Supplementary Figures

Figure S1. The methylation status of the identified CpGs was analyzed by bisulfite sequencing of the *KLK6* proximal promoter region in normal and breast tumor tissue specimens, as well as in the following breast cancer cell lines: 21PT primary breast cancer cell line that highly overexpresses *KLK6* and in the *KLK6*-nonexpressing BT-474, MDA-MB-436 and ZR-75-1 metastatic breast cancer cell lines. For analysis of tissue specimens, formalin fixed paraffin-embedded breast carcinomas were obtained from patients diagnosed with breast cancer. Patients were admitted at the Department of Medical Oncology, University General Hospital of Heraklion, Heraklion, Crete, Greece. Clinicopathological features for all five patients are available (not shown). Specimens derived from reduction mammoplasties (histologically cancer-free) were used as normal breast tissue controls (N1-N3). Tumor samples (T1-T5) were collected at diagnosis prior to chemotherapy, all patients gave their informed consent and the study was approved by the Institute’s Ethical and Scientific Committees. Tissue sections of 10 μm containing >80% of tumor cells were cut and used for DNA extraction. Genomic DNA was isolated with High Pure PCR Template Preparation (Roche, Germany) and its concentration was determined in the Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies, USA). Subsequently, 1 μg of extracted DNA was modified with sodium bisulfite using EZ DNA Methylation Gold (ZYMO Research Co., Orange, CA), according to manufacturer’s instructions, PCR-amplified and sequenced as described in Materials and Methods. Each row represents one sequenced allele. Each circle represents a CpG dinucleotide: methylated (●) or unmethylated (○). Numbering was based on GenBank™ sequence AY804248.
**Figure S2.** KLK6 inhibits tumor formation *in vivo*. *Top*, parental, mock- and *KLK6*-transfected cells were orthotopically implanted bilaterally into the mammary fat pad of 6-week old SCID mice. Mice were examined on alternate days for the presence of palpable tumors and tumor sizes were measured. Tumors were allowed to grow, then, mice were sacrificed and photographed. *Bottom*, tumor growth rates for parental, mock, and *KLK6*-transfected MDA-MB-231 xenografts in SCID mice. Tumor volumes were calculated using the formula: ½*(height)*(width)*(length).