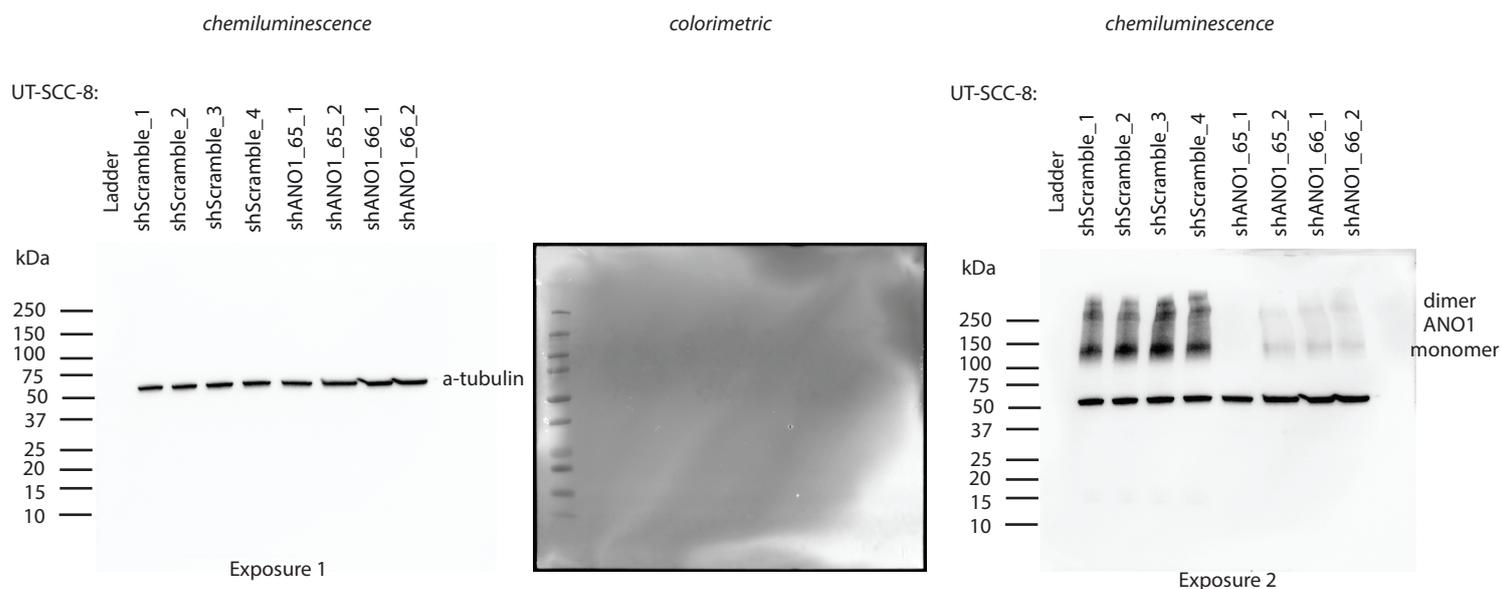
AZD-5991-treated	Intensity of each band (background adjusted)							
	UT-SCC-8 DMSO	UT-SCC-8 0.625 μ M	UT-SCC-8 2.5 μ M	UT-SCC-8 10 μ M	UT-SCC-14 DMSO	UT-SCC-14 0.625 μ M	UT-SCC-14 2.5 μ M	UT-SCC-14 10 μ M
MCL1	674694	1607502	2045739	1519667	577321	2225212	1972098	2007980
BCL-XL	7978149	5708129	7218642	7232210	6729603	4966260	3572365	4846508
α -tubulin	1961259	2071485	1889649	1740564	1730898	1963104	1591766	1856926
Intensity ratio (MCL1/ α -tubulin)	0.34	0.78	1.08	0.87	0.33	1.13	1.24	1.08
Intensity ratio (BCL-XL/ α -tubulin)	4.07	2.76	3.82	4.16	3.89	2.53	2.24	2.61



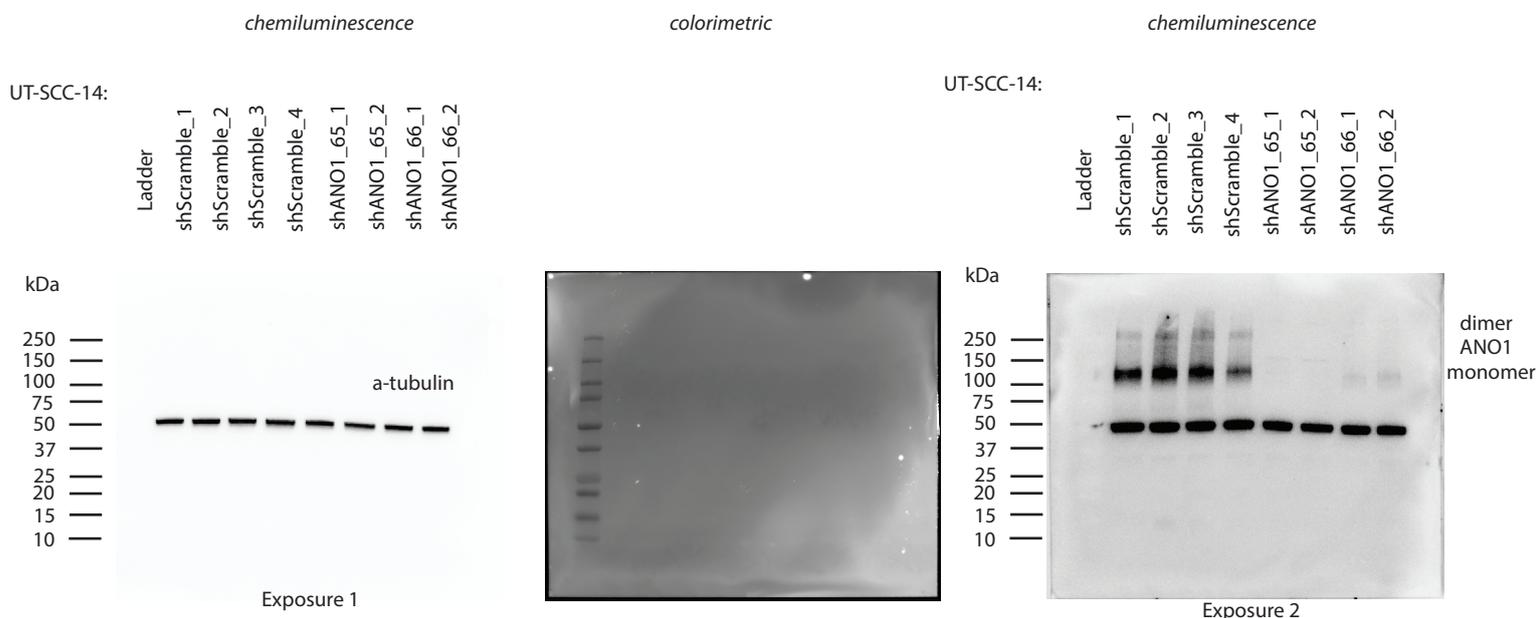
AZD-5991-treated	Intensity of each band (background adjusted)							
	UT-SCC-8 DMSO	UT-SCC-8 0.625 μ M	UT-SCC-8 2.5 μ M	UT-SCC-8 10 μ M	UT-SCC-14 DMSO	UT-SCC-14 0.625 μ M	UT-SCC-14 2.5 μ M	UT-SCC-14 10 μ M
Cleaved-PARP	-48534	-63401	-94361	10784	52453	515492	902968	1112333
α -tubulin	2441657	2155564	1765976	1409903	1320234	1602544	1554180	1673707
Intensity ratio (PARP/ α -tubulin)	0.00	0.00	0.00	0.01	0.04	0.32	0.58	0.66

Figure S7 Uncropped blots of Figure S2A.

Immunoblot analysis shows ANO1 and α -tubulin protein levels following lentiviral transductions. Two different shRNA constructs targeting ANO1, as well as two technical replicates were tested. shScramble indicates control lentivirus constructs. Cell lines used were UT-SCC-8 and UT-SCC-14. Densitometry readings and normalized values are presented in the tables under the respective whole blots.



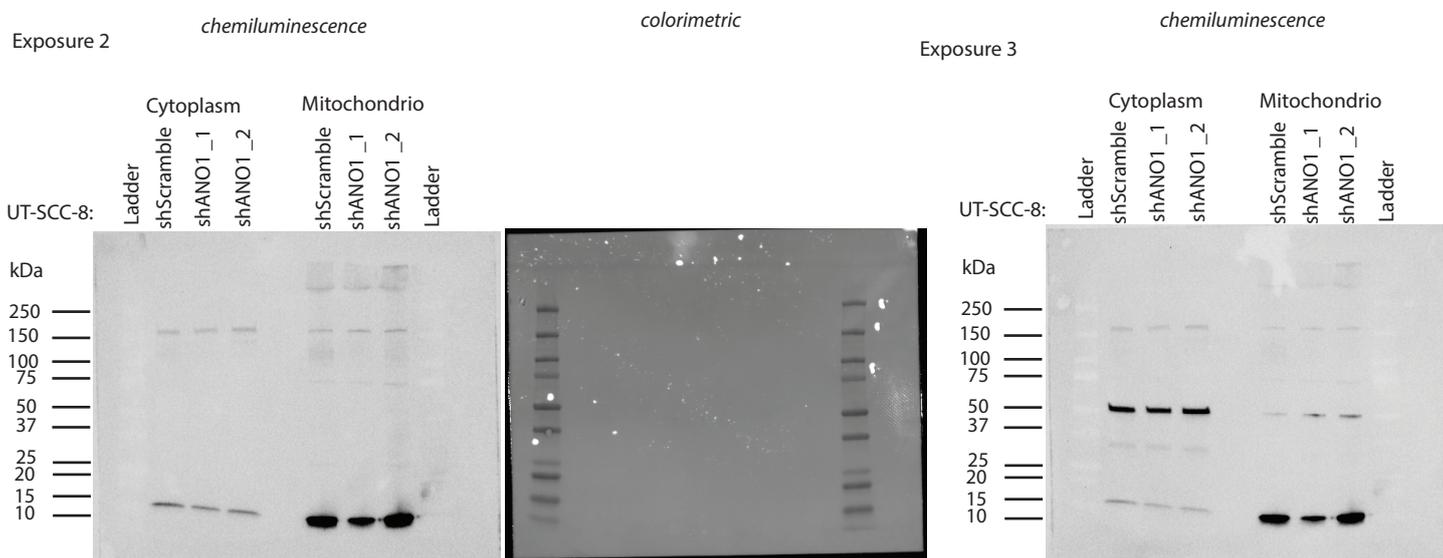
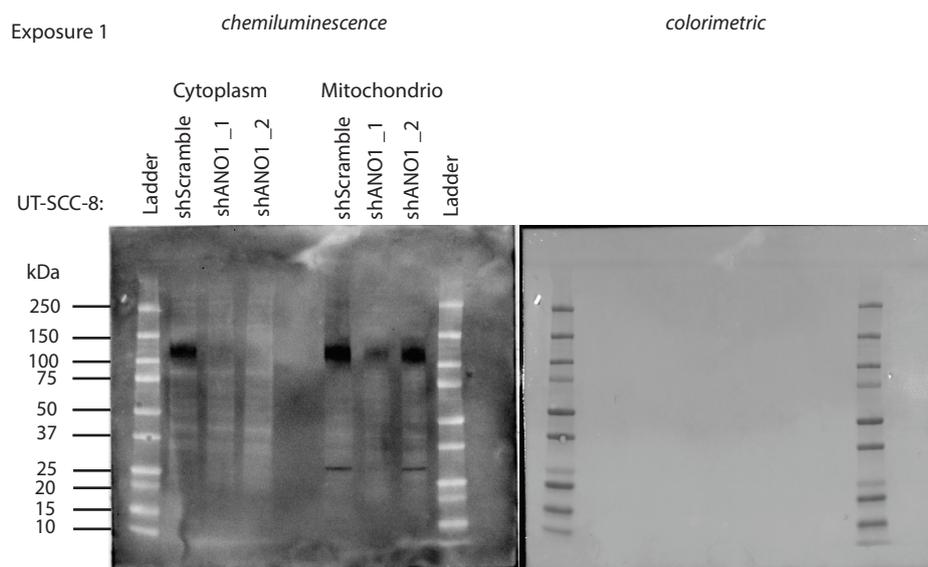
	Intensity of each band (background adjusted)							
	UT-SCC-8 shScramble-1	UT-SCC-8 shScramble-2	UT-SCC-8 shScramble-3	UT-SCC-8 shScramble-4	UT-SCC-8 shANO1_65-1	UT-SCC-8 shANO1_65-2	UT-SCC-8 shANO1_66-1	UT-SCC-8 shANO1_66-2
ANO1	12077201	13846237	14155545	10275488	137207	770529	1683514	1192792
α -tubulin	11312051	11827842	14064242	14297874	14445017	14808878	15155762	16039669
Intensity ratio	1.07	1.17	1.01	0.72	0.01	0.05	0.11	0.07



	Intensity of each band (background adjusted)							
	UT-SCC-14 shScramble-1	UT-SCC-14 shScramble-2	UT-SCC-14 shScramble-3	UT-SCC-14 shScramble-4	UT-SCC-14 shANO1_65-1	UT-SCC-14 shANO1_65-2	UT-SCC-14 shANO1_66-1	UT-SCC-14 shANO1_66-2
ANO1	5614103	6002751	5212174	3357209	89603	12904	298802	512510
α -tubulin	18575333	16319536	13843395	14311993	12855591	10660942	11556502	10008511
Intensity ratio	0.30	0.37	0.38	0.23	0.01	0.00	0.03	0.05

Figure S7 Uncropped blots of Figure S3A.

Immunoblot analysis of changes in proteins ANO1, COXIV and a-tubulin in cytoplasmic and mitochondrial fractions of the cell line UT-SCC-8. Densitometry readings and intensity ratios (normalized values) are presented in the table under the whole blots.

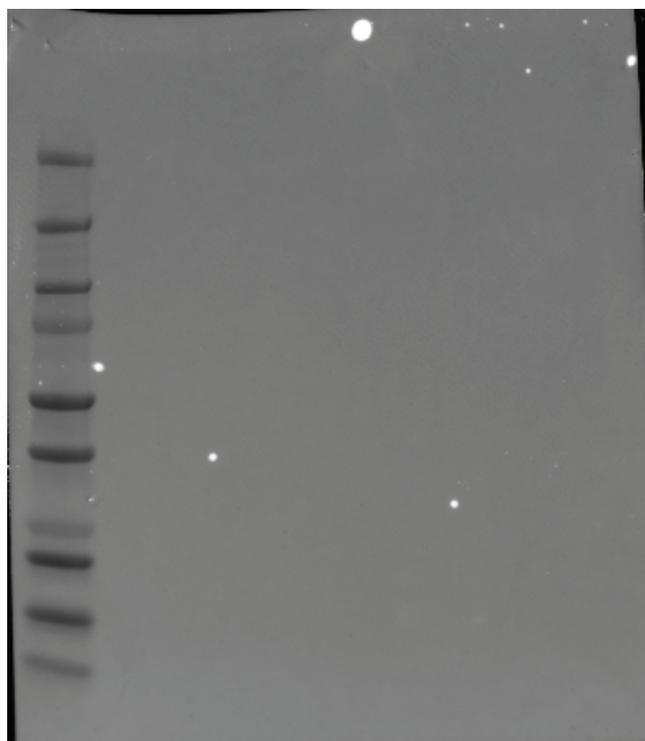


	Intensity of each band (background adjusted)					
	UT-SCC-8 shScramble cytoplasmic	UT-SCC-8 shANO1_1 cytoplasmic	UT-SCC-8 shANO1_2 cytoplasmic	UT-SCC-8 shScramble mitochondrio	UT-SCC-8 shANO1_1 mitochondrio	UT-SCC-8 shANO1_2 mitochondrio
ANO1	1708467	142562	10719	2423751	789525	1635683
a-tubulin	848404	684063	1013428	59593	136652	151321
COXIV	251119	156889	205156	2307407	1123599	2702501
Intensity ratio (to a-tubulin)	2.01	0.21	0.01	40.67	5.78	10.81
Intensity ratio (to COXIV)	6.80	0.91	0.05	1.05	0.70	0.61

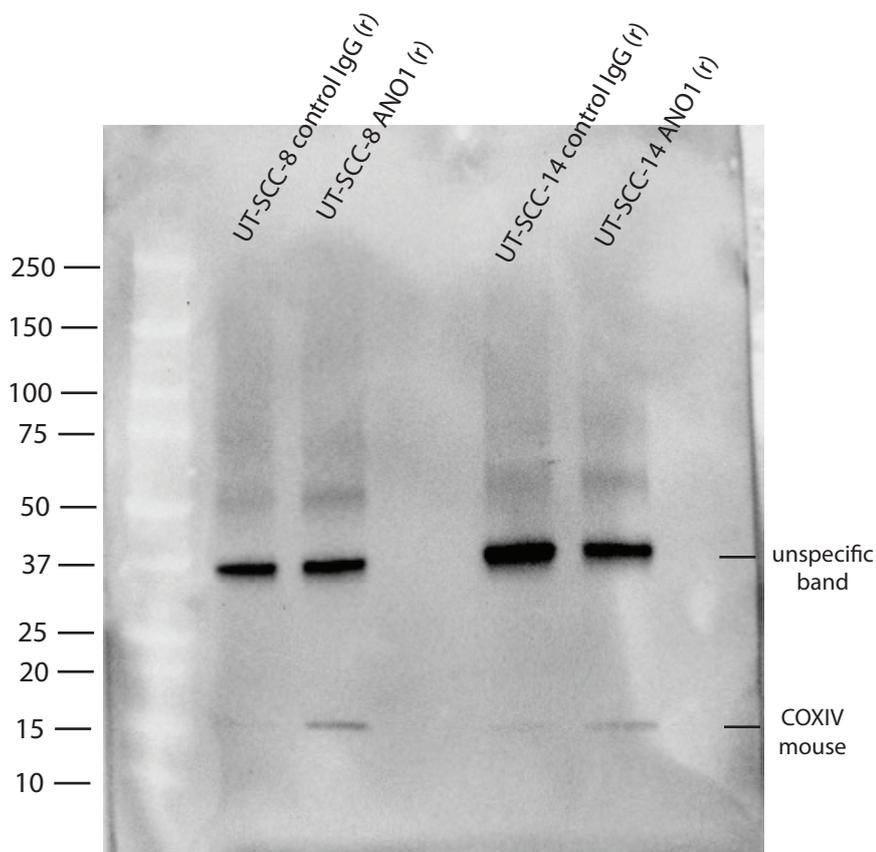
Figure S7 Uncropped blots of Figure S3B.

Immunoblot analysis of the proteins COXIV and α -tubulin from co-immunoprecipitated samples with ANO1 antibody, as well as their corresponding inputs samples. Cell lines utilized were UT-SCC-8 and UT-SCC-14. COXIV antibody used was raised in mouse (Abcam).

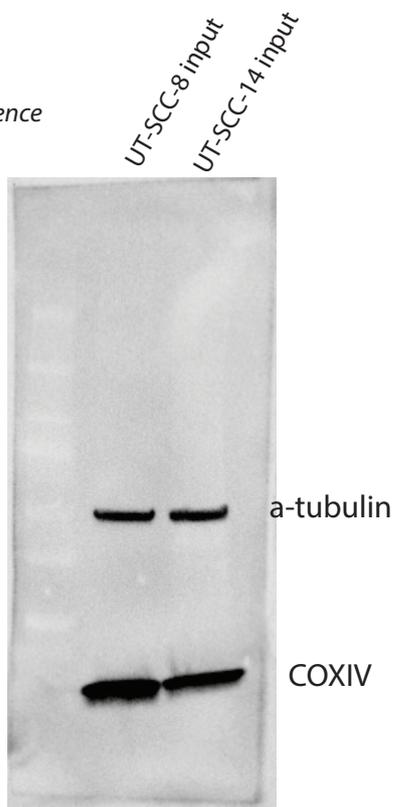
colorimetric



chemiluminescence



chemiluminescence



colorimetric

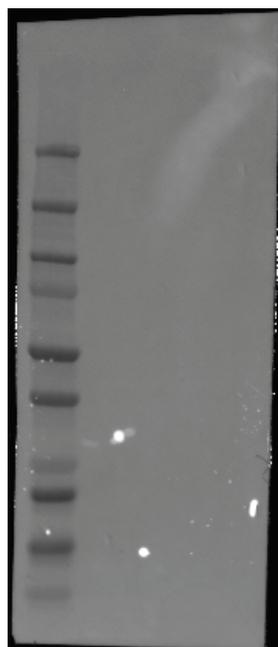
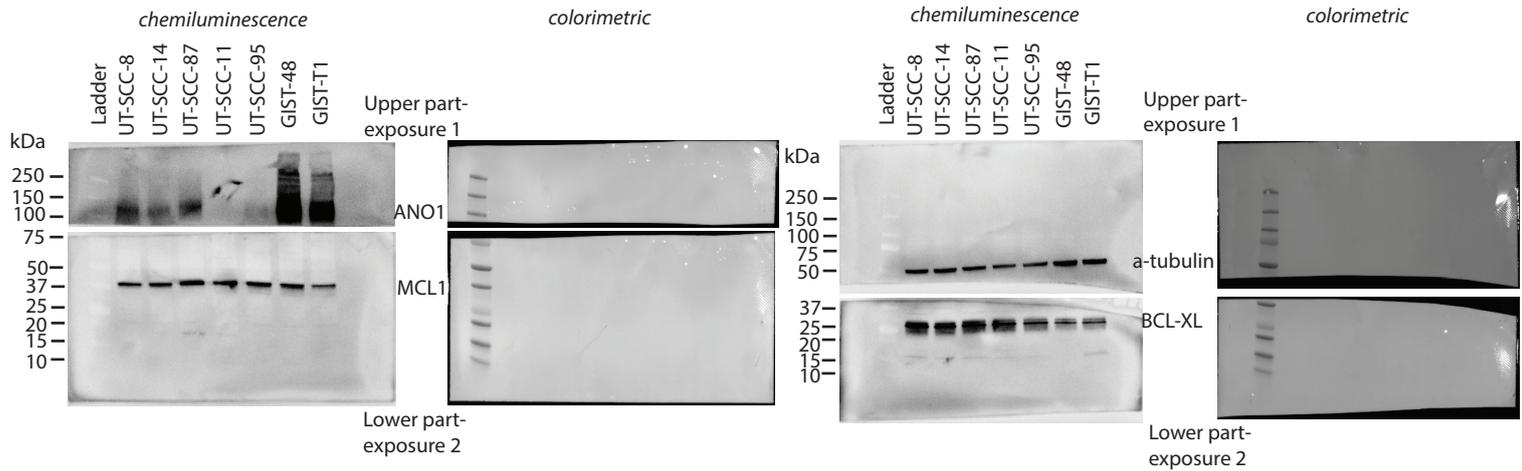


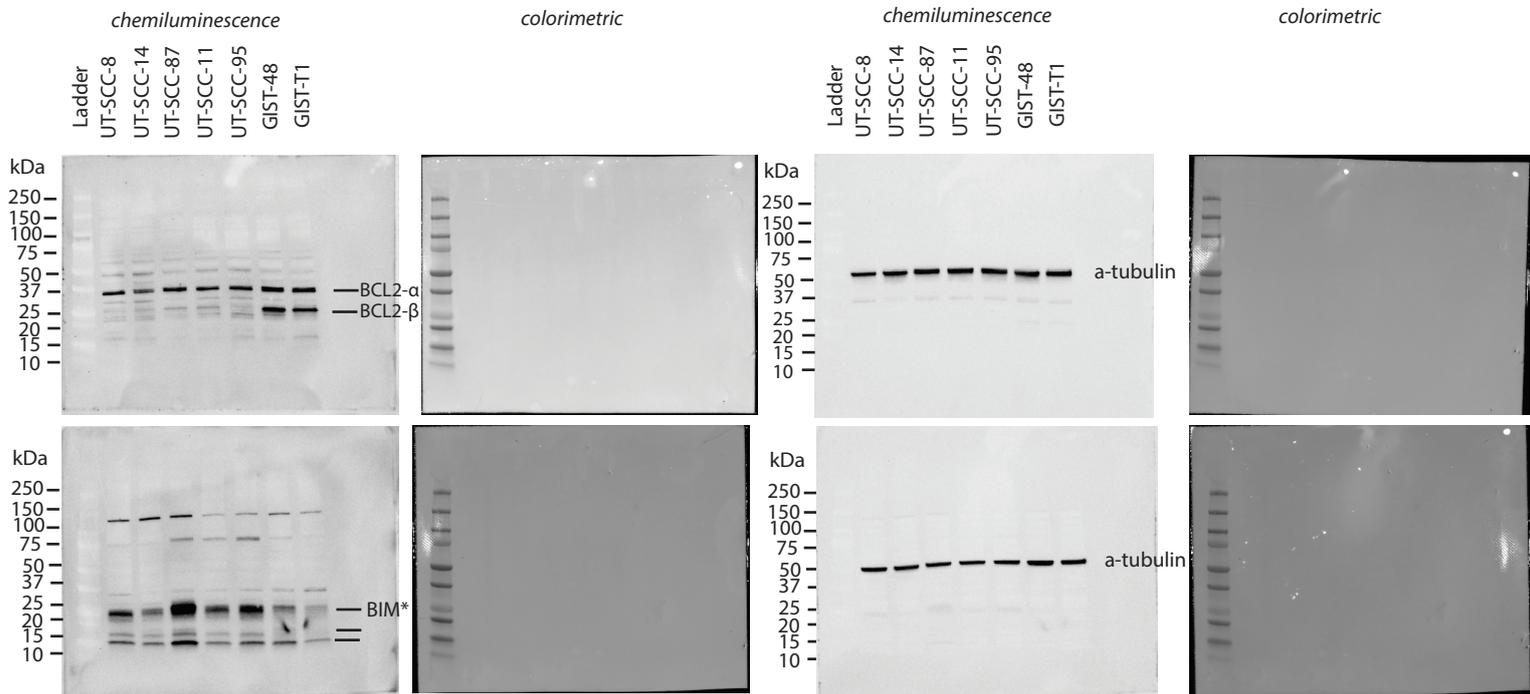
Figure S7 Uncropped blots of Figure S3C.

Immunoblot analysis of the proteins ANO1, MCL1, BCL-XL, BCL2, BIM and α -tubulin from cell lysates of a panel of UTSCC cell lines. Alpha-tubulin was used as the loading control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the respective blots.



The two gels above were run simultaneously in the sds-page cassette, after which the two mini-gels were transferred in parallel using a midi-PVDF membrane.

	Intensity of each band (background adjusted)						
	UT-SCC-8	UT-SCC-14	UT-SCC-87	UT-SCC-11	UT-SCC-95	GIST-48	GIST-T1
ANO1	1557644	1087278	1139776	370644	677492	5937297	4030323
MCL1	1096911	1227031	1657176	1711423	1600784	1355426	779095
BCL-XL	4124391	3602105	3908531	3812586	2906652	1824880	2112793
α -tubulin	1273000	1329923	1128754	840036	907972	1754374	2047973
Intensity ratio (ANO1/ α -tubulin)	1.22	0.82	1.01	0.44	0.75	3.38	1.97
Intensity ratio (MCL1/ α -tubulin)	0.86	0.92	1.47	2.04	1.76	0.77	0.38
Intensity ratio (BCL-XL/ α -tubulin)	3.24	2.71	3.46	4.54	3.20	1.04	1.03

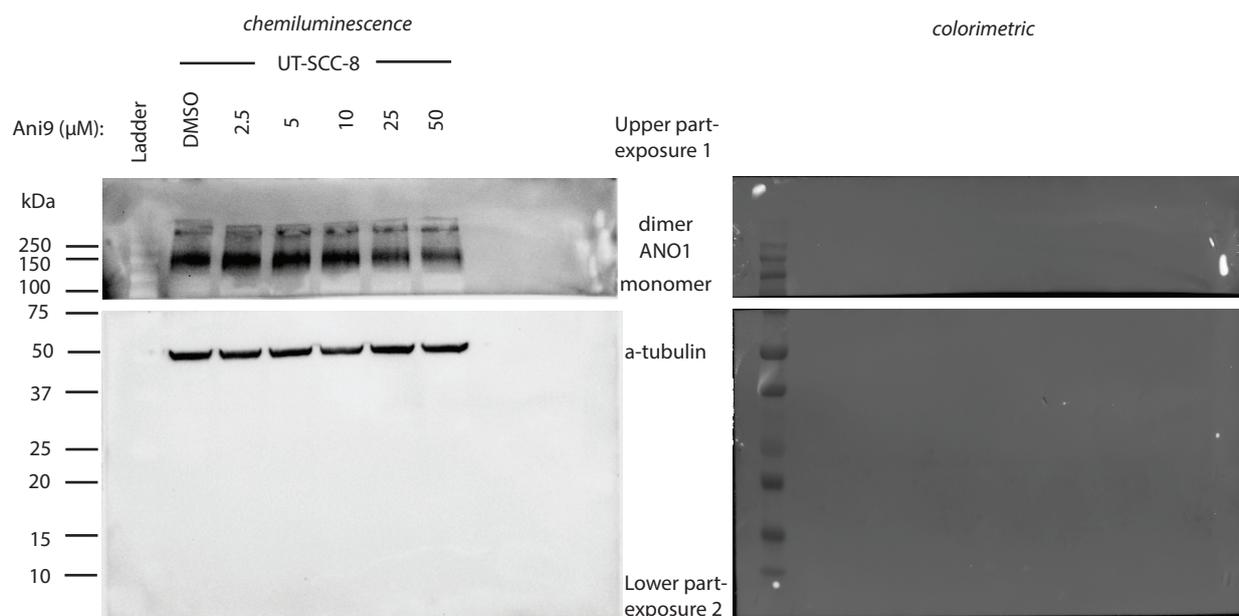


*BIM-specific bands: 23, 16, 12 kDa. Dnsitometry was measured for the main, 23 kDa band.

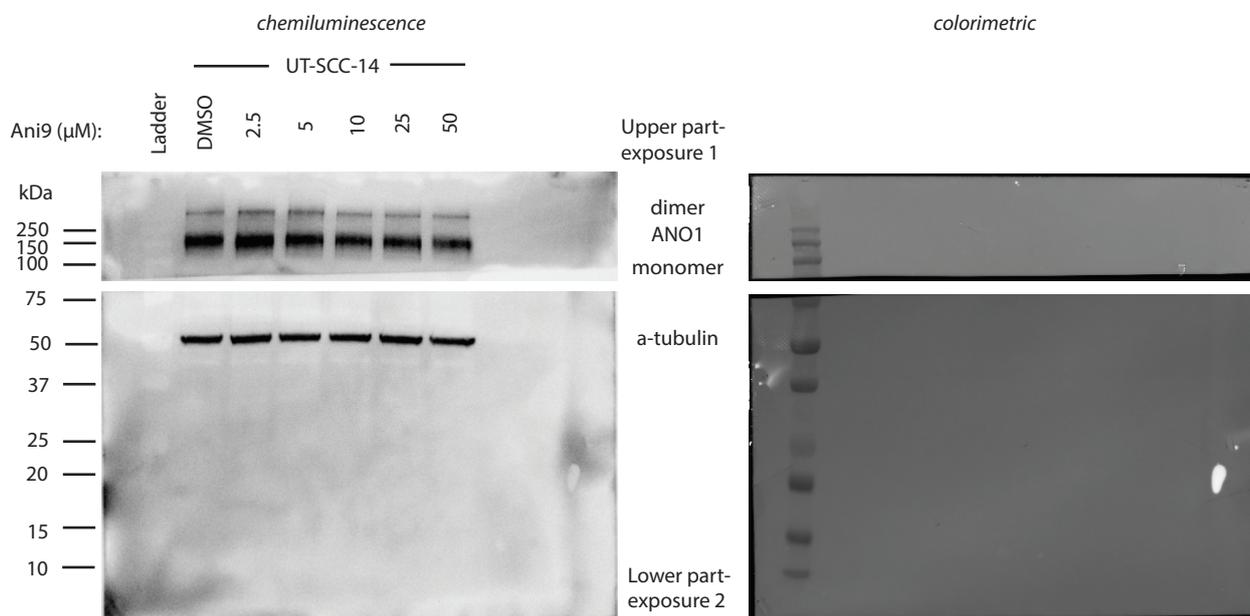
	Intensity of each band (background adjusted)						
	UT-SCC-8	UT-SCC-14	UT-SCC-87	UT-SCC-11	UT-SCC-95	GIST-48	GIST-T1
BCL2- α	1005709	597373	1204262	974539	1113073	1544510	1455693
BCL2- β	66430	80284	183876	158980	69084	1530632	1110605
α -tubulin	1562656	1807257	1711540	1610574	1709107	1913249	2154470
Intensity ratio (BCL2- α / α -tubulin)	0.64	0.33	0.70	0.61	0.65	0.81	0.68
Intensity ratio (BCL2- β / α -tubulin)	0.04	0.04	0.11	0.10	0.04	0.80	0.52
BIM	1556109	791182	4124364	1519685	2188691	871609	360657
α -tubulin	1389433	1154068	1109790	1079964	1333818	1929931	1860979
Intensity ratio (BIM/ α -tubulin)	1.12	0.69	3.72	1.41	1.64	0.45	0.19

Figure S7 Uncropped blots of Figure S4B.

Immunoblot analysis of the proteins ANO1 and α -tubulin from cell lysates of UT-SCC-8 and UT-SCC-14 treated with a range of concentrations of Ani9 inhibitor. Alpha-tubulin was used as the control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the respective blots.



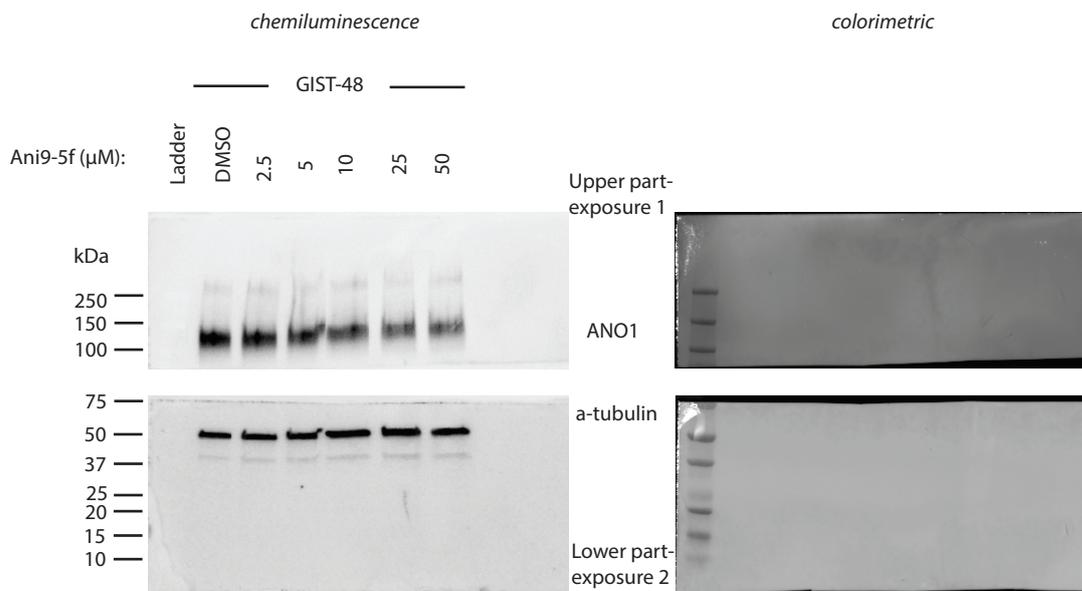
	Intensity of each band (background adjusted)					
	UT-SCC-8 DMSO	UT-SCC-8 2.5 μ M Ani9	UT-SCC-8 5 μ M Ani9	UT-SCC-8 10 μ M Ani9	UT-SCC-8 25 μ M Ani9	UT-SCC-8 50 μ M Ani9
ANO1 (monomer)	3076860	3389209	3453302	3385514	2884734	2801066
a-tubulin	2800540	2347174	2492055	1983652	3086486	2774190
Intensity ratio (to a-tubulin)	1.10	1.44	1.39	1.71	0.93	1.01



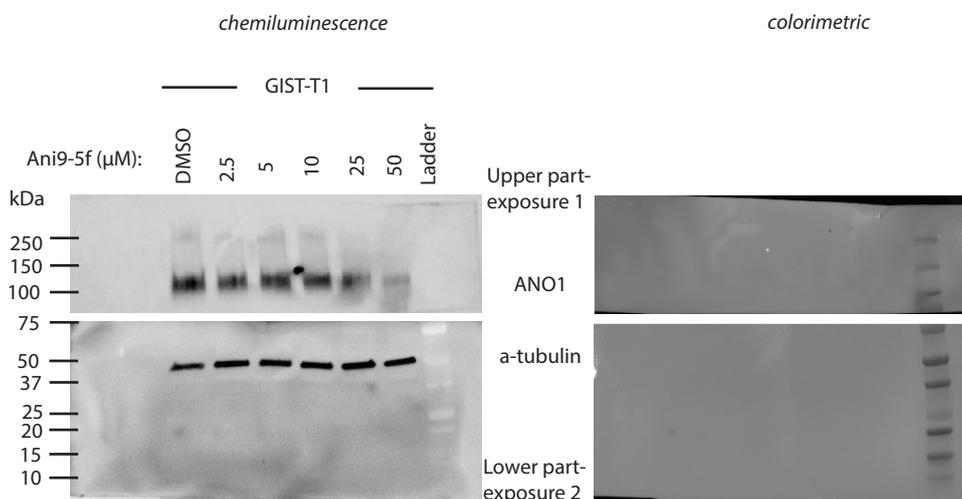
	Intensity of each band (background adjusted)					
	UT-SCC-14 DMSO	UT-SCC-14 2.5 μ M Ani9	UT-SCC-14 5 μ M Ani9	UT-SCC-14 10 μ M Ani9	UT-SCC-14 25 μ M Ani9	UT-SCC-14 50 μ M Ani9
ANO1 (monomer)	3120427	3491869	2990948	2697955	2776385	2757160
a-tubulin	2231352	2400024	2053325	2280005	2420889	2233379
Intensity ratio (to a-tubulin)	1.40	1.45	1.46	1.18	1.15	1.23

Figure S7 Uncropped blots of Figure S6B.

Immunoblot analysis of the proteins ANO1 and a-tubulin of cell lysates from GIST-48 and GIST-T1 treated with a range of concentrations of Ani9-5f inhibitor. Alpha-tubulin was used as the control to normalize the quantities of the proteins. Densitometry readings and normalized values are presented in the tables under the respective blots.



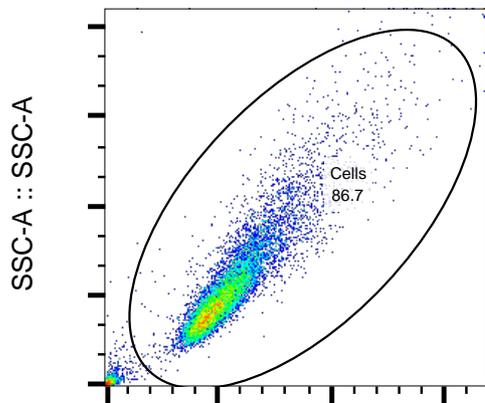
	Intensity of each band (background adjusted)					
	GIST-48 DMSO	GIST-48 2.5 μM Ani9-5f	GIST-48 5 μM Ani9-5f	GIST-48 10 μM Ani9-5f	GIST-48 25 μM Ani9-5f	GIST-48 50 μM Ani9-5f
ANO1 (monomer)	4103574	4148841	3423658	2861404	2992919	2876292
a-tubulin	1403925	1682958	1553548	2096217	2379447	1887867
Intensity ratio (to a-tubulin)	2.92	2.47	2.20	1.37	1.26	1.52



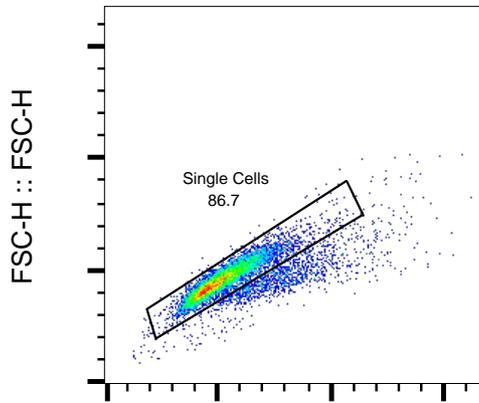
	Intensity of each band (background adjusted)					
	GIST-T1 DMSO	GIST-T1 2.5 μM Ani9-5f	GIST-T1 5 μM Ani9-5f	GIST-T1 10 μM Ani9-5f	GIST-T1 25 μM Ani9-5f	GIST-T1 50 μM Ani9-5f
ANO1 (monomer)	1409509	1089275	866654	343499	729478	384773
a-tubulin	1095759	1701096	1548198	1382456	1756769	1595450
Intensity ratio (to a-tubulin)	1.29	0.64	0.56	0.25	0.42	0.24

Figure S8

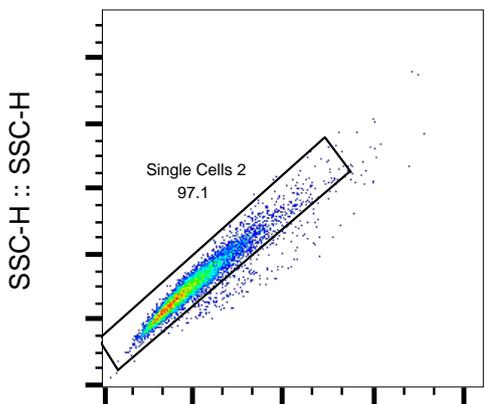
Run 1-UT-SCC-8



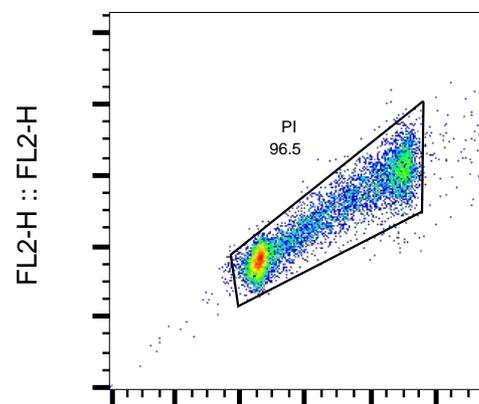
FSC-A :: FSC-A
A04 UTSCC8 shscramble.fcs
Ungated



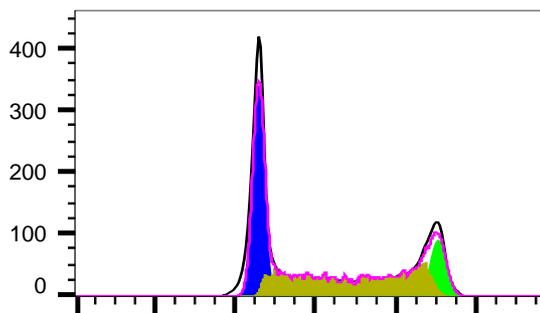
FSC-A :: FSC-A
A04 UTSCC8 shscramble.fcs
Cells



SSC-A :: SSC-A
A04 UTSCC8 shscramble.fcs
Single Cells

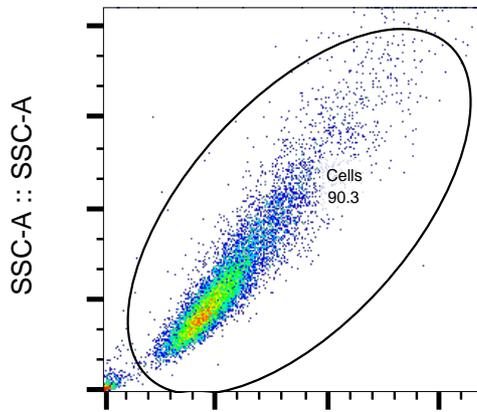


FL2-A :: FL2-A
A04 UTSCC8 shscramble.fcs
Single Cells 2

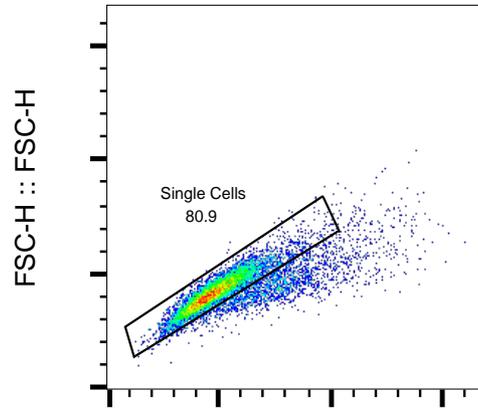


: 1.69
%G1 : 41.3
%S : 42.2
%G2 : 14.5
G1 Mean: 4.58E5
G2 Mean: 9.05E5
G1 CV: 4.48
G2 CV: 2.99
% less G1: 3.18
% greater G2: -0.16

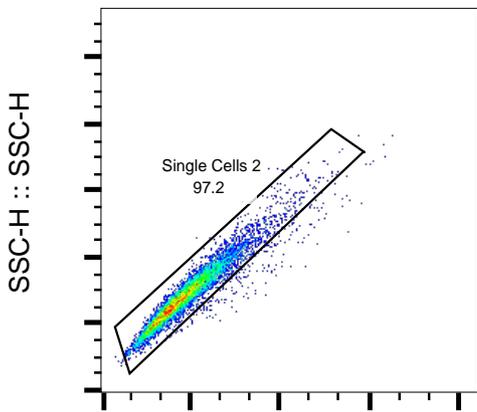
FL2-A :: FL2-A
A04 UTSCC8 shscramble.fcs
Cell Cycle



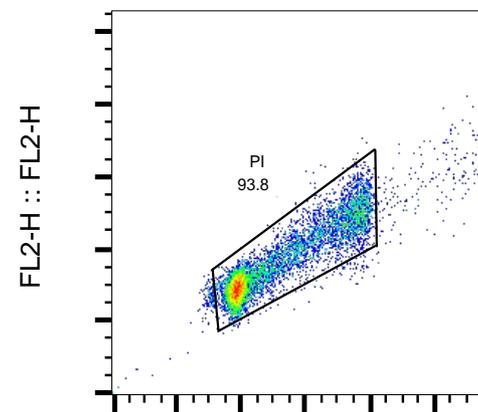
FSC-A :: FSC-A
A05 UTSCC8 shANO1 65.fcs
Ungated



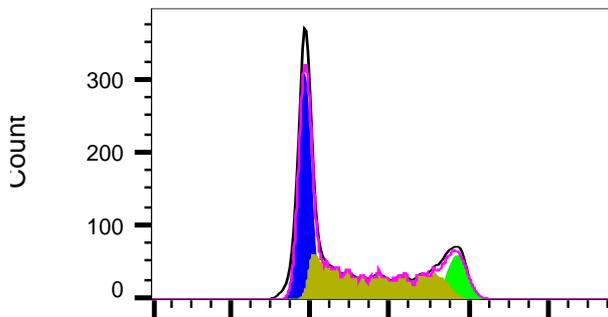
FSC-A :: FSC-A
A05 UTSCC8 shANO1 65.fcs
Cells



SSC-A :: SSC-A
A05 UTSCC8 shANO1 65.fcs
Single Cells

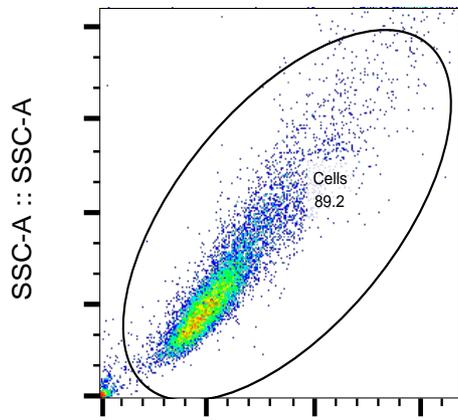


FL2-A :: FL2-A
A05 UTSCC8 shANO1 65.fcs
Single Cells 2

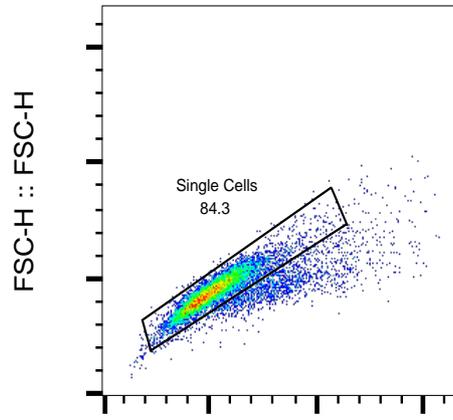


FL2-A :: FL2-A
A05 UTSCC8 shANO1 65.fcs
Cell Cycle

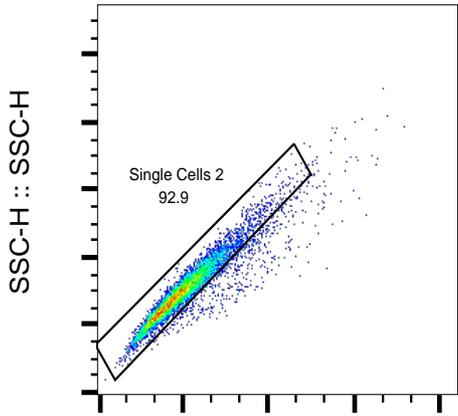
: 1.02
%G1: 43.8
%S: 41.6
%G2: 13.4
G1 Mean: 386630
G2 Mean: 7.71E5
G1 CV: 5.71
G2 CV: 4.56
% less G1: 2.19
% greater G2: -0.87



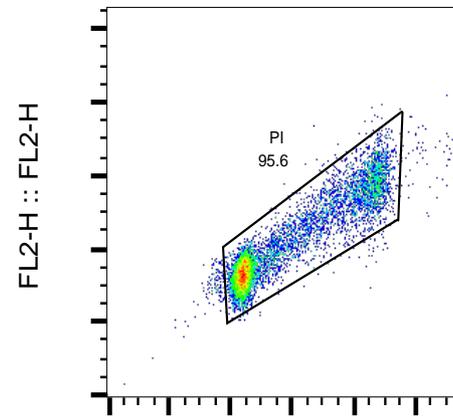
FSC-A :: FSC-A
A06 UTSCC8 shANO1 66.fcs
Ungated



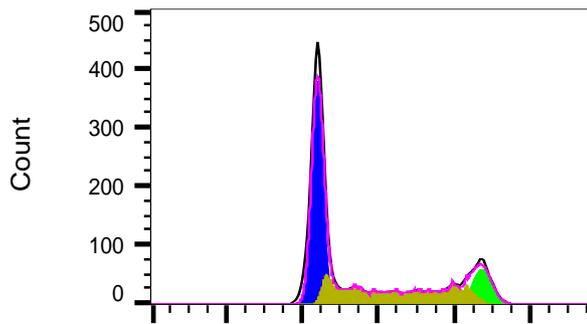
FSC-A :: FSC-A
A06 UTSCC8 shANO1 66.fcs
Cells



SSC-A :: SSC-A
A06 UTSCC8 shANO1 66.fcs
Single Cells



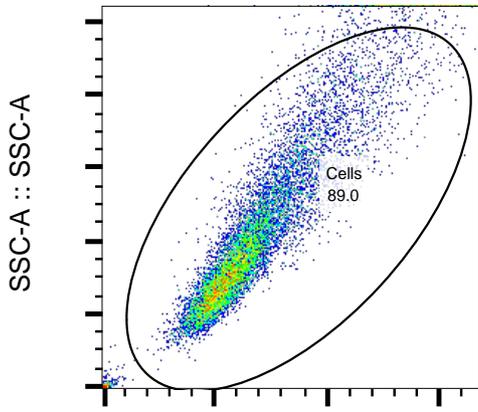
FL2-A :: FL2-A
A06 UTSCC8 shANO1 66.fcs
Single Cells 2



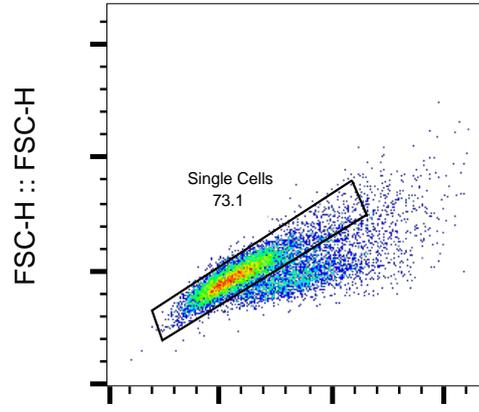
: 1.04
%G1: 51.0
%S: 33.9
%G2: 13.3
G1 Mean: 4.40E5
G2 Mean: 8.74E5
G1 CV: 4.89
G2 CV: 4.07
% less G1: 1.87
% greater G2: -0.13

FL2-A :: FL2-A
A06 UTSCC8 shANO1 66.fcs
Cell Cycle

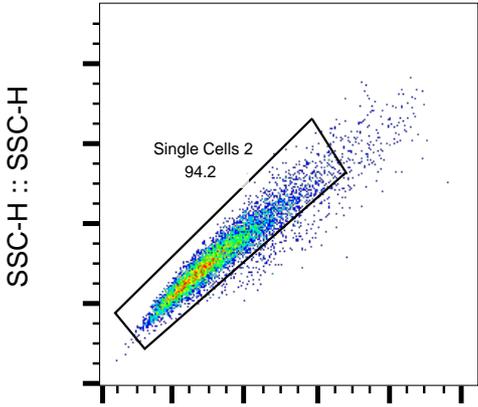
Run 2- UT-SCC-8



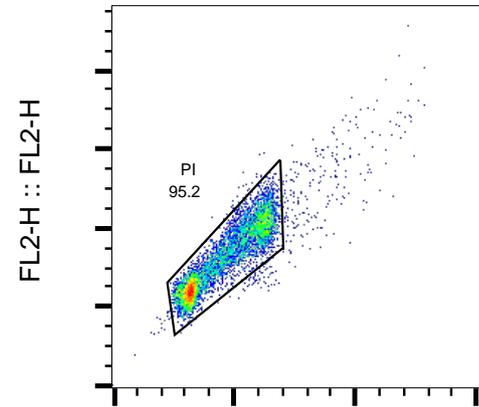
FSC-A :: FSC-A
A02 8 shscramble.fcs
Ungated



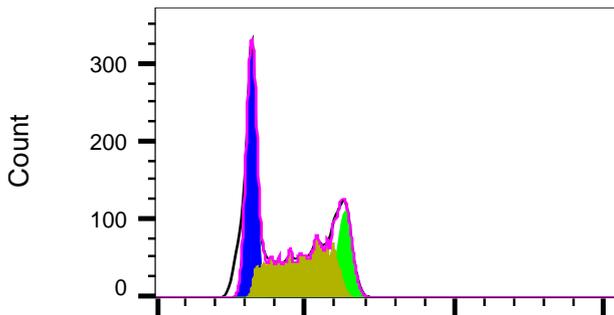
FSC-A :: FSC-A
A02 8 shscramble.fcs
Cells



SSC-A :: SSC-A
A02 8 shscramble.fcs
Single Cells

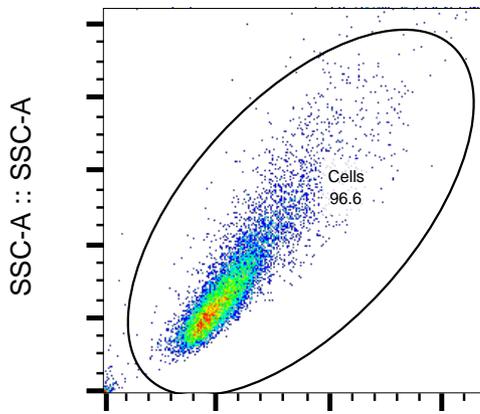


FL2-A :: FL2-A
A02 8 shscramble.fcs
Single Cells 2

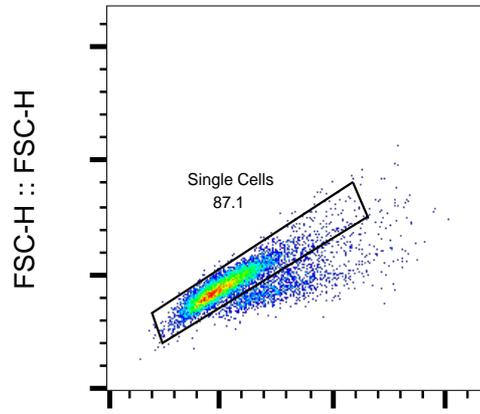


: 2.48
%G1: 35.9
%S: 43.0
%G2: 17.8
G1 Mean: 321850
G2 Mean: 6.36E5
G1 CV: 7.42
G2 CV: 5.33
% less G1: 4.76
% greater G2: -0.16

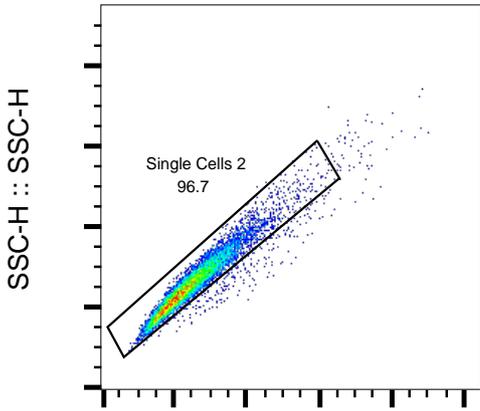
FL2-A :: FL2-A
A02 8 shscramble.fcs
Cell Cycle



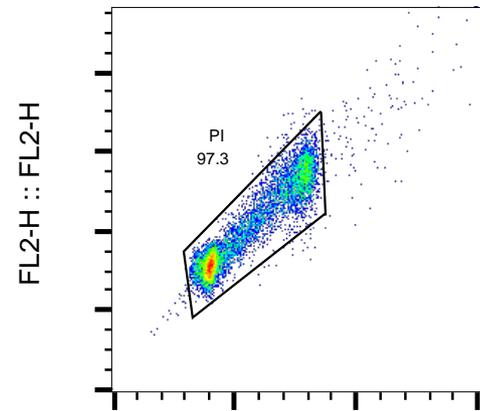
FSC-A :: FSC-A
A01 8 KD65.fcs
Ungated



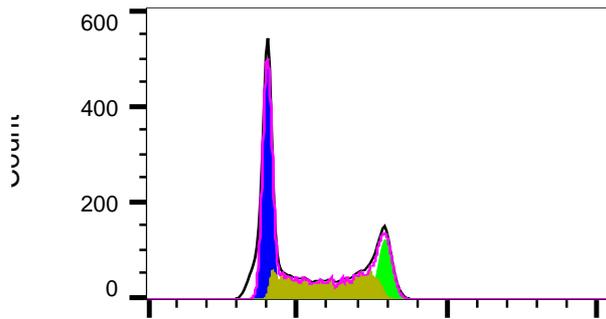
FSC-A :: FSC-A
A01 8 KD65.fcs
Cells



SSC-A :: SSC-A
A01 8 KD65.fcs
Single Cells

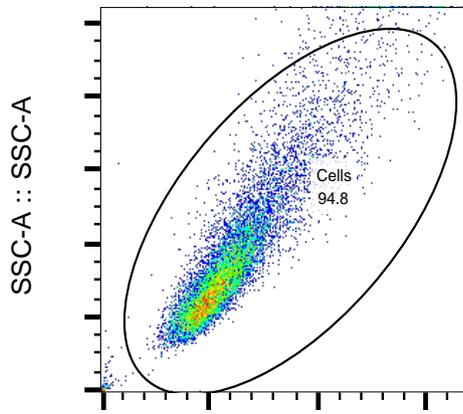


FL2-A :: FL2-A
A01 8 KD65.fcs
Single Cells 2

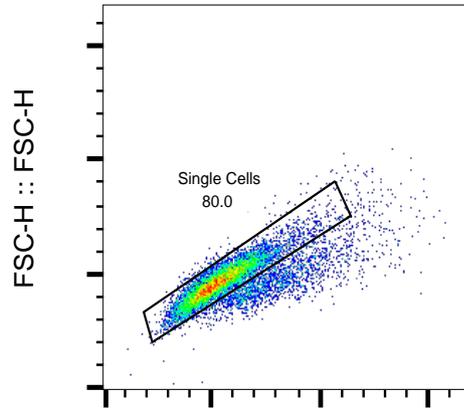


FL2-A :: FL2-A
A01 8 KD65.fcs
Cell Cycle

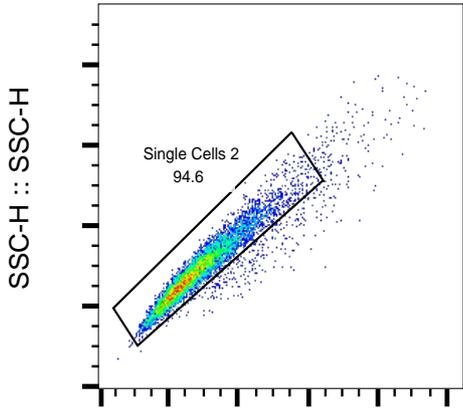
: 2.84
%G1: 41.6
%S: 37.4
%G2: 15.9
G1 Mean: 4.03E5
G2 Mean: 7.95E5
G1 CV: 5.15
G2 CV: 3.91
% less G1: 5.49
% greater G2: 0.21



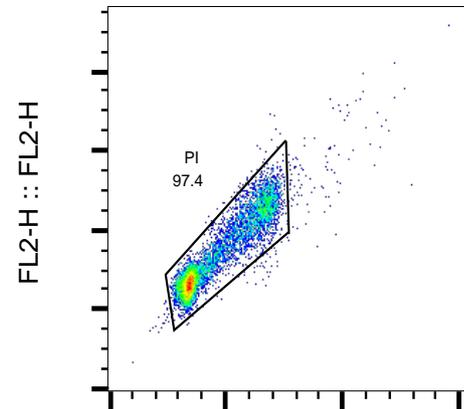
FSC-A :: FSC-A
A03 8 KD66.fcs
Ungated



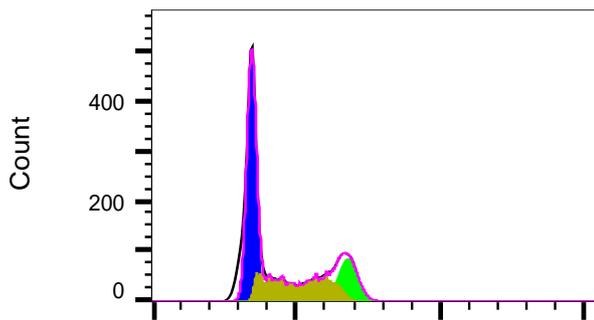
FSC-A :: FSC-A
A03 8 KD66.fcs
Cells



SSC-A :: SSC-A
A03 8 KD66.fcs
Single Cells



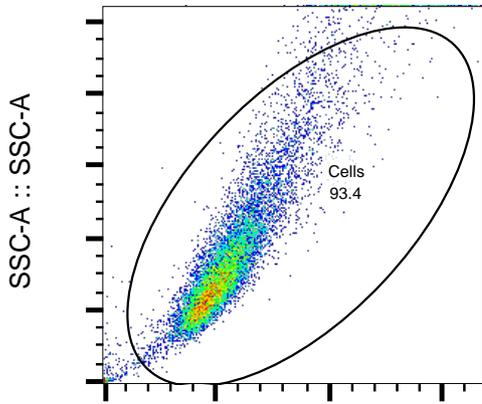
FL2-A :: FL2-A
A03 8 KD66.fcs
Single Cells 2



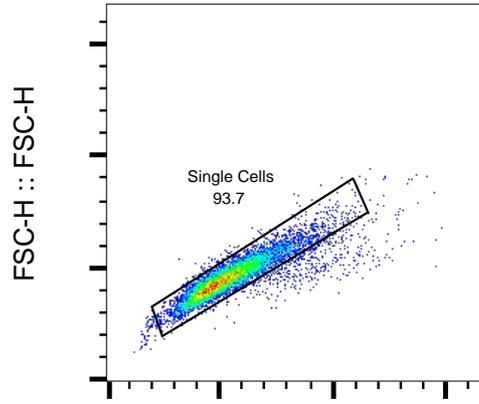
:2.90
%G1 : 47.4
%S : 32.1
%G2 : 17.1
G1 Mean : 346892
G2 Mean : 6.81E5
G1 CV : 6.42
G2 CV : 6.87
% less G1 : 5.11
% greater G2 : -0.52

FL2-A :: FL2-A
A03 8 KD66.fcs
Cell Cycle

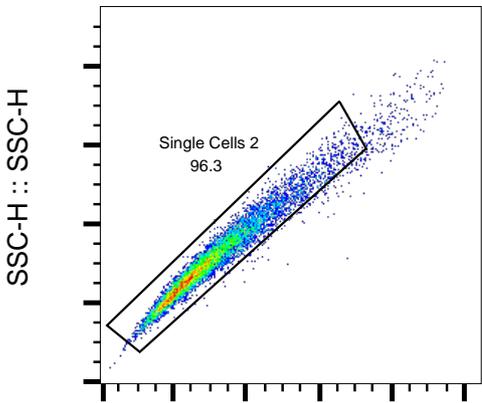
Run 1- UT-SCC-14



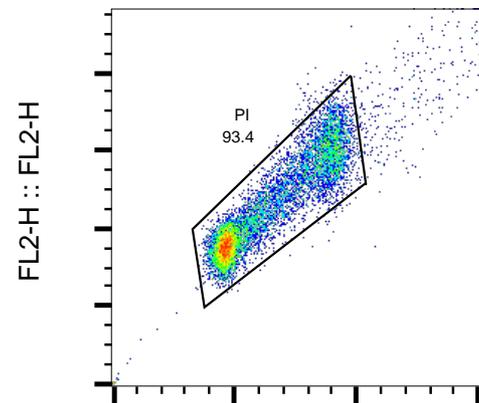
FSC-A :: FSC-A
A04 14 shscramble.fcs
Ungated



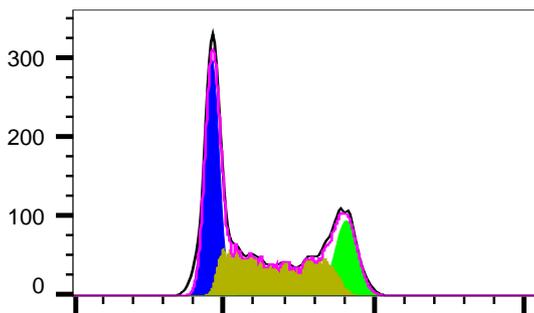
FSC-A :: FSC-A
A04 14 shscramble.fcs
Cells



SSC-A :: SSC-A
A04 14 shscramble.fcs
Single Cells

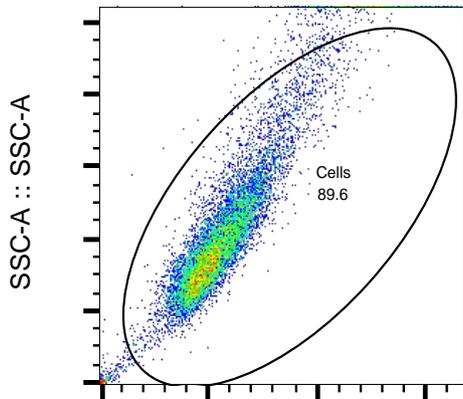


FL2-A :: FL2-A
A04 14 shscramble.fcs
Single Cells 2



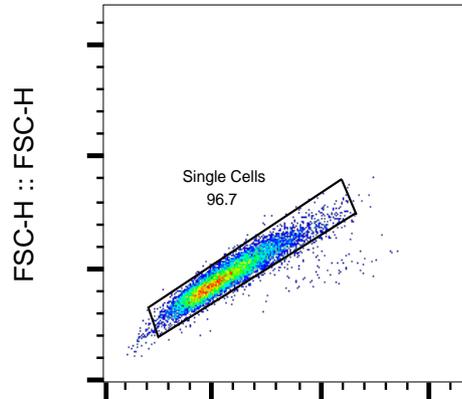
FL2-A :: FL2-A
A04 14 shscramble.fcs
Cell Cycle

: 1.16
%G1: 38.6
%S: 40.4
%G2: 18.8
G1 Mean: 4.62E5
G2 Mean: 9.08E5
G1 CV: 7.27
G2 CV: 5.71
% less G1: 1.71
% greater G2: 0.41



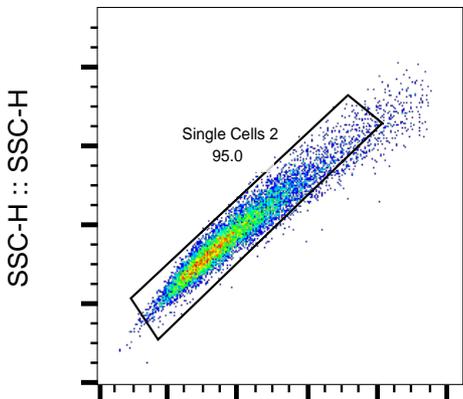
FSC-A :: FSC-A

A05 14 KD65.fcs
Ungated



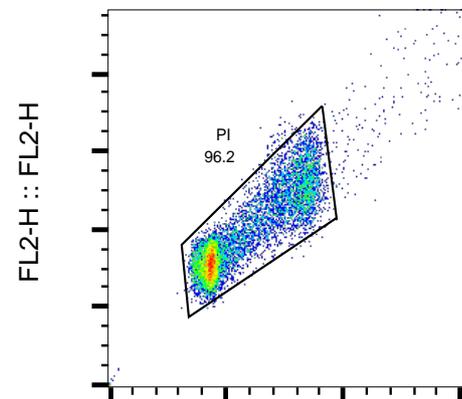
FSC-A :: FSC-A

A05 14 KD65.fcs
Cells



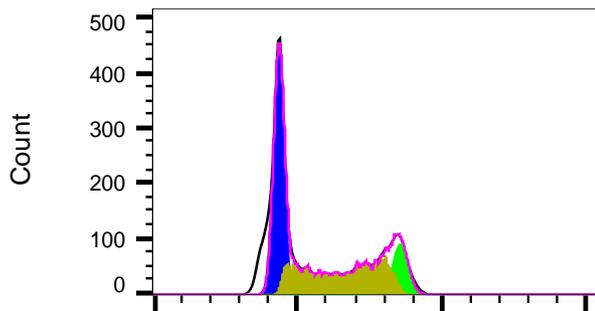
SSC-A :: SSC-A

A05 14 KD65.fcs
Single Cells



FL2-A :: FL2-A

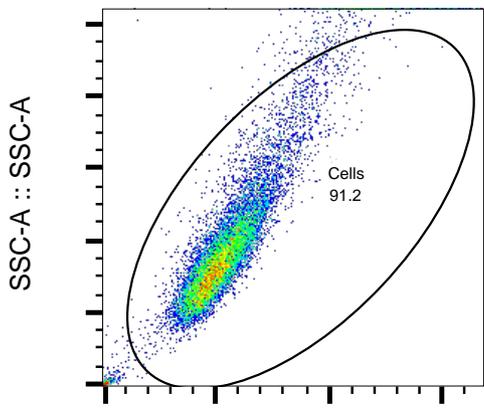
A05 14 KD65.fcs
Single Cells 2



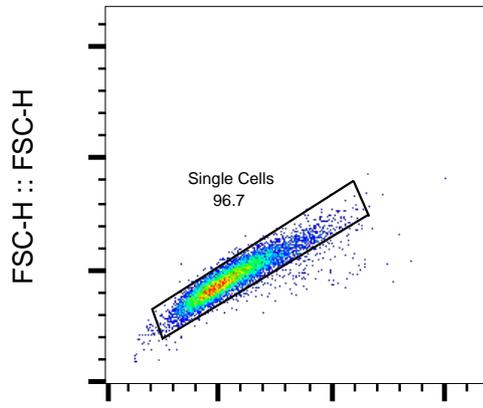
: 4.12
%G1: 41.5
%S: 38.9
%G2: 12.3
G1 Mean: 4.37E5
G2 Mean: 8.57E5
G1 CV: 6.02
G2 CV: 4.38
% less G1: 7.35
% greater G2: 0.58

FL2-A :: FL2-A

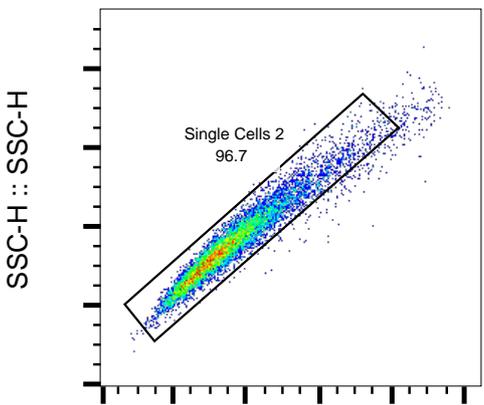
A05 14 KD65.fcs
Cell Cycle



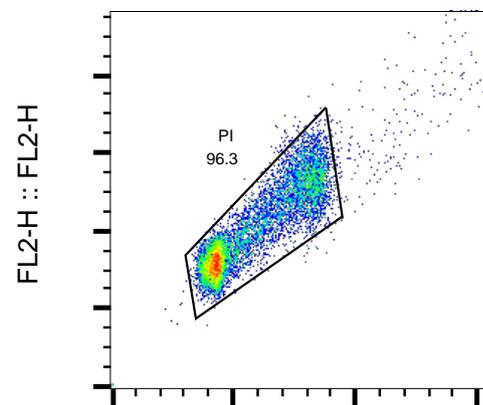
FSC-A :: FSC-A
B06 14 KD66 repeat.fcs
Ungated



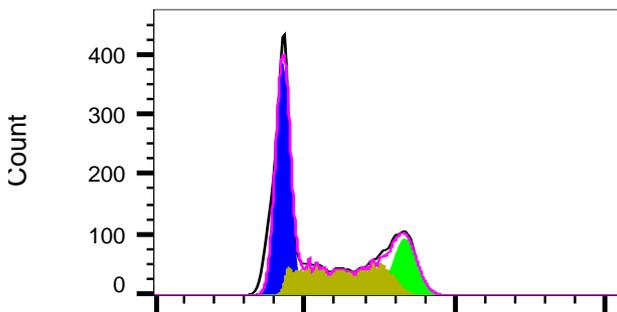
FSC-A :: FSC-A
B06 14 KD66 repeat.fcs
Cells



SSC-A :: SSC-A
B06 14 KD66 repeat.fcs
Single Cells



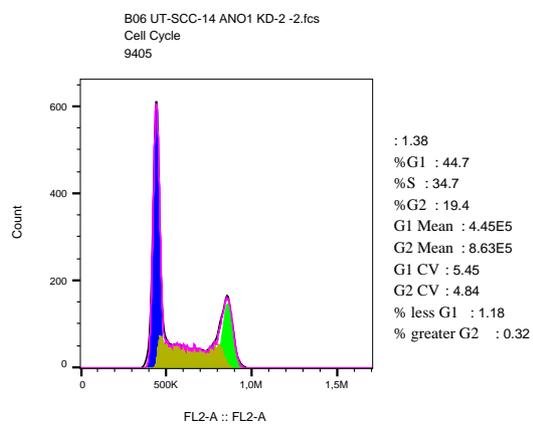
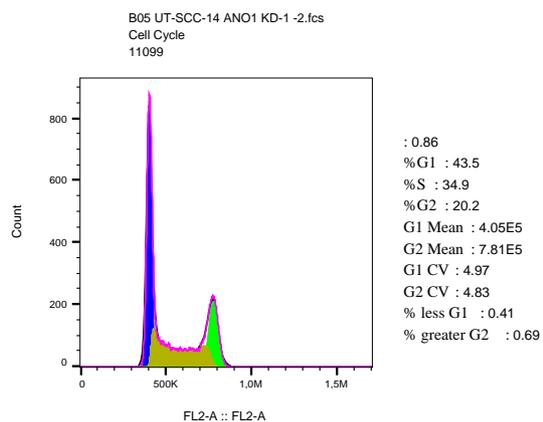
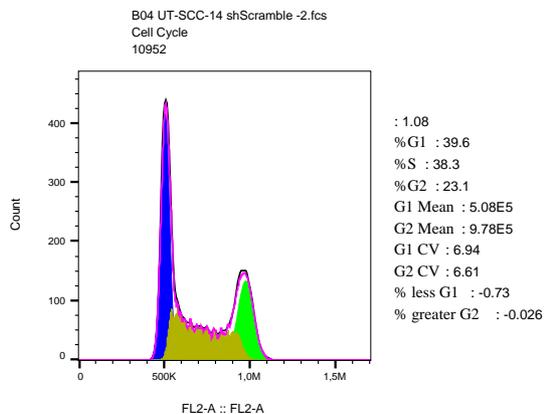
FL2-A :: FL2-A
B06 14 KD66 repeat.fcs
Single Cells 2



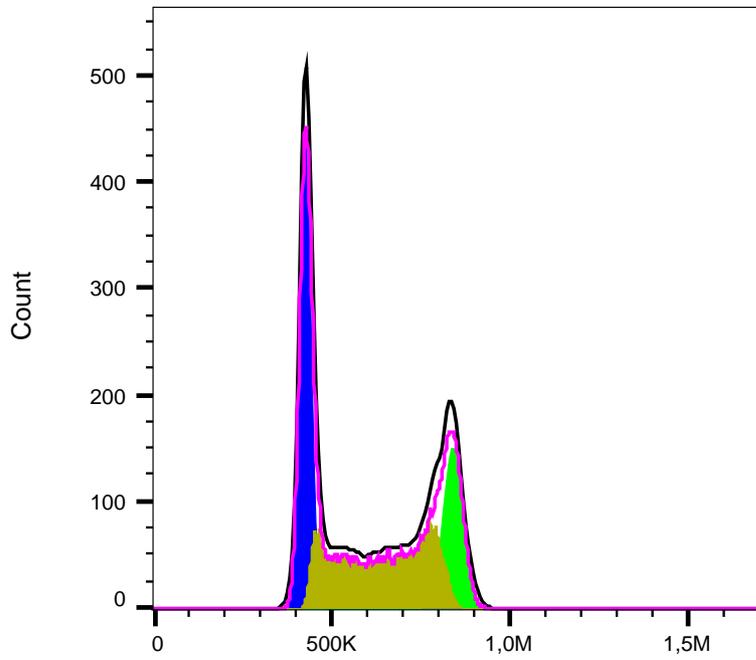
: 3.37
%G1: 46.3
%S: 34.5
%G2: 18.2
G1 Mean: 4.28E5
G2 Mean: 8.34E5
G1 CV: 7.76
G2 CV: 6.45
% less G1: 3.63
% greater G2: -0.74

FL2-A :: FL2-A
B06 14 KD66 repeat.fcs
Cell Cycle

Run 2- UT-SCC-14

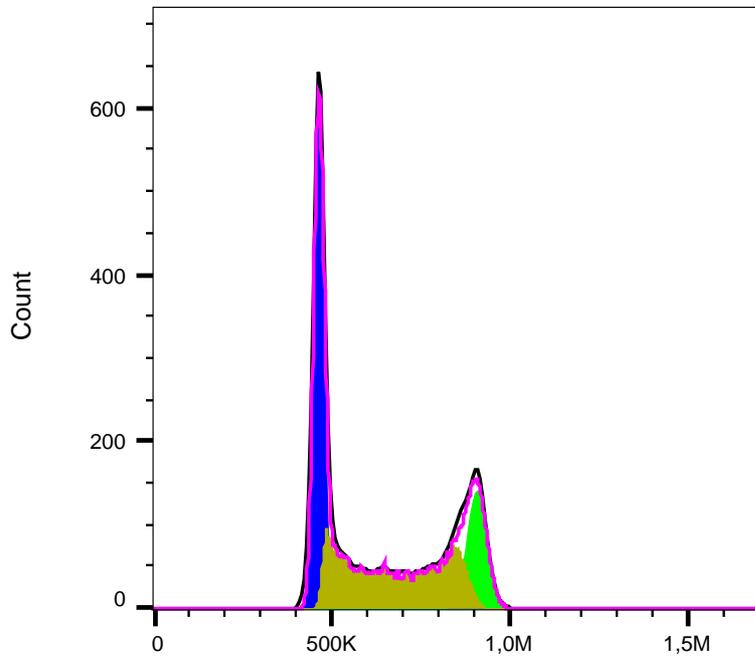


Run 3- UT-SCC-8



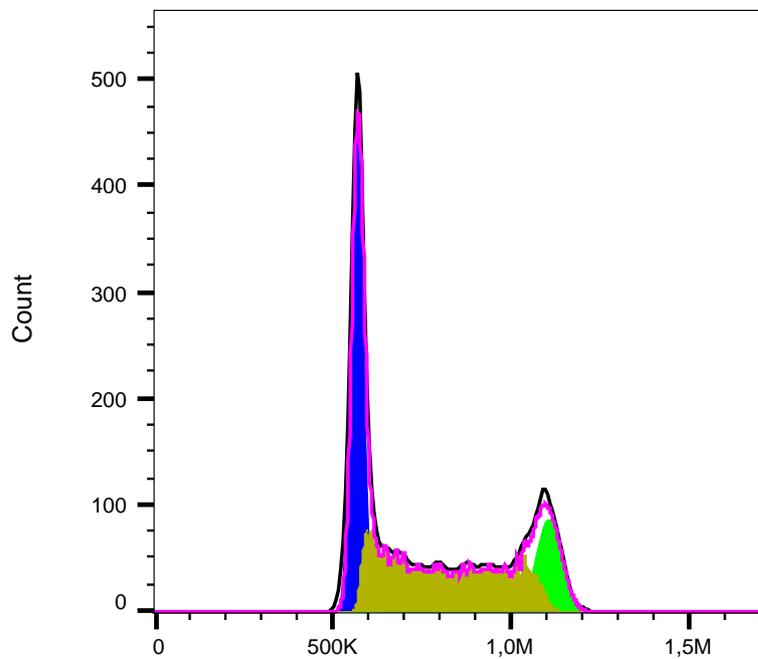
: 0,92
%G1 : 35,0
%S : 43,0
%G2 : 20,3
G1 Mean : 4,29E5
G2 Mean : 8,43E5
G1 CV : 5,30
G2 CV : 4,55
% less G1 : 0,13
% greater G2 : 0,91

FL2-A :: FL2-A
A01 UT-SCC-8 shScramble.fcs
Cell Cycle
9499



: 1,17
%G1 : 39,1
%S : 42,0
%G2 : 18,0
G1 Mean : 4,66E5
G2 Mean : 9,10E5
G1 CV : 4,26
G2 CV : 4,29
% less G1 : 0,90
% greater G2 : -0,19

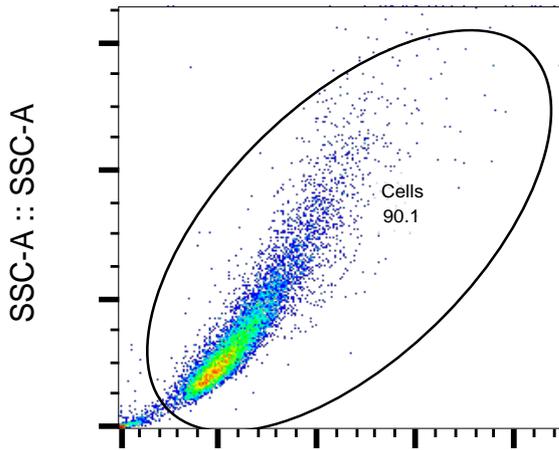
FL2-A :: FL2-A
A02 UT-SCC-8 ANO1 KD-1.fcs
Cell Cycle
9418



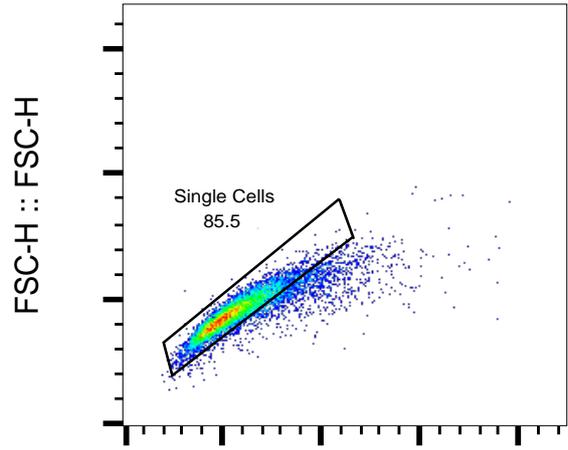
: 1,21
 %G1 : 37,9
 %S : 46,2
 %G2 : 15,1
 G1 Mean : 5,72E5
 G2 Mean : 1,11E6
 G1 CV : 4,19
 G2 CV : 4,48
 % less G1 : 0,99
 % greater G2 : -0,028

FL2-A :: FL2-A
 A06 UT-SCC-8 ANO1 KD2- 2.fcs
 Cell Cycle
 8940

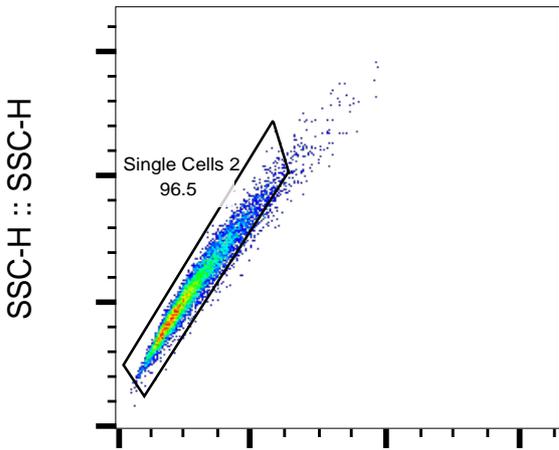
Run 3- UT-SCC-14



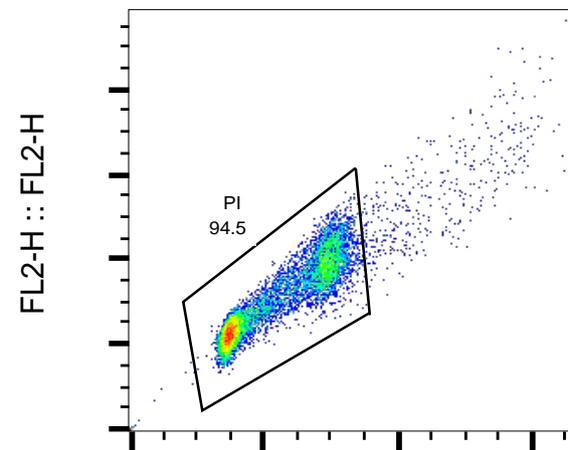
FSC-A :: FSC-A
A04 14 shscramble.fcs
Ungated



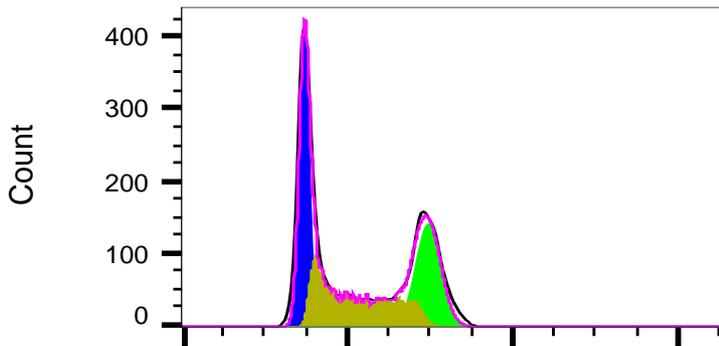
FSC-A :: FSC-A
A04 14 shscramble.fcs
Cells



SSC-A :: SSC-A
A04 14 shscramble.fcs
Single Cells

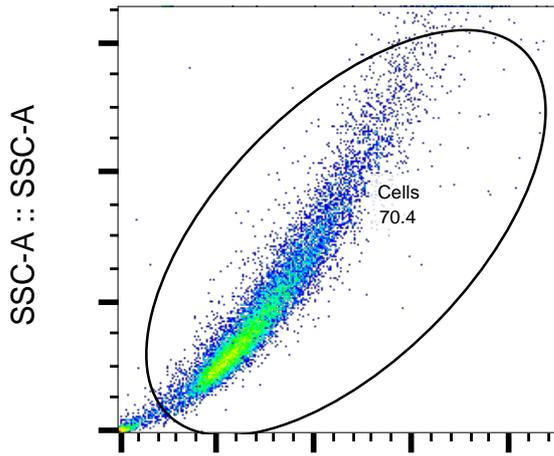


FL2-A :: FL2-A
A04 14 shscramble.fcs
Single Cells 2

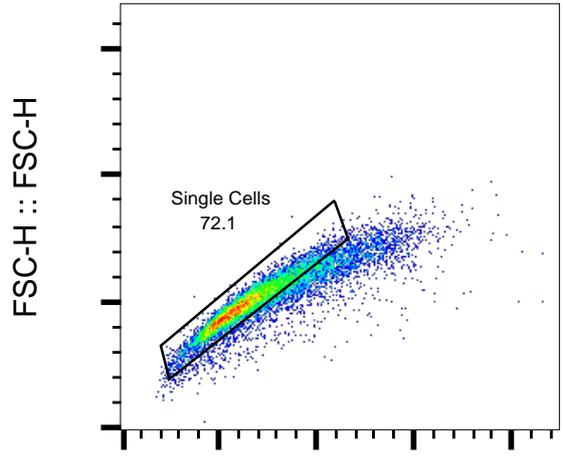


FL2-A :: FL2-A
A04 14 shscramble.fcs
Cell Cycle

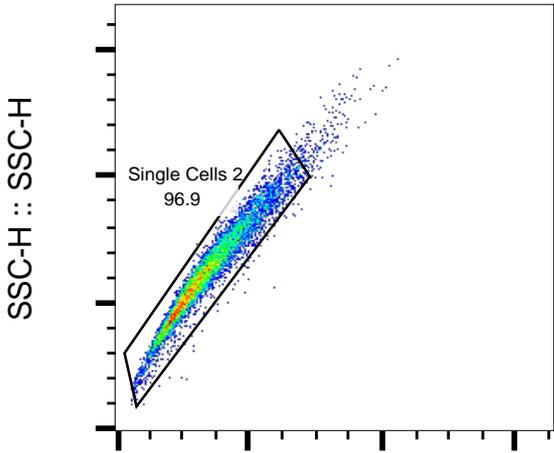
: 1.79
%G1: 34.3
%S: 34.8
%G2: 28.7
G1 Mean: 148789
G2 Mean: 298472
G1 CV: 5.97
G2 CV: 7.19
% less G1: -1.73
% greater G2: 3.61



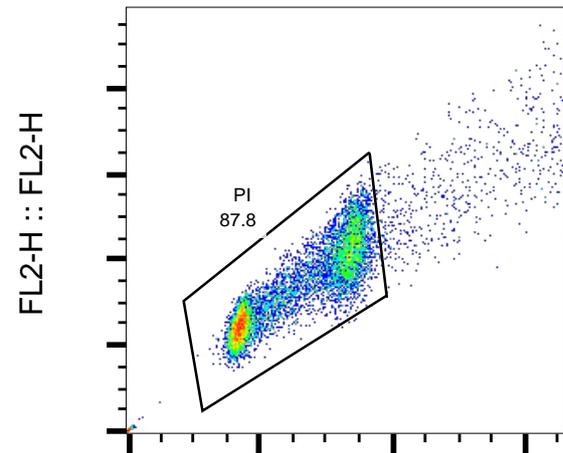
FSC-A :: FSC-A
A05 14 KD65.fcs
Ungated



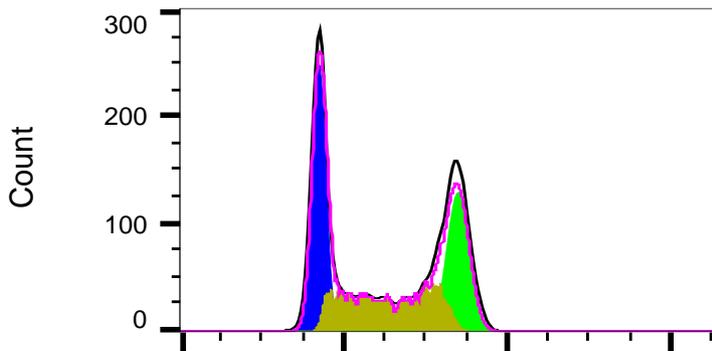
FSC-A :: FSC-A
A05 14 KD65.fcs
Cells



SSC-A :: SSC-A
A05 14 KD65.fcs
Single Cells

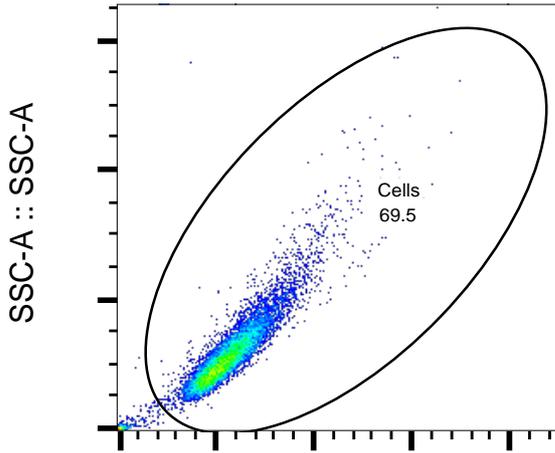


FL2-A :: FL2-A
A05 14 KD65.fcs
Single Cells 2

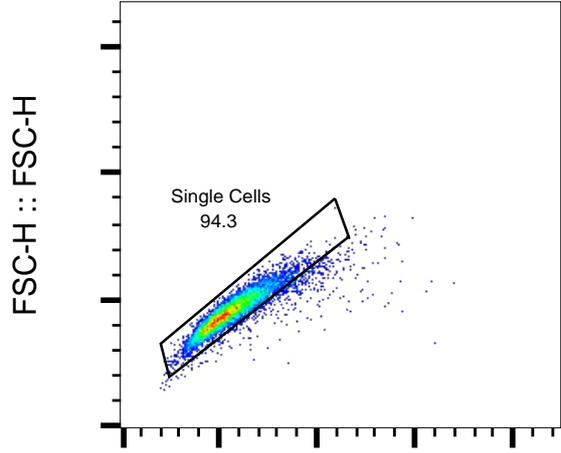


: 0.91
%G1: 35.3
%S: 33.8
%G2: 29.2
G1 Mean: 170331
G2 Mean: 340101
G1 CV: 6.99
G2 CV: 5.61
% less G1: 0.32
% greater G2: 1.86

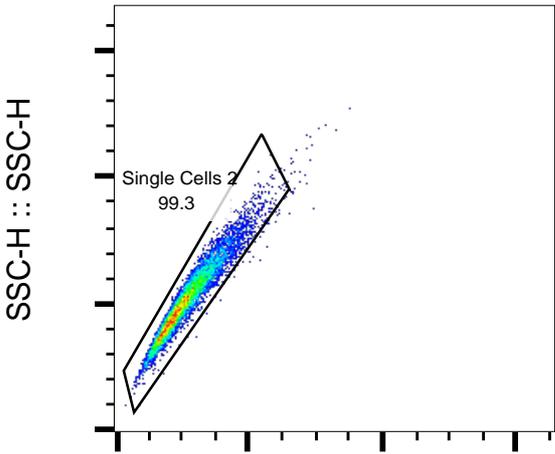
FL2-A :: FL2-A
A05 14 KD65.fcs
Cell Cycle



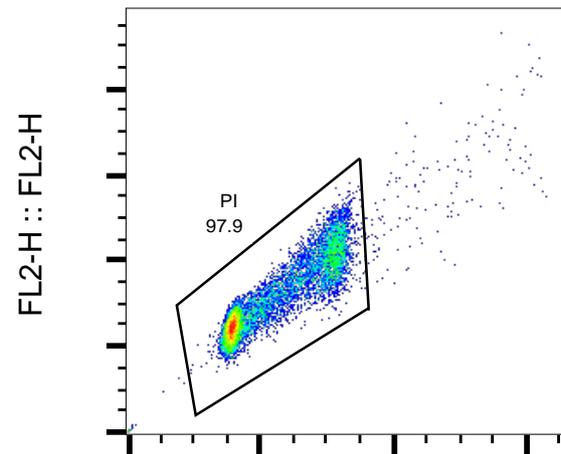
FSC-A :: FSC-A
A06 14 KD66.fcs
Ungated



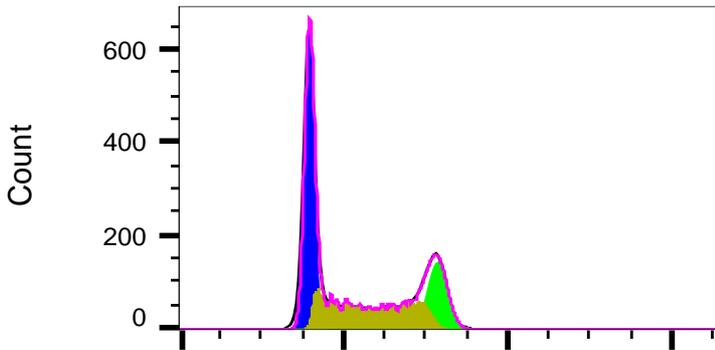
FSC-A :: FSC-A
A06 14 KD66.fcs
Cells



SSC-A :: SSC-A
A06 14 KD66.fcs
Single Cells



FL2-A :: FL2-A
A06 14 KD66.fcs
Single Cells 2



: 1.12
%G1 : 44.4
%S : 36.2
%G2 : 19.0
G1 Mean : 158774
G2 Mean : 314884
G1 CV : 5.37
G2 CV : 5.25
% less G1 : 0.65
% greater G2 : 0.14

FL2-A :: FL2-A
A06 14 KD66.fcs
Cell Cycle