

Supplementary material

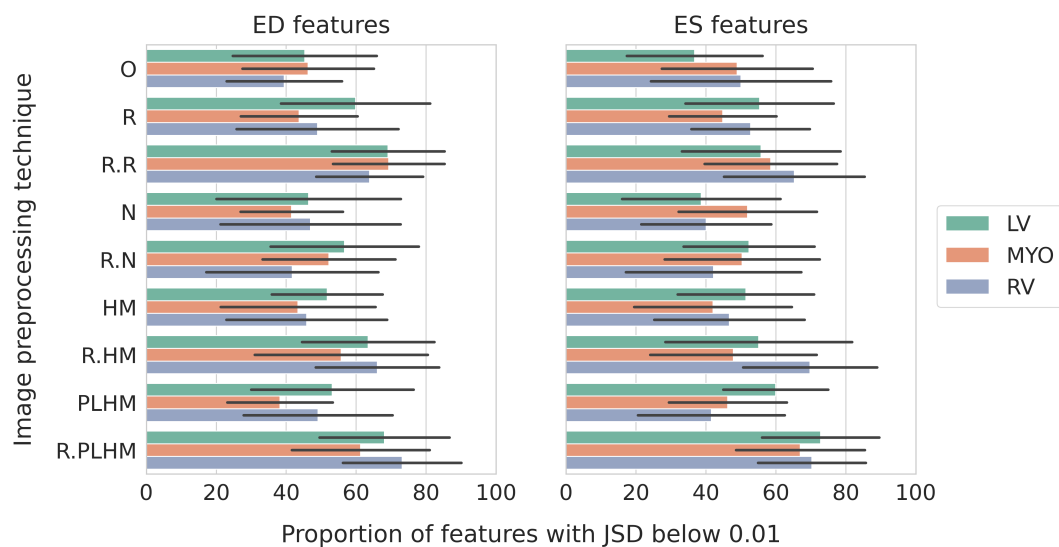


Figure S1. Percentage of texture features below the 0.01 JSD threshold for each ROI for healthy subjects. Results are averaged over feature types and centre pairs and separated in ED and ES frames. Only features with square cross-correlation below 0.9 were considered. The black lines represent the standard deviation. O: original images (without normalisation), R: image intensity recaling, N: image intensity normalisation, HM: histogram matching and PLHM: piecewise linear histogram matching. An “R.” in front of a method means that it is applied at ROI level.

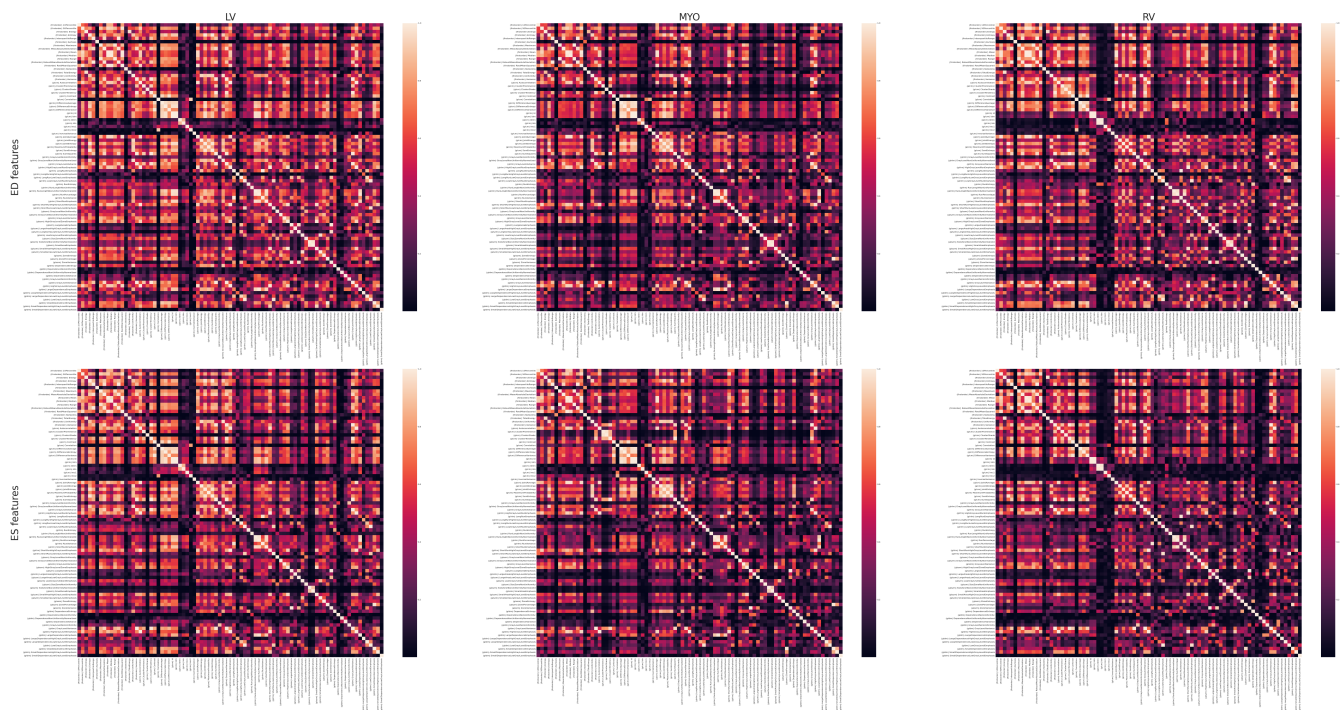


Figure S2. Pairwise square correlation for features extracted from the three different ROIs without the application of any normalisation technique. The correlation between features was very similar for the different preprocessing techniques, showing a negligible standard deviation. Zoom in to see in more detail.

Table S1. List of radiomic features extracted with PyRadiomics. We refer the reader to the library documentation (<https://pyradiomics.readthedocs.io/>) for the specific definition and interpretation of each feature.

Family	Index	Feature	Family	Index	Feature
Shape	1	Elongation	GLCM	51	InverseVariance
	2	Flatness		52	MaximumProbability
	3	LeastAxisLength		53	SumEntropy
	4	MajorAxisLength		54	SumSquares
	5	Maximum2DDiameterColumn	GLRLM	55	GrayLevelNonUniformity
	6	Maximum2DDiameterRow		56	GrayLevelNonUniformityNormalized
	7	Maximum2DDiameterSlice		57	GrayLevelVariance
	8	Maximum3DDiameter		58	HighGrayLevelRunEmphasis
	9	MeshVolume		59	LongRunEmphasis
	10	MinorAxisLength		60	LongRunHighGrayLevelEmphasis
	11	Sphericity		61	LongRunLowGrayLevelEmphasis
	12	SurfaceArea		62	LowGrayLevelRunEmphasis
	13	SurfaceVolumeRatio		63	RunEntropy
	14	VoxelVolume		64	RunLengthNonUniformity
First order	15	10Percentile		65	RunLengthNonUniformityNormalized
	16	90Percentile		66	RunPercentage
	17	Energy		67	RunVariance
	18	Entropy		68	ShortRunEmphasis
	19	InterquartileRange		69	ShortRunHighGrayLevelEmphasis
	20	Kurtosis		70	ShortRunLowGrayLevelEmphasis
	21	Maximum	GLSZM	71	GrayLevelNonUniformity
	22	MeanAbsoluteDeviation		72	GrayLevelNonUniformityNormalized
	23	Mean		73	GrayLevelVariance
	24	Median		74	HighGrayLevelZoneEmphasis
	25	Minimum		75	LargeAreaEmphasis
	26	Range		76	LargeAreaHighGrayLevelEmphasis
	27	RobustMeanAbsoluteDeviation		77	LargeAreaLowGrayLevelEmphasis
	28	RootMeanSquared		78	LowGrayLevelZoneEmphasis
	29	Skewness		79	SizeZoneNonUniformity
	30	TotalEnergy		80	SizeZoneNonUniformityNormalized
	31	Uniformity		81	SmallAreaEmphasis
	32	Variance		82	SmallAreaHighGrayLevelEmphasis
GLCM	33	Autocorrelation		83	SmallAreaLowGrayLevelEmphasis
	34	JointAverage		84	ZoneEntropy
	35	ClusterProminence		85	ZonePercentage
	36	ClusterShade		86	ZoneVariance
	37	ClusterTendency	GLDM	87	DependenceEntropy
	38	Contrast		88	DependenceNonUniformity
	39	Correlation		89	DependenceNonUniformityNormalized
	40	DifferenceAverage		90	DependenceVariance
	41	DifferenceEntropy		91	GrayLevelNonUniformity
	42	DifferenceVariance		92	GrayLevelVariance
	43	JointEnergy		93	HighGrayLevelEmphasis
	44	JointEntropy		94	LargeDependenceEmphasis
	45	Imc1		95	LargeDependenceHighGrayLevelEmphasis
	46	Imc2		96	LargeDependenceLowGrayLevelEmphasis
	47	Idm		97	LowGrayLevelEmphasis
	48	Idmn		98	SmallDependenceEmphasis
	49	Id		99	SmallDependenceHighGrayLevelEmphasis
	50	Idn		100	SmallDependenceLowGrayLevelEmphasis

GLCM: Gray Level Co-occurrence Matrix, GLRLM: Gray Level Run Length Matrix, GLSZM: Gray Level Size Zone Matrix and GLDM: Gray Level Dependence Matrix.

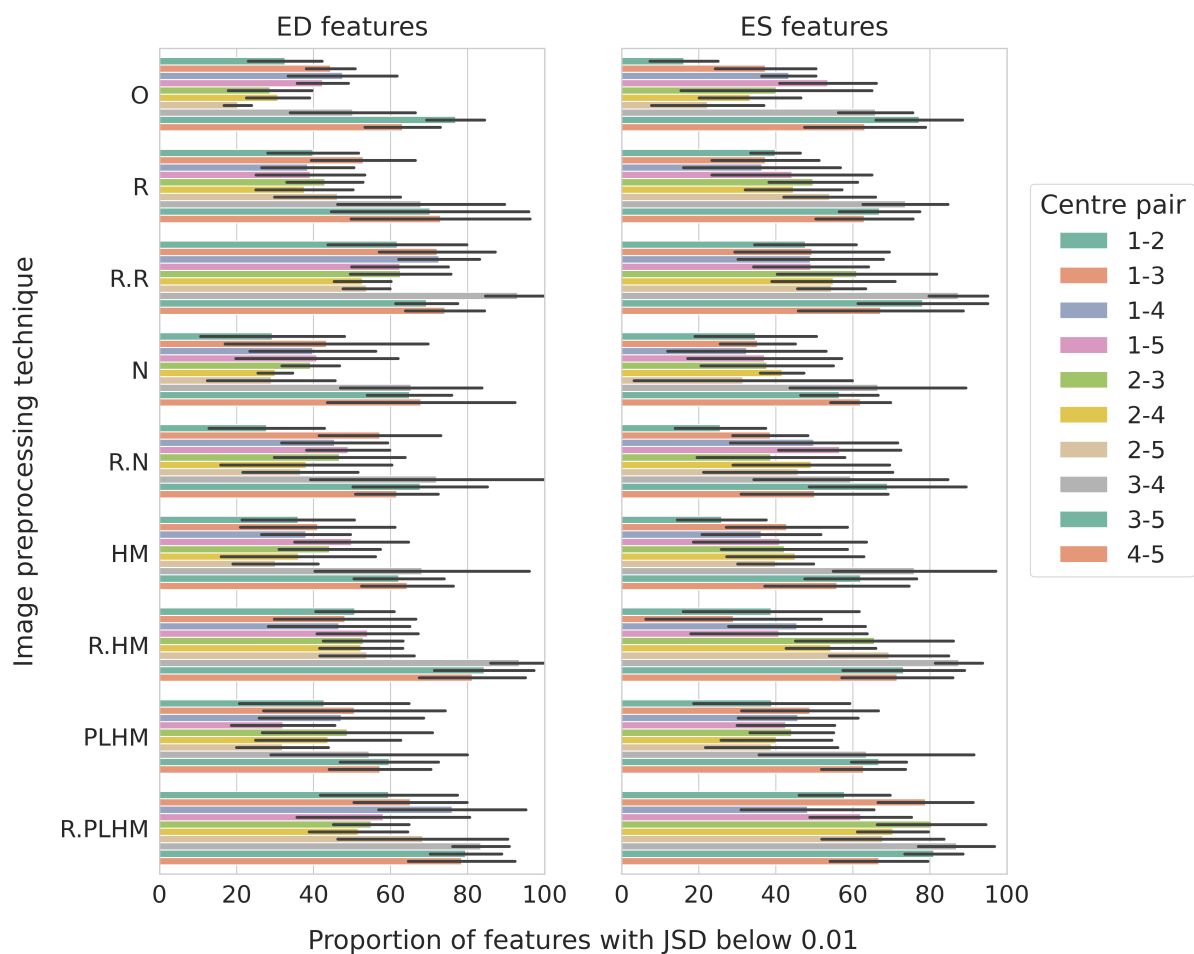


Figure S3. Percentage of texture features below the 0.01 JSD threshold for each centre pair, indexed in alphabetical order as in Table 2, for healthy subjects. Results are averaged over feature types and ROIs and separated in ED and ES frames. Only features with square cross-correlation below 0.9 were considered. The black lines represent the standard deviation. O: original images (without normalisation), R: image intensity recaling, N: image intensity normalisation, HM: histogram matching and PLHM: piecewise linear histogram matching. An "R." in front of a method means that it is applied at ROI level.

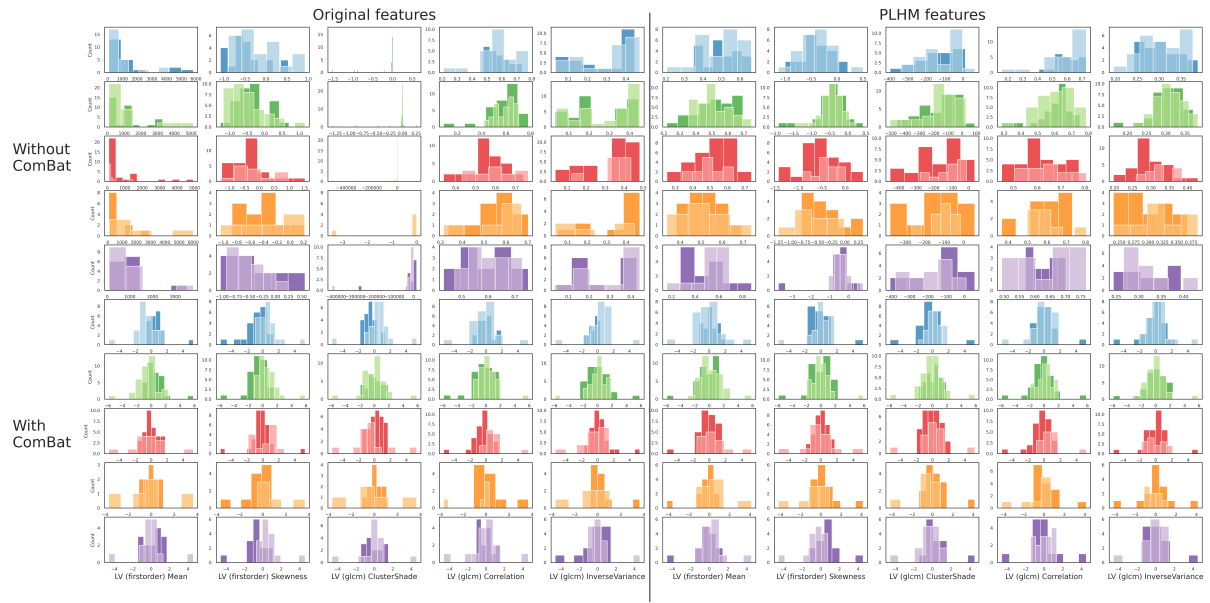


Figure S4. Comparison of histograms of five different radiomic features from the LV across centres and for different normalisation methods. Histograms and separated for healthy (brighter color) and HCM subjects (lighter color). Centres are presented in different colors and different rows following the ordering in Table 3. The first five rows correspond for methods without ComBat harmonisation, while the last five rows represent the same features with ComBat harmonisation. The first five columns are distributions of features extracted from original images, while the last five are features extracted after PLHM.

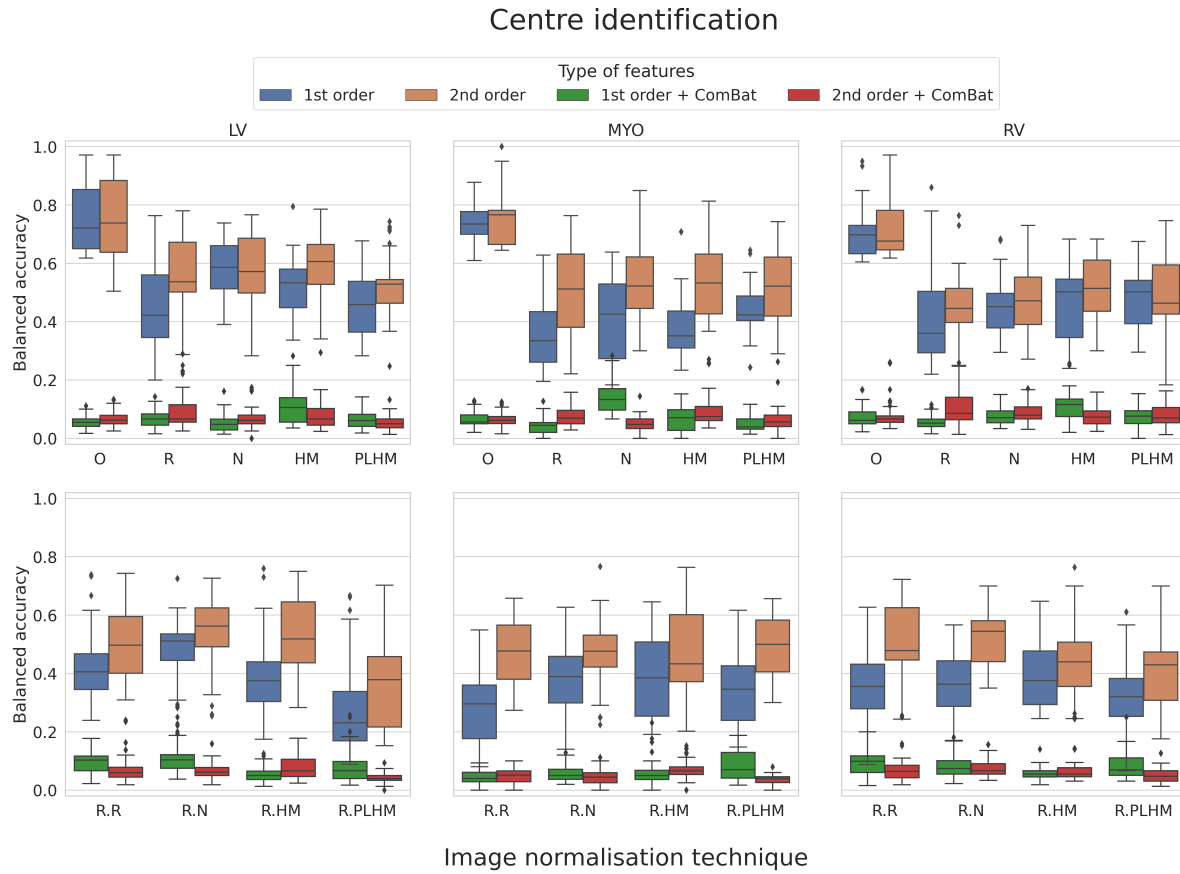


Figure S5. Balanced accuracy of random forest models when predicting the centre of origin of HCM subjects for first and second order texture features before and after the application of ComBat harmonisation. The row above corresponds to image preprocessing techniques applied at the whole image level, while in the row below they are applied at the ROI level. O: original images (without normalisation), R: image intensity recaling, N: image intensity normalisation, HM: histogram matching and PLHM: piecewise linear histogram matching. An “R.” in front of a method means that it is applied at ROI level.

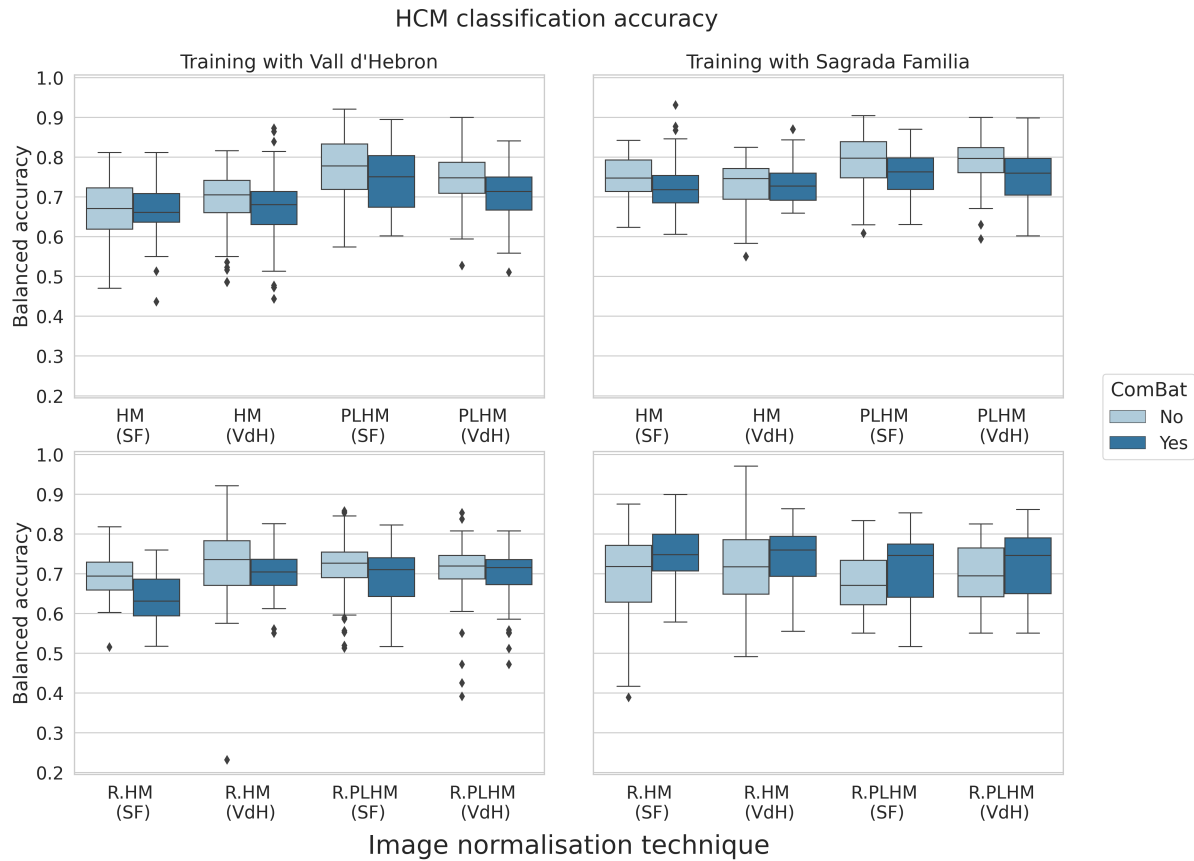


Figure S6. Comparison of balanced accuracy for models trained with two different reference templates from Vall d'Hebron (VdH) and Sagrada Familia (SF) on the HCM classification task. All models were trained with a combination of first and second order texture features from all ROIs. The first column corresponds to models trained with features extracted from Vall d'Hebron studies, while models in the second column were trained with features from Sagrada Familia studies. The row above corresponds to image preprocessing techniques applied at the whole image level, while in the row below they are applied at the ROI level. HCM: Hypertrophic cardiomyopathy, VdH: Vall d'Hebron, SF: Sagrada Familia, HM: histogram matching and PLHM: piecewise linear histogram matching. An "R." in front of a method means that it is applied at ROI level.

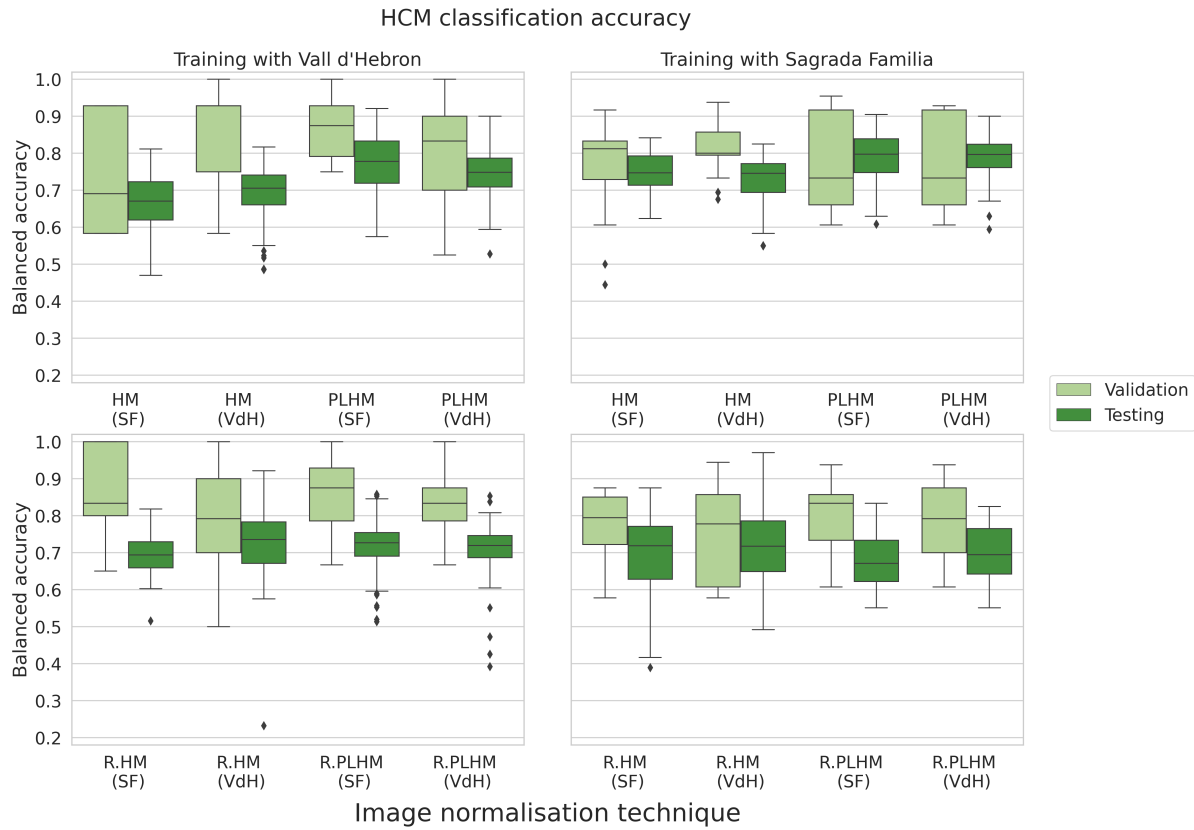


Figure S7. Comparison of validation (same domain) and testing (unseen centres) balanced accuracy for models trained with two different reference templates from Vall d’Hebron (VdH) and Sagrada Familia (SF) on the HCM classification task. Results are presented without ComBat harmonisation. All models were trained with a combination of first and second order texture features from all ROIs. The first column corresponds to models trained with features extracted from Vall d’Hebron studies, while models in the second column were trained with features from Sagrada Familia studies. The row above corresponds to image preprocessing techniques applied at the whole image level, while in the row below they are applied at the ROI level. HCM: Hypertrophic cardiomyopathy, O: original images (without normalisation), R: image intensity recaling, N: image intensity normalisation, HM: histogram matching and PLHM: piecewise linear histogram matching. An “R.” in front of a method means that it is applied at ROI level.