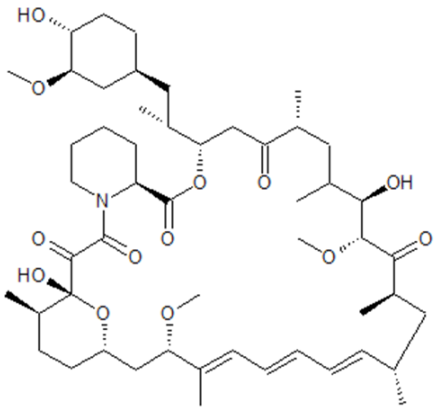
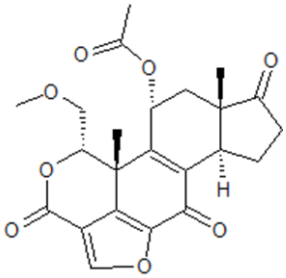
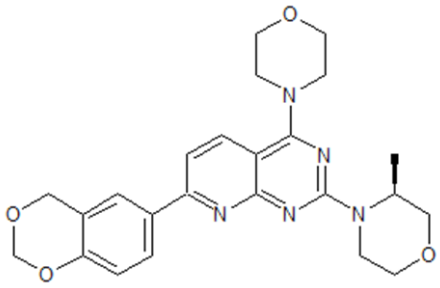
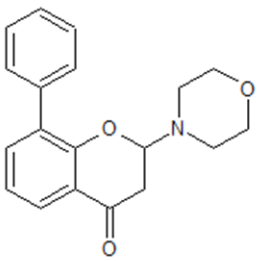
Supplementary Tables

Supplementary Table 1. REDD1 inhibitors identified by computational screen and selected for study

Compound	Structure	No of cell lines	No of assays	Specific down-regulated target
Rapamycin		30	135	mTORC1
Wortmannin		14	131	PI3K
AZD-8055		24	55	mTORC1/mTORC2/Akt/PI3K
LY294002		6	28	PI3K

To identify small molecule compounds that can inhibit REDD1 expression, we analyzed the transcriptional profiles induced by FDA-approved and experimental drugs from the LINCS library

(http://lincsproject.org/LINCS/) comprised of the results of ~1 million experiments in which the global effect of >20,000 unique compounds on human cell transcriptome was accessed across 50 cell types of varied lineage using custom-made DNA arrays. The molecular signature of each compound in each experiment is presented at LINCS as a list of DEGs - differentially expressed genes (compound-treated versus solvent-treated), ordered by descending expression fold-change. The top putative REDD1 inhibitors were selected according to the number of LINCS experiments in which REDD1 was within 100 most down-regulated genes in treated cells. For statistical computing, we used the R project version 3.2.5 (https://www.r-project.org/).

Supplementary Table 2. Primer sets for Q-PCR analysis

Gene symbol		Primer sequence: sense/antisense (5'-3')
Mouse	**Human**	
Rankl		CAGCATCGCTCTGTTCCTGTA CTGCGTTTTCATGGAGTCTCA
Opg		ACCCAGAAACTGGTCATCAGC CTGCAATACACACACTCATCACT
Rpl27		GCCCTGGTGGCTGGAATTGACC TTGCGCTTCAAAGCTGGGTCCC
	CCND1	CTACCTTCCGCAGTGCTCCTA CCCAGCCAAGAAACGGTCC
	CCND2	GCTGGAGCCCGTGAAAAAGA CTCCGCCTCTGGCATTTTG
	CD86	CTGCTCATCTATACACGGTTACC GGAAACGTCGTACAGTTCTGTG
	FKBP51	GAATGGTGAGGAAACGCCGAT TGCCAAGACTAAAGACAAATGGT
	GILZ	AACACCGAAATGTATCAGACCC TGTCCAGCTTAACGGAAACCA
	IL7R	CGTCTATCGGGAAGGAGCCAAT GCTGGATAAATTCACATGCGTCCA
	KLF9	GAAACACGCCTCCGAAAAGAGG GAAAGGGCCGTTCACCTGTATG
	MKP1	ACCACCACCGTGTTCAACTTC TGGGAGAGGTCGTAATGGGG
	REDD1	TAGCCTTTGGGACCGCTTCTCGT CAGGTAAGCCGTGTCTTCCTCCG
	RPL27	ACCGCTACCCCCGCAAAGTG CCCGTCGGGCCTTGCGTTTA

Supplementary Table 3. Cytotoxicity of WM, LY294002, AZD8055 (IC50 value after 24 h of incubation, uM)

Compound	IC50, CEM, uM	IC50, Granta, uM
Wortmannin	9,145	11,944
LY294002	61,969	77,588
AZD8055	1,358	2,015

To calculate IC50 values, CEM and Granta cells were pretreated with solvent, LY294002 (1-500 uM), WM (0,1-25 uM) and AZD8055 (0,05-5 uM) for 6 h and treated with either solvent or glucocorticoid Dex (1 uM) for 24 h. After the treatment, 20 ul of MTT solution (5 mg/ml) was added to each well and the plates were incubated for another 3 hours. After incubation with MTT, the medium was removed and 150 µL of 100% DMSO was added to each well. Optical density was read at 495 nm using a microplate reader MultiScan MCC 340 (Labsystems). Relative cell viability was determined respectively to the untreated cells. The IC50 values was calculated using Quest Graph™ IC50 Calculator software.