Supplementary Table 2: Comparative Analysis of AGO2 mRNA and Protein Levels Against Clinicopathological Parameters and Their Prognostic Significance in TCGA-ACC and an Independent ACC Cohort.

Parameters	TCGA-ACC cohort (n=79)	AGO2 mRNA expression in TCGA (log2)	p-value	Collected-ACC cohort (n=15) (Kollings Tumour bank)	AGO2 Protein concentration in collected cohort (ng/ml)	p-value
Diagnosis Age	46.7 ± 15.77		0.672	46.27 ± 15.47		0.833
<49	39	6.64 ± 0.77		9	6.66 ± 2.71	
>49	40	6.72 ± 0.9		6	7.03 ± 4.14	
Sex			0.254			0.484
Female	48	6.59 ± 0.8		8	6.24 ± 2.97	
Male	31	6.82 ± 0.88		7	7.46 ± 3.6	
Overall survival status			<0.001			0.009
Alive	51	6.44 ± 0.7		9	5.16 ± 2.42	
Deceased	28	7.11 ± 0.89		6	9.28 ± 2.72	
Weiss score			0.003			0.008
Weiss score (2-5)	30	6.32 ± 0.8		4	3.43 ± 1.86	
Weiss score (6-9)	31	6.9 ± 0.83		11	8.04 ± 2.69	
Pathologic stage			0.011			0.004
Stage I-II	46	6.49 ± 0.78		5	3.76 ± 1.77	
Stage III-IV	31	6.93 ± 0.87		10	8.33 ± 2.64	
Cluster of clusters (CoCs)	n=76		0.036 (COC1 vs COC3)			
COC1 (Disease progression rate: (7%)	33	-0.16 ± 0.91				
COC2 (Disease progression rate: (56%)	19	-0.18 ± 1.14				
COC3 (Disease progression rate: (96%)	24	0.31 ± 1.01				

The data are presented as the means ± SDs or n (numbers).
Abbreviations: TCGA, The Cancer Genome Atlas