Supplementary Table 2. Associations between fusion status or *RAS* mutation status and DNA methylation subsets in RMS discovery and validation cohorts

	Fusion-positive Cluster				Fusion-negative Cluster			
Cohort	**Fusion**	**FP-1 (No./ total No., %)**	**FP-2 (No./ total No., %)**	**P Value**	**Mutations**	**FN-1 (No./ total No., %)**	**FN-2 (No./ total No., %)**	**P Value**
Discovery								
	PAX3-FOXO1	4/12 (33%)	8/9 (89%)	0.024	*RAS* family	0/5 (0%)	7/12 (58%)	0.044
	PAX7-FOXO1	8/12 (67%)	1/9 (11%)	0.024				
Validation								
	PAX3-FOXO1	0/7 (0%)	14/16 (88%)	<0.001	*RAS* family	2/12 (17%)	8/13 (62%)	0.041
	PAX7-FOXO1	4/7 (57%)	1/16 (6%)	0.017				