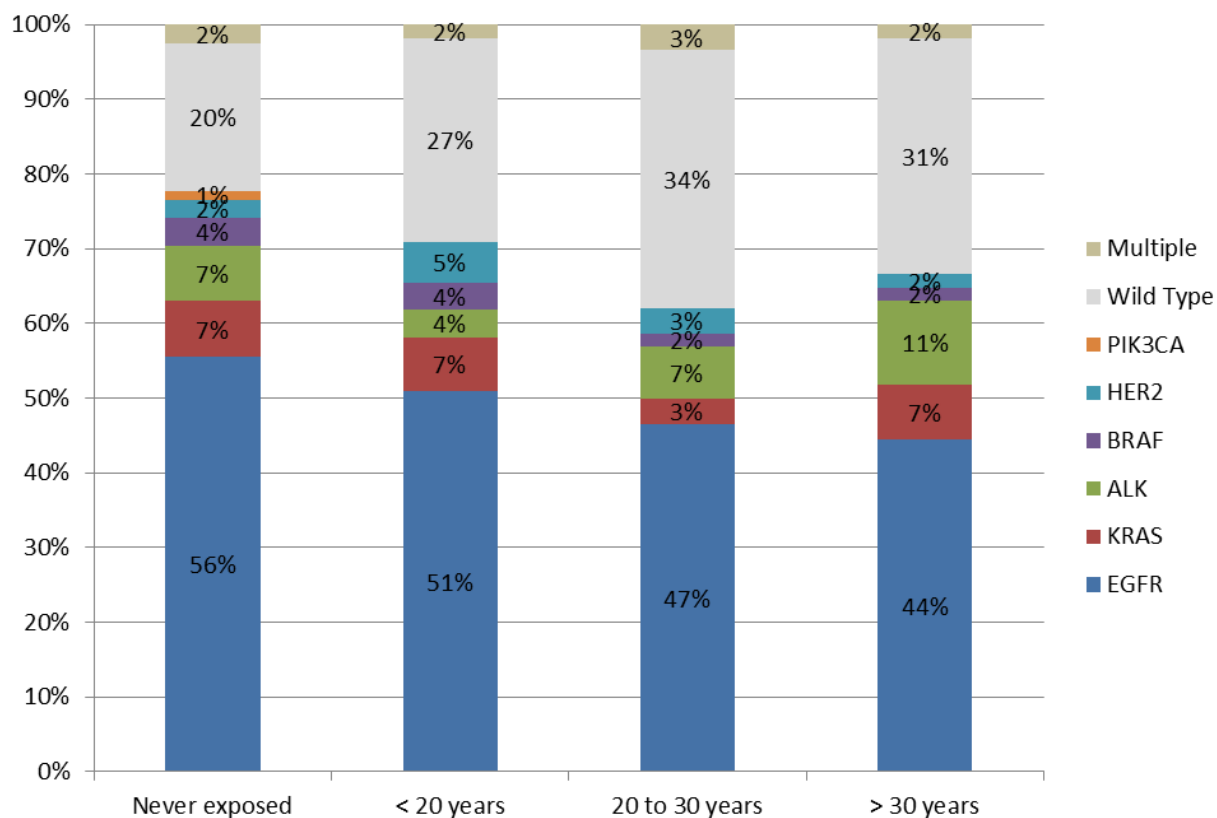


**Table S1** – Somatic mutation profile according to exposure to passive smoking in univariate analysis

		Mut. in HER2 (n=174)			Mut. in BRAF (n=196)			Mut. in PIK3CA (n=164)		
		n	% [95%CI]	P value	n	% [95%CI]	P value	n	% [95%CI]	P value
<b>Exposure to Passive Smoking</b>	Never	2	4% [1%-13%]	1,0*	4	6% [2%-15%]	0.741*	2	4% [<1%-14%]	0.586*
	Ever	6	5% [2%-11%]		6	5% [2%-10%]		2	2% [<1%-6%]	
<b>Cumulative duration of exposure</b>	Never	2	4%	NC	4	6%	NC	2	4%	NC
	≤20 years	3	8%		3	7%		1	3%	
	20 to 30years	2	5%		1	2%		1	3%	
	>30 years	1	3%		2	5%		0	0%	
<b>Time of exposure</b>	Never	2	3%	NC	5	6%	NC	2	4%	NC
	Childhood	2	3%		2	3%		0	0%	
	Adulthood only	4	10%		3	7%		2	2%	
<b>Exposure at workplace</b>	Never	8	6%	0.225*	9	5%	0.568*	4	3%	0.559*
	Ever	0	0%		1	4%		0	0%	
<b>Domestic exposure</b>	Never	2	3%	0.330*	5	6%	0.359*	2	3.5%	0.433*
	Ever	6	6%		5	4%		2	1.9%	

Mut.: mutation; Rearr.: rearrangement; NC: not computable

\*Fisher test; others are Chi-squared tests



**Figure S1** – Biomarker pattern according to cumulative duration of exposure (CDE) to overall passive smoking in the 248 patients with full main biomarker analysis. Wild-type means that all biomarkers tested – with at least EGFR, KRAS, and ALK – were wild-type. Multiple means that more than one mutation – in different gene – was found in the same patient