Step 1)   For all human genes, identify their co-expression trends.
            Previous experiments show that genes positively correlated in their
            co-expression levels (Figure S1), tend to be related by function,
            phenotype, and disease relevance. Not all genes have expression data

Step 2)   For genes of unknown function, identify the 20 genes with the strongest
            co-expression correlation (Figure S2 - only 3 genes shown here for simplicity)

Step 3)   To identify what the co-expressed genes have in common, text-mining
            software is used (IRIDESCENT) to analyze what diseases, phenotypes,
            chemicals and other genes appear in the literature with each of the co-expressed
            genes. These are the inferred associations for the unknown gene. (Figure S3)

Step 4)   After all genes are analyzed, the list is shortened to include only those that
            are inferred to be associated with gliomas, are plasma-membrane bound, and
            have commercial antibodies available. Experiments are then conducted to see
            if these proteins are differentially present in gliomas.

Figure S1: For every experiment where 2 genes, alox5ap and itgb2, are expressed, this is quantified by Pearson's
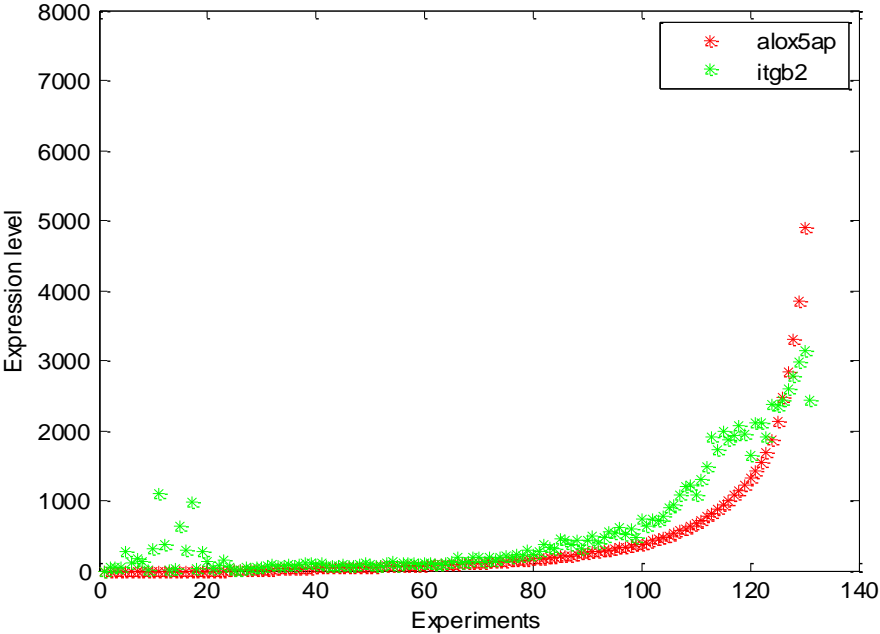

Figure S2: For genes of unknown function, a set of co-expressed genes are analyzed in their place
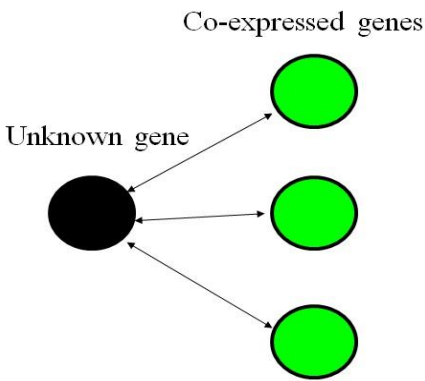

Figure S3: The set of co-expressed genes is searched for reported commonalities in the peer-reviewed literature