Supplemental Figure 1: *MGMT* promoter methylation and response to temozolomide in GBMs. In the entire cohort, 106 GBMs had known *MGMT* promoter methylation status and were treated with temozolomide (TMZ) as part of the postsurgical adjuvant regimen. 33 (31.1%) were negative for methylation, 29 (27.4%) had low-level methylation, and 44 (41.5%) had high-level methylation. No significant survival differences were seen (*P* = 0.89). Likewise, *MGMT* promoter methylation was not an independent prognostic factor on multivariate Cox regression analysis using the same variables as in the upper portion of Table 3 (hazard ratio = 0.92; 95% CI = 0.61—1.4; *P* = 0.71; N = 140).
Supplemental Figure 2: Schematic of region covered by *EGFR* FISH probe. The FISH probe used in this study (see Methods) covers the entire *EGFR* gene on chromosome 7p12, extending toward the centromere of chromosome 7. The closest nearby gene, *LANCL2*, is not covered. (Schematic adapted from Abbott Molecular; gene lengths and intervals derived from UCSD Genome Browser.)
Supplemental Figure 3: No difference in EGFR-amplified GBM survival stratified by LANCL2 co-amplification. 169 GBMs with EGFR amplification (log2 ratio > 1.0) were retrieved from The Cancer Genome Atlas (TCGA) repository and stratified according to whether LANCL2 was co-amplified (N = 96) or not (N = 73), as determined by Affymetrix Genome-Wide Human SNP Array 6.0. $P = 0.94$. 
Supplemental Figure 4: GBMs from The Cancer Genome Atlas dataset stratified by SNP

**EGFR copy ratio.** 372 GBMs were retrieved from TCGA with survival stratified by degree of **EGFR** copy gain as determined by Affymetrix Genome-Wide Human SNP Array 6.0. Overall $P = 0.01$, $*P < 0.05$ versus both < 1.0 and 3.0+; $P = 0.10$ between 1.0-2.9 and 3.0+. N = 203 for non-amplified cases (< 1.0), N = 44 for 1.0-2.9, and N = 125 for 3.0+. 