

## **Supplemental legends**

**Supplemental table 1. Quantification of amplification and overexpression of SEC61 $\gamma$  and EGFR in GBMs by Q-PCR.**

**Supplemental figure 1. Identification of consensus SEC61 $\gamma$  and EGFR co-amplification by Illumina hap550K in GBMs.** Each line corresponds to an individual GBM sample. The light grey bars represent the gain of copy number. The dark grey bars represent high copy-number gains. The arrow indicates the drill-down SNP view of the particular sample at the corresponding loci. Dots represent the LogR ratio call value of an individual SNP. The black bar represents the call value for that segment as determined by Nexus rank segmentation algorithm. The two vertical lines encapsulate the consensus region of copy number gains revealed from 35 GBMs. Interstitial deletions of EGFR are shown in the first two samples.

**Supplemental figure 2. There is no association of SEC61 $\gamma$  amplification and the survival of GBM patients.** We examined the survival of 43 GBM patients between ages 51 and 80. Kaplan–Meier survival curves were plotted, and the survival distributions were compared with the use of the Mantel–Cox log-rank test and the Wilcoxon test.

**Supplemental figure 3. SEC61 $\gamma$  is overexpressed in GBM xenografts.** Western blotting shows that SEC61 $\gamma$  is overexpressed in six of eight GBM xenografts. N, normal brain; T, GBM xenografts.

**Supplemental figure 4. SEC61 $\gamma$  is expressed at low levels in secondary GBMs.** SEC61 $\gamma$  expression was measured by Q-PCR in three secondary GBMs without *EGFR* amplifications.

**Supplemental figure 5. Human GeneChip array U133A heatmap shows SEC61 $\alpha$ , SEC61 $\beta$ , and SEC61 $\gamma$  expression in normal brain tissue and GBMs.** To visualize the increased expression of SEC61 $\alpha$ , SEC61 $\beta$ , and SEC61 $\gamma$  in cancer samples, the internally normalized expression value was further normalized against the mean expression value of the normal tissues (N), which showed the fold of increase over normal tissues. Hierarchical clustering was then performed on the samples. The tree and heat map were drawn by using dChip.

**Supplemental figure 6. SEC61 $\gamma$  is induced by ER stress.** H80 cells were treated with tunicamycin for the indicated number of hours, and the expression of ATF4, ATF6, Xbp1, EGFR, cyclin D, SEC61 $\alpha$ , SEC61 $\beta$ , SEC61 $\gamma$ , GRP78, and CHOP was measured by Q-PCR.

**Supplemental figure 7. SEC61 $\gamma$  is required for EGFR/AKT cell survival signaling.** HeLa cells were cultured under serum starvation. Cells were transfected with scrambled siRNA or SEC61 $\gamma$  siRNA, treated with 0 or 50 ng/mL EGF. SEC61 $\gamma$  siRNA treatment inhibited EGF-induced EGFR and AKT phosphorylation, but had little effect on ERK phosphorylation.