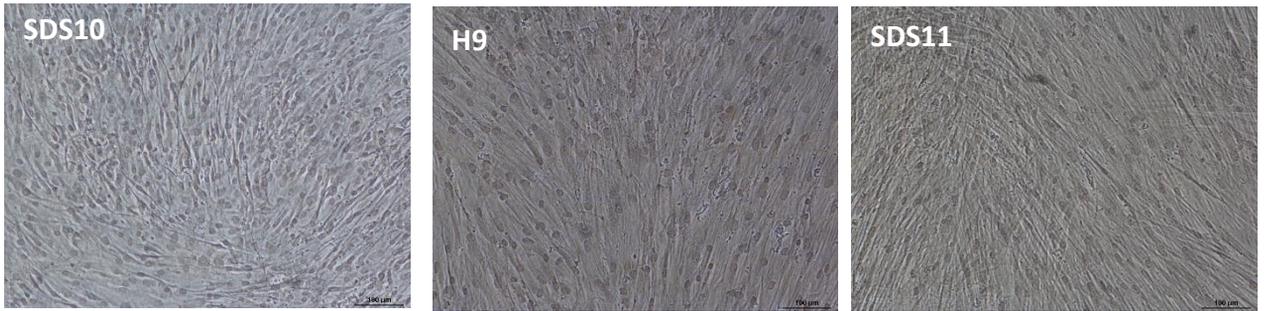
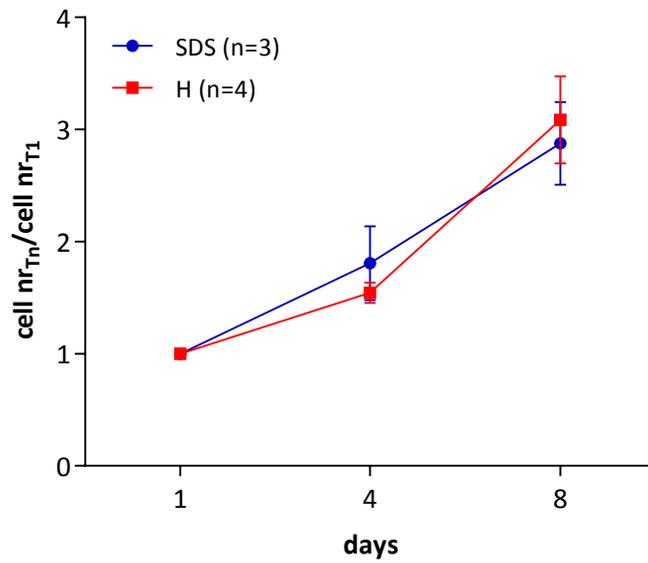


Figure S1

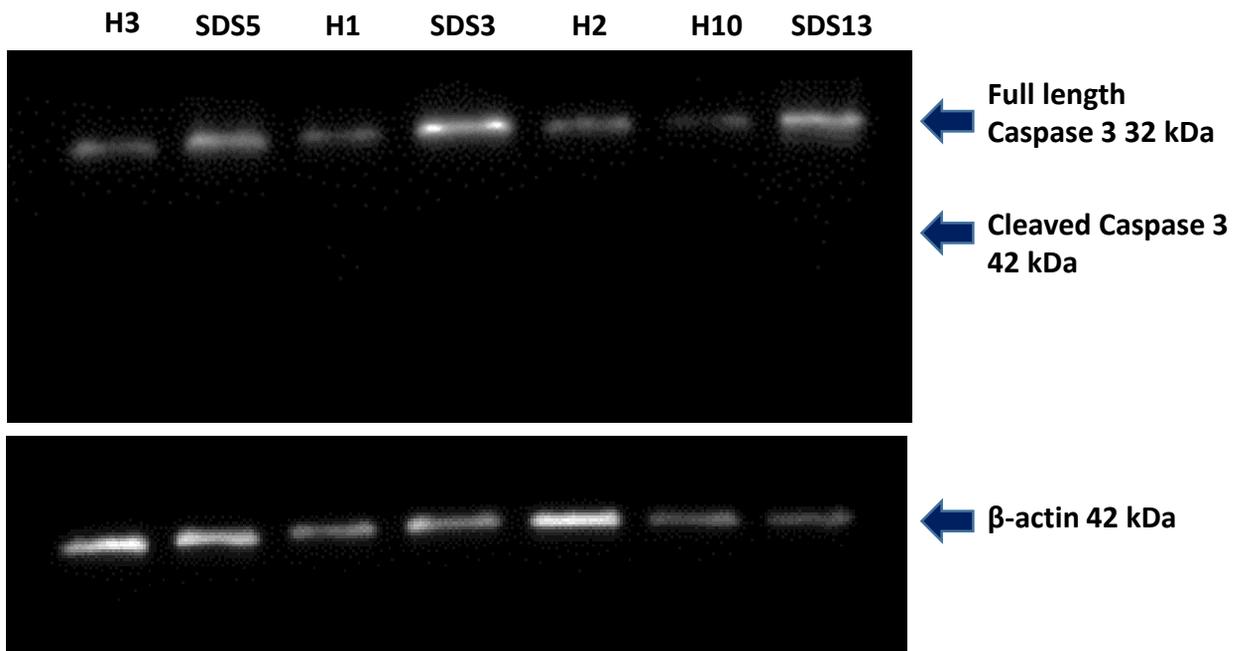
a

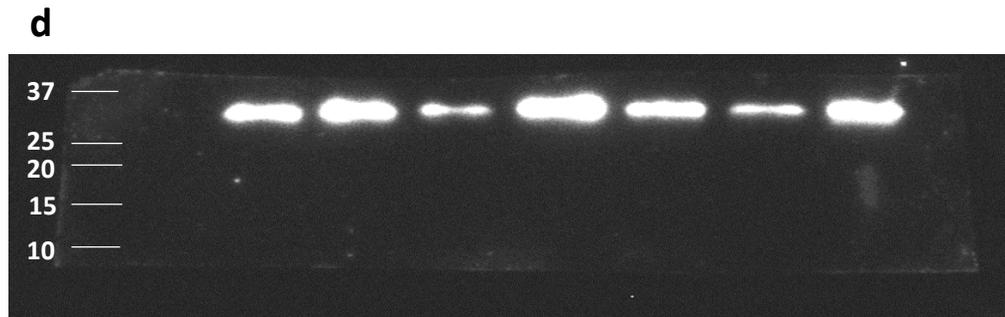


b



c





e

Antibody #9668 Cell Signaling Technologies.
 Western blot analysis of HeLa cell extracts treated with 1uM staurosporine (3hrs)

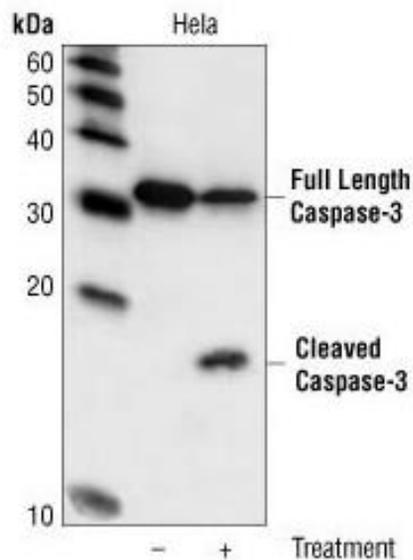


Figure S1: **a.** Image of osteoblast derived from Shwachman Diamond Syndrome subjects (SDS10, SDS11) and from a healthy subject (H9), magnification 10x. **b.** Proliferation of osteoblast derived from Shwachman Diamond Syndrome subjects (SDS=3) and from healthy subjects (n=4). **c.** Representative image of Western blot analysis of full length and cleaved caspase 3 protein expression in osteoblasts from healthy subjects (H3,H1, H2) and SDS patients (SDS5,SDS3,SDS13) **d.** Over-exposed image of the western blot did not reveal the presence of cleaved caspase 3 **e.** Characteristics of the antibody used for the detection of full length and cleaved caspase. all these data indicate that SDS-OBs has comparable proliferation and apoptotic activities as H-OBs.

Figure S2

(a)

>Human SBDS chromosome:GRCh37:7:66452064:66461188

1	aattagcttggcgtggccgctcacacctgtagtcccagctacttgggaagctaacgctgg	60
61	aagatcgctcgaaccaggaggtcgaagctgcagtgggggccatgaccctgccactgcact	120
121	ccagcctgggtgacagagtgagactgacttaaaaaaaaaaactgtaaataaaaaagcaaca	180
181	aaaaaatgaaaaagaataaaaacaaggatggcaaaatggtgatagcgggggatgggtac	240
241	atagaaggttcattacacttttttgtctacattttatgttataaatatttctattataaaa	300
301	gggtgagtaaataaaaaatatttattataaaaataattctattataaaaaatatttatatta	360
361	taaagtgggtctggcccttgaattccgcggaacgaggtgggtgccaacgctgtgttttaac	420
421	ccggtcactaaacatccgcgagcatcctgtcagagctctcagctcattggcgaaagtaaa	480
481	tacgccaaggaaaagcacctcccttttggcgtggaaagatggcgtaaaaagccacaat	540
541	acgcaggcgtcatcgctcacttttccctcccggtctctgctccacctgacgctgcgca	600
601	GTAAGTAAGCCTGCCAGACACACTGTGACGGCTGCCTGAAGCTAGTGAGTCGCGGGCGCCG	660 exon 1
661	CGCACTGGTGGTTGGGTGAGTGCCGCGCGCCGATCGGTCGTTACCGCGAGGCGCTGGTGG	720
721	CCTTCAGGCTGGACGGCGGGTCCAGCCCTGGTTCGCCGGTCTTGGGTCTTTGAACAGC	780
781	CGCGATGTCGATCTTCACCCCAACCAACCAGATCCGCTAACCAATGTGGCCGTGGTACG	840
841	GATGAAGCGTGCCGGGAAGCGCTTCGAAATCGCCTGCTACAAAAACAAGGTGCTCGGCTG	900
901	GCGGAGCGGCGT gtgagtagccccctccctcgggcctgggcctgggcctgagccgtcacC	960
961	tccgaggcggcctgtctctgcccaagtgcagtgaaatgggcccaggctgggggtgttggccgg	1020
1021	ggaggaaatggaacatttctgctgtgagcatgagacgtcgtctgctccgagcttggcgcceta	1080
1081	agccaagggtttcttctttatattggttgggttcggattgggttgggttgggttgggtt	1140
1141	tttgttgggtgtcataaaagctgcagccaagaaatctcgtaattgtgggtccttttctaga	1200
1201	ataatgatggctgagaacctagtcttacgaataactgtcatagttgtgggtacatctgggtg	1260
1261	tcatagatctcagtacccatgacagtttaaaagtgcgtagtgtcttctactgctgccatcta	1320
1321	gggactggcattccgtggcagcagctgtctgcacccccacccttgtgtttcttacg	1380
1381	tctcccatgacatttttctccagtgcacaaatggtaaggcaaatacgggttctgagtttt	1440
1441	gaaaatgttccctcaggccgatgcgggcagttcacttgaggccaggagttcgaggccagc	1500
1501	ctggccaacatgaaacccatctctactaaaaatacaaaagttagccgggtgtggtggcgc	1560
1561	atgcctgtaatcccagttactcaggaggetgaggcgaggagaatcacttgaaccgggagg	1620
1621	ctgaggttacagtgaccgagatcgcgccattgcactccagcctgggcaaaaacagtga	1680
1681	attccatctaggggccccgggttggggggtaagaaaagaaaactgccctctacactaaag	1740
1741	gtcatcaggggatttggttgtgtcttggcgttcatgttggttgccatctcgtatttaaatg	1800
1801	taaatgcatgtccaagtttcaagtatattcacataggactttctctcctgccctcacaag	1860
1861	GGAAAAAGACCTCGATGAAGTTCTGCAGACCCACTCAGTGTGTTGTAATGTTTCTAAAGG	1920 exon 2
1921	TCAGGTTGCCAAAAAGGAAGATCTCATCAGTGCGTTTGAACAGATGACCAAACCTGAAAT	1980
1981	CTCTAAGCAG gtgggtaacagctgcagcatagctaaccctaataaccattttataacgtat	2040
	▼ c. 258+2T>C	
	del 8 bp	
2041	ttgtagatatattaacattaaaggctgtttttctggaggaaagactaaccaagcaataa	2100
2101	tgtgaactgcacagtgctcacttctaataataaagaacttgggtgggtttgtttgtttttg	2160
2161	tggtttttttttttttttttttggcaaaacctcctgaaatcagattttctactaaattac	2220
2221	ctcattttttctataaattgccccatttatagaatgtggtataacctgaaaactgaatttgt	2280
2281	tttcaagtatttcatctttcagatccttttttttttgggtggggggacagagtcttgcctc	2340
2341	tgttggccaggctggagtgacgtgcacttcaactgcactcagctcactgcaacctctgcct	2400
2401	cctggattcaagcgatttctcttgcctcagcttccagggtagctgggattacaggtgcca	2460
2461	ccacctgcctggctaatttttggatttttagtagagatggggtttcccatgttggcca	2520
2521	ggttgggtctcaaactcctgaccttgggtgatatgccgccttagccacccaaagtgtgg	2580
2581	gattacagatgtgagccactgagcccagccaaaagattcttgcatttttgggcaagct	2640
2641	caaaccattacttacatattgatagctggagaggatgaaattttaattttctctccatcca	2700
2701	gttactcattttttatggttagttataaatagtggtgtgatagagaaagatagtgatttc	2760
2761	ttaaagtgttggcatttttttag ATTTTGACTAAAGGAGAAGTTCAAGTATCAGATAAA	2820 exon3
2821	GAAAGACACACAACCTGGAGCAGATGTTTAGGGACATTGCAACTATTGTGGCAGACAAA	2880
2881	TGTGTGAATCCTGAAACAAAGAGACCATAACCCGTGATCCTTATTGAGAGAGCCATGAAG	2940
2941	GACATCCACTATTCCGTTGAAAACCAACAAGAGTACAAAAACAGCAG gtgagtggtttctca	3000

(b)

WT	<u>ATGTCGATCTT</u> CACCCCCACCAACCAGATCCGCCTAACCAATGTGGCCGTGGTACGGATG	exon1
258+2T>C	<u>ATGTCGATCTT</u> CACCCCCACCAACCAGATCCGCCTAACCAATGTGGCCGTGGTACGGATG	
WT pep	M S I F T P T N Q I R L T N V A V V R M	
Alt pep	M S I F T P T N Q I R L T N V A V V R M	
WT	<u>AAGCGTGCCGGAAGCGCTT</u> CGAAATCGCCTGCTACAAAAACAAGGTCGTCCGCTGGCGG	
258+2T>C	<u>AAGCGTGCCGGAAGCGCTT</u> CGAAATCGCCTGCTACAAAAACAAGGTCGTCCGCTGGCGG	
Wt pep	K R A G K R F E I A C Y K N K V V G W R	
Alt pep	K R A G K R F E I A C Y K N K V V G W R	
WT	<u>AGCGGCGTGG</u> AAAAAGACCTCGATGAAGTTCTGCAGACCCACTCAGTGTGGTAAATGTT	exon2
258+2T>C	<u>AGCGGCGTGG</u> AAAAAGACCTCGATGAAGTTCTGCAGACCCACTCAGTGTGGTAAATGTT	
WT pep	S G V E K D L D E V L Q T H S V F V N V	
Alt pep	S G V E K D L D E V L Q T H S V F V N V	
WT	TCTAAAGGTCAGGTTGCCAAAAAGGAAGATCTCATCAGTGCCTTT <u>GGAACAGATGACCAA</u>	
258+2T>C	TCTAAAGGTCAGGTTGCCAAAAAGGAAGATCTCATCAGTGCCTTT <u>GGAACAGATGACCAA</u>	forw ►
WT pep	S K G Q V A K K E D L I S A F G T D D Q	
Alt pep	S K G Q V A K K E D L I S A F G T D D Q	
WT	<u>ACTGAAATC</u> TGTAAGCAGATTTT <u>GACTAAAGGAGAAGTTCAAGTATCAGATAAAGAAAGA</u>	exon3
258+2T>C	<u>ACTGAAATC</u> T-----ATTTT <u>GACTAAAGGAGAAGTTCAAGTATCAGATAAAGAAAGA</u>	
WT pep	T E I C K Q I L T K G E V Q V S D K E R	
Alt pep	T E I Y F D X	
WT	CACACACA <u>ACTGGAGCAGATGTTT</u> AGGGACATTGCAACTATTGTGGCAGACAAATGTGTG	
258+2T>	CACACACA <u>ACTGGAGCAGATGTTT</u> AGGGACATTGCAACTATTGTGGCAGACAAATGTGTG	
WT pep	H--T--Q--L--E--Q--M--F--R--D--I--A--T--I--V--A--D--K--C--V-	
WT	AATCCTGAAACAAAGAGAC <u>CCATACACCGTGATCCTTATTG</u> AGAGGCCATGAAGGACATC	
258+2T>C	AATCCTGAAACAAAGAGAC <u>CCATACACCGTGATCCTTATTG</u> AGAGGCCATGAAGGACATC	◀ rev
WT pep	N--P--E--T--K--R--P--Y--T--V--I--L--I--E--R--A--M--K--D--I	

Figure S2. Splice site mutation in the *SBDS* gene

(a) Genomic sequence of the gene *SBDS* showing the first 3 exons (capital letters) and introns (lowercase letters). It is indicate the position of the mutation c.258+2T>C (▼) that abrogates the classical 3' splice site GT and creates the mutated and weak splice site GC, and the position (▼) of the alternative splice site used in the alternative transcript, resulting in the deletion of 8 nucleotides.

(b) The alignment of wild type (WT), mutated (258+2T>C) nucleotide sequences and the amino acids sequence of the alternative transcript (alt pep) and the wild type protein at the mutation level (WT pep). Primer sequences (forward and reverse) used for the RT-PCR are underlined and in bold.