

**SUPPLEMENTAL TABLE S2.** Best bivariate radiomic models for Deauville Score prediction (whole cohort)

<b>Covariate 1</b>	<b>Covariate 2</b>	<b>mAUC*</b>	<b>SD<sup>†</sup> AUC</b>
Lesion_A.F_cm_2.5D.corr	Lesion_B.F_cm.joint.entr	0.782	0.0535
Lesion_A.F_cm.2.5Dmerged.corr	Lesion_B.F_cm.joint.entr	0.778	0.0792
Lesion_A.F_szm_2.5D.lze	Lesion_B.F_cm.joint.entr	0.773	0.1103
Lesion_A.F_rlm.glnu	Lesion_B.F_cm.joint.entr	0.772	0.1166
Lesion_A.F_rlm.lre	Lesion_B.F_cm_2.5D.corr	0.770	0.0811
Lesion_A.F_rlm.rlnu	Lesion_A.F_stat.uniformity	0.769	0.1395
TMTV <sup>‡</sup>	Lesion_A.F_rlm.lgre	0.763	0.0849
TMTV	Lesion_A.F_morph.surface	0.761	0.0979
TMTV	Lesion_B.F_cm_2.5D.joint.entr	0.756	0.0909
Lesion_A.F_cm_2.5D.corr	Lesion_A.F_rlm.2.5Dmerged.rlnu	0.752	0.0454
* Mean area under the ROC curve.			
† Standard deviation.			
‡ Total metabolic tumor volume.			