Glioblastoma is a devastating disease and despite extensive treatment, overall survival (OS) for these patients remains poor. Yet, a small proportion of glioblastoma patients present relatively long survival over 3 years, but the underlying molecular background separating these long-term survivors (LTS) from short-term survivors (STS) are still insufficiently understood. The purpose of this study was to identify independent prognostic variables for survival by examining molecular profiles of LTS and STS in a clinically well characterized cohort of glioblastoma patients. The cohort consisted of 93 patients diagnosed with primary glioblastoma and treated with radiation therapy plus concomitant and adjuvant chemotherapy as well as bevacizumab administered in the first-line setting or at time of recurrence. Among these, 14 STS (OS >36 months) were identified, which were all confirmed being IDHwt. For all patients, RNA had previously been purified from microdissected tumor tissue of the diagnostic specimen and analyzed for expression levels by a customized NanoString platform. This covered 800 genes related to glioblastoma cancer hallmarks, including regulation of angiogenesis and immune response. When comparing expression of these genes in LTS vs. STS using a Welsh’s t-test, 14 candidate genes ended up significant (P < 0.05).