

Supplemental Material:

Figure 1S:

A heat-map of all the expression data (770 genes vs. 40 samples) is shown, which is based on supervised clustering. The columns represent the 40 samples with nevocellular nevi (NCN) shown under the green bars and Spitz nevi (SN) shown under the blue bars. The cohort includes a training set (orange bar) and a validation set (red bar). The training set consisted of 7 NCN, and 7 SN derived from the same patients to minimize interindividual genomic noise. The validation set consisted of 8 NCN and 18 SN. Higher expression levels are shown in red and lower expression levels are shown in blue color (yellow staining represents an intermediate expression level).

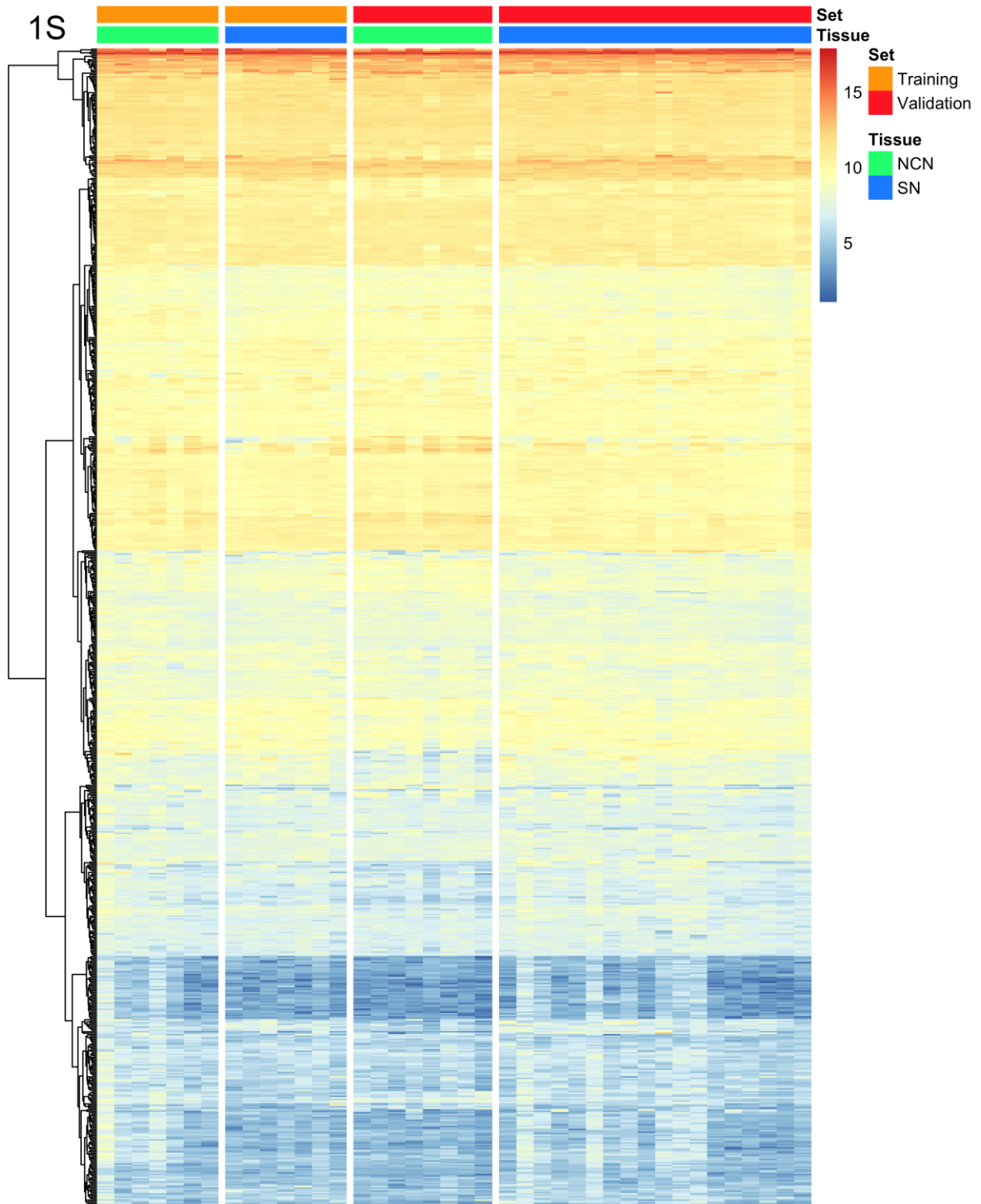


Figure 2S:

Manhattan plot based on the training data results. Data on chromosomal coordinates were from the University of Santa Cruz (UCSC) Genome Browser (version hg19). The validated genes are shown in green colored dots. The name of the most significant gene per chromosome is shown.

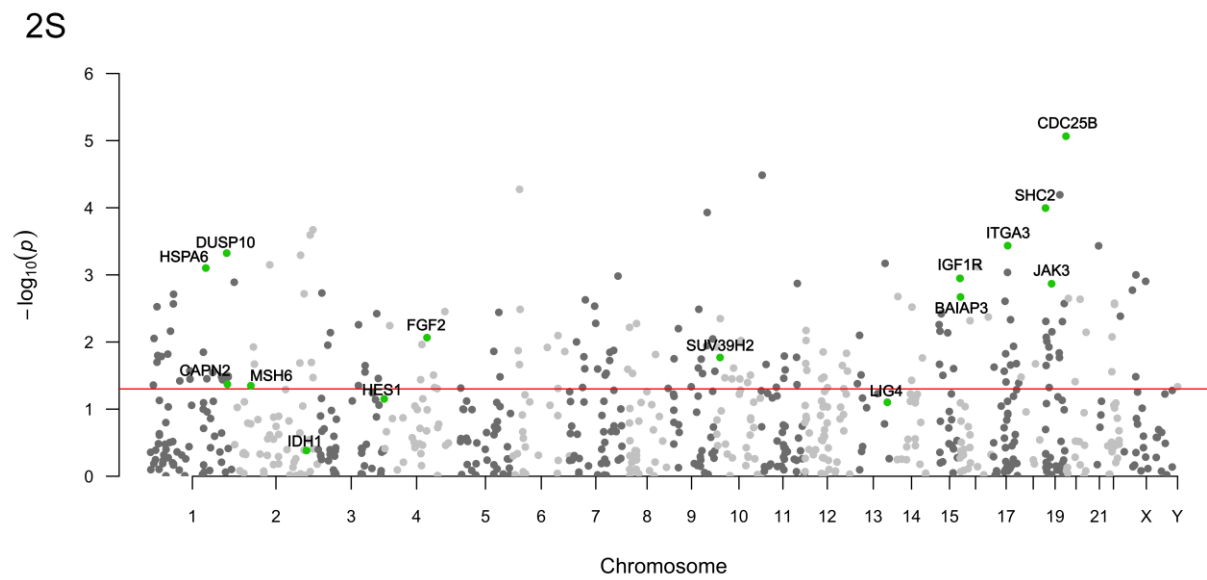


Table 1S: Characteristics of Identified Gene Pathways

The SN group corresponding genomic pathways as determined by the camera method. The upregulated gene sets in the table have a p-value < 0.05.

Pathway	# of genes	Direction	P-value	FDR Q-value	Description
Hallmark IL6 JAK STAT3 Signaling	33	Up-regulation	0.0000	0.0001	Immune category: IL6 STAT3 signaling during acute phase response
Hallmark Interferon Gamma Response	26	Up-regulation	0.0001	0.0012	Immune category: interferon gamma response
Hallmark Inflammatory Response	33	Up-regulation	0.0003	0.0040	Immune category: inflammation
KEGG Cytokine Cytokine Receptor Interaction	93	Up-regulation	0.0004	0.0183	Cytokine-cytokine receptor interaction
KEGG ECM Receptor Interaction	40	Up-regulation	0.0003	0.0183	Cellular differentiation category: ECM-receptor interaction
KEGG Hematopoietic Cell Lineage	31	Up-regulation	0.0005	0.0183	Immune category: Hematopoietic cell lineage
Reactome Integrin Cell Surface Interactions	30	Up-regulation	0.0001	0.0169	Cellular differentiation category: Integrin Cell Surface Interactions
Reactome NCAM1 Interactions	14	Up-regulation	0.0001	0.0197	Cellular differentiation category: NCAM-1 interactions
Reactome Metabolism of mRNA	8	Down-regulation	0.010	0.0547	Genes involved in metabolism of mRNA

Legend to Table 1S:

FDR = False Discovery Rate, # of genes = Number of Genes attributed to the Pathway