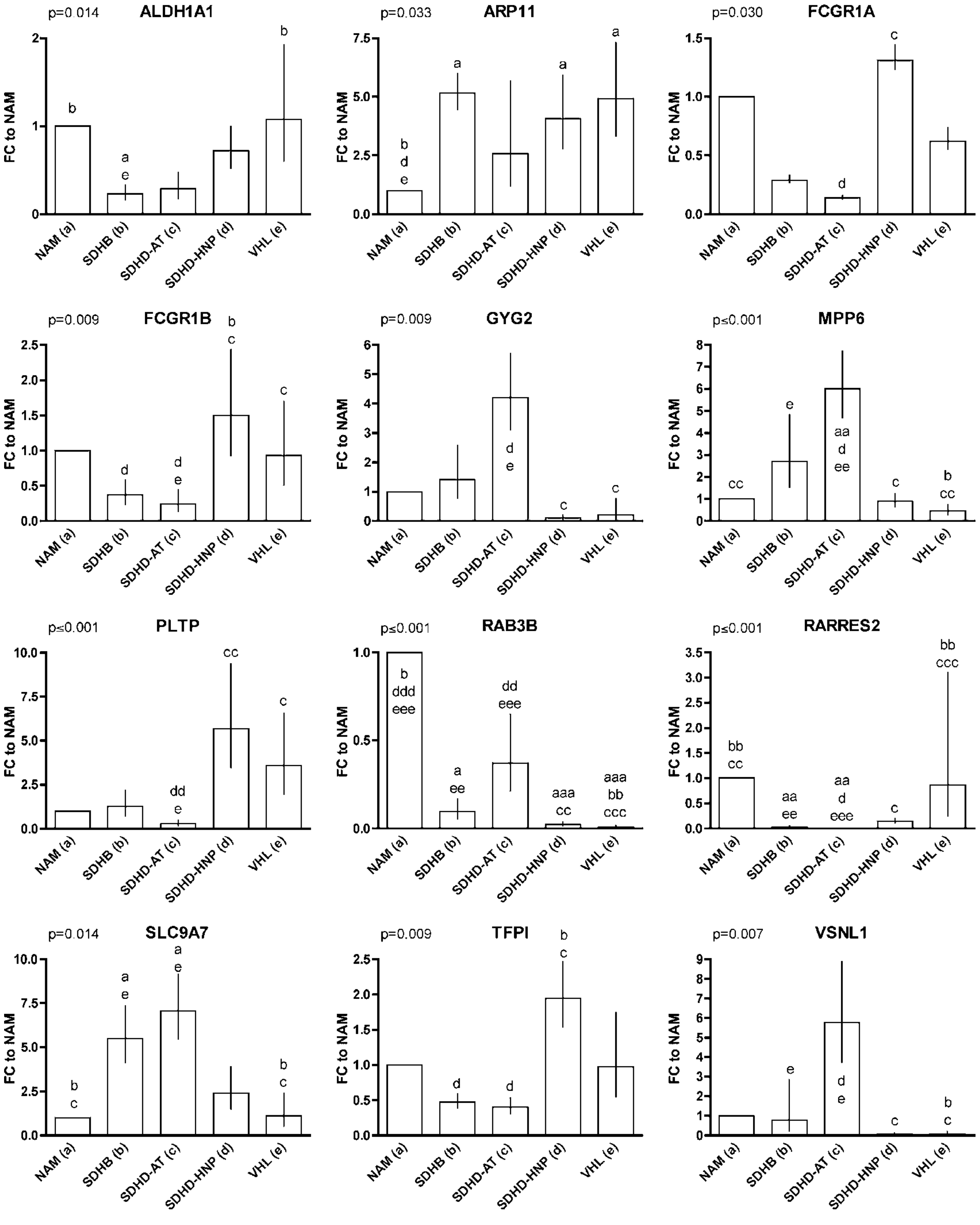

Figure W1. Relative expression of 12 genes of the minimum subset of 35 genes to NAM, which did not confirm the expression pattern predicted by the microarray. Overall significance has been evaluated for each gene by ANOVA (value given for each gene in the upper left corner). Significant differences between each group and (a) NAM, (b) SDHB, (c) SDHD-AT, (d) SDHD-HN, and (e) VHL are indicated above each applicable column. Replications of the letter specify the level of significance (xxx, $P < .001$; xx, $P < .01$; x, $P < .05$).

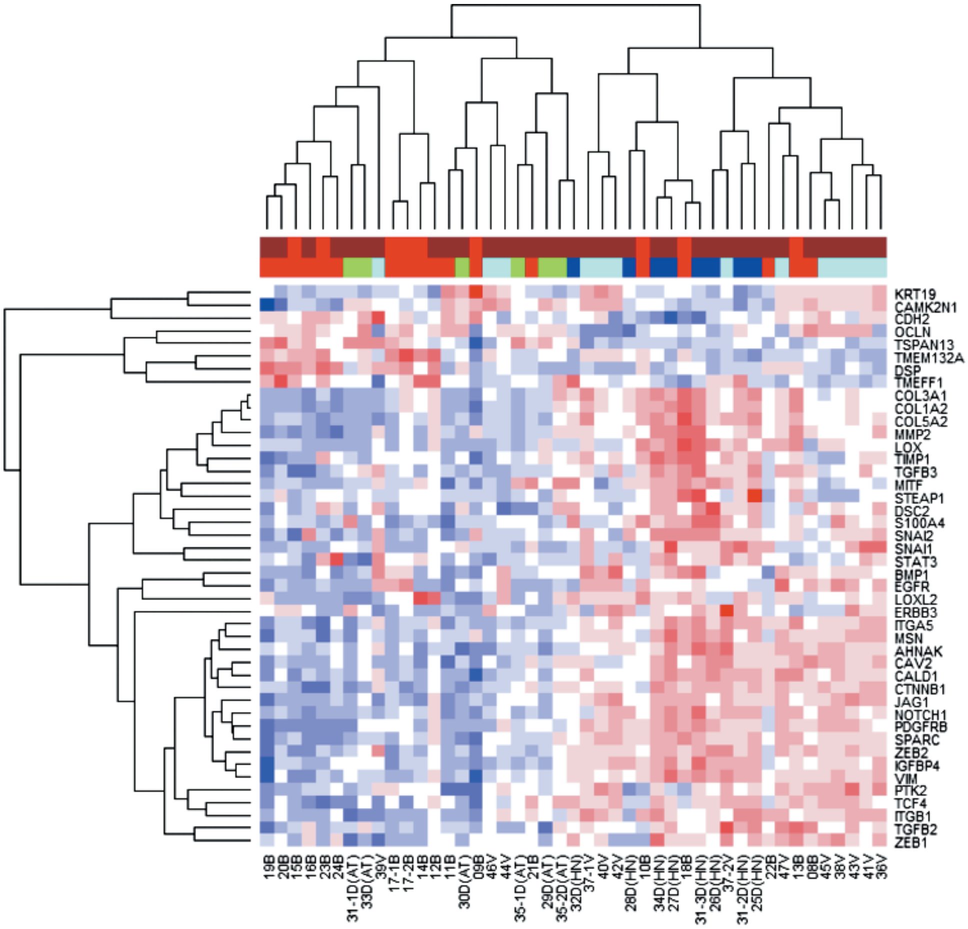

Figure W2. Unsupervised hierarchical clustering of EMT genes. Forty-four of 92 EMT genes provided by Loriot et al. [24] were significantly differentially expressed between the mutation/location types ($P \leq .05$) and led to separation of the samples into two main clusters. Color blocks above the heatmap indicate tumor behavior (top row) and mutation/location (bottom row). In the top row, brown and red indicate non-metastatic and metastatic samples, respectively. The colors in the second row indicate the following: red, SDHB; green, SDHD-AT; blue, SDHD-HN; cyan, VHL.

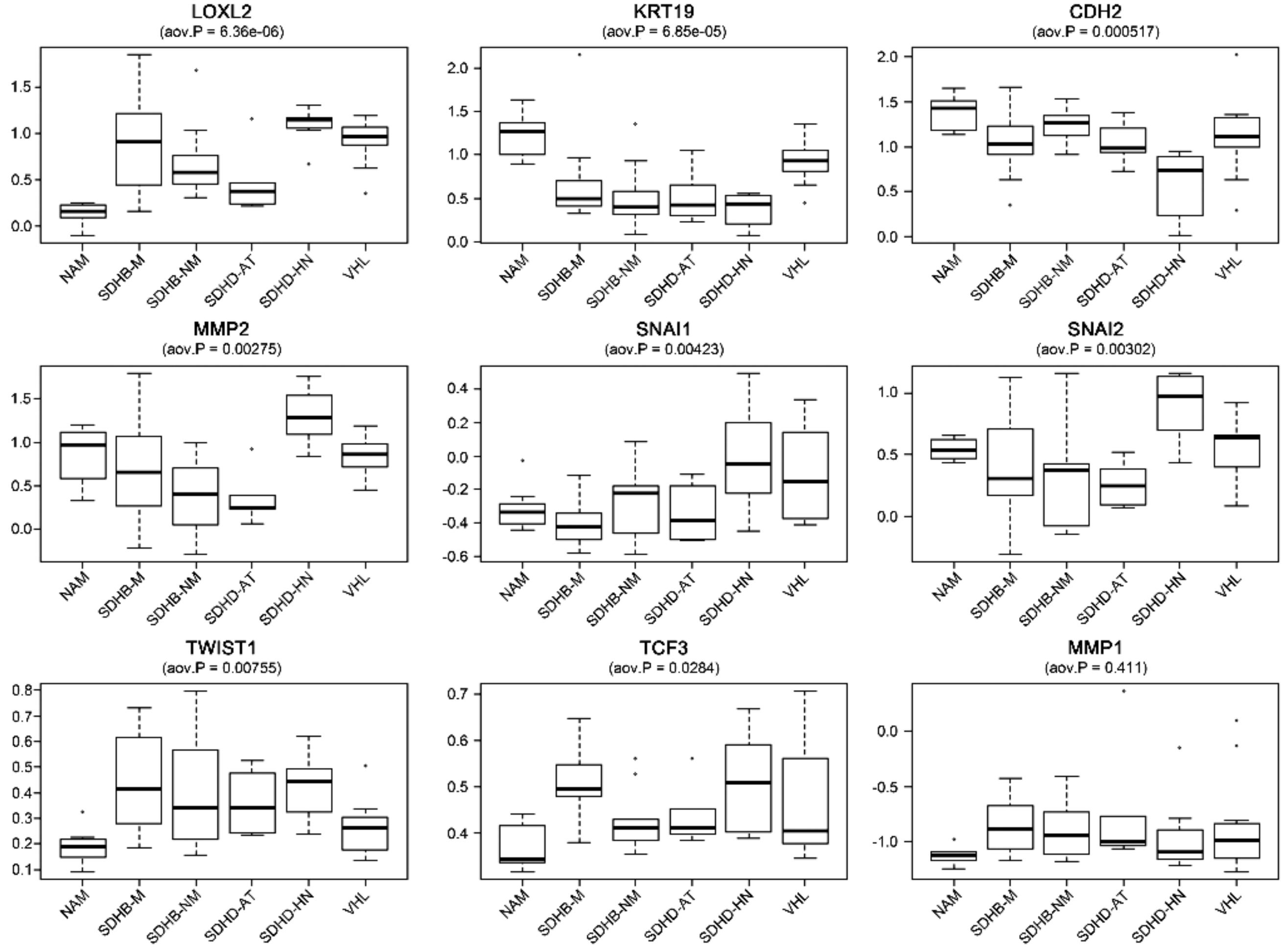

Figure W3. Boxplots of relative expression levels of selected EMT genes as determined by microarray of our sample set. Our sample set does not reproduce the findings of Loriot et al., reporting decreased expression of *CDH2* and *KRT19* and increased expression of *LOXL2*, *TWIST1*, *MMP1*, and *MMP2* in SDHB-metastatic samples compared to all non-metastatic samples [24]. Differential expression of *TWIST1*, *TCF3*, and *MMP1* between the groups lacked statistical significance by SAM at a threshold *P* value of .05. This may be because SDHB samples were not subgrouped into metastatic and non-metastatic previous to SAM. In agreement with Loriot et al., we did not observe elevated *SNAI1* and *SNAI2* mRNA expression in SDHB tumors. Nonetheless, the localization or level of the protein snail and slug may differ between metastatic and non-metastatic PHEOs/PGLs as has been previously reported [23,24].

Table W3. Classification and Cross-Validated Misclassification Error Rates for the Shrunken Centroid Model Including Subgrouping of SDHB Samples into Metastatic (n = 9) and Non-Metastatic (n = 9).

	SDHB–NM	SDHB-M	SDHD-AT	SDHD-HN	VHL	Class Error Rate
SDHB–NM	5	3	0	0	1	0.44
SDHB-M	3	4	0	1	1	0.56
SDHD-AT	1	0	5	0	0	0.17
SDHD-HN	0	0	0	8	0	0.00
VHL	0	0	1	2	10	0.23
Overall error rate						0.28