ABSTRACT
Neuroblastoma is the most common extra-cranial cancer of childhood. Genome-wide expression profiles of solid tumor biopsies have been associated with prognosis and hold promise for guiding therapy. Bone marrow aspirates potentially provide an important source of information, for example, when it is important to capture variation over time or between anatomical sites. Unlike solid tumors, however, neuroblastoma cells may be represented in the bone marrow by less than 1% of cells so isolation is essential. We show that patient-specific neuroblastoma gene expression profiles can be obtained from bone marrow aspirates using FACS ($p < 0.002$) method. Patient-specific variation is highly correlated between these two methods method ($rho = 0.75$, $p = 0.15$). These profiles reflect variation between patients that has been associated with a biological process (deregulation of Wnt/beta-catenin signaling) and clinical outcome (high-risk, non-MYCN-amplified neuroblastoma tumors). These results suggest a novel neuroblastoma target: Melanoma antigen family A, 4 (MAGEA4) expression level is the most significantly differentially expressed gene across patients (independent of method) ($p = 10e-5$).