Oropharyngeal squamous cell carcinoma: radiomic machine-learning classifiers from multiparametric MR images for determination of HPV infection status

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Supplementary Table 1. Selected features from various combinations of each sequence

Sequence	Selected features			
ADC	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	ADC	Wavelet_HHH	GLCM_dist_3	Correlation
	ADC	Wavelet_HLH	GLCM_dist_3	Correlation
	ADC	Original	GLCM_dist_3	Entropy_std
	ADC	Original	GLCM_dist_1	Cluster Shade std
T1WI	T1	Original	GLCM_dist_1	Autocorrelation_std
	T1	Wavelet_LHL	GLCM_dist_3	Correlation
	T1	Wavelet_LHH	Firstorder	Median
	T1	Wavelet_HLH	GLCM_dist_2	Correlation
	T1	Wavelet_LLH	GLCM_dist_3	Correlation
T2WI	T2	Wavelet_LLH	Firstorder	Median
	T2	Wavelet_LLH	GLCM_dist_1	Cluster Prominence
	T2	Wavelet_HLH	GLRLM	HGRE
	T2	Wavelet_LHH	Firstorder	Skewness
	T2	Wavelet_HLH	GLCM_dist_3	Correlation
CE-T1WI	T1CE	Wavelet_LLH	GLCM_dist_1	Cluster Shade std
	T1CE	Wavelet_LHL	GLCM_dist_1	Cluster Prominence
	T1CE	Wavelet_HLL	GLCM_dist_2	Cluster Prominence std
	T1CE	Wavelet_LLH	Firstorder	Max
	T1CE	Original	Firstorder	Range Cover
ADC+T1WI	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	T1	Original	GLCM_dist_1	Autocorrelation_std
	ADC	Wavelet_HHH	GLCM_dist_3	Correlation
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Wavelet_LLH	GLCM_dist_1	Homogeneity1 std
ADC+T2WI	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	ADC	Wavelet_LLH	GLCM_dist_1	Homogeneity1 std
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Original	GLCM_dist_3	Entropy_std
	T2	Wavelet_HLH	GLRLM	HGRE
ADC+CE-T1WI	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Wavelet_LLH	GLCM_dist_1	Homogeneity1 std
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Original	GLCM_dist_3	Entropy_std
T1WI+T2WI	T1	Original	GLCM_dist_1	Autocorrelation_std
	T1	Wavelet_LHL	GLCM_dist_3	Correlation
	T2	Wavelet_LLH	GLCM_dist_1	Cluster Prominence std
	T1	Wavelet_LLH	GLCM_dist_3	Correlation
	T1	Original	GLCM_dist_1	Sum average std
T1WI+CE-T1WI	T1	Original	GLCM_dist_1	Autocorrelation_std
	T1	Wavelet_LHL	GLCM_dist_3	Correlation
	T1	Wavelet_LLH	GLCM_dist_3	Correlation
	T1	Original	GLRLM	GLN
	T1	Wavelet_HHL	GLCM_dist_1	Correlation
T2WI+CE-T1WI	T1CE	Wavelet_LLH	GLCM_dist_1	Cluster Shade std
	T2	Wavelet_HLH	GLRLM	HGRE
	T2	Original	Firstorder	Max
	T1CE	Wavelet_LHH	GLCM_dist_1	Cluster Prominence
	T1CE	Wavelet_LHL	GLCM_dist_1	Cluster Prominence
ADC+T1WI+T2WI	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	T1	Original	GLCM_dist_1	Autocorrelation_std
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Wavelet_LLH	GLCM_dist_1	Homogeneity1 std
	ADC	Wavelet_HHH	GLCM_dist_3	Correlation

ADC+T1WI+CE-T1WI	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	T1	Original	GLCM_dist_1	Autocorrelation_std
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Wavelet_LLH	GLCM_dist_1	Homogeneity1 std
	ADC	Wavelet_HHH	GLCM_dist_3	Correlation
ADC+T2WI+CE-T1WI	ADC	Wavelet_LLL	GLCM_dist_2	Entropy_std
	ADC	Wavelet_LLH	GLCM_dist_1	Homogeneity1 std
	ADC	Wavelet_HLH	GLCM_dist_2	Correlation_std
	ADC	Original	GLCM_dist_3	Entropy_std
	ADC	Wavelet_HLH	GLCM_dist_3	Correlation
T1WI+T2WI+ CE-T1WI	T1	Original	GLCM_dist_1	Autocorrelation_std
	T1	Wavelet_LHL	GLCM_dist_3	Correlation
	T1	Wavelet_LLH	GLCM_dist_3	Correlation
	T1	Wavelet_HHL	GLCM_dist_1	Correlation
	T1	Wavelet_LHL	Firstorder	Range Cover

Abbreviations: ADC = apparent diffusion coefficient, T1WI = T1-weighted imaging, T2WI = fat-suppressed T2-weighted imaging, CE-T1WI = fat-suppressed contrast-enhanced T1-weighted imaging, GLCM = gray-level co-occurrence matrix, GLRLM = gray-level run-length matrix.

Supplementary Table 2. Number of extracted features from each sequence

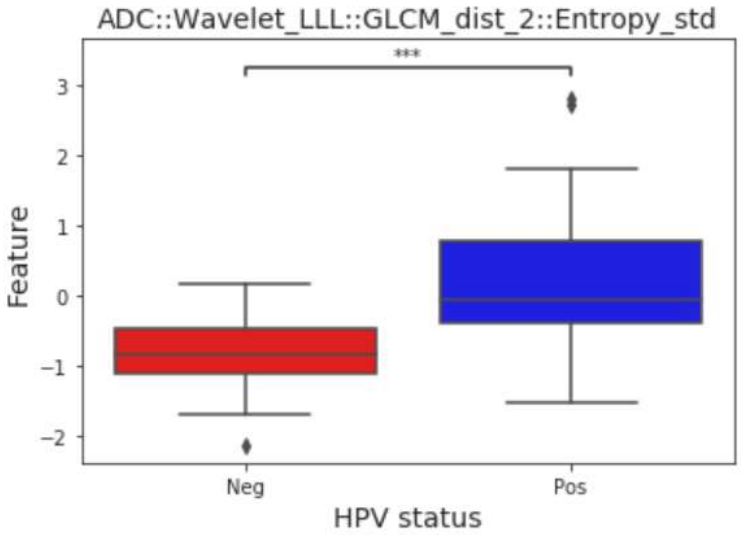
Class	Original	3D Wavelets	Total
First order	17	136	153
GLCM_dist_1	46	368	414
GLCM_dist_2	46	368	414
GLCM_dist_3	46	368	414
GLRLM	24	192	216
Shpae/vol	7	-	7
Total	186	1432	1618

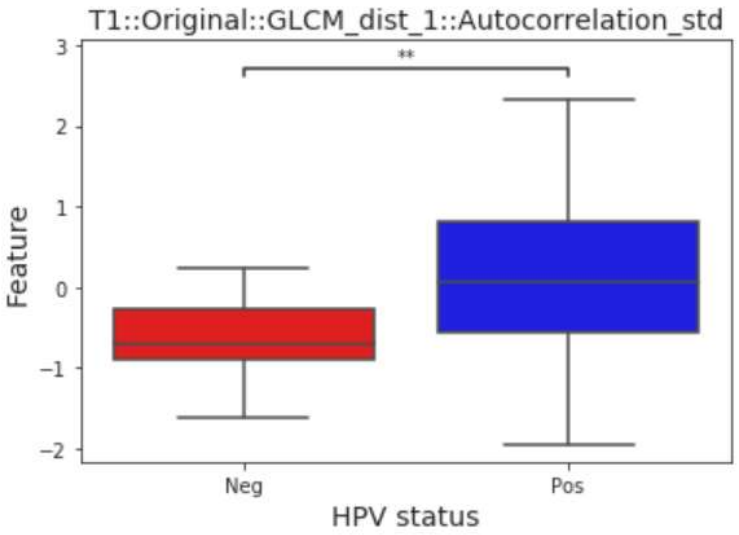
Abbreviations: GLCM = gray-level co-occurrence matrix, GLRLM = gray-level run-length matrix

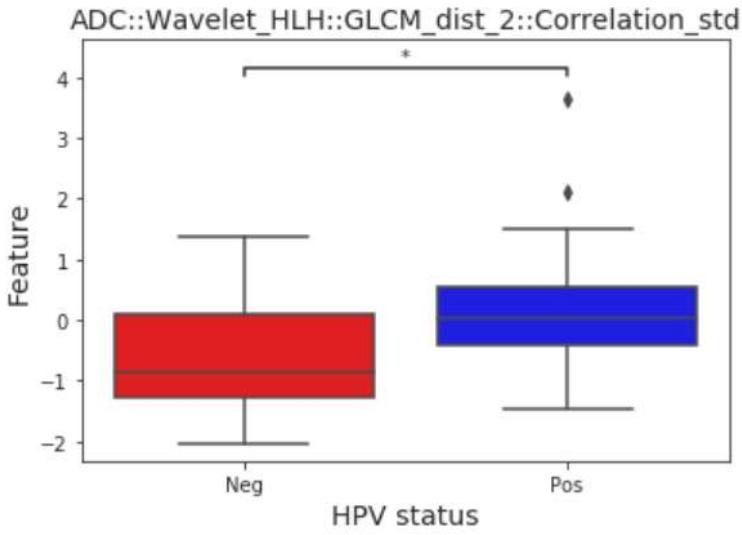
Supplementary Table 3. Hyperparameters of each classifier

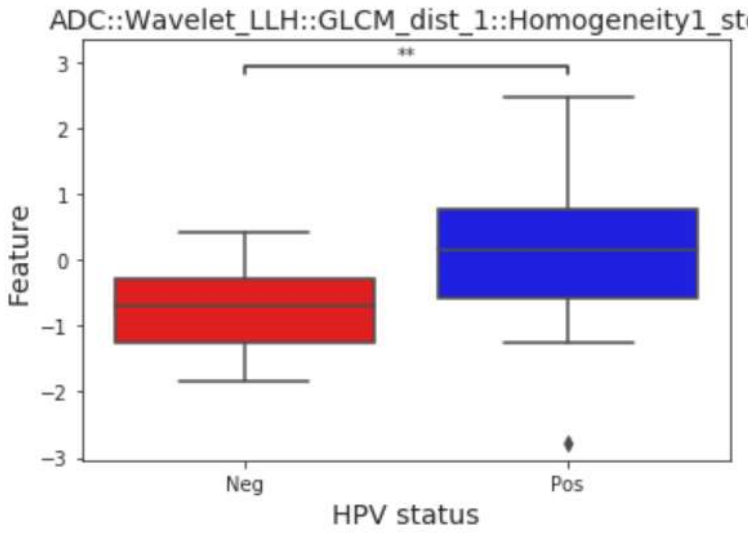
Classifier	Hyperparameters
Logistic regression	C = 0.01 penalty = l2 class_weight = balanced
Random forest	criterion = gini n_estimators = 300 max_features = 1 min_sample_split = 2 class_weight = balanced
XG boost	objective = binary:logistic n_estimators = 1000 max_depth = 1 subsample = 0.4 colsample_bytree = 0.5

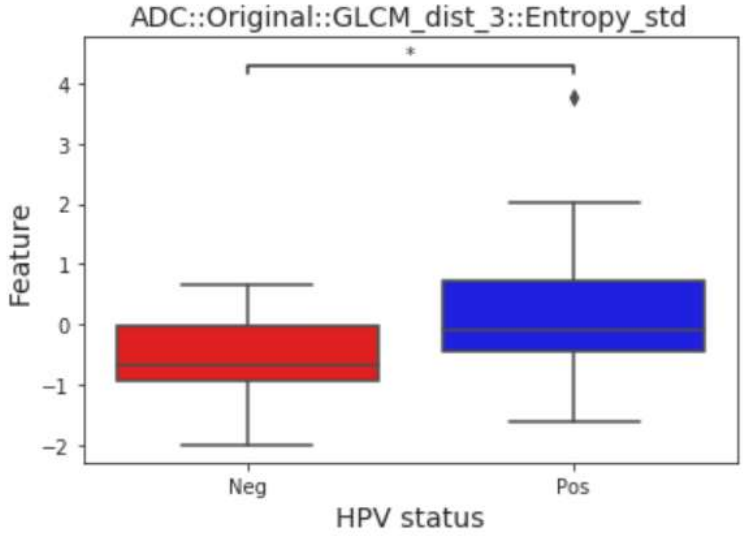
Supplementary Figure 1: Box plots of selected features extracted from four magnetic resonance sequences



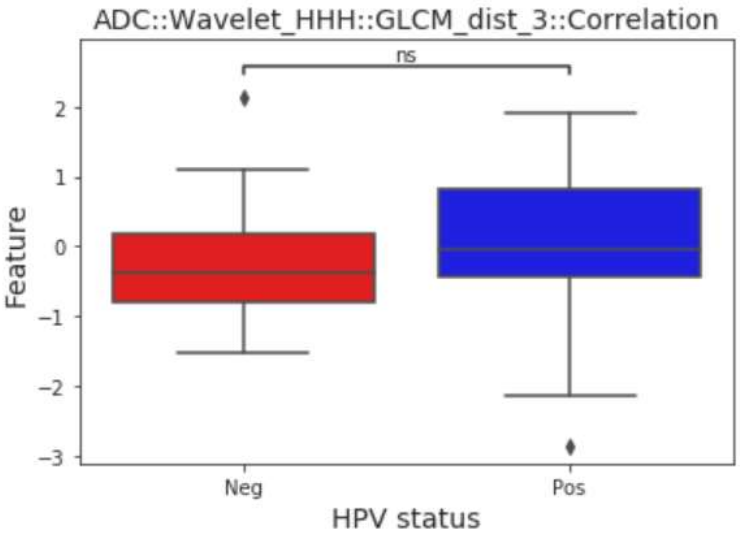


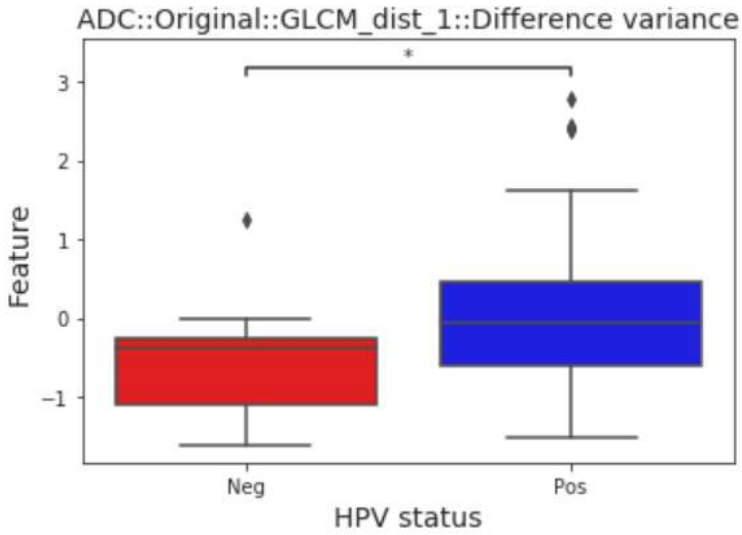






ns: $0.05 < p \leq 1.$
*: $0.01 < p \leq 0.05$
**: $0.001 < p \leq 0.01$
***: $0.0001 < p \leq 0.001$
****: $p \leq 0.0001$

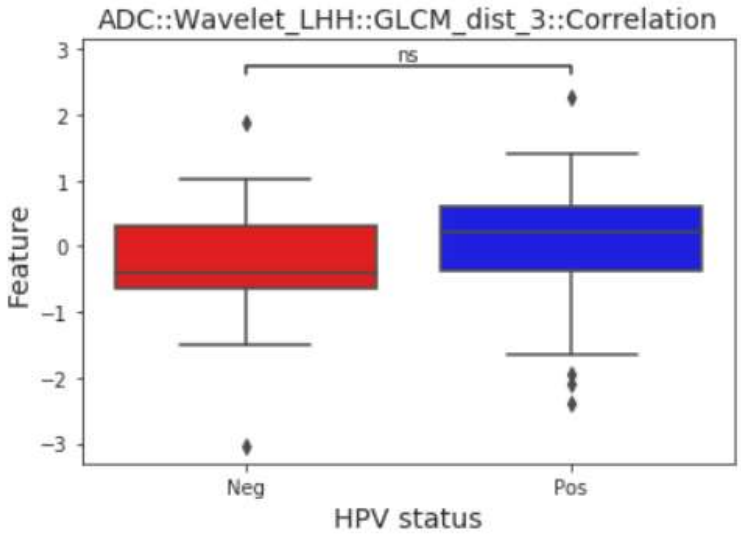


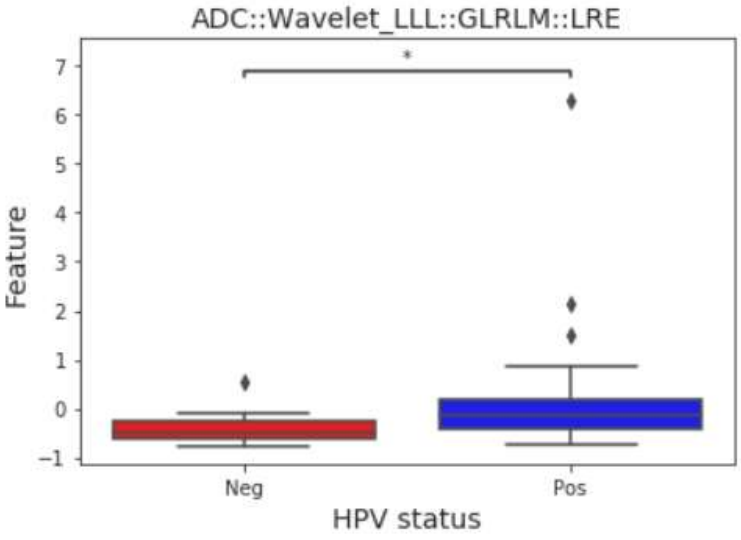


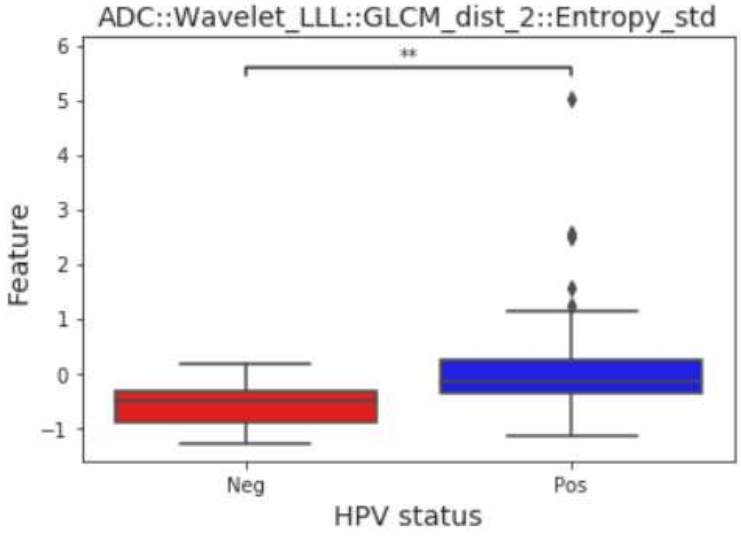
ns: $0.05 < p \leq 1.$
*: $0.01 < p \leq 0.05$
**: $0.001 < p \leq 0.01$
***: $0.0001 < p \leq 0.001$
****: $p \leq 0.0001$

Supplementary Figure 2: Box plots of selected features extracted from ADC map of tumor (T) mask and lymph node (N) mask. (a) Features from T mask. (b) Features from N mask

a.







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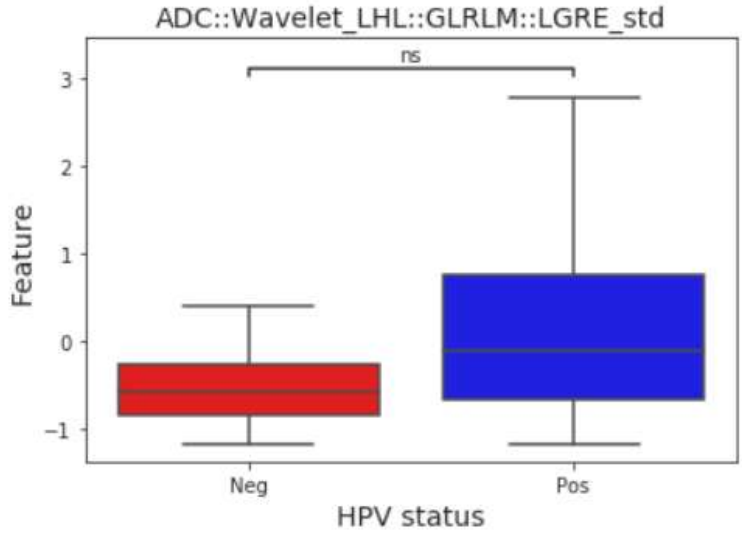
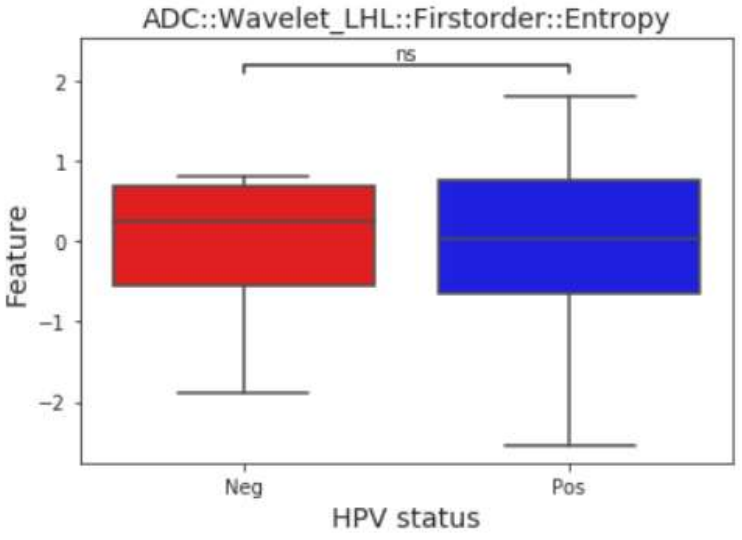
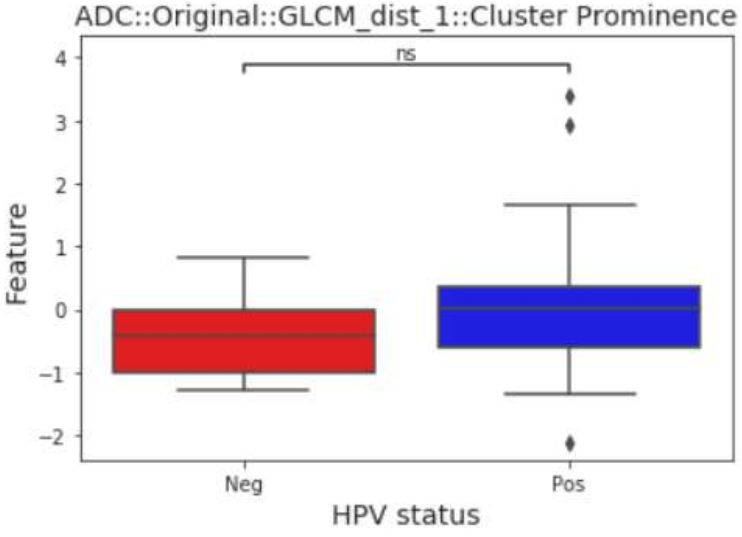
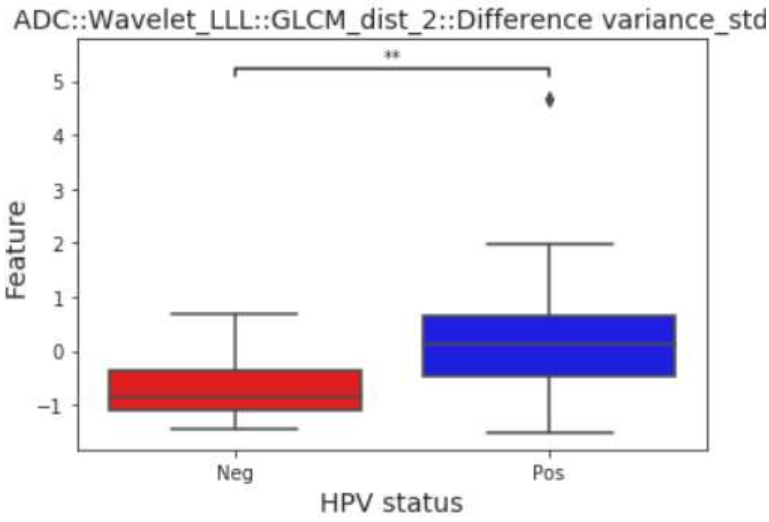
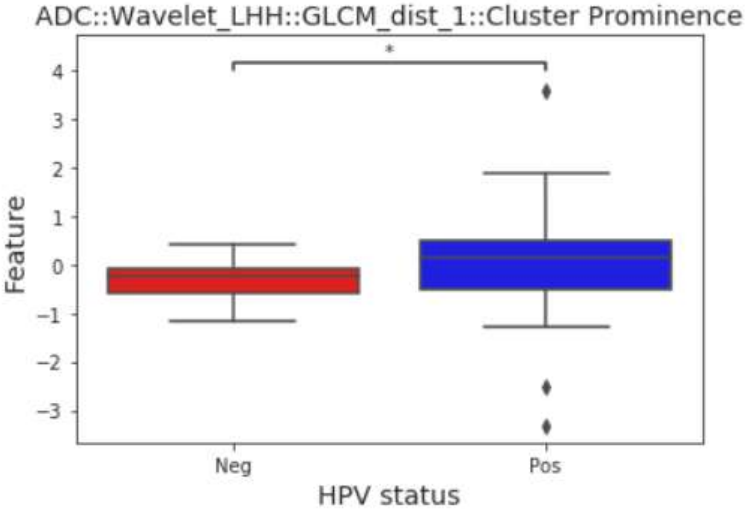




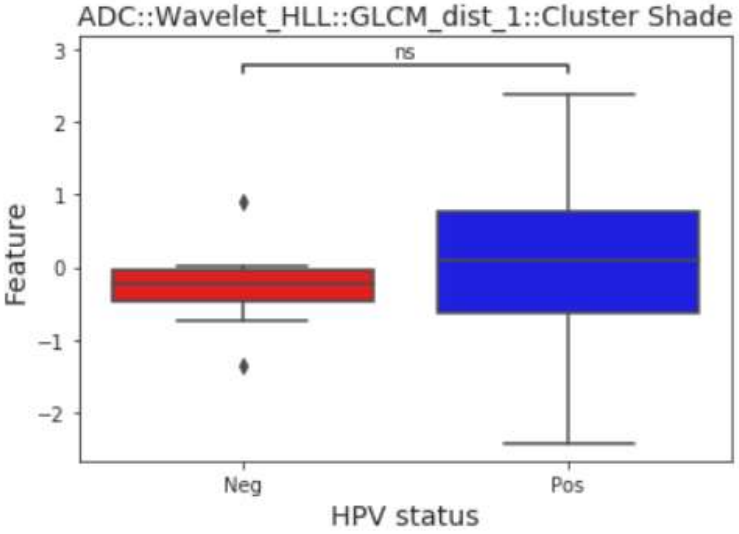


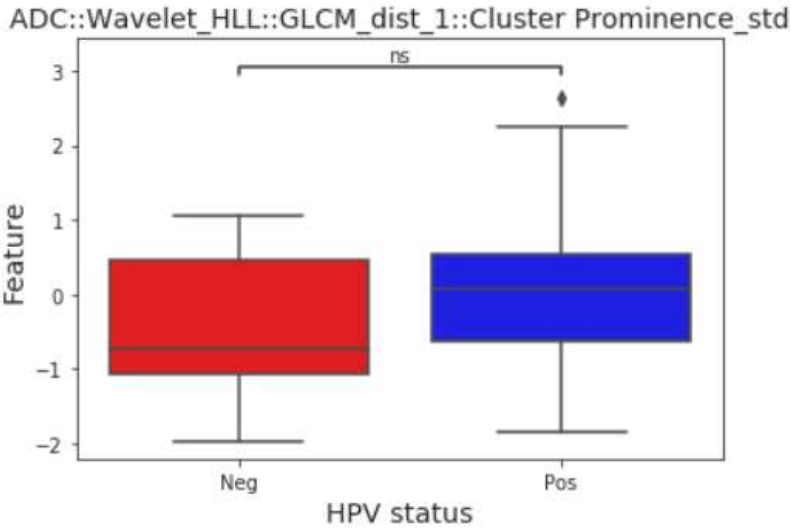
a.





b.





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