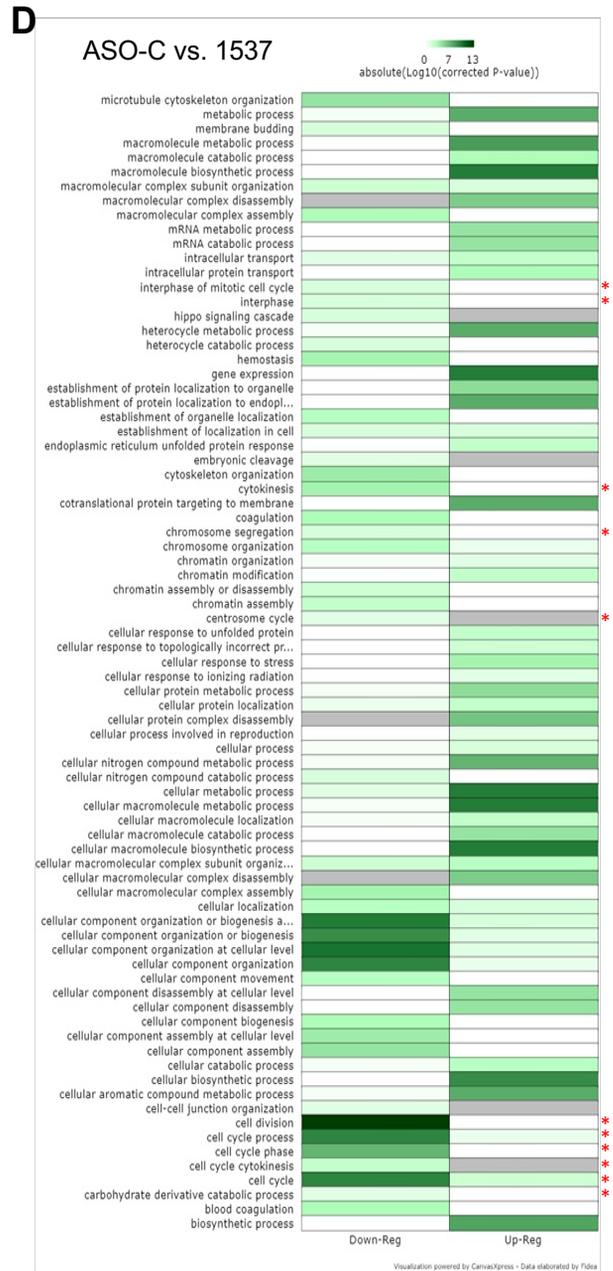
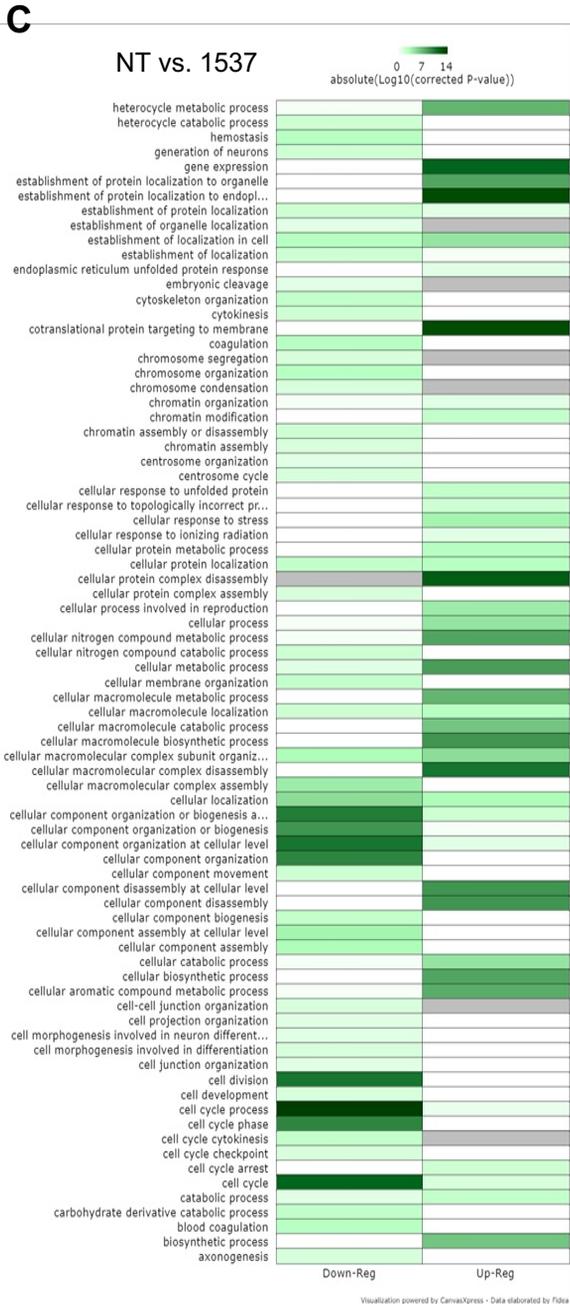
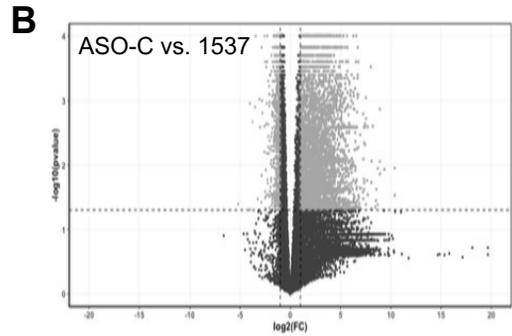
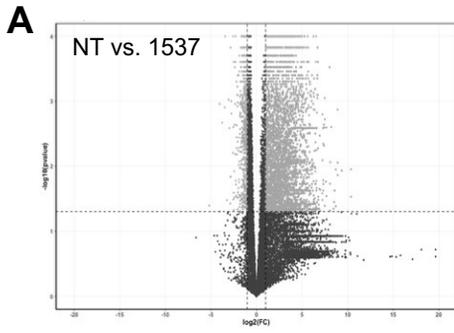
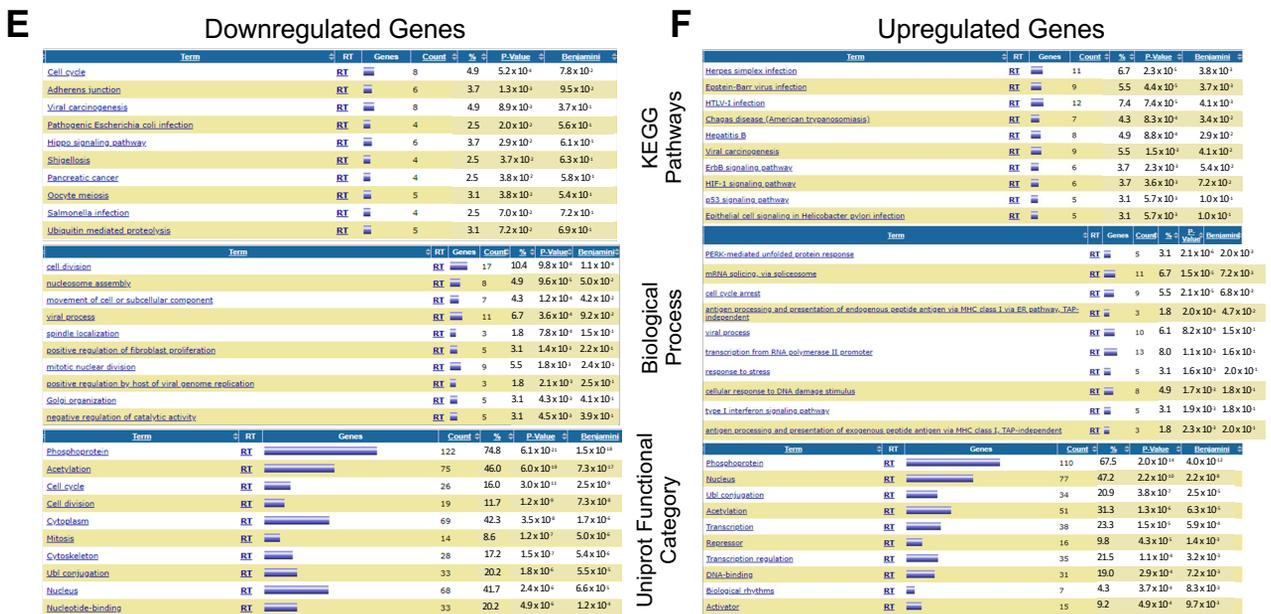


**Table S1:** Sequence of primers used for qPCR

GENE NAME	Forward/Reverse	Sequence (5' – 3')
AURKA	Forward	GTCAAGTCCCCTGTTCGGTTC
	Reverse	AGTGAGACCCTCTAGCTGTAAT
TOP2A	Forward	AGTGGAGCTCTCCTAACCGA
	Reverse	CATTTACAGGCTGCAATGGTGA
COX5B	Forward	ATCTGGAGGTGGTGTTCCTCA
	Reverse	CCAGACGACGCTGGTATTGT
TIMM50	Forward	CAGATCAGGCCGCAGAGATCG
	Reverse	TATGTCCGGCGCAACTGCT
18S	Forward	GTAACCCGTTGAACCCCAT
	Reverse	CATCCAATCGGTAGTAGCG





**Figure S1:** Transcriptome data analysis. **A, B**, volcano plots of data comparison between NT and Andes-1537 (**A**) and between ASO-C and Andes-1537 (**B**) showing  $p$ -value and fold-change data. **C, D**,  $p$ -value heatmaps of most significant differentially-expressed genes between NT and Andes-1537 (**C**) and between ASO-C and Andes-1537 (**D**) according to biological function. Categories directly related to cell cycle progression are marked with red asterisks. E, F, Gene ontology analysis of differentially-expressed genes for NT vs Andes-1537 and ASO-C vs Andes-1537 (see Fig. 1C). **E**, downregulated genes; **F**, upregulated genes. The first 10 results for each (Kegg Pathways, biological process and Uniprot functional category) are shown.

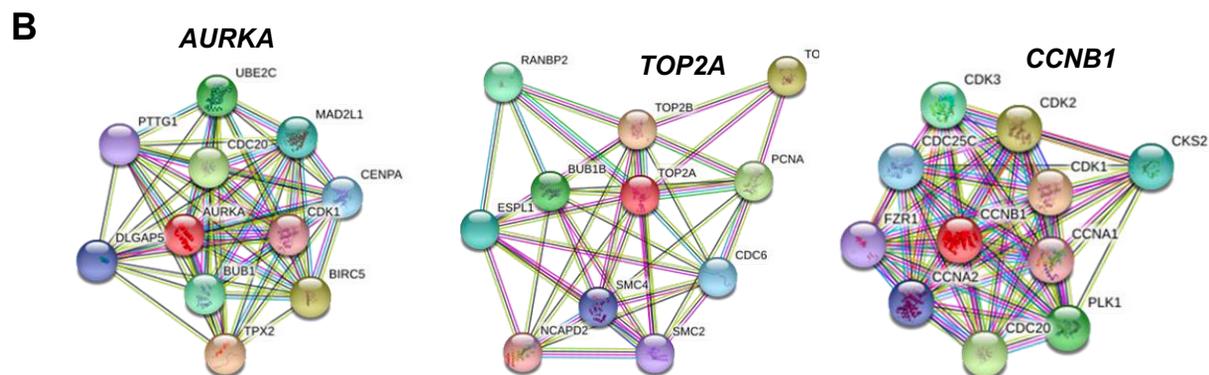
**A**

### Down-regulated Genes

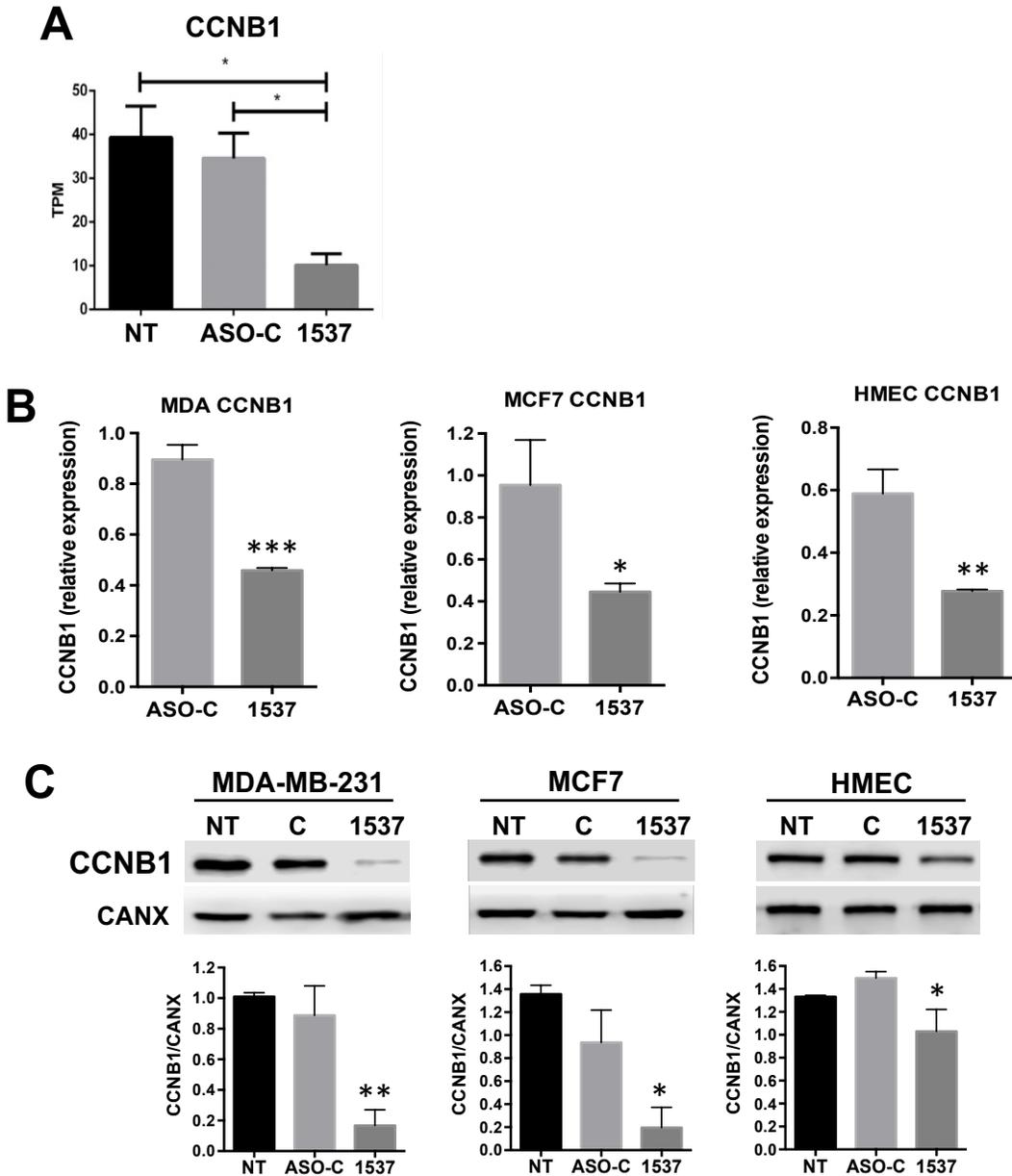
N°	ENSEMBL_ID	Official_name	Description	CB_rank	CB_peak
1	ENSG0000087586	AURKA	aurora kinase A	4	M
2	ENSG0000134690	CDCA8	cell division cycle associated 8	5	G2
3	ENSG0000175063	UBE2C	ubiquitin conjugating enzyme E2 C	8	G2
4	ENSG0000088325	TPX2	TPX2, microtubule nucleation factor	9	M
5	ENSG0000131747	TOP2A	topoisomerase (DNA) II alpha	14	G2
6	ENSG0000169679	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	15	M
7	ENSG0000126787	DLGAP5	DLG associated protein 5	20	M
8	ENSG0000138160	KIF11	kinesin family member 11	30	G2
9	ENSG0000156970	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	33	G2/M
10	ENSG0000134057	CCNB1	cyclin B1	49	M
11	ENSG0000136108	CKAP2	cytoskeleton associated protein 2	50	G2/M
12	ENSG0000134222	PSRC1	proline and serine rich coiled-coil 1	81	G2
13	ENSG0000011426	ANLN	anillin actin binding protein	89	M
14	ENSG0000157456	CCNB2	cyclin B2	96	M

### Up-regulated Genes

N°	ENSEMBL_ID	Official_name	Description	CB_rank	CB_peak
1	ENSG0000177606	JUN	Jun proto-oncogene, AP-1 transcription factor subunit	393	non-periodic
2	ENSG0000175197	DDIT3	DNA damage inducible transcript 3	1568	non-periodic
3	ENSG0000116717	GADD45A	growth arrest and DNA damage inducible alpha	2092	non-periodic
4	ENSG0000165891	E2F7	E2F transcription factor 7	4207	non-periodic
5	ENSG0000125347	IRF1	interferon regulatory factor 1	4357	non-periodic



**Figure S2:** Selection of genes of interest. **A**, final list of pre-selected genes for RT-qPCR validation, generated using CycleBase and selecting only cell cycle-related genes. **B**, Interactions of the final 3 genes selected after RT-qPCR validation, obtained using the STRING platform (see Methods).



**Figure S3:** Changes in *CCNB1* expression after ASncmtRNA KD. **A**, Relative *CCNB1* levels in MDA-MB-231 cells after a 24 h treatment with Andes-1537, ASO-C or non-treated (NT), obtained from transcriptomic data and expressed in TPM. **B**, *CCNB1* mRNA levels are decreased 2-fold in MDA-MB-231, MCF7 and HMEC, as evidenced by RT-qPCR. Data is presented relative to NT cells. **C**, Cells treated as in B were subjected to Western blot analysis, which showed a reduction in *CCNB1* protein levels in all three cell types, but much more marked in both tumor cell lines compared to normal HMECs. Calnexin (*CANX*) was used as loading control. \* $p < 0,05$ , \*\* $p < 0,01$ , \*\*\* $p < 0,001$ .