HCC-001_Blood

KU-cHCC-001

KU-cHCC-001-Kidney

KU-cHCC-002

KU-cHCC-003

KU-cHCC-004

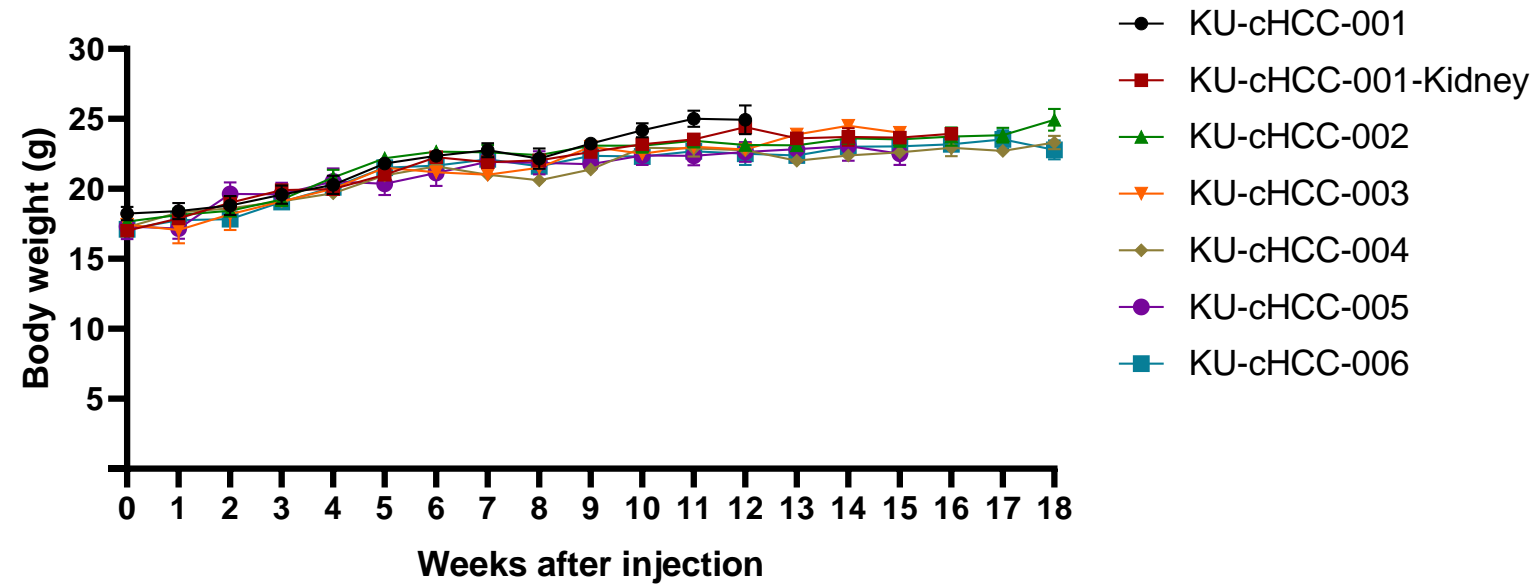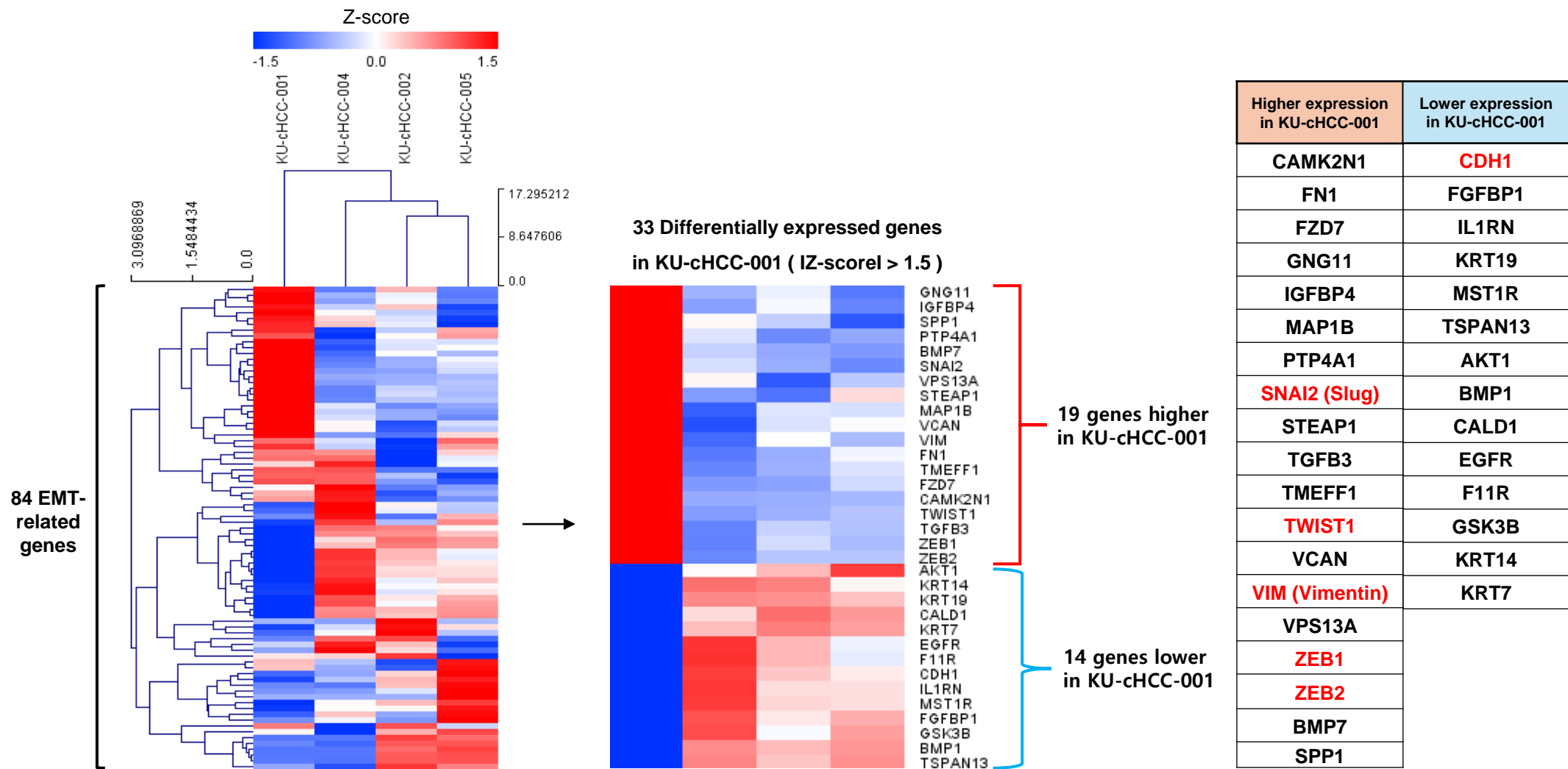

KU-cHCC-005

KU-cHCC-006

Supplementary Figure 1. STR analysis to authenticate cell lines. All cell lines showed canine-specific loci in a heterozygous pattern depending on the patients from which they were derived. The profile conformed that KU-CTCC-001 and KU-CTCC-001-Kideny were originated from the same patient without cross-contamination. HCC-001-Blood represents blood sample derived from patient HCC-001.

Supplementary Figure 2. Body weight of xenograft mice after inoculation of canine HCC cell lines. Tumor growth at the injection site was not observed in the mice inoculated with KU-cHCC-002, KU-cHCC-003, KU-cHCC-004, KU-cHCC-005 and KU-cHCC-006. Mice with no tumor growth were euthanized at 16 or 18 weeks after injection. No significant body weight loss was observed. Error bars represent the standard error of the mean (SEM).

Supplementary Figure 3. Hierarchical clustering heatmap analysis of 84 EMT-related genes using RNA-seq data of control cells (KU-cHCC-001, KU-cHCC-002, KU-cHCC-004 and KU-cHCC-005). For the identification of 84 EMT-related genes, a list of genes previously implicated in EMT* was employed. Z-score of each gene was calculated using normalized data (Log2(FPKM+Geometric Normalized RC+1)). Hierarchical clustering heatmap analysis was conducted by Euclidean distance metrics, using MeV software* (2) (ver. 4.9.0). Differentially expressed genes (|Z-score| > 1.5) of KU-cHCC-001 were listed (right).