

**(-)-Sativan inhibits tumor development and regulates
miR-200c/PD-L1 in triple negative breast cancer cells**

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Table S1. The primers used for Real-time PCR

CD247	(F) TGCCGACTACAAGCGAATTACTG
	(R) CTGCTTGTCCAGATGACTTCGG
GAPDH	(F) GACTCATGACCACAGTCCATGC
	(R) AGAGGCAGGGATGATGTTCTG
U6	(F) CTCGCTTCGGCAGCACCA
	(R) AACGCTTCACGAATTGCGT

Table S2. The primers used for colony PCR

CD247	(F) CGCGCTCGAGGTTGGTCATGCTGGGGA
wide-type	(R) CGCGAAGCTTCTTCTCCCTGTCACAGGCG
CD247	(F) ATTATCACTCTGGTCTATGACATTGGAGGTCTGCTAATCCAGCATTG GAACTTCTGATC
mut	(R) CATAGACCAGAGTGATAATAGTATATTAAATTCATGGGAAG

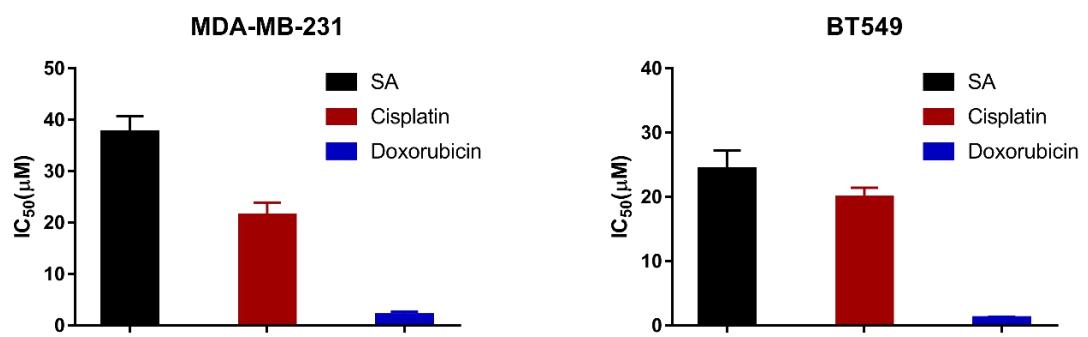


Fig S1. The IC₅₀ values of MDA-MB-231 and BT549 cells with the treatment of SA, cisplatin, and doxorubicin for 24 h.

PhenomiR 2.0

Study information	
Study design:	Patient study phenotype-control
Patients:	55
Control:	55
Samples information:	
Tissue/Cell line:	breast epithelium
Tissue comment:	

Detailed information about selected miRNA	
miRNA:	hsa-mir-200c
miRNA comment:	
Method:	array CGH
Further methods:	
Evidence:	miRNA overexpression
Foldchange:	

Study information	
Study design:	Cell culture study
Patients:	
Control:	
Samples information:	
Tissue/Cell line:	MDA-MB-231 cell
Tissue comment:	

Detailed information about selected miRNA	
miRNA:	hsa-mir-200c
miRNA comment:	
Method:	quantitative PCR
Further methods:	
Evidence:	miRNA downregulation
Foldchange:	5.882

Fig S2. PhenomiR 2.0 (<http://mips.helmholtz-muenchen.de/phenomir>) showed that miR-200c was highly expressed in normal breast epithelium, and was lowly expressed in TNBC cell line.



Fig S3. MicroRNA.org (<http://www.microrna.org/microrna/getGeneForm.do>) predicted that CD247 was one of the most potential targets of miR-200c with the relatively high prediction scores.