

Table S1

Healthy donors characteristics

Donors	Age	Sex	Skin biopsy location
NHF-Ad17	93	M	Abdomen
NHF-Ad19	60	M	Abdomen
NHF-Br15	84	F	Arm
NHF-D16	36	M	Dorsum
NHF-D24	40	M	Dorsum
NHF-D27	39	M	Dorsum
NHF-G9	63	F	Leg
NHF-G13	77	M	Leg
NHF-Ing5	96	M	Inguinal
NHF-Pa6	55	F	Occipital area
NHF-S16	62	F	Breast
NHF-Sp2	29	M	Schiuder

Table S2

BCC patients characteristics

Patients	Age	Sex	Skin biopsy location
BCC-233	78	M	Leg
BCC-748SF	78	F	Scalp
BCC-800AN	87	F	Dorsum
BCC-1000NA	67	F	Dorsum
BCC-1PE	66	M	Abdomen
BCC-2TW	75	M	Neck
BCC-4CS	70	M	Dorsum

Table S3

Primers for Real Time Quantitative Polymerase Chain Reaction

Target Gene	Foward Primer	Reverse primer
<i>β-Actin</i>	5'-GACAGGATGCAGAAGGAGATTACT-3'	5'-TGATCCACATCTGCTGGAAGGT-3'
<i>TCF1</i>	5'-CCA AGA ATC CAC CAC AGG AGG-3'	5'-GCA GCC TAG AGC ACT GTC AT-3'
<i>TCF4</i>	5'-AAG ACT GGA TGA TGC TAT TC-3'	5'-CTG TTG GCT GAA AGA AGG-3'
<i>Lef1</i>	5'-TTC CTT GGT GAA CGA GTC-3'	5'-GGG TCC CTT GTT GTA GAG-3'
<i>PDGFRα</i>	5'-GTG TGG GAC ATT CAT TGC GG-3'	5'-TAG GCT CAG CCC TGT GAG AA-3'
<i>PDGFRβ</i>	5'-GGA GAG GGC AGT AAG GAG GA-3'	5'-GAA GCC GCA TGG TGT CCT TG-3'
<i>FSP1</i>	5'-CTT GGT TTG GTG CTT CTG AGA-3'	5'-TGG ACA CCA TCA CAT CCA GG-3'

Fig. S1

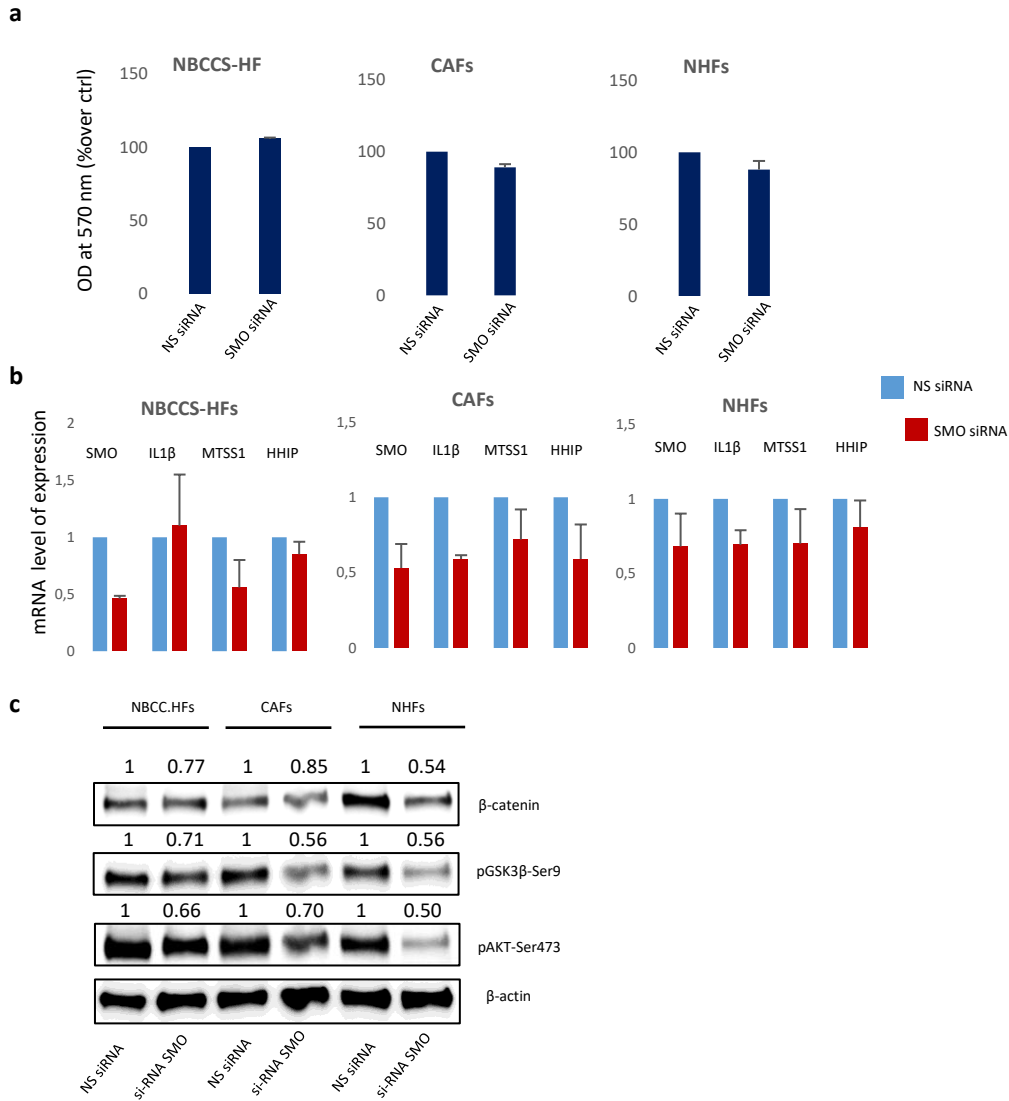


Table S4 Gene expression analysis

Gene	NBCCS-HF NS-siRNA	NBCCS-HF SMO-siRNA	CAF NS-siRNA	CAF SMO-siRNA	NHF NS-siRNA	NHF SMO-siRNA
<i>SMO</i>	4.9±5.4	2.2±0.11	9.6±9.5	5.1±1.5	1.0	0.68±0.22
<i>IL18</i>	6457.7±9666.3	7102.3±2905.3	30.3±23.5	17.9±5.0	1.0	0.69±0.10
<i>MTSS1</i>	7.5±3.4	4.2±1.79	4.73±3.4	3.40±0.9	1.0	0.70±0.23
<i>HHIP</i>	873.3±1192.4	733.6±87.3	38.3±37.0	22.8±8.9	1.0	0.81±0.18

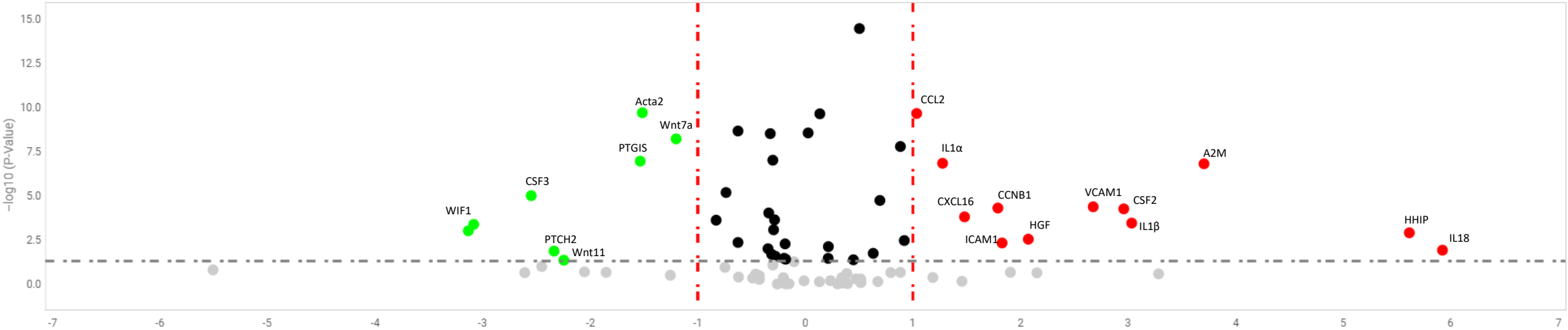
**Figure S1:** (a) MTT assay of NBCCS-HFs, CAFs and NHFs transfected with specific SMO siRNA for 72h. Data represent the average of experiments performed with 2 different SMO siRNA. (b) Semi-quantitative RT-PCR was performed to assess the level of SMO, IL1β, MTSS1 and HHIP level of expression in cells transfected with SMO siRNA (72h). Histograms report mean ± SD of 2 set of experiments performed with 2 different SMO siRNA. (c) One representative western blot detecting β-catenin, pSer9-GSK3β and pSer473-AKT after 72h treatment with siRNA (NS siRNA or SMO siRNA).

Fig. S2

a

Group : NBCCS-HFs Vis (2 week) vs NBCCS-HFs Ctrl

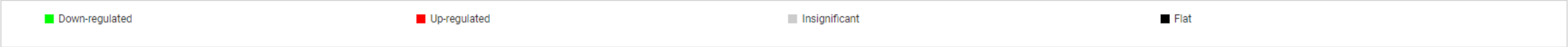
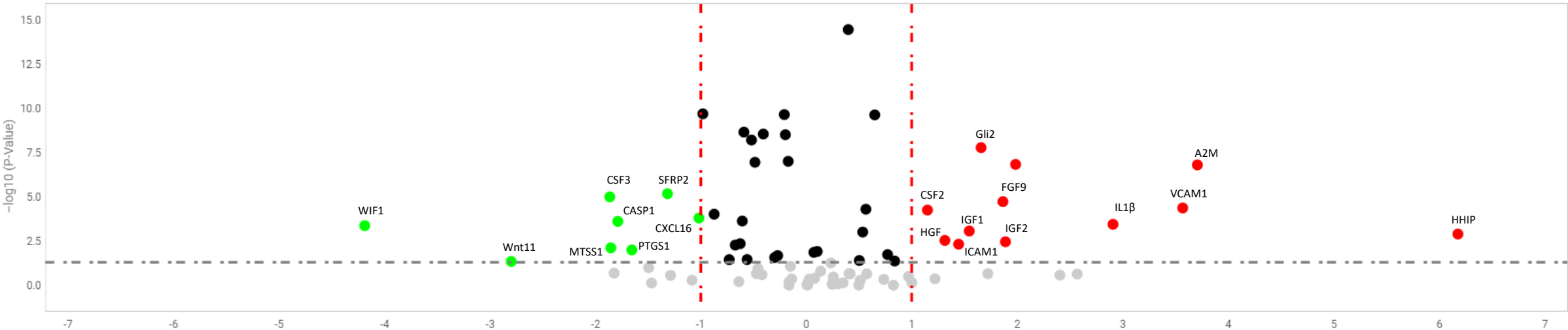
Reference : A    Fold Change Boundary :     P-Value Boundary :    



b

Group : NBCCS-HFs Son (2 week) vs NBCCS-HFs Ctrl

Reference : A    Fold Change Boundary :     P-Value Boundary :    



**Figure S2:** Volcano plot represents gene expression analysis comparing NBCCS-HFs treated with vismodegib (a) and sonidegib (b) for 2 weeks (n=9). (b) Analysis was performed using three different housekeeping genes ( $\beta$ -actin, GAPDH and 18S). One-way ANOVA statistical test with thresholds  $>2.0$  fold-change and  $p < 0.05$  defined significant increase are reported in red; significant decrease  $<0.5$  fold-change and  $p < 0.05$  reported in green; any fold-difference with  $p \geq 0.5$ , *e.g.* insignificant are reported in grey;  $\leq 2.0$  or  $\geq 0.5$  difference *e.g.* flat reported in black.