Additional file 2 - Associations of the presence/absence and degree of methylation and the clinical and molecular parameters

		Discovery cohort				Validation cohort				
					p-value				p-value	
Gene	Clinicopathological factor	Methylation Status		Odds ratio (95% CI)	Fisher	Non-parametric	Methylation Status		Odds ratio (95% CI)	Fisher	Non-parametric

Gene	Clinicopathological factor	Methylation Status		Odds ratio (95% CI)	Fisher	Non-parametric	Methylation Status		Odds ratio (95% CI)	Fisher	Non-parametric
Histological grade											
PPP2R2B_3		Unmethylated	Methylated				Unmethylated	Methylated			
	Grade 1	8	9				1	3			
	Grade 2	6	26	NA	0.019	0.02	25	68	NA	0.008	0.013
	Grade 3	9	7				25	22			
Treatment response											
ABCB1_2		Unmethylated	Methylated				Unmethylated	Methylated			
	Progressive disease	6	1	13.50 (1.52-119.6)	0.0076	0.04	NA	NA	NA	NA	NA
	PR,MD or SD	20	45				NA	NA			
***TP53* mutations**											
ABCB1_2		Unmethylated	Methylated				Unmethylated	Methylated			
	Mutant	11	8	3.58 (1.17-10.35)	0.028	0.031	25	17	2.49 (1.21-5.14)	0.018	0.012
	Wild type	15	38				43	73			
PPP2R2B_3		Unmethylated	Methylated				Unmethylated	Methylated			
	Mutant	11	7	4.58 (1.44-14.5)	0.010	0.028	23	16	3.81 (1.79-8.22)	0.001	0.006
	Wild type	12	35				29	77			
Estrogen receptor											
PPP2R2B		Unmethylated	Methylated				Unmethylated	Methylated			

		Unmethylated	Methylated	OR (95% CI)	p-value	p-value		Unmethylated	Methylated	OR (95% CI)	p-value	p-value
_3	Negative	9	1	15.65 (1.88-131.5)	0.004	0.02		21	17	3.01 (1.39-6.48)	0.006	0.004
	Positive	23	40					30	73			
ErbB2												
ABCB1_2		Unmethylated	Methylated					Unmethylated	Methylated			
	Positive	9	2	10.50 (1.88-58.6)	0.005	0.0019		NA	NA	NA	NA	NA
	Negative	9	21					NA	NA			
IGF2_DMR2		Hypo / Hyper	Meth					Unmethylated	Methylated			
	Negative	20 / 4	8	NA	0.007	0.036		NA	NA	NA	NA	NA
	Positive	2 / 6	2					NA	NA			

Associations of the presence/absence and degree of methylation and the clinical and molecular parameters of the samples by Fisher's exact test (2 categorical variables) or χ^2 analysis (3 categorical variables) with odds ratio (OR) and 95 % Confidence interval (CI) and their respective p-value in the validation cohort. Statistical significance of the differences in the distribution of the degree of methylation is assessed by the non-parametric Mann-Whitney and Kruskal-Wallis test. Samples are called methylated if the methylation degree exceeded 5 % and the average methylation degree of the healthy tissue samples plus at least two times the standard deviation of the healthy tissues.