Supplemental Table *3*: Correlation of *TNFRSF9* methylation and mRNA expression with lymphocyte score and with regard to tumor tissue type. Spearman’s rank correlations of *TNFRSF9* methylation and mRNA expression with lymphocyte score in melanoma patients stratified according to the stage (all sites/mRNA: *N* = 328, all sites/methylation: *N* = 329, primary tumor/mRNA: *N* = 65, primary tumor/methylation: *N* = 66, regional lymph node metastases: *N* = 165, distant metastases: *N* = 35, regional cutaneous or subcutaneous tissue: *N* = 61, missing information: *N* = 2). Significant features are shown in boldface.

		All Sites		**Primary Tumors**		**Regional Lymph Nodes**		**Distant Metastases**		**Regional Cutaneous or Subcutaneous Tissues**	
Analyte	**CpG site no.**	**Spearman’s *ρ***	***P*-Value**	**Spearman’s *ρ***	***P*-Value**	**Spearman’s *ρ***	***P*-Value**	**Spearman’s *ρ***	***P*-Value**	**Spearman’s *ρ***	***P*-Value**
mRNA	NA	**0.51**	**<0.001**	0.20	0.12	**0.57**	**<0.001**	**0.52**	**0.001**	**0.38**	**0.003**
cg16839093	1	0.08	0.13	**0.36**	**0.003**	0.07	0.40	0.08	0.63	**-0.26**	**0.043**
cg27305704	2	-0.07	0.21	**0.26**	**0.033**	-0.08	0.29	-0.02	0.90	**-0.27**	**0.037**
cg18859763	3	-0.02	0.67	0.15	0.24	-0.06	0.43	-0.10	0.59	-0.07	0.57
cg07836592	4	-0.03	0.58	0.07	0.57	-0.03	0.74	0.24	0.17	-0.11	0.40
cg23959705	5	**0.14**	**0.012**	0.24	0.051	0.10	0.20	0.05	0.80	0.11	0.40
cg06956444	6	**-0.31**	**<0.001**	-0.15	0.24	**-0.31**	**<0.001**	**-0.37**	**0.031**	**-0.27**	**0.038**
cg14614416	7	**-0.22**	**<0.001**	-0.24	0.052	-0.14	0.070	-0.33	0.051	-0.14	0.28
cg18025409	8	-0.04	0.44	0.16	0.21	0.01	0.89	-0.20	0.25	-0.09	0.49
cg14153654	9	0.07	0.20	0.19	0.13	0.11	0.18	-0.15	0.38	-0.03	0.84
cg08840010	10	**-0.23**	**<0.001**	-0.04	0.77	**-020**	**0.012**	**-0.39**	**0.020**	**-0.29**	**0.024**
cg17123655	11	**-0.18**	**0.001**	-0.02	0.89	**-0.16**	**0.041**	-0.27	0.11	-0.22	0.091
cg16117781	12	**-0.23**	**<0.001**	0.06	0.63	**-0.31**	**<0.001**	**-0.34**	**0.044**	0.00	1.0

NA: Not Applicable