Low-grade (WHO I-II) gliomas represent the most frequent primary tumors of the central nervous system in children. They often have a good prognosis following total resection, however they can create many neurological complications due to mass effect, and may be difficult to resect depending on anatomic location. MicroRNAs have been identified as molecular regulators of protein expression that can repress multiple mRNAs concurrently through base pairing. Specific microRNAs are often suppressed during early cell differentiation to promote the expression of mitogenic proteins that are associated with the maintenance of specific stem cell types, a mechanism for growth and survival that is frequently exploited in cancer cells. Identification of these microRNA signatures present in low grade glioma and glioneuronal tumor sub-types could therefore lead to a wealth of candidate biomarkers. We used NanoString technology to analyze the expression levels of 800 microRNAs in nine low-grade glial and glioneuronal tumor subtypes (n = 45) using formalin-fixed paraffin-embedded tissue. We then generated hierarchical clusters following evaluation via significant analysis of microarrays (SAMs). Hierarchical clustering separated tumors from non-neoplastic brain. When looking at individual tumors, subependymal giant cell astrocytomas (SEGA) clustered sharply together, consistent with a unique microRNA expression signature in this tuberous sclerosis associated tumor subtype, compared to other low grade glial and glioneuronal tumors. Candidate microRNAs were validated using qRT-PCR. In SEGAs, microRNAs miR-219-5p, miR-129-2-3p, miR-338-3p, miR-487b, miR-885-5p, and miR-323-3p were significantly down-regulated by more than 15 fold as compared to normal brain and were also significantly down-regulated as compared to other low grade gliomas. In summary, altered microRNA expression is a feature of low grade glial and glioneuronal tumors. MicroRNA profiling may therefore be useful in subtyping these tumors and to provide important insights into their biology.