Supplementary Material

Patch-Based and Single-Cell-Based Analysis of Peripheral Blood and Bone Marrow Histology for CHIP Detection

1 Peripheral Blood

1.1 Patches with QC

Table S1: Validation and test results presenting the metrics for PB patches using the UNI encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.4063	0.4000	0.5000	0.6667	0.4000	0.4000
1	0.0000	0.5714	0.4000	0.5556	0.6667	0.6667
2	0.9167	0.8571	0.8333	0.0667	0.3077	0.1818
3	0.0000	0.0000	0.1818	0.5000	0.4000	0.5000
4	0.6563	0.7778	0.6667	0.2500	0.4000	0.2500

Table S2: Validation and test results presenting the metrics for PB patches using the UNI encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.5000	0.6667	0.5833	0.5833	0.6000	0.6000
1	0.0833	0.5714	0.4000	0.4444	0.5714	0.5000
2	0.8056	0.6667	0.5833	0.1833	0.3077	0.1818
3	0.1667	0.0000	0.0909	0.6250	0.7143	0.6667
4	0.5938	0.7059	0.5833	0.1563	0.2857	0.1667

Table S3: Validation and test results presenting the metrics for PB patches using the DinoBloom encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.7188	0.7692	0.7500	0.7083	0.6667	0.6000
1	0.2500	0.5714	0.4000	0.2500	0.5714	0.5000
2	0.8611	0.9231	0.9167	0.4000	0.5000	0.4546
3	0.1000	0.0000	0.1818	0.6250	0.4000	0.5000
4	0.3750	0.3077	0.2500	0.9688	0.8571	0.8333

Table S4: Validation and test results presenting the metrics for PB patches using the DinoBloom encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.4688	0.5333	0.4167	0.7083	0.6667	0.6000
1	0.3333	0.6667	0.5000	0.3611	0.6667	0.5833
2	0.9167	0.9231	0.9167	0.3000	0.4615	0.3636
3	0.1333	0.3636	0.3636	0.3438	0.3077	0.2500
4	0.4063	0.5000	0.3333	0.4375	0.5000	0.5000

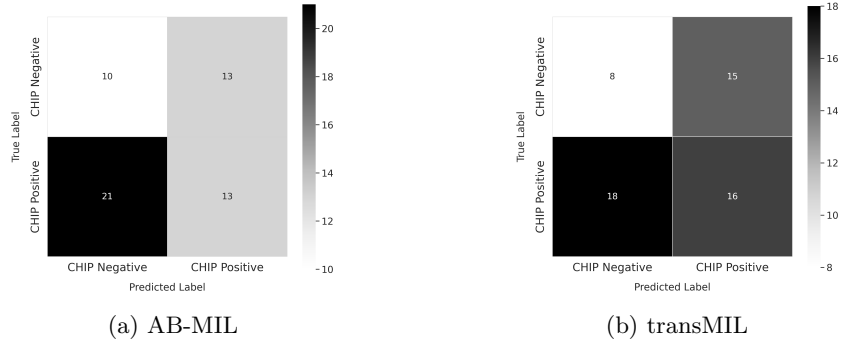**Confusion Matrices for PB Patches (UNI)**

(a) AB-MIL

(b) transMIL

Figure S1: Comparison of confusion matrices for PB patch classification using UNI encoder.
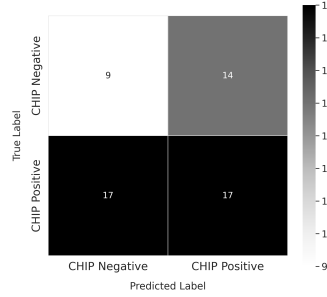
Confusion Matrix for PB Patches (DinoBloom + TransMIL)

Figure S2: Confusion matrix for PB patch classification using DinoBloom encoder and TransMIL aggregator.

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1.2 Patches without QC

Table S5: Validation and test results presenting the metrics for PB patches without QC using the UNI encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.2813	0.4000	0.5000	0.7917	0.5000	0.6000
1	0.0000	0.4615	0.3000	0.3611	0.4286	0.3333
2	0.8333	0.7692	0.7500	0.0333	0.3077	0.1818
3	0.0000	0.0000	0.1818	0.5313	0.4000	0.5000
4	0.3438	0.5882	0.4167	0.1250	0.1667	0.1667

Table S6: Validation and test results presenting the metrics for PB patches without QC using the UNI encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.8125	0.7778	0.6667	0.5833	0.7273	0.7000
1	0.0000	0.3333	0.2000	0.5000	0.5714	0.5000
2	0.7500	0.6667	0.5000	0.1333	0.4286	0.2727
3	0.0667	0.0000	0.1818	0.5313	0.4000	0.5000
4	0.5000	0.6667	0.5000	0.4375	0.5333	0.4167

Table S7: Validation and test results presenting the metrics for PB patches without QC using the DinoBloom encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.7813	0.6667	0.6667	0.6250	0.6154	0.5000
1	0.3333	0.5714	0.4000	0.3333	0.4615	0.4167
2	0.8888	0.9230	0.9167	0.4000	0.5000	0.4545
3	0.1333	0.0000	0.1818	0.2500	0.3636	0.4167
4	0.2500	0.3077	0.2500	1.0000	1.0000	1.0000

Table S8: Validation and test results presenting the metrics for PB patches without QC using the DinoBloom encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.7188	0.6154	0.5833	0.5417	0.6667	0.6000
1	0.0417	0.4615	0.3000	0.4444	0.4615	0.4167
2	1.0000	0.7500	0.6667	0.3333	0.4286	0.2727
3	0.1333	0.3636	0.3636	0.3125	0.3077	0.2500
4	0.3438	0.4286	0.3333	0.6563	0.5000	0.5000

Confusion Matrices for PB Patches Without QC (UNI)
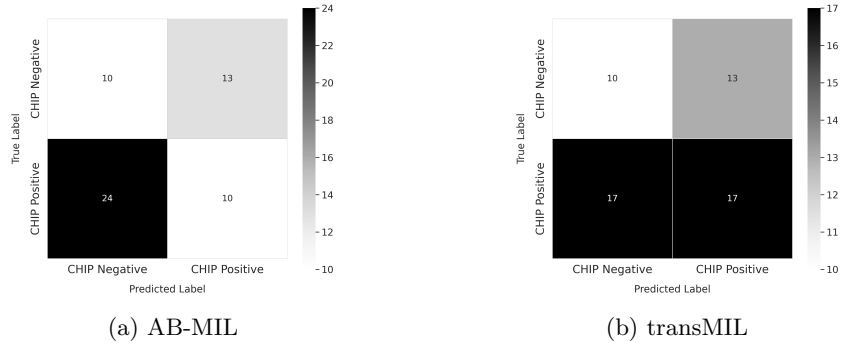

(a) AB-MIL

(b) transMIL

Figure S3: Comparison of confusion matrices for PB patch without QC classification using UNI encoder.

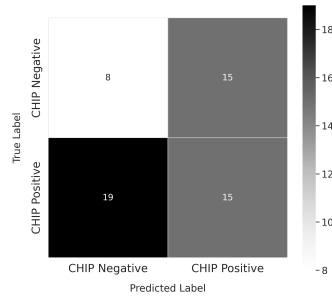## Confusion Matrix for PB Patches Without QC (DinoBloom + TransMIL)

Figure S4: Confusion matrix for PB patch without QC classification using DinoBloom encoder and TransMIL aggregator.

1.3   40 × 40 segmentation

Table S9: Validation and test results presenting the metrics for PB white blood cell segmentation using the UNI encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.1563	0.1818	0.2500	0.5000	0.6667	0.7000
1	0.1667	0.3333	0.2000	0.3333	0.5714	0.5000
2	0.6667	0.5714	0.5000	0.3667	0.5000	0.4546
3	0.2000	0.2000	0.2727	0.6875	0.4615	0.4167
4	0.3750	0.8000	0.6667	0.2188	0.5333	0.4167

Table S10: Validation and test results presenting the metrics for PB white blood cell segmentation using the UNI encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.1875	0.3077	0.2500	0.7083	0.8000	0.8000
1	0.2083	0.3333	0.2000	0.3333	0.5714	0.5000
2	0.3889	0.6667	0.5833	0.3667	0.6667	0.5455
3	0.2333	0.5000	0.4546	0.3438	0.4286	0.3333
4	0.4063	0.6250	0.5000	0.2500	0.5333	0.4167

Table S11: Validation and test results presenting the metrics for PB white blood cell segmentation using the DinoBloom encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.4063	0.5714	0.5000	0.4167	0.4000	0.4000
1	0.2500	0.4000	0.4000	0.4167	0.6154	0.5833
2	0.8611	0.8571	0.8333	0.4000	0.3636	0.3636
3	0.1667	0.3636	0.3636	0.6250	0.8235	0.7500
4	0.4375	0.7500	0.6667	0.1250	0.3077	0.2500

Table S12: Validation and test results presenting the metrics for PB white blood cell segmentation using the DinoBloom encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.4063	0.4286	0.3333	0.5417	0.6000	0.6000
1	0.0833	0.3333	0.2000	0.3056	0.5714	0.5000
2	0.8611	0.7500	0.6667	0.2667	0.5000	0.4546
3	0.1333	0.2000	0.2727	0.5938	0.7778	0.6667
4	0.3438	0.6667	0.5000	0.2500	0.4000	0.2500

Confusion Matrices for PB 40 × 40 Segmentation (UNI)
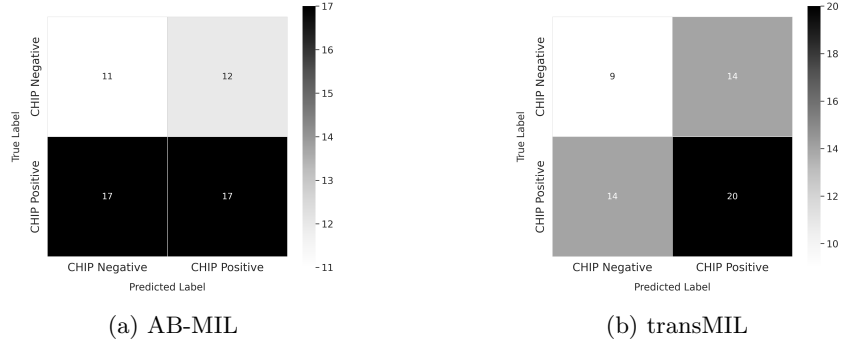

(a) AB-MIL

(b) transMIL

Figure S5: Comparison of confusion matrices for PB 40 × 40 segmentation classification using UNI encoder.

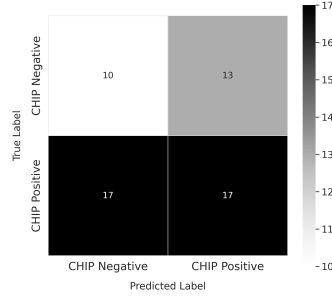**Confusion Matrix for PB Segmentation (DinoBloom + AB-MIL)**

Figure S6: Confusion matrix for PB 40 × 40 segmentation classification using DinoBloom encoder and AB-MIL aggregator.

1.4 224 × 224 segmentation

Table S13: Validation and test results presenting the metrics for PB 224×224 resized white blood cell segmentation using the UNI encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.2188	0.3636	0.4167	0.6250	0.6667	0.7000
1	0.1667	0.3333	0.2000	0.3333	0.5714	0.5000
2	0.6667	0.5714	0.5000	0.4000	0.5000	0.4546
3	0.1333	0.2000	0.2727	0.6875	0.5714	0.5000
4	0.5000	0.8235	0.7500	0.3125	0.4615	0.4167

Table S14: Validation and test results presenting the metrics for PB 224×224 resized white blood cell segmentation using the UNI encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.5625	0.5714	0.5000	0.5417	0.5455	0.5000
1	0.2083	0.5714	0.4000	0.3056	0.6250	0.5000
2	0.8056	0.7500	0.6667	0.1667	0.5714	0.4546
3	0.0667	0.1818	0.1818	0.5313	0.3333	0.3333
4	0.4063	0.4615	0.4167	0.5313	0.7059	0.5833

Table S15: Validation and test results presenting the metrics for PB 224×224 resized white blood cell segmentation using the DinoBloom encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.5938	0.3636	0.4167	0.6667	0.6667	0.7000
1	0.2500	0.5000	0.4000	0.3611	0.3333	0.3333
2	0.7222	0.5455	0.5833	0.2667	0.3636	0.3636
3	0.2000	0.3636	0.3636	0.5625	0.6667	0.5833
4	0.4688	0.6250	0.5000	0.4688	0.2222	0.4167

Table S16: Validation and test results presenting the metrics for PB 224×224 resized white blood cell segmentation using the DinoBloom encoder and Trans-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.4688	0.5333	0.4167	0.5833	0.6000	0.6000
1	0.0833	0.3333	0.2000	0.3889	0.5714	0.5000
2	0.8056	0.6667	0.6667	0.1667	0.3636	0.3636
3	0.1333	0.2000	0.2727	0.9063	0.7778	0.6667
4	0.3750	0.6667	0.5000	0.2500	0.4000	0.2500

Confusion Matrices for PB 224 × 224 Resized Segmentation (UNI)
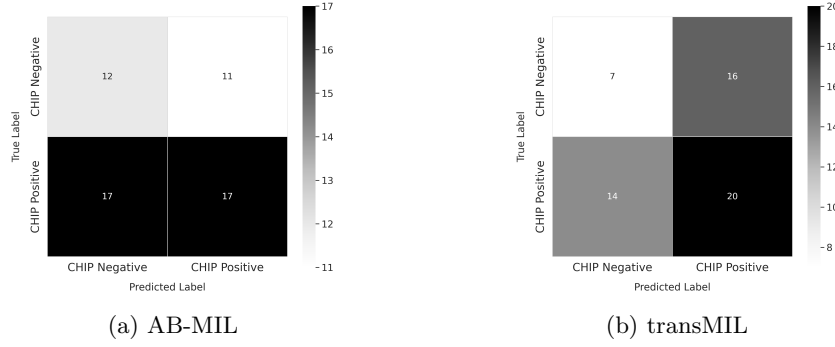

(a) AB-MIL

(b) transMIL

Figure S7: Comparison of confusion matrices for PB 224 × 224 resized segmentation classification using UNI encoder.

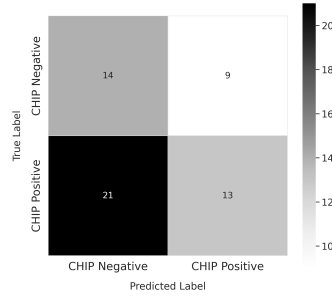**Confusion Matrix for PB Resized Segmentation (DinoBloom + AB-MIL)**

Figure S8: Confusion matrix for PB 224 × 224 resized segmentation classification using DinoBloom encoder and AB-MIL aggregator.

2 Bone Marrow

Table S17: Validation and test results presenting the metrics for BM patches using the UNI encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.040	0.000	0.067	0.302	0.480	0.350
1	0.542	0.714	0.600	0.771	0.867	0.789
2	0.563	0.875	0.789	0.219	0.533	0.364
3	0.657	0.765	0.636	0.273	0.667	0.500
4	0.080	0.621	0.450	0.980	0.889	0.867

Table S18: Validation and test results presenting the metrics for BM patches using the UNI encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.160	0.421	0.267	0.490	0.690	0.550
1	0.635	0.769	0.700	0.750	0.800	0.684
2	0.458	0.839	0.737	0.267	0.500	0.364
3	0.724	0.800	0.682	0.172	0.621	0.450
4	0.091	0.667	0.500	0.980	0.947	0.933

Table S19: Validation and test results presenting the metrics for BM patches using the DinoBloom encoder and AB-MIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.320	0.167	0.333	0.417	0.500	0.400
1	0.469	0.741	0.650	0.792	0.786	0.684
2	0.542	0.714	0.579	0.067	0.095	0.136
3	0.667	0.800	0.682	0.313	0.667	0.500
4	0.200	0.538	0.400	0.920	0.824	0.800

Table S20: Validation and test results presenting the metrics for BM patches using the DinoBloom encoder and TransMIL aggregator.

kfold	Validation			Test		
	AUC	F1-score	ACC	AUC	F1-score	ACC
0	0.020	0.000	0.067	0.229	0.643	0.500
1	0.500	0.714	0.600	0.688	0.759	0.632
2	0.542	0.714	0.579	0.305	0.552	0.409
3	0.610	0.800	0.682	0.152	0.667	0.500
4	0.323	0.667	0.500	0.880	0.737	0.667

Confusion Matrices for BM Patches (DinoBloom)
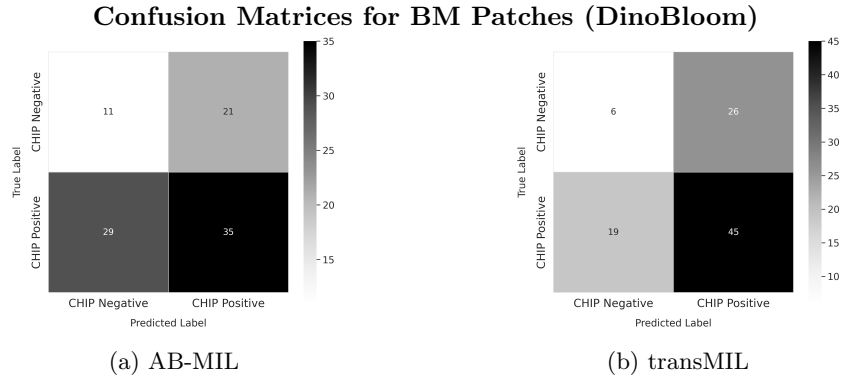

(a) AB-MIL

(b) transMIL

Figure S9: Comparison of confusion matrices for BM patch classification using DinoBloom encoder.