

Table S1: Comparison of AI-based BRAF mutation prediction with confirmed PCR result based on sample quality and specific histomorphological features.

PCR				
AI prediction (all samples)				
	Positive	Negative	Total	
Positive	40	10	50	
Negative	29	17	46	
Total	69	27	96	SE 58%, SP 63%
AI prediction (high quality samples)				
Positive	24	4	28	
Negative	3	3	6	
Total	27	7	34	SE 89%, SP 43%
AI prediction (standard quality samples)				
Positive	7	1	8	
Negative	8	3	11	
Total	15	4	19	SE 47%, SP 75%
AI prediction (poor quality samples)				
Positive	9	5	14	
Negative	18	11	29	
Total	27	16	43	SE 33%, SP 69%
AI prediction (classic urothelial only)				
Positive	34	8	42	
Negative	6	2	8	
Total	40	10	50	SE 85%, SP 20%
AI prediction (non classic urothelial only)				
Positive	6	2	8	
Negative	23	15	38	
Total	29	17	46	SE 21%, SP 88%
AI prediction (invasive only)				
Positive	8	2	10	
Negative	15	9	24	
Total	23	11	34	SE 35%, SP 82%
AI prediction (non-invasive)				
Positive	16	3	19	
Negative	3	1	4	
Total	19	4	23	SE 84%, SP 25%
AI prediction (inflammatory)				
Positive	8	3	11	
Negative	20	8	28	
Total	28	11	39	
AI prediction (non-inflammatory)				SE 29%, SP, 73%
Positive	32	7	39	
Negative	8	9	17	
Total	40	16	56	

Table S2: Extension of Table 4. Assessing the AI tool reliability for correct *BRAF* mutation prediction based on specific features across different sample cohorts. A Chi-square test was performed for categorical data (urothelial differentiation, inflammation, slide quality, invasive growth, and mutation status) and a 2-sided t-test for continuous data (sample size). For each feature, p values are indicated for PCR positive and negative cases, as well as separately for true positive and true negative prediction. P values of <0.05 were considered significant (in bold).

Feature	BRAF PCR	All samples	Standard and high quality samples only	High quality samples only
Urothelial differentiation	Pos and neg	<0.01	>0.1	>0.9
	Pos	<0.00001	<0.001	>0.19
	Neg	<0.001	<0.006	<0.009
Inflammation	Pos and neg	<0.01	<0.03	>0.7
	Pos	<0.00001	<0.0005	>0.48
	Neg	>0.38	>0.15	NA
Slide quality	Pos and neg	<0.02	NA	NA
	Pos	<0.0001		
	Neg	>0.42		
Sample size (ROI)	Pos and neg	<0.02	>0.08	>0.3
	Pos	<0.003	>0.09	>0.2
	Neg	>0.3	>0.5	>0.9
Invasive growth	Pos and neg	>0.08	>0.3	>0.2
	Pos	<0.002	>0.23	>0.28
	Neg	<0.04	>0.57	>0.68
Mutation status (PCR)	NA	>0.6	>0.1	<0.02