Supplemental Tables

Adaptation to spindle assembly checkpoint inhibition through the selection of specific aneuploidies

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Cell line	Tissue	Phenotype	Sex	Culture Medium	Source
hTERT-RPE1	Retina epithelial	Adherent	Female	DMEM (Sigma-Aldrich) + 2 mmol L-Glutamine (Gibco) + 1mM Natrium-Pyruvate (Sigma-Aldrich)	I. M. Cheeseman (University of California, USA)
hTERT-HME1	Mammary gland epithelial	Adherent	Female	MEBM (Lonza) + 2 mmol L-Glutamine (Gibco) + 1mM Natrium-Pyruvate (Sigma-Aldrich)	Evercyte (Cat#: CHT-044-0236)
DLD1	Colorectal cancer	Adherent	Male	RPMI-1640 (ATCC) (Sigma-Aldrich)	M. Baccarini (Max Perutz Labs, Austria)
HCT116	Colorectal cancer	Adherent	Male	McCoy's 5A (Sigma-Aldrich) + 2 mmol L-Glutamine (Gibco) + 1mM Natrium-Pyruvate (Sigma-Aldrich)	B. Vogelstein (The Johns Hopkins Oncology Center, USA)
diploid HAP1 (dipHAP1)	Chronic myeloid leukemia (CML)	Adherent	Male	IMDM (Sigma-Aldrich)	J.I. Loizou (CeMM, Austria)
EEB	Acute myeloid leukemia (AML)	Suspension	Male	SFEM (STEMCELL Technologies)	Riken (RCB2345)

All culture media were supplemented with 10% FBS and 1% Penicillin-Streptomycin.

Supplemental Table 1. Cell lines used in this study and their culture medium.

Cell line	Karyotype deviations from euploidy
parental RPE1	Segmental chr. 10q gain
RPE1 TP53 KO	Segmental chr. 10q gain
parental HME1	segmental loss of 3p, loss of chr. 4, segmental gain & loss of chr. 7q, chr. 10 isochromosome, chr. 12p gain
HME1 TP53 KO	segmental gain of 3p, loss of chr. 4p, gain of chr. 4q, segmental gain & loss of chr. 7q, chr. 10 isochromosome, chr. 12p gain
parental HAP1	Segmental chr. 15q gain
dipHAP1 TP53 KO	Segmental chr. 15q gain
parental EEB	none
EEB TP53 KO	none
parental DLD1	Segmental chr. 2p gain
DLD1 TP53 KO	Segmental chr. 2p gain
parental HCT116	Segmental gains of chromosomes 8q, 10q 16q and 17q
HCT116 TP53 KO	Segmental gains of chromosomes 8q, 10q, 16q and 17q, segmental 4q loss (above 1.6 threshold)

Supplemental Table 2. Karyotype deviations of the parental cell lines used in this study.

Name	Sequence	Reference
Chromosome arm 6p deletion		
sgRNA 6p A	ACGGTTTCATTAGTCATACC	This paper
sgRNA 6p B	GGGACCGTCACCCTAATAGG	This paper
sgRNA 6p C	TGGAATATTGTTCACCTTTA	This paper
Chromosome arm 13q deletion		
sgRNA 13q A	GGGGGAGTGAATGTGAGTGA	This paper
sgRNA 13q B	ATATATGGGGTATACGTATA	This paper
sgRNA 13q C	TGGGTTACTTACCGACCGTG	This paper
sgRNA 13q D	GATAATACGATAGGCCAGTG	This paper

Supplemental Table 3. sgRNAs that were used for the generation of whole or partial chromosome deletions. Further Illustration in Figure S10 B.

Name		Sequence	Reference	
Chromosome 6p deletions				
EXOC2	fw	ATGTCTCGATCACGACAACCC	PrimerBank, ID: 30581133c1	Spandidos et al. 2010
	rev	GGCCAGTCCCCAGATTTTCT		
DST	fw	CTACCAGCACTCGAACCAGTC	PrimerBank, ID: 291290967c1	
	rev	GCCGAAGCTAATGCAAGAGTTG		
Chromosome 13q deletions				
ZMYM5	fw	AGAGTTGACTGAACAGACTCCT	PrimerBank ID: 218083691c1	
	rev	GACCAAATGAATCCCCTATGTCC		
GPC5	fw	GGTGTGACTGACAGTTCCCTG	PrimerBank, ID: 215272348c3	
	rev	TGCAGATAGTCTGTGGTGTTGAT		
Control primer				
ALB **(chr4)**	fw	TGTTGCATGAGAAAACGCCA	Bremer et al. 2015	
	rev	GTCGCCTGTTCAACCAAGGAT		

Supplemental Table 4. QPCR primers used to identify whole and partial chromosome deletions. Primer binding sites for chr. 6p and 13q are illustrated in Figure S10 B.

Name	Sequence		Reference
p53	fw	CACCGACTTCCTGAAAACAACGTTC	Giacomelli et al. 2018
	rev	AAACGAACGTTGTTTTCAGGAAGTC	
p21	fw	CACCGCCGCGACTGTGATGCGCTAA	McKinley and Cheeseman 2017
	rev	AAACTTAGCGCATCACAGTCGCGGC	
p31^{comet}	fw	CACCGACTTGAGACAAGCTCTACGC	Thu et al. 2018
	rev	AAACGCGTAGAGCTTGTCTCAAGTC	
CDC16	fw	CACCGCTCTAGATAACCGAACCC	This paper
	rev	AAACGGGTTCGGTTATCTAGAGC	

Supplemental Table 5. SgRNAs used in this study for the generation of heterozygous and homozygous knockout cell lines. Underlined sequence represents added overhangs for the creation of dsDNA oligos that can be cloned into the gRNA/Cas9 plasmid, see Methods.

Name	Sequence	
p53	fw	TTATAGGGAGGTCAAATAAGCAGCA
	rev	ATCTACAAGCAGTCACAGCACAT
p21	fw	GCCCGGCCAGGTAACATAGTG
	rev	GTGACAGGTCCACATGGTCTTC
p31^{comet}	fw	GCGTATGTCGGAGTGCCTGC
	rev	GTGCTTAAGCTGTTCATAGG
CDC16	fw	CTATGATCGCACCACTGAACTC
	rev	TGTCAGCATGTGATGTGATGTT

Supplemental Table 6. Genotyping primers used for the identification and analysis of generated knockout cell lines.

Name	Sequence
Scrambled	Scramble siRNA (Dharmacon/smartpool format - D-001810-10-05)
MAD2	siMAD2 (Dharmacon/smartpool format – L-003271-00-0005)

Supplemental Table 7. SiRNA used in this study for the depletion of MAD2.

Name	gRNA Sequence	Reference
p31^{comet}	GCGTCGCCGCAGTGTGGGGG	This paper, gRNAs were selected using CHOPCHOP, (https://chopchop.cbu.uib.no, (Labun et al. 2019))
	GCGCGGGCCCCGTGCTCAAG	
	GTAACCTAGCGTAGTCACAGT	
CDC16	GTGGGCTTCTGGTTGCCTTG	Horlbeck et al. 2016

Supplemental Table 8. gRNAs used for the overexpression of *p31^{comet}* and *CDC16* via CRISPRa, see Fig. S15A.

Name	Sequence	
p31^{comet}	fw	GAGAAGTCCGAAGAAACTCACG
	rev	CCGAAGCGTTGAGAGGTTCC
CDC16	fw	TCCTGTGTCTTGGTTTGCAG
	rev	CAGAGCTTGGCTGAAGAACC
GAPDH	fw	TTGACCTCAACTACATGGTTTAC
	rev	AGGAGGCATTGCTGATGATC

Supplemental Table 9. RT-qPCR primers used for the identification of the fold change of p31comet and CDC16 in the dCas9-VPR-mCherry WT cell line, see Fig. S15C.

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