SUPPLEMENTARY MATERIALS

Assessment of *HMGA2* and *PLAG1* rearrangements in breast adenomyoepitheliomas

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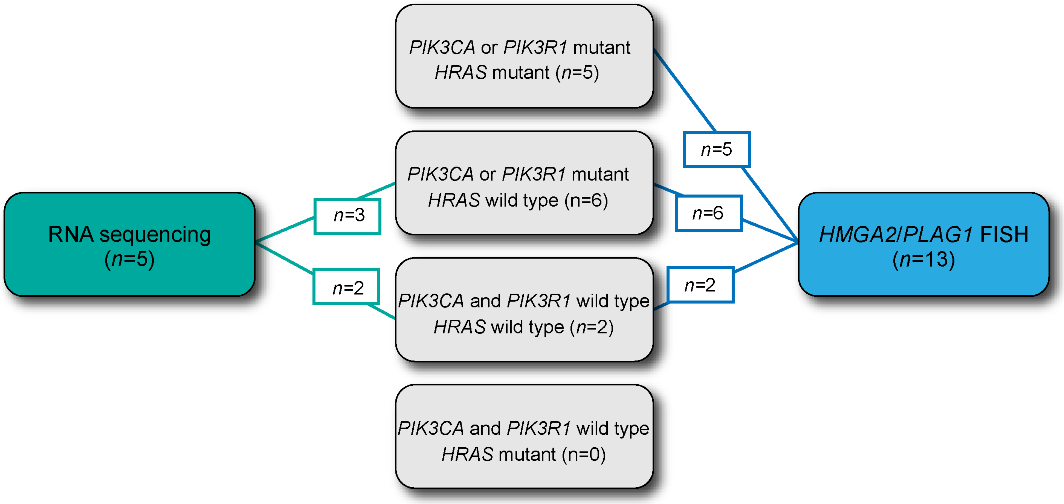
Supplementary Figure 1

Supplementary Table 1

Supplementary Figure 1



Supplementary Figure 1: Schematic representation of the cases and analyses conducted in this study.

Depiction of the *PIK3CA*, *PIK3R1* and *HRAS* status of the breast adenomyopitheliomas included in this series, and the analyses conducted in this study. FISH, fluorescence *in situ* hybridization.

Supplementary Table 1: List of fusion genes and/or read-throughs identified by RNA-sequencing analysis of breast adenomyoepitheliomas.

Sample ID	Fusion caller*	5' gene	3' gene	Mapping 5'	Mapping 3'	Spanning reads	Encompassing reads	In-frame	Type	Driver probability (Oncofuse)	Remarks
AM16	INTEGRATE	HMGA2	WIF1	chr12:66358254	chr12:65476942	8	13	Yes	Intra-Chromosomal	0.082892348	No start codon for 3' partner gene
AM2	INTEGRATE	EEF1A1	PAN3	chr6:74229617	chr13:28788787	4	3	Yes	Inter-Chromosomal	0.288187631	Intronic breakpoint
AM7	INTEGRATE	RRP7B	KCTD19	chr22:42961117	chr16:67355607	22	8	No	Inter-Chromosomal	0.047062962	
AM7	INTEGRATE	GRM5	SCARNA9	chr11:88345973	chr11:93454952	4	2	No	Intra-Chromosomal	0.021825573	
AM7	INTEGRATE	GRM5	KIAA1731	chr11:88345973	chr11:93454952	3	2	No	Intra-Chromosomal	0.021825573	

*deFuse did not identify any candidates not found in normal breast or that can be mapped to RefSeq genes.