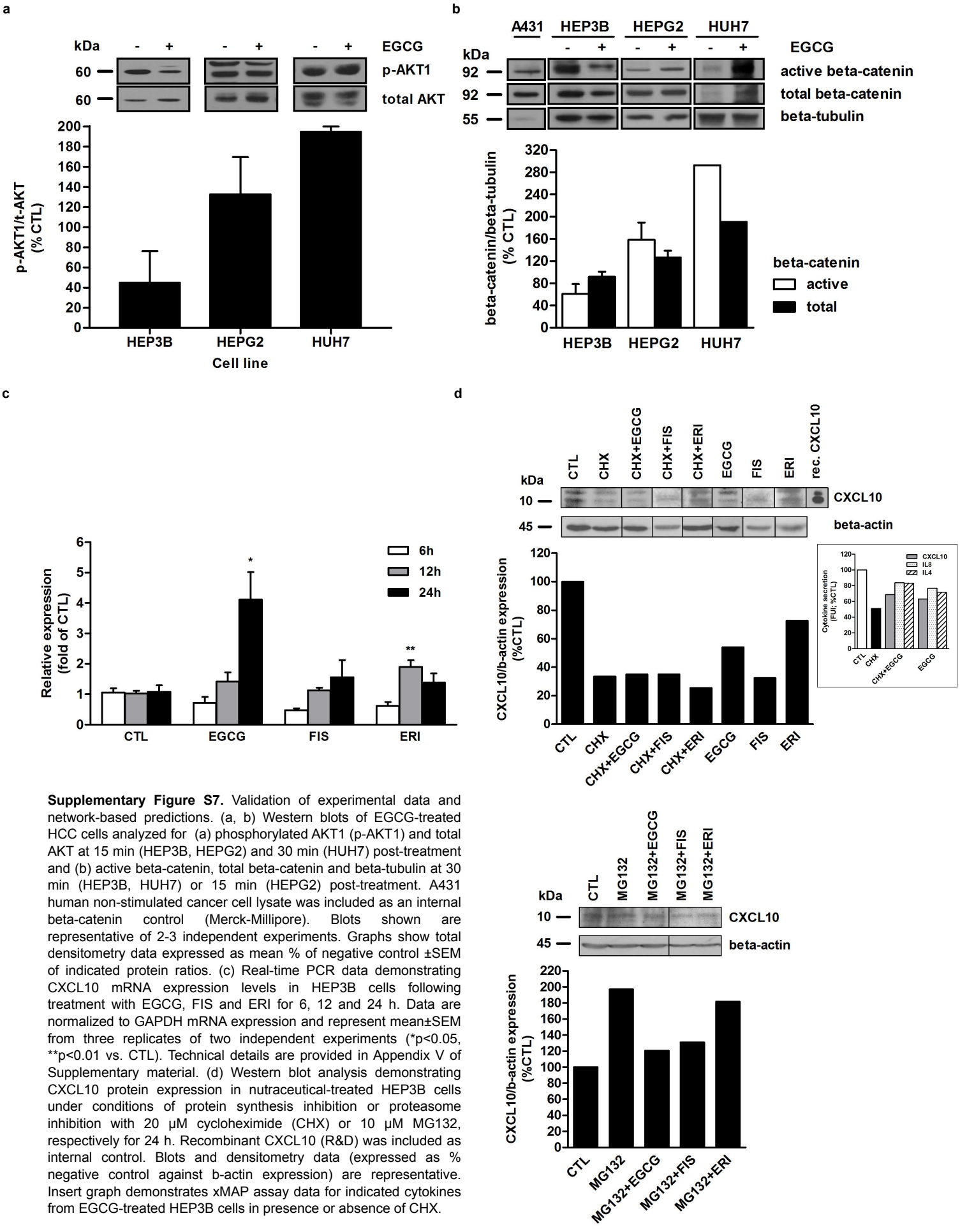

Supplementary Figure S7. Validation of experimental data and network-based predictions. (a, b) Western blots of EGCG-treated HCC cells analyzed for (a) phosphorylated AKT1 (p-AKT1) and total AKT at 15 min (HEP3B, HEPG2) and 30 min (HUH7) post-treatment and (b) active beta-catenin, total beta-catenin and beta-tubulin at 30 min (HEP3B, HUH7) or 15 min (HEPG2) post-treatment. A431 human non-stimulated cancer cell lysate was included as an internal beta-catenin control (Merck-Millipore). Blots shown are representative of 2-3 independent experiments. Graphs show total densitometry data expressed as mean % of negative control ±SEM of indicated protein ratios. (c) Real-time PCR data demonstrating CXCL10 mRNA expression levels in HEP3B cells following treatment with EGCG, FIS and ERI for 6, 12 and 24 h. Data are normalized to GAPDH mRNA expression and represent mean±SEM from three replicates of two independent experiments (*p<0.05, **p<0.01 vs. CTL). Technical details are provided in Appendix V of Supplementary material. (d) Western blot analysis demonstrating CXCL10 protein expression in nutraceutical-treated HEP3B cells under conditions of protein synthesis inhibition or proteasome inhibition with 20 μM cycloheximide (CHX) or 10 μM MG132, respectively for 24 h. Recombinant CXCL10 (R&D) was included as internal control. Blots and densitometry data (expressed as % negative control against b-actin expression) are representative. Insert graph demonstrates xMAP assay data for indicated cytokines from EGCG-treated HEP3B cells in presence or absence of CHX.