

Supplementary Information

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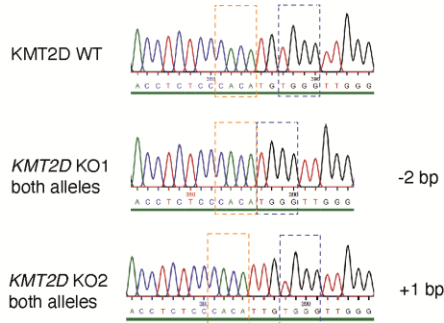
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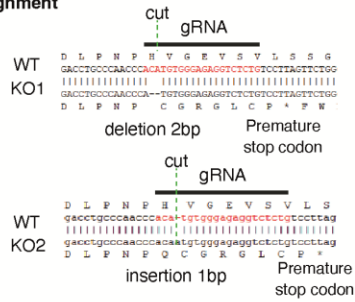
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KMT2D KO in parental MCF10A

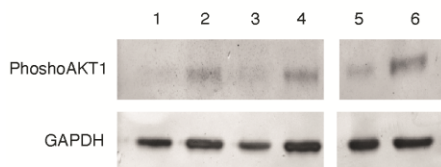
Sequencing



Alignment



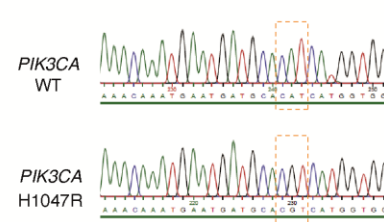
PIK3CA H1047R results in increased PhosphoAKT1



- 1 MCF10A
- 2 PI3KCA + H1047R (Horizon)
- 3 KMT2D KO
- 4 Double mutant
- 5 KMT2D KO (clone 2)
- 6 Double mutant (clone2)

PIK3CA H1047R/+

Sequencing

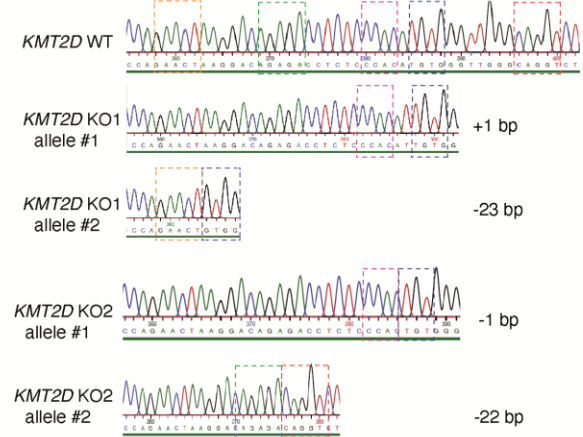


Alignment



KMT2D KO in *PIK3CA* H1047R/+

Sequencing



Alignment

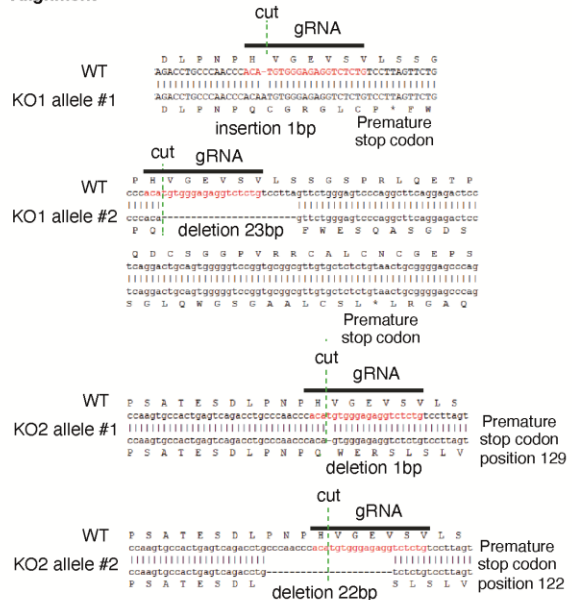


Figure S1. Characterization of *PIK3CA* H1047R and *KMT2D* KO alleles in the MCF10A cell lines. For the *KMT2D* KO, clones were selected based on the loss of the PciI restriction site (ACATGT) in the Cas9 cutting site and confirmed by sequencing when a frameshift results in the formation of a premature stop codon. Clones harboring *PIK3CA* H1047R displayed phosphorylated AKT1 on Ser 473, as expected upon constitutively active PI-3 kinase activity.

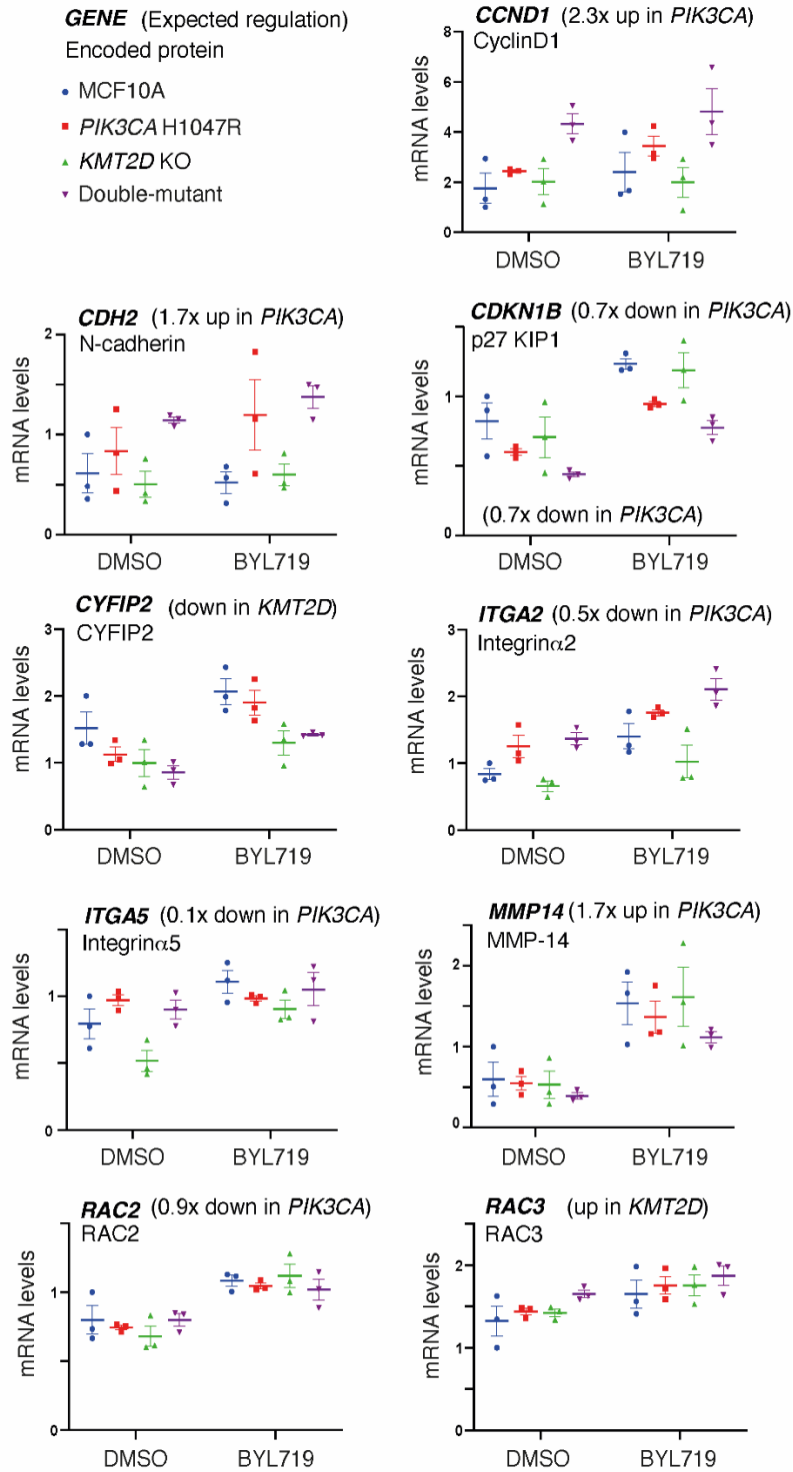


Figure S2. Genes, whose expression is measured and is not found to be significantly deregulated in MCF10A cells by *PIK3CA* H1047R or *KMT2D* inactivation. qRT-PCR analysis of gene expression is performed from MCF10A, *PIK3CA* H1047R, *KMT2D* KO and double-mutant cells in the presence or absence of 5 μ M BYL719. Mean \pm SEM, n=3 biological repeats. The variations that are previously reported in the references cited in the main text are indicated in parentheses.

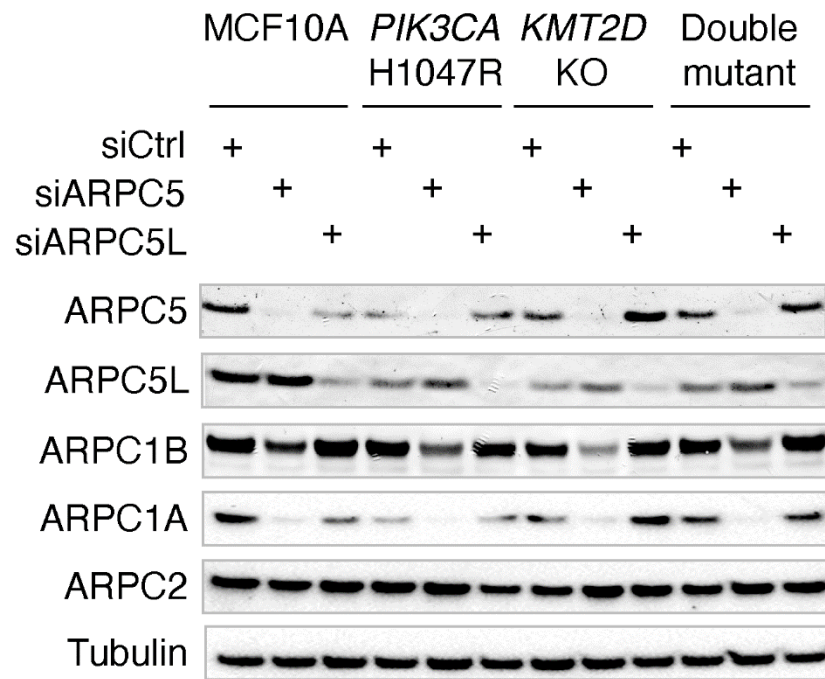


Figure S3. Western blots of MCF10A, *PIK3CA* H1047R, *KMT2D* KO and double-mutant cells when transfected with siRNAs targeting ARPC5 or ARPC5L or non-targeting siRNAs. The same depleted cells are assayed for single cell migration and results are displayed in Figure 6 and Figure S4.

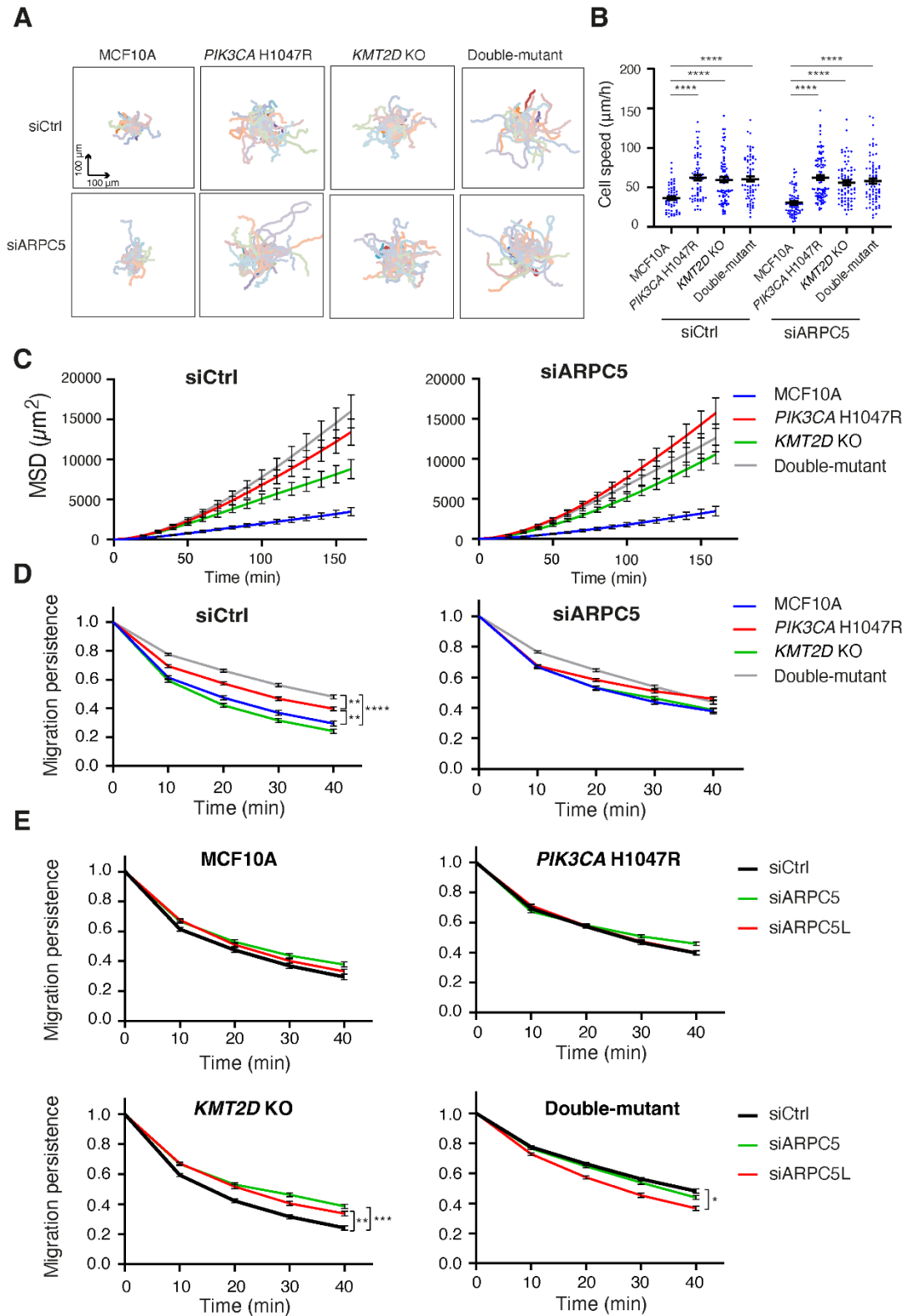


Figure S4. Single cell migration analysis. MCF10A, *PIK3CA* H1047R, *KMT2D* KO and double-mutant cells transfected with siRNAs targeting ARPC5 or ARPC5L or non-targeting siRNAs. **A** Trajectories of 56 MCF10A, *PIK3CA* H1047R, *KMT2D* KO and double-mutant cells, depleted of ARPC5 or not. The origin of each track is registered at the center of the plot. **B** Cell speed (mean \pm SEM). **C** Mean Square Displacement (MSD). **D** Migration persistence. **E** Migration persistence in all cell lines when depleted of either ARPC5 or ARPC5L. Three independent experiments are performed, overall number of cells ranges from 56 to 78 for each condition. ** $p < 0.01$, **** $p < 0.0001$ (1-way ANOVA on non linear mixed-effect models for each condition). This supplementary figure displays additional results from the same experiment whose main results are displayed in Figure 6.

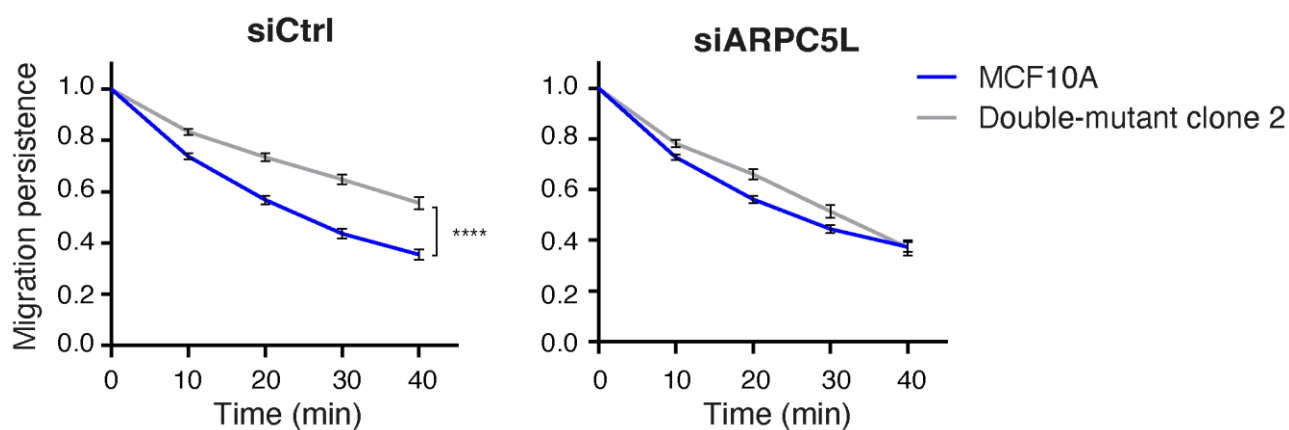


Figure S5. Confirmation of the enhanced ARPC5L-dependent migration persistence of a second double-mutant. MCF10A and double-mutant clone 2 were transfected with siRNA targeting ARPC5L or non-targeting siRNAs and analyzed for single cell migration. The overall number of cells analyzed ranges from 46 to 22 for each condition. **** $p < 0.0001$ (1-way ANOVA on non linear mixed-effect models for each condition).

Video legends

Video S1. Collective migration of parental MCF10A cells is observed using phase contrast microscopy in the presence of 5 μ M BYL719 or not. Displacement vectors obtained using Particle Image Velocimetry are overlaid in green.

Video S2. Collective migration of *PIK3CA* H1047R cells is observed using phase contrast microscopy in the presence of 5 μ M BYL719 or not. Displacement vectors obtained using Particle Image Velocimetry are overlaid in green.

Video S3. Collective migration of *KMT2D* KO cells is observed using phase contrast microscopy in the presence of 5 μ M BYL719 or not. Displacement vectors obtained using Particle Image Velocimetry are overlaid in green.

Video S4. Collective migration of double-mutant cells is observed using phase contrast microscopy in the presence of 5 μ M BYL719 or not. Displacement vectors obtained using Particle Image Velocimetry are overlaid in green.

Video S5. Single cell migration of parental, *PIK3CA* H1047R, *KMT2D* KO or double-mutant cell lines when depleted or not of ARPC5L.

Table S1. Primers used for qRT-PCR of genes described to be regulated by either *PIK3CA* H1047R or *KMT2D* mutations in breast cancer.

Gene name	Regulated by	Primer forward	Primer reverse
<i>CYFIP2</i>	KMT2D mut	CCCACGTCATGGAGGTGTACTCT	TAATTGTAGCGTGTGGCTCTCTCA
<i>RAC3</i>	KMT2D mut	CGTGGGGAAGACATGCTTGCT	GGCAGAGTAGTTGTCAAAAACGGTG
<i>CCND1</i>	PI3KCA (H1047R)	GGATGCTGGAGGTCTGCGA	AGAGGCCACGAACATGCAAG
<i>CDKN1B</i>	PI3KCA (H1047R)	GAGGGATCAAAGCCTGGAACAT	CGATTCTGTACCTCAACATCCCAT
<i>PLAUR</i>	PI3KCA (H1047R)	ACGGGGTTAGCGGAGCAAT	TGTTTTGAGTAGAAGAATCGTCGGT
<i>MMP14</i>	PI3KCA (H1047R)	ACACCTGCGTCCCAGCCTCT	CGCACTCTTCCACACGGCA
<i>ITGA2</i>	PI3KCA (H1047R)	CAACATTGGAGGAGACACCCACT	CCAGGAAGATGTCATTTCCATTCA
<i>ITGA3</i>	PI3KCA (H1047R)	AGGTGCCTGCAGAAGAATATGGT	GACAACATCAGAGGGCTCCTGTAT
<i>ITGA5</i>	PI3KCA (H1047R)	ACCCTGCCGCTCAGATTTC	ACCTAAAACCACACGGCCAGTCT
<i>ARPC5L</i>	PI3KCA (H1047R)	CATGCAGCCTTGCGGAACCTCT	CCCTGGGCTCGCTCCTTCA
<i>RAC2</i>	PI3KCA (H1047R)	TGGCCAAGGAGATTGACTCGGT	GGCCTCTCTGGGTGAGAGCTGA
<i>VIM</i>	PI3KCA (H1047R)	TCAGACAGGATGTTGACAATGCGT	CTGCAGCTCCTGGATTTCCTCTT
<i>ZEB1</i>	PI3KCA (H1047R)	ACAGTGTTACCAGGGAGGAGCAGT	TTTCTTGCCCTTCCTTTCTGTCAT