Supplementary Materials

List of Figures

Supplementary Fig. 1: ROC plots of the trained VarMIL networks in the (A) discovery, (B) BC validation, and (C) CC validation sets.

Supplementary Fig. 2: DSS and PFS KM curves associated with NSMP, *p53abn-like NSMP*, and p53abn cases in the (A) discovery set and the (B) BC validation set. The reported p-values compare the significance between p53abn-like NSMP and p53abn, computed using a two-sided log-rank statistical test.

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Supplementary Figure 4: Performance benchmarking of Vanilla (A), IDaRS (B), Histogram (C), DeepMIL (D), VLAD (E), CLAM-MB (F), CLAM-SB (G), and TransMIL(H) models for the discovery and validation sets.

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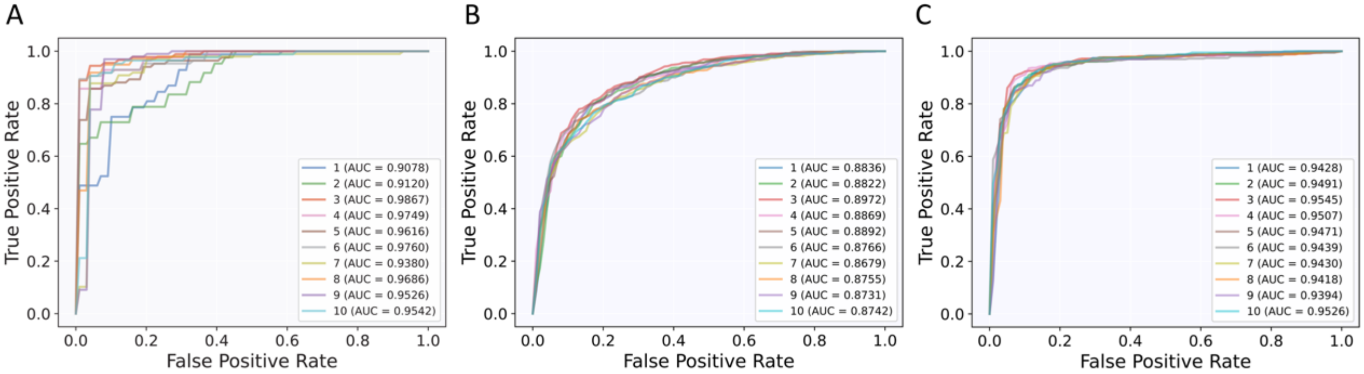
List of Tables



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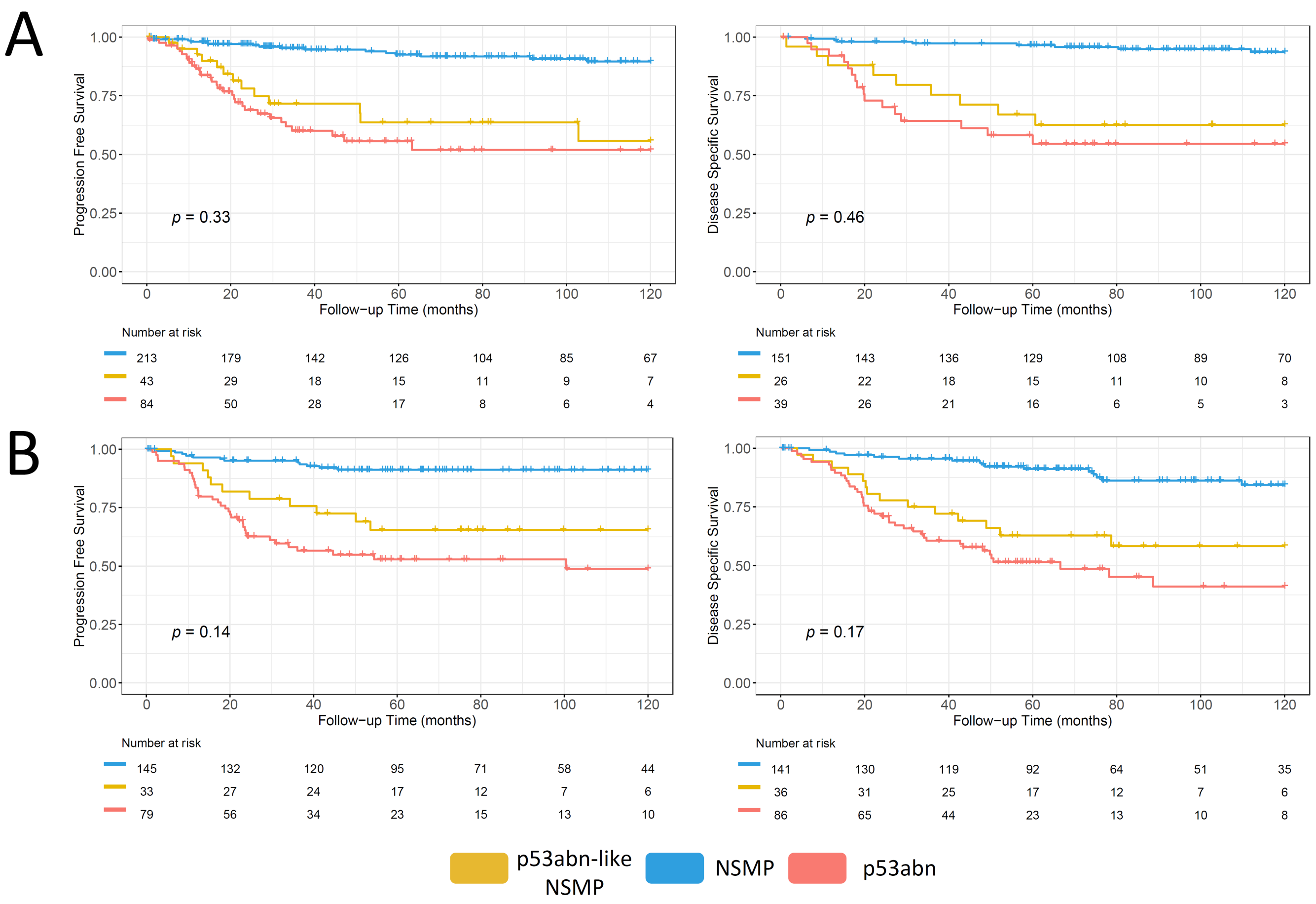

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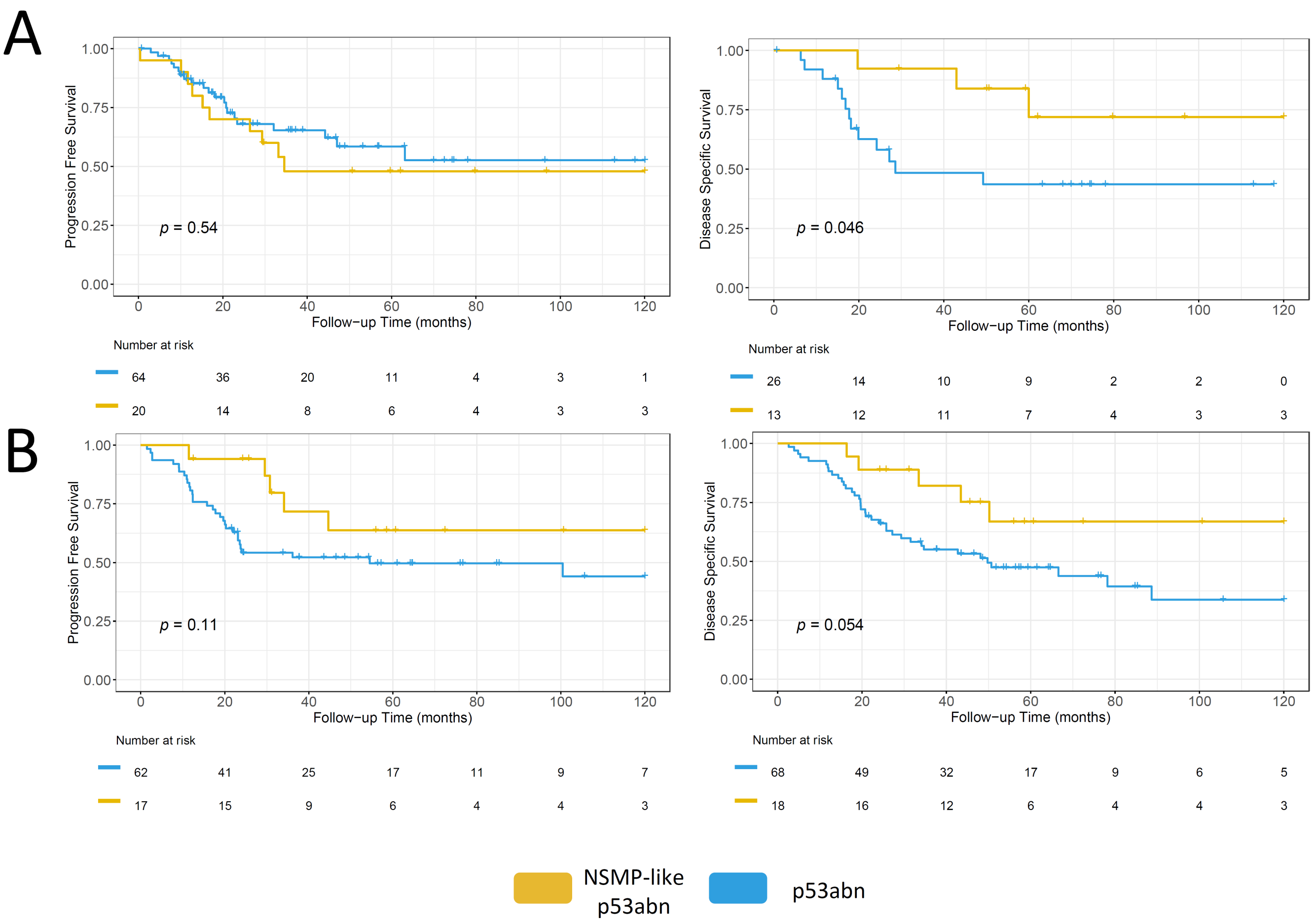

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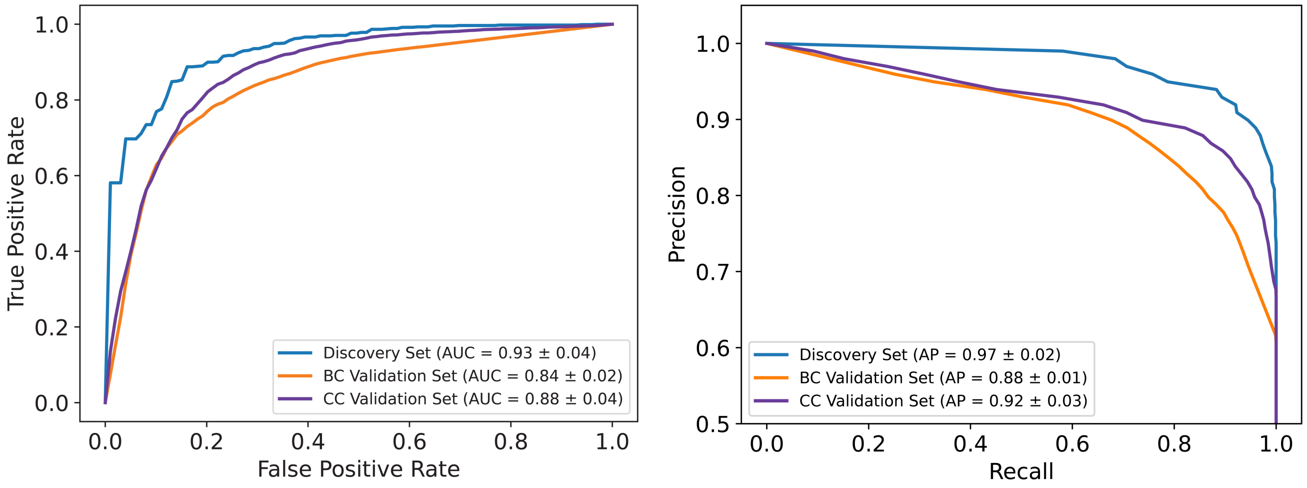

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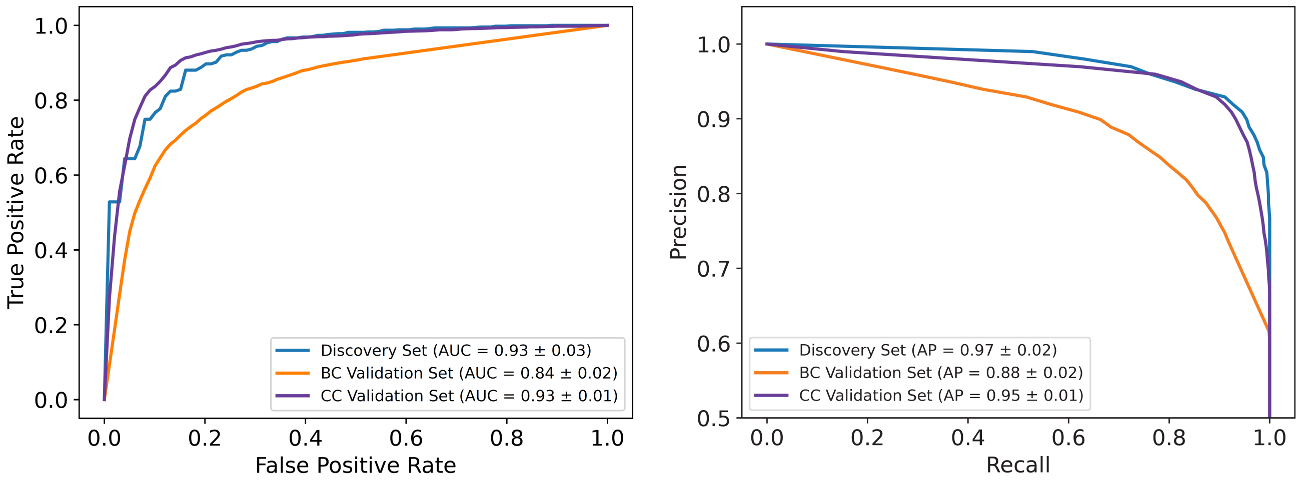

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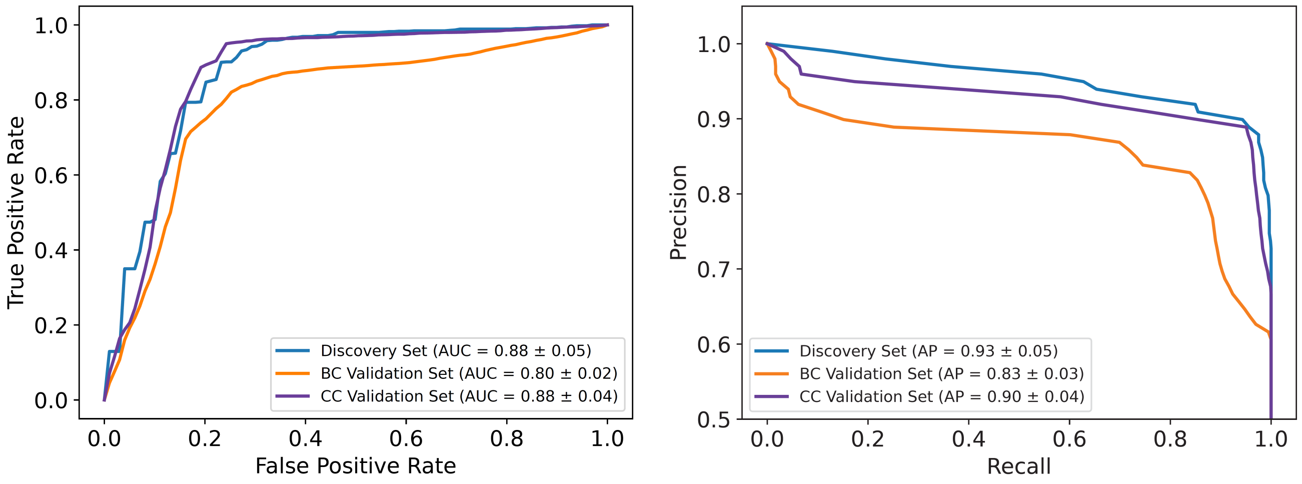

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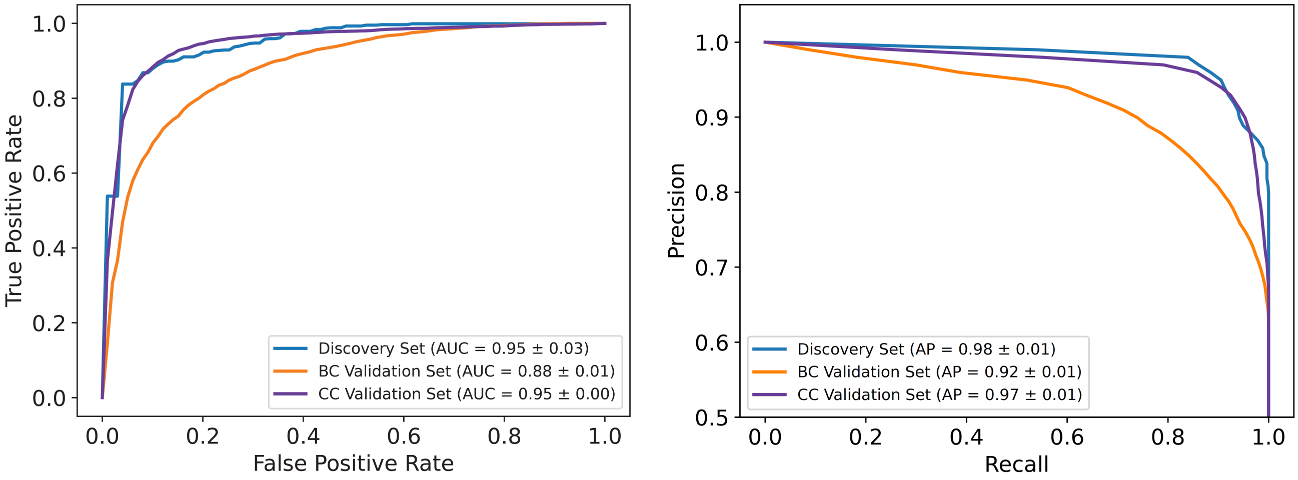

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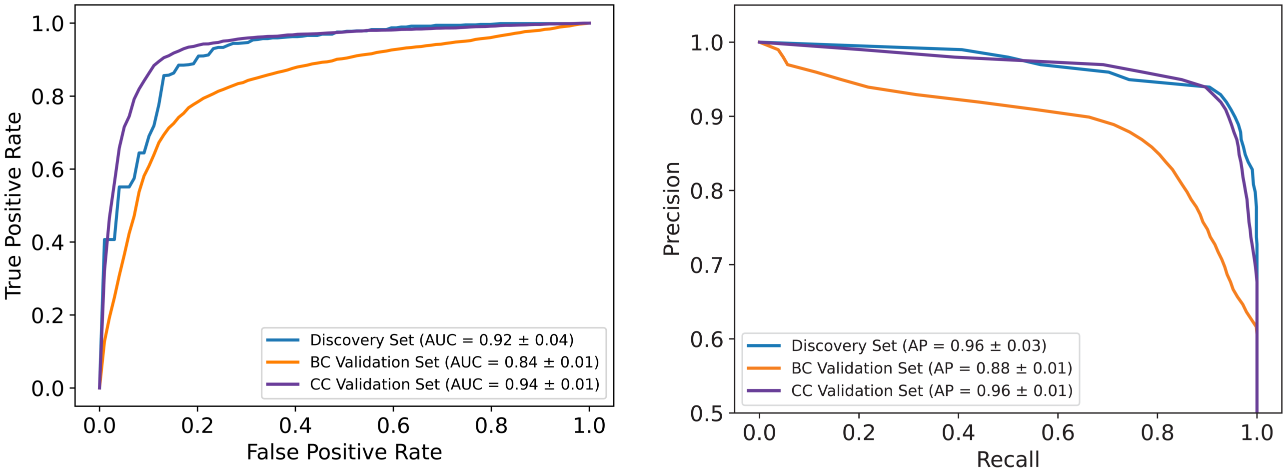

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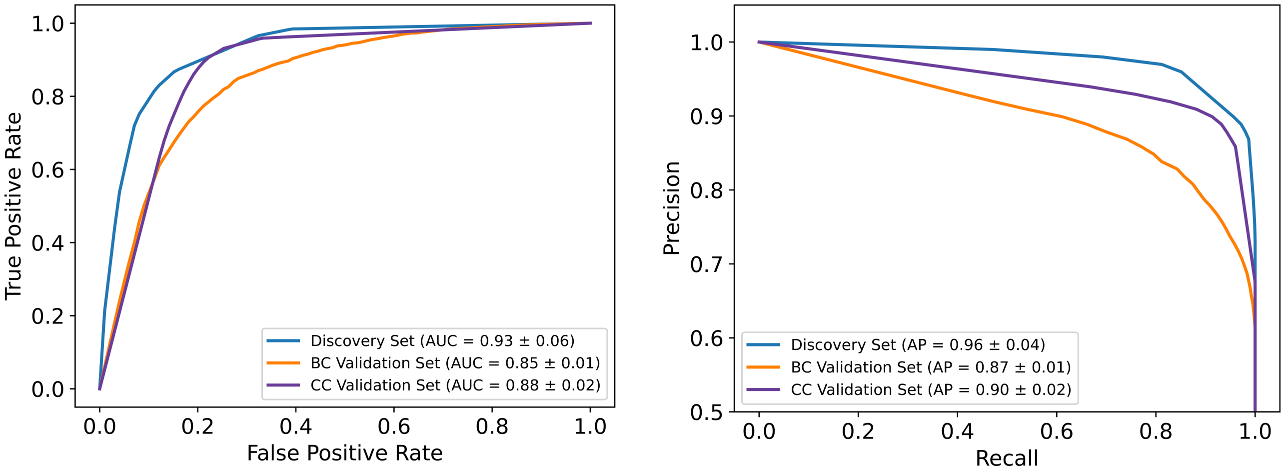

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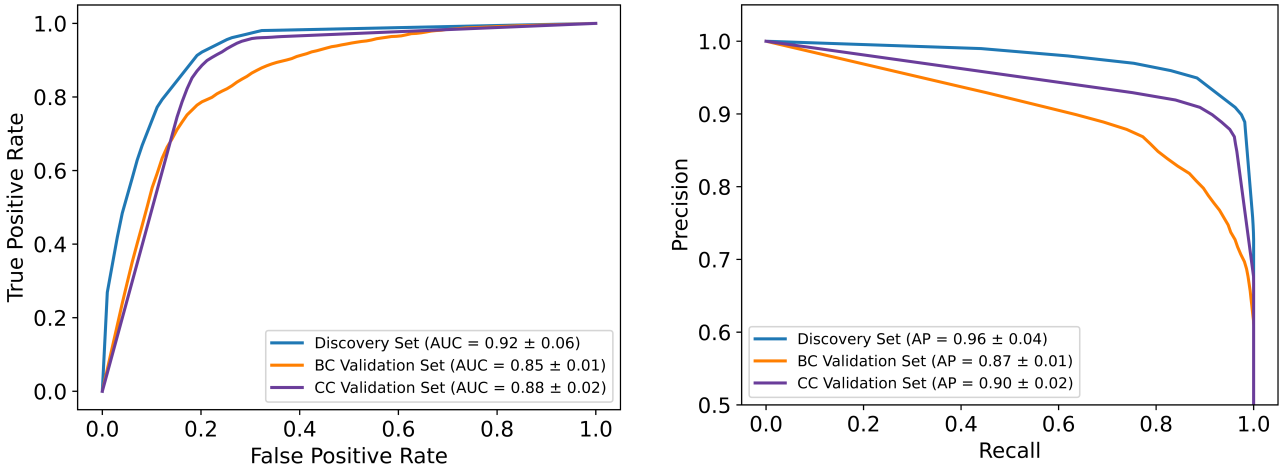

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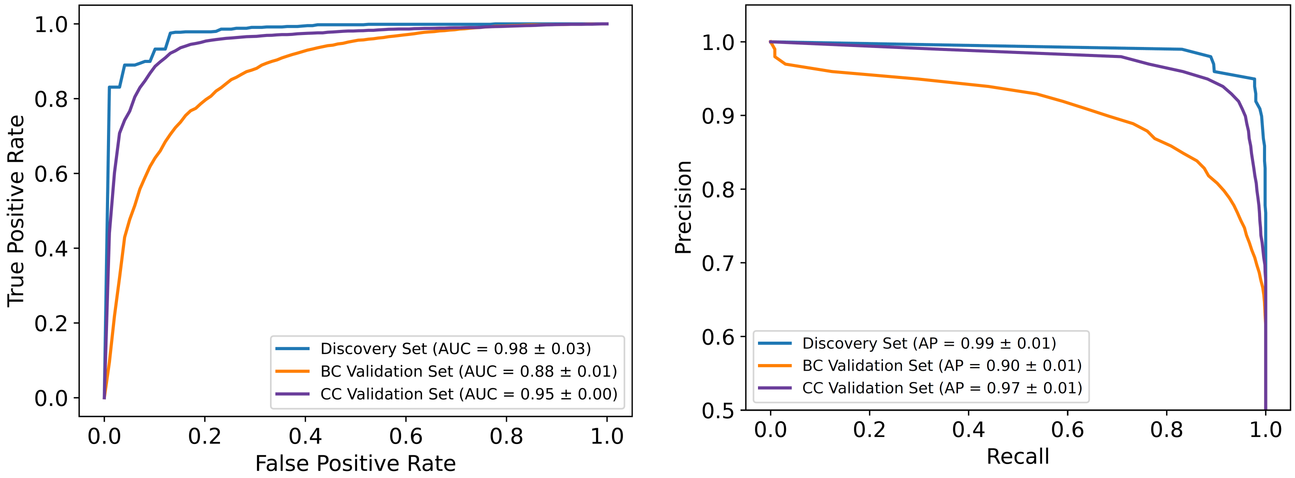

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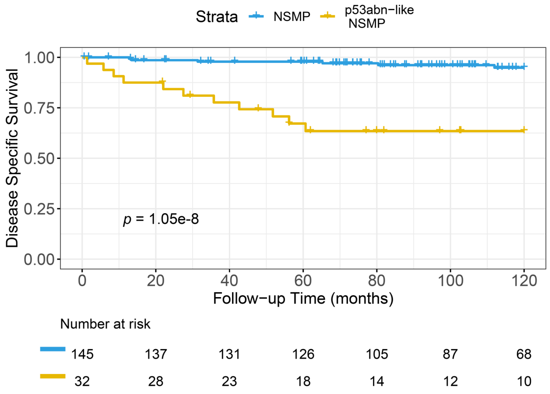
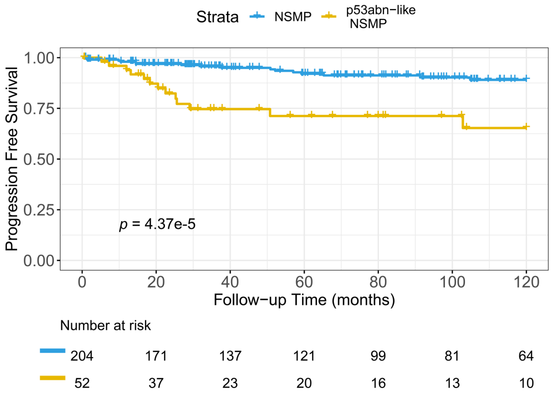
A: Discovery cohort

DSS **PFS**

Vanilla





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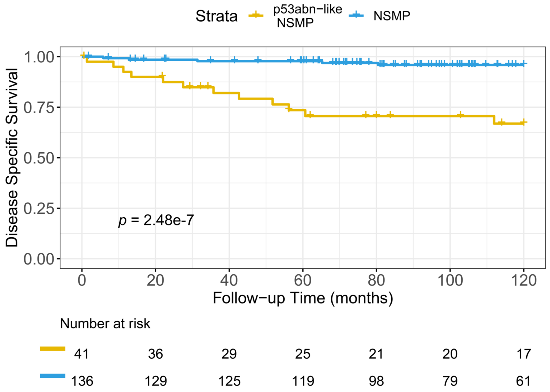

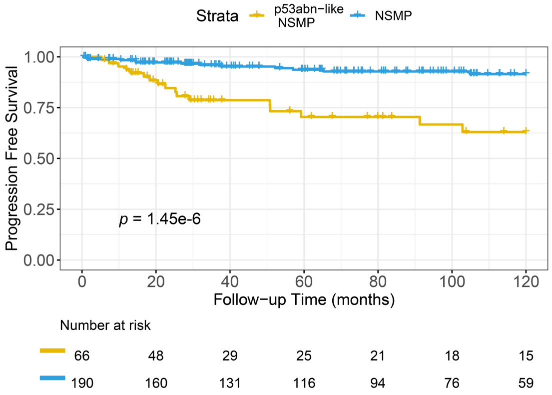

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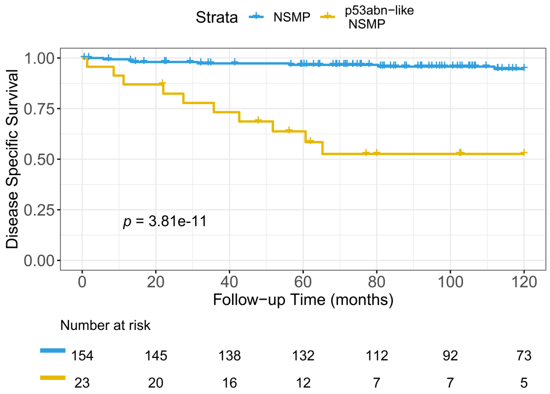

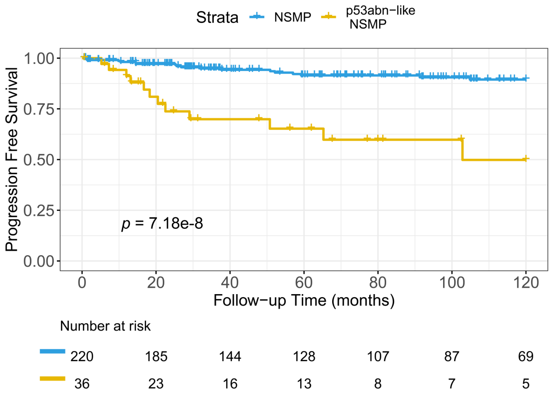

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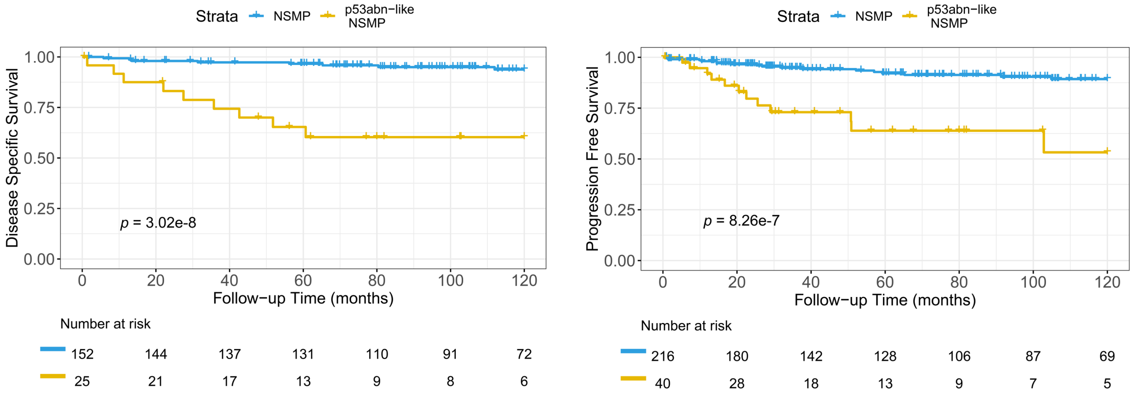

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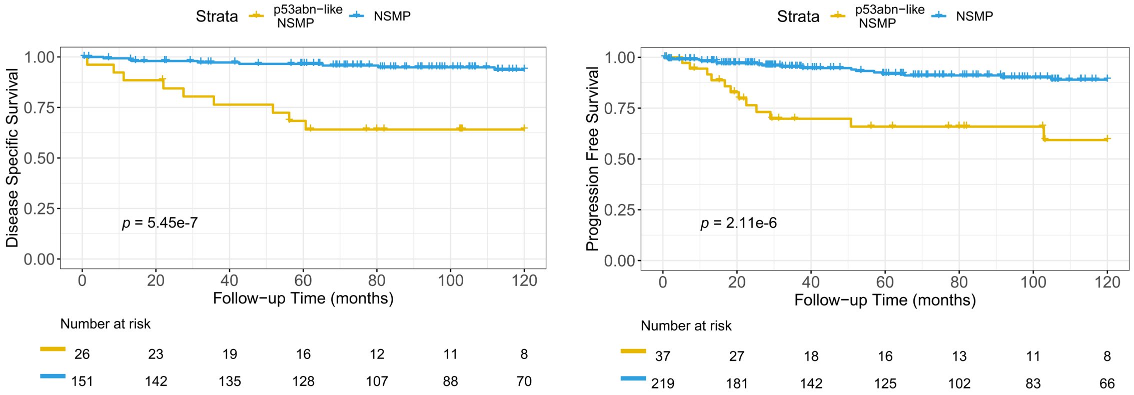

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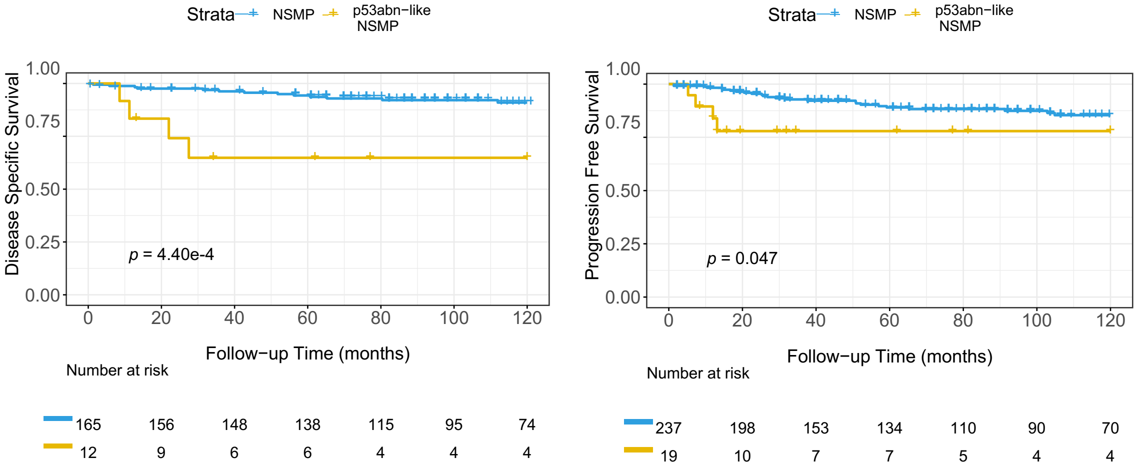

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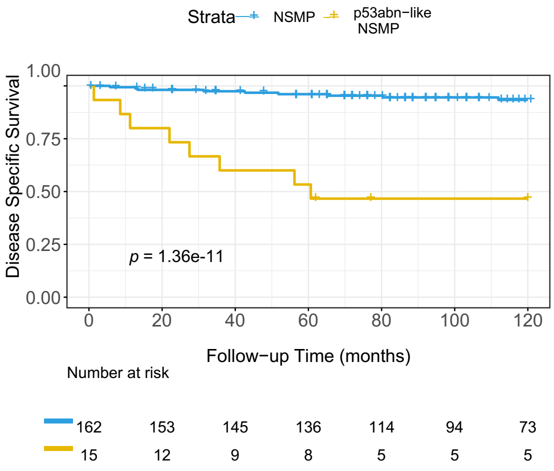

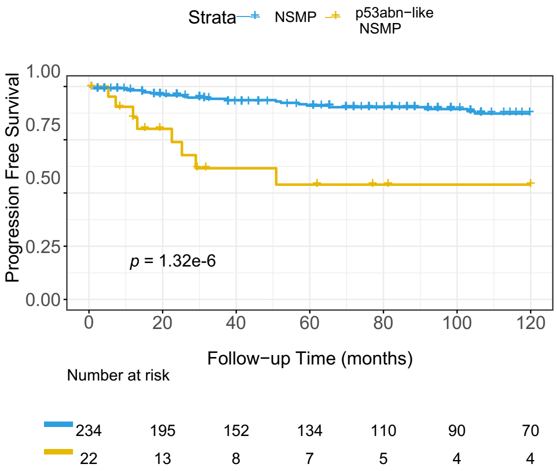

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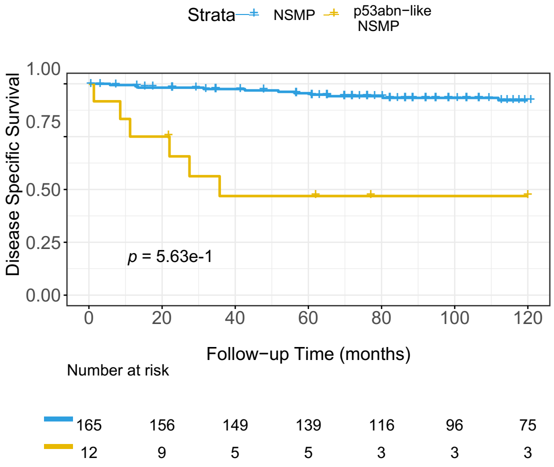
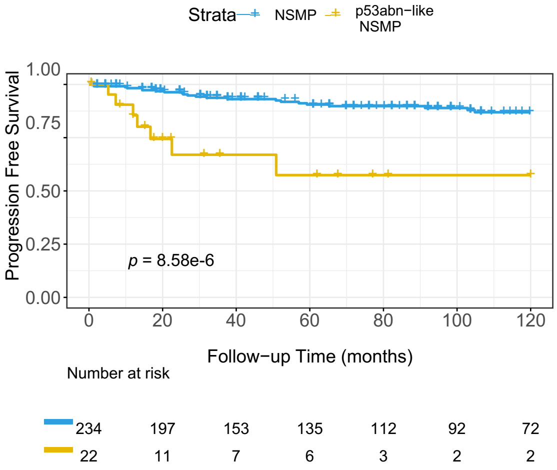


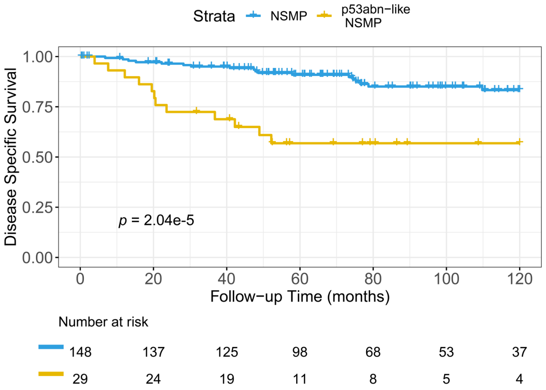


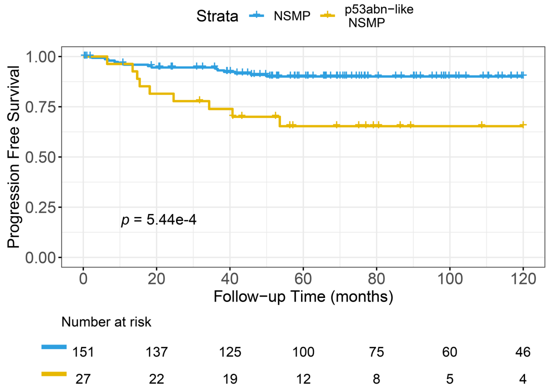
B: BC validation cohort

DSS

PFS

Vanilla





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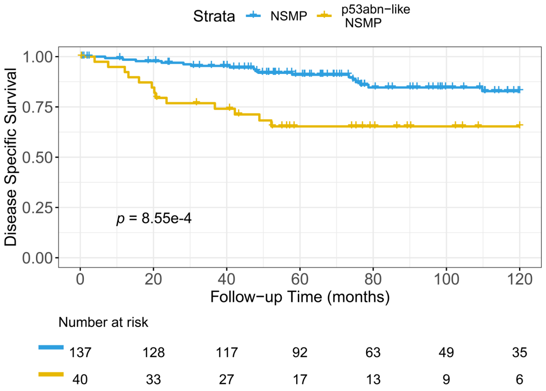

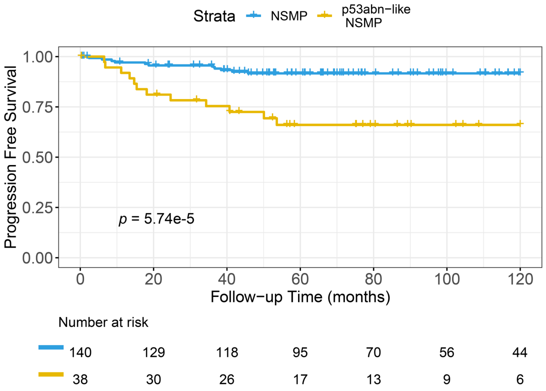

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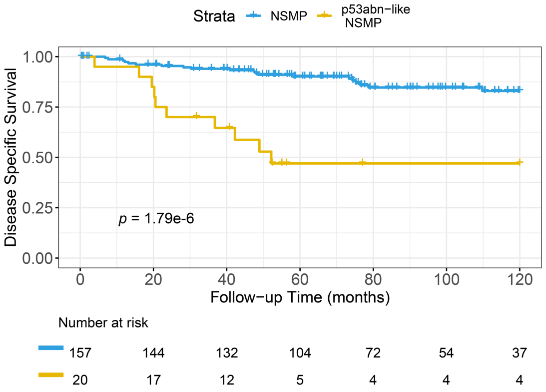

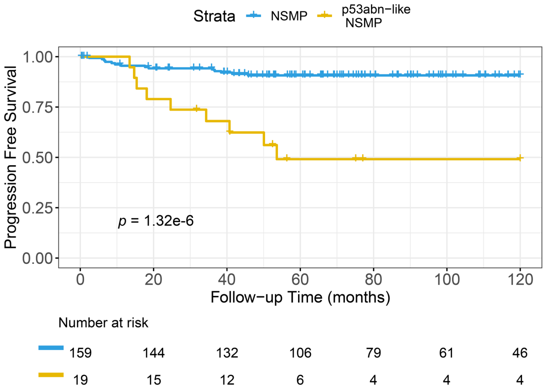

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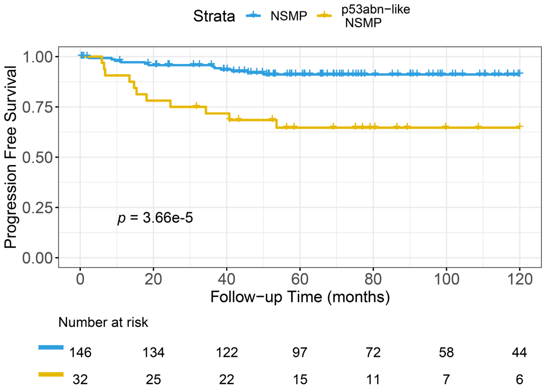
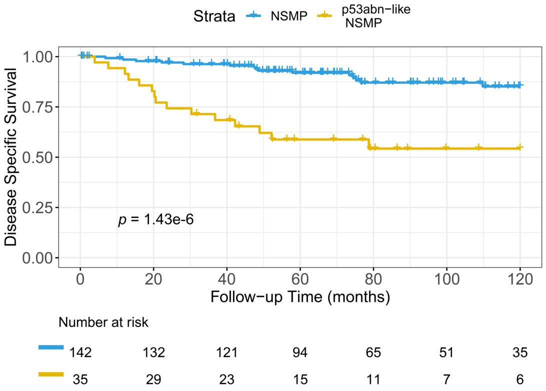
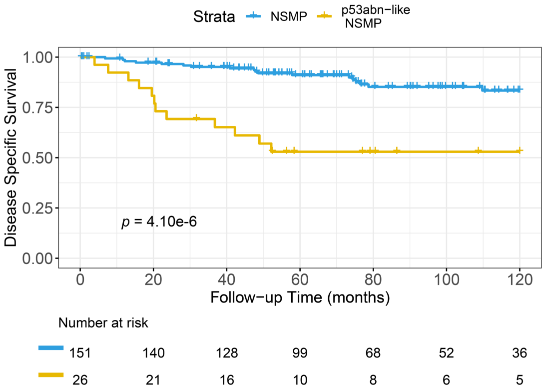
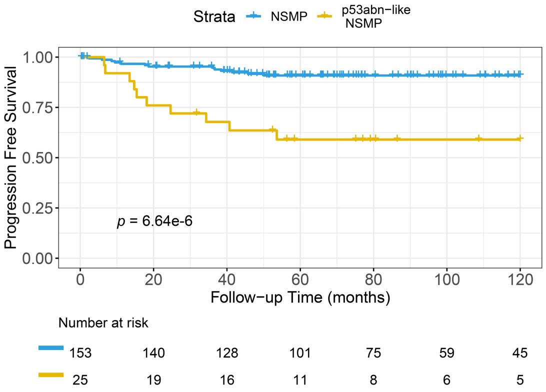


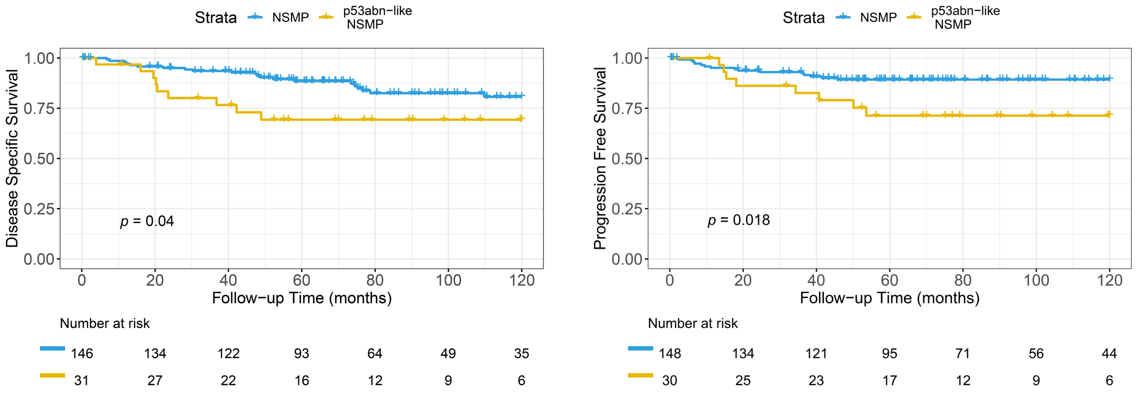


VLAD





CLAM-MB



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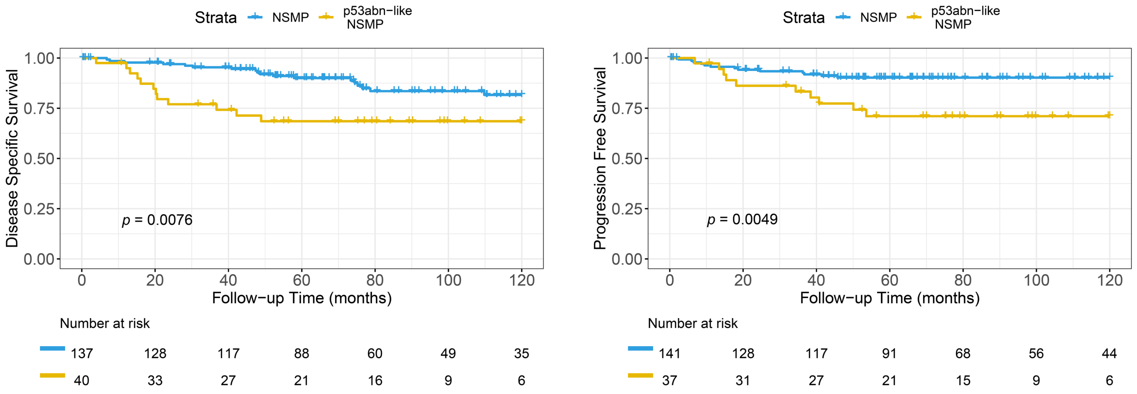

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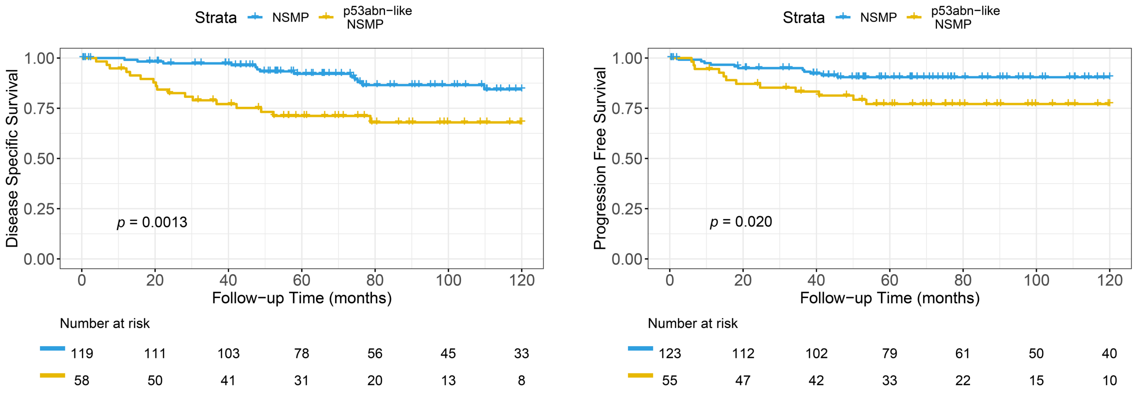
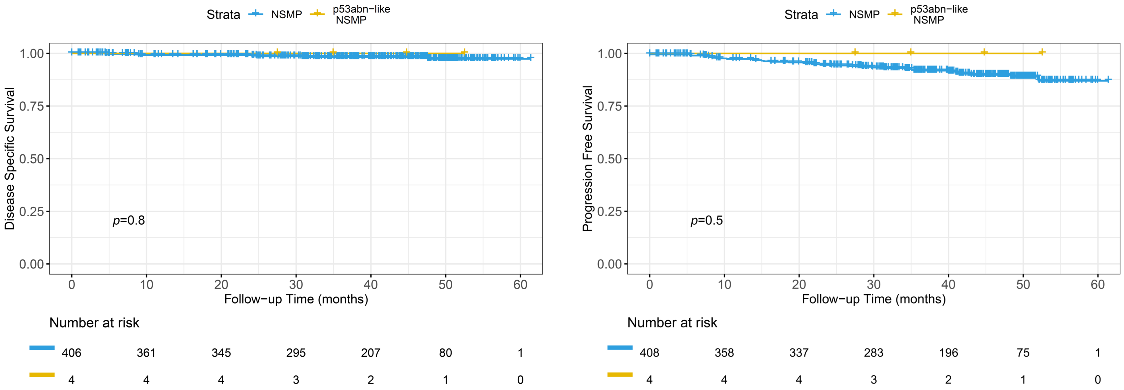


C: CC validation cohort

Vanilla



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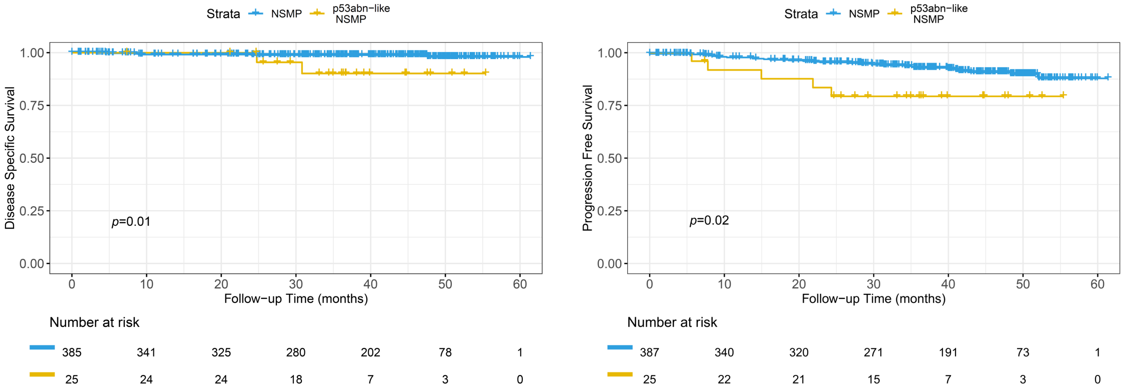
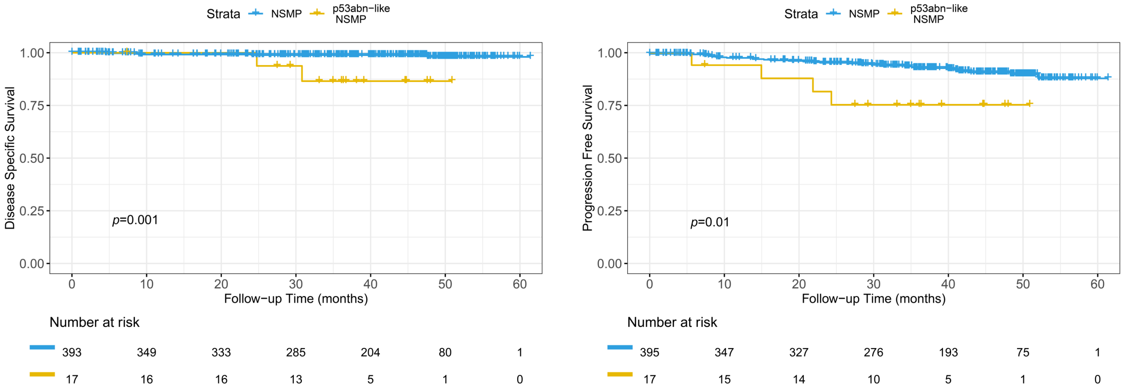
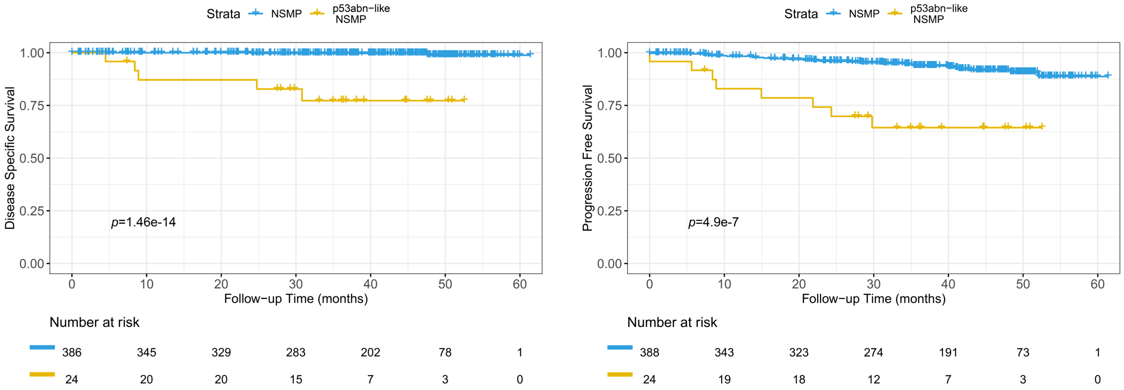


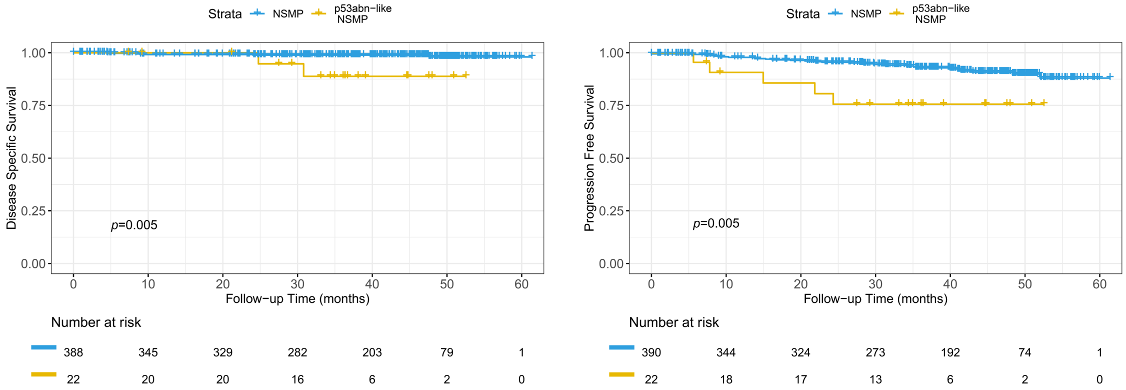
Histogram-based



DeepMIL



VLAD



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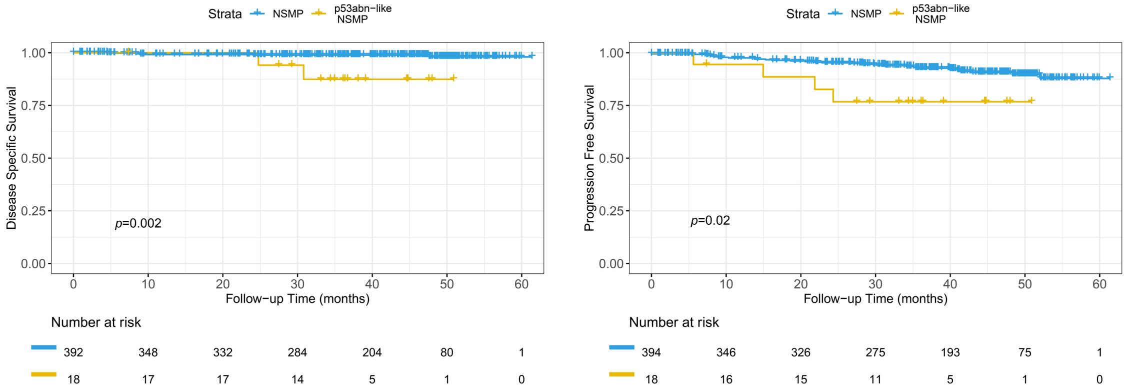

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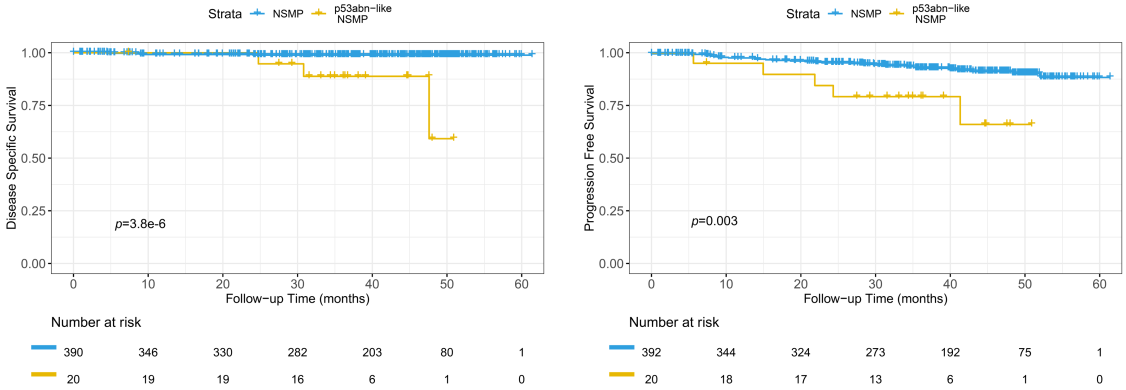

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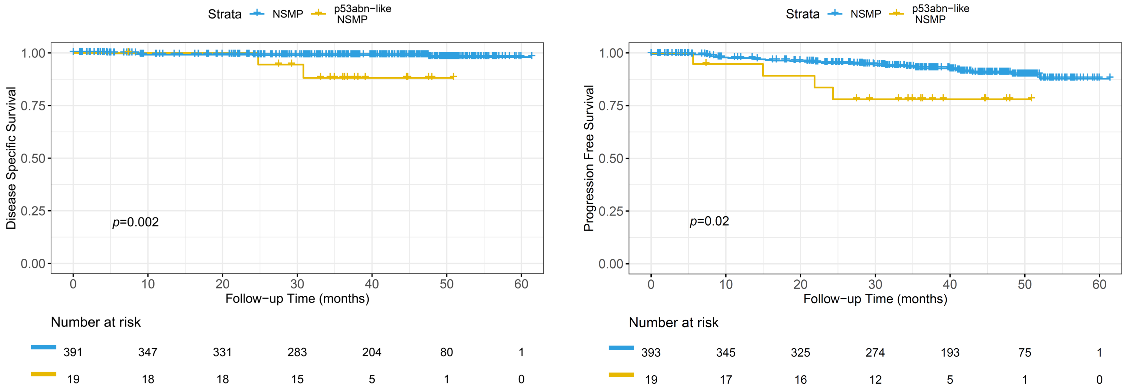

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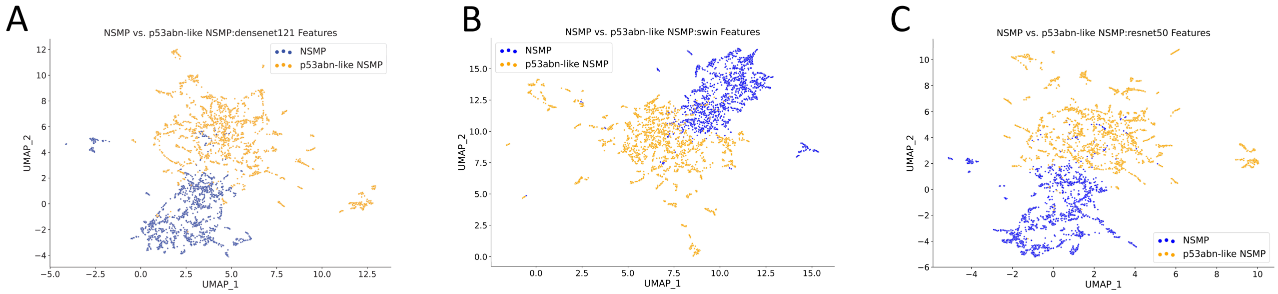

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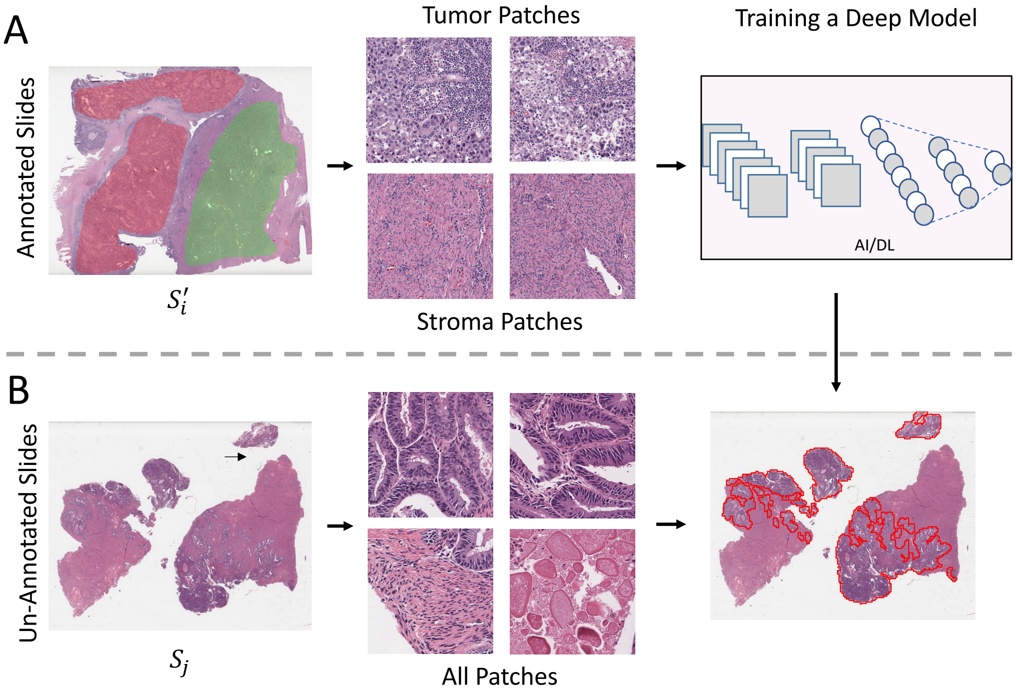

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Supplementary Table 1: Overview of cohorts.

Dataset	Unit	Subtype	
		NSMP	p53abn
TCGA (WSIs)	Patients	90	56
	Slides	94	61
	Manually Annotated Slides by Pathologists	14	13
	512×512 Pixel Patches at 20x	162,998	82,655
German (WSIs)	Patients	182	40
	Slides	355	76
	Manually Annotated Slides by Pathologists	0	0
	512×512 Pixel Patches at 20x	576,553	125,376
Vancouver (TMAs)	Patients	195	95
	Slides	670	422
	512×512 Pixel Patches at 20x with 65% Overlap	15,584	10,251
Cross Canada (WSIs)	Patients	416	198
	Slides	432	208
	Manually Annotated Slides by Pathologists	0	0
	512×512 Pixel Patches at 20x	696,340	414,019

Supplementary Table 2: Outcome information of the discovery and validation cohorts.

Source			**NSMP**	***p53abn-like NSMP***	**p53abn**
Discovery Cohort	Disease Specific (German)	Total	155 (69.82%)	27 (12.16%)	40 (18.02%)
		Censored	143 (92.26%)	17 (62.96%)	23 (57.50%)
		Event	8 (5.16%)	9 (33.33%)	16 (40.00%)
		Unk	4 (2.58%)	1 (3.70%)	1 (2.50%)
	Progression Free (German and TCGA)	Total	221 (60.88%)	47 (12.95%)	95 (26.17%)
		Censored	197 (89.14%)	30 (63.82%)	53 (55.79%)
		Event	16 (7.24%)	13 (27.66%)	31 (32.63%)
		Unk	8 (3.62%)	4 (8.51%)	11 (11.58%)
BC Validation Cohort	Disease Specific	Total	155 (53·82%)	38 (13·19%)	95 (32·99%)
		Censored	125 (80.65%)	22 (57.89%)	44 (46.32%)
		Event	16 (10.32%)	14 (36.84%)	42 (44.21%)
		Unk	14 (9.03%)	2 (5.26%)	9 (9.47%)
	Progression Free	Total	155 (53·82%)	38 (13·19%)	95 (32·99%)
		Censored	133 (85.81%)	22 (57.89%)	43 (45.26%)
		Event	12 (7.74%)	11 (28.95%)	36 (37.89%)
		Unk	10 (6.45%)	5 (13.16%)	16 (16.82%)
CC Validation Cohort	Disease Specific	Total	390 (63.52%)	26 (4.23%)	198 (32.25%)
		Censored	382 (97.95%)	21 (80.87%)	165 (80.05%)
		Event	2 (0.51%)	5 (19.23%)	29 (14.95%)
		Unk	6 (1.54%)	0	4 (2.06%)
	Progression Free	Total	390 (63.52%)	26 (4.23%)	198 (32.25%)
		Censored	360 (92.31%)	18 (69.23%)	135 (68.18%)
		Event	26 (6.67%)	8 (30.77%)	63 (31.82%)
		Ukn	4 (1.03%)	0	0

Supplementary Table 3: Treatment information of the discovery and validation cohorts.

	Treatment	Total	NSMP	p53abn
Discovery Cohort (German)	Total	217	178	39
	None	76 (32.02)	68 (37.99%)	8 (20.51%)
	RT only	8 (3.69%)	6 (3.35%)	2 (5.13%)
	brachy only	66 (30.41%)	63 (35.20%)	3 (7.69%)
	brachy+RT	4 (1.84%)	3 (1.68%)	1 (2.56%)
	chemo only	23 (10.60%)	9 (5.03%)	14 (35.90%)
	chemo+RT	5 (2.30%)	3 (1.68%)	2 (5.13%)
	chemo+brach+RT	1 (0.46%)	1 (0.56%)	0
	chemo+brachy	3 (1.38%)	1 (0.56%)	2 (5.13%)
	N / A	31 (14.29%)	24 (13.41%)	7 (17.95%)
BC Validation Cohort	Total	288	193	95
	None	158 (54.86%)	128 (66.32%)	30 (31.58%)
	Rt only	47 (16.32%)	31 (16.06%)	16 (16.84%)
	Brachy only	5 (1.74%)	4 (2.07%)	1 (1.05%)
	Chemo only	27 (9.38%)	6 (3.11%)	21 (22.11%)
	Chemo + RT	43 (14.93%)	21 (10.88%)	22 (23.16%)
	N / A	8 (2.78%)	3 (1.55%)	5 (5.26%)
CC Validation Cohort	Total	614	416	198
	None	342 (55.7%)	284 (68.27%)	58 (29.29%)
	RT only	28 (4.56%)	21 (5.05%)	7 (3.54%)
	brachy only	66 (10.75%)	53 (12.74%)	13 (6.57%)
	chemo+brachy+RT	26 (4.23%)	10 (2.4%)	16 (8.08%)
	chemo+brachy	33 (5.37%)	5 (1.2%)	28 (14.14%)
	chemo+RT	56 (9.12%)	20 (4.81%	36 (18.18%)
	brachy+RT	13 (2.12%)	9 (2.16%)	4 (2.02%)
	chemo only	46 (7.49%)	11 (2.64%)	35 (17.68%)
	chemo+brachy+RT+boost	3 (0.49%)	2 (0.48%)	1 (0.51%)
	horm only	1 (0.16%)	1 (0.24%)	0

Supplementary Table 4: Distribution of samples across different centres in the CC validation cohort.

Center	Total	NSMP	P53abn
Total	614	416	198
LGH	5 (0.81%)	4 (0.96%)	1 (0.51%)
HAM	65 (10.59%)	25 (6.01%)	40 (20.2%)
ARH	8 (1.3%)	8 (1.92%)	0 (0.0%)
CHM	19 (3.09%)	14 (3.37%)	5 (2.53%)
CMX	1 (0.16%)	1 (0.24%)	0 (0.0%)
LAV	104 (16.94%)	75 (18.03%)	29 (14.65%)
RGH	3 (0.49%)	3 (0.72%)	0 (0.0%)
PEN	2 (0.33%)	2 (0.48%)	0 (0.0%)
NAN	6 (0.98%)	5 (1.2%)	1 (0.51%)
RJH	27 (4.4%)	21 (5.05%)	6 (3.03%)
SSK	18 (2.93%)	12 (2.88%)	6 (3.03%)
KAM	4 (0.65%)	3 (0.72%)	1 (0.51%)
BBY	2 (0.33%)	2 (0.48%)	0 (0.0%)
VER	1 (0.16%)	1 (0.24%)	0 (0.0%)
JGH	39 (6.35%)	26 (6.25%)	13 (6.57%)
KEL	4 (0.65%)	4 (0.96%)	0 (0.0%)
WPG	19 (3.09%)	15 (3.61%)	4 (2.02%)
CRN	1 (0.16%)	1 (0.24%)	0 (0.0%)
UNH	5 (0.81%)	5 (1.2%)	0 (0.0%)
RCH	12 (1.95%)	12 (2.88%)	0 (0.0%)
NSH	56 (9.12%)	47 (11.3%)	9 (4.55%)
SUN	115 (18.73%)	55 (13.22%)	60 (30.3%)
VGH	81 (13.19%)	58 (13.94%)	23 (11.62%)
SPH	8 (1.3%)	8 (1.92%)	0 (0.0%)
TRL	2 (0.33%)	2 (0.48%)	0 (0.0%)
SMH	7 (1.14%)	7 (1.68%)	0 (0.0%)

Supplementary Table 5: Accuracy and other performance measures of the binary tumor-stroma classifier.

Non-tumor Accuracy	Tumor Accuracy	Kappa	F1 Score	AUC	Balanced Accuracy
99·89%	99·61%	0·9952	0·9976	0·9994	99·75%

Supplementary Table 6: Performance metrics of the deep learning model for p53abn vs. NSMP classifier (based on VarMIL method). The results are based on mean ± std of 10 cross-validation splits.

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	87·17 ± 10·86	91·59 ± 3·58	0·75 ± 0·09	0·87 ± 0·05	0·95 ± 0·03	89·38 ± 5·49
BC Validation Set	81·99 ± 4·56	77·61 ± 5·62	0·58 ± 0·03	0·79 ± 0·02	0·88 ± 0·01	79·80 ± 1·34
CC Validation Set	84.76 ± 3.48	92.24 ± 2.1	0.77 ± 0.02	0.88 ± 0.01	0.95 ± 0.0	88.5 ± 1.08

Supplementary Table 7: Detailed accuracy and other performance measures of the VarMIL network.

Source	Split	Metrics					
		p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Average Score (%)
Discovery Set	1	70·97	90·48	0·6208	0·8104	0·9078	80·72
	2	64·52	89·41	0·5506	0·7752	0·9120	76·96
	3	96·00	93·33	0·8332	0·9164	0·9867	94·67
	4	92·59	91·67	0·7928	0·8961	0·9749	92·13
	5	96·30	85·71	0·7205	0·8586	0·9616	91·01
	6	96·30	89·41	0·7784	0·8885	0·9760	92·85
	7	96·15	87·76	0·7262	0·8617	0·9380	91·95
	8	88·46	94·90	0·8107	0·9053	0·9686	91·68
	9	80·77	97·98	0·8225	0·9112	0·9526	89·37
	10	89·66	95·29	0·8400	0·9200	0·9542	92·47
BC Validation Set	1	85·78	75·82	0·5897	0·7930	0·8836	80·80
	2	81·28	81·19	0·6121	0·8057	0·8822	81·24
	3	81·52	82·24	0·6263	0·8129	0·8972	81·88
	4	89·34	70·60	0·5619	0·7767	0·8869	79·97
	5	79·86	81·49	0·6032	0·8013	0·8892	80·68
	6	76·07	81·79	0·5733	0·7866	0·8766	78·93
	7	90·05	64·03	0·4974	0·7403	0·8679	77·04
	8	78·67	79·70	0·5722	0·7857	0·8755	79·19
	9	77·96	79·70	0·5660	0·7826	0·8731	78·83
	10	79·38	79·55	0·5767	0·7879	0·8742	79·47
CC Validation Set	1	81.07	94.17	0.7659	0.8829	0.9428	87.62
	2	84.47	93.01	0.7767	0.8883	0.9491	88.74
	3	85.92	93.24	0.7916	0.8958	0.9545	89.58
	4	89.81	91.38	0.7957	0.8978	0.9507	90.59
	5	78.64	94.64	0.7527	0.8762	0.9471	86.64
	6	86.41	91.14	0.7658	0.8829	0.9439	88.77
	7	89.32	88.34	0.7502	0.8748	0.9430	88.83
	8	85.92	91.84	0.7718	0.8859	0.9418	88.88
	9	85.44	89.51	0.7356	0.8677	0.9394	87.47
	10	80.58	95.10	0.7755	0.8876	0.9526	87.84

Supplementary Table 8: Statistics of NSMP and *p53abn-like NSMP* patients based on p53abn vs. NSMP classifiers.

Source	Number of patients	NSMP	*p53abn-like NSMP*
Discovery Set	272	224 (82·35%)	48 (17·65%)
BC Validation Set	195	156 (80%)	39 (20%)
CC Validation Set	416	390 (93.75%)	26 (6.25%)

Supplementary Table 9: Performance benchmarking of Vanilla (A), IDaRS (B), Histogram (C), DeepMIL (D), VLAD (E), CLAM-MB (F), CLAM-SB (G), and TransMIL (H) models for the discovery and validation sets.

A: Vanilla

Source	P53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	74.80 ± 11.91	92.28 ± 5.51	0.68 ± 0.10	0.84 ± 0.05	0.93 ± 0.04	83.54 ± 5.69
BC Validation Set	79.46 ± 7.51	75.22 ± 11.43	0.53 ± 0.07	0.76 ± 0.04	0.84 ± 0.02	77.34 ± 2.85
CC Validation Set	57.96 ± 30.74	74.69 ± 34.19	0.34 ± 0.18	0.62 ± 0.15	0.88 ± 0.04	66.32 ± 8.6

B: IDaRS

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	81.63 ± 9.78	88.61 ± 5.22	0.66 ± 0.07	0.83 ± 0.04	0.93 ± 0.03	85.12 ± 3.98
BC Validation Set	83.41 ± 5.21	71.19 ± 10.90	& 0.52 ± 0.08	0.75 ± 0.05	0.84 ± 0.02	77.30 ± 3.34
CC Validation Set	86.07± 3.56	86.20± 10.41	0.7024± 0.1	0.85± 0.06	0.93± 0.01	86.13± 3.56

C: Histogram

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	72.38 ± 10.26	94.83 ± 2.64	0.70 ± 0.10	0.85 ± 0.05	0.88 ± 0.05	83.60 ± 5.34
BC Validation Set	75.88 ± 5.58	81.04 ± 4.95	0.56 ± 0.04	0.78 ± 0.02	0.80 ± 0.02	78.46 ± 1.77
CC Validation Set	80.68 ± 5.65	93.68 ± 1.72	0.76 ± 0.03	0.88 ± 0.02	0.92 ± 0.01	87.18 ± 2.29

D: DeepMIL

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	85.72 ± 11.55	91.45 ± 4.31	0.74 ± 0.12	0.87 ± 0.06	0.95 ± 0.03	88.58 ± 6.60
BC Validation Set	82.84 ± 4.15	77.60 ± 5.65	0.59 ± 0.03	0.79 ± 0.02	0.88 ± 0.01	80.22 ± 1.32
CC Validation Set	83.69± 1.77	93.26± 0.83	0.7741± 0.01	0.89± 0	0.95± 0	88.48± 0.61

E: VLAD

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	79.11 ± 6.67	93.43 ± 2.45	0.73 ± 0.08	0.86 ± 0.04	0.92± 0.04	86.27 ± 3.87
BC Validation Set	77.48 ± 4.56	80.36 ± 3.50	0.57 ± 0.03	0.78 ± 0.01	0.84 ± 0.01	78.92 ± 1.53
CC Validation Set	83.18 ± 2.09	92.27 ± 1.14	0.76 ± 0.02	0.88 ± 0.01	0.93 ± 0.01	87.72 ± 1.05

F: CLAM-MB

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	86.53 ± 11.8	97.72 ± 1.42	0.86 ± 0.1	0.93 ± 0.05	0.93 ± 0.06	92.12 ± 6.06
BC Validation Set	77.15 ± 7.05	79.63 ± 7.93	0.56 ± 0.04	0.78 ± 0.02	0.85 ± 0.01	78.39 ± 1.33
CC Validation Set	78.59 ± 5.61	94.22 ± 2.29	0.75 ± 0.03	0.87 ± 0.01	0.88 ± 0.02	86.41 ± 1.94

G: CLAM-SB

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	86.97 ± 10.36	97.51 ± 2.78	0.86 ± 0.1	0.93 ± 0.05	0.92 ± 0.06	92.24 ± 5.56
BC Validation Set	78.13 ± 6.8	79.65 ± 6.49	0.57 ± 0.03	0.78 ± 0.01	0.85 ± 0.01	78.89 ± 1.12
CC Validation Set	78.25 ± 5.1	94.97 ± 1.32	0.75 ± 0.03	0.88 ± 0.01	0.88 ± 0.02	86.61 ± 1.99

H: TransMIL

Source	p53abn Accuracy (%)	NSMP Accuracy (%)	Kappa	F1 score	AUC	Balanced Accuracy (%)
Discovery Set	92.45 ± 8.39	97.46 ± 2.8	0.90 ± 0.	0.95 ± 0.05	0.98 ± 0.03	94.95 ± 5.29
BC Validation Set	82.44 ± 13.93	70.39 ± 13.97	0.5 ± 0.09	0.74 ± 0.05	0.88 ± 0.01	76.41 ± 4.32
CC Validation Set	81.46 ± 4.59	94.48 ± 1.64	0.77 ± 0.02	0.89 ± 0.01	0.95 ± 0	87.97 ± 1.54

Supplementary Table 10: Statistics of NSMP and p53abn-like NSMP patients based on p53abn vs. NSMP Vanilla (A), IDaRS (B), Histogram (C), DeepMIL (D), VLAD (E), CLAM-MB (F), CLAM-SB (G), and TransMIL (H) models for the discovery and validation sets.

A: Vanilla

Source	**Number of patients**	**NSMP**	**p53abn-like NSMP**
Discovery Set	272	213 (78.31%)	59 (21.69%)
BC Validation Set	195	163 (83.59%)	32 (16.41%)
CC Validation Set	416	412 (99.04%)	4 (0.96%)

B: IDaRS

Source	**Number of patients**	**NSMP**	**p53abn-like NSMP**
Discovery Set	272	200 (73.53%)	72 (26.47%)
BC Validation Set	195	152 (77.95%)	43 (22.05%)
CC Validation Set	416	391 (93.99%)	25 (6.01%)

C: Histogram

Source	**Number of patients**	**NSMP**	**p53abn-like NSMP**
Discovery Set	272	232 (85.29%)	40 (14.71%)
BC Validation Set	195	172 (88.21%)	23 (11.79%)
CC Validation Set	416	399 (95.91%)	17 (4.09%)

D: DeepMIL

Source	**Number of patients**	**NSMP**	**p53abn-like NSMP**
Discovery Set	272	228 (83.82%)	44 (16.18%)
BC Validation Set	195	157 (80.51%)	38 (19.49%)
CC Validation Set	416	392 (94.23%)	24 (5.77%)

E: VLAD

Source	**Number of patients**	**NSMP**	**p53abn-like NSMP**
Discovery Set	272	232 (85.29%)	40 (14.71%)
BC Validation Set	195	166 (85.13%)	29 (14.87%)
CC Validation Set	416	394 (94.71%)	22 (5.29%)

F: CLAM-MB

Source	**Number of patients**	**NSMP**	**p53abn-like NSMP**
Discovery Set	272	251 (92.28%)	21 (7.72%)

BC Validation Set	195	161 (82.56%)	34 (17.44%)
CC Validation Set	416	398 (95.67%)	18 (4.33%)

F: CLAM-SB

Source	Number of patients	NSMP	p53abn-like NSMP
Discovery Set	272	247 (90.81%)	25 (9.19%)
BC Validation Set	195	152 (77.95%)	43 (22.05%)
CC Validation Set	416	396 (95.19%)	20 (4.81%)

F: TransMIL

Source	Number of patients	NSMP	p53abn-like NSMP
Discovery Set	272	248 (91.18%)	24 (8.82%)
BC Validation Set	195	131 (67.18%)	64 (32.82%)
CC Validation Set	416	397 (95.43%)	19 (4.57%)

Supplementary Table 11: Clinicopathologic features of the *p53abn-like NSMP* group in the discovery set.

Variable	Total	NSMP	*p53abn-like NSMP*	p53abn
Total	363	221 (60·88%)	47 (12·95%)	95 (26·17%)
Age at diagnosis				
<60 yrs	121 (33·33%)	90 (40·72%)	20 (42·55%)	11 (11·58%)
≥60 yrs	242 (66·67%)	131 (59·28%)	27 (57·45%)	84 (88·42%)
Histotype				
Endometrioid	288 (79·34%)	220 (99·55%)	42 (89·36%)	26 (27·37%)
Non-endometrioid	75 (20·66%)	1 (0·45%)	5 (10·64%)	69 (72·63%)
Tumour grade				
Low grade (G1–2)	258 (71·07%)	215 (97·29%)	31 (65·96%)	12 (12·63%)
High grade (G3)	105 (28·93%)	6 (2·71%)	16 (34·04%)	83 (87·37%)
FIGO stage				
I-II	291 (80·17%)	203 (91·86%)	36 (76·60%)	52 (54·74%)
III-IV	71 (19·56%)	18 (8·14%)	10 (21·28%)	43 (45·26%)
Unknown	1 (0·28%)	0	1 (2·13%)	0

Supplementary Table 12: Clinicopathologic features of the *p53abn-like NSMP* group in the BC validation set without excluding any patients.

Variable	Total	NSMP	***p53abn-like NSMP***	p53abn
Total	288	155 (53·82%)	38 (13·19%)	95 (32·99%)
Age at diagnosis				
<60 yrs	81 (28·13%)	61 (39·36%)	11 (28·95%)	9 (9·47%)
≥60 yrs	205 (71·18%)	92 (59·35%)	27 (71·05%)	86 (90·53%)
Unknown	2 (0·69%)	2 (1·29%)	0	0
Histotype				
Endometrioid	195 (67·71%)	145 (93·55%)	27 (71·05%)	23 (24·21%)
Non-endometrioid	91 (31·60%)	8 (5·16%)	11 (28·95%)	72 (75·79%)
Unknown	2 (0·69%)	2 (1·29%)	0	0
Tumour grade				
Low grade (G1–2)	151 (52·43%)	140 (90·32%)	6 (15·79%)	5 (5·26%)
High grade (G3)	137 (47·57%)	15 (9·68%)	32 (84·21%)	90 (94·74%)
FIGO stage				
I-II	216 (75·00%)	138 (89·03%)	28 (73·68%)	50 (52·63%)
III-IV	69 (23·96%)	14 (9·03%)	10 (26·32%)	45 (47·37%)
Unknown	3 (1·04%)	3 (1·94%)	0	0

Supplementary Table 13: Clinicopathologic features of the *p53abn-like NSMP* group in the CC validation set without excluding any patients.

Variable	Total	NSMP	***p53abn-like NSMP***	p53abn
Total	614	390 (63.52%)	26 (4.23%)	198 (32.25%)
Age at diagnosis				
<60 yrs	199 (32.41%)	158 (40.51%)	10 (38.46%)	31 (15.66%)
≥60 yrs	415 (67.59%)	232 (59.49%)	16 (61.54%)	167 (84.34%)
Unknown	0	0	0	0
Histotype				
Endometrioid	419 (68.24%)	367 (94.1%)	13 (50.0%)	39 (19.7%)
Non-endometrioid	195 (31.76%)	23 (5.9%)	13 (50.0%)	159 (80.3%)
Unknown	0	0	0	0
Tumour grade				
Low grade (G1–2)	390 (63.52%)	371 (95.13%)	5 (19.23%)	14 (7.07%)
High grade (G3)	199 (32.41%)	19 (4.87%)	19 (73.08%)	161 (81.31%)
Unknown	25 (4.07%)	0	2 (7.69%)	23 (11.62%)
FIGO stage				
I-II	487 (79.32%)	350 (89.74%)	19 (73.08%)	118 (59.6%)
III-IV	127 (20.68%)	40 (10.26%)	7 (26.92%)	80 (40.4%)
Unknown	0	0	0	0

Supplementary Table 14: Multi-variate Cox regression analysis showing the prognostic significance of *p53abn-like NSMP* group PFS for the entire cohort.

Variable	Hazard ratio	*p*
Grade	2·35	0·04
Stage	3·94	1.2e-5
Histology (endometrioid vs. non-endometrioid)	1.1	0.82
p53abn-like NSMP	2·53	0·01