Supplementary Figure 1. Immunohistochemical analysis of GLAST protein expression in NF1 and sporadic PA. GLAST protein expression is shown for a representative positive NF1-PA (top left panel) and a representative negative NF1-PA (top right panel). GLAST protein expression is shown for a representative positive sporadic PA (bottom right panel) and a representative negative sporadic PA (bottom left panel). Scale bars = 50 μM.

Supplementary Figure 2. Hierarchical cluster analysis of PA specimens using genes differentially expressed in forebrain and hindbrain. **(A)** Hierarchical clustering of developmental marker transcripts involved in neocortical (forebrain) versus cerebellar (hindbrain) development. The genes involved in forebrain development (GO ID-GO:0030900) and hindbrain development (GO ID-GO:0030902) were obtained from AmiGO[9]. The probe sets that represent these genes in our microarray data sets were obtained using the Function Express algorithm[10] (Siteman Cancer Center Bioinformatics Core). Gene expression data was filtered, z-score normalized (standard deviation of 1 across all samples for each gene), and the resultant 160 probe sets were subjected to hierarchical cluster analysis as described in the Material and Methods section. The dendrogram on the top displays the relationship of the samples based on their pattern of gene expression. On the bottom of the dendrogram is a "heat map" representing gene expression, with each of the 10 supratentorial PA (marked by red rectangle) and 27 posterior fossa PA (samples not marked by red rectangle) represented in a column, each probe set represented as a horizontal line, and the relative expression of any one gene in any one sample in continuous color scale from low (yellow) to high (dark blue)

[9] http://www.godatabase.org
[10] http://bioinformatics.wustl.edu/webTools/FunctionExpressClient.do

expression. This class of developmentally-regulated transcripts themselves could not distinguish PAs by site of origin. **(B)** Expression data for all normal human tissues available as Human U133A GeneChip microarray datasets (gcRMA-condensed) from the GeneAtlas project at the Genomics Institute of the Novartis Research Foundation[11] was obtained to identify genes that exhibit either differential gene expression in normal human brain (neocortex) versus cerebellum. The median expression value for each available probe set over all the tissues was calculated and the probe sets that had either 10 fold higher or 10 fold lower values in whole brain (cortex) or cerebellum compared to the calculated median were selected. The PA microarray data set was used to obtain the expression data for each of these probe sets. Gene expression data was filtered, z-score normalized (standard deviation of 1 across all samples for each gene), and the resultant 856 probe sets were subjected to hierarchical cluster analysis as described in the Material and Methods section. Hierarchical clustering was performed using this set of transcripts to determine whether genes that are either upregulated or downregulated in neocortex (forebrain) versus cerebellum (hindbrain) would distinguish supratentorial from posterior fossa PAs. The dendrogram on the top displays the relationship of the samples based on their pattern of gene expression. On the bottom of the dendrogram is a "heat map" representing gene expression, with each of the 10 supratentorial PA (marked by red rectangle) and 27 posterior fossa PA (samples not marked by red rectangle) represented in a column, each probe set represented as a horizontal line, and the relative expression of any one gene in any one sample in continuous color scale from low (yellow) to high (dark blue) expression. The results demonstrate that this class of transcripts themselves could also not distinguish PAs by site of origin.

[11] http://wombat.gnf.org/index.html