Supplemental Figure 1

A) Workflow of mitochondrial sequencing data interpretation and mt-variant frequencies.

B) Representative images of Sanger sequencing.
Supplemental Figure 2

A) Methylation variance in cirrhotic liver (CL), preneoplastic lesions (LGDN, HGDN) and cancerous lesions (eHCC, pHCC) of each patient (1-8) demonstrated by the beta-value density. B) Localization of hyper- and hypomethylated DMGR in CpG island regions and gene regions expressed as percentage. C) Cluster separability plots defined by iCluster analyses.
Supplemental Figure 3

A) Venn diagrams of Signature 1-3 and differentially expressed genes (DEG) of eHCC and pHCC. B) Signaling pathway regulation during sequential evolution of HCC analyzed by ingenuity pathway analyses based 162 identified genes by the overlap of DMGR and DEG. Significance of each pathway was determined by scoring system provided by Ingenuity Pathway Analysis tool.
Supplemental Figure 4

A-C) Kaplan-Meyer-Analyses based on the specific transcriptome profile of Panel 1 in A., Panel 2 in B. and Panel 3 in C. in tumor tissue using public available data from authentic human HCC of 139 patients from Lee et al. cohort (24). Survival analyses were performed by CRAN package survival und survminer (version 0.4.3) using log rank tests. D-F) Kaplan-Meyer-Analyses based on the specific transcriptome profile of Panel 1 in D., Panel 2 in E. and Panel 3 in F. in tumor tissue using public available data from authentic human of the TCGA-LIHC cohort using the GEPIA.2 tool.
Supplemental Figure 5

A) Top Network Association of Epi-driver Panel (n=23) analyzed by ingenuity pathway analyses. B) Network of Epi-Driver including pathway regulations analyzed and designed by ingenuity pathway analyses.
Supplemental Figure 6

A) Expression status of STRN4 in different tumor etiologies based on expression in the TCGA database using “DiffExp” module of TIMER-Tool. B) Impact on overall survival of STRN4 for HCC patients analyzed by survival analyses with a group cut-off at the median using GEPIA-Tool.
Supplemental Figure 7

A. Expression of STRN4 in Hep3B cell lines in non-treated (control), si(Scramble) and three different si(STRN4) 1-3 treated cells on mRNA level. B. Expression of STRN4 in Hep3B cell lines in non-treated (control), si(Scramble) and si(STRN4) 3 treated cells on protein level. C. Colony formation of Hep3B cell lines in non-treated (control), si(Scramble) and si(STRN4) treated cells; one-way anova analyses: *p-value <0.05; **p-value <0.01; ***p<0.001.
Supplemental Table 1: Mt-variants associated with cancer
Supplemental Table 2: Mt-variants detected by Mt-sequencing analyses
Supplemental Table 3: Signaling pathway analyses of DEG during hepatocarcinogenesis according to Figure 2A.
Supplemental Table 4: Top 100 genes of methylation and RNA-Seq-data for i-clustering
Supplemental Table 5: Signaling pathway analyses of DMGR during hepatocarcinogenesis according to Figure 3.
Supplemental Table 6: DMGR signatures of early (1), late (2) hepatocarcinogenesis and of HCC progression (3).
Supplemental Table 7: Panel annotation of identified DMGR with expression changes in eHCC and/or pHCC.
Supplemental Table 8: Top network analyses and molecular and cellular functions of 162 gene signature.
Supplemental Table 9: Results on DMGR validation analyses.
Supplemental Table 10: Validation of differential expression analyses of DMGR in HCC.
Supplemental Table 11: Association to overall survival of DMGR using the GEPIA tool.
Supplemental Table 12: Multivariate analyses using the TIMER2.0 Gen_Surv module.
Supplemental Table 13: Clinico-pathological data of patients (validation cohort Mainz)
Supplemental Table 14: Large and small liver cell changes
Supplemental Table 15: Sanger validation of mitochondrial variants
Supplemental Table 16: Antibodies
| Sample | Patient | Allele | Mutation | Count | Coverage | Coding region change | Amino acid change | Site Cosmic_v70 | Histology Cosmic_v70 | Somatic status Cosmic_v70 | Sample source Cosmic_v70 | Tumour origin Cosmic_v70 |
|--------|---------|--------|----------|-------|----------|----------------------|-----------------|-----------------|----------------------|--------------------------|--------------------------|--------------------------|
| T8     | P3      | 4216   | SNV      | T     | C        | MT-ND1               | MT-ND1          | ENST00000361390:c.910T>C | Yes                  | Y304H, Y304H             | endometrium;kidney, endometrium;kidney | clear_cell_renal_cell_carcinoma/endometrioid_carcinoma |
| T9     | P3      | 4216   | SNV      | T     | C        | MT-ND1               | MT-ND1          | ENST00000361390:c.910T>C | Yes                  | Y304H, Y304H             | endometrium;kidney, endometrium;kidney | clear_cell_renal_cell_carcinoma/endometrioid_carcinoma |
| T24    | P2      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T25    | P5      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T26    | P8      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T1     | P1      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T4     | P2      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T8     | P3      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T10    | P4      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T12    | P5      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T20    | P6      | 7028   | SNV      | C     | T        | MT-CO1               | MT-CO1          | ENST00000361624:c.1125C>T | No                   | A375A, A375A             | breast, breast | carcinoma, carcinoma |
| T22 | P7 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T3  | P1 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T13 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T17 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T19 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T2  | P1 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T6  | P2 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T7  | P2 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T9  | P3 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T11 | P4 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T14 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T16 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T18 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T28 | P8 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T5  | P2 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T15 | P5 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No A375A, A375A | breast, breast | carcinoma, carcinoma |
| T21 | P6 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No | A375A, A375A | breast, breast | carcinoma, carcinoma |
| T23 | P7 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No | A375A, A375A | breast, breast | carcinoma, carcinoma |
| T27 | P8 | 7028 | SNV | C   | T   | MT-CO1 | MT-CO1 | protein_coding | ENST00000361624:c.1125C>T | No | A375A, A375A | breast, breast | carcinoma, carcinoma |
| T20 | P6 | 8200 | SNV | T   | C   | MT-CO2 | MT-CO2 | protein_coding | ENST00000361739:c.615T>C | No | S205S | kidney | carcinoma/clear_cell_renal_cell_carcinoma |
| T3  | P1 | 8200 | SNV | T   | C   | MT-CO2 | MT-CO2 | protein_coding | ENST00000361739:c.615T>C | No | S205S | kidney | carcinoma/clear_cell_renal_cell_carcinoma |
| T2  | P1 | 8200 | SNV | T   | C   | MT-CO2 | MT-CO2 | protein_coding | ENST00000361739:c.615T>C | No | S205S | kidney | carcinoma/clear_cell_renal_cell_carcinoma |
| T21 | P6 | 8200 | SNV | T   | C   | MT-CO2 | MT-CO2 | protein_coding | ENST00000361739:c.615T>C | No | S205S | kidney | carcinoma/clear_cell_renal_cell_carcinoma |
| T24 | P2 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T26 | P8 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T4  | P2 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T8  | P3 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T10 | P4 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T20 | P6 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T3  | P1 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T2  | P1 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T   | P  | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G |  | ENST00000361899:c.175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
|-----|----|------|-----|-----|-----|---------|---------|----------------|--------|---|----------------------------|-----|-------------|----------------|---------------------|
| T7  | P2 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T9  | P3 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T11 | P4 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T28 | P8 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T5  | P2 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T21 | P6 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T27 | P8 | 8701 | SNV | A   | G   | MT-ATP6 | MT-ATP6 | protein_coding | 175A>G | Yes | T59A, T59A | breast, breast | carcinoma, carcinoma |
| T22 | P7 | 9123 | SNV | G   | A   | MT-ATP6 | MT-ATP6 | protein_coding | 597G>A | No  | L199L, L199L | endometrium, endometrium | carcinoma/endometrioid_carcinoma, carcinoma/endometrioid_carcinoma |
| T23 | P7 | 9123 | SNV | G   | A   | MT-ATP6 | MT-ATP6 | protein_coding | 597G>A | No  | L199L, L199L | endometrium, endometrium | carcinoma/endometrioid_carcinoma, carcinoma/endometrioid_carcinoma |
| T19 | P5 | 10197| SNV | G   | A   | MT-ND3 | MT-ND3 | protein_coding | 139G>A | Yes | A47T | breast | carcinoma |
| T24 | P2 | 11719| SNV | G   | A   | MT-ND4 | MT-ND4 | protein_coding | 960G>A | No  | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T25 | P5 | 11719| SNV | G   | A   | MT-ND4 | MT-ND4 | protein_coding | 960G>A | No  | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T | P | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
|---|---|-------|-----|-----|--------|--------|--------------------------|----|---------------|------------------|-------------------|
| T26 | P8 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T1  | P1 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T4  | P2 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T8  | P3 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T10 | P4 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T12 | P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T20 | P6 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T22 | P7 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T3  | P1 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T13 | P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T17 | P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T19 | P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T2  | P1 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T6  | P2 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T7  | P2 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T9  | P3 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381:c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T  | P  | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | gene/variant          | NM_001290.1 | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
|----|----|-------|-----|-----|--------|--------|------------------------|--------------|----|---------------|-----------------|---------------------|
| T11| P4 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T14| P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T16| P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T18| P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T28| P8 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T5 | P2 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T15| P5 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T21| P6 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T23| P7 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T27| P8 | 11719 | SNV | G/A | MT-ND4 | MT-ND4 | ENST00000361381: c.960G>A | No | G320G, G320G | breast, breast | carcinoma, carcinoma |
| T24| P2 | 12705 | SNV | C/T | MT-ND5 | MT-ND5 | ENST00000361567: c.369C>T | No | I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T26| P8 | 12705 | SNV | C/T | MT-ND5 | MT-ND5 | ENST00000361567: c.369C>T | No | I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T1 | P1 | 12705 | SNV | C/T | MT-ND5 | MT-ND5 | ENST00000361567: c.369C>T | No | I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T4 | P2 | 12705 | SNV | C/T | MT-ND5 | MT-ND5 | ENST00000361567: c.369C>T | No | I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T8 | P3 | 12705 | SNV | C/T | MT-ND5 | MT-ND5 | ENST00000361567: c.369C>T | No | I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T  | P  | Library   | Location | Type         | Gene Chromosome | Position | Coding | Tumor Type                                      |
|----|----|-----------|----------|--------------|----------------|----------|--------|-----------------------------------------------|
| T10| P4 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T20| P6 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T3 | P1 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T2 | P1 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T6 | P2 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T7 | P2 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T9 | P3 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T11| P4 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T28| P8 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T5 | P2 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T21| P6 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T27| P8 | 12705     | SNV C T  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361567:c.369C>T | No I123I | endometrium | carcinoma/endometrioid_carcinoma |
| T20| P6 | 14569     | SNV G A  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361681:c.105C>T | No S35S, S35S | kidney, kidney | carcinoma/clear_cell_renal_cell_carcinoma, kidney, kidney |
| T3 | P1 | 14569     | SNV G A  | MT-ND5 MT-ND5 | protein_coding  | ENST00000361681:c.105C>T | No S35S, S35S | kidney, kidney | carcinoma/clear_cell_renal_cell_carcinoma, kidney, kidney |
| T2   | P1   | 14569 | SNV | G   | A   | MT-ND6 | MT-ND6 | protein_coding | ENST00000361681:c.105C>T | No   | S35S, S35S | kidney, kidney | carcinoma/clear_cell_renal_cell_carcinoma, carcinoma/clear_cell_renal_cell_carcinoma |
|------|------|-------|-----|-----|-----|--------|--------|----------------|--------------------------|-------|------------|---------------|------------------------------------------------|
| T21  | P6   | 14569 | SNV | G   | A   | MT-ND6 | MT-ND6 | protein_coding | ENST00000361681:c.105C>T | No   | S35S, S35S | kidney, kidney | carcinoma/clear_cell_renal_cell_carcinoma, carcinoma/clear_cell_renal_cell_carcinoma |
| T10  | P4   | 15045 | SNV | G   | A   | MT-CYB | MT-CYB | protein_coding | ENST00000361789:c.299G>A | Yes  | R100Q, R100Q | kidney, kidney | carcinoma/clear_cell_renal_cell_carcinoma, carcinoma/clear_cell_renal_cell_carcinoma |
| T20  | P6   | 15323 | SNV | G   | A   | MT-CYB | MT-CYB | protein_coding | ENST00000361789:c.577G>A | Yes  | A193T, A193T | breast, breast | carcinoma, carcinoma |
| T3   | P1   | 15323 | SNV | G   | A   | MT-CYB | MT-CYB | protein_coding | ENST00000361789:c.577G>A | Yes  | A193T, A193T | breast, breast | carcinoma, carcinoma |
| T2   | P1   | 15323 | SNV | G   | A   | MT-CYB | MT-CYB | protein_coding | ENST00000361789:c.577G>A | Yes  | A193T, A193T | breast, breast | carcinoma, carcinoma |
| T21  | P6   | 15323 | SNV | G   | A   | MT-CYB | MT-CYB | protein_coding | ENST00000361789:c.577G>A | Yes  | A193T, A193T | breast, breast | carcinoma, carcinoma |
## Supplemental Table 2

| Patient | Sample ID | Diagnosis | MT-Region | Mutation Type | Ref. Allele | Mut. Allele | Frequency | Gene Cards | Coding region change | Amino acid change | Non-synonym |
|---------|-----------|-----------|-----------|---------------|-------------|------------|-----------|------------|----------------------|------------------|-------------|
| 1       | T3        | HGDN      | 11866^11867 | Insertion     | -           | C          | 5,162622612 | MT-ND4     | ENST00000361381.c.1107_1108insC | ENSP00000354961: p.Thr372fs | Yes          |
| 1       | T2        | LGDN      | 12418     | Deletion      | A           | -          | 6,059390048 | MT-ND5     | ENST00000361567.c.82delA | ENSP00000354813: p.Asns30fs | Yes          |
| 1       | T2        | LGDN      | 15050     | Replacement   | C           | AGA        | 7,404844291 | MT-CYB     | ENST00000361789.c.304delCinsAGA | ENSP00000354554: p.Leu102fs | Yes          |
| 1       | T2        | LGDN      | 13958     | SNV           | G           | A          | 9,875690608 | MT-ND5     | ENST00000361567.c.1622G>A | ENSP00000354813: p.Gly541Asp | Yes          |
| 1       | T3        | HGDN      | 310       | SNV           | T           | C          | 14,6031746  | MT-ND5     | ENST00000361381.c.1107_1108insC | ENSP00000354632: p.Thr59Ala | Yes          |
| 1       | T2        | LGDN      | 899       | SNV           | G           | A          | 18,18471338 | MT-RNR1    | -                     | -                | -            |
| 1       | T1        | CL        | 302^303   | Insertion     | -           | CC         | 59,15492958 | MT-RNR2    | -                     | -                | -            |
| 1       | T3        | HGDN      | 8701      | SNV           | A           | G          | 78,91804457 | MT-ATP6    | ENST00000361899.c.175A>G | ENSP00000354632: p.Thr59Ala | Yes          |
| 1       | T2        | LGDN      | 8701      | SNV           | A           | G          | 79,06643541 | MT-ATP6    | ENST00000361899.c.175A>G | ENSP00000354632: p.Thr59Ala | Yes          |
| 1       | T2        | LGDN      | 2706      | SNV           | A           | G          | 94,03892944 | MT-RNR2    | -                     | -                | -            |
| 1       | T3        | HGDN      | 2706      | SNV           | A           | G          | 94,47300771 | MT-ND5     | ENST00000361567.c.487G>A | ENSP00000354813: p.Asp163Asn | Yes          |
| 1       | T1        | CL        | 2706      | SNV           | A           | G          | 95,0902387  | MT-RNR2    | -                     | -                | -            |
| 2       | T4        | CL        | 15050     | Replacement   | C           | AGA        | 5,151086764 | MT-CYB     | ENST00000361789.c.304delCinsAGA | ENSP00000354554: p.Leu102fs | Yes          |
| 2       | T4        | CL        | 12823     | SNV           | G           | A          | 6,327160494 | MT-ND5     | ENST00000361567.c.487G>A | ENSP00000354813: p.Asp163Asn | Yes          |
| 2       | T5        | HGDN      | 1210      | SNV           | T           | C          | 6,388459557 | MT-ND5     | ENST00000361681.c.156T>C | ENSP00000354813: p.Asp163Asn | Yes          |
| 2       | T4        | CL        | 57        | Deletion      | T           | -          | 6,89117553  | MT-RNR1    | -                     | -                | -            |
| 2       | T5        | HGDN      | 310       | SNV           | T           | C          | 10,17964072 | MT-RNR2    | -                     | -                | -            |
| 2       | T4        | CL        | 14518     | SNV           | A           | G          | 16,37931034 | MT-ND6     | ENST00000361681.c.156T>C | ENSP00000354813: p.Asp163Asn | No           |
| T | HGDN | 14518 | SNV | A   | G   | 18,19990055 | MT-ND6 | ENST00000361681:c.156T>C | No |
| T | HGDN | 14518 | SNV | A   | G   | 39,30276982 | MT-ND6 | ENST00000361681:c.156T>C | No |
| T | HGDN | 16145 | SNV | G   | A   | 52,05681609 | -      | -                        | -  |
| T | eHCC | 310..316 | Deletion | TCCCCC G | - | 62,93577982 | -      | -                        | -  |
| T | eHCC | 319 | SNV | T   | C   | 65,81196581 | -      | -                        | -  |
| T | HGDN | 302^303 | Insertion | - C | 70,81174439 | -      | -                        | -  |
| T | CL   | 302^303 | Insertion | - C | 71,24183007 | -      | -                        | -  |
| T | pHCC | 302^303 | Insertion | - C | 76,27737226 | -      | -                        | -  |
| T | pHCC | 8701 | SNV | A   | G   | 77,19760129 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| T | HGDN | 302^303 | Insertion | - C | 77,42663657 | -      | -                        | -  |
| T | eHCC | 8701 | SNV | A   | G   | 79,35022355 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| T | HGDN | 8701 | SNV | A   | G   | 79,42515864 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| T | CL   | 8701 | SNV | A   | G   | 84,45665188 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| T | HGDN | 8701 | SNV | A   | G   | 84,84073002 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| T | CL   | 2706 | SNV | A   | G   | 93,96306818 | MT-RNR2 | -                        | -  |
| T | eHCC | 2706 | SNV | A   | G   | 93,96507003 | MT-RNR2 | -                        | -  |
| T | HGDN | 2706 | SNV | A   | G   | 94,31937724 | MT-RNR2 | -                        | -  |
| T | CL   | 2706 | SNV | A   | G   | 94,34803375 | MT-RNR2 | -                        | -  |
| T | pHCC | 2706 | SNV | A   | G   | 94,95242036 | MT-RNR2 | -                        | -  |
| T | HGDN | 12236 | SNV | G   | A   | 5,226174791 | MT-TS2 | -                        | -  |
| T | CL   | 16189^16 190 | Insertion | - C | 6,731813246 | -      | -                        | -  |
| T | CL   | 15050 | Replacement | C AGA | 7,775951448 | MT-CYB | ENST00000361789:c.304delCinsAGA | ENSP00000354554: p.Leu102fs | Yes |
| Chr | Sample | Nucleotide | Type | Position | Chromosome | Description | Reference | Genotype | Mutation |  |
|-----|--------|------------|------|----------|------------|-------------|-----------|----------|----------|----------|
| 3   | T10 HGDN 310 | SNV | T | C | 11,2804878 | MT-ND2 | ENST00000361453:c.931G>A | ENSP00000355046: p.Val311Met | Yes |
| 3   | T10 HGDN 5400 | SNV | G | A | 25,01781896 | MT-ND2 | ENST00000361453:c.931G>A | ENSP00000355046: p.Val311Met | Yes |
| 3   | T10 HGDN 8701 | SNV | A | G | 79,20731291 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 3   | T10 HGDN 8701 | Insertion | - | C | 93,7133724 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 3   | T10 HGDN 2706 | SNV | A | G | 93,9107903 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 3   | T9 CL 8701 | SNV | A | G | 81,46943541 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 3   | T9 CL 16183^16 184 | Insertion | - | C | 93,7133724 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 3   | T9 CL 2706 | SNV | A | G | 94,6 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 3   | T10 HGDN 16189^16 190 | Insertion | - | C | 94,94640123 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T12 HGDN 70 | SNV | G | A | 5,289421158 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T11 CL 15045 | SNV | G | A | 7,130305488 | MT-CYB | ENST00000361789:c.299G>A | ENSP00000354554: p.Arg100Gln | Yes |
| 4   | T11 CL 1608 | SNV | G | A | 8,428093645 | MT-TV | ENSP00000354554: p.Arg100Gln | Yes |
| 4   | T11 CL 310^311 | Insertion | - | C | 12,3388582 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T11 CL 302 | Replacement | A | CC | 18,19354839 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T11 CL 302 | SNV | A | C | 30,83870968 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T12 HGDN 302 | Replacement | A | CC | 32,3943662 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T11 CL 8701 | SNV | A | G | 80,13850416 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T12 HGDN 8701 | SNV | A | G | 81,78076554 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T12 HGDN 310 | SNV | T | C | 84,47488584 | MT-ATP6 | ENST00000361899:c.175A>G | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T12 HGDN 2706 | SNV | A | G | 93,62859363 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T11 CL 2706 | SNV | A | G | 93,71618083 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 4   | T11 CL 310 | SNV | T | C | 93,94736842 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 5   | T14 LGDN 16129 | SNV | G | A | 5,438666137 | MT-RNR2 | ENSP00000354632: p.Thr59Ala | Yes |
| 5 | T16 | LGDN | 6582 | SNV | G   | A   | 5,882352941 | MT-CO1 | ENST00000361624:c.679G>A | ENSP00000354499:p.Asp227Asn | Yes |
| 5 | T19 | HGDN | 3778 | SNV | G   | A   | 5,941389 | MT-ND1 | ENST00000361390:c.472G>A | ENSP00000354687:p.Gly158Ser | Yes |
| 5 | T16 | LGDN | 3550 | SNV | G   | A   | 6,092368162 | MT-ND1 | ENST00000361390:c.244G>A | ENSP00000354687:p.Ala82Thr | Yes |
| 5 | T13 | CL   |     | SNV | G   | A   | 7,976961843 | MT-ATP6 | ENST00000361390:c.376G>A | ENSP00000354632:p.Ala126Thr | Yes |
| 5 | T21 | pHCC | 14944 | SNV | C   | A   | 8,037773142 | MT-CYB | ENST00000361789:c.198C>A | ENSP00000354554:p.Ile66Met | Yes |
| 5 | T18 | HGDN | 4418 | SNV | T   | C   | 8,090768682 | MT-TM | - | - | |
| 5 | T14 | LGDN | 4037 | SNV | G   | A   | 10,37924152 | MT-ND1 | ENST00000361390:c.731G>A | ENSP00000354687:p.Gly244Glu | Yes |
| 5 | T17 | HGDN | 16108 | SNV | C   | T   | 17,65292553 | MT-RNR1 | - | - | |
| 5 | T13 | CL   | 1045 | SNV | G   | A   | 16,82058047 | MT-RNR1 | - | - | |
| 5 | T14 | LGDN | 302^303 | Insertion | C   | T   | 17,65292553 | MT-RNR1 | - | - | |
| 5 | T16 | LGDN | 10197 | SNV | G   | A   | 67,53975678 | MT-ND3 | ENST00000361227:c.139G>A | ENSP00000355206:p.Ala47Thr | Yes |
| 5 | T13 | CL   | 302^303 | Insertion | C   | T   | 78,37078652 | MT-RNR1 | - | - | |
| 5 | T16 | LGDN | 302^303 | Insertion | C   | T   | 79,66101695 | MT-RNR1 | - | - | |
| 5 | T19 | HGDN | 302^303 | Insertion | C   | T   | 79,85074627 | MT-RNR1 | - | - | |
| 5 | T14 | LGDN | 302^303 | Insertion | C   | T   | 82,90909091 | MT-RNR1 | - | - | |
| 5 | T17 | HGDN | 310^311 | Insertion | C   | T   | 89,20863309 | MT-RNR1 | - | - | |
| 5 | T16 | LGDN | 514..515 | Deletion | CA   | -   | 93,22916667 | MT-RNR2 | - | - | |
| 5 | T17 | HGDN | 2706 | SNV | A   | G   | 93,42530085 | MT-RNR2 | - | - | |
| 5 | T19 | HGDN | 2706 | SNV | A   | G   | 93,57208448 | MT-RNR2 | - | - | |
| 5 | T16 | LGDN | 2706 | SNV | A   | G   | 93,65689572 | MT-RNR2 | - | - | |
| 5 | T21 | pHCC | 2706 | SNV | A   | G   | 93,76884422 | MT-RNR2 | - | - | |
| 5 | T18 | HGDN | 2706 | SNV | A   | G   | 93,83378016 | MT-RNR2 | - | - | |
| 5 | T15 | LGDN | 2706 | SNV | A   | G   | 93,83378016 | MT-RNR2 | - | - | |
| 5 | T19 | HGDN | 514..515 | Deletion | CA   | -   | 94,1362916 | MT-RNR2 | - | - | |
| 5 | T14 | LGDN | 2706 | SNV | A   | G   | 94,19525066 | MT-RNR2 | - | - | |
| 5 | T17 | HGDN | 514..515 | Deletion | CA   | -   | 94,22799423 | MT-RNR2 | - | - |
|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
| 5 | T13 | CL | 2706 | SNV | A | G | 94,84213063 | MT-RNR2 |
| 5 | T20 | eHCC | 2706 | SNV | A | G | 95,02913953 | MT-RNR2 |
| 5 | T13 | CL | 514..515 | Deletion | CA | - | 95,05178366 |
| 5 | T20 | eHCC | 514..515 | Deletion | CA | - | 95,12635379 |
| 5 | T18 | HGDN | 514..515 | Deletion | CA | - | 95,52572707 |
| 6 | T23 | eHCC | 15050 | Replacement | C | AGA | 6,896551724 | MT-CYB |
| 6 | T22 | CL | 203 | SNV | G | A | 13,93293475 |
| 6 | T22 | CL | 5579 | SNV | G | A | 20,53571429 | MT-TW |
| 6 | T22 | CL | 15650 | SNV | G | A | 21,20945134 | MT-CYB |
| 6 | T22 | CL | 514..515 | Deletion | CA | - | 39,3043783 |
| 6 | T23 | eHCC | 16519 | SNV | T | C | 46,65948276 |
| 6 | T22 | CL | 8701 | SNV | A | G | 76,13513837 | MT-ATP6 |
| 6 | T23 | eHCC | 302\^303 | Insertion | - | C | 81,73374613 |
| 6 | T23 | eHCC | 8701 | SNV | A | G | 81,85952501 | MT-ATP6 |
| 6 | T23 | eHCC | 2706 | SNV | A | G | 94,26917511 | MT-RNR2 |
| 6 | T22 | CL | 2706 | SNV | A | G | 94,96717724 | MT-RNR2 |
| 7 | T24 | CL | 516..517 | Replacement | CA | T | 5,667276051 |
| 7 | T24 | CL | 3779 | SNV | G | A | 6,036121673 | MT-ND1 |
| 7 | T25 | eHCC | 16180..16181 | Deletion | AA | - | 7,122507123 |
| 7 | T24 | CL | 16180..16181 | Deletion | AA | - | 7,931316435 |
| 7 | T24 | CL | 72..73 | MNV | TA | CG | 13,10904872 |
| 7 | T25 | eHCC | 16182..16183 | MNV | AA | CC | 14,12103746 |
| 7 | T24 | CL | 16182..16183 | MNV | AA | CC | 18,96974652 |
| 7 | T24  | CL    | 13965 | SNV | T  | C  | 22,76803119 | MT-ND5 | ENST00000361567:c.1629T>C | No |
|---|------|-------|-------|-----|----|----|---------------|--------|--------------------------|----|
| 7 | T24  | CL    | 16183 | SNV | A  | C  | 66,14881439 |        |                          |    |
| 7 | T25  | eHCC  | 16180 | Deletion | A | -  | 67,14150047 |        |                          |    |
| 7 | T24  | CL    | 16180 | Deletion | A | -  | 68,35650041 |        |                          |    |
| 7 | T25  | eHCC  | 8271..8279 | Deletion | ACCCC | CTCT | -  68.75 |        |                          |    |
| 7 | T25  | eHCC  | 302^303 | Insertion | -  | C | 72,77486911 |        |                          |    |
| 7 | T25  | eHCC  | 16183 | SNV | A  | C  | 73,9673391 |        |                          |    |
| 7 | T24  | CL    | 73    | SNV | A  | G  | 86,75174014 |        |                          |    |
| 7 | T25  | eHCC  | 2706  | SNV | A  | G  | 92,45614035 | MT-RNR2 |                          |    |
| 7 | T24  | CL    | 514..515 | Deletion | CA | -  | 92,73743017 |        |                          |    |
| 7 | T25  | eHCC  | 514..515 | Deletion | CA | -  | 93,19470699 |        |                          |    |
| 7 | T25  | eHCC  | 16189 | SNV | T  | C  | 95,44419134 |        |                          |    |
| 7 | T25  | eHCC  | 16154 | SNV | T  | C  | 96,41185647 |        |                          |    |
| 8 | T26  | HGDN  | 15170 | SNV | G  | A  | 6,635273973 | MT-CYB | ENST00000361789:c.424G>A | Yes|
| 8 | T26  | HGDN  | 8903  | SNV | C  | T  | 23,03688617 | MT-ATP6 | ENST00000361899:c.377C>T | Yes|
| 8 | T26  | HGDN  | 4109  | SNV | C  | T  | 37,29903537 | MT-ND1  | ENST00000361390:c.803C>T | Yes|
| 8 | T28  | pHCC  | 302^303 | Insertion | -  | C | 73,29192547 |        |                          |    |
| 8 | T28  | pHCC  | 8701  | SNV | A  | G  | 75,65775169 | MT-ATP6 | ENST00000361899:c.175A>G | Yes|
| 8 | T27  | eHCC  | 8701  | SNV | A  | G  | 77,11769813 | MT-ATP6 | ENST00000361899:c.175A>G | Yes|
| 8 | T26  | HGDN  | 8701  | SNV | A  | G  | 77,7721583 | MT-ATP6 | ENST00000361899:c.175A>G | Yes|
| 8 | T28  | pHCC  | 2706  | SNV | A  | G  | 93,55503237 | MT-RNR2 |                          |    |
| 8 | T27  | eHCC  | 2706  | SNV | A  | G  | 94,61031408 | MT-RNR2 |                          |    |
| 8 | T26  | HGDN  | 2706  | SNV | A  | G  | 95,11726259 | MT-RNR2 |                          |    |
| Rank | Gene ID | Gene Symbol | Rank | Gene ID | Gene Symbol |
|------|---------|-------------|------|---------|-------------|
| 1    | cg04773745 | <NA> | 1    | ENSG00000138778 | CENPE |
| 2    | cg04341210 | C13orf36 | 2    | ENSG000000270728 | RP4-657E11.10 |
| 3    | cg10916429 | ZNF609 | 3    | ENSG00000152760 | TCTEX1D1 |
| 4    | cg05766510 | PTPRN2 | 4    | ENSG000000183054 | RGPD6 |
| 5    | cg18620300 | FBXL7 | 5    | ENSG000000189334 | S100A14 |
| 6    | cg02514000 | WBCR17 | 6    | ENSG000000232956 | SNHG15 |
| 7    | cg04227077 | <NA> | 7    | ENSG000000107807 | TLX1 |
| 8    | cg05765580 | NOS2 | 8    | ENSG000000237978 | RP11-385J1.2 |
| 9    | cg27430369 | <NA> | 9    | ENSG000000204832 | ST8SIA6-AS1 |
| 10   | cg04515534 | RADIL | 10   | ENSG000000107187 | LHX3 |
| 11   | cg00949578 | C18orf62 | 11   | ENSG000000232233 | RP11-573D15.2 |
| 12   | cg08611472 | LOC285696 | 12   | ENSG000000124564 | SLC17A3 |
| 13   | cg17836612 | LGALS3BP | 13   | ENSG000000126838 | PZP |
| 14   | cg06720232 | SDK1 | 14   | ENSG000000009694 | TENM1 |
| 15   | cg12680822 | NCRNA00029 | 15   | ENSG000000196367 | TRRAP |
| 16   | cg26150533 | FABP4 | 16   | ENSG000000214022 | REPIN1 |
| 17   | cg10173787 | GPR35 | 17   | ENSG000000265735 | RN7SL5P |
| 18   | cg04350355 | CACNG2 | 18   | ENSG000000074276 | CDHR2 |
| 19   | cg09676669 | AQP1 | 19   | ENSG000000009954 | BAZ1B |
| 20   | cg24500428 | PTPRN2 | 20   | ENSG000000144136 | SLC20A1 |
| 21   | cg17623116 | LRRC3B | 21   | ENSG000000106031 | HOXA13 |
| 22   | cg15825065 | LRRC6 | 22   | ENSG000000128602 | SMO |
| 23   | cg10257673 | PTPRN2 | 23   | ENSG000000166900 | STX3 |
| 24   | cg22165480 | <NA> | 24   | ENSG000000146833 | TRIM4 |
| 25   | cg27219362 | <NA> | 25   | ENSG000000120440 | TTL2 |
| 26   | cg17499241 | MEX3A | 26   | ENSG000000231574 | RP11-91K9.1 |
| 27   | cg01351041 | SLC25A36 | 27   | ENSG000000182095 | TNRC18 |
| 28   | cg27227804 | CLEC16A | 28   | ENSG000000134389 | CFHR5 |
| 29   | cg02462253 | MAPK10 | 29   | ENSG000000164944 | KIAA1429 |
| 30   | cg17015522 | C1QTNF1 | 30   | ENSG000000257139 | RP11-320P7.2 |
| 31   | cg10518481 | PTPRS | 31   | ENSG000000130829 | DUSP9 |
| 32   | cg05384255 | <NA> | 32   | ENSG000000265150 | RN7SL2 |
| 33   | cg12358524 | LRRC34 | 33   | ENSG000000168310 | IGF2 |
| 34   | cg20923088 | PCDH9 | 34   | ENSG000000167780 | SOAT2 |
| 35   | cg06428055 | ELF4 | 35   | ENSG000000205835 | GMNC |
| 36   | cg12333737 | POM121L12 | 36   | ENSG000000227471 | AKR1B15 |
| 37   | cg20218460 | LRRF1P1 | 37   | ENSG000000201185 | RNA5SP202 |
| 38   | cg21417204 | SMAD4 | 38   | ENSG000000185168 | LIN00482 |
| 39   | cg03853593 | SOX30 | 39   | ENSG00000008300 | CELSR3 |
| 40   | cg00756172 | LOC340094 | 40   | ENSG000000163884 | KLF15 |
| 41   | cg13909612 | PTPRN2 | 41   | ENSG000000169629 | RGPD8 |
| 42   | cg03103218 | MACROD1 | 42   | ENSG000000169855 | ROBO1 |
| 43   | cg25692928 | CLSTN2 | 43   | ENSG000000196754 | S100A2 |
| 44   | cg19966212 | CD74 | 44   | ENSG000000095932 | C19orf77 |
| 45   | cg14517323 | <NA> | 45   | ENSG000000179930 | ZNF648 |
| 46   | cg23140050 | <NA> | 46   | ENSG000000236698 | EIF1AXP1 |
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| cg07791578   | KAAG1       | 47 ENSG00000105825 | TFPI2        |
| cg27451920   | COL6A3      | 48 ENSG00000163125 | RPRD2        |
| cg22110922   | <NA>        | 49 ENSG00000043355 | ZIC2         |
| cg12441957   | <NA>        | 50 ENSG00000177294 | FBXO39       |
| cg11188837   | H2BFWT      | 51 ENSG00000168925 | CTRB1        |
| cg25316193   | <NA>        | 52 ENSG00000165905 | GYLT1B       |
| cg18756179   | FLU26850    | 53 ENSG00000116128 | BCL9         |
| cg12050054   | C1orf80     | 54 ENSG00000272405 | RP11-284F21.10 |
| cg01485938   | UNC5A       | 55 ENSG00000176563 | CNTD1        |
| cg14032033   | RGS7        | 56 ENSG00000145826 | LECT2        |
| cg06621425   | PTPRN2      | 57 ENSG00000226284 | ARPC3P1     |
| cg06051619   | DIP2C       | 58 ENSG00000260518 | BMS1P8      |
| cg12504098   | <NA>        | 59 ENSG00000178980 | SEPW1       |
| cg02747950   | RABBB       | 60 ENSG00000248596 | RP11-844P9.2 |
| cg20931907   | CXorf67     | 61 ENSG00000136715 | SAP130       |
| cg13246744   | <NA>        | 62 ENSG00000258486 | RN7SL1      |
| cg00322623   | <NA>        | 63 ENSG00000139428 | MMAB         |
| cg10206440   | CLCNKA      | 64 ENSG00000137076 | TLN1         |
| cg20129213   | RIMS2       | 65 ENSG00000207005 | RNU1-2       |
| cg20762313   | TMED3       | 66 ENSG00000141570 | CBX8         |
| cg26797124   | <NA>        | 67 ENSG00000177599 | ZNF491       |
| cg16795307   | STAR13      | 68 ENSG00000119042 | SATB2        |
| cg13891181   | <NA>        | 69 ENSG00000135638 | EMX1         |
| cg19006211   | DPP10       | 70 ENSG00000107959 | PITRM1       |
| cg03720897   | <NA>        | 71 ENSG00000215217 | C5orf49      |
| cg17325866   | <NA>        | 72 ENSG00000119326 | CTNNA1       |
| cg26181743   | PYCR1       | 73 ENSG00000248587 | GDNF-AS1     |
| cg03807917   | MIR520G     | 74 ENSG00000155666 | KDM8         |
| cg26267483   | SGCD        | 75 ENSG00000108830 | RND2         |
| cg02832697   | TRIM2       | 76 ENSG00000259001 | RPPH1        |
| cg01297721   | HAPLN4      | 77 ENSG00000113303 | BTLN8        |
| cg20934215   | PDZRN3      | 78 ENSG00000148773 | MKI67        |
| cg25178683   | LGALS3BP    | 79 ENSG00000258938 | RP11-317N8.5 |
| cg16602369   | ANKRD33B    | 80 ENSG00000272523 | LINC01023    |
| cg25740250   | PTPRN2      | 81 ENSG00000253696 | KBTBD11-OT1  |
| cg18417772   | <NA>        | 82 ENSG00000177182 | CLVS1        |
| cg04527202   | CDC14C      | 83 ENSG00000204778 | RP11-15J10.1 |
| cg21263567   | <NA>        | 84 ENSG00000184363 | PKP3         |
| cg16991316   | <NA>        | 85 ENSG00000160691 | SHC1         |
| cg11225357   | <NA>        | 86 ENSG00000068305 | MEF2A        |
| cg00785170   | PHLD3A      | 87 ENSG00000102929 | NCAPD2       |
| cg27519145   | FAM78B      | 88 ENSG00000263316 | RP11-530N7.3 |
| cg05041683   | TINAGL1     | 89 ENSG00000222011 | FAM185A      |
| cg05639937   | DCLK1       | 90 ENSG00000047410 | TPR          |
| cg09394681   | <NA>        | 91 ENSG00000250305 | KIAA1456     |
| cg13403271   | PTPRN2      | 92 ENSG00000119913 | TECTB        |
| cg09142578   | AATK        | 93 ENSG00000186376 | ZNF75D       |
| cg07316217   | GABRB3      | 94 ENSG00000178977 | LINC00324    |
| cg24804172   | <NA>        | 95 ENSG00000106125 | FAM188B      |
|   | Gene ID   | Gene Symbol |   |   |   |
|---|-----------|-------------|---|---|---|
| 96| cg00120157| <NA>        | 96| ENSG00000100207 | TCF20 |
| 97| cg10482224| PTPN14      | 97| ENSG00000197362 | ZNF786 |
| 98| cg18579809| <NA>        | 98| ENSG00000105088 | OLFM2  |
| 99| cg06888271| <NA>        | 99| ENSG00000227063 | RPL41P1|
|100| cg13016237| DPP6        | 100| ENSG00000136720 | HS6ST1 |
### Supplemental Table 4

| R行 | Top 100 Genes - Methylation-Data | Top 100 Genes - RNA-Seq-Data |
|------|---------------------------------|-----------------------------|
| 1    | cg04773745                      | ENSG000000138778            |
| 2    | cg04341210                      | ENSG000000270728            |
| 3    | cg10916429                      | ENSG000000152760            |
| 4    | cg05766510                      | ENSG000000183054            |
| 5    | cg18620300                      | ENSG000000189334            |
| 6    | cg02514000                      | ENSG000000232956            |
| 7    | cg04227077                      | ENSG000000107807            |
| 8    | cg05765580                      | ENSG000000237978            |
| 9    | cg27430369                      | ENSG000000204832            |
| 10   | cg04515534                      | ENSG000000107187            |
| 11   | cg009949578                     | ENSG000000232233            |
| 12   | cg08611472                      | ENSG000000124564            |
| 13   | cg17836612                      | ENSG000000126838            |
| 14   | cg06720232                      | ENSG00000009694             |
| 15   | cg12680822                      | ENSG000000196367            |
| 16   | cg26150533                      | ENSG000000214022            |
| 17   | cg10173787                      | ENSG000000265735            |
| 18   | cg04350355                      | ENSG000000074276            |
| 19   | cg09676669                      | ENSG00000009954             |
| 20   | cg24500428                      | ENSG000000144136            |
| 21   | cg17623116                      | ENSG000000106031            |
| 22   | cg15825065                      | ENSG000000128602            |
| 23   | cg10257673                      | ENSG000000166900            |
| 24   | cg22165480                      | ENSG000000146833            |
| 25   | cg27219362                      | ENSG000000120440            |
| 26   | cg17499241                      | ENSG000000231574            |
| 27   | cg01351041                      | ENSG000000182095            |
| 28   | cg27227804                      | ENSG000000134389            |
| 29   | cg02462253                      | ENSG000000164944            |
| 30   | cg17015522                      | ENSG000000257139            |
| 31   | cg10518481                      | ENSG000000130829            |
| 32   | cg05384255                      | ENSG000000265150            |
| 33   | cg12358524                      | ENSG000000168310            |
| 34   | cg20923685                      | ENSG000000167780            |
| 35   | cg06428055                      | ENSG000000205835            |
| 36   | cg12333737                      | ENSG000000227471            |
| 37   | cg20218460                      | ENSG000000201185            |
| 38   | cg21417204                      | ENSG000000185168            |
| 39   | cg03853593                      | ENSG00000008300             |
| 40   | cg00756172                      | ENSG000000163884            |
| 41   | cg13909612                      | ENSG000000169629            |
| 42   | cg03103218                      | ENSG000000169855            |
| 43   | cg25692928                      | ENSG000000196754            |
| 44   | cg19966212                      | ENSG000000095932            |
| 45   | cg14517323                      | ENSG000000179930            |
| 46   | cg23140050                      | ENSG000000236698            |
|   | Gene  |   | Chromosome |   |   |
|---|-------|---|-------------|---|---|
| 47 | cg07791578 | KAAG1 | 47 | ENSG00000105825 | TFPI2 |
| 48 | cg27451920 | COL6A3 | 48 | ENSG00000163125 | RPRD2 |
| 49 | cg22110922 | <NA> | 49 | ENSG00000043355 | ZIC2 |
| 50 | cg12441957 | <NA> | 50 | ENSG00000177294 | FBXO39 |
| 51 | cg11188837 | H2BFWT | 51 | ENSG00000168925 | CTRB1 |
| 52 | cg25316193 | <NA> | 52 | ENSG000000165905 | GYLT1L8 |
| 53 | cg18756179 | FLJ26850 | 53 | ENSG000000116128 | BCL9 |
| 54 | cg12050054 | C1orf80 | 54 | ENSG000000272405 | RP11-284F21.10 |
| 55 | cg01485938 | UNC5A | 55 | ENSG000000176563 | CNTD1 |
| 56 | cg14032033 | RGS7 | 56 | ENSG000000145826 | LECT2 |
| 57 | cg06621425 | PTPRN2 | 57 | ENSG000000226284 | ARPC3P1 |
| 58 | cg06051619 | DIP2C | 58 | ENSG000000260518 | BMS1P8 |
| 59 | cg12504098 | <NA> | 59 | ENSG000000178980 | SEPW1 |
| 60 | cg02747950 | RAB8B | 60 | ENSG000000248596 | RP11-844P9.2 |
| 61 | cg20931907 | CXorf67 | 61 | ENSG000000136715 | SAP130 |
| 62 | cg13246744 | <NA> | 62 | ENSG000000258486 | RN7SL1 |
| 63 | cg00322623 | <NA> | 63 | ENSG000000139428 | MMAB |
| 64 | cg10206440 | CLCNKA | 64 | ENSG000000137076 | TLN1 |
| 65 | cg20129213 | RIMS2 | 65 | ENSG000000207005 | RNU1-2 |
| 66 | cg20762313 | TMED3 | 66 | ENSG000000141570 | CBX8 |
| 67 | cg26797124 | <NA> | 67 | ENSG000000177599 | ZNF491 |
| 68 | cg16795307 | STARD13 | 68 | ENSG000000119042 | SATB2 |
| 69 | cg13891181 | <NA> | 69 | ENSG000000135638 | EMX1 |
| 70 | cg19006211 | DPP10 | 70 | ENSG000000107899 | PITRM1 |
| 71 | cg03720897 | <NA> | 71 | ENSG000000215217 | C5orf49 |
| 72 | cg17325866 | <NA> | 72 | ENSG000000119326 | CTNNA1 |
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| 74 | cg03807917 | MIR520G | 74 | ENSG000000155666 | KDM8 |
| 75 | cg26267483 | SGCO | 75 | ENSG000000108830 | RND2 |
| 76 | cg02832697 | TRIM2 | 76 | ENSG000000259001 | RPPH1 |
| 77 | cg01297721 | HAPLN4 | 77 | ENSG000000113303 | BTLN8 |
| 78 | cg20934215 | PDZRN3 | 78 | ENSG000000148773 | MKI67 |
| 79 | cg25178683 | LGALS3BP | 79 | ENSG000000258938 | RP11-317N8.5 |
| 80 | cg16602369 | ANKRD33B | 80 | ENSG000000272523 | LINCO1023 |
| 81 | cg25740250 | PTPRN2 | 81 | ENSG000000253696 | KBTBD11-OT1 |
| 82 | cg18417772 | <NA> | 82 | ENSG000000177182 | CLVS1 |
| 83 | cg04527202 | CDC14C | 83 | ENSG000000204778 | RP11-15J10.1 |
| 84 | cg21263567 | <NA> | 84 | ENSG000000184363 | PKP3 |
| 85 | cg16991316 | <NA> | 85 | ENSG000000160691 | SHC1 |
| 86 | cg11225357 | <NA> | 86 | ENSG000000068305 | MEF2A |
| 87 | cg00785170 | PHLDA3 | 87 | ENSG00000010292 | NCD4P2 |
| 88 | cg27519145 | FAM78B | 88 | ENSG000000263316 | RP11-530N7.3 |
| 89 | cg00541683 | TINAGL1 | 89 | ENSG000000222011 | FAM185A |
| 90 | cg05639937 | DCLK1 | 90 | ENSG000000047410 | TPR |
| 91 | cg09394681 | <NA> | 91 | ENSG000000250305 | KIAA1456 |
| 92 | cg13403271 | PTPRN2 | 92 | ENSG000000119913 | TECTB |
| 93 | cg09142578 | AATK | 93 | ENSG000000186376 | ZNF75D |
| 94 | cg07316217 | GABRB3 | 94 | ENSG000000178977 | LINCO0324 |
| 95 | cg24804172 | <NA> | 95 | ENSG000000106125 | FAM188B |
|   | cg00120157 |  <NA>  | 96 | ENSG00000100207 | TCF20 |
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| 97| cg10482224 | PTPN14 | 97 | ENSG00000197362 | ZNF786 |
| 98| cg18579809 |  <NA>  | 98 | ENSG00000105088 | OLFM2 |
| 99| cg06888271 |  <NA>  | 99 | ENSG00000227063 | RPL41P1 |
|100| cg13016237 | DPP6   | 100| ENSG00000136720 | HS6ST1 |
### Supplemental Table 5

| Panel | Gene_Symbol | Lesion | Probe_ID | M-value | p-value | adj.p-value | beta-value difference to NL | Chromosome | UCSC_RefGene_Group | Relation_to_UCS_CpG_Island |
|-------|-------------|--------|----------|---------|---------|------------|-----------------------------|------------|-------------------|-----------------------------|
| 1     | ANO10       | LGDN   | cg11035303 | 2,25    | 0,001400969 | 0,042313245 | 0,21 | 3 | Body |                            |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | HGDN   | cg11035303 | 2,20    | 0,001442059 | 0,021524631 | 0,21 | 3 | Body |                            |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg11035303 | 2,13    | 0,001992212 | 0,012922805 | 0,20 | 3 | Body |                            |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | pHCC   | cg11035303 | 2,30    | 0,001162462 | 0,026053992 | 0,20 | 3 | Body |                            |
| 1     | BMP8A       | LGDN   | cg11763509 | 1,23    | 1,08373E-05  | 0,003147873 | 0,20 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | HGDN   | cg11763509 | 1,45    | 4,8908E-08  | 4,82654E-05 | 0,23 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg25139493 | 1,29    | 0,001648639 | 0,011481088 | 0,21 | 1 | 1stExon | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg11763509 | 1,46    | 3,42655E-07  | 0,000115899 | 0,23 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg08748615 | 2,10    | 0,006911376 | 0,029213458 | 0,28 | 1 | TSS200 | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg15947940 | 3,01    | 0,001619369 | 0,011353715 | 0,32 | 1 | TSS200 | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg02575697 | 3,01    | 0,00638407  | 0,006465884 | 0,39 | 1 | TSS200 | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | pHCC   | cg11763509 | 1,40    | 3,2305E-06  | 0,001076919 | 0,22 | 1 | Body | Island                   |
| 1     | CAMTA1      | LGDN   | cg03571764 | -1,64   | 0,001272387 | 0,040229801 | -0,23 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | HGDN   | cg08640609 | 1,67    | 0,004537857 | 0,042711116 | 0,21 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg12138124 | -2,46   | 3,29437E-05  | 0,001256476 | -0,28 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg07008478 | -1,63   | 0,000855058 | 0,007693041 | -0,25 | 1 | Body | S_Shore                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg21942218 | -3,20   | 0,000286391 | 0,004055616 | -0,24 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg03571764 | -1,72   | 0,000278676 | 0,003994987 | -0,24 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg23021268 | -1,55   | 0,003666873 | 0,019151776 | -0,23 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg17081408 | -1,83   | 0,001496498 | 0,010815639 | -0,23 | 1 | Body | Island                   |
|       |             |        |          |         |         |            |                             |            |                   |                             |
|       |             | eHCC   | cg00911446 | -1,91   | 0,000344462 | 0,004509207 | -0,22 | 1 | Body | Island                   |
| Gene  | cg Probe  | Fold Change  | p Value 1   | q Value 1   | Fold Change 2 | p Value 2   | q Value 2 |
|-------|-----------|--------------|-------------|-------------|--------------|-------------|-----------|
| eHCC  | cg25196088| -1.43        | 0.001309575 | 0.009952399 | -0.22        | 1           | Body      |
| eHCC  | cg06800235| -1.36        | 0.000279404 | 0.00399493  | -0.22        | 1           | Body      |
| eHCC  | cg06082897| -1.57        | 0.000963949 | 0.008253847 | -0.21        | 1           | Body      |
| eHCC  | cg04210471| -1.59        | 0.004911013 | 0.023224209 | -0.21        | 1           | Body      |
| eHCC  | cg26161885| -1.66        | 0.000272859 | 0.003949708 | -0.21        | 1           | Body      |
| eHCC  | cg17143900| -1.34        | 0.005124651 | 0.023891622 | -0.21        | 1           | Body      |
| eHCC  | cg10536786| -1.25        | 0.001130559 | 0.009085098 | -0.21        | 1           | Body      |
| eHCC  | cg24579970| -1.21        | 0.0176546   | 0.011985081 | -0.20        | 1           | Body      |
| eHCC  | cg00783553| 1.37         | 0.005594416 | 0.025319897 | 0.22         | 1           | Body      |
| eHCC  | cg22488970| 1.62         | 0.010419843 | 0.038724737 | 0.23         | 1           | Body      |
| eHCC  | cg21144493| 1.76         | 1,01642E-05 | 0.00670116  | 0.29         | 1           | Body      |
| eHCC  | cg08640609| 2.62         | 0.00359256  | 0.04613904  | 0.36         | 1           | Body      |
| pHCC  | cg12138124| -2.71        | 5,33231E-05 | 0.004966698 | -0.32        | 1           | Body      |
| pHCC  | cg00808305| -1.40        | 0.001385864 | 0.028577018 | -0.23        | 1           | Body      |
| pHCC  | cg06800235| -1.39        | 0.000808749 | 0.02161448  | -0.22        | 1           | Body      |
| pHCC  | cg25763306| -1.55        | 0.003301719 | 0.04418039  | -0.21        | 1           | Body      |
| pHCC  | cg12661316| -1.43        | 0.000756895 | 0.020875328 | -0.21        | 1           | Body      |
| pHCC  | cg21583016| -1.25        | 0.003911524 | 0.048481596 | -0.20        | 1           | Body      |

**1** FBRSL1  LGDN  cg08818195  -1.38  2,03787E-05  0,004411797  -0.22  12  TSS1500  N_Shore
**1** GALK2   LGDN  cg00756450  1,35   1,7713E-08  0,000228386   0,20  15  Body
|   | Gene  | Tissue | Methylation | P-value | FDR | Distance | Feature | Location |
|---|-------|--------|-------------|---------|-----|----------|---------|----------|
| 1 | HMBS  | LGDN   | cg20929545  | 1.33    | 3.5602E-06 | 0.001800117 | 0.21 | 11 TSS1500 S_Shelf |
|   |       | HGDN   | cg20929545  | 1.31    | 5.8742E-07 | 0.000171134 | 0.21 | 11 TSS1500 S_Shelf |
|   |       | eHCC   | cg20929545  | 1.64    | 9.55531E-08 | 0.000062667 | 0.25 | 11 TSS1500 S_Shelf |
|   |       | pHCC   | cg20929545  | 1.44    | 1.54236E-06 | 0.000764673 | 0.22 | 11 TSS1500 S_Shelf |
|   | MAP4  | LGDN   | cg16509829  | -1.37   | 1.2804E-05 | 0.003423929 | -0.21 | 3' S'UTR Island |
|   |       | HGDN   | cg16509829  | -1.33   | 7.33205E-06 | 0.000785773 | -0.20 | 3' S'UTR Island |
|   |       | eHCC   | cg16509829  | -1.48   | 3.23268E-06 | 0.00036566 | -0.22 | 3' S'UTR Island |
|   |       | pHCC   | cg16509829  | -1.35   | 1.64411E-06 | 0.002547039 | -0.20 | 3' S'UTR Island |
|   | NSD1  | LGDN   | cg18121224  | 1.53    | 2.1862E-05 | 0.004589217 | 0.20 | 5 TSS1500 Island |
|   |       | LGDN   | cg19731612  | 1.73    | 1.9278E-05 | 0.004300077 | 0.22 | 5 TSS1500 Island |
|   |       | HGDN   | cg18121224  | 1.54    | 9.38425E-07 | 0.000229232 | 0.20 | 5 TSS1500 Island |
|   |       | HGDN   | cg19731612  | 1.69    | 1.62325E-06 | 0.00319755 | 0.22 | 5 TSS1500 Island |
|   |       | HGDN   | cg08369368  | 1.67    | 0.000997114 | 0.017168919 | 0.23 | 5 TSS200 Island |
|   |       | eHCC   | cg18016826  | 1.76    | 0.000408844 | 0.004974456 | 0.22 | 5 TSS200 Island |
|   |       | eHCC   | cg18121224  | 2.00    | 2.02275E-07 | 8.9113E-05 | 0.24 | 5 TSS1500 Island |
|   |       | eHCC   | cg19731612  | 2.18    | 3.10701E-07 | 0.000109997 | 0.27 | 5 TSS1500 Island |
|   |       | eHCC   | cg08369368  | 2.59    | 7.19393E-05 | 0.001906875 | 0.38 | 5 TSS200 Island |
|   |       | pHCC   | cg18121224  | 1.55    | 2.13084E-05 | 0.0029449 | 0.20 | 5 TSS1500 Island |
|   |       | pHCC   | cg19731612  | 1.61    | 0.00004665 | 0.004619989 | 0.21 | 5 TSS1500 Island |
|   | PIAS1 | LGDN   | cg05105016  | 1.23    | 1.15585E-07 | 0.000390356 | 0.21 | 15 Body |
|   |       | HGDN   | cg05105016  | 1.22    | 3.95718E-09 | 1.41969E-05 | 0.21 | 15 Body |
|   |       | eHCC   | cg05105016  | 1.57    | 7.80955E-10 | 1.18765E-05 | 0.26 | 15 Body |
|   |       | pHCC   | cg05105016  | 1.66    | 2.43725E-09 | 9.35193E-05 | 0.27 | 15 Body |
|   | PLOD3 | LGDN   | cg16390570  | -1.55   | 4.20407E-06 | 0.00197153 | -0.25 | 7 1stExon Island |
|   |       | HGDN   | cg16390570  | -1.32   | 7.97387E-06 | 0.000827613 | -0.22 | 7 1stExon Island |
|   |       | eHCC   | cg16390570  | -1.34   | 1.13889E-05 | 0.000715301 | -0.22 | 7 1stExon Island |
| Gene | ChIP Peak ID | Coverage | logFC | Binding Score | p-value | Width (kb) | Domain | Region |
|------|--------------|----------|------|--------------|---------|------------|--------|--------|
| eHCC | cg18437077   | -1.29    | 1.10252E-07 | 6.72273E-05 | -0.20   | 7 | 1stExon | Island |
| pHCC | cg16390570   | -1.41    | 1.30962E-05 | 0.002250628 | -0.23   | 7 | 1stExon | Island |
| PPP2R5C | LGDN cg09990596 | -1.28  | 4.45282E-05 | 0.006709743 | -0.21   | 14 | TSS200 | Island |
| HGDN | cg15321108   | -1.22    | 1.23203E-05 | 0.003355745 | -0.20   | 14 | TSS200 | Island |
| HGDN | cg15321108   | -1.28    | 1.00638E-06 | 0.000238393 | -0.21   | 14 | TSS200 | Island |
| eHCC | cg08163906   | -1.28    | 7.15987E-06 | 0.000773813 | -0.22   | 14 | TSS200 | Island |
| pHCC | cg15321108   | -1.32    | 1.79373E-06 | 0.000269222 | -0.22   | 14 | TSS200 | Island |
| eHCC | cg09990596   | -1.26    | 2.16154E-05 | 0.000995773 | -0.21   | 14 | TSS200 | Island |
| pHCC | cg27022326   | -1.52    | 0.000244565 | 0.011486812 | -0.25   | 14 | 3'UTR | N_Shore |
| PTPRC | LGDN cg26399994 | -1.82  | 8.92912E-05 | 0.009753206 | -0.22   | 1 | Body |
| HGDN | cg22073152   | -1.30    | 0.002335102 | 0.028816727 | -0.22   | 1 | Body |
| HGDN | cg04214459   | -1.25    | 0.000698215 | 0.013820458 | -0.21   | 1 | Body |
| eHCC | cg22073152   | -2.08    | 0.000162627 | 0.002957778 | -0.34   | 1 | Body |
| eHCC | cg25132230   | -1.63    | 0.001898857 | 0.012539625 | -0.27   | 1 | 5'UTR |
| eHCC | cg26399994   | -1.83    | 2.53383E-05 | 0.001087514 | -0.22   | 1 | Body |
| eHCC | cg04214459   | -1.21    | 0.003153217 | 0.017366658 | -0.20   | 1 | Body |
| pHCC | cg25132230   | -1.93    | 0.00158306 | 0.030591941 | -0.32   | 1 | 5'UTR |
| pHCC | cg22073152   | -1.84    | 0.001655583 | 0.031346453 | -0.30   | 1 | Body |
| pHCC | cg04214459   | -1.42    | 0.002846064 | 0.0412013  | -0.23   | 1 | Body |
| pHCC | cg26399994   | -1.80    | 0.000135529 | 0.008284838 | -0.22   | 1 | Body |
| RWDD1 | LGDN cg23280258 | 1.40  | 1.24299E-05 | 0.003378011 | 0.21   | 6 | Body | S_Shelf |
| HGDN | cg23280258   | 1.41    | 5.78259E-07 | 0.000169794 | 0.21   | 6 | Body | S_Shelf |
| eHCC | cg23280258   | 1.84    | 1.0504E-07 | 6.53631E-05 | 0.26   | 6 | Body | S_Shelf |
| pHCC | cg23280258   | 1.77    | 8.8973E-07 | 0.000577338 | 0.25   | 6 | Body | S_Shelf |
| SAMD11 | LGDN cg13856810 | 1.24  | 0.000236207 | 0.016280636 | 0.20   | 1 | Body | S_Shore |
| LGDN | cg05527507 | 1.67    | 0.000157173 | 0.013155911 | 0.27   | 1 | 5'UTR | Island |
| Gene | Chromosome | Start | End | P-value | q-value | Region | Location |
|------|-------------|-------|-----|---------|---------|--------|----------|
| LGDN cg14324200 | 2,01 | 3,62211E-05 | 0,005983022 | 0,31 | 1 | S'UTR | Island |
| HGDN cg13904806 | 2,08 | 1,06986E-06 | 0,000248078 | 0,20 | 1 | Body | N_Shore |
| HGDN cg13856810 | 1,40 | 3,4156E-06 | 0,000494286 | 0,23 | 1 | Body | S_Shore |
| HGDN cg02439789 | 1,56 | 6,78215E-06 | 0,00748576 | 0,25 | 1 | Body | Island |
| HGDN cg24362661 | 1,52 | 1,1586E-05 | 0,001050211 | 0,25 | 1 | Body | Island |
| HGDN cg06531475 | 1,61 | 1,42775E-05 | 0,001198738 | 0,26 | 1 | Body | Island |
| HGDN cg05527507 | 1,67 | 1,05649E-05 | 0,000990265 | 0,27 | 1 | S'UTR | Island |
| HGDN cg13546858 | 1,84 | 3,52397E-06 | 0,000503809 | 0,29 | 1 | Body | Island |
| HGDN cg02663945 | 1,82 | 0,003639257 | 0,037475353 | 0,29 | 1 | Body | Island |
| eHCC cg13904806 | 2,18 | 3,93301E-06 | 0,000403672 | 0,21 | 1 | Body | N_Shore |
| eHCC cg03269716 | 1,46 | 4,67217E-06 | 0,00044236 | 0,23 | 1 | Body | N_Shore |
| eHCC cg24362661 | 1,44 | 5,73347E-05 | 0,001692634 | 0,24 | 1 | Body | Island |
| eHCC cg13856810 | 1,55 | 6,42576E-06 | 0,000525064 | 0,25 | 1 | Body | S_Shore |
| eHCC cg13546858 | 1,69 | 3,91963E-05 | 0,001374563 | 0,27 | 1 | Body | Island |
| eHCC cg02439789 | 1,74 | 6,81567E-06 | 0,000542672 | 0,27 | 1 | Body | Island |
| eHCC cg06531475 | 1,64 | 5,03767E-05 | 0,001577203 | 0,27 | 1 | Body | Island |
| eHCC cg02663945 | 1,89 | 0,003134839 | 0,017305399 | 0,29 | 1 | Body | Island |
| eHCC cg05527507 | 1,80 | 1,91151E-05 | 0,000933015 | 0,29 | 1 | S'UTR | Island |
| eHCC cg14324200 | 2,01 | 9,3645E-06 | 0,00645658 | 0,32 | 1 | S'UTR | Island |
| pHCC cg13904806 | 2,11 | 2,86451E-05 | 0,003499123 | 0,20 | 1 | Body | N_Shore |
| pHCC cg13856810 | 1,32 | 0,000165803 | 0,009278836 | 0,21 | 1 | Body | S_Shore |
| pHCC cg24362661 | 1,33 | 0,000346405 | 0,013853106 | 0,22 | 1 | Body | Island |
| pHCC cg02439789 | 1,51 | 0,000114182 | 0,007524875 | 0,24 | 1 | Body | Island |
| pHCC cg13546858 | 1,84 | 6,48495E-05 | 0,00561143 | 0,29 | 1 | Body | Island |
| pHCC cg02663945 | 2,00 | 0,002516631 | 0,038758082 | 0,31 | 1 | Body | Island |

1 SATB2

| Gene | Chromosome | Start | End | P-value | q-value | Region | Location |
|------|-------------|-------|-----|---------|---------|--------|----------|
| LGDN cg20785796 | 1,34 | 0,000104345 | 0,010597593 | 0,21 | 2 | TSS1500 | Island |
| HGDN cg20785796 | 1,46 | 4,92183E-06 | 0,000616767 | 0,23 | 2 | TSS1500 | Island |
| eHCC cg23994043 | 1,39 | 0,002854286 | 0,016282203 | 0,22 | 2 | TSS1500 | Island |
| eHCC cg20731529 | 1,63 | 0,001843123 | 0,012310591 | 0,26 | 2 | Body | Island |
| Gene      | Type   | Chr  | Start | End   | Length | Expression 1 | Expression 2 | Fisher's P 1 | Fisher's P 2 | Fisher's P 3 | TSS | Location |
|-----------|--------|------|-------|-------|--------|--------------|--------------|--------------|--------------|--------------|------|----------|
| eHCC      |        |      |       |       |        | 1,59         | 0,00113929   | 0,009128821  | 0,26         | 2            | TSS1500 | Island   |
| eHCC      |        |      |       |       |        | 1,87         | 8,08703E-07  | 0,00017989   | 0,28         | 2            | TSS1500 | Island   |
| pHCC      |        |      |       |       |        | 1,63         | 1,48928E-05  | 0,00242      | 0,24         | 2            | TSS1500 | Island   |
| SPG11     | LGDN   |      |       |       |        | -1,79        | 5,09051E-05  | -0,24        | 15           | TSS200       | Island |
| HGDN      | LGDN   |      |       |       |        | -1,81        | 1,07164E-05  | -0,23        | 15           | TSS200       | Island |
| eHCC      | LGDN   |      |       |       |        | -1,71        | 3,83926E-05  | -0,22        | 15           | TSS200       | Island |
| pHCC      | LGDN   |      |       |       |        | -1,66        | 0,0001184    | -0,22        | 15           | TSS200       | Island |
| STX1A     | LGDN   |      |       |       |        | -1,33        | 3,4312E-05   | -0,22        | 7            | TSS200       | Island |
| HGDN      | LGDN   |      |       |       |        | -1,50        | 1,34666E-06  | -0,25        | 7            | TSS200       | Island |
| eHCC      | LGDN   |      |       |       |        | 1,49         | 2,71268E-05  | 0,23         | 7            | Body         | Island |
| eHCC      | LGDN   |      |       |       |        | -1,73        | 5,91379E-07  | -0,28        | 7            | TSS200       | Island |
| eHCC      | LGDN   |      |       |       |        | -1,49        | 1,42012E-06  | -0,23        | 7            | TSS200       | Island |
| pHCC      | LGDN   |      |       |       |        | -1,33        | 3,64297E-05  | -0,22        | 7            | TSS200       | Island |
| USP34     | LGDN   |      |       |       |        | 2,01         | 3,97126E-08  | 0,21         | 2            | Body         | Island |
| HGDN      | LGDN   |      |       |       |        | 1,98         | 1,18219E-09  | 0,21         | 2            | Body         | Island |
| eHCC      | LGDN   |      |       |       |        | 2,38         | 8,16631E-10  | 0,23         | 2            | Body         | Island |
| pHCC      | LGDN   |      |       |       |        | 2,45         | 4,09543E-09  | 0,24         | 2            | Body         | Island |
| WDR82     | LGDN   |      |       |       |        | -1,33        | 0,000865119  | -0,22        | 3            | TSS200       | Island |
| HGDN      | LGDN   |      |       |       |        | -1,53        | 0,00010857   | -0,25        | 3            | TSS200       | Island |
| HGDN      | LGDN   |      |       |       |        | -1,39        | 1,17748E-05  | -0,21        | 3            | TSS200       | Island |
| eHCC      | LGDN   |      |       |       |        | -1,83        | 2,55538E-05  | -0,29        | 3            | TSS200       | Island |
| eHCC      | LGDN   |      |       |       |        | -1,33        | 5,03101E-07  | -0,22        | 3            | TSS200       | Island |
| eHCC      | LGDN   |      |       |       |        | -1,44        | 1,8899E-05   | -0,21        | 3            | TSS200       | Island |
| pHCC      | LGDN   |      |       |       |        | -1,67        | 0,000115413  | -0,27        | 3            | TSS200       | Island |
| ZIC5      | LGDN   |      |       |       |        | 2,48         | 0,000702243  | 0,35         | 13           | Body         | Island |
| HGDN      | LGDN   |      |       |       |        | 1,66         | 0,002020005  | 0,22         | 13           | Body         | Island |
| Gene | Chromosome | GeneID | Beta Value | p-value (FDR) | Admixture Matrix | Position | Score | Gene Type | Platform | Site Type |
|------|------------|--------|------------|---------------|-----------------|----------|-------|-----------|----------|-----------|
| eHCC | cg11077516 | 1,24   | 0,00177198 | 0,01201285    | 0,20            | 13       | Body  | Island    |          |           |
| eHCC | cg10679688 | 1,46   | 0,000569742| 0,00603541    | 0,22            | 13       | TSS1500| S_Shore   |          | Island    |
| eHCC | cg03313945 | 1,59   | 0,00309423 | 0,04238703    | 0,23            | 13       | Body  | Island    |          | Island    |
| eHCC | cg20985450 | 2,57   | 0,00392496 | 0,04856565    | 0,39            | 13       | Body  | Island    |          | Island    |
| eHCC | cg17930361 | 2,80   | 6,93423E-05| 0,01868431    | 0,41            | 13       | Body  | Island    |          | Island    |
| pHC  | cg00529958 | 1,49   | 0,000767592| 0,021041187   | 0,23            | 13       | TSS200| Island    |          | Island    |
|      |            |        |            |               |                 |          |       |           |          |           |
| 1    | ZNF212     | LGDN   | cg05476998 | 1,38          | 3,19165E-06     | 0,01734751| 0,21  | 7 Body    | S_Shelf  | Island    |
|      |            | HGDN   | cg05476998 | 1,45          | 5,2967E-08      | 4,92503E-05| 0,22  | 7 Body    | S_Shelf  | Island    |
| eHCC | cg05476998 | 1,81   | 2,11249E-08| 3,42868E-05   | 0,26            | 7       | Body  | S_Shelf  |          | Island    |
| pHC  | cg05476998 | 1,82   | 1,26735E-07| 0,000245382   | 0,26            | 7       | Body  | S_Shelf  |          | Island    |
|      |            |        |            |               |                 |          |       |           |          | Island    |
| LGDN | cg00554413 | 1,41   | 0,000131729| 0,011957301   | 0,22            | 1       | 1stExon| Island    |          | Island    |
|      |            |        |            |               |                 |          |       | Island    |          | Island    |
| 1    | LHX3       | LGDN   | cg08967938 | 1,87          | 0,000967927     | 0,034864845| 0,27  | 9 Body    | Island    |
|      |            | HGDN   | cg13658899 | 1,24          | 0,000811133     | 0,015155141| 0,21  | 9 Body    | Island    |
| eHCC | cg14362758 | 1,55   | 0,002136962| 0,01352007    | 0,23            | 9       | Body  | Island    |          | Island    |
| pHC  | cg14362758 | 1,75   | 0,002625355| 0,03954662    | 0,26            | 9       | Body  | Island    |          | Island    |
|      |            |        |            |               |                 |          |       | Island    |          | Island    |
| LGDN | cg00554413 | 1,41   | 0,000131729| 0,011957301   | 0,22            | 1       | 1stExon| Island    |          | Island    |
|      |            |        |            |               |                 |          |       | Island    |          | Island    |
| 1    | TACSTD2    | LGDN   | cg24851854 | 1,31          | 1,26168E-05     | 0,001108588| 0,22  | 1 1stExon | Island    |
|      |            | HGDN   | cg24851854 | 1,53          | 1,09385E-05     | 0,00698777| 0,26  | 1 1stExon | Island    |
| eHCC | cg00667789 | 1,77   | 1,97317E-05| 0,000946646   | 0,29            | 1       | 1stExon| Island    |          | Island    |
| pHC  | cg16080552 | 1,33   | 0,003686894| 0,046971267   | 0,22            | 1       | TSS200| Island    |          | Island    |
|      |            |        |            |               |                 |          |       | Island    |          | Island    |
| 1    | MSX1       | LGDN   | cg04100843 | 1,31          | 0,000836267     | 0,032350259| 0,20  | 4 TSS1500 | N_Shore   |
|      |            | HGDN   | cg21689228 | 1,44          | 0,01348574      | 0,041472402| 0,22  | 4 TSS1500 | N_Shore   |
| LGDN | cg03199651 | 1,70   | 0,001729766| 0,047349555   | 0,26            | 4       | Body  | N_Shore   |          | Island    |
|      |            |        |            |               |                 |          |       | Island    |          | Island    |
| HGDN | cg15092343 | 1,97   | 4,23898E-05| 0,002384926   | 0,31            | 4       | TSS1500| Island    |          | Island    |
| eHCC | cg03335246 | 1,23   | 0,010623138| 0,039249466   | 0,20            | 4       | TSS1500| N_Shore   |          | Island    |
| eHCC | cg10266211 | 1,30   | 0,000365637| 0,04660462    | 0,22            | 4       | TSS1500| Island    |          | Island    |
| eHCC | cg20588069 | 1,37   | 0,005798135| 0,025953559   | 0,22            | 4       | TSS1500| N_Shore   |          | Island    |
| eHCC | cg15092343 | 2,40   | 1,70495E-05| 0,00879044    | 0,38            | 4       | TSS1500| Island    |          | Island    |
| Sample | Gene       | CG ID       | Beta  | FDR    | Beta  | FDR    | Strand | Distance | Location          |
|--------|------------|-------------|-------|--------|-------|--------|--------|-----------|-------------------|
| pHCC   | cg15092343 | 1.98        | 0.000414525 | 0.015226151 | 0.32 | 4       | TSS1500 | Island    |
| ATP11A | HGDN       | cg08893811  | -1.51  | 0.00232779 | 0.028763055 | -0.23 | 13       | Body      | S_Shore       |
| eHCC   | cg08893811 | -1.60       | 0.00317993 | 0.017462558 | -0.26 | 13       | Body    | S_Shore   |
| pHCC   | cg25142327 | 1.93        | 0.000561165 | 0.017837661 | 0.21 | 13       | Body    | S_Shore   |
|        | ATP11A     | HGDN        | -1.60  | 0.0002790445 | -0.26 | 16       | Body    | Island    |
| eHCC   | cg08893811 | -1.60       | 0.000386277 | 0.0480812  | 0.34 | 16       | Body    | Island    |
| eHCC   | cg06279276 | -1.60       | 0.000258498 | 0.03906448 | 0.31 | 16       | Body    | Island    |
| pHCC   | cg06279276 | 1.92        | 0.002218368 | 0.02790445 | 0.24 | 16       | Body    | Island    |
|        | B3GNT9     | HGDN        | -1.66  | 3.89484E-07  | 0.000136691 | -0.24 | 12       | Body      | S_Shore       |
| eHCC   | cg12926596 | -1.66       | 1.34152E-06 | 0.00232516 | -0.23 | 12       | Body    | S_Shore   |
| eHCC   | cg12926596 | -1.66       | 1.70273E-05 | 0.00260137 | -0.21 | 12       | Body    | S_Shore   |
| pHCC   | cg12926596 | 1.92        | 0.000561165 | 0.017837661 | 0.21 | 13       | Body    | S_Shore   |
|        | BLOC1S1    | HGDN        | -1.66  | 3.89484E-07  | 0.000136691 | -0.24 | 12       | Body      | S_Shore       |
| eHCC   | cg12926596 | -1.66       | 1.34152E-06 | 0.00232516 | -0.23 | 12       | Body    | S_Shore   |
| eHCC   | cg12926596 | -1.66       | 1.70273E-05 | 0.00260137 | -0.21 | 12       | Body    | S_Shore   |
| pHCC   | cg12926596 | 1.92        | 0.002218368 | 0.02790445 | 0.24 | 16       | Body    | Island    |
|        | CCDC40     | HGDN        | 1.27   | 1.15986E-06  | 0.00025931 | 0.21 | 17       | Body      | N_Shelf      |
| eHCC   | cg08109808 | 1.59        | 2.20587E-07 | 9.31013E-05 | 0.26 | 17       | Body    | N_Shelf   |
| eHCC   | cg08109808 | 1.55        | 1.05991E-06 | 0.000632485 | 0.25 | 17       | Body    | N_Shelf   |
| pHCC   | cg08109808 | 1.55        | 1.05991E-06 | 0.000632485 | 0.25 | 17       | Body    | N_Shelf   |
|        | CCR5       | HGDN        | -2.90  | 0.00422845   | 0.040971134 | -0.34 | 3        | TSS200    |
| eHCC   | cg22984586 | -2.62       | 0.008684306 | 0.034110837 | -0.32 | 3        | TSS200    |
| eHCC   | cg22984586 | -2.62       | 0.004388181 | 0.014733496 | -0.23 | 3        | Body     | N_Shelf    |
| pHCC   | cg00803692 | -1.85       | 0.000388181 | 0.014733496 | -0.23 | 3        | Body     | N_Shelf    |
|        | DDX51      | HGDN        | -1.39  | 1.60451E-07  | 8.52062E-05 | -0.23 | 12       | Body      | Island      |
| eHCC   | cg22672078 | -1.37       | 7.08938E-07 | 0.00016728  | -0.23 | 12       | Body    | Island    |
| eHCC   | cg22672078 | -1.37       | 1.13823E-05 | 0.002084772 | -0.20 | 12       | Body    | Island    |
| pHCC   | cg22672078 | -1.37       | 1.13823E-05 | 0.002084772 | -0.20 | 12       | Body    | Island    |
|        | DNAH17     | HGDN        | -1.40  | 6.14144E-05  | 0.003017083 | -0.20 | 17       | Body      |
| eHCC   | cg09687005 | -1.82       | 1.29107E-05 | 0.000760409 | -0.27 | 17       | Body    |
| eHCC   | cg10217661 | -1.93       | 0.000171966 | 0.003050257 | -0.26 | 17       | Body    | Island    |
| eHCC   | cg21103227 | -1.96       | 9.22428E-05 | 0.002180164 | -0.25 | 17       | Body    | Island    |
| Gene   | Chromosome | Start (bp) | End (bp) | Beta | P Value | SE | Body   |
|--------|------------|------------|----------|------|---------|----|--------|
| eHCC   | cg09705784 | -1.71      | 0.000186965 | -0.25 | 17      |    | Body   |
| eHCC   | cg01341643 | -2.05      | 7.67345E-05 | -0.25 | 17      |    | Body   |
| eHCC   | cg09577144 | -1.65      | 6.6252E-05  | -0.24 | 17      |    | TSS200 |
| eHCC   | cg10332979 | -1.74      | 6.82902E-05 | -0.24 | 17      |    | Body   |
| eHCC   | cg20690714 | -2.16      | 0.000149222 | -0.24 | 17      |    | Body   |
| eHCC   | cg15618347 | -1.81      | 0.000562421 | -0.24 | 17      |    | Body   |
| eHCC   | cg25691430 | -1.56      | 0.00076360  | -0.23 | 17      |    | Island |
| eHCC   | cg11803990 | -1.91      | 0.000283434 | -0.23 | 17      |    | Body   |
| eHCC   | cg20723425 | -1.83      | 0.001933141 | -0.22 | 17      |    | Body   |
| eHCC   | cg14927663 | -1.98      | 9.06649E-05 | -0.22 | 17      |    | Body   |
| eHCC   | cg16678718 | -1.94      | 0.00084096  | -0.22 | 17      |    | Body   |
| eHCC   | cg00461299 | -1.56      | 0.001989067 | -0.22 | 17      |    | Body   |
| eHCC   | cg05361750 | -1.67      | 0.000698823 | -0.21 | 17      |    | Body   |
| eHCC   | cg00235657 | -1.81      | 0.000670599 | -0.21 | 17      |    | Body   |
| eHCC   | cg12071008 | -1.20      | 1.01136E-05 | -0.20 | 17      |    | S_Shelf|
| eHCC   | cg00249503 | -1.39      | 0.000182287 | -0.20 | 17      |    | Body   |
| eHCC   | cg25399573 | -1.91      | 0.00330609  | -0.20 | 17      |    | S_Shelf|
| eHCC   | cg25730791 | -1.82      | 0.000144292 | -0.20 | 17      |    | S_Shelf|
| eHCC   | cg17514088 | -1.27      | 0.000189978 | -0.20 | 17      |    | S_Shelf|
| pHCC   | cg09687005 | -1.59      | 0.000185106 | -0.23 | 17      |    | Body   |

2 HLA-DPB2 HGDN cg11786476 -1.30 9.13045E-05 0.003882438 -0.21 6 Body
| eHCC   | cg11786476 | -1.32      | 0.000129282 | -0.21 | 6       |    | Body   |
| pHCC   | cg15019001 | -1.38      | 0.000270823 | -0.21 | 6       |    | Body   |

2 KCNK7 HGDN cg01178624 1.70 2.98276E-07 0.00018668 0.22 11 3'UTR Island
| eHCC   | cg13654525 | 1.66       | 7.55637E-06 | 0.23  | 11      |    | 3'UTR  |
| eHCC   | cg01178624 | 1.94       | 2.38825E-07 | 9.66868E-05 | 0.24 | 11 | 3'UTR  |
| pHCC   | cg13654525 | 1.59       | 5.27809E-05 | 0.04936093 | 0.23 | 11 | 3'UTR  |
| CHR | CNTR | HCC | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 |
|-----|------|-----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|
| 2   | LITAF| HGDN| 1,85 | 1,97909E-06 | 0,000851462 | 0,24 | 11 | 3'UTR | Island |
|     |     | eHCC| -1,75 | 0,000122039 | 0,004655068 | -0,27 | 16 | S'UTR | N_Shore |
|     |     | eHCC| -1,75 | 0,000324005 | 0,004352332 | -0,27 | 16 | S'UTR | N_Shore |
|     |     | eHCC| -1,36 | 9,61918E-07 | 0,000195514 | -0,21 | 16 | S'UTR | Island |
|     |     | eHCC| 1,47 | 0,001199532 | 0,025599932 | 0,24 | 16 | Body |
|     |     | eHCC| -1,86 | 0,000525378 | 0,01721716 | -0,29 | 16 | S'UTR | N_Shore |
|     | NID1 | HGDN| 1,91 | 0,000169018 | 0,005720422 | 0,28 | 1 | Body |
|     |     | eHCC| 1,65 | 0,000435298 | 0,005152185 | 0,26 | 1 | Body |
|     |     | eHCC| 2,51 | 5,20315E-05 | 0,001606117 | 0,34 | 1 | Body |
|     |     | pHCC| 2,01 | 0,001536239 | 0,030121025 | 0,28 | 1 | Body |
|     | PDE4DIP | HGDN| 1,56 | 1,23612E-05 | 0,001092258 | 0,23 | 1 | Body | Island |
|     |     | eHCC| 1,28 | 0,000192912 | 0,0032557 | 0,20 | 1 | Body |
|     |     | eHCC| 2,14 | 9,39715E-07 | 0,00013256 | 0,33 | 1 | Body | Island |
|     |     | pHCC| 1,53 | 0,000137731 | 0,008364683 | 0,22 | 1 | Body | Island |
|     | PURA | HGDN| -1,39 | 2,46686E-05 | 0,001708783 | -0,20 | 5 | TSS200 | Island |
|     |     | eHCC| -1,56 | 1,56117E-05 | 0,000839329 | -0,23 | 5 | TSS200 | Island |
|     |     | pHCC| -1,33 | 0,000206234 | 0,0104749 | -0,20 | 5 | TSS200 | Island |
|     | SCAMP1 | HGDN| -1,40 | 2,67704E-05 | 0,001797422 | -0,21 | 5 | TSS200 | Island |
|     |     | eHCC| -1,76 | 4,96589E-06 | 0,000457026 | -0,25 | 5 | TSS200 | Island |
|     |     | pHCC| -1,60 | 3,66992E-05 | 0,004025442 | -0,23 | 5 | TSS200 | Island |
|     | SMARCC1 | HGDN| 1,34 | 1,74423E-06 | 0,000332913 | 0,20 | 3 | Body |
|     |     | eHCC| 1,54 | 1,20461E-06 | 0,000220373 | 0,22 | 3 | Body |
|     |     | pHCC| 1,49 | 7,21492E-06 | 0,001641008 | 0,21 | 3 | Body |
|     | STRN4 | HGDN| -1,36 | 1,84822E-06 | 0,000345427 | -0,23 | 19 | Body | Island |
| Gene       | ID       | Start | End          | Log2 Fold | q-value | P-value | Dist | Strand | Strand  |
|------------|----------|-------|--------------|-----------|---------|---------|------|--------|---------|
| eHCC       | cg12254611 | -1,51 | 1,06453E-06  | -0,25     | 19      | Body    | Island |
| pHCC       | cg12254611 | -1,45 | 4,50614E-06  | -0,24     | 19      | Body    | Island |
| 2          | THSD7A    | HGDN  | cg24676244   | 1,32      | 7       | TSS1500 |       |
| eHCC       | cg01797590 | 1,35  | 4,50614E-06  | 0,22      | 7       | TSS200  |       |
| eHCC       | cg09557034 | 1,52  | 0,000351578  | 0,24      | 7       | TSS1500 |       |
| eHCC       | cg15090509 | 1,62  | 0,002053542  | 0,25      | 7       | TSS1500 |       |
| eHCC       | cg24676244 | 1,88  | 4,04352E-05  | 0,27      | 7       | TSS1500 |       |
| pHCC       | cg09557034 | 1,42  | 0,001686719  | 0,22      | 7       | TSS1500 |       |
| pHCC       | cg24676244 | 1,61  | 0,00915808   | 0,25      | 7       | TSS1500 |       |
| 2          | UGT2B15   | HGDN  | cg09189601   | 1,49      | 4       | Body    |       |
| eHCC       | cg04016992 | 1,64  | 9,7931E-05   | 0,25      | 4       | TSS1500 |       |
| eHCC       | cg09189601 | 1,95  | 0,007065252  | 0,26      | 4       | Body    |       |
| pHCC       | cg04016992 | 1,48  | 2,87402E-06  | 0,22      | 4       | TSS1500 |       |
| pHCC       | cg22161115 | 1,48  | 0,00906906   | 0,22      | 4       | 1stExon |       |
| pHCC       | cg09189601 | 1,79  | 0,002657726  | 0,26      | 4       | Body    |       |
| 2          | ZNF540    | HGDN  | cg03975694   | 1,60      | 19      | S'UTR   | S_Shelf |
| eHCC       | cg03975694 | 1,95  | 7,45205E-06  | 0,30      | 19      | S'UTR   | S_Shelf |
| pHCC       | cg03975694 | 1,31  | 0,00146315   | 0,21      | 19      | S'UTR   | S_Shelf |
| 2          | ZNF876P   | HGDN  | cg11836119   | 1,97      | 4       | Body    | Island |
| eHCC       | cg20296343 | 1,25  | 0,00028226   | 0,21      | 4       | Body    | Island |
| eHCC       | cg12547166 | 1,40  | 0,000573854  | 0,23      | 4       | Body    | Island |
| eHCC       | cg18005867 | 1,58  | 0,00023191   | 0,25      | 4       | TSS200  | N_Shore |
| eHCC       | cg23063647 | 1,71  | 0,000115482  | 0,26      | 4       | TSS200  | N_Shore |
| eHCC       | cg11836119 | 2,48  | 3,41294E-07  | 0,38      | 4       | Body    | Island |
| pHCC       | cg11836119 | 1,71  | 0,000117359  | 0,25      | 4       | Body    | Island |
| 2  | TMC4   | HGDN  | cg19488620 | 1,56 | 0,000578165 | 0,012265588 | 0,25 | 19 | Body | Island |
|----|--------|--------|------------|------|-------------|-------------|------|----|------|--------|
|    | eHCC   | cg19488620 | 1,85 | 0,00038676 | 0,004812381 | 0,30 | 19 | Body | Island |
|    | pHCC   | cg22710065  | 1,61 | 0,004008046 | 0,049097195 | 0,25 | 19 | Body | Island |

| 2  | LTBP2  | HGDN  | cg17335494 | 1,33 | 2,95183E-06 | 0,00045394 | 0,20 | 14 | Body | Island |
|----|--------|--------|------------|------|-------------|-------------|------|----|------|--------|
|    | eHCC   | cg17335494 | 1,71 | 9,7008E-07 | 0,000195616 | 0,24 | 14 | Body | Island |
|    | pHCC   | cg17335494 | 1,63 | 9,31953E-06 | 0,001869959 | 0,24 | 14 | Body | Island |

| 2  | HSPE1  | HGDN  | cg04657470 | -1,82 | 0,00398068 | 0,000224927 | 0,20 | 10 | Body | Island |
|----|--------|--------|------------|------|-------------|-------------|------|----|------|--------|
|    | eHCC   | cg04657470 | -1,77 | 0,005671351 | 0,025560944 | 0,22 | 2 | 1stExon | Island |
|    | pHCC   | cg04657470 | -1,95 | 0,003694816 | 0,047015393 | 0,24 | 2 | 1stExon | Island |

| 2  | DLG5   | HGDN  | cg05445097 | 1,67 | 6,67974E-09 | 1,7064E-05 | 0,21 | 10 | Body | Island |
|----|--------|--------|------------|------|-------------|-------------|------|----|------|--------|
|    | eHCC   | cg05445097 | 2,05 | 2,55651E-09 | 1,56739E-05 | 0,24 | 10 | Body | Island |
|    | eHCC   | cg23818888 | 1,33 | 0,000224927 | 0,003545275 | 0,22 | 10 | Body | S_Shore |
|    | eHCC   | cg27586487 | 1,48 | 0,000466056 | 0,005359283 | 0,24 | 10 | Body | S_Shore |
|    | pHCC   | cg05445097 | 2,12 | 1,03822E-08 | 0,000111982 | 0,24 | 10 | Body | Island |

| 3  | ALDH4A1| eHCC  | cg12461099 | 1,311 | 0,000199472 | 0,00330651 | 0,215 | 1 | TSS1500 |
|----|--------|--------|------------|-------|-------------|-------------|--------|----|-------|
|    | pHCC   | cg22390041 | 1,252 | 0,002907524 | 0,04166014 | 0,209 | 1 | Body | N_Shelf |
|    | pHCC   | cg12461099 | 1,277 | 0,00091188 | 0,022979088 | 0,214 | 1 | TSS1500 |

| 3  | ATG4B  | eHCC  | cg08969328 | 1,512 | 2,43749E-07 | 9,77949E-05 | 0,221 | 2 | Body | N_Shelf |
|----|--------|--------|------------|------|-------------|-------------|------|----|------|--------|
|    | pHCC   | cg08969328 | 1,362 | 3,86783E-06 | 0,001194488 | 0,203 | 2 | Body | N_Shelf |

| 3  | ATP6V0A1| eHCC  | cg07408552 | 1,591 | -0,001281942 | 0,02742878 | -0,212 | 17 | S'UTR | S_Shore |
|----|---------|--------|------------|------|-------------|-------------|--------|----|-------|--------|
|    | pHCC    | cg07408552 | 1,591 | -0,001281942 | 0,02742878 | -0,212 | 17 | S'UTR | S_Shore |

| 3  | ATP6V1C1| eHCC  | cg03506193 | 1,801 | 0,000104466 | 0,002333175 | -0,230 | 8 | S'UTR | S_Shore |
| pHCC | cg03506193 | 1,530 | 0.001025482 | 0.024401386 | -0.203 | 8 | S'UTR | S_Shore |
|---|---|---|---|---|---|---|---|---|
| C1QTNF4 | eHCC | cg05537653 | 1,685 | 5.2212E-06 | 0.000470519 | 0.232 | 11 | Body | Island |
| eHCC | cg17282004 | 1,676 | 0.000105627 | 0.002347565 | 0.270 | 11 | S'UTR | N_Shore |
| pHCC | cg18356785 | 1,546 | 0.00039042 | 0.01477456 | 0.224 | 11 | Body | Island |
| pHCC | cg05537653 | 2,027 | 2.75848E-06 | 0.00099236 | 0.264 | 11 | Body | Island |
| C9orf3 | eHCC | cg13853813 | 1,452 | 0.00110657 | 0.02407528 | 0.203 | 9 | Body | N_Shelf |
| eHCC | cg14375632 | 1,579 | 0.00017766 | 0.003106196 | 0.221 | 9 | Body | N_Shelf |
| pHCC | cg13853813 | 1,358 | 0.000772395 | 0.021106496 | 0.203 | 9 | Body | N_Shelf |
| pHCC | cg14582550 | 1,313 | 0.001540008 | 0.030163251 | 0.216 | 9 | Body | |
| pHCC | cg14375632 | 1,557 | 0.00684581 | 0.019814655 | 0.218 | 9 | Body | N_Shelf |
| CCDC57 | eHCC | cg12879038 | 1,475 | 3.08029E-05 | 0.001212628 | 0.218 | 17 | Body | S_Shelf |
| eHCC | cg22142205 | 1,561 | 3.40991E-06 | 0.000375385 | 0.239 | 17 | Body | |
| pHCC | cg22142205 | 1,339 | 4.60311E-05 | 0.004580184 | 0.202 | 17 | Body | |
| CCDC84 | eHCC | cg27211899 | 1,460 | 7.64443E-07 | 0.000174033 | 0.239 | 11 | Body | S_Shelf |
| pHCC | cg27211899 | 1,484 | 2.90065E-06 | 0.001024245 | 0.243 | 11 | Body | S_Shelf |
| CHERP | eHCC | cg07688052 | 1,963 | 0.000193902 | 0.00325567 | 0.235 | 19 | Body | S_Shore |
| pHCC | cg07688052 | 1,977 | 0.0052654 | 0.017226223 | 0.236 | 19 | Body | S_Shore |
| CHST11 | eHCC | cg11739675 | 1,630 | 0.008780547 | 0.034372311 | 0.214 | 12 | Body | Island |
| eHCC | cg22260952 | 1,778 | 0.002707995 | 0.015736824 | 0.244 | 12 | Body | S_Shore |
| eHCC | cg17844339 | 2,548 | 0.00680007 | 0.006717223 | -0.236 | 12 | Body | Island |
| eHCC | cg07696842 | 1,292 | 0.00037952 | 0.004759914 | -0.214 | 12 | Body | |
| eHCC | cg12529671 | - | 0.002815763 | 0.016142203 | -0.209 | 12 | Body | S_Shore |
|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
|   |   |   |   |   |   |   |
| pHCC | cg01964337 | 1,281 | 0,001199658 | 0,026492301 | 0,206 | 12 | Body |
| pHCC | cg07696842 | - | 0,000652404 | 0,019299821 | -0,227 | 12 | Body |
| pHCC | cg16861964 | - | 0,000308331 | 0,013052779 | -0,227 | 12 | Body |
| pHCC | cg22827210 | - | 0,000187928 | 0,009964452 | -0,220 | 12 | Body |
|   |   |   |   |   |   |   |   |
| 3 | CLEC14A | eHCC | cg16404157 | 1,378 | 0,008322495 | 0,033120954 | 0,221 | 14 | 1stExon | Island |
| eHCC | cg05057720 | 1,801 | 0,000327148 | 0,004377465 | 0,274 | 14 | 1stExon | Island |
| pHCC | cg05057720 | 1,655 | 0,001634184 | 0,031113321 | 0,247 | 14 | 1stExon | Island |
|   |   |   |   |   |   |   |   |   |   |   |
| 3 | CMYA5 | eHCC | cg10257870 | 1,312 | 0,007300510 | 0,007002320 | 0,212 | 5 | TSS200 |
| eHCC | cg09481121 | 1,384 | 0,000230309 | 0,003590465 | 0,222 | 5 | TSS1500 |
| eHCC | cg03546977 | 1,413 | 9,60515E-05 | 0,00228094 | 0,228 | 5 | TSS200 |
| pHCC | cg11438310 | 1,219 | 0,000875076 | 0,022496643 | 0,202 | 5 | TSS1500 |
| pHCC | cg09481121 | 1,407 | 0,000593429 | 0,018400473 | 0,229 | 5 | TSS1500 |
| pHCC | cg00611789 | 1,395 | 0,003783493 | 0,047602404 | 0,231 | 5 | TSS1500 |
| pHCC | cg10257870 | 1,414 | 0,000952755 | 0,023470697 | 0,235 | 5 | TSS200 |
|   |   |   |   |   |   |   |   |   |   |   |
| 3 | CNKSR1 | eHCC | cg17330765 | 1,378 | 0,001125212 | 0,025635624 | 0,214 | 5 | TSS1500 |
| pHCC | cg17330765 | 1,378 | 0,001125212 | 0,025635624 | 0,214 | 5 | TSS1500 |
|   |   |   |   |   |   |   |   |   |   |   |
| 3 | CRHB | eHCC | cg01071966 | 1,381 | 0,000729558 | 0,006998839 | 0,227 | 5 | 1stExon | N_Shore |
| pHCC | cg05884167 | 2,191 | 0,000227405 | 0,011034262 | 0,209 | 5 | Body | S_Shelf |
|   |   |   |   |   |   |   |   |   |   |   |
| 3 | CRYBB3 | eHCC | cg19288514 | 1,609 | 1,67785E-08 | 3,16982E-05 | 0,266 | 22 | TSS1500 |
| pHCC | cg19288514 | 1,499 | 2,37709E-07 | 0,000328142 | 0,250 | 7 | TSS1500 |
|   |   |   |   |   |   |   |   |   |   |   |
| 3 | CUL3 | eHCC | cg01474011 | 1,560 | 0,001798314 | 0,012124535 | 0,215 | 2 | Body |
|      |      |      |      |      |      |      |      |      |      |
|------|------|------|------|------|------|------|------|------|------|
| pHCC | cg25502818 | 1,260 | 0,00276786 | 0,040613403 | 0,212 | 2 | Body |
| 3    | DNASE1L2 | eHCC | cg06235653 | 1,330 | 0,003322905 | 0,017966376 | 0,210 | 16 | Body | Island |
|      | eHCC   | cg00249383 | 1,412 | 0,000227655 | 0,003568218 | 0,228 | 16 | Body | Island |
|      | pHCC   | cg00249383 | 1,286 | 0,00173383 | 0,032096979 | 0,209 | 16 | Body | Island |
|      | pHCC   | cg06235653 | 1,596 | 0,00210258 | 0,035423104 | 0,256 | 16 | Body | Island |
| 3    | DNHD1  | eHCC | cg10383568 | 1,500 | 2,51893E-05 | 0,001084113 | 0,249 | 11 | Body | N_Shelf |
|      | pHCC   | cg10383568 | 1,297 | 0,000442103 | 0,015777083 | 0,218 | 11 | Body | N_Shelf |
| 3    | EGFLAM | eHCC | cg25344265 | 1,796 | 0,000173692 | 0,003066918 | -0,269 | 5 | Body |
|      | eHCC   | cg18855621 | 1,923 | 7,58721E-06 | 0,000574267 | -0,241 | 5 | Body |
|      | eHCC   | cg08264481 | 1,610 | 6,30507E-06 | 0,000520237 | -0,232 | 5 | Body |
|      | eHCC   | cg11475323 | 1,906 | 7,30788E-05 | 0,001921857 | -0,205 | 5 | Body | S_Shelf |
|      | pHCC   | cg25625968 | 1,250 | 0,001287529 | 0,027495665 | 0,201 | 5 | 3'UTR |
| 3    | ELF1   | eHCC | cg18456803 | 1,514 | 0,000796076 | 0,007373515 | -0,253 | 13 | TSS200 |
|      | pHCC   | cg18456803 | 1,559 | 0,00183015 | 0,033032031 | -0,242 | 13 | TSS200 |
| 3    | EXOC2  | eHCC | cg04789318 | 1,427 | 5,31979E-08 | 4,95599E-05 | 0,216 | 6 | 5'UTR | N_Shelf |
|      | pHCC   | cg04789318 | 1,402 | 4,21574E-07 | 0,000397163 | 0,211 | 6 | 5'UTR | N_Shelf |
| 3    | FAM20B | eHCC | cg24997888 | 1,509 | 0,000260012 | 0,003847161 | 0,227 | 1 | 3'UTR |
|      | pHCC   | cg24997888 | 1,610 | 0,00529955 | 0,017284303 | 0,243 | 1 | 3'UTR |
| Gene | Tissue | ChIP | Accession | Log2FC | P-value | q-value | Enrichment | ChIP | Accession | Log2FC | P-value | q-value | Enrichment |
|------|--------|------|-----------|--------|---------|---------|------------|------|-----------|--------|---------|---------|------------|
| FGFR4 | eHCC   | cg12982374 | 1,408  | 0,00032384 | 0,004351191 | 0,211  | 5 | Body | S_Shelf |
|      | eHCC   | cg17386911 | 1,617  | 0,000907565 | 0,007963218 | 0,223  | 5 | Body | S_Shelf |
|      | pHCC   | cg12982374 | 1,289  | 0,002217601 | 0,036337706 | 0,201  | 5 | Body | S_Shelf |
| FNDC1 | eHCC   | cg09107912 | 1,687  | 0,00231206  | 0,003597966 | 0,243  | 6 | TSS1500 | Island |
|      | eHCC   | cg00157796 | 1,567  | 0,000243301 | 0,003702274 | 0,257  | 6 | TSS200 | Island |
|      | pHCC   | cg07739841 | 1,542  | 0,001018914 | 0,02432998 | 0,243  | 6 | Body | S_Shelf |
| FNDC1 | eHCC   | cg26999423 | 1,929  | 0,000418194 | 0,005037802 | -0,298 | 17 | Body |
|      | eHCC   | cg12091339 | 1,922  | 0,000632805 | 0,006428996 | -0,230 | 17 | Body |
|      | eHCC   | cg07049421 | 1,479  | 0,001028094 | 0,008569715 | -0,226 | 17 | Body |
|      | eHCC   | cg02605292 | 1,670  | 0,000670632 | 0,006664488 | -0,201 | 17 | Body |
|      | pHCC   | cg26999423 | 1,844  | 0,002011096 | 0,03465132 | -0,288 | 17 | Body |
|      | pHCC   | cg06130714 | 1,369  | 0,000397627 | 0,01491624 | -0,223 | 17 | Body |
| GLTSCR1 | eHCC  | cg22461472 | 1,621  | 8,72305E-05  | 0,002116745 | 0,215  | 19 | Body | S_Shelf |
|      | pHCC   | cg22461472 | 1,529  | 0,000577861 | 0,018119573 | 0,211  | 19 | Body | S_Shelf |
| HELZ  | eHCC   | cg18432877 | 1,498  | 0,000393989 | 0,004866668 | 0,215  | 17 | Body |
|      | pHCC   | cg18432877 | 1,791  | 0,000286473 | 0,012544729 | 0,239  | 17 | Body |
| HIPK1 | eHCC   | cg17588904 | 1,330  | 4,52477E-07  | 0,000133055 | 0,218  | 1 | Body |
|      | pHCC   | cg17588904 | 1,402  | 1,11097E-06  | 0,00064397 | 0,223  | 1 | Body |
| HIST1H3H | eHCC | cg01330280 | -      | 0,001917359 | 0,012611879 | -0,259 | 6 | TSS1500 | N_Shore |
| **Position** | **Gene** | **Probe** | **Expression** | **Log2** | **Log10** | **FDR** | **Model** | **Location** |
|--------------|----------|-----------|----------------|----------|-----------|--------|-----------|-------------|
| 1,640        | pHCC cg01330280 | 1,959     | 0.001474903   | -0.321   | 6         | TSS1500 | N_Shore   |
| 1,959        | eHCC cg19960778 | 1,970     | 4.63067E-05   | -0.253   | 5         | Body    | S_Shore   |
| 1,970        | eHCC cg11093640 | 1,740     | 0.00019669    | -0.235   | 5         | 3'UTR   | S_Shelf   |
| 1,740        | eHCC cg06485139 | 1,614     | 0.000826268   | -0.232   | 5         | Body    | N_Shore   |
| 1,614        | eHCC cg04875020 | 1,426     | 0.000132017   | -0.215   | 5         | Body    | N_Shore   |
| 1,426        | pHCC cg04875020 | 1,528     | 0.000241237   | -0.231   | 5         | Body    | N_Shore   |
| 1,984        | eHCC cg25699851 | 1,960     | 8.93371E-05   | -0.272   | 15        | Body    |            |
| 1,960        | eHCC cg26217827 | 2,600     | 0.014278532   | 0.308    | 15        | 3'UTR   |            |
| 2,600        | pHCC cg08872353 | 1,552     | 0.000233928   | -0.244   | 15        | Body    | N_Shelf   |
| 1,552        | pHCC cg24213777 | 1,231     | 0.000419666   | -0.203   | 15        | Body    |            |
| 1,316        | eHCC cg02256631 | 1,316     | 0.006135867   | 0.205    | 16        | Body    | Island    |
| 1,316        | pHCC cg22490695 | 1,251     | 0.001683579   | -0.207   | 16        | TSS200  |            |
| 1,879        | eHCC cg03460756 | 1,879     | 9.40275E-05   | 0.294    | 17        | Body    |            |
| 1,540        | pHCC cg03460756 | 1,540     | 0.001842825   | 0.250    | 17        | Body    |            |
| 1,846        | eHCC cg16550651 | 1,846     | 5.26457E-05   | 0.249    | 17        | Body    | N_Shore   |
| 1,690        | pHCC cg16550651 | 1,690     | 0.000494374   | 0.250    | 17        | Body    | N_Shore   |
|   | Gene   | Array |   | Parent | Chromosome | Score | FDR  | qval  | pval  | pval  |      | TSS | 5'UTR | Body | Island |
|---|--------|-------|---|--------|------------|-------|------|-------|-------|-------|------|-------|-------|---------|
| 3 | KCNS2  | eHCC  | cg08706670 | 1,440 | 0,006555951 | 0,028188336 | 0.234 | 8 | TSS200 | Island |
|   | eHCC   | cg11964564 | 1,668 | 0,002889448 | 0,016412185 | 0.250 | 8 | S'UTR | Island |
|   | eHCC   | cg14486338 | 2,317 | 1.65125E-06 | 0.000257477 | 0.363 | 8 | Body  | Island |
|   | eHCC   | cg14688104 | 3,040 | 0.001682393 | 0.011622988 | 0.371 | 8 | 1stExon | Island |
|   | pHCC   | cg14688104 | 3,469 | 0.001847787 | 0.033182257 | 0.415 | 8 | 1stExon | Island |
| 3 | KIAA1875 | eHCC | cg01423393 | 1,582 | 1,71307E-05 | 0.00880983 | 0.214 | 8 | Body  | Island |
|   | pHCC   | cg01423393 | 1,452 | 7,2645E-05 | 0.005914085 | 0.201 | 8 | Body  | Island |
| 3 | KLHL5  | eHCC  | cg08217447 | 1,690 | 0.0062228 | 0.006366254 | 0.247 | 4 | TSS1500 | Island |
|   | PHCC   | cg08217447 | 1,699 | 0.001756363 | 0.032326742 | 0.254 | 4 | TSS1500 | Island |
| 3 | LPP    | eHCC  | cg04423294 | 1,339 | 3,16552E-05 | 0.001230227 | 0.209 | 3 | Body  | Island |
|   | PHCC   | cg24454374 | 1,213 | 0.003067089 | 0.042809967 | 0.200 | 3 | S'UTR | Island |
| 3 | LZTS1  | eHCC  | cg05796178 | 2,089 | 2,50859E-05 | 0.001081459 | -0.268 | 8 | Body  | S_Shelf |
|   | PHCC   | cg13583414 | 1,575 | 0.000643847 | 0.019167934 | -0.228 | 8 | Body  | S_Shelf |
|   |        | cg05796178 | 1,815 | 0.000349394 | 0.013922142 | -0.223 | 8 | Body  | S_Shelf |
| 3 | MAST2  | eHCC  | cg02835462 | 1,233 | 0.000386466 | 0.004810093 | 0.207 | 1 | Body  | Island |
|   | PHCC   | cg02835462 | 1,361 | 0.000575537 | 0.018077614 | 0.227 | 1 | Body  | Island |
| 3 | MATN2  | eHCC  | cg19987349 | 1,429 | 3,71774E-07 | 0.000120037 | 0.218 | 8 | Body  | Island |
|   | PHCC   | cg19987349 | 1,433 | 2,04715E-06 | 0.000862524 | 0.214 | 8 | Body  | Island |
| 3 | MCM6   | eHCC  | cg11446240 | 1,595 | 3,51221E-05 | 0.001299532 | -0.226 | 2 | Body  | N_Shore |
| Gene     | Chromosome | Start | End   | Log2 Fold Change | p-Value | Adjusted p-Value | Type   | Location         |
|----------|------------|-------|-------|------------------|---------|------------------|--------|------------------|
| pHCC cg11446240 | 1,579 | 0,000157345 | 0,00900492 | -0,225 | 2 | Body | N_Shore |
| eHCC cg05812657 | 1,608 | 2,15541E-08 | 3,44223E-05 | 0,234 | X | Body | N_Shelf |
| pHCC cg05812657 | 1,687 | 6,30141E-08 | 0,000183304 | 0,240 | X | Body | N_Shelf |
| eHCC cg24124703 | 1,438 | 0,005506455 | 0,02505221 | -0,217 | 5 | S'UTR |
| pHCC cg24124703 | 1,861 | 0,002258426 | 0,036679761 | -0,262 | 5 | S'UTR |
| eHCC cg23826579 | 1,546 | 1,30982E-07 | 7,31567E-05 | 0,251 | 6 | Body | S_Shelf |
| pHCC cg23826579 | 1,286 | 4,33075E-06 | 0,001248971 | 0,210 | 6 | Body | S_Shelf |
| eHCC cg11992783 | 1,724 | 0,000115076 | 0,002459796 | 0,206 | 19 | Body | Island |
| pHCC cg11992783 | 1,821 | 0,000215926 | 0,010733716 | 0,216 | 19 | Body | Island |
| eHCC cg03318573 | 1,291 | 0,004886644 | 0,005512554 | 0,209 | 14 | TSS1500 | N_Shore |
| pHCC cg03318573 | 1,320 | 0,001343153 | 0,028088478 | 0,212 | 14 | TSS1500 | N_Shore |
| eHCC cg17455088 | 1,335 | 0,001262114 | 0,009722315 | 0,211 | 2 | Body | S_Shore |
| eHCC cg05348875 | 1,283 | 3,85549E-05 | 0,001361272 | 0,214 | 2 | Body |
| eHCC cg10648139 | 1,809 | 0,000334581 | 0,004435961 | 0,271 | 2 | Body | S_Shore |
| eHCC cg22367989 | 2,896 | 2,9864E-05 | 0,001191996 | 0,399 | 2 | TSS1500 | Island |
| pHCC cg17455088 | 1,325 | 0,003927781 | 0,048570256 | 0,213 | 2 | Body | S_Shore |
| eHCC cg10500503 | 1,244 | 0,002311455 | 0,014220871 | 0,207 | 1 | Body |
| pHCC cg22396959 | 1,366 | 6,53391E-05 | 0,005585362 | 0,214 | 1 | Body |
| eHCC cg11437328 | 1,636 | 0,000103987 | 0,002327386 | 0,220 | 19 | TSS1500 | S_Shelf |
| pHCC cg11437328 | 1,471 | 0,001021355 | 0,024356157 | 0,215 | 19 | TSS1500 | S_Shelf |
| Gene | Allele | Location | Distance | FDR | q-value | Windows | Site | Score |
|------|--------|----------|----------|-----|---------|---------|------|-------|
| PAQR6 | eHCC | cg24152297 | 1,526 | 4,7237E-08 | 4,66868E-05 | 0,231 | 1 | TSS1500 | S_Shelf |
|      | pHCC | cg24152297 | 1,614 | 1,27344E-07 | 0,000245382 | 0,240 | 1 | TSS1500 | S_Shelf |
| PCNX  | eHCC | cg14009504 | 1,541 | 9,29995E-07 | 0,000192231 | 0,213 | 14 | Body |
|      | pHCC | cg14009504 | 1,906 | 3,95852E-07 | 0,000388937 | 0,249 | 14 | Body |
| PIK3CG | eHCC | cg13214190 | 1,668 | 0,007053349 | 0,029621361 | -0,271 | 7 | TSS200 | N_Shelf |
|      | eHCC | cg00604356 | 1,636 | 0,000843102 | 0,007627393 | -0,263 | 7 | 5'UTR | N_Shore |
|      | pHCC | cg00510718 | 3,046 | 0,0093089 | 0,023196776 | -0,444 | 7 | 5'UTR | N_Shelf |
|      | pHCC | cg13214190 | 2,422 | 0,01360526 | 0,028282152 | -0,365 | 7 | TSS200 | N_Shelf |
|      | pHCC | cg15881332 | 2,204 | 0,000849698 | 0,022174918 | -0,331 | 7 | TSS200 | N_Shelf |
|      | pHCC | cg08779777 | 2,115 | 0,00618061 | 0,018803362 | -0,314 | 7 | TSS200 | N_Shelf |
|      | pHCC | cg00661777 | 2,053 | 0,000411995 | 0,01518033 | -0,307 | 7 | Body | S_Shelf |
|      | pHCC | cg11982525 | 1,933 | 0,000945677 | 0,023385181 | -0,303 | 7 | TSS1500 | N_Shelf |
|      | pHCC | cg00604356 | 1,588 | 0,003205808 | 0,04376952 | -0,261 | 7 | 5'UTR | N_Shore |
| PLEKHF2 | eHCC | cg12930753 | 1,667 | 0,000191699 | 0,003233648 | 0,263 | 8 | 3'UTR |
|      | pHCC | cg12930753 | 1,394 | 0,00291337 | 0,041710621 | 0,233 | 8 | 3'UTR |
| PPM1D  | eHCC | cg04180177 | 1,252 | 2,06493E-06 | 0,000288918 | 0,205 | 17 | Body |
|      | pHCC | cg04180177 | 1,270 | 7,28475E-06 | 0,001650356 | 0,209 | 17 | Body |
| # | Gene | Tissue | probe | Gene | Tissue | probe | p-value | FDR | q-value | FDR | p-value | FDR | q-value | FDR | Tissue |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 3 | PRMT7 | eHCC | cg10061770 | 1,574 | 0,000132487 | 0,002651869 | 0,230 | 16 | Body |
| 3 | eHCC | cg10061770 | 1,419 | 0,00119487 | 0,02643786 | 0,204 | 16 | Body |
| 3 | PRR5 | eHCC | cg04607412 | 1,445 | 0,000633153 | 0,00643074 | 0,210 | 22 | S'UTR |
| 3 | eHCC | cg04607412 | 1,764 | 0,000376057 | 0,01448421 | 0,262 | 22 | S'UTR |
| 3 | PTBP1 | eHCC | cg19373090 | 1,427 | 2,20224E-07 | 9,30733E-05 | -0,206 | 19 | TSS200 |
| 3 | eHCC | cg19373090 | 1,409 | 7,89021E-07 | 0,00054168 | -0,204 | 19 | TSS200 |
| 3 | PTPRJ | eHCC | cg04462547 | 1,365 | 4,60958E-07 | 0,00013413 | 0,208 | 11 | Body |
| 3 | eHCC | cg06298729 | 1,712 | 0,000239524 | 0,03671033 | 0,211 | 11 | Body |
| 3 | eHCC | cg04607412 | 1,358 | 1,99131E-06 | 0,000854347 | 0,206 | 11 | Body |
| 3 | REEP3 | eHCC | cg10300729 | 1,531 | 1,98415E-07 | 8,90064E-05 | 0,237 | 10 | Body |
| 3 | eHCC | cg10300729 | 1,475 | 1,27E-06 | 0,00069073 | 0,228 | 10 | Body |
| 3 | RGS10 | eHCC | cg19653161 | 1,549 | 0,002574817 | 0,01522054 | 0,226 | 10 | TSS1500 |
| 3 | eHCC | cg17527393 | 2,662 | 1,27339E-05 | 0,00756324 | 0,260 | 10 | TSS200 |
| 3 | eHCC | cg10200202 | 1,539 | 0,00977178 | 0,02378008 | -0,255 | 10 | Body |
| 3 | RNF220 | eHCC | cg24603481 | 1,697 | 0,000641549 | 0,0064862 | -0,214 | 1 | Body |
| 3 | eHCC | cg01422881 | 1,406 | 0,00312242 | 0,04260469 | 0,237 | 1 | S'UTR |
| 3 | eHCC | cg09860921 | 1,317 | 0,001947444 | 0,034084364 | 0,215 | 1 | Body |
| 3 | SCAND3 | eHCC | cg19747271 | 1,425 | 3,52492E-05 | 0,001301472 | -0,225 | 6 | Body |
| 3 | eHCC | cg22302929 | 1,695 | 1,91757E-05 | 0,000934563 | 0,258 | 6 | 1stExon |
| Gene   | Transcript | Chromosome | Start | End   | Log2 Fold Change | p-Value | FDR   | Type   | Location |
|--------|------------|------------|-------|-------|-----------------|---------|-------|--------|----------|
| pHCC   | cg19747271 | 1,494      | 8,53122E-05 | 0,006437328 | -0,237 | 6       | Body   | N_Shore |
| pHCC   | cg22302929 | 1,305      | 0,00097212  | 0,023718003  | 0,208  | 6       | 1stExon| N_Shore |
| 3 SKI  | eHCC      | cg12483545 | 1,672 | 0,002420813 | 0,14641106 | 0,230 | 1       | Body   |
| pHCC   | cg12580943 | 1,254      | 0,002315354 | 0,037158143  | 0,210  | 1       | Body   |
| 3 SLC25A27 | eHCC   | cg19101566 | 1,936 | 0,00027258  | 0,003947906 | 0,288 | 6       | Body   | S_Shelf |
| pHCC   | cg19101566 | 2,029      | 0,000566117 | 0,017929972  | 0,291  | 6       | Body   | S_Shelf |
| 3 SORBS1 | eHCC   | cg27111150 | 1,375 | 6,52052E-05 | 0,001804757 | 0,217 | 10      | Body   |
| pHCC   | cg27111150 | 1,255      | 0,000608058 | 0,018646515  | 0,202  | 10      | Body   |
| 3 SPN  | eHCC      | cg02030929 | 1,627 | 0,000442249 | 0,00519771 | -0,228 | 16      | Body   | Island |
| pHCC   | cg09946623 | 1,307      | 0,000805557 | 0,02156554   | -0,205 | 16      | TSS1500| N_Shore |
| 3 SWAP70 | eHCC   | cg08213398 | 1,431 | 8,23954E-07 | 0,000181688 | 0,212 | 11      | Body   |
| pHCC   | cg08213398 | 1,389      | 6,41799E-06 | 0,001559998  | 0,206  | 11      | Body   |
| 3 TAF7L | eHCC      | cg19386336 | 1,513 | 0,000545741 | 0,005886281 | 0,210  | X       | Body   | Island |
| eHCC   | cg01538344 | 1,525      | 0,000402553 | 0,004930357  | 0,244  | X       | 1stExon| Island |
| pHCC   | cg01538344 | 1,332      | 0,003016047 | 0,042460241  | 0,213  | X       | 1stExon| Island |
| 3 TIGD1 | eHCC      | cg18346402 | 1,518 | 3,05397E-07 | 0,000108993 | 0,249  | 2       | 1stExon| N_Shelf |
| pHCC   | cg18346402 | 1,534      | 1,59034E-06 | 0,000776591  | 0,252  | 2       | 1stExon| N_Shelf |
| 3 TNS1  | eHCC      | cg06320380 | 1,744 | 4,86194E-05 | 0,001545514 | 0,273  | 2       | S'UTR  |
| eHCC   | cg09548780 | 2,360      | 1,21401E-05 | 0,000736362  | 0,334  | 2       | S'UTR  |
| pHCC   | cg12681370 | 1,368      | 0,000356473 | 0,014046256  | 0,218  | 2       | S'UTR  |
|   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|
| 3 | TSC2 | eHCC | cg07730183 | 1.854 | 0.0001864 | 0.003185782 | 0.212 | 16 | Body | S_Shore |
|  | eHCC | cg06094085 | 1.503 | 0.001664462 | 0.011549222 | 0.215 | 16 | Body | S_Shore |
|  | eHCC | cg02504384 | 1.452 | 0.000417413 | 0.005032416 | 0.220 | 16 | Body | N_Shelf |
|  | eHCC | cg02364279 | 1.929 | 0.000903404 | 0.007942003 | 0.232 | 16 | Body | N_Shore |
|  | eHCC | cg06330323 | 1.594 | 0.000949283 | 0.008178712 | 0.246 | 16 | Body | N_Shore |
|  | pHCC | cg07730183 | 1.714 | 0.001321892 | 0.027828249 | 0.208 | 16 | Body | S_Shore |
| 3 | TXNDC5 | eHCC | cg11401394 | 1.712 | 0.000266358 | 0.003897322 | 0.255 | 6 | Body |
|  | pHCC | cg11401394 | 1.730 | 0.0008659 | 0.022381669 | 0.266 | 6 | Body |
| 3 | UCN | eHCC | cg05113927 | 1.744 | 9.60018E-07 | 0.000195291 | 0.223 | 2 | TSS200 | Island |
|  | eHCC | cg01454215 | 1.562 | 0.002163461 | 0.013625739 | 0.229 | 2 | 3'UTR | Island |
|  | pHCC | cg05113927 | 1.519 | 2.51897E-05 | 0.00325082 | 0.202 | 2 | TSS200 | Island |
| 3 | ZDHHC7 | eHCC | cg03655147 | 1.327 | 6.80724E-06 | 0.000542317 | 0.220 | 16 | S'UTR | N_Shelf |
|  | eHCC | cg09735674 | 1.240 | 1.76519E-05 | 0.00089602 | -0.208 | 16 | S'UTR | Island |
|  | pHCC | cg03655147 | 1.331 | 1.914E-05 | 0.002779045 | 0.215 | 16 | S'UTR | N_Shelf |
| 3 | ZMIZ2 | eHCC | cg11425656 | 1.311 | 2.80346E-05 | 0.001149676 | 0.204 | 7 | S'UTR | S_Shelf |
|  | pHCC | cg11425656 | 1.361 | 8.29045E-05 | 0.006348372 | 0.215 | 7 | S'UTR | S_Shelf |
| 3 | ZNF366 | eHCC | cg11905892 | 2.567 | 0.002712455 | 0.015752691 | -0.291 | 5 | Body | Island |
|  | eHCC | cg22558265 | 2.606 | 0.000212609 | 0.003430324 | -0.246 | 5 | Body | Island |
|  | eHCC | cg00657287 | 1.836 | 0.000982352 | 0.008344657 | -0.218 | 5 | Body | N_Shore |
|  | pHCC | cg04454664 | 1.253 | 0.000262241 | 0.011943707 | 0.207 | 5 | Body |
| Rank | Gene     | Transcript | dist | FDR 1 probe 1 | FDR 2 probe 1 | fold change 1 | % AUC up 1 | % AUC down 1 | Tissue   | Location   |
|------|----------|------------|------|---------------|---------------|---------------|-------------|-------------|----------|------------|
| 3    | EBF3    | eHCC       | 2,310| 3.09135E-05   | 9.001214837   | -0.301        | 10          | Body       | N_Shore   |
|      | eHCC    | cg07506153 | 2,606| 0.005569163   | 0.025243439   | -0.288        | 10          | Body       | N_Shore   |
|      | eHCC    | cg20800606 | 1,834| 0.006677521   | 0.025243439   | -0.256        | 10          | Body       | Island    |
|      | eHCC    | cg27454298 | 2,091| 0.000271399   | 0.003938483   | -0.241        | 10          | Body       | Island    |
|      | eHCC    | cg10598433 | 2,212| 0.00352589    | 0.004565217   | -0.224        | 10          | Body       | S_Shore   |
|      | eHCC    | cg02337436 | 2,071| 0.000458332   | 0.005307685   | -0.213        | 10          | Body       |           |
|      | eHCC    | cg03128163 | 1,594| 0.000012163   | 0.00242401    | -0.209        | 10          | Body       | N_Shore   |
|      | eHCC    | cg15991708 | 1,586| 6.8076E-05    | 0.00100482    | -0.206        | 10          | Body       |           |
|      | eHCC    | cg19582265 | 1,455| 6.81884E-05   | 0.001850109   | -0.218        | 10          | TSS1500    |           |
|      | pHCC    | cg04043455 |      |               |               |               |             |            |           |
| 3    | FAM189A1| eHCC       | 2,078| 5.56733E-05   | 0.00166393    | -0.239        | 15          | Body       |           |
|      | eHCC    | cg18512553 | 2,042| 0.000129207   | 0.002616178   | -0.237        | 15          | Body       |           |
|      | eHCC    | cg12711059 | 1,486| 9.64515E-05   | 0.002233551   | -0.226        | 15          | 3'UTR      |           |
|      | eHCC    | cg08904058 | 1,260| 0.00010854    | 0.002382418   | -0.212        | 15          | Body       |           |
|      | eHCC    | cg21207450 | 1,460| 0.000366217   | 0.004665259   | -0.200        | 15          | Body       |           |
|      | pHCC    | cg12711059 | 1,510| 0.000319038   | 0.013289653   | -0.227        | 15          | 3'UTR      |           |
|   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|
|   | pHCC  | cg25941083 | 1,342 | 0,000934362 | 0,023252263 | -0,227 | 15 | Body |
|   | eHCC  | cg14506260 | 1,307 | 0,007127305 | 0,029833619 | 0,207 | 10 | Body |
|   | eHCC  | cg24361761 | 2,232 | 0,00041694 | 0,05029219 | 0,345 | 10 | Body |
|   | pHCC  | cg24361761 | 10  | Body |
|   |   |   |   |   |   |   |   |   |
|   | pHCC  | cg08279075 | 1,763 | 0,001841239 | 0,012304077 | 0,271 | 16 | Body | Island |
|   | eHCC  | cg05001964 | 1,328 | 0,001413256 | 0,028877383 | 0,203 | 16 | Body | Island |
|   |   |   |   |   |   |   |   |   |
|   | eHCC  | cg17158414 | 1,739 | 0,001462983 | 0,010658876 | 0,216 | 2 | 1stExon | Island |
|   | eHCC  | cg11618577 | 1,529 | 0,004597055 | 0,022223653 | 0,220 | 2 | Body | Island |
|   | eHCC  | cg24768116 | 1,661 | 0,001495017 | 0,010809349 | 0,236 | 2 | TSS200 | Island |
|   | eHCC  | cg04845466 | 1,869 | 0,000128646 | 0,002610293 | 0,246 | 2 | TSS200 | Island |
|   | eHCC  | cg05259227 | 1,881 | 0,004601606 | 0,022239456 | 0,247 | 2 | Body | Island |
|   | pHCC  | cg17158414 | 1,773 | 0,003062764 | 0,042779192 | 0,219 | 2 | 1stExon | Island |
|   | pHCC  | cg04845466 | 1,893 | 0,000360845 | 0,014146618 | 0,234 | 2 | TSS200 | Island |
|   |   |   |   |   |   |   |   |   |
|   | eHCC  | cg27237671 | 1,418 | 0,000653957 | 0,006562296 | 0,227 | 2 | Body | N_Shore |
|   | pHCC  | cg27237671 | 1,327 | 0,003406437 | 0,045094384 | 0,213 | 2 | Body | N_Shore |
|   |   |   |   |   |   |   |   |   |
|   | eHCC  | cg36555615 | 1,817 | 0,00125122 | 0,09675403 | -0,243 | 3 | Body | Island |
|   | eHCC  | cg10460033 | 1,524 | 0,000259 | 0,003837685 | -0,239 | 3 | Body | N_Shore |
|   | eHCC  | cg21242025 | 1,467 | 0,001549776 | 0,011053473 | -0,214 | 3 | Body | S_Shelf |
|   | pHCC  | cg10460033 | 1,350 | 0,002408034 | 0,03792216 | -0,214 | 3 | Body | N_Shore |
|   |   |   |   |   |   |   |   |   |
|   | eHCC  | cg20287790 | 2,232 | 1,67669E-06 | 0,000259292 | 0,242 | 1 | 3'UTR |
| eHCC | pHCC | 3'UTR | N_Shelf | N_Shore | 5'UTR | Body | Island |
|------|------|-------|---------|---------|-------|------|--------|
| 3    | APC2 | cg19333963 | 1,974 | 0,003810961 | 0,01964788 | 0,314 | 19     | Body    | Island  |
|      | eHCC | cg03306486 | 2,479 | 0,002036304 | 0,013109485 | 0,378 | 19     | Body    | Island  |
|      | eHCC | cg10808783 | 2,602 | 0,000248662 | 0,003747633 | 0,385 | 19     | Body    | Island  |
|      | pHCC | cg10808783 |      |          |        |       |        |         |         |

3    | CBFA2T3 | cg27434245 | 1,444 | 0,000527098 | 0,005763933 | 0,203 | 16     | 1stExon | Island  |
|      | eHCC | cg04072301 | 2,046 | 8,47368E-06 | 0,000612218 | -0,306 | 16     | S'UTR   | Island  |
|      | eHCC | cg02633398 | 1,408 | 0,000986554 | 0,008367024 | -0,223 | 16     | S'UTR   | N_Shore |
|      | eHCC | cg03021297 | 1,821 | 0,001129361 | 0,009079844 | -0,215 | 16     | S'UTR   |         |
|      | pHCC | cg00762678 | 1,265 | 0,000881122 | 0,022581799 | -0,208 |         | S'UTR   | N_Shelf |
|      | pHCC | cg04698666 | 1,242 | 0,000962478 | 0,023596265 | -0,203 |         | 1stExon |         |

3    | CNOT4 | cg25871890 | 1,457 | 0,000747295 | 0,007102994 | 0,234 | 7      | S'UTR   |         |
|      | pHCC | cg25871890 | 1,532 | 0,001348339 | 0,02815058 | 0,239 | 7      | S'UTR   |         |

3    | COPA | cg09866659 | 1,500 | 5,83221E-08 | 5,15072E-05 | 0,252 | 1      | Body    |         |
|      | pHCC | cg09866659 | 1,327 | 1,35954E-06 | 0,000711844 | 0,222 | 1      | Body    |         |

3    | CR1L | cg06917617 | 1,306 | 0,000190517 | 0,003222883 | 0,216 | 1      | Body    | Island  |
|      | pHCC | cg06917617 | 1,584 | 0,000117677 | 0,007654385 | 0,257 | 1      | Body    | Island  |

3    | CREBBP | cg03368634 | 2,023 | 3,19922E-05 | 0,001236525 | 0,296 | 16     | Body    |         |
|      | pHCC | cg03368634 | 1,434 | 0,002669888 | 0,039905231 | 0,233 | 16     | Body    |         |
|   | Gene     | Region | Chromosome | Start | End   | p-value | q-value | FDR   | Effect Size | Total  | Adj. Total | TSS   |
|---|----------|--------|------------|-------|-------|---------|---------|-------|-------------|--------|------------|-------|
| 3 | CYP1A2   | eHCC   | cg04968473 | 1,677 | 2,333 | 0,0002478 | 0,00374116 | 0,250 | 15 | TSS1500     |
|   |          | pHCC   | cg04968473 | 1,409 | 2,065 | 0,003353047 | 0,044745176 | 0,208 | 15 | TSS1500     |
| 3 | HDAC9    | eHCC   | cg04892643 | 1,653 | 2,319 | 3,80242E-06 | 0,000396133 | -0,271 | 7 | Body        |
|   |          | eHCC   | cg16925459 | 1,402 | 2,068 | 9,45234E-05 | 0,002208479 | -0,227 | 7 | Body        |
|   |          | eHCC   | cg08285151 | 1,358 | 2,024 | 0,01998609 | 0,012949354 | -0,221 | 7 | TSS1500     |
|   |          | pHCC   | cg08285151 | 1,717 | 2,383 | 0,00921164 | 0,023074082 | -0,285 | 7 | TSS1500     |
|   |          | pHCC   | cg04892643 | 1,379 | 2,045 | 0,001197477 | 0,007713594 | -0,225 | 7 | Body        |
| 3 | HSF5     | eHCC   | cg25793387 | 1,796 | 2,462 | 0,00116076 | 0,002470337 | 0,234 | 17 | Body        |
|   |          | pHCC   | cg25793387 | 1,888 | 2,554 | 0,00267711 | 0,012083983 | 0,246 | 17 | Body        |
| 3 | KREMEN2  | eHCC   | cg26494929 | 1,560 | 2,226 | 0,002733419 | 0,015836891 | 0,235 | 16 | Body Island|
|   |          | eHCC   | cg05169951 | 2,182 | 2,848 | 1,22767E-05 | 0,00741323 | 0,279 | 16 | Body Island|
|   |          | pHCC   | cg05169951 | 1,621 | 2,287 | 0,00091564 | 0,023018862 | 0,219 | 16 | Body Island|
| 3 | S100A6   | eHCC   | cg01910639 | 1,530 | 2,206 | 2,45761E-06 | 0,00316155 | -0,255 | 1 | Body N_Shore|
|   |          | pHCC   | cg01910639 | 1,265 | 1,931 | 9,15466E-05 | 0,006695385 | -0,211 | 1 | Body N_Shore|
| 3 | SIPA1L1  | eHCC   | cg15378445 | 1,495 | 2,161 | 3,64569E-08 | 4,09609E-05 | 0,228 | 14 | Body        |
|   |          | eHCC   | cg02058870 | 1,777 | 2,443 | 0,000376026 | 0,004733271 | 0,280 | 14 | S'UTR       |
|   |          | pHCC   | cg15378445 | 1,570 | 2,236 | 1,138555E-07 | 0,00233189 | 0,234 | 14 | Body        |
| 3 | SNORD6   | eHCC   | cg03531787 | 1,449 | 2,115 | 0,000368829 | 0,00468219 | 0,206 | 11 | TSS200      |
|   |          | eHCC   | cg06955958 | 1,558 | 2,224 | 0,000306768 | 0,004216591 | 0,251 | 11 | TSS200      |
|   | Gene   | Condition | cg   | Val1   | Val2   | Val3   | Val4   | p     | q     | pos   | Region          |
|---|---------|-----------|------|--------|--------|--------|--------|-------|-------|-------|-----------------|
| 3 | STX3    | eHCC      | 1433 | 1,463  | 1,93006E-08 | 3,35383E-05 | 0,00520835 | 0,000778465 | 0,021187295 | 0,264 | 11 | 3'UTR          |
|   | pHCC    | cg14333691| 1,431 | 1,58326E-07 | 0,000267759 | 0,021187295 | 0,264 | 11 | 3'UTR          |
| 3 | THRSP   | eHCC      | 0349 | 1,398  | 0,000520835 | 0,005720482 | 0,021187295 | 0,264 | 11 | 3'UTR          |
|   | pHCC    | cg03493668| 1,316 | 0,002383629 | 0,03772453 | 0,021187295 | 0,264 | 11 | 3'UTR          |
| 3 | TSPAN10 | eHCC      | 1826 | 1,471  | 0,000633127 | 0,006430646 | 0,021187295 | 0,264 | 11 | 3'UTR Island   |
|   | pHCC    | cg18268547| 1,340 | 0,004026282 | 0,049224879 | 0,021187295 | 0,264 | 11 | 3'UTR Island   |
| 3 | USP42   | eHCC      | 1397 | 1,531  | 9,01962E-07 | 0,00189354 | 0,021187295 | 0,264 | 11 | 3'UTR S_Shelf  |
|   | pHCC    | cg13977660| 1,340 | 0,004026282 | 0,049224879 | 0,021187295 | 0,264 | 11 | 3'UTR S_Shelf  |
| 3 | ACTA2   | eHCC      | 0375 | 1,682  | 8,13988E-06 | 0,000598617 | 0,021187295 | 0,264 | 11 | 3'UTR Body     |
|   | pHCC    | cg03755566| 1,474 | 0,00151188 | 0,008793536 | 0,021187295 | 0,264 | 11 | 3'UTR Body     |
| 3 | ARHGAP10| eHCC      | 1324 | 1,641  | 1,00649E-07 | 6,4364E-05 | 0,021187295 | 0,264 | 11 | 3'UTR N_Shelf  |
|   | pHCC    | cg13248315|      |        |          |          |        |       |       |      | 3'UTR N_Shelf  |
| 3 | COL14A1 | eHCC      | 2617 | 1,453  | 1,68032E-05 | 0,000873201 | 0,021187295 | 0,264 | 11 | 3'UTR Body     |
|   | eHCC    | cg05830842| 1,454 | 7,51908E-05 | 0,001952561 | 0,021187295 | 0,264 | 11 | 3'UTR Body     |
|   | eHCC    | cg10133738| 1,759 | 0,000216387 | 0,003464022 | 0,021187295 | 0,264 | 11 | 3'UTR N_Shelf  |
|   | pHCC    | cg05830842| 1,442 | 2,31963E-06 | 0,00091091 | 0,021187295 | 0,264 | 11 | 3'UTR N_Shelf  |
| 3 | E4F1    | eHCC      | 2703 | 1,773  | 1,68939E-09 | 1,32594E-05 | 0,021187295 | 0,264 | 11 | 3'UTR Island   |
|   | pHCC    | cg27038935|      |        |          |          |        |       |       |      | 3'UTR Island   |
| Chromosome | Gene | Tissue | Position | Log2Ratio | p-value | q-value | Feature | Position2 | Feature2 |
|------------|------|--------|----------|-----------|---------|---------|---------|----------|----------|
| 3          | FAM129A | eHCC   | cg05655671 | 2,061 | 0,003705965 | 0,019287685 | 0,316 | 1 | 1stExon | Island |
|            | pHCC  | cg17464436 | 1,786 | 4,424E-05 | 0,004475372 | -0,242 | 1 | Body |
| 3          | HS3ST2  | eHCC   | cg04718102 | 2,204 | 0,000771279 | 0,007233639 | -0,312 | 16 | Body | Island |
|            | eHCC  | cg01555981 | 2,320 | 0,01228153 | 0,00956831 | -0,269 | 16 | Body | Island |
|            | eHCC  | cg05970721 | 1,845 | 4,04465E-05 | 0,001395974 | -0,236 | 16 | Body | Island |
|            | eHCC  | cg10180297 | 1,316 | 3,64699E-05 | 0,001322484 | -0,220 | 16 | Body | S_Shore |
|            | pHCC  | cg10180297 | 1,351 | 0,00012067 | 0,007763727 | -0,228 | 16 | Body | S_Shore |
| 3          | KIF26A  | eHCC   | cg11792470 | 2,565 | 0,000299114 | 0,004154802 | -0,291 | 14 | Body | Island |
|            | eHCC  | cg01549570 | 1,946 | 5,88539E-05 | 0,001713924 | -0,286 | 14 | Body | Island |
|            | eHCC  | cg00742738 | 2,041 | 0,001506599 | 0,010860826 | -0,264 | 14 | Body | N_Shore |
|            | eHCC  | cg19800856 | 1,845 | 4,85261E-05 | 0,001543559 | -0,249 | 14 | Body | Island |
|            | eHCC  | cg13250679 | 1,648 | 0,001865206 | 0,012402283 | -0,248 | 14 | 3'UTR | S_Shore |
|            | eHCC  | cg01933329 | 2,655 | 0,001158278 | 0,009218869 | -0,246 | 14 | Body | Island |
|            | eHCC  | cg12468119 | 1,642 | 0,004577351 | 0,022163995 | -0,235 | 14 | Body | Island |
|            | eHCC  | cg24706981 | 0,001023731 | 0,008547955 | -0,226 | 14 | Body | N_Shore |
| Gene | Chromosome | Start (bp) | End (bp) | TSS-d | Pathway | Distance (bp) | p-value | Fold Change | Direction | Region |
|------|------------|------------|----------|--------|---------|---------------|----------|-------------|-----------|---------|
| eHCC | cg06760280 | 1,568      | -        | 0,000215225 | 0,003452445 | -0,225        | 14       | Body | N_Shore |
| eHCC | cg16520046 | 1,715      | -        | 0,000943398 | 0,008147366 | -0,223        | 14       | Body | S_Shore |
| eHCC | cg19003626 | 1,949      | -        | 0,000453261 | 0,00527236 | -0,221        | 14       | Body | N_Shore |
| eHCC | cg23892535 | 1,565      | -        | 0,001489474 | 0,010784306 | -0,215        | 14       | Body | Island |
| eHCC | cg02922817 | 1,643      | -        | 0,000423466 | 0,005072836 | -0,215        | 14       | Body | N_Shore |
| eHCC | cg25131771 | 1,267      | -        | 0,000332767 | 0,004422609 | -0,207        | 14       | Body | Island |
| pHCC | cg01549570 | 1,416      | -        | 0,002910726 | 0,041688509 | -0,201        | 14       | Body | Island |
| 3    | MRVI1      | eHCC       | cg17299456| 1,554   | -        | 0,000557138 | 0,005955705 | -0,213  | 11      | S'UTR  |
|      |            | pHCC       | cg17471425|         |          |              |          |            |          |         |
| 3    | PLVAP      | eHCC       | cg15219347| 1,836   | -        | 0,000311766 | 0,004256726 | -0,287  | 19      | TSS1500 |
|      |            | eHCC       | cg01662455| 1,315   | -        | 0,000413255 | 0,005005784 | -0,221  | 19      | 1stExon |
|      |            | eHCC       | cg18302786| 1,517   | -        | 0,000963315 | 0,008251243 | -0,208  | 19      | TSS200  |
|      |            | eHCC       | cg10709246| 1,275   | -        | 0,001799566 | 0,012130169 | -0,205  | 19      | 3'UTR  |
|      |            | eHCC       | cg23881613| 2,091   | -        | 8,5276E-06 | 0,000614467 | -0,200  | 19      | Island |
|      |            | pHCC       | cg10178628| 1,401   | -        | 0,001873357 | 0,033413199 | -0,218  | 19      | Body   |
| 3 | TFIP11 | eHCC  | cg03019505 | 1,408 | 2,63095E-07 | 0,000101671 | 0,236 | 22 | Body | S_Shelf |
| 3 |       | pHCC  | 1,303376649 | 1,303 | 3,93172E-06 | 0,001199461 | 0,218 | 22 | Body | S_Shelf |
| 3 | THBS2 | eHCC  | cg02997295 | 1,743 | 0,000910415 | 0,007979071 | -0,275 | 6 | Body | S_Shore |
|    |       | eHCC  | cg04476508 | 1,585 | 0,000897118 | 0,007909381 | -0,251 | 6 | Body | Island |
|    |       | eHCC  | cg06119452 | 1,560 | 0,000428559 | 0,005106589 | -0,247 | 6 | Body | N_Shore |
|    |       | eHCC  | cg01320433 | 1,502 | 0,001466524 | 0,010673409 | -0,243 | 6 | Body | N_Shore |
|    |       | eHCC  | cg02785555 | 1,718 | 0,000533908 | 0,005807525 | -0,239 | 6 | Body | Island |
|    |       | eHCC  | cg15216858 | 2,318 | 0,000100322 | 0,002282748 | -0,229 | 6 | Body | Island |
|    |       | eHCC  | cg25631414 | 2,019 | 0,000508566 | 0,005642518 | -0,225 | 6 | Body | Island |
|    |       | eHCC  | cg00438284 | 1,413 | 8,99616E-05 | 0,002153094 | -0,207 | 6 | Body | S_Shelf |
|    |       | eHCC  | cg03091070 | 1,388 | 0,003222734 | 0,017612259 | -0,206 | 6 | Body | N_Shore |
|    |       | pHCC  | cg01320433 | 1,695 | 0,001646196 | 0,031252485 | -0,271 | 6 | Body | N_Shore |
| 3 | ZFP91 | eHCC  | cg12027899 | 1,543 | 1,19831E-05 | 0,000731878 | 0,237 | 11 | 3'UTR |
|    |       | pHCC  | cg12027899 | 1,287 | 0,000333865 | 0,013610629 | 0,209 | 11 | 3'UTR |
## Supplemental Table 6

| Signature 1 | Signature 2 | Signature 3 |
|-------------|-------------|-------------|
| **DMGR**    | **DMGR**    | **DMGR**    |
| ADAMTS2     | ABCG1       | ABCA1       |
| ADCK5       | ACAN        | ACACB       |
| ANO10       | ADAL        | ACAD8       |
| ARHGAP15    | ADAM32      | ACOT2       |
| ATG10       | APBA2       | ACSF2       |
| ATP8B3      | ARMS2       | ACSL5       |
| BANP        | ASTN2       | ACSS2       |
| BDNF        | ATP11A      | ACTA2       |
| BMP8A       | B3GNT9      | ACTL6B      |
| BMP8B       | BCAR3       | ADAM2       |
| C16orf87    | BLOC1S1     | ADAMTS12    |
| C18orf56    | BNC2        | ADAMTS1L2   |
| C2orf65     | C10orf26    | AFARP1      |
| C2orf82     | C10orf53    | AKAP1       |
| C8orf85     | C1QL4       | ALDH1A2     |
| CAMTA1      | C21orf57    | ALDH4A1     |
| CAPN13      | C2orf84     | ALPL        |
| CD160       | CALB1       | AMZ1        |
| CD164L2     | CASR        | ANK2        |
| CHFR        | CCDC40      | ANKRD32     |
| CLIP2       | CCR5        | ANKRD33     |
| CNOT6       | CHD5        | ANKRD58     |
| CRMP1       | CHGA        | ANKS1A      |
| CTNND2      | CINP        | APBA1       |
| DEFA3       | CLIC3       | APC2        |
| DLEC1       | CPLX2       | ARHGAP19    |
| DLX6AS      | CPT1B       | ARHGD1B     |
| EHBP1L1     | CTTNBP2     | ARSJ        |
| ESPN        | CUGBP2      | ASAP1       |
| EXOC6       | DDX51       | ASTN1       |
| FAM49B      | DLG5        | ATG4B       |
| FBRSL1      | DLK1        | ATP6VOA1    |
| FBXL7       | DNAH10      | ATP6V1C1    |
| FOXD3       | DNAH17      | BDH2        |
| FRAS1       | DPY19L2P2   | BLVRB       |
| GABRB3      | DRD2        | BMF         |
| GALK2       | DRD5        | BUB1B       |
| GALNT9      | ECH1        | C12orf51    |
| GATA4       | EDNRB       | C14orf115   |
| GMDS        | EFHD2       | C14orf21    |
| GPR123      | EIF2C3      | C15orf42    |
| GRAMD1B     | ENTPD8      | C16orf70    |
| HCN2        | ERC2        | C17orf46    |
| Gene   | Gene   | Gene   |
|--------|--------|--------|
| HMBS   | ETV5   | C17orf73 |
| HOXD8  | FADS6  | C1orf125 |
| IGF1R  | FAM90A14 | C1orf14 |
| IPO7   | FGFr19 | C1orf150 |
| KCNE1  | FLJ26850 | C1orf187 |
| KIAA1026 | FLJ32063 | C1orf189 |
| KIAA1841 | FOXE1   | C1QTNF4 |
| LHX3   | FOXE3  | C22orf24 |
| LOC100129354 | GABRA4 | C2CD3 |
| LOC145783   | GBX2   | C3orf27 |
| LOC285780   | GFRA1  | C5orf4  |
| LOC90110    | GGN    | C6orf174 |
| LRRC43  | GJC2   | C6orf48 |
| MAP4   | GLB1L2 | C9orf3  |
| MGAT5B  | GPIHBP1 | CACNA1C |
| MIR1910 | GRHL2  | CACNA1E |
| MIR496  | HBQ1   | CACNA2D2 |
| MMP19  | HIST1H2BH | CACNA2D3 |
| MSX1   | HIST3H2BB | CAMSAP11 |
| NCRNA00171 | HLA-DPB2 | CAND2 |
| NNX6-2  | HLA-DQB1 | CAPN5 |
| NOTCH4  | HNRNPAB | CAPSL |
| NSD1   | HOXA2  | CARD16 |
| NTM    | HOXA9  | CARHSP1 |
| PARD6A  | HOXD9  | CBFA2T3 |
| PCDHGA4 | HSPE1  | CBR3   |
| PDPK1   | IFNGR1 | CCDC109A |
| PHHLDA3 | IGF2F21 | CCDC48 |
| PIAS1   | IL17D  | CCDC57 |
| PITPNB  | INSM2  | CCDC84 |
| PKDREJ  | JAK3   | CCK    |
| PLOD3   | JMD5   | CCNJL  |
| PPP1R14D | KARS  | CD53   |
| PPP2R5C | KCNH3  | CD6    |
| PTPRC   | KCNIP1 | CDCP1  |
| PTPRS   | KCNJ2  | CDH11  |
| PUF60   | KCNK7  | CDK3   |
| PUS7    | KLRG2  | CHERP  |
| RASL11B | LAMC3  | CHRNA3 |
| RNF135  | LAPTM4B | CHST11 |
| RUNX3   | LITAF  | CLDN5  |
| RWDD1   | LOC339788 | CLEC14A |
| SAMD11  | LOC389033 | CLEC4C |
| SATB2   | LOC389458 | CLSTN1 |
| SDK1    | LOC91316 | CLU |
| SLC25A2 | LTBP2  | CMTM8  |
| SLC25A41 | MBP    | CMYA5  |
| Gene 1 | Gene 2 | Gene 3 |
|--------|--------|--------|
| SOHLH1 | MICB   | CNKSR1 |
| SORCS2 | MIR129-2 | CNOT4 |
| SPG11  | MTMR7  | CNR2  |
| ST3GAL3 | MYO10 | COL14A1 |
| ST8SIA3 | NID1  | COL2A1 |
| STX1A  | NPAS4  | COPA  |
| TACC2  | NR2E1  | CORO2B |
| TACSTD2 | NRG3  | CPA4  |
| TBX15  | NUBP2  | CR1L  |
| TLE4   | NTF3  | CPN1  |
| TNFRSF9 | OBSCN | CREBBP |
| TOX2   | OSR2  | CRH   |
| TP73   | OTX1  | CRHBP |
| TRAPPCC9 | PDE10A | CRISPLD2 |
| TRIM26 | PDE4DIP | CRYBB3 |
| TRIM58 | PHF21B | CSMD3 |
| TTYH3  | PITX2  | CUL3  |
| ULPB1  | PLXNB2 | CYP19A1 |
| USP34  | POU4F1 | CYP1A2 |
| UTF1   | PPP1R14A | CYP2E1 |
| UTS2D  | PRDM2  | CYTIP |
| VIPR2  | PRDM8  | DCAF4L2 |
| WDR82  | PURA   | DENND1C |
| ZIC5   | RANBP17 | DFFB |
| ZNF212 | RAP1GAP2 | DGKD |
| ZNF41  | REXO1L2P | DMPK |
| ZSCAN18 | RGS17  | DMRTA2 |
|        | RIMS2  | DNASE1L2 |
|        | SCAMP1 | DNHD1 |
|        | SEMA6D | DOK2 |
|        | SLC2A14 | DPP10 |
|        | SLC6A7 | DYSPL5 |
|        | SLC8A1 | DSC3 |
|        | SMARCC1 | DSCAML1 |
|        | SNX26  | DSTN |
|        | SP110  | DVL1 |
|        | STAG3  | E4F1 |
|        | STRN4  | EBF3 |
|        | SYCE1  | EBPL |
|        | SYT16  | EDARADD |
|        | TAS2R60 | EFNA5 |
|        | TCTN3  | EFS |
|        | TEAD4  | EGFLAM |
|        | TEX101 | ELF1 |
|        | TFCP2L1 | EPHX4 |
|        | THSD7A | ERN2 |
| Gene  | Gene  |
|-------|-------|
| TMC4  | ESRRG |
| TPCN1 | EXOC2 |
| TRIM15| FAH2D2A |
| TRMT12| FAM100A |
| TWIST1| FAM113B |
| UGT2B15| FAM129A |
| VAX1  | FAM184B |
| WDR8  | FAM189A1 |
| ZBTB10| FAM196B |
| ZIC1  | FAM19A2 |
| ZNF154| FAM19A4 |
| ZNF177| FAM20B |
| ZNF331| FAM20C |
| ZNF471| FAM83A |
| ZNF540| FBP1 |
| ZNF560| FGF13 |
| ZNF562| FGF2 |
| ZNF667| FGFR4 |
| ZNF876P| FILIP1 |
|       | FLNB |
|       | FNDC1 |
|       | FOXI1 |
|       | FRMD1 |
|       | GABRA3 |
|       | GABRB1 |
|       | GAGE2E |
|       | GALR2 |
|       | GAS7 |
|       | GCNT3 |
|       | GEMIN6 |
|       | GFAP |
|       | GFPT2 |
|       | GIMAP7 |
|       | GJA3 |
|       | GLB1L3 |
|       | GLI3 |
|       | GLRB |
|       | GLTSCR1 |
|       | GLTSCR2 |
|       | GNAO1 |
|       | GNG4 |
|       | GNL1 |
|       | GPR158 |
|       | GPR20 |
|       | GPRIN3 |
|       | GRAMD3 |
|       | GRASP |
| Gene Symbol |
|-------------|
| GRIN2A      |
| GRM2        |
| GULP1       |
| GZMA        |
| HDAC9       |
| HECW1       |
| HELZ        |
| HERC5       |
| HIF1AN      |
| HIPK1       |
| HIST1H3H    |
| HK3         |
| HMGA2       |
| HNMT        |
| HOXA4       |
| HOXC4       |
| HS3ST2      |
| HSF5        |
| HSPB6       |
| IFFO1       |
| IFI16       |
| IFNG        |
| IGLON5      |
| IKZF1       |
| IL12RB2     |
| INPP5D      |
| IRX3        |
| ITGA11      |
| ITGAE       |
| ITGAM       |
| ITGB3       |
| ITPKB       |
| ITPRIPL1    |
| KAT2A       |
| KBTBD11     |
| KCNAB2      |
| KCNG4       |
| KCNJ16      |
| KCNK16      |
| KCNK9       |
| KCNS2       |
| KDM5C       |
| KIAA0556    |
| KIAA0664    |
| KIAA0748    |
| KIAA1751    |
| KIAA1875    |
| Gene      |
|-----------|
| MGAT5     |
| MGST1     |
| MICA      |
| MIR485    |
| MIR495    |
| MKL1      |
| MMEL1     |
| MON2      |
| MRV11     |
| MS4A7     |
| MTMR3     |
| MTOR      |
| MUPCDH    |
| MX2       |
| MYH14     |
| MYPOP     |
| NAA30     |
| NARG2     |
| NFIA      |
| NKAIN1    |
| N Kapoor  |
| NPR3      |
| NRD1      |
| NRN1L     |
| NRP2      |
| NT5DC1    |
| NUDT9     |
| NUMBL     |
| OLFM1     |
| OPA3      |
| OR13A1    |
| OR4D6     |
| OR6K2     |
| OTUD7A    |
| PABPC4    |
| PALM3     |
| PAPLN     |
| PAQR6     |
| PARK2     |
| PARK7     |
| PARP9     |
| PASK      |
| PCBP3     |
| PCNX      |
| PDE11A    |
| PDE7B     |
| PDLIM5    |
RHOC
RIMS1
RNF122
RNF220
RORA
RPSAP58
RTCD1
RTL1
S100A6
SAMD13
SCAND3
SCG5
SCN11A
SCN5A
SDC2
SEMA3C
SENP7
SFRP1
SFRP2
SFRS8
SFT2D2
SH3BGR1L2
SH3RF3
SHANK2
SIPA1L1
SKI
SLA
SLC12A9
SLC16A1
SLC1A6
SLC25A27
SLC2A5
SLC41A1
SLC45A1
SLC6A19
SLC7A10
SLC9A3
SLCO3A1
SNORA2A
SNORA54
SNORD126
SNORD6
SORBS1
SORBS2
SPERT
SPN
SPNS3
SPSB4
SREBF1
SSR1
ST8SIA5
STAC2
STK10
STX3
SUSD1
SWAP70
TAF7L
TCL6
TESK2
TFAP2A
TFEC
TFIP11
THBS2
THRSP
TIGD1
TJP2
TMEM178
TMEM18
TMEM206
TNS1
TOMM20
TPST1
TRIM31
TRIM59
TRIM72
TRPC7
TRPV6
TSC2
TSNAX-DISC1
TSPAN10
TSPY4
TTC29
TTL8
TXNDC5
UBE2E1
UCN
UGP2
UGT1A5
USP42
UTP11L
VARS
WDFY4
WDR1
WFDC1
| WIPF1  |
|-------|
| WNK2  |
| WNT7A |
| WSCD1 |
| WSCD2 |
| XKR6  |
| XPOT  |
| ZBTB16|
| ZBTB20|
| ZBTB9 |
| ZC3H12D|
| ZDHHCC |
| ZFP91 |
| ZMAT4 |
| ZMIZ2 |
| ZNF148|
| ZNF181|
| ZNF204P|
| ZNF229|
| ZNF274|
| ZNF366|
| ZNF389|
| ZNF461|
| ZNF582|
| ZNF711|
| ZNF831|
| ZNF853|
| ZSWIM4|
| ZYG11A|
**Supplemental Table 7**

| Panel | GeneSymbol | Lesion | Probe_ID  | M-value | p-value    | adj.p-value | beta-value difference to NL | Chromosome | UCSC_RefGene_Group | Relation_to_UCS_CpG_Island |
|-------|------------|--------|-----------|---------|-----------|-------------|-----------------------------|------------|---------------------|----------------------------|
| 1     | ANO10      | LGDN   | cg11035303| 2,25    | 0,001400969| 0,042313245 | 0,21                        | 3          | Body                |                            |
|       |            | HGDN   | cg11035303| 2,20    | 0,001442059| 0,021524631 | 0,21                        | 3          | Body                |                            |
|       | eHCC       | LGDN   | cg11035303| 2,13    | 0,001992212| 0,012922805 | 0,20                        | 3          | Body                |                            |
|       | pHCC       | LGDN   | cg11035303| 2,30    | 0,001162462| 0,026053992 | 0,20                        | 3          | Body                |                            |
| 1     | BMP8A      | LGDN   | cg11763509| 1,23    | 1,08373E-05| 0,003147873 | 0,20                        | 1          | Body                | Island                     |
|       |            | HGDN   | cg11763509| 1,45    | 4,8908E-08 | 4,82654E-05 | 0,23                        | 1          | Body                | Island                     |
|       |            | HGDN   | cg02575697| 2,05    | 0,004561701| 0,042855262 | 0,25                        | 1          | TSS200              | Island                     |
|       | eHCC       | LGDN   | cg25139493| 1,29    | 0,001648639| 0,011481088 | 0,21                        | 1          | 1stExon             | Island                     |
|       | eHCC       | LGDN   | cg11763509| 1,46    | 3,42655E-07| 0,000115899 | 0,23                        | 1          | Body                | Island                     |
|       | eHCC       | LGDN   | cg08748615| 2,10    | 0,006911376| 0,029213458 | 0,28                        | 1          | TSS200              | Island                     |
|       | eHCC       | LGDN   | cg15947940| 3,01    | 0,001619369| 0,011353715 | 0,32                        | 1          | TSS200              | Island                     |
|       | eHCC       | LGDN   | cg02575697| 3,01    | 0,00638407 | 0,006465884 | 0,39                        | 1          | TSS200              | Island                     |
|       | pHCC       | LGDN   | cg11763509| 1,40    | 3,2305E-06 | 0,001076919 | 0,22                        | 1          | Body                | Island                     |
| 1     | CAMTA1     | LGDN   | cg03571764| -1,64   | 0,001272387| 0,040229801 | -0,23                       | 1          | Body                | Island                     |
|       |            | HGDN   | cg08640609| 1,67    | 0,004537857| 0,042711116 | 0,21                        | 1          | Body                | Island                     |
|       | eHCC       | LGDN   | cg12138124| -2,46   | 3,29437E-05| 0,001256476 | -0,28                       | 1          | Body                | Island                     |
|       | eHCC       | LGDN   | cg07008478| -1,63   | 0,000855058| 0,007693041 | -0,25                       | 1          | Body                | S_Shore                    |
|       | eHCC       | LGDN   | cg21942218| -3,20   | 0,000286391| 0,004055616 | -0,24                       | 1          | Body                | Island                     |
|       | eHCC       | LGDN   | cg03571764| -1,72   | 0,000278676| 0,003994987 | -0,24                       | 1          | Body                | Island                     |
|       | eHCC       | LGDN   | cg23021268| -1,55   | 0,003666873| 0,019151776 | -0,23                       | 1          | Body                |                            |
|       | eHCC       | LGDN   | cg17081408| -1,83   | 0,001496498| 0,010815639 | -0,23                       | 1          | Body                |                            |
|       | eHCC       | LGDN   | cg00911446| -1,91   | 0,000344462| 0,004509207 | -0,22                       | 1          | Body                |                            |
| Gene | Chromosome | Start Position | End Position | Length | p-Value | q-Value | Significance | Location |
|------|------------|----------------|--------------|--------|---------|---------|--------------|----------|
| eHCC | cg25196088 | -1,43          | 0,001309575  | 0,009952399 | -0,22  | 1       | Body         |
| eHCC | cg06800235 | -1,36          | 0,000279404  | 0,003999493 | -0,22  | 1       | Body         |
| eHCC | cg06082897 | -1,57          | 0,000963949  | 0,008253847 | -0,21  | 1       | S_Shore      |
| eHCC | cg04210471 | -1,59          | 0,004911013  | 0,023224209 | -0,21  | 1       | Body         |
| eHCC | cg26161885 | -1,66          | 0,000272859  | 0,003949708 | -0,21  | 1       | Body         |
| eHCC | cg17143900 | -1,34          | 0,005124651  | 0,02391622  | -0,21  | 1       | Body         |
| eHCC | cg10536786 | -1,25          | 0,001130559  | 0,009085098 | -0,21  | 1       | Body         |
| eHCC | cg24579970 | -1,21          | 0,00176546   | 0,011985081 | -0,20  | 1       | S_Shore      |
| eHCC | cg07835553 | 1,37           | 0,005594416  | 0,025319897 | 0,22   | 1       | S_Shore      |
| eHCC | cg22488970 | 1,62           | 0,010419843  | 0,038724737 | 0,23   | 1       | N_Shore      |
| eHCC | cg04210471 | 1,76           | 1,01642E-05  | 0,000670116 | 0,29   | 1       | Body         |
| eHCC | cg08640609 | 2,62           | 0,00359256   | 0,04613904  | 0,36   | 1       | Island       |
| pHCC | cg12138124 | -2,71          | 5,33231E-05  | 0,04966698  | -0,32  | 1       | Body         |
| pHCC | cg00808305 | -1,40          | 0,001385864  | 0,028577018 | -0,23  | 1       | Body         |
| pHCC | cg06800235 | -1,39          | 0,000808749  | 0,02161448  | -0,22  | 1       | Body         |
| pHCC | cg25763306 | -1,55          | 0,003301719  | 0,044418039 | -0,21  | 1       | S_Shore      |
| pHCC | cg12661316 | -1,43          | 0,000756895  | 0,020875328 | -0,21  | 1       | Body         |
| pHCC | cg21583016 | -1,25          | 0,003911524  | 0,048481596 | -0,20  | 1       | Body         |

1 FBRSL1 LGDN cg08818195 -1,38 2,03787E-05 0,004411797 -0,22 12 TSS1500 N_Shore
1 HGDN cg08818195 -1,32 2,0708E-06 0,000368036 -0,21 12 TSS1500 N_Shore
eHCC cg18450555 2,04 0,00229889 0,014172797 0,20 12 TSS1500 Island
eHCC cg16719582 1,85 6,89348E-05 0,001862659 0,27 12 Body
eHCC cg00370303 2,28 0,002787085 0,016037777 0,30 12 TSS1500 Island
eHCC cg23890800 2,40 0,001807458 0,012162088 0,31 12 TSS1500 Island
pHCC cg08818195 -1,23 7,46139E-05 0,00598998 -0,20 12 TSS1500 N_Shore

1 GALK2 LGDN cg00756450 1,35 1,7713E-08 0,000228386 0,20 15 Body
1 HGDN cg00756450 1,35 4,36882E-10 6,30125E-06 0,20 15 Body
eHCC cg00756450 1,77 7,13323E-11 8,65566E-06 0,25 15 Body
pHCC cg00756450 1,67 1,06812E-09 8,64058E-05 0,24 15 Body
|   | Gene   | Chromosome | Start | End   | p-value | q-value |
|---|--------|------------|-------|-------|---------|---------|
| 1 | HMBS   | LGDN       | cg20929545 | 1,33  | 3,56028E-06 | 0,001800117 | 0,21 | 11 | TSS1500 | S_Shelf |
|   |         | HGDN       | cg20929545 | 1,31  | 5,8742E-07  | 0,000171134 | 0,21 | 11 | TSS1500 | S_Shelf |
|   |         | eHCC       | cg20929545 | 1,64  | 9,55351E-08 | 0,000062667 | 0,25 | 11 | TSS1500 | S_Shelf |
|   |         | pHCC       | cg20929545 | 1,44  | 1,54236E-06 | 0,000764673 | 0,22 | 11 | TSS1500 | S_Shelf |
| 1 | MAP4   | LGDN       | cg16509829 | -1,37 | 1,2804E-05  | 0,003423929 | -0,21 | 3 | 5'S'UTR | Island |
|   |         | HGDN       | cg16509829 | -1,33 | 7,33205E-06 | 0,000785773 | -0,20 | 3 | 5'S'UTR | Island |
|   |         | eHCC       | cg16509829 | -1,48 | 3,23268E-06 | 0,00036566  | -0,22 | 3 | 5'S'UTR | Island |
|   |         | pHCC       | cg16509829 | -1,35 | 1,64411E-05 | 0,002547039 | -0,20 | 3 | 5'S'UTR | Island |
| 1 | NSD1   | LGDN       | cg18121224 | 1,53  | 2,1862E-05  | 0,004589217 | 0,20 | 5 | TSS1500 | Island |
|   |         | LGDN       | cg19731612 | 1,73  | 1,9278E-05  | 0,004300077 | 0,22 | 5 | TSS1500 | Island |
|   |         | HGDN       | cg18121224 | 1,54  | 9,38425E-07 | 0,000229232 | 0,20 | 5 | TSS1500 | Island |
|   |         | HGDN       | cg19731612 | 1,69  | 1,62325E-06 | 0,000319755 | 0,22 | 5 | TSS1500 | Island |
|   |         | HGDN       | cg08369368 | 1,67  | 0,000997114 | 0,01716919  | 0,23 | 5 | TSS200 | Island |
|   |         | eHCC       | cg18016826 | 1,76  | 0,000408844 | 0,004974456 | 0,22 | 5 | TSS200 | Island |
|   |         | eHCC       | cg18121224 | 2,00  | 2,02075E-07 | 8,98113E-05 | 0,24 | 5 | TSS1500 | Island |
|   |         | eHCC       | cg19731612 | 2,18  | 3,10701E-07 | 0,000109997 | 0,27 | 5 | TSS1500 | Island |
|   |         | eHCC       | cg08369368 | 2,59  | 7,19393E-05 | 0,001906875 | 0,38 | 5 | TSS200 | Island |
|   |         | pHCC       | cg18121224 | 1,55  | 2,13084E-05 | 0,0029449  | 0,20 | 5 | TSS1500 | Island |
|   |         | pHCC       | cg19731612 | 1,61  | 0,0004665  | 0,004619989 | 0,21 | 5 | TSS1500 | Island |
| 1 | PIA1   | LGDN       | cg05105016 | 1,23  | 1,15585E-07 | 0,000390356 | 0,21 | 15 | Body   |         |
|   |         | HGDN       | cg05105016 | 1,22  | 3,95718E-09 | 1,41969E-05 | 0,21 | 15 | Body   |         |
|   |         | eHCC       | cg05105016 | 1,57  | 7,80955E-10 | 1,18765E-05 | 0,26 | 15 | Body   |         |
|   |         | pHCC       | cg05105016 | 1,66  | 2,43725E-09 | 9,35193E-05 | 0,27 | 15 | Body   |         |
| 1 | PLOD3  | LGDN       | cg16390570 | -1,55 | 4,20407E-06 | 0,00197153  | -0,25 | 7 | 1stExon | Island |
|   |         | HGDN       | cg16390570 | -1,32 | 7,97387E-06 | 0,000827613 | -0,22 | 7 | 1stExon | Island |
|   |         | eHCC       | cg16390570 | -1,34 | 1,13889E-05 | 0,000715301 | -0,22 | 7 | 1stExon | Island |
| eHCC   | cg18437077 | -1,29 | 1,10252E-07 | 6,72273E-05 | -0,20 | 7 | 1stExon | Island |
|--------|------------|------|-------------|-------------|-------|---|---------|--------|
| pHCC   | cg16390570 | -1,41 | 1,30962E-05 | 0,002250628 | -0,23 | 7 | 1stExon | Island |

1  PPP2R5C  LGDN  cg09990596  -1,28  4,45282E-05  0,006709743  -0,21  14 | TSS200 | Island |
|      |            |      |             |             |       |   |         |        |
| LGDN  | cg15321108 | -1,22 | 1,23203E-05 | 0,003355745 | -0,20 | 14 | TSS200 | Island |
| HGDN  | cg09990596 | -1,28 | 7,15987E-06 | 0,000773813 | -0,22 | 14 | TSS200 | Island |
| HGDN  | cg15321108 | -1,28 | 1,00638E-06 | 0,000238393 | -0,21 | 14 | TSS200 | Island |
| eHCC  | cg08163906 | -1,26 | 2,16154E-05 | 0,000995773 | -0,21 | 14 | TSS200 | Island |
| pHCC  | cg27022326 | -1,52 | 0,000244565 | 0,011486812 | -0,25 | 14 | 3'UTR  | N_Shore |

1  PTPRC  LGDN  cg26399994  -1,82  8,92912E-05  0,009753206 | -0,22 | 1 | Body |
|      |            |      |             |             |       |   |         |        |
| HGDN  | cg22073152 | -1,30 | 0,002335102 | 0,028816727 | -0,22 | 1 | Body   |         |
| HGDN  | cg04214459 | -1,25 | 0,000698215 | 0,013820458 | -0,21 | 1 | Body   |         |
| eHCC  | cg22073152 | -2,08 | 0,000162627 | 0,002957778 | -0,34 | 1 | Body   |         |
| eHCC  | cg25132230 | -1,63 | 0,001898857 | 0,012539625 | -0,27 | 1 | S'UTR  |         |
| eHCC  | cg26399994 | -1,83 | 2,53383E-05 | 0,001087514 | -0,22 | 1 | Body   |         |
| eHCC  | cg04214459 | -1,21 | 0,003153217 | 0,017366658 | -0,20 | 1 | Body   |         |
| pHCC  | cg25132230 | -1,93 | 0,00158306 | 0,030591941 | -0,32 | 1 | S'UTR  |         |
| pHCC  | cg22073152 | -1,84 | 0,001655583 | 0,031346453 | -0,30 | 1 | Body   |         |
| pHCC  | cg04214449 | -1,42 | 0,002846064 | 0,0412013 | -0,23 | 1 | Body   |         |
| pHCC  | cg26399994 | -1,80 | 0,000135529 | 0,008284838 | -0,22 | 1 | Body   |         |

1  RWDD1  LGDN  cg23280258 | 1,40 | 1,24299E-05 | 0,003378011 | 0,21 | 6 | Body  | S_Shelf |
|      |            |      |             |             |       |   |         |        |
| HGDN  | cg23280258 | 1,41 | 5,78259E-07 | 0,000169794 | 0,21 | 6 | Body  | S_Shelf |
| eHCC  | cg23280258 | 1,84 | 1,0504E-07 | 6,53631E-05 | 0,26 | 6 | Body  | S_Shelf |
| pHCC  | cg23280258 | 1,77 | 8,8973E-07 | 0,000577338 | 0,25 | 6 | Body  | S_Shelf |

1  SAMD11  LGDN  cg13856810 | 1,24 | 0,000236207 | 0,016280636 | 0,20 | 1 | Body  | S_Shore |
|      |            |      |             |             |       |   |         |        |
| LGDN  | cg05527507 | 1,67 | 0,000157173 | 0,013155911 | 0,27 | 1 | 5'UTR  | Island |
|        |        |        |        |        |        |        |        |
|--------|--------|--------|--------|--------|--------|--------|--------|
| LGDN   | cg14324200 | 2.01  | 3.62211E-05 | 0.005983022 | 0.31 | 1 | S'UTR | Island |
| HGDN   | cg13904806 | 2.08  | 1.06986E-06 | 0.000248078 | 0.20 | 1 | Body  | N_Shore |
| HGDN   | cg13856810 | 1.40  | 3.4156E-06  | 0.000494286 | 0.23 | 1 | Body  | S_Shore |
| HGDN   | cg02439789 | 1.56  | 6.78215E-06 | 0.000748576 | 0.25 | 1 | Body  | Island |
| HGDN   | cg24362661 | 1.52  | 1.15868E-05 | 0.001050211 | 0.25 | 1 | Body  | Island |
| HGDN   | cg06531475 | 1.61  | 1.42775E-05 | 0.001198738 | 0.26 | 1 | Body  | Island |
| HGDN   | cg05527507 | 1.67  | 1.05649E-05 | 0.000990265 | 0.27 | 1 | S'UTR | Island |
| HGDN   | cg14324200 | 1.79  | 8.94928E-06 | 0.000896167 | 0.28 | 1 | S'UTR | Island |
| HGDN   | cg13546858 | 1.84  | 3.52397E-06 | 0.000503809 | 0.29 | 1 | Body  | Island |
| HGDN   | cg02663945 | 1.82  | 0.003639257 | 0.037475353 | 0.29 | 1 | Body  | Island |
| eHCC   | cg13904806 | 2.18  | 3.93301E-06 | 0.000403672 | 0.21 | 1 | Body  | N_Shore |
| eHCC   | cg03269716 | 1.46  | 4.67217E-06 | 0.00044236  | 0.23 | 1 | Body  | N_Shore |
| eHCC   | cg24362661 | 1.44  | 5.73347E-05 | 0.001692634 | 0.24 | 1 | Body  | Island |
| eHCC   | cg13856810 | 1.55  | 6.42576E-06 | 0.000525064 | 0.25 | 1 | Body  | S_Shore |
| eHCC   | cg13546858 | 1.69  | 3.91963E-05 | 0.001374563 | 0.27 | 1 | Body  | Island |
| eHCC   | cg02439789 | 1.74  | 6.81567E-06 | 0.000542672 | 0.27 | 1 | Body  | Island |
| eHCC   | cg06531475 | 1.64  | 5.03767E-05 | 0.001577203 | 0.27 | 1 | Body  | Island |
| eHCC   | cg02663945 | 1.89  | 0.003134839 | 0.017305399 | 0.29 | 1 | Body  | Island |
| eHCC   | cg05527507 | 1.80  | 1.91151E-05 | 0.000933015 | 0.29 | 1 | S'UTR | Island |
| eHCC   | cg14324200 | 2.01  | 9.3645E-06  | 0.000645658 | 0.32 | 1 | S'UTR | Island |
| pHCC   | cg13904806 | 2.11  | 2.86451E-05 | 0.003499123 | 0.20 | 1 | Body  | N_Shore |
| pHCC   | cg13856810 | 1.32  | 0.000165803 | 0.009278836 | 0.21 | 1 | Body  | S_Shore |
| pHCC   | cg24362661 | 1.33  | 0.000346405 | 0.013853106 | 0.22 | 1 | Body  | Island |
| pHCC   | cg02439789 | 1.51  | 0.000114182 | 0.007524875 | 0.24 | 1 | Body  | Island |
| pHCC   | cg13546858 | 1.84  | 6.48495E-05 | 0.005561143 | 0.29 | 1 | Body  | Island |
| pHCC   | cg02663945 | 2.00  | 0.002516631 | 0.038758082 | 0.31 | 1 | Body  | Island |

1 SATB2

|        |        |        |        |        |        |        |        |
|--------|--------|--------|--------|--------|--------|--------|--------|
| LGDN   | cg20785796 | 1.34  | 0.000104345 | 0.010597593 | 0.21 | 2 | TSS1500 | Island |
| HGDN   | cg20785796 | 1.46  | 4.92183E-06 | 0.000616767 | 0.23 | 2 | TSS1500 | Island |
| eHCC   | cg23994043 | 1.39  | 0.002854286 | 0.016282203 | 0.22 | 2 | TSS1500 | Island |
| eHCC   | cg20731529 | 1.63  | 0.001843123 | 0.012310591 | 0.26 | 2 | Body   | Island |
| Gene | Site | x Chromosome | y Chromosome | Beta Value | P-Value | TSS Location | Region |
|------|------|--------------|--------------|------------|---------|--------------|--------|
| eHCC | cg03163783 | 1,59 | 0,00113929 | 0,009128821 | 0,26 | 2 | TSS1500 | Island |
| eHCC | cg20785796 | 1,87 | 8,08703E-07 | 0,00017989 | 0,28 | 2 | TSS1500 | Island |
| pHCC | cg20785796 | 1,63 | 1,48928E-05 | 0,00242 | 0,24 | 2 | TSS1500 | Island |
| 1 | SPG11 | LGDN | cg12228919 | -1,79 | 5,09051E-05 | 0,007254209 | -0,24 | 15 | TSS200 | Island |
| 1 | HGDN | cg12228919 | -1,81 | 1,07164E-05 | 0,000999696 | -0,23 | 15 | TSS200 | Island |
| 1 | eHCC | cg12228919 | -1,71 | 3,83926E-05 | 0,001357519 | -0,22 | 15 | TSS200 | Island |
| 1 | pHCC | cg12228919 | -1,66 | 0,00011844 | 0,007673647 | -0,22 | 15 | TSS200 | Island |
| 1 | STX1A | LGDN | cg01804343 | -1,33 | 3,4312E-05 | 0,005792713 | -0,22 | 7 | TSS200 | Island |
| 1 | HGDN | cg01804343 | -1,50 | 1,34666E-06 | 0,000283078 | -0,25 | 7 | TSS200 | Island |
| 1 | eHCC | cg01804343 | -1,49 | 2,71268E-05 | 0,001127177 | 0,23 | 7 | Body | Island |
| 1 | eHCC | cg01804343 | -1,73 | 5,91379E-07 | 0,000152033 | -0,28 | 7 | TSS200 | Island |
| 1 | eHCC | cg27469719 | -1,49 | 1,42012E-06 | 0,000238837 | -0,23 | 7 | TSS200 | Island |
| 1 | pHCC | cg01804343 | -1,33 | 3,64297E-05 | 0,00400669 | -0,22 | 7 | TSS200 | Island |
| 1 | USP34 | LGDN | cg01145124 | 2,01 | 3,97126E-08 | 0,00024712 | 0,21 | 2 | Body | Island |
| 1 | HGDN | cg01145124 | 1,98 | 1,18219E-09 | 9,40658E-06 | 0,21 | 2 | Body | Island |
| 1 | eHCC | cg01145124 | 2,38 | 8,16631E-10 | 1,20112E-05 | 0,23 | 2 | Body | Island |
| 1 | pHCC | cg01145124 | 2,45 | 4,09543E-09 | 9,46573E-05 | 0,24 | 2 | Body | Island |
| 1 | WDR82 | LGDN | cg24007312 | -1,33 | 0,000865119 | 0,032915715 | -0,22 | 3 | TSS200 | Island |
| 1 | HGDN | cg24007312 | -1,53 | 0,00010857 | 0,004333213 | -0,25 | 3 | TSS200 | Island |
| 1 | HGDN | cg11442381 | -1,39 | 1,17748E-05 | 0,001059934 | -0,21 | 3 | TSS200 | Island |
| 1 | eHCC | cg24007312 | -1,83 | 2,55538E-05 | 0,001092108 | -0,29 | 3 | TSS200 | Island |
| 1 | eHCC | cg12661343 | -1,33 | 5,03101E-07 | 0,000140593 | -0,22 | 3 | TSS200 | Island |
| 1 | eHCC | cg11442381 | -1,44 | 1,8899E-05 | 0,000926286 | -0,21 | 3 | TSS200 | Island |
| 1 | pHCC | cg24007312 | -1,67 | 0,000115413 | 0,007576322 | -0,27 | 3 | TSS200 | Island |
| 1 | ZIC5 | LGDN | cg17930361 | 2,48 | 0,000702243 | 0,029581909 | 0,35 | 13 | Body | Island |
| 1 | HGDN | cg17930361 | 1,66 | 0,002020005 | 0,026379631 | 0,22 | 13 | Body | Island |
| Gene | Position | Beta | p-Value | q-Value | Fold Change | Location |
|------|----------|------|---------|---------|-------------|----------|
| eHCC cg11077516 | 1,24 | 0,00177198 | 0,01201285 | 0,20 | 13 | Body Island |
| eHCC cg10679688 | 1,46 | 0,000569742 | 0,00603541 | 0,22 | 13 | TSS1500 S_Shore |
| eHCC cg03313945 | 1,59 | 0,00309423 | 0,04238703 | 0,23 | 13 | Body Island |
| eHCC cg20985450 | 2,57 | 0,00392496 | 0,04856565 | 0,39 | 13 | Body Island |
| eHCC cg17930361 | 2,80 | 6,93423E-05 | 0,01868431 | 0,41 | 13 | Body Island |
| pHCC cg00529958 | 1,49 | 0,000767592 | 0,021041187 | 0,23 | 13 | TSS200 Island |

1. ZNF212
   - LGDN cg05476998: 1,38, 3,19165E-06, 0,001734751, 0,21 | 7 | Body | S_Shelf
   - HGDN cg05476998: 1,45, 5,2967E-08, 4,92503E-05, 0,22 | 7 | Body | S_Shelf
   - eHCC cg05476998: 1,81, 2,11249E-08, 3,42868E-05, 0,26 | 7 | Body | S_Shelf
   - pHCC cg05476998: 1,82, 1,26735E-07, 0,000245382, 0,26 | 7 | Body | S_Shelf

1. LHX3
   - LGDN cg08967938: 1,87, 0,000967927, 0,034864845, 0,27 | 9 | Body | Island
   - HGDN cg13658899: 1,24, 0,00811133, 0,015155141, 0,21 | 9 | Body | Island
   - eHCC cg14362758: 1,55, 0,002136962, 0,01352007, 0,23 | 9 | Body | Island
   - pHCC cg14362758: 1,75, 0,002625355, 0,03954662, 0,26 | 9 | Body | Island

LGDN cg00554413: 1,41, 0,000131729, 0,011957301, 0,22 | 1 | 1stExon | Island

1. TACSTD2
   - HGDN cg24851854: 1,31, 1,26168E-05, 0,001108588, 0,22 | 1 | 1stExon | Island
   - eHCC cg24851854: 1,53, 1,09385E-05, 0,00069877, 0,26 | 1 | 1stExon | Island
   - eHCC cg00667789: 1,77, 1,97317E-05, 0,000946646, 0,29 | 1 | 1stExon | Island
   - pHCC cg16080552: 1,33, 0,003686894, 0,046971267, 0,22 | 1 | TSS200 | Island

1. MSX1
   - LGDN cg04100843: 1,31, 0,000836267, 0,032350259, 0,20 | 4 | TSS1500 | N_Shore
   - LGDN cg21689228: 1,44, 0,001348574, 0,041472402, 0,22 | 4 | TSS1500 | N_Shore
   - LGDN cg03199651: 1,70, 0,001729766, 0,047349555, 0,26 | 4 | Body | N_Shore
   - HGDN cg15092343: 1,97, 4,23898E-05, 0,002384926, 0,31 | 4 | TSS1500 | Island
   - eHCC cg03335246: 1,23, 0,010623138, 0,039249466, 0,20 | 4 | TSS1500 | N_Shore
   - eHCC cg10266211: 1,30, 0,000365637, 0,004660462, 0,22 | 4 | TSS1500 | Island
   - eHCC cg20588069: 1,37, 0,005798135, 0,025953559, 0,22 | 4 | TSS1500 | N_Shore
   - eHCC cg15092343: 2,40, 1,70495E-05, 0,000879044, 0,38 | 4 | TSS1500 | Island
| Sample | Gene        | Chromosome | start | end  |strand | ID | tissue | location |
|--------|-------------|------------|-------|------|-------|----|--------|----------|
| eHCC   | ATP11A      | 2          | -1,51 | -1   | -     | cg08893811 | 13 | Body   | S_Shore  |
| eHCC   | ATP11A      | 2          | -1,60 | -1   | -     | cg08893811 | 13 | Body   | S_Shore  |
| pHCC   | ATP11A      | 2          | 1,93  | 1    | +     | cg25142327 | 13 | Body   | S_Shore  |
| pHCC   | B3GNT9      | 2          | 1,45  | 1    | +     | cg06279276 | 16 | Body   | Island   |
| eHCC   | B3GNT9      | 2          | -1,66 | -1   | -     | cg06279276 | 12 | Body   | S_Shore  |
| eHCC   | B3GNT9      | 2          | -1,66 | -1   | -     | cg06279276 | 12 | Body   | S_Shore  |
| pHCC   | B3GNT9      | 2          | 1,92  | 1    | +     | cg06279276 | 16 | Body   | Island   |
| pHCC   | BLOC1S1     | 2          | -1,66 | -1   | -     | cg12962696 | 12 | Body   | S_Shore  |
| eHCC   | BLOC1S1     | 2          | -1,66 | -1   | -     | cg12962696 | 12 | Body   | S_Shore  |
| pHCC   | BLOC1S1     | 2          | -1,49 | -1   | -     | cg12962696 | 12 | Body   | S_Shore  |
| eHCC   | CCDC40      | 2          | 1,27  | 1    | +     | cg08109808 | 17 | Body   | N_Shelf  |
| eHCC   | CCDC40      | 2          | 1,59  | 1    | +     | cg08109808 | 17 | Body   | N_Shelf  |
| pHCC   | CCDC40      | 2          | 1,55  | 1    | +     | cg08109808 | 17 | Body   | N_Shelf  |
| eHCC   | CCR5        | 2          | -2,90 | -2   | -     | cg22984586 | 3  | TSS200 | N_Shelf  |
| eHCC   | CCR5        | 2          | -2,62 | -2   | -     | cg22984586 | 3  | TSS200 | N_Shelf  |
| pHCC   | CCR5        | 2          | -1,85 | -1   | -     | cg00803692 | 3  | TSS200 | N_Shelf  |
| eHCC   | DDX51       | 2          | -1,39 | -1   | -     | cg22672078 | 12 | Body   | Island   |
| eHCC   | DDX51       | 2          | -1,37 | -1   | -     | cg22672078 | 12 | Body   | Island   |
| pHCC   | DDX51       | 2          | -1,21 | -1   | -     | cg22672078 | 12 | Body   | Island   |
| eHCC   | DNAH17      | 2          | -1,40 | -1   | -     | cg09687005 | 17 | Body   | Island   |
| eHCC   | DNAH17      | 2          | -1,82 | -1   | -     | cg09687005 | 17 | Body   | Island   |
| eHCC   | DNAH17      | 2          | -1,93 | -1   | -     | cg10217661 | 17 | Body   | Island   |
| eHCC   | DNAH17      | 2          | -1,96 | -1   | -     | cg21103227 | 17 | Body   | Island   |
| Gene  | Chromosome | Position  | Beta   | SE   | p-Value   | Distance | Feature  |
|-------|------------|-----------|--------|------|-----------|----------|----------|
| eHCC  | cg09705784 | -1.71     | 0.000186965 | 0.003191535 | -0.25 | 17 | Body     |
| eHCC  | cg01341643 | -2.05     | 7.67345E-05 | 0.001976056 | -0.25 | 17 | Body     |
| eHCC  | cg09577144 | -1.65     | 6.6252E-05  | 0.001820993 | -0.24 | 17 | TSS200   |
| eHCC  | cg10332979 | -1.74     | 6.82902E-05 | 0.00185215  | -0.24 | 17 | Body     |
| eHCC  | cg20690714 | -2.16     | 0.00149222  | 0.002828448 | -0.24 | 17 | Body     |
| eHCC  | cg10375710 | -1.48     | 0.003666226 | 0.004665259 | -0.24 | 17 | Body     |
| eHCC  | cg15618347 | -1.81     | 0.00562421  | 0.005989096 | -0.24 | 17 | Body     |
| eHCC  | cg25691430 | -1.56     | 0.007636    | 0.007192077 | -0.23 | 17 | Body     |
| eHCC  | cg11803990 | -1.91     | 0.00283434  | 0.004031729 | -0.23 | 17 | Body     |
| eHCC  | cg14927663 | -1.98     | 9.06649E-05 | 0.002161082 | -0.22 | 17 | Body     |
| eHCC  | cg16678718 | -1.94     | 0.0084096   | 0.007615679 | -0.22 | 17 | Body     |
| eHCC  | cg00461299 | -1.56     | 0.01989067  | 0.012908616 | -0.22 | 17 | Body     |
| eHCC  | cg05361750 | -1.67     | 0.00698823  | 0.006824991 | -0.21 | 17 | Body     |
| eHCC  | cg00235657 | -1.81     | 0.00670599  | 0.00664404  | -0.21 | 17 | Body     |
| eHCC  | cg12071008 | -1.20     | 1.01136E-05 | 0.00668985  | -0.20 | 17 | Body     |
| eHCC  | cg00249503 | -1.39     | 0.00182287  | 0.003146066 | -0.20 | 17 | Body     |
| eHCC  | cg25399573 | -1.91     | 0.00330609  | 0.004405026 | -0.20 | 17 | Body     |
| eHCC  | cg25730791 | -1.82     | 0.00144292  | 0.002776676 | -0.20 | 17 | Body     |
| eHCC  | cg17514088 | -1.27     | 0.00189978  | 0.00321883  | -0.20 | 17 | Body     |
| eHCC  | cg09687005 | -1.59     | 0.00185106  | 0.009873074 | -0.23 | 17 | Body     |
| 2     | HLA-DPB2   | HGDN      | cg11786476 | -1.30 | 9.13045E-05 | 0.003882438 | -0.21 | 6 | Body     |
| pHCC  | cg11786476 | -1.32     | 0.00129282  | 0.002616638 | -0.21 | 6 | Body     |
| pHCC  | cg15019001 | -1.38     | 0.00207082  | 0.035173009 | -0.21 | 6 | Body     |
| pHCC  | cg11786476 | -1.31     | 0.00260193  | 0.011893961 | -0.21 | 6 | Body     |
| 2     | KCNK7      | HGDN      | cg01178624 | 1.70  | 2.98276E-07 | 0.000118668 | 0.22 | 11 | 3'UTR    |
| eHCC  | cg13654525 | 1.66      | 7.55637E-06 | 0.000573029 | 0.23 | 11 | 3'UTR    |
| eHCC  | cg11188624 | 1.94      | 2.38825E-07 | 9.66868E-05 | 0.24 | 11 | 3'UTR    |
| pHCC  | cg13654525 | 1.59      | 5.27809E-05 | 0.004936093 | 0.23 | 11 | 3'UTR    |
| Gene   | Position | Fold Change | p-value | q-value | Tissue | Location |
|---------|----------|-------------|---------|---------|--------|----------|
| pHCC cg01178624 | 1,85 | 1,97909E-06 | 0,000851462 | 0,24 | 11 | 3'UTR | Island |
| 2 LITAF HGDN cg08767044 | -1,75 | 0,000122039 | 0,004655068 | -0,27 | 16 | S'UTR | N_Shore |
| eHCC cg08767044 | -1,75 | 0,000324005 | 0,004352332 | -0,27 | 16 | S'UTR | N_Shore |
| eHCC cg07994696 | -1,36 | 9,61918E-07 | 0,000195514 | -0,21 | 16 | S'UTR | Island |
| pHCC cg04359558 | 1,47 | 0,001119953 | 0,025569993 | 0,24 | 16 | 3'UTR | Island |
| pHCC cg08767044 | -1,86 | 0,000525378 | 0,01721716 | -0,29 | 16 | S'UTR | N_Shore |
| 2 NID1 HGDN cg26837399 | 1,91 | 0,000169018 | 0,004352332 | 0,28 | 1 | Body |
| eHCC cg18765906 | 1,65 | 0,000435298 | 0,00512185 | 0,26 | 1 | Body |
| eHCC cg26837399 | 2,51 | 5,20315E-05 | 0,000160617 | 0,34 | 1 | Body |
| pHCC cg26837399 | 2,01 | 0,001536239 | 0,030121025 | 0,28 | 1 | Body |
| 2 PDE4DIP HGDN cg19084726 | 1,56 | 1,23612E-05 | 0,001092258 | 0,23 | 1 | Body | Island |
| eHCC cg15743907 | 1,28 | 0,000193912 | 0,0032557 | 0,20 | 1 | Body |
| eHCC cg19084726 | 2,14 | 9,39715E-07 | 0,000193256 | 0,33 | 1 | Body | Island |
| pHCC cg19084726 | 1,53 | 0,000137731 | 0,003864683 | 0,22 | 1 | Body | Island |
| 2 PURA HGDN cg21778810 | -1,39 | 2,46686E-05 | 0,001078583 | -0,20 | 5 | TSS200 | Island |
| eHCC cg21778810 | -1,56 | 1,56117E-05 | 0,000839329 | -0,23 | 5 | TSS200 | Island |
| pHCC cg21778810 | -1,33 | 0,000206234 | 0,0104749 | -0,20 | 5 | TSS200 | Island |
| 2 SCAMP1 HGDN cg03056766 | -1,40 | 2,67704E-05 | 0,001797422 | -0,21 | 5 | TSS200 | Island |
| eHCC cg03056766 | -1,76 | 4,96589E-06 | 0,000457026 | -0,25 | 5 | TSS200 | Island |
| pHCC cg03056766 | -1,60 | 3,66992E-05 | 0,004025442 | -0,23 | 5 | TSS200 | Island |
| 2 SMARCC1 HGDN cg19134770 | 1,34 | 1,74423E-06 | 0,000332913 | 0,20 | 3 | Body |
| eHCC cg19134770 | 1,54 | 1,20461E-06 | 0,000220373 | 0,22 | 3 | Body |
| pHCC cg19134770 | 1,49 | 7,21492E-06 | 0,001641008 | 0,21 | 3 | Body |
| 2 STRN4 HGDN cg12254611 | -1,36 | 1,84822E-06 | 0,000345427 | -0,23 | 19 | Body | Island |
| eHCC | cg12254611 | -1,51 | 1,06453E-06 | 0,000206487 | -0,25 | 19 | Body | Island |
|------|------------|-------|--------------|-------------|--------|----|------|--------|
| pHCC | cg12254611 | -1,45 | 4,50614E-06 | 0,001282109 | -0,24 | 19 | Body | Island |

2 | THSD7A | HGDN | cg24676244 | 1,32 | 0,000493582 | 0,011099535 | 0,21 | 7 | TSS1500 |
|----|--------|------|------------|-------|--------------|-------------|--------|----|------|
| eHCC | cg01797590 | 1,35 | 0,003258392 | 0,017732131 | 0,22 | 7 | TSS200 |
| eHCC | cg09557034 | 1,52 | 0,000351578 | 0,004559064 | 0,24 | 7 | TSS1500 |
| eHCC | cg15090509 | 1,62 | 0,002053542 | 0,01318321 | 0,25 | 7 | TSS1500 |
| eHCC | cg24676244 | 1,88 | 4,04352E-05 | 0,001395682 | 0,30 | 7 | TSS1500 |
| pHCC | cg09557034 | 1,42 | 0,001686719 | 0,03163698 | 0,22 | 7 | TSS1500 |
| pHCC | cg24676244 | 1,61 | 0,00051808 | 0,017128325 | 0,25 | 7 | TSS1500 |
| pHCC | cg01797590 | 1,57 | 0,002863191 | 0,04133531 | 0,25 | 7 | TSS200 |

2 | UGT2B15 | HGDN | cg09189601 | 1,49 | 0,003971787 | 0,03949362 | 0,22 | 4 | Body |
|----|--------|------|------------|-------|--------------|-------------|--------|----|------|
| eHCC | cg04016992 | 1,64 | 2,44741E-07 | 9,7931E-05 | 0,25 | 4 | TSS1500 |
| eHCC | cg09189601 | 1,95 | 0,00765252 | 0,07201589 | 0,26 | 4 | Body |
| pHCC | cg04016992 | 1,48 | 2,87402E-06 | 0,001018849 | 0,22 | 4 | TSS1500 |
| pHCC | cg22161115 | 1,48 | 0,000906906 | 0,022917989 | 0,22 | 4 | 1stExon |
| pHCC | cg09189601 | 1,79 | 0,002657726 | 0,039809857 | 0,26 | 4 | Body |

2 | ZNF540 | HGDN | cg03975694 | 1,60 | 1,19877E-05 | 0,001072227 | 0,24 | 19 | S'UTR | S_Shelf |
|----|--------|------|------------|-------|--------------|-------------|--------|----|------|---------|
| eHCC | cg03975694 | 1,95 | 7,45205E-06 | 0,00056898 | 0,30 | 19 | S'UTR | S_Shelf |
| pHCC | cg03975694 | 1,31 | 0,00146315 | 0,029389607 | 0,21 | 19 | S'UTR | S_Shelf |

2 | ZNF876P | HGDN | cg11836119 | 1,97 | 9,34657E-07 | 0,00022915 | 0,29 | 4 | Body | Island |
|----|--------|------|------------|-------|--------------|-------------|--------|----|------|---------|
| eHCC | cg20296343 | 1,25 | 0,002082226 | 0,0307653 | 0,21 | 4 | Body | Island |
| eHCC | cg12547166 | 1,40 | 0,00573854 | 0,00601744 | 0,23 | 4 | Body | Island |
| eHCC | cg18005867 | 1,58 | 0,0003191 | 0,03604759 | 0,25 | 4 | TSS200 | N_Shore |
| eHCC | cg23063647 | 1,71 | 0,000115482 | 0,002463327 | 0,26 | 4 | TSS200 | N_Shore |
| eHCC | cg11836119 | 2,48 | 3,41294E-07 | 0,00011561 | 0,38 | 4 | Body | Island |
| pHCC | cg11836119 | 1,71 | 0,000117359 | 0,00764703 | 0,25 | 4 | Body | Island |
|   | Gene   | Plate Type | GeneSymbol | Expression Level | p-Value | q-Value | Body Region | Island Region |
|---|---------|------------|------------|------------------|---------|---------|-------------|---------------|
| 2 | TMC4    | eHCC       | cg19488620 | 1.56             | 0.000578165 | 0.012265588 | 0.25         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 2 | LTBP2   | eHCC       | cg19488620 | 1.85             | 0.0038676 | 0.004812381 | 0.30         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 2 | HSPE1   | eHCC       | cg19488620 | 1.65             | 0.00398068 | 0.004812381 | 0.30         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 2 | DLG5    | eHCC       | cg19488620 | 1.85             | 0.00398068 | 0.004812381 | 0.30         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 3 | ALDH4A1 | eHCC       | cg19488620 | 1.56             | 0.000578165 | 0.012265588 | 0.25         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 3 | ATG4B   | eHCC       | cg19488620 | 1.56             | 0.000578165 | 0.012265588 | 0.25         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 3 | ATP6V0A1| eHCC       | cg19488620 | 1.56             | 0.000578165 | 0.012265588 | 0.25         | 19            |
|   |         | phCC       | cg22710065 | 1.61             | 0.004008046 | 0.049097195 | 0.25         | 19            |
| 3 | ATP6V1C1| eHCC       | cg19488620 | 1.56             | 0.000578165 | 0.012265588 | 0.25         | 19            |
| Rank | Gene   | Chromosome | Gene Coordinates | Start Gene | End Gene | p-Value | q-Value | Adj p-Value | Adj q-Value | Function | Region |
|------|--------|------------|------------------|------------|----------|---------|---------|------------|------------|----------|--------|
|     | pHCC   | cg03506193 | 1,530            | 0.001025482| 0.024401386| -0.203  | 8       | S'UTR      | S_Shore    | Body     | Island |
| 3   | C1QTNF4| cg05537653 | 1,685            | 5,2212E-06  | 0.000470519| 0.232   | 11      | Body       | Island     | Body     | Island |
| 3   | C9orf3 | cg13853813 | 1,452            | 0.000110657| 0.002407528| 0.203   | 9       | Body       | N_Shelf    | Body     | N_Shelf |
| 3   | CCDC57 | cg12879038 | 1,475            | 3,08029E-05| 0.001212628| 0.218   | 17      | Body       | S_Shelf    | Body     | S_Shelf |
| 3   | CCDC84 | cg27211899 | 1,460            | 7,64443E-07| 0.000174033| 0.239   | 17      | Body       | S_Shelf    | Body     | S_Shelf |
| 3   | CHERP  | cg07688052 | 1,963            | 0.000193902| 0.00325567 | 0.235   | 19      | Body       | S_Shore    | Body     | S_Shore |
| 3   | CHST11 | cg11739675 | 1,630            | 0.008780547| 0.034372311| 0.214   | 12      | Body       | Island     | Body     | Island |
|     | eHCC   | cg12529671 | -                | 0.002815763| 0.016142203| -0.209  | 12      | Body       | S_Shore    | Body     | S_Shore |
| Gene | Tissue | Transcript | Fold Change | p-value | q-value | 1st | Feature |
|------|--------|-------------|-------------|---------|---------|------|---------|
| pHCC cg01964337 | 1,281 | 0.001199658 | 0.026492301 | 0.206 | 12 | Body |
| pHCC cg07696842 | - | 0.000652404 | 0.019299821 | -0.227 | 12 | Body |
| pHCC cg16861964 | - | 0.00308331 | 0.013052779 | -0.227 | 12 | Body |
| pHCC cg22827210 | - | 0.00187928 | 0.009964452 | -0.220 | 12 | Body |

3 CLEC14A eHCC cg16404157 | 1,378 | 0.008322495 | 0.033120954 | 0.221 | 14 | 1stExon Island |
| eHCC cg05057720 | 1,801 | 0.000327148 | 0.004377465 | 0.274 | 14 | 1stExon Island |
| pHCC cg05057720 | 1,655 | 0.00163418 | 0.03111332 | 0.247 | 14 | 1stExon Island |

3 CMYA5 eHCC cg10257870 | 1,312 | 0.000730051 | 0.00700232 | 0.212 | 5 | TSS200 |
| eHCC cg09481121 | 1,384 | 0.000230309 | 0.003590465 | 0.222 | 5 | TSS1500 |
| eHCC cg03546977 | 1,413 | 0.002228094 | 0.228 | 5 | TSS200 |
| pHCC cg11438310 | 1,219 | 0.00875076 | 0.022496643 | 0.202 | 5 | TSS1500 |
| pHCC cg09481121 | 1,407 | 0.00593429 | 0.18400473 | 0.229 | 5 | TSS1500 |
| pHCC cg00611789 | 1,395 | 0.003783493 | 0.047602404 | 0.231 | 5 | TSS1500 |
| pHCC cg10257870 | 1,414 | 0.00952755 | 0.023470697 | 0.235 | 5 | TSS200 |

3 CNKSR1 eHCC cg17330765 | 1,378 | 0.001125212 | 0.025635624 | 0.214 | 1 | TSS1500 |
| pHCC cg17330765 | 1,378 | 0.001125212 | 0.025635624 | 0.214 | 1 | TSS1500 |

3 CRHB BP eHCC cg01071966 | 1,381 | 0.000729558 | 0.006998839 | 0.227 | 5 | 1stExon N_Shore |
| pHCC cg05884167 | 2,191 | 0.000227405 | 0.011034262 | 0.209 | 5 | Body S_Shelf |

3 CRYBB3 eHCC cg19288514 | 1,609 | 1.67785E-08 | 3.16982E-05 | 0.266 | 22 | TSS1500 |
| pHCC cg19288514 | 1,499 | 2.37709E-07 | 0.000328142 | 0.250 | 22 | TSS1500 |

3 CUL3 eHCC cg01474011 | 1,560 | 0.001798314 | 0.012124535 | 0.215 | 2 | Body |
|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
| pHCC | cg25502818 | 1,260 | 0,00276786 | 0,040613403 | 0,212 | 2 | Body |
| 3 | DNASE1L2 | eHCC | cg06235653 | 1,336 | 0,003322905 | 0,040613403 | 0,212 | 16 | Body | Island |
|   | eHCC | cg00249383 | 1,412 | 0,000227655 | 0,03568218 | 0,228 | 16 | Body | Island |
|   | pHCC | cg00249383 | 1,286 | 0,03123383 | 0,032096978 | 0,209 | 16 | Body | Island |
|   | pHCC | cg06235653 | 1,596 | 0,01210258 | 0,035423104 | 0,256 | 16 | Body | Island |
| 3 | DNHD1 | eHCC | cg10383568 | 1,500 | 2,51893E-05 | 0,001084113 | 0,249 | 11 | Body | N_Shelf |
|   | pHCC | cg10383568 | 1,297 | 0,000442103 | 0,01577083 | 0,218 | 11 | Body | N_Shelf |
| 3 | EGFLAM | eHCC | cg25344265 | 1,796 | 0,000173692 | 0,0406918 | -0,269 | 5 | Body |
|   | eHCC | cg18855621 | 1,923 | 7,5821E-06 | 0,000574267 | -0,241 | 5 | Body |
|   | eHCC | cg08264481 | 1,610 | 6,30507E-06 | 0,000520237 | -0,233 | 5 | Body |
|   | eHCC | cg11475323 | 1,906 | 7,30788E-05 | 0,001921857 | -0,205 | 5 | Body | S_Shelf |
|   | pHCC | cg25625968 | 1,250 | 0,00287529 | 0,02749665 | 0,201 | 5 | 3'UTR |
| 3 | ELF1 | eHCC | cg18456803 | 1,514 | 0,000796076 | 0,007373515 | -0,253 | 13 | TSS200 |
|   | pHCC | cg18456803 | 1,559 | 0,00083015 | 0,03032031 | -0,242 | 13 | TSS200 |
| 3 | EXOC2 | eHCC | cg04789318 | 1,427 | 5,31979E-08 | 4,95599E-05 | 0,216 | 6 | S'UTR | N_Shelf |
|   | pHCC | cg04789318 | 1,402 | 4,21574E-07 | 0,000397163 | 0,211 | 6 | S'UTR | N_Shelf |
| 3 | FAM20B | eHCC | cg24997888 | 1,509 | 0,000260012 | 0,03847161 | 0,227 | 1 | 3'UTR |
|   | pHCC | cg24997888 | 1,610 | 0,000529955 | 0,017284303 | 0,243 | 1 | 3'UTR |
|   | Gene | Tissue | cgID | Gene-centric Log2 fold change | Body-centric Log2 fold change | Body-centric p-value | Tissue-centric p-value | Location |
|---|------|--------|------|-------------------------------|-------------------------------|----------------------|----------------------|----------|
| 3 | FGFR4 | eHCC   | cg12982374 | 1,408 | 0,00032384 | 0,004351191 | 0,211 | 5 | Body | S_Shelf |
|   |      |        | cg17386911 | 1,617 | 0,000907565 | 0,007963218 | 0,223 | 5 | Body | S_Shelf |
|   |      | phHCC  | cg12982374 | 1,289 | 0,002217601 | 0,036337706 | 0,201 | 5 | Body | S_Shelf |
| 3 | FNDC1 | eHCC   | cg09107912 | 1,687 | 0,000231206 | 0,003597966 | 0,243 | 6 | TSS1500 | Island |
|   |      |        | cg00157796 | 1,567 | 0,000243301 | 0,003702274 | 0,257 | 6 | TSS200 | Island |
|   |      | phHCC  | cg07739841 | 1,542 | 0,001018914 | 0,02432998 | -0,243 | 6 | Body | S_Shelf |
| 3 | GAS7  | eHCC   | cg26999423 | 1,929 | 0,000418194 | 0,005037802 | -0,298 | 17 | Body |
|   |      |        | cg12091339 | 1,922 | 0,000632805 | 0,006428996 | -0,230 | 17 | Body |
|   |      | eHCC   | cg07049421 | 1,479 | 0,001028094 | 0,008569715 | -0,226 | 17 | Body |
|   |      | phHCC  | cg02605292 | 1,670 | 0,000670632 | 0,006664488 | -0,201 | 17 | Body |
|   |      |        | cg26999423 | 1,844 | 0,002011096 | 0,03465132 | -0,288 | 17 | Body |
|   |      | phHCC  | cg06130714 | 1,369 | 0,000397627 | 0,01491624 | -0,223 | 17 | Body |
| 3 | GLTSCR1 | eHCC  | cg22461472 | 1,621 | 8,72305E-05 | 0,002116745 | 0,215 | 19 | Body | S_Shelf |
|   |      | phHCC  | cg22461472 | 1,529 | 0,000577861 | 0,018119573 | 0,211 | 19 | Body | S_Shelf |
| 3 | HELZ  | eHCC   | cg18432877 | 1,498 | 0,000393989 | 0,004866668 | 0,215 | 17 | Body |
|   |      | phHCC  | cg18432877 | 1,791 | 0,000286473 | 0,012544729 | 0,239 | 17 | Body |
| 3 | HIPK1 | eHCC   | cg17588904 | 1,330 | 4,52477E-07 | 0,000133055 | 0,218 | 1 | Body |
|   |      | phHCC  | cg17588904 | 1,402 | 1,11097E-06 | 0,00064397 | 0,223 | 1 | Body |
| 3 | HIST1H3H | eHCC | cg01330280 | - | 0,001917359 | 0,012611879 | -0,259 | 6 | TSS1500 | N_Shore |
| Gene | Type | cg ID | Start | End | FDR | q-value | Status | Dist | Region |
|------|------|-------|-------|-----|-----|---------|--------|------|--------|
| ITGA11 | eHCC | cg25699851 | 1,984 | - | 8,93371E-05 | 0,00214507 | -0,272 | 15 | Body |
| ITGA11 | eHCC | cg26217827 | 2,600 | - | 0,01427853 | 0,04815242 | 0,308 | 15 | 3'UTR |
| ITGA11 | pHCC | cg08872353 | 1,552 | - | 0,00233928 | 0,01120301 | -0,244 | 15 | Body |
| ITGA11 | pHCC | cg24213777 | 1,231 | - | 0,00041966 | 0,01533492 | -0,203 | 15 | Body |
| ITGM | eHCC | cg02256631 | 1,316 | - | 0,00613586 | 0,02695865 | 0,205 | 16 | Body |
| ITGM | pHCC | cg22490695 | 1,251 | - | 0,00168357 | 0,03161132 | -0,207 | 16 | TSS200 |
| ITGB3 | eHCC | cg03460756 | 1,879 | - | 9,40275E-05 | 0,00220198 | 0,294 | 17 | Body |
| ITGB3 | pHCC | cg03460756 | 1,540 | - | 0,00184282 | 0,03314158 | 0,250 | 17 | Body |
| KAT2A | eHCC | cg16550651 | 1,846 | - | 5,26457E-05 | 0,00161582 | 0,249 | 17 | Body |
| KAT2A | pHCC | cg16550651 | 1,690 | - | 0,00049437 | 0,01674492 | 0,250 | 17 | Body |
| Chrom | Gene | Tissue | cgID   | Distance | Real_Freq | Freq | p_val | Fold_Change | Localised Reggie | Annotation  |
|-------|------|--------|--------|----------|-----------|------|-------|-------------|-----------------|-------------|
| 3     | KCNS2| eHCC   | cg08706670 | 1,440    | 0,006555951  | 0,028188336 | 0,234 | 8 | TSS200 | Island |
| eHCC  | cg11964564 | 1,668 | 0,002889448  | 0,016412185 | 0,250 | 8 | S'UTR | Island |
| eHCC  | cg14486338 | 2,317 | 1,65125E-06 | 0,000257477 | 0,363 | 8 | Body | Island |
| eHCC  | cg14688104 | 3,040 | 0,01682393  | 0,011622988 | 0,371 | 8 | 1stExon | Island |
| pHCC  | cg14688104 | 3,469 | 0,01847787  | 0,033182257 | 0,415 | 8 | 1stExon | Island |
| 3     | KIAA1875 | eHCC | cg01423393 | 1,582    | 1,71307E-05 | 0,000880983 | 0,214 | 8 | Body | Island |
| pHCC  | cg01423393 | 1,452 | 7,2645E-05 | 0,005914085 | 0,201 | 8 | Body | Island |
| 3     | KLHL5  | eHCC   | cg08217447 | 1,690    | 0,0066228  | 0,006366254 | 0,247 | 4 | TSS1500 | Island |
| pHCC  | cg08217447 | 1,699 | 0,015756363 | 0,032326742 | 0,254 | 4 | TSS1500 | Island |
| 3     | LPP    | eHCC   | cg04423294 | 1,339    | 3,16552E-05 | 0,001230227 | 0,209 | 3 | Body | 5'UTR |
| pHCC  | cg24454374 | 1,213 | 0,003067089 | 0,042809967 | 0,200 | 3 | 5'UTR | Island |
| 3     | LZTS1  | eHCC   | cg05796178 | -        | 2,50859E-05 | 0,001081459 | -0,268 | 8 | Body | S_Shelf |
| pHCC  | cg13583414 | 1,575 | 0,00643847  | 0,019167934 | -0,228 | 8 | Body | S_Shelf |
|       | cg05796178 | 1,815 | 0,00349394  | 0,013922142 | -0,223 | 8 | Body | S_Shelf |
| 3     | MAST2  | eHCC   | cg02835462 | 1,233    | 0,000386466 | 0,004810093 | 0,207 | 1 | Body | 5'UTR |
| pHCC  | cg02835462 | 1,361 | 0,000575537 | 0,018077614 | 0,227 | 1 | Body | 5'UTR |
| 3     | MATN2  | eHCC   | cg19987349 | 1,429    | 3,71774E-07 | 0,000120037 | 0,218 | 8 | Body | 5'UTR |
| pHCC  | cg19987349 | 1,433 | 2,04715E-06 | 0,000862524 | 0,214 | 8 | Body | 5'UTR |
| 3     | MCM6   | eHCC   | cg11446240 | 1,595    | 3,51221E-05 | 0,001299532 | -0,226 | 2 | Body | N_Shore |

**Notes:**
- The table lists promoter methylation marks of three genes (KCNS2, KIAA1875, KLHL5) with their corresponding genomic locations and significance levels.
- Each row represents a different gene and its specific methylation mark details.
- The columns include Chromosome, Gene, Tissue Type, cgID, Distance, Real-Frequency, Frequency, p-value, Fold Change, Regulatory Localisation, and Annotation.
|   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|
|   | pHCC | cg11446240 | 1,579 | 0,000157345 | 0,00900492 | -0,225 | 2 | Body | N_Shore |
| 3 | MED14 | eHCC | cg05812657 | 1,608 | 2,15541E-08 | 3,44223E-05 | 0,234 | X | Body | N_Shelf |
|   | pHCC | cg05812657 | 1,687 | 6,30141E-08 | 0,000183304 | 0,240 | X | Body | N_Shelf |
| 3 | MEF2C | eHCC | cg24124703 | 1,438 | 0,005506455 | 0,02505221 | -0,217 | 5 | S'UTR |
|   | pHCC | cg24124703 | 1,861 | 0,002258426 | 0,036679761 | -0,262 | 5 | S'UTR |
| 3 | MICA | eHCC | cg23826579 | 1,546 | 1,30982E-07 | 7,31567E-05 | 0,251 | 6 | Body | S_Shelf |
|   | pHCC | cg23826579 | 1,286 | 4,33075E-06 | 0,001248971 | 0,210 | 6 | Body | S_Shelf |
| 3 | MYH14 | eHCC | cg11992783 | 1,724 | 0,000115076 | 0,002459796 | 0,206 | 19 | Body | Island |
|   | pHCC | cg11992783 | 1,821 | 0,00215926 | 0,010733716 | 0,216 | 19 | Body | Island |
| 3 | NAA30 | eHCC | cg03318573 | 1,291 | 0,000488664 | 0,005512554 | 0,209 | 14 | TSS1500 | N_Shore |
|   | pHCC | cg03318573 | 1,320 | 0,001343153 | 0,028088478 | 0,212 | 14 | TSS1500 | N_Shore |
| 3 | NRP2 | eHCC | cg17455088 | 1,335 | 0,001262114 | 0,009722315 | 0,211 | 2 | Body | S_Shore |
|   | eHCC | cg05348875 | 1,283 | 3,85549E-05 | 0,001361272 | 0,214 | 2 | Body |
|   | eHCC | cg10648139 | 1,809 | 0,000334581 | 0,004435961 | 0,271 | 2 | Body | S_Shore |
|   | eHCC | cg22367989 | 2,896 | 2,9864E-05 | 0,00191996 | 0,399 | 2 | TSS1500 | Island |
|   | pHCC | cg17455088 | 1,325 | 0,003927781 | 0,048570256 | 0,213 | 2 | Body | S_Shore |
| 3 | PPAP2B | eHCC | cg10500503 | 1,244 | 0,002311455 | 0,014220871 | 0,207 | 1 | Body |
|   | pHCC | cg22396959 | 1,366 | 6,53391E-05 | 0,005585362 | 0,214 | 1 | Body |
| 3 | PALM3 | eHCC | cg11437328 | 1,636 | 0,000103987 | 0,002327386 | 0,220 | 19 | TSS1500 | S_Shelf |
|   | pHCC | cg11437328 | 1,471 | 0,001021355 | 0,024356157 | 0,215 | 19 | TSS1500 | S_Shelf |
| Row | Gene  | Model | cgID  | Fold Change | p-value | q-value | Feature | Region |
|-----|-------|-------|-------|-------------|---------|---------|---------|--------|
| 3   | PAQR6 | eHCC  | cg24152297 | 1,526 | 4.7237E-08 | 4.6686E-05 | 0.231 | TSS1500 | S_Shelf |
|     |       | pHCC  | cg24152297 | 1,614 | 1.27344E-07 | 0.000245382 | 0.240 | TSS1500 | S_Shelf |
| 3   | PCNX  | eHCC  | cg14009504 | 1,541 | 9.29995E-07 | 0.000192231 | 0.213 | Body   |
|     |       | pHCC  | cg14009504 | 1,906 | 3.95852E-07 | 0.000388937 | 0.249 | Body   |
| 3   | PIK3CG| eHCC  | cg13214190 | 1,668 | 0.007053349 | 0.029621361 | -0.271 | TSS200 | N_Shelf |
|     |       | eHCC  | cg00604356 | 1,636 | 0.00843102 | 0.007627393 | -0.263 | S'UTR  | N_Shore |
|     |       | pHCC  | cg00510718 | 3,046 | 0.0093089 | 0.023196776 | -0.444 | S'UTR  | N_Shelf |
|     |       | pHCC  | cg13214190 | 2,422 | 0.01360526 | 0.028282152 | -0.365 | TSS200 | N_Shelf |
|     |       | pHCC  | cg15881332 | 2,204 | 0.00849698 | 0.022174918 | -0.331 | TSS200 | N_Shelf |
|     |       | pHCC  | cg08779777 | 2,115 | 0.00618061 | 0.018803362 | -0.314 | TSS200 | N_Shelf |
|     |       | pHCC  | cg00661777 | 2,053 | 0.00411995 | 0.01518033 | -0.307 | Body   | S_Shelf |
|     |       | pHCC  | cg11982525 | 1,933 | 0.00945677 | 0.023385181 | -0.303 | TSS1500 | N_Shelf |
|     |       | pHCC  | cg00604356 | 1,588 | 0.03205808 | 0.04376952 | -0.261 | S'UTR  | N_Shore |
| 3   | PLEKHF2| eHCC  | cg12930753 | 1,667 | 0.0001916999 | 0.003233648 | 0.263 | 3'UTR  |
|     |       | pHCC  | cg12930753 | 1,394 | 0.0291337 | 0.041710621 | 0.233 | 3'UTR  |
| 3   | PPM1D | eHCC  | cg04180177 | 1,252 | 2.06493E-06 | 0.000288918 | 0.205 | Body   |
|     |       | pHCC  | cg04180177 | 1,270 | 7.28475E-06 | 0.001650356 | 0.209 | Body   |
| Rank | Gene Symbol | Tissue | cgID | Distance to Promoter | Beta 1 | Beta 2 | q-value 1 | q-value 2 | p-value 1 | p-value 2 | annotation 1 | annotation 2 |
|------|-------------|--------|------|----------------------|-------|-------|----------|----------|----------|----------|-------------|-------------|
| 3    | PRMT7       | eHCC   | cg10061770 | 1,574 | 0,000132487 | 0,002651869 | 0,230 | 16 | Body |
|      |             | pHCC   | cg10061770 | 1,419 | 0,00119487 | 0,026433786 | 0,204 | 16 | Body |
| 3    | PRR5        | eHCC   | cg04607412 | 1,445 | 0,000633153 | 0,006430784 | 0,210 | 22 | 5'UTR |
|      |             | pHCC   | cg04607412 | 1,764 | 0,000376057 | 0,014484217 | 0,262 | 22 | 5'UTR |
| 3    | PTBP1       | eHCC   | cg19373090 | 1,427 | 2,20224E-07 | 9,30733E-05 | -0,206 | 19 | TSS200 Island |
|      |             | pHCC   | cg19373090 | 1,409 | 7,89021E-07 | 0,00054168 | -0,204 | 19 | TSS200 Island |
| 3    | PTPRJ       | eHCC   | cg04462547 | 1,365 | 4,60958E-07 | 0,000134134 | 0,208 | 11 | Body S_Shelf |
|      |             | eHCC   | cg06298729 | 1,712 | 0,000239524 | 0,003671033 | 0,211 | 11 | Body |
|      |             | pHCC   | cg04462547 | 1,358 | 1,99131E-06 | 0,000854347 | 0,206 | 11 | Body S_Shelf |
| 3    | REEP3       | eHCC   | cg10300729 | 1,561 | 1,98415E-07 | 8,90064E-05 | 0,237 | 10 | Body S_Shelf |
|      |             | pHCC   | cg10300729 | 1,475 | 1,27E-06 | 0,000690733 | 0,228 | 10 | S_Shelf |
| 3    | RGS10       | eHCC   | cg19653161 | 1,549 | 0,002574817 | 0,01522054 | 0,226 | 10 | TSS1500 Island |
|      |             | eHCC   | cg17527393 | 2,662 | 1,27339E-05 | 0,000756324 | 0,260 | 10 | TSS200 Island |
|      |             | pHCC   | cg10200202 | 1,539 | 0,00977178 | 0,02378008 | -0,225 | 10 | Body |
| 3    | RNF220      | eHCC   | cg24603481 | 1,697 | 0,000641549 | 0,0064862 | -0,214 | 1 | Body S_Shore |
|      |             | eHCC   | cg01422881 | 1,406 | 0,000312242 | 0,004260469 | 0,237 | 1 | S'UTR Island |
|      |             | pHCC   | cg09860921 | 1,317 | 0,001947444 | 0,034084364 | 0,215 | 1 | Body N_Shelf |
| 3    | SCAND3      | eHCC   | cg19747271 | 1,425 | 3,52492E-05 | 0,001301472 | -0,225 | 6 | Body N_Shore |
|      |             | eHCC   | cg22302929 | 1,695 | 1,91757E-05 | 0,000934563 | 0,258 | 6 | 1stExon N_Shore |
| Gene  | Ensembl ID | CHR | Start | End | Score | Fold | P-Value | Q-Value | Tissue | Location  |
|-------|------------|-----|-------|-----|-------|------|---------|---------|--------|----------|
| pHCC  | cg19747271 | 1   | 1,494 | 8,531,222 | -0,237 | 6 | 0,006437328 | 0,00397212 | Body | N_Shore  |
| pHCC  | cg22302929 | 1   | 1,305 | 0,00097212 | 0,208 | 6 | 0,023718003 | 0,0097212 | 1stExon | N_Shore  |
| pHCC  | cg12483545 | 1   | 1,305 | 0,0002420813 | 0,230 | 1 | 0,014641106 | 0,002420813 | Body |          |
| pHCC  | cg12580943 | 1   | 1,254 | 0,002315354 | 0,210 | 1 | 0,037158143 | 0,002315354 | Body |          |
| pHCC  | cg19101566 | 1   | 1,936 | 0,00027258 | 0,288 | 6 | 0,00397212 | 0,0027258 | Body | S_Shelf  |
| pHCC  | cg19101566 | 1   | 2,029 | 0,00566117 | 0,291 | 6 | 0,017929972 | 0,00566117 | Body | S_Shelf  |
| pHCC  | cg19111150 | 1   | 1,375 | 6,520,522 | 0,217 | 10 | 0,001804757 | 0,001375 | Body |          |
| pHCC  | cg19111150 | 1   | 1,255 | 0,00608058 | 0,202 | 10 | 0,018646515 | 0,00608058 | Body |          |
| pHCC  | cg02030929 | 1   | 1,627 | 0,000442249 | 0,228 | 16 | 0,00519771 | 0,000442249 | Body | Island  |
| pHCC  | cg09946623 | 1   | 1,307 | 0,000805557 | 0,205 | 16 | 0,02156554 | 0,000805557 | TSS1500 | N_Shore  |
| pHCC  | cg08213398 | 1   | 1,431 | 8,239,542 | 0,212 | 11 | 0,00181688 | 0,001431 | Body |          |
| pHCC  | cg08213398 | 1   | 1,389 | 6,417,999 | 0,206 | 11 | 0,01555998 | 0,001389 | Body |          |
| pHCC  | cg19386336 | 1   | 1,513 | 0,000545741 | 0,210 | X | 0,005886281 | 0,000545741 | Body | Island  |
| pHCC  | cg01538344 | 1   | 1,525 | 0,00402553 | 0,244 | X | 0,04930357 | 0,00402553 | 1stExon | Island  |
| pHCC  | cg01538344 | 1   | 1,332 | 0,003016047 | 0,213 | X | 0,042460241 | 0,003016047 | 1stExon | Island  |
| pHCC  | cg18346402 | 1   | 1,518 | 3,053,977 | 0,249 | 2 | 0,00108993 | 0,001518 | 1stExon | N_Shelf |
| pHCC  | cg18346402 | 1   | 1,534 | 1,590,341 | 0,252 | 2 | 0,00776591 | 0,001534 | 1stExon | N_Shelf |
| pHCC  | cg06320380 | 1   | 1,744 | 4,861,942 | 0,273 | 2 | 0,001545514 | 0,001744 | S'UTR  |
| pHCC  | cg09548780 | 2   | 2,360 | 1,214,014 | 0,334 | 2 | 0,00736362 | 0,002360 | S'UTR  |
| pHCC  | cg12681370 | 1   | 1,368 | 0,000356473 | 0,218 | 2 | 0,014046256 | 0,001368 | S'UTR  |
|   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|
| 3 | TSC2 | eHCC | cg07730183 | 1,854 | 0,0001864 | 0,003185782 | 0,212 | 16 | Body | S_Shore |
|   | eHCC | cg06094085 | 1,503 | 0,001664462 | 0,011549222 | 0,215 | 16 | Body | S_Shore |
|   | eHCC | cg02504384 | 1,452 | 0,000417413 | 0,005032416 | 0,220 | 16 | Body | N_Shelf |
|   | eHCC | cg02364279 | 1,929 | 0,000903404 | 0,007942003 | 0,232 | 16 | Body | N_Shore |
|   | eHCC | cg06330323 | 1,594 | 0,000949283 | 0,008178712 | 0,246 | 16 | Body | N_Shore |
|   | pHCC | cg07730183 | 1,714 | 0,001321892 | 0,027828249 | 0,208 | 16 | Body | S_Shore |
| 3 | TXNDC5 | eHCC | cg11401394 | 1,712 | 0,000266358 | 0,003897322 | 0,255 | 6 | Body |
|   | pHCC | cg11401394 | 1,730 | 0,0008659 | 0,022381669 | 0,266 | 6 | Body |
| 3 | UCN | eHCC | cg05113927 | 1,744 | 9,60018E-07 | 0,00195291 | 0,223 | 2 | TSS200 | Island |
|   | eHCC | cg01454215 | 1,562 | 0,002163461 | 0,013625739 | 0,229 | 2 | 3'UTR | Island |
|   | pHCC | cg05113927 | 1,519 | 2,51897E-05 | 0,00325082 | 0,202 | 2 | TSS200 | Island |
| 3 | ZDHHC7 | eHCC | cg03655147 | 1,327 | 6,80724E-06 | 0,000542317 | 0,220 | 16 | S'UTR | N_Shelf |
|   | eHCC | cg09735674 | 1,240 | 1,76519E-05 | 0,00089602 | -0,208 | 16 | S'UTR | Island |
|   | pHCC | cg03655147 | 1,331 | 1,914E-05 | 0,002779045 | 0,215 | 16 | S'UTR | N_Shelf |
| 3 | ZMIZ2 | eHCC | cg11425656 | 1,311 | 2,80346E-05 | 0,001149676 | 0,204 | 7 | S'UTR | S_Shelf |
|   | pHCC | cg11425656 | 1,361 | 8,29045E-05 | 0,006348372 | 0,215 | 7 | S'UTR | S_Shelf |
| 3 | ZNF366 | eHCC | cg11905892 | 2,567 | 0,002712455 | 0,015752691 | -0,291 | 5 | Body | Island |
|   | eHCC | cg22558265 | 2,606 | 0,000212609 | 0,003430324 | -0,246 | 5 | Body | Island |
|   | eHCC | cg00657287 | 1,836 | 0,000982352 | 0,008344657 | -0,218 | 5 | Body | N_Shore |
|   | pHCC | cg04454664 | 1,253 | 0,000262241 | 0,011943707 | 0,207 | 5 | Body |
|   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 3 | EBF3 | eHCC | cg22952849 | 2,310 | 3,09135E-05 | 0,001214837 | -0,301 | 10 | Body | N_Shore |
|   | eHCC | cg07506153 | 2,606 | 0,005569163 | 0,025243439 | -0,288 | 10 | Body | N_Shore |
|   | eHCC | cg20800606 | 1,834 | 0,006677521 | 0,006677521 | -0,256 | 10 | Body | Island |
|   | eHCC | cg27454298 | 2,091 | 0,000271399 | 0,003938483 | -0,241 | 10 | Body | Island |
|   | eHCC | cg10598433 | 2,212 | 0,000352589 | 0,004565217 | -0,224 | 10 | Body | S_Shore |
|   | eHCC | cg02337436 | 2,071 | 0,000458332 | 0,005307685 | -0,213 | 10 | Body |   |
|   | eHCC | cg03128163 | 1,594 | 0,000112163 | 0,00242401 | -0,209 | 10 | Body | N_Shore |
|   | eHCC | cg15991708 | 1,586 | 6,8076E-05 | 0,0018482 | -0,206 | 10 | Body |   |
|   | eHCC | cg19582265 | 1,455 | 6,81884E-05 | 0,001850109 | -0,218 | 10 | TSS1500 |   |
|   | pHCC | cg04043455 |   |   |   |   |   |   |   |   |   |

|   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 3 | FAM189A1 | eHCC | cg19263124 | 2,078 | 5,56733E-05 | 0,00166393 | -0,239 | 15 | Body |   |
|   | eHCC | cg18512553 | 2,042 | 0,000129207 | 0,002616178 | -0,237 | 15 | Body |   |
|   | eHCC | cg12711059 | 1,486 | 9,64515E-05 | 0,002233551 | -0,226 | 15 | 3'UTR |   |
|   | eHCC | cg08904058 | 1,260 | 0,00010854 | 0,002382418 | -0,212 | 15 | Body |   |
|   | eHCC | cg21207450 | 1,460 | 0,000366217 | 0,004665259 | -0,200 | 15 | Body |   |
|   | pHCC | cg12711059 | 1,510 | 0,00319038 | 0,013289653 | -0,227 | 15 | 3'UTR |   |
|    | PHC   | ECHC    | cg    |   |   |   |   |   |   |   |   |   |
|----|-------|---------|-------|---|---|---|---|---|---|---|---|---|
| 3  | GPR158| eHCC    | cg14506260 | 1,307 | 0,007127305 | 0,029833619 | 0,207 | 10 | Body |
|    | eHCC  | cg24361761 | 2,232 | 0,00041694 | 0,05029219 | 0,345 | 10 | Body |
|    | pHCC  | cg24361761 | 10 | Body |
| 3  | IRX3  | eHCC    | cg08279075 | 1,763 | 0,001841239 | 0,012304077 | 0,271 | 16 | Body |
|    | pHCC  | cg05001964 | 1,328 | 0,001413256 | 0,028877383 | 0,203 | 16 | Body |
| 3  | KRTCAP3| eHCC    | cg17158414 | 1,739 | 0,001462983 | 0,010658876 | 0,216 | 2 | 1stExon |
|    | eHCC  | cg11618577 | 1,529 | 0,004597055 | 0,022223653 | 0,220 | 2 | Body |
|    | eHCC  | cg24768116 | 1,661 | 0,001495017 | 0,010809349 | 0,236 | 2 | TSS200 |
|    | eHCC  | cg04845466 | 1,869 | 0,000128646 | 0,002610293 | 0,246 | 2 | TSS200 |
|    | eHCC  | cg02592271 | 1,881 | 0,004601606 | 0,022239456 | 0,247 | 2 | Body |
|    | pHCC  | cg17158414 | 1,773 | 0,003062764 | 0,042779192 | 0,219 | 2 | 1stExon |
|    | pHCC  | cg04845466 | 1,893 | 0,000360845 | 0,014146618 | 0,234 | 2 | TSS200 |
| 3  | TMEM18 | eHCC    | cg27237671 | 1,418 | 0,000653957 | 0,006562296 | 0,227 | 2 | Body |
|    | pHCC  | cg27237671 | 1,327 | 0,003406437 | 0,045094384 | 0,213 | 2 | Body |
| 3  | WNT7A | eHCC    | cg23655615 | 1,817 | 0,00125122 | 0,009675403 | -0,243 | 3 | Body |
|    | eHCC  | cg10460033 | 1,524 | 0,000259 | 0,003837685 | -0,239 | 3 | Body |
|    | eHCC  | cg21224025 | 1,467 | 0,001549776 | 0,011053473 | -0,214 | 3 | Body |
|    | pHCC  | cg10460033 | 1,350 | 0,002408034 | 0,03792216 | -0,214 | 3 | Body |
| 3  | ZYG11A| eHCC    | cg20287790 | 2,232 | 1,67669E-06 | 0,000259292 | 0,242 | 1 | 3'UTR |
| Gene  | Chromosome | Position | Log2 Fold Change | p-value   | Adjusted p-value | Feature | Location      |
|-------|------------|----------|-----------------|-----------|------------------|---------|---------------|
| pHCC  | cg20287790 | 1,688    | 0,000170838     | 0,217     | 1                | 3'UTR   |               |
| 3     | APC2       | eHCC     | 1,974           | 0,003810961| 0,314            | 19      | Body Island   |
| eHCC  | cg03306486 | 2,479    | 0,002036304     | 0,378     | 19               | Body Island   |
| eHCC  | cg10808783 | 2,602    | 0,00248662      | 0,385     | 19               | Body Island   |
| pHCC  | cg10808783 |          |                 |           |                  |         |               |
| 3     | CBFA2T3    | eHCC     | 1,444           | 0,000527098| 0,203            | 16      | 1stExon Island |
| eHCC  | cg04072301 | 2,046    | 8,47368E-06     | -0,306    | 16               | S'UTR Island |
| eHCC  | cg02633398 | 1,408    | 0,000986554     | -0,223    | 16               | S'UTR N_Shore |
| eHCC  | cg03021297 | 1,821    | 0,001129361     | -0,215    | 16               | S'UTR |
| pHCC  | cg00762678 | 1,265    | 0,000881122     | -0,208    | S'UTR N_Shelf    |
| pHCC  | cg04699663 | 1,242    | 0,000962478     | -0,203    | 1stExon          |
| 3     | CNOT4      | eHCC     | 1,457           | 0,000747295| 0,234            | 7       | S'UTR         |
| pHCC  | cg25871890 | 1,532    | 0,001348339     | 0,239     | 7                | S'UTR |
| 3     | COPA       | eHCC     | 1,500           | 5,83221E-08| 0,252            | 1       | Body          |
| PHCC  | cg09866659 | 1,327    | 1,35954E-06     | 0,222     | 1                | Body |
| 3     | CR1L       | eHCC     | 1,306           | 0,000190517| 0,216            | 1       | Body Island   |
| PHCC  | cg06917617 | 1,584    | 0,000117677     | 0,257     | 1                | Body Island   |
| 3     | CREBBP     | eHCC     | 2,023           | 3,19922E-05| 0,296            | 16      | Body          |
| PHCC  | cg03368634 | 1,434    | 0,00266988      | 0,233     | 16               | Body |
| 3  | CYP1A2 | eHCC | cg04968473 | 1,677 | 0.0002478 | 0.00374116 | 0.250 | 15 | TSS1500 |
|----|--------|------|------------|------|------------|------------|-------|----|--------|
|    | pHCC   | cg04968473 | 1,409 | 0.003353047 | 0.044745176 | 0.208 | 15 | TSS1500 |
| 3  | HDAC9  | eHCC | cg04892643 | 1,653 | 3.80242E-06 | 0.000396133 | -0.271 | 7 | Body   |
|    | eHCC   | cg16925459 | 1,402 | 9.45234E-05 | 0.002208479 | -0.227 | 7 | Body   |
|    | eHCC   | cg08285151 | 1,358 | 0.01998609 | 0.012949354 | -0.221 | 7 | TSS1500 |
|    | pHCC   | cg08285151 | 1,717 | 0.000921164 | 0.023074082 | -0.285 | 7 | TSS1500 |
|    | pHCC   | cg04892643 | 1,379 | 0.00119477 | 0.007713594 | -0.225 | 7 | Body   |
| 3  | HSF5   | eHCC | cg25793387 | 1,796 | 0.000116076 | 0.002470337 | 0.234 | 17 | Body   |
|    | pHCC   | cg25793387 | 1,888 | 0.000267711 | 0.012083983 | 0.246 | 17 | Body   |
| 3  | KREME2  | eHCC | cg26494929 | 1,560 | 0.002733419 | 0.015836891 | 0.235 | 16 | Body   |
|    | eHCC   | cg05169951 | 2,182 | 1.22767E-05 | 0.000741323 | 0.279 | 16 | Body   |
|    | pHCC   | cg05169951 | 1,621 | 0.00091564 | 0.023018862 | 0.219 | 16 | Body   |
|    |         |         |         |       |            |            |       |    | Island |
| 3  | S100A6 | eHCC | cg01910639 | 1,530 | 2.45761E-06 | 0.000316155 | -0.255 | 1 | Body   |
|    | pHCC   | cg01910639 | 1,265 | 9.15466E-05 | 0.006695385 | -0.211 | 1 | Body   |
| 3  | SIPA1L1  | eHCC | cg15378445 | 1,495 | 3.64569E-08 | 4.09609E-05 | 0.228 | 14 | Body   |
|    | eHCC   | cg02058870 | 1,777 | 0.000376026 | 0.004733271 | 0.280 | 14 | S'UTR  |
|    | pHCC   | cg15378445 | 1,570 | 1.13855E-07 | 0.00233189 | 0.234 | 14 | Body   |
| 3  | SNORD6 | eHCC | cg03531787 | 1,449 | 0.000368829 | 0.00468219 | 0.206 | 11 | TSS200 |
|    | eHCC   | cg06955958 | 1,558 | 0.000306768 | 0.004216591 | 0.251 | 11 | TSS200 |
|   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|
|   | pHCC | cg06955958 | 1,617 | 0,000778465 | 0,021187295 | 0,264 | 11 | TSS200 |
| 3 | STX3 | eHCC | cg14333691 | 1,463 | 1,93006E-08 | 3,35383E-05 | 0,224 | 11 | 3'UTR |
|   | pHCC | cg14333691 | 1,431 | 1,58326E-07 | 0,000267759 | 0,217 | 11 | 3'UTR |
| 3 | THRSP | eHCC | cg03493668 | 1,398 | 0,000520835 | 0,0006430646 | 0,236 | 17 | Island |
| 3 | TSPAN10 | eHCC | cg18268547 | 1,471 | 0,000633127 | 0,049224879 | 0,214 | 17 | Island |
|   | pHCC | cg18268547 | 1,340 | 0,004026282 | 0,049224879 | 0,214 | 17 | Island |
| 3 | USP42 | eHCC | cg13977660 | 1,531 | 9,01962E-07 | 0,00189354 | 0,252 | 7 | 5'UTR |
|   | pHCC | cg13977660 | 1,340 | 0,004026282 | 0,049224879 | 0,214 | 7 | 5'UTR |
| 3 | ACTA2 | eHCC | cg03755566 | 1,682 | 8,13988E-06 | 0,000598617 | 0,271 | 10 | Body |
|   | pHCC | cg03755566 | 1,474 | 0,00151188 | 0,008793536 | 0,235 | 10 | Body |
| 3 | ARHGAP10 | eHCC | cg13248315 | 1,641 | 1,00649E-07 | 6,4364E-05 | 0,244 | 10 | Body |
|   | pHCC | cg13248315 | 1,400 | 0,004026282 | 0,049224879 | 0,214 | 10 | Body |
| 3 | COL14A1 | eHCC | cg26179069 | 1,453 | 1,68032E-05 | 0,000873201 | -0,233 | 8 | Body |
|   | eHCC | cg05830842 | 1,454 | 7,51908E-05 | 0,001952561 | -0,228 | 8 | Body |
|   | eHCC | cg10133738 | 1,759 | 0,000216387 | 0,003465422 | -0,207 | 8 | 3'UTR |
|   | pHCC | cg05830842 | 1,442 | 2,31963E-06 | 0,00091091 | 0,215 | 8 | Body |
| 3 | E4F1 | eHCC | cg27038935 | 1,773 | 1,68939E-09 | 1,32594E-05 | -0,224 | 16 | Island |
|   | pHCC | cg27038935 | - | 2,30428E-08 | 0,000133146 | -0,215 | 16 | Island |
| Chrom | Gene   | Type | Start | End   | Beta   | P      | Fold Change | Location |
|-------|--------|------|-------|-------|--------|--------|-------------|----------|
| 3     | FAM129A| eHCC | 1,689 | 2,061 | 0.003705965 | 0.019287685 | 0.316 | 1 | 1stExon | Island |
|       | pHCC   |      |       |       | - | 4.424E-05 | 0.004475372 | -0.242 | 1 | Body    |        |
| 3     | HS3ST2 | eHCC | 2,204 | 2,061 | 0.00771279 | 0.007233639 | -0.312 | 16 | Body | Island |
|       | eHCC   |      |       |       | - | 0.001228153 | 0.00956831 | -0.269 | 16 | Body | Island |
|       | eHCC   |      |       |       | - | 4.04465E-05 | 0.001395974 | -0.236 | 16 | Body | Island |
|       | eHCC   |      |       |       | - | 3.64699E-05 | 0.001322484 | -0.220 | 16 | Body | S_Shore |
|       | pHCC   |      |       |       | - | 0.00012067 | 0.007763727 | -0.228 | 16 | Body | S_Shore |
| 3     | KIF26A | eHCC | 2,565 | 2,061 | 0.00299114 | 0.004154802 | -0.291 | 14 | Body | Island |
|       | eHCC   |      |       |       | - | 5.88539E-05 | 0.001713924 | -0.286 | 14 | Body | Island |
|       | eHCC   |      |       |       | - | 0.001506599 | 0.010860826 | -0.264 | 14 | Body | N_Shore |
|       | eHCC   |      |       |       | - | 4.85261E-05 | 0.001543559 | -0.249 | 14 | Body | Island |
|       | eHCC   |      |       |       | - | 0.001865206 | 0.012402283 | -0.248 | 14 | 3'UTR | S_Shore |
|       | eHCC   |      |       |       | - | 0.001158278 | 0.009218869 | -0.246 | 14 | Body | Island |
|       | eHCC   |      |       |       | - | 0.004577351 | 0.022163995 | -0.235 | 14 | Body | Island |
|       | eHCC   |      |       |       | - | 0.001023731 | 0.008547955 | -0.226 | 14 | Body | N_Shore |
|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
|   |   |   |   |   |   |   |
| 1,889 | eHCC | cg06760280 | 1,568 | 0,000215225 | 0,003452445 | -0,225 | 14 | Body | N_Shore |
| 1,715 | eHCC | cg16520046 | 1,715 | 0,000943398 | 0,008147366 | -0,223 | 14 | Body | S_Shore |
| 1,949 | eHCC | cg19003626 | 1,949 | 0,000453261 | 0,00527236 | -0,221 | 14 | Body | N_Shore |
| 1,565 | eHCC | cg23892535 | 1,565 | 0,001489474 | 0,010784306 | -0,215 | 14 | Body | Island |
| 1,643 | eHCC | cg02922817 | 1,643 | 0,000423466 | 0,005072836 | -0,215 | 14 | Body | N_Shore |
| 1,267 | eHCC | cg25131771 | 1,267 | 0,00032767 | 0,004422609 | -0,207 | 14 | Body | Island |
| 3   |   | pHCC | cg01549570 | 1,416 | 0,002910726 | 0,041688509 | -0,201 | 14 | Body | Island |
| 1,554 | eHCC | cg17299456 | 1,554 | 0,000557138 | 0,005955705 | -0,213 | 11 | S'UTR |
| 1,416 |   | pHCC | cg17471425 |   |   |   |   |   |   |
| 3   |   |   |   |   |   |   |
| 1,836 | eHCC | cg15219347 | 1,836 | 0,000311766 | 0,004256726 | -0,287 | 19 | TSS1500 | S_Shore |
| 1,315 | eHCC | cg01662455 | 1,315 | 0,000413255 | 0,005005784 | -0,221 | 19 | 1stExon | Island |
| 1,517 | eHCC | cg18302786 | 1,517 | 0,000963315 | 0,008251243 | -0,208 | 19 | TSS200 | S_Shore |
| 1,275 | eHCC | cg10709246 | 1,275 | 0,001799566 | 0,012130169 | -0,205 | 19 | 3'UTR | Island |
| 2,091 | eHCC | cg23881613 | 2,091 | 8,5276E-06 | 0,000614467 | -0,200 | 19 | 3'UTR | Island |
| 1,401 | pHCC | cg10178628 | 1,401 | 0,001873357 | 0,033413199 | -0,218 | 19 | Body |   |
| 1,416 |   | pHCC | cg18319645 | 1,416 | 0,000413255 | 0,005005784 | -0,221 | 19 | 1stExon | Island |
| 2,091 | eHCC | cg23881613 | 2,091 | 8,5276E-06 | 0,000614467 | -0,200 | 19 | 3'UTR | Island |
| 1,889 | eHCC | cg06760280 | 1,889 | 0,000215225 | 0,003452445 | -0,225 | 14 | Body | N_Shore |
| 1,715 | eHCC | cg16520046 | 1,715 | 0,000943398 | 0,008147366 | -0,223 | 14 | Body | S_Shore |
| 1,949 | eHCC | cg19003626 | 1,949 | 0,000453261 | 0,00527236 | -0,221 | 14 | Body | N_Shore |
| 1,565 | eHCC | cg23892535 | 1,565 | 0,001489474 | 0,010784306 | -0,215 | 14 | Body | Island |
| 1,643 | eHCC | cg02922817 | 1,643 | 0,000423466 | 0,005072836 | -0,215 | 14 | Body | N_Shore |
| 1,267 | eHCC | cg25131771 | 1,267 | 0,00032767 | 0,004422609 | -0,207 | 14 | Body | Island |
| 1,416 |   | pHCC | cg17471425 | 1,416 | 0,002910726 | 0,041688509 | -0,201 | 14 | Body | Island |
| 1,554 | eHCC | cg17299456 | 1,554 | 0,000557138 | 0,005955705 | -0,213 | 11 | S'UTR |
| 1,416 |   | pHCC | cg18319645 | 1,416 | 0,000413255 | 0,005005784 | -0,221 | 19 | 1stExon | Island |
| 2,091 | eHCC | cg23881613 | 2,091 | 8,5276E-06 | 0,000614467 | -0,200 | 19 | 3'UTR | Island |
| 1,401 | pHCC | cg10178628 | 1,401 | 0,001873357 | 0,033413199 | -0,218 | 19 | Body |   |
| 1,416 |   | pHCC | cg18319645 | 1,416 | 0,000413255 | 0,005005784 | -0,221 | 19 | 1stExon | Island |
| 2,091 | eHCC | cg23881613 | 2,091 | 8,5276E-06 | 0,000614467 | -0,200 | 19 | 3'UTR | Island |
| 1,889 | eHCC | cg06760280 | 1,889 | 0,000215225 | 0,003452445 | -0,225 | 14 | Body | N_Shore |
| 1,715 | eHCC | cg16520046 | 1,715 | 0,000943398 | 0,008147366 | -0,223 | 14 | Body | S_Shore |
| 1,949 | eHCC | cg19003626 | 1,949 | 0,000453261 | 0,00527236 | -0,221 | 14 | Body | N_Shore |
| 1,565 | eHCC | cg23892535 | 1,565 | 0,001489474 | 0,010784306 | -0,215 | 14 | Body | Island |
| 1,643 | eHCC | cg02922817 | 1,643 | 0,000423466 | 0,005072836 | -0,215 | 14 | Body | N_Shore |
| 1,267 | eHCC | cg25131771 | 1,267 | 0,00032767 | 0,004422609 | -0,207 | 14 | Body | Island |
| 1,416 |   | pHCC | cg17471425 | 1,416 | 0,002910726 | 0,041688509 | -0,201 | 14 | Body | Island |
| Rank | Gene | Chromosome | Gene Symbol | Transcript ID | Log2FoldChange | p-value | FDR | TSS Location | Tissue Type | Location |
|------|------|------------|-------------|---------------|----------------|---------|-----|--------------|-------------|----------|
| 3    | TFIP11 | eHCC | cg03019505 | 1,408 | 2,63095E-07 | 0,000101671 | 0,236 | 22 | Body | S_Shelf |
|      |       | pHCC | 1,30337664 | 1,303 | 3,93172E-06 | 0,001199461 | 0,218 | 22 | Body | S_Shelf |
| 3    | THBS2 | eHCC | cg02997295 | 1,743 | 0,000910415 | 0,007979071 | -0,275 | 6 | Body | S_Shore |
|      |       | eHCC | cg04476508 | 1,585 | 0,000897118 | 0,007909381 | -0,251 | 6 | Body | Island |
|      |       | eHCC | cg06119452 | 1,560 | 0,00428559 | 0,005106589 | -0,247 | 6 | Body | N_Shore |
|      |       | eHCC | cg01320433 | 1,502 | 0,001466524 | 0,010673409 | -0,243 | 6 | Body | N_Shore |
|      |       | eHCC | cg02785555 | 1,718 | 0,000533908 | 0,005807525 | -0,239 | 6 | Body | Island |
|      |       | eHCC | cg15216858 | 2,318 | 0,000100322 | 0,002282748 | -0,229 | 6 | Body | Island |
|      |       | eHCC | cg25631414 | 2,019 | 0,000508566 | 0,005642518 | -0,225 | 6 | Body | Island |
|      |       | eHCC | cg00438284 | 1,413 | 8,99616E-05 | 0,002153094 | -0,207 | 6 | Body | S_Shelf |
|      |       | eHCC | cg03091070 | 1,388 | 0,003222734 | 0,017612259 | -0,206 | 6 | Body | N_Shore |
|      |       | pHCC | 1,695 | 0,001646196 | 0,031252485 | -0,271 | 6 | Body | N_Shore |
| 3    | ZFP91 | eHCC | cg12027899 | 1,543 | 1,19831E-05 | 0,000731878 | 0,237 | 11 | 3'UTR |
|      |       | pHCC | 1,287 | 0,000333865 | 0,013610629 | 0,209 | 11 | 3'UTR |
### Supplemental Table 8

#### Top Networks

| ID | Associated Network Functions                                                                 | Score |
|----|-----------------------------------------------------------------------------------------------|-------|
| 1  | Connective Tissue Development and Function, Connective Tissue Disorders, Organ Morphology      | 43    |
| 2  | Cellular Development, Cellular Growth and Proliferaton, Embryonic Development                  | 35    |
| 3  | Cell-To-Cell Signaling and Interaction, Tissue Development, Connective Tissue Development and Function | 30    |
| 4  | Cancer, Organismal Injury and Abnormalities, Cellular Assembly and Organization                | 30    |
| 5  | Behavior, Inflammatory Disease                                                                 | 30    |

#### Molecular and Cellular Functions

| Name                              | p-value range         | # molecules |
|-----------------------------------|-----------------------|-------------|
| Cellular Movement                 | 6.97E-03 – 3.29E-06   | 46          |
| Cell Morphology                   | 6.97E-03 – 1.52E-05   | 37          |
| Cell Signaling                    | 5.59E-03 – 2.66E-05   | 23          |
| Cell-to-Cell Signaling and Interaction | 6.97E-03 – 5.70E-05   | 24          |
| Cellular Development              | 6.97E-03 – 1.04E-04   | 55          |
| Gene_ Symbol | Panel | Probe_ID | HCC_Mean_Beta | NL_Mean_Beta | Mean_Beta_Diff. | Mean_Log2_Quotient | P-value | FDR P-value | min. 0.2 delta beta | FDR P<0.05 | Status in HCC |
|--------------|-------|----------|----------------|---------------|-----------------|-------------------|---------|-------------|-------------------|------------|---------------|
| EGFLAM       | List_3 | cg25344265 | 0.409967781    | 0.892152377   | -0.48           | -                 | 1.103092478 | 1.28E-62 | 6.46E-60 | Yes         | Yes | Hypomethylated in HCC |
| LZTS1        | List_3 | cg13583414 | 0.423408301    | 0.846738917   | -0.42           | -                 | 0.983128839 | 7.40E-35 | 2.54E-33 | Yes         | Yes | Hypomethylated in HCC |
| ATP6V0A1     | List_3 | cg07408552 | 0.117444216    | 0.323434138   | -0.21           | -                 | 1.38753592  | 3.67E-34 | 1.18E-32 | Yes         | Yes | Hypomethylated in HCC |
| LZTS1        | List_3 | cg05796178 | 0.47957211     | 0.887568016   | -0.41           | -                 | 0.874499893 | 2.52E-33 | 7.50E-32 | Yes         | Yes | Hypomethylated in HCC |
| DNAH17       | List_2 | cg12071008 | 0.324331228    | 0.616963242   | -0.29           | -                 | 0.907102747 | 3.76E-31 | 9.04E-30 | Yes         | Yes | Hypomethylated in HCC |
| FAM189A1     | List_3 | cg12711059 | 0.420513191    | 0.82788456    | -0.41           | -                 | 0.960528563 | 1.20E-29 | 7.50E-29 | Yes         | Yes | Hypomethylated in HCC |
| HK3          | List_3 | cg19960778 | 0.585752362    | 0.909082329   | -0.32           | -                 | 0.625481333 | 5.32E-29 | 1.02E-27 | Yes         | Yes | Hypomethylated in HCC |
| DNAH17       | List_2 | cg25691430 | 0.568599408    | 0.914092755   | -0.35           | -                 | 0.675472828 | 2.41E-28 | 4.33E-27 | Yes         | Yes | Hypomethylated in HCC |
| HK3          | List_3 | cg06485139 | 0.557341962    | 0.889660212   | -0.33           | -                 | 0.665161647 | 3.60E-28 | 6.33E-27 | Yes         | Yes | Hypomethylated in HCC |
| GAS7         | List_3 | cg12091339 | 0.578969104    | 0.927306719   | -0.35           | -                 | 0.670329268 | 4.43E-28 | 7.73E-27 | Yes         | Yes | Hypomethylated in HCC |
| GAS7         | List_3 | cg07049421 | 0.472863733    | 0.849913159   | -0.38           | -                 | 0.832574861 | 3.16E-27 | 5.04E-26 | Yes         | Yes | Hypomethylated in HCC |
| DNAH17       | List_2 | cg09705784 | 0.422492216    | 0.864495172   | -0.44           | -                 | 1.015776253 | 1.49E-26 | 2.22E-25 | Yes         | Yes | Hypomethylated in HCC |
| DNAH17       | List_  | cg11803990 | 0.539566666    | 0.884823881   | -0.35           | -                 | 2.30E-26   | 3.36E-25 | 3.36E-25 | Yes         | Yes | Hypomethylated in HCC |
| Gene  | List_ | cg     | TSS (log2) | p-value (log10) | FDR  | Hypomethylated in HCC |
|-------|-------|--------|------------|--------------|------|-----------------------|
| DNAH17 | List_2 | cg09687005 | 0.43302694 | 0.795687382 | 0.703309258 | Yes, Yes |
| ITGA11 | List_3 | cg25699851 | 0.531798061 | 0.913411396 | 0.703309258 | Yes, Yes |
| DNAH17 | List_2 | cg10375710 | 0.405588052 | 0.789004985 | 0.703309258 | Yes, Yes |
| CAMTA1 | List_1 | cg17143900 | 0.527163973 | 0.869862178 | 0.703309258 | Yes, Yes |
| CAMTA1 | List_1 | cg23021268 | 0.546600152 | 0.855672153 | 0.703309258 | Yes, Yes |
| HK3    | List_3 | cg11093640 | 0.555667054 | 0.872346157 | 0.703309258 | Yes, Yes |
| DNAH17 | List_2 | cg15618347 | 0.528183589 | 0.921089717 | 0.703309258 | Yes, Yes |
| CAMTA1 | List_1 | cg24579970 | 0.399969814 | 0.761984604 | 0.703309258 | Yes, Yes |
| CAMTA1 | List_1 | cg26161885 | 0.63110525 | 0.932053367 | 0.703309258 | Yes, Yes |
| DNAH17 | List_2 | cg25399573 | 0.588370774 | 0.949534441 | 0.703309258 | Yes, Yes |
| DNAH17 | List_2 | cg01341643 | 0.627660003 | 0.934551055 | 0.703309258 | Yes, Yes |
| EGFLAM | List_3 | cg11475323 | 0.615334267 | 0.945301741 | 0.703309258 | Yes, Yes |
| DNAH17 | List_2 | cg21103227 | 0.550404361 | 0.915761217 | 0.703309258 | Yes, Yes |
| WNT7A  | List_3 | cg23655615 | 0.53014866 | 0.864194864 | 0.703309258 | Yes, Yes |
| LITAF  | List_  | cg08767044 | 0.37741795 | 0.72630788 | 0.703309258 | Yes, Yes |
| Gene    | List  | cgID     | FDR  | Nominal p-value | Log2 fold change | FDR-adjusted p-value | Fold change | Hypomethylated in HCC |
|---------|-------|----------|------|-----------------|------------------|----------------------|-------------|-----------------------|
| HK3     | List 3 | cg04875020 | 0.535950744 | 0.806599021   | -0.27            | -0.58085704        | 1.62E-23    | Yes                   |
| CAMTA1  | List 1 | cg21583016 | 0.421635047 | 0.773786036   | -0.35            | -0.86064786        | 2.50E-23    | Yes                   |
| DNAH17  | List 2 | cg25730791 | 0.52515205  | 0.880586623   | -0.36            | 0.734807087        | 3.21E-23    | Yes                   |
| DNAH17  | List 2 | cg00461299 | 0.508637152 | 0.837538481   | -0.33            | 0.708553317        | 1.40E-22    | Yes                   |
| WNT7A   | List 3 | cg21224025 | 0.539480607 | 0.8661206     | -0.33            | 0.673060911        | 1.49E-22    | Yes                   |
| WNT7A   | List 3 | cg10460033 | 0.221803999 | 0.477416134   | -0.26            | 1.072248549        | 1.97E-22    | Yes                   |
| DNAH17  | List 2 | cg10332979 | 0.474277816 | 0.870048587   | -0.40            | 0.861748258        | 2.49E-22    | Yes                   |
| EGFLAM  | List 3 | cg08264481 | 0.46570847  | 0.819064781   | -0.35            | 0.801407121        | 3.20E-21    | Yes                   |
| DNAH17  | List 2 | cg10217661 | 0.566533023 | 0.907440883   | -0.34            | 0.670211952        | 5.42E-21    | Yes                   |
| CAMTA1  | List 1 | cg12138124 | 0.539106196 | 0.919118307   | -0.38            | 0.758777119        | 3.31E-20    | Yes                   |
| DNAH17  | List 2 | cg05361750 | 0.572059338 | 0.91657028    | -0.34            | 0.670734173        | 4.18E-20    | Yes                   |
| HLA-DPB2| List 2 | cg15019001 | 0.487527695 | 0.81390218    | -0.33            | 0.727696225        | 4.66E-20    | Yes                   |
| CAMTA1  | List 1 | cg06082897 | 0.572077438 | 0.901284218   | -0.33            | 0.646689984        | 5.09E-20    | Yes                   |
| EGFLAM  | List 3 | cg18855621 | 0.524367615 | 0.816333923   | -0.29            | 0.628892318        | 5.89E-20    | Yes                   |
| DNAH17  | List  | cg16678718 | 0.655016462 | 0.934843996   | -0.28            | 6.88E-20           | 5.10E-19    | Yes                   |
| List_ | cg11786476 | 0.412696491 | 0.733545236 | -0.32 | - | 0.814798381 | 2.12E-19 | 1.49E-18 | Yes | Yes | Hypomethylated in HCC |
|-------|-------------|-------------|-------------|-------|---|-------------|----------|----------|-----|-----|-------------------|
| CAMTA1 | List_ | cg07008478 | 0.548488103 | 0.881201873 | -0.33 | - | 0.674225716 | 2.15E-19 | 1.51E-18 | Yes | Yes | Hypomethylated in HCC |
| CAMTA1 | List_ | cg00911446 | 0.64609296 | 0.950942104 | -0.30 | - | 0.550549271 | 4.53E-19 | 3.08E-18 | Yes | Yes | Hypomethylated in HCC |
| DNAH17 | List_ | cg20723425 | 0.600003866 | 0.908066883 | -0.31 | - | 0.589780876 | 4.14E-18 | 2.55E-17 | Yes | Yes | Hypomethylated in HCC |
| CAMTA1 | List_ | cg25196088 | 0.567670094 | 0.868398765 | -0.30 | - | 0.604630219 | 2.38E-17 | 1.36E-16 | Yes | Yes | Hypomethylated in HCC |
| DNAH17 | List_ | cg09577144 | 0.508213014 | 0.745553346 | -0.24 | - | 0.543988375 | 6.68E-17 | 3.63E-16 | Yes | Yes | Hypomethylated in HCC |
| DNAH17 | List_ | cg00235657 | 0.535186818 | 0.905927299 | -0.37 | - | 0.748482412 | 7.42E-17 | 4.02E-16 | Yes | Yes | Hypomethylated in HCC |
| DNAH17 | List_ | cg20690714 | 0.597755487 | 0.922732124 | -0.32 | - | 0.617971792 | 7.89E-17 | 4.26E-16 | Yes | Yes | Hypomethylated in HCC |
| DNAH17 | List_ | cg00249503 | 0.569669839 | 0.87864422 | -0.31 | - | 0.61637451 | 1.28E-16 | 6.79E-16 | Yes | Yes | Hypomethylated in HCC |
| CAMTA1 | List_ | cg06800235 | 0.343503347 | 0.640900093 | -0.30 | - | 0.880712244 | 1.87E-16 | 9.72E-16 | Yes | Yes | Hypomethylated in HCC |
| CAMTA1 | List_ | cg00808305 | 0.280769908 | 0.563846296 | -0.28 | - | 0.980786394 | 2.14E-16 | 1.10E-15 | Yes | Yes | Hypomethylated in HCC |
| PTPRC | List_ | cg26399994 | 0.603438957 | 0.900290235 | -0.30 | - | 6.83E-16 | 3.36E-15 | 5.06E-18 | Yes | Yes | Hypomethylated |
|   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|
| 1 | DNAH17 | List_2 | cg17514088 | 0,466747917 | 0,778802439 | -0,31 | - | 0,726437377 | 7,19E-16 | 3,52E-15 | Yes | Yes | Hypomethylated in HCC |
|   | DNAH17 | List_2 | cg14927663 | 0,59178536 | 0,932090945 | -0,34 | - | 0,646617328 | 1,67E-15 | 7,90E-15 | Yes | Yes | Hypomethylated in HCC |
|   | ZNF366 | List_3 | cg11905892 | 0,638268465 | 0,93561169 | -0,30 | - | 0,544656476 | 1,43E-14 | 6,14E-14 | Yes | Yes | Hypomethylated in HCC |
|   | FAM189A1 | List_3 | cg25941083 | 0,382626383 | 0,602034132 | -0,22 | - | 0,640459949 | 2,58E-14 | 1,08E-13 | Yes | Yes | Hypomethylated in HCC |
|   | CAMTA1 | List_1 | cg04210471 | 0,635847272 | 0,90986939 | -0,27 | - | 0,51023599 | 5,06E-14 | 2,06E-13 | Yes | Yes | Hypomethylated in HCC |
|   | CAMTA1 | List_1 | cg10536786 | 0,437267224 | 0,695212755 | -0,26 | - | 0,656921526 | 2,16E-13 | 8,27E-13 | Yes | Yes | Hypomethylated in HCC |
|   | GAS7 | List_3 | cg02605292 | 0,58206587 | 0,876365564 | -0,29 | - | 0,582144143 | 5,06E-13 | 1,87E-12 | Yes | Yes | Hypomethylated in HCC |
|   | CCR5 | List_2 | cg22984586 | 0,192909335 | 0,38874862 | -0,20 | - | 0,974644285 | 9,10E-13 | 3,28E-12 | Yes | Yes | Hypomethylated in HCC |
|   | PIK3CG | List_3 | cg00604356 | 0,321812459 | 0,562223201 | -0,24 | - | 0,786210087 | 7,69E-12 | 2,54E-11 | Yes | Yes | Hypomethylated in HCC |
|   | ITGA11 | List_3 | cg08872353 | 0,530051459 | 0,73186379 | -0,20 | - | 0,458057445 | 6,54E-09 | 1,65E-08 | Yes | Yes | Hypomethylated in HCC |
|   | GAS7 | List_3 | cg06130714 | 0,48003765 | 0,685119818 | -0,21 | - | 0,504203884 | 3,02E-08 | 7,16E-08 | Yes | Yes | Hypomethylated in HCC |
|   | CAMTA1 | List_1 | cg12661316 | 0,558753034 | 0,770590196 | -0,21 | - | 0,456763007 | 8,47E-08 | 1,93E-07 | Yes | Yes | Hypomethylated in HCC |
|   | CAMTA1 | List_1 | cg17081408 | 0,521348459 | 0,78588637 | -0,26 | - | 0,582904176 | 3,22E-07 | 6,94E-07 | Yes | Yes | Hypomethylated in HCC |
|   | ZNF366 | List_3 | cg22558265 | 0,695090957 | 0,907243944 | -0,21 | - | 0,379496095 | 5,62E-07 | 1,19E-06 | Yes | Yes | Hypomethylated in HCC |
|   | SORBS1 | List_2 | cg27111150 | 0,710314508 | 0,354447604 | 0,36 | - | 0,982915545 | 2,47E-89 | 4,21E-85 | Yes | Yes | Hypermethylated |
| Gene   | List_ | cgID     | fnmtp   | fmlpt   | pval   | qval   | FPKM   | TPM    | Methyl | MethylStatus |
|--------|-------|----------|---------|---------|--------|--------|--------|--------|--------|--------------|
| EXOC2  | List_3| cg04789318| 0,931068733| 0,735436413| 0,20 | 0,336214803 | 8,55E-77 | 2,10E-73 | Yes   | Yes          |
| CHERP  | List_3| cg07688052| 0,938035206| 0,710800503| 0,23 | 0,395340619 | 1,63E-69 | 1,71E-66 | Yes   | Yes          |
| CCDC40 | List_2| cg08109808| 0,814395144| 0,417772738| 0,40 | 0,395340619 | 1,63E-69 | 1,71E-66 | Yes   | Yes          |
| PCNX   | List_3| cg14009504| 0,601948096| 0,135358361| 0,47 | 0,210390516 | 4,33E-55 | 9,91E-53 | Yes   | Yes          |
| TNS1   | List_3| cg09548780| 0,854931506| 0,517316203| 0,34 | 0,713917561 | 1,26E-67 | 7,08E-61 | Yes   | Yes          |
| SATB2  | List_1| cg20785796| 0,618555001| 0,235704173| 0,38 | 0,13511663 | 1,95E-54 | 7,97E-51 | Yes   | Yes          |
| ZNF212 | List_1| cg05476998| 0,888560757| 0,646782788| 0,24 | 0,452199737 | 3,79E-54 | 7,97E-51 | Yes   | Yes          |
| SATB2  | List_1| cg23994043| 0,618555001| 0,235704173| 0,38 | 0,13511663 | 1,95E-54 | 7,97E-51 | Yes   | Yes          |
| TSC2   | List_3| cg02364279| 0,822441921| 0,550747747| 0,27 | 0,569997719 | 2,03E-53 | 4,00E-53 | Yes   | Yes          |
| TNS1   | List_3| cg06320380| 0,61725925| 0,254981103| 0,37 | 0,297249116 | 2,76E-53 | 5,34E-51 | Yes   | Yes          |
| FBRSL1 | List_1| cg16719582| 0,823837672| 0,519785365| 0,30 | 0,654358562 | 2,79E-53 | 5,39E-51 | Yes   | Yes          |
| CCDC84 | List_3| cg271121899| 0,81860105| 0,479364003| 0,34 | 0,759768665 | 2,04E-52 | 3,62E-50 | Yes   | Yes          |
| TSC2   | List_3| cg06330323| 0,690211769| 0,266269106| 0,42 | 1,341717076 | 2,78E-51 | 4,42E-49 | Yes   | Yes          |
| PDE4DIP| List_2| cg19084726| 0,457368622| 0,106526394| 0,35 | 2,003904109 | 9,04E-51 | 1,38E-48 | Yes   | Yes          |
| C1QTNF4| List_5| cg05537653| 0,794568195| 0,515360672| 0,28 | 0,614906504 | 5,18E-50 | 7,36E-48 | Yes   | Yes          |
| Gene  | List  | CG Probe   | Methylation Index | P-value | FDR-corrected P-value | Ctrl Methylation Index | FDR-corrected P-value | Status   | Hypermethylated in HCC |
|-------|-------|------------|------------------|---------|-----------------------|------------------------|-----------------------|---------|------------------------|
| KCNS2 | List_3 | cg14486338 | 0.665524873      | 0.45    | 1.564802889           | 1.09E-49               | 1.50E-47               | Yes     | Yes                    |
| ZNF876P | List_2 | cg20296343 | 0.644563286      | 0.41    | 1.42293614            | 3.67E-46               | 3.65E-44               | Yes     | Yes                    |
| ZNF540 | List_2 | cg16550651 | 0.849765267      | 0.33    | 0.697200774           | 8.13E-45               | 7.14E-43               | Yes     | Yes                    |
| SWAP70 | List_3 | cg08213398 | 0.809485469      | 0.24    | 0.497999713           | 1.55E-44               | 1.33E-42               | Yes     | Yes                    |
| C1QTNF4 | List_3 | cg18356785 | 0.689352312      | 0.38    | 1.595748017           | 1.70E-40               | 1.00E-38               | Yes     | Yes                    |
| MICA | List_3 | cg23826579 | 0.826849097      | 0.23    | 0.45730737            | 5.89E-40               | 3.29E-38               | Yes     | Yes                    |
| ZNF876P | List_2 | cg12547166 | 0.620881746      | 0.35    | 1.163596702           | 8.58E-40               | 4.72E-38               | Yes     | Yes                    |
| STX1A | List_1 | cg02610600 | 0.752121494      | 0.27    | 0.6369817            | 5.76E-39               | 2.93E-37               | Yes     | Yes                    |
| CRYBB3 | List_3 | cg19288514 | 0.782474951      | 0.24    | 0.517569554           | 8.53E-39               | 4.28E-37               | Yes     | Yes                    |
| SKI | List_3 | cg12483545 | 0.774560615      | 0.34    | 0.831699141           | 1.54E-38               | 7.55E-37               | Yes     | Yes                    |
| MYH14 | List_3 | cg11992783 | 0.839163187      | 0.21    | 0.399381805           | 2.41E-38               | 1.16E-36               | Yes     | Yes                    |
| NSD1 | List_1 | cg19731612 | 0.820886314      | 0.24    | 0.487979277           | 7.77E-38               | 3.56E-36               | Yes     | Yes                    |
| NSD1 | List_1 | cg18121224 | 0.798646384      | 0.28    | 0.61593001            | 1.20E-37               | 5.41E-36               | Yes     | Yes                    |
| PIAS1 | List_3 | cg05105016 | 0.810493124      | 0.21    | 0.427481553           | 1.11E-35               | 4.12E-34               | Yes     | Yes                    |
| Gene   | List_ | cgID    | FDR   | q-value | Log2FoldChange | p-value | Hypermethylated |
|--------|-------|---------|-------|---------|----------------|---------|----------------|
| TSC2   | List_3| cg02504384 | 0,713408243 | 0,478814879 | 0,23 | 0,565521837 | 1,14E-34 | Yes | Yes | Hypermethylated in HCC |
| SATB2  | List_1| cg03163783 | 0,705856705 | 0,350653797 | 0,36 | 0,989056217 | 1,84E-33 | Yes | Yes | Hypermethylated in HCC |
| CREBBP | List_3| cg03368634 | 0,806100634 | 0,547139182 | 0,26 | 0,550709285 | 1,19E-29 | Yes | Yes | Hypermethylated in HCC |
| BMP8A  | List_1| cg11763509 | 0,610124936 | 0,356974472 | 0,25 | 0,756879194 | 2,39E-28 | Yes | Yes | Hypermethylated in HCC |
| ZIC5   | List_1| cg00529958 | 0,798182307 | 0,584677802 | 0,21 | 1,608768079 | 1,29E-28 | Yes | Yes | Hypermethylated in HCC |
| TSC2   | List_3| cg06094085 | 0,704929759 | 0,50345437 | 0,20 | 0,442572545 | 1,34E-28 | Yes | Yes | Hypermethylated in HCC |
| KCNK7  | List_2| cg01178624 | 0,760506407 | 0,475527623 | 0,28 | 0,666253578 | 1,18E-26 | Yes | Yes | Hypermethylated in HCC |
| NSD1   | List_1| cg08369368 | 0,389943673 | 0,0667812 | 0,32 | 2,380971817 | 1,53E-26 | Yes | Yes | Hypermethylated in HCC |
| KIAA1875| List_3| cg01423393 | 0,704929759 | 0,50345437 | 0,20 | 0,477565433 | 3,61E-25 | Yes | Yes | Hypermethylated in HCC |
| NID1   | List_2| cg18765906 | 0,655432968 | 0,311083841 | 0,34 | 1,051343284 | 1,07E-24 | Yes | Yes | Hypermethylated in HCC |
| B3GNT9 | List_2| cg05333146 | 0,775671284 | 0,519994988 | 0,26 | 0,567947115 | 1,63E-24 | Yes | Yes | Hypermethylated in HCC |
| NRP2   | List_3| cg17455088 | 0,605659829 | 0,284969232 | 0,32 | 1,061568961 | 1,96E-24 | Yes | Yes | Hypermethylated in HCC |
| RNF220 | List_3| cg09860921 | 0,734378346 | 0,519913671 | 0,21 | 0,49027874 | 6,64E-24 | Yes | Yes | Hypermethylated in HCC |
| CNKSR1 | List_3| cg17330765 | 0,77744123 | 0,557484073 | 0,22 | 0,47259235 | 1,51E-22 | Yes | Yes | Hypermethylated in HCC |
| NSD1   | List_ | cg18016826 | 0,397282969 | 0,076097884 | 0,32 | 2,2419818 | 4,46E-22 | Yes | Yes | Hypermethylated in HCC |
|   | ZNF876P | List_2 | cg23063647 | 0.673270819 | 0.389906354 | 0.28 | 0.772795312 | 1.00E-21 | 9.04E-21 | Yes | Yes | Hypermethylated in HCC |
|---|---------|--------|------------|-------------|-------------|------|-------------|----------|----------|-----|-----|----------------------|
|   | RNF220  | List_3 | cg01422881 | 0.596173945 | 0.344472108 | 0.25 | 0.774059731 | 3.06E-21 | 2.61E-20 | Yes | Yes | Hypermethylated in HCC |
|   | KCNS2   | List_3 | cg11964564 | 0.346491116 | 0.068382504 | 0.28 | 2.185262564 | 5.28E-19 | 3.57E-18 | Yes | Yes | Hypermethylated in HCC |
|   | ZIC5    | List_1 | cg20985450 | 0.488580889 | 0.129077099 | 0.36 | 1.841942709 | 6.27E-19 | 4.21E-18 | Yes | Yes | Hypermethylated in HCC |
|   | KRTCAP3 | List_3 | cg17158414 | 0.740277812 | 0.511463141 | 0.23 | 0.524859614 | 3.06E-18 | 3.60E-17 | Yes | Yes | Hypermethylated in HCC |
|   | CUL3    | List_3 | cg01474011 | 0.764520444 | 0.556137474 | 0.21 | 0.452150898 | 5.94E-18 | 3.60E-17 | Yes | Yes | Hypermethylated in HCC |
|   | ZIC5    | List_1 | cg11077516 | 0.599715291 | 0.320782721 | 0.28 | 0.882251853 | 1.29E-17 | 7.57E-17 | Yes | Yes | Hypermethylated in HCC |
|   | ZIC5    | List_1 | cg17930361 | 0.345200547 | 0.087500019 | 0.26 | 1.865159401 | 7.85E-17 | 4.24E-16 | Yes | Yes | Hypermethylated in HCC |
|   | THRSP   | List_3 | cg03493668 | 0.736262396 | 0.488954783 | 0.25 | 0.580773911 | 9.86E-17 | 5.27E-16 | Yes | Yes | Hypermethylated in HCC |
|   | KRTCAP3 | List_3 | cg02592271 | 0.721665637 | 0.480438096 | 0.24 | 0.577113456 | 2.38E-16 | 1.22E-15 | Yes | Yes | Hypermethylated in HCC |
|   | KRTCAP3 | List_3 | cg24768116 | 0.690346477 | 0.425956627 | 0.26 | 0.683884223 | 6.24E-16 | 3.08E-15 | Yes | Yes | Hypermethylated in HCC |
|   | CLEC14A | List_3 | cg05057720 | 0.487230336 | 0.161023624 | 0.33 | 1.539718694 | 1.48E-15 | 7.05E-15 | Yes | Yes | Hypermethylated in HCC |
|   | KRTCAP3 | List_3 | cg11618577 | 0.668759807 | 0.444573698 | 0.22 | 0.578386928 | 1.09E-14 | 4.74E-14 | Yes | Yes | Hypermethylated in HCC |
|   | TMEM18  | List_3 | cg27237671 | 0.678177853 | 0.481159473 | 0.20 | 0.486589938 | 1.11E-14 | 4.81E-14 | Yes | Yes | Hypermethylated in HCC |
|   | NRP2    | List_  | cg10648139 | 0.453029416 | 0.139796015 | 0.31 | 1.628104602 | 4.18E-14 | 1.72E-13 | Yes | Yes | Hypermethylated in HCC |
| Gene  | List  | cg   | FDR  | P-value       | Log2 Fold  | Log10 P-value | Hypermethylated in HCC |
|-------|-------|------|------|---------------|------------|---------------|------------------------|
| KCNS2 | List_3 | cg14688104 | 0.340469027 | 0.051581203 | 2.508724992 | 4.53E-13 | Yes | Yes | Hypermethylated in HCC |
| ZIC5  | List_1 | cg03313945 | 0.408715413 | 0.126902156 | 1.612824854 | 3.24E-13 | Yes | Yes | Hypermethylated in HCC |
| C1QTNF4 | List_3 | cg17282004 | 0.498449663 | 0.293001854 | 0.746778334 | 2.84E-12 | Yes | Yes | Hypermethylated in HCC |
| CAMTA1 | List_1 | cg00783553 | 0.338542896 | 0.11602324 | 1.467646413 | 5.87E-12 | Yes | Yes | Hypermethylated in HCC |
| ITGB3 | List_3 | cg03460756 | 0.548670946 | 0.315251923 | 0.780441206 | 3.24E-12 | Yes | Yes | Hypermethylated in HCC |
| CLEC14A | List_3 | cg16404157 | 0.520833052 | 0.236168222 | 1.108613667 | 6.55E-11 | Yes | Yes | Hypermethylated in HCC |
| NRP2 | List_3 | cg22367989 | 0.264060408 | 0.067335986 | 1.825282126 | 4.24E-10 | Yes | Yes | Hypermethylated in HCC |
| CRHBP | List_3 | cg01071966 | 0.504392151 | 0.215658561 | 0.996732713 | 7.71E-09 | Yes | Yes | Hypermethylated in HCC |
| SIPA1L1 | List_3 | cg02058870 | 0.615702868 | 0.380122038 | 0.681552218 | 2.73E-09 | Yes | Yes | Hypermethylated in HCC |
| B3GNT9 | List_2 | cg06279276 | 0.378888095 | 0.162566599 | 1.172201818 | 3.28E-09 | Yes | Yes | Hypermethylated in HCC |
| ZIC5  | List_1 | cg10679688 | 0.440296176 | 0.215658561 | 0.996732713 | 7.71E-09 | Yes | Yes | Hypermethylated in HCC |
| ITGAM | List_3 | cg02256631 | 0.373541446 | 0.156235655 | 1.206152639 | 4.50E-08 | Yes | Yes | Hypermethylated in HCC |
| KCNS2 | List_3 | cg08706670 | 0.298003746 | 0.092566222 | 1.586392218 | 9.48E-08 | Yes | Yes | Hypermethylated in HCC |
| CAMTA1 | List_1 | cg08640609 | 0.260589976 | 0.052173929 | 2.121726745 | 1.01E-07 | Yes | Yes | Hypermethylated in HCC |
| FAM189A1 | List_ | cg04283162 | 0.338508981 | 0.110882162 | 1.52759447 | 4.99E-07 | Yes | Yes | Hypermethylated |
| Gene   | List_3 | cg    | Freq in 1 | Freq in 2 | Freq in 3 | p-value 1   | p-value 2   | p-value 3   | Fold Change | Methylated in HCC | Methylated in HCC |
|--------|--------|-------|-----------|-----------|-----------|------------|------------|------------|-------------|-------------------|-------------------|
| FNDC1  | List_3 | cg00157796 | 0,370065262 | 0,158200882 | 0,21 | 1,176061894 | 4,35E-05 | 7,70E-05 | Yes | Yes | Hypermethylated in HCC |
| CHST11 | List_3 | cg22260952 | 0,298001159 | 0,099722053 | 0,20 | 1,48908226 | 0,000180 824 | 0,000301 492 | Yes | Yes | Hypermethylated in HCC |
| ZYG11A | List_3 | cg20287790 | 0,934964064 | 0,755239011 | 0,18 | 0,304349044 | 3,00E-60 | 1,18E-57 | No | Yes | - |
| STX3   | List_3 | cg14333691 | 0,298001159 | 0,099722053 | 0,20 | 1,48908226 | 0,000180 824 | 0,000301 492 | Yes | Yes | Hypermethylated in HCC |
| TSC2   | List_3 | cg07730183 | 0,906570667 | 0,736849713 | 0,17 | 0,295428154 | 1,04E-44 | 9,08E-43 | No | Yes | - |
| USP34  | List_1 | cg01145124 | 0,945206472 | 0,804028251 | 0,14 | 0,230733748 | 2,08E-43 | 1,61E-41 | No | Yes | - |
| PURA   | List_2 | cg21778810 | 0,051399191 | 0,110706167 | -0,06 | - | - | - | No | Yes | - |
| TIGD1  | List_3 | cg18346402 | 0,884184946 | 0,701563923 | 0,18 | 0,329579892 | 3,02E-37 | 1,31E-35 | No | Yes | - |
| MCM6   | List_3 | cg11446240 | 0,10837107 | 0,227701444 | -0,13 | 1,100709706 | 3,20E-34 | 1,03E-32 | No | Yes | - |
| ATG4B  | List_3 | cg08969328 | 0,834563402 | 0,691109919 | 0,14 | 0,268565086 | 1,28E-32 | 3,56E-31 | No | Yes | - |
| HIPK1  | List_3 | cg17588904 | 0,738368521 | 0,574953476 | 0,16 | 0,355426991 | 1,25E-27 | 2,08E-26 | No | Yes | - |
| COPA   | List_3 | cg09866659 | 0,731941546 | 0,558522958 | 0,17 | 0,38408692 | 3,41E-27 | 5,43E-26 | No | Yes | - |
| SMARCC1 | List_2 | cg19134770 | 0,871949202 | 0,751782304 | 0,12 | 0,211316787 | 3,43E-23 | 3,60E-22 | No | Yes | - |
| ATP6V1C1 | List_3 | cg03506193 | 0,117463086 | 0,232190326 | -0,11 | 0,926061747 | 4,02E-23 | 4,19E-22 | No | Yes | - |
| SCAMP1 | List_3 | cg03056766 | 0,047314261 | 0,088288621 | -0,04 | - | 4,75E-21 | 3,98E-20 | No | Yes | - |
| Gene    | List_ | RefGene       | EPI | TSS | p-value | Adjusted p-value | Expression | Log2| Direction | Fold Change | CNA | Methylated | UCH | Interpreted |
|---------|-------|---------------|-----|-----|---------|------------------|------------|-----|-----------|-------------|-----|-------------|-----|-------------|
| KRTCAP3| List_ 3 | cg04845466    | 0,809672269 | 0,626041083 | 0,18 | 0,365927234 | 2,02E-19 | 1,43E-18 | No | Yes | - |
| RWDD1  | List_ 1 | cg23280258    | 0,798702495 | 0,65202233 | 0,15 | 0,288729182 | 2,55E-19 | 1,78E-18 | No | Yes | - |
| SIPA1L1 | List_ 3 | cg15378445    | 0,849480726 | 0,74420309 | 0,11 | 0,188512227 | 3,59E-19 | 2,23E-17 | No | Yes | - |
| SPG11  | List_ 1 | cg12228919    | 0,055413 | 0,088353072 | -0,03 | 0,588392733 | 2,83E-17 | 1,60E-16 | No | Yes | - |
| WDR82  | List_ 1 | cg24007312    | 0,085243635 | 0,13562583 | -0,05 | 0,612571681 | 9,78E-17 | 5,23E-16 | No | Yes | - |
| MATN2  | List_ 3 | cg19987349    | 0,055413 | 0,088353072 | -0,03 | 0,588392733 | 2,83E-17 | 1,60E-16 | No | Yes | - |
| MAST2  | List_ 3 | cg02835462    | 0,75448421 | 0,565267608 | 0,19 | 0,410253465 | 5,16E-16 | 2,56E-15 | No | Yes | - |
| ATP11A | List_ 2 | cg25142327    | 0,90869295 | 0,836702534 | 0,07 | 0,117727552 | 6,18E-16 | 3,05E-15 | No | Yes | - |
| C9orf3 | List_ 3 | cg14375632    | 0,780249875 | 0,606065739 | 0,17 | 0,359224596 | 1,94E-14 | 8,22E-14 | No | Yes | - |
| LITAF  | List_ 2 | cg07994696    | 0,245123056 | 0,367814378 | -0,12 | -0,56648432 | 2,34E-13 | 8,92E-13 | No | Yes | - |
| EGFLAM | List_ 3 | cg25625968    | 0,227390933 | 0,372038342 | -0,14 | 0,686452601 | 3,27E-13 | 1,23E-12 | No | Yes | - |
| REEP3  | List_ 3 | cg10300729    | 0,846646079 | 0,737493761 | 0,11 | 0,196637744 | 3,76E-13 | 1,41E-12 | No | Yes | - |
| CAMTA1 | List_ 1 | cg25763306    | 0,224250829 | 0,377114345 | -0,15 | 0,724705617 | 4,47E-13 | 1,66E-12 | No | Yes | - |
| DNASE1L2 | List_ 3 | cg06235653    | 0,267645994 | 0,085694524 | 0,18 | 1,536738307 | 5,57E-13 | 2,05E-12 | No | Yes | - |
| BLOC1S1 | List_ 3 | cg12926596    | 0,622507743 | 0,80660363 | -0,18 | -0,36855284 | 7,61E-13 | 2,76E-12 | No | Yes | - |
| Gene       | List | cg   | p1  | p2  | p3  | p4  | p5  | p6  | p7  | p8  | p9  | p10 | p11 | p12 | p13 | p14 |
|------------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MAP4       | List | cg16509829 | 0,046585042 | 0,065199503 | -0,02 | - | 0,410302385 | 9,24E-13 | 3,33E-12 | No | Yes | - |
| KREMEN2    | List | cg05169951 | 0,718138921 | 0,555005779 | 0,16 | 0,365948105 | 2,98E-12 | 1,02E-11 | No | Yes | - |
| PPM1D      | List | cg04180177 | 0,680597373 | 0,575556353 | 0,11 | 0,238036825 | 3,41E-12 | 1,16E-11 | No | Yes | - |
| SLC25A27   | List | cg19101566 | 0,745685061 | 0,584730673 | 0,16 | 0,345548618 | 8,91E-12 | 2,93E-11 | No | Yes | - |
| UCN        | List | cg01454215 | 0,238859715 | 0,078353474 | 0,16 | 1,493973936 | 1,22E-11 | 3,96E-11 | No | Yes | - |
| PTPRJ      | List | cg04462547 | 0,842334313 | 0,764846197 | 0,08 | 0,137509441 | 1,60E-11 | 5,12E-11 | No | Yes | - |
| LHX3       | List | cg14362758 | 0,236705782 | 0,09081312 | 0,15 | 1,291108125 | 7,90E-11 | 2,37E-10 | No | Yes | - |
| KCNK7      | List | cg13654525 | 0,74123877 | 0,618940086 | 0,12 | 0,25634893 | 1,68E-10 | 4,88E-10 | No | Yes | - |
| ITGA11     | List | cg24213777 | 0,546432215 | 0,730242923 | -0,18 | 0,411792844 | 4,69E-10 | 1,31E-09 | No | Yes | - |
| UCN        | List | cg05113927 | 0,684324195 | 0,543460273 | 0,14 | 0,327129681 | 5,28E-10 | 1,47E-09 | No | Yes | - |
| DNASE1L2   | List | cg00249383 | 0,565807123 | 0,382333069 | 0,18 | 0,553506693 | 7,34E-10 | 2,02E-09 | No | Yes | - |
| SPN        | List | cg02030929 | 0,40367796 | 0,566807672 | -0,16 | - | 0,479582257 | 2,86E-09 | 7,44E-09 | No | Yes | - |
| PPAP2B     | List | cg22396959 | 0,234977672 | 0,330506079 | -0,10 | - | 0,475030292 | 4,26E-09 | 1,09E-08 | No | Yes | - |
| ALDH4A1    | List | cg12461099 | 0,696785944 | 0,565615784 | 0,13 | 0,296167196 | 7,29E-09 | 1,83E-08 | No | Yes | - |
| GALK2      | List | cg00756450 | 0,925907947 | 0,89955543 | 0,03 | 0,041205076 | 1,61E-08 | 3,92E-08 | No | Yes | - |
| Gene   | List | Probe ID 1 | Unlogged Expression 1 | Log2 Fold Change 1 | P-Value 1 | No  | Yes  | Value | Log2 Fold Change 2 | P-Value 2 | No  | Yes  |
|--------|------|------------|------------------------|-------------------|----------|-----|------|-------|-------------------|----------|-----|------|
| STRN4  | List 2 | cg12254611 | 0.075840667            | 0.097755043       | -0.02    | 0.328022205 | 2.44E-08 | 5.83E-08 | No     | Yes    |       |
| FGFR4  | List 3 | cg12982374 | 0.677065318            | 0.541387018       | 0.14     | 0.317381959 | 2.54E-08 | 6.05E-08 | No     | Yes    |       |
| CBFA2T3| List 3 | cg27434245 | 0.284072086            | 0.101544065       | 0.18     | 1.398556099 | 4.14E-08 | 9.69E-08 | No     | Yes    |       |
| FBRSL1 | List 1 | cg08818195 | 0.077274438            | 0.099616982       | -0.02    | 0.328840242 | 6.27E-08 | 1.44E-07 | No     | Yes    |       |
| CAMTA1 | List 1 | cg21144493 | 0.537033269            | 0.382300133       | 0.15     | 0.479670751 | 7.70E-08 | 1.76E-07 | No     | Yes    |       |
| KLHL5  | List 3 | cg08217447 | 0.684486869            | 0.558404238       | 0.13     | 0.289030105 | 1.52E-07 | 3.37E-07 | No     | Yes    |       |
| ZNF876P| List 2 | cg18005867 | 0.431292247            | 0.246811795       | 0.18     | 0.781022935 | 1.79E-07 | 3.95E-07 | No     | Yes    |       |
| PAQR6  | List 3 | cg24152297 | 0.847531709            | 0.810614354       | 0.04     | 0.06348563  | 2.24E-07 | 4.90E-07 | No     | Yes    |       |
| STX1A  | List 1 | cg01804343 | 0.061146318            | 0.076623107       | -0.02    | 0.283962829 | 2.66E-07 | 5.78E-07 | No     | Yes    |       |
| UGT2B15| List 2 | cg09189601 | 0.662704734            | 0.544713026       | 0.12     | 0.278231806 | 2.84E-07 | 6.17E-07 | No     | Yes    |       |
| CCR5   | List 2 | cg00803692 | 0.637517069            | 0.811068312       | -0.17    | 0.342584035 | 4.97E-07 | 1.05E-06 | No     | Yes    |       |
| ANO10  | List 1 | cg11035303 | 0.062528227            | 0.115899744       | -0.05    | 0.795660861 | 6.00E-07 | 1.26E-06 | No     | Yes    |       |
| LPP    | List 3 | cg04423294 | 0.66720779             | 0.562807848       | 0.10     | 0.24154731  | 7.07E-07 | 1.48E-06 | No     | Yes    |       |
| LPP    | List 3 | cg24454374 | 0.460828831            | 0.59085185        | -0.13    | 0.351806648 | 1.35E-06 | 2.75E-06 | No     | Yes    |       |
| ZDHHC7 | List  _| cg03655147 | 0.812896754            | 0.757532365       | 0.06     | 0.100483846 | 1.46E-06 | 2.97E-06 | No     | Yes    |       |
| Gene   | List. | cgID      | Distance | p-value  | MDR value | MDN value | Transmitter | \%
|--------|-------|-----------|----------|----------|-----------|------------|-------------|
| WDR82  | List_1 | cg11442381 | 0,08479947 | 0,069998077 | 0,01 | 0,244845187 | 1,59E-06 | 3,23E-06 | No | Yes |
| ZMIZ2  | List_3 | cg11425656 | 0,70278203 | 0,607282664 | 0,10 | 0,20754209 | 2,22E-06 | 4,44E-06 | No | Yes |
| PTPRJ  | List_3 | cg06298729 | 0,79510556 | 0,732511102 | 0,06 | 0,116745925 | 3,14E-06 | 6,18E-06 | No | Yes |
| DNHD1  | List_3 | cg10383568 | 0,579499761 | 0,420951412 | 0,16 | 0,45166007 | 4,27E-06 | 8,30E-06 | No | Yes |
| ALDH4A1| List_3 | cg22390041 | 0,430733428 | 0,55383528 | -0,12 | 0,355367429 | 4,81E-06 | 9,32E-06 | No | Yes |
| CCDC57 | List_3 | cg22142205 | 0,817943387 | 0,77065436 | 0,05 | 0,08484195 | 5,53E-06 | 1,07E-05 | No | Yes |
| NAA30  | List_3 | cg03318573 | 0,619499362 | 0,502407094 | 0,12 | 0,296914465 | 5,94E-06 | 1,14E-05 | No | Yes |
| CHST11 | List_3 | cg16861964 | 0,491036366 | 0,624053302 | -0,13 | 0,339688805 | 6,58E-06 | 1,26E-05 | No | Yes |
| CCDC57 | List_3 | cg12879038 | 0,71298492 | 0,62580394 | 0,09 | 0,18589033 | 7,38E-06 | 1,41E-05 | No | Yes |
| FAM189A1| List_3 | cg13942157 | 0,249280407 | 0,084682412 | 0,16 | 1,453344822 | 7,62E-06 | 1,45E-05 | No | Yes |
| PDE4DIP| List_2 | cg15743907 | 0,58259746 | 0,501865782 | 0,08 | 0,211286878 | 8,30E-06 | 1,57E-05 | No | Yes |
| IRX3   | List_3 | cg05001964 | 0,238524117 | 0,091124563 | 0,15 | 1,297252384 | 1,10E-05 | 2,05E-05 | No | Yes |
| CYP1A2 | List_3 | cg04968473 | 0,775359789 | 0,698272751 | 0,08 | 0,149048693 | 1,38E-05 | 2,57E-05 | No | Yes |
| CAMTA1 | List_1 | cg22488970 | 0,271708519 | 0,08786246 | 0,18 | 1,525373086 | 1,70E-05 | 3,13E-05 | No | Yes |
| CHST11 | List_ | cg22827210 | 0,501172514 | 0,634660128 | -0,13 | - | 1,73E-05 | 3,18E-05 | No | Yes |
| Gene   | List_ | cg       | FDR  | FCP   | p-value  | q-value  | Class | Status |
|--------|-------|----------|------|-------|----------|----------|-------|--------|
| CBFA2T3 | 3     | cg00762678 | 0,396770224 | 0,518248868 | -0,12 | 0,377003695 | 2,12E-05 | 3,87E-05 | No      | Yes     | -       |
| GLTSCR1  | List_ | cg22461472 | 0,789181993 | 0,728576133 | 0,06 | 0,113777433 | 2,28E-05 | 4,15E-05 | No      | Yes     | -       |
| FNDC1    | List_ | cg09107912 | 0,231033585 | 0,090726663 | 0,14 | 1,258788554 | 3,11E-05 | 5,57E-05 | No      | Yes     | -       |
| FBRSL1   | List_ | cg00370303 | 0,175111528 | 0,046924432 | 0,13 | 1,701274843 | 4,12E-05 | 7,31E-05 | No      | Yes     | -       |
| CHST11   | List_ | cg07696842 | 0,411900814 | 0,539050524 | -0,13 | 0,380035041 | 4,46E-05 | 7,89E-05 | No      | Yes     | -       |
| SAMD11   | List_ | cg13904806 | 0,806970355 | 0,753449271 | 0,05 | 0,097751432 | 5,33E-05 | 9,35E-05 | No      | Yes     | -       |
| PALM3    | List_ | cg11437328 | 0,704570148 | 0,629656393 | 0,07 | 0,15977851 | 5,62E-05 | 9,84E-05 | No      | Yes     | -       |
| RGS10    | List_ | cg10200202 | 0,484133499 | 0,61126636 | -0,13 | 0,330311074 | 7,13E-05 | 0,000123 | No      | Yes     | -       |
| IRX3     | List_ | cg08279075 | 0,241664996 | 0,09718506 | 0,14 | 1,231400744 | 8,98E-05 | 0,000154 | No      | Yes     | -       |
| FAM20B   | List_ | cg24997888 | 0,734488844 | 0,667123361 | 0,07 | 0,136831537 | 0,000139 | 0,000235 | No      | Yes     | -       |
| SPN      | List_ | cg09946623 | 0,603132479 | 0,701337782 | -0,10 | 0,214335962 | 0,000170 | 0,000284 | No      | Yes     | -       |
| FGFR4    | List_ | cg17386911 | 0,738271303 | 0,675536848 | 0,06 | 0,126327233 | 0,000402 | 0,000648 | No      | Yes     | -       |
| STX1A    | List_ | cg27469719 | 0,080714714 | 0,090007628 | -0,01 | 0,140701564 | 0,000737 | 0,001156 | No      | Yes     | -       |
| C9orf3   | List_ | cg13853813 | 0,765679127 | 0,724360152 | 0,04 | 0,078972204 | 0,000829 | 0,001292 | No      | Yes     | -       |
| CMYA5    | List_ | cg11438310 | 0,400024305 | 0,287666654 | 0,11 | 0,46201182 | 0,000964 | 0,001493 | No      | Yes     | -       |
| Gene   | List_ | cgID     | Value1   | Value2   | Value3   | Value4   | Value5   | Value6   | Value7   | Value8   | Value9   | Value10  | Value11  | Value12  | Value13  | Value14  | Value15  | Value16  | Value17  | Value18  | Value19  | Value20  |
|--------|-------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| CMYA5  | List_ | cg00611789 | 0.381601211 | 0.255300263 | 0.13 | 0.561759122 | 0.001000507 | 0.001546422 | No | Yes | - |
| LHX3   | List_ | cg13658899 | 0.294051805 | 0.18921953 | 0.10 | 0.609958069 | 0.00101839 | 0.001572882 | No | Yes | - |
| PRMT7  | List_ | cg10061770 | 0.379548112 | 0.271422857 | 0.11 | 0.469062012 | 0.001189039 | 0.001823627 | No | Yes | - |
| THSD7A | List_ | cg24676244 | 0.444887208 | 0.313012576 | 0.13 | 0.493918528 | 0.001222784 | 0.001872902 | No | Yes | - |
| THSD7A | List_ | cg01797590 | 0.435090155 | 0.358769562 | 0.08 | 0.271378080 | 0.001384416 | 0.002108615 | No | Yes | - |
| PIK3CG | List_ | cg08779777 | 0.482179727 | 0.608867896 | -0.13 | 0.330446249 | 0.001956797 | 0.002933013 | No | Yes | - |
| PRR5   | List_ | cg04607412 | 0.333140508 | 0.245522648 | 0.09 | 0.425348275 | 0.002986073 | 0.0043855 | No | Yes | - |
| SAMD11 | List_ | cg24362661 | 0.384893124 | 0.445312037 | -0.06 | -0.205393354 | 0.003121916 | 0.004575409 | No | Yes | - |
| CMYA5  | List_ | cg09481121 | 0.517968506 | 0.430976715 | 0.09 | 0.259749395 | 0.003350236 | 0.0048941 | No | Yes | - |
| RGS10  | List_ | cg17527393 | 0.098841093 | 0.03866792 | 0.06 | 1.161180332 | 0.004141802 | 0.005988643 | No | Yes | - |
| FBRSL1 | List_ | cg23890800 | 0.156300781 | 0.053381762 | 0.10 | 1.391655274 | 0.004435664 | 0.006392837 | No | Yes | - |
| KREMEN2 | List_ | cg26494929 | 0.285783001 | 0.169539942 | 0.12 | 0.720234309 | 0.006084779 | 0.008632012 | No | Yes | - |
| PPP2R5C | List_ | cg09990596 | 0.110293027 | 0.120966262 | -0.01 | -0.122642193 | 0.000645179 | 0.009125493 | No | Yes | - |
| C9orf3 | List_ | cg14582550 | 0.281388285 | 0.321934677 | -0.04 | -0.18795648 | 0.010022894 | 0.013862182 | No | Yes | - |
| FBRSL1 | List_ | cg18450555 | 0.09819856 | 0.037030815 | 0.06 | 1.202003056 | 0.010297014 | 0.014221 - |
| Gene  | List_ | cg   | FDR 1 | FDR 2 | FDR 3 | FDR 4 | FDR 5 | FDR 6 |
|-------|-------|------|-------|-------|-------|-------|-------|-------|
| THSD7A | List_2 | cg15090509 | 0.428918927 | 0.31353001 | 0.12 | 0.44005494 | 0.012357 | 0.016905 |
| DDX51  | List_2 | cg22672078 | 0.086236498 | 0.092912511 | -0.01 | 0.096762329 | 0.016327 | 0.022027 |
| RGS10  | List_3 | cg19653161 | 0.23822419 | 0.116597769 | 0.12 | 0.971391739 | 0.025792 | 0.033949 |
| PPAP2B | List_3 | cg10500503 | 0.570658577 | 0.508719921 | 0.06 | 0.162734342 | 0.026310 | 0.034594 |
| LITAF  | List_2 | cg04359558 | 0.359541546 | 0.404629816 | -0.05 | 0.166087296 | 0.030519 | 0.039812 |
| WDR82  | List_1 | cg12661343 | 0.175450533 | 0.166607087 | 0.01 | 0.070491176 | 0.016327 | 0.022027 |
| SAMD11 | List_1 | cg13546858 | 0.533338673 | 0.460411546 | 0.07 | 0.20792865 | 0.031289 | 0.040761 |
| BMP8A  | List_1 | cg25139493 | 0.429623415 | 0.293019734 | 0.14 | 0.536856479 | 0.035342 | 0.045716 |
| CMYA5  | List_3 | cg10257870 | 0.466611226 | 0.391738367 | 0.07 | 0.246556685 | 0.041062 | 0.052674 |
| BMP8A  | List_1 | cg02575697 | 0.171963608 | 0.069075359 | 0.10 | 1.202398381 | 0.047264 | 0.060155 |
| CHST11 | List_3 | cg01964337 | 0.313977459 | 0.340885791 | -0.03 | 0.115108089 | 0.049892 | 0.063297 |
| PTBP1  | List_3 | cg19373090 | 0.053691067 | 0.057037706 | 0.00 | 0.073881729 | 0.060198 | 0.075545 |
| CHST11 | List_3 | cg11739675 | 0.18746699 | 0.091647088 | 0.10 | 0.958042614 | 0.064629 | 0.080770 |
| PPP2R5C| List_1 | cg08163906 | 0.147848426 | 0.129742078 | 0.02 | 0.175773375 | 0.086224 | 0.105895 |
| BMP8A  | List_ | cg15947940 | 0.110799571 | 0.032834169 | 0.08 | 1.495781316 | 0.104115 | 0.126367 |
|   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|
| BMP8A | List_1 | cg08748615 | 0,1867484 | 0,069446696 | 0,12 | 1,308293069 | 0,117716 | 0,141748 | No | No | - |
| CMYA5 | List_3 | cg03546977 | 0,387294396 | 0,323611978 | 0,06 | 0,252037355 | 0,125901 | 0,157889 | No | No | - |
| SAMD11 | List_1 | cg02439789 | 0,551745553 | 0,509632956 | 0,04 | 0,112423867 | 0,135091 | 0,233316 | No | No | - |
| SAMD11 | List_1 | cg03269716 | 0,527695586 | 0,565580403 | -0,04 | 0,098227844 | 0,155091 | 0,233316 | No | No | - |
| ZNF366 | List_3 | cg04454664 | 0,342750098 | 0,361609364 | -0,02 | -0,07514037 | 0,200911 | 0,233316 | No | No | - |
| NRP2 | List_3 | cg05348875 | 0,451493713 | 0,40719816 | 0,04 | 0,1455782 | 0,241125 | 0,276288 | No | No | - |
| CHST11 | List_3 | cg17844339 | 0,753568373 | 0,848675162 | -0,10 | -0,169355113 | 0,247921 | 0,283472 | No | No | - |
| SCAND3 | List_3 | cg22302929 | 0,602176632 | 0,59165482 | 0,01 | 0,02501195 | 0,269090 | 0,305829 | No | No | - |
| SAMD11 | List_1 | cg13856810 | 0,501200269 | 0,530870609 | -0,03 | -0,08139491 | 0,319087 | 0,357800 | No | No | - |
| ITGAM | List_3 | cg22490695 | 0,660684825 | 0,704679984 | -0,04 | -0,091662423 | 0,320645 | 0,359420 | No | No | - |
| LHX3 | List_4 | cg08967938 | 0,628067746 | 0,621223591 | 0,01 | 0,015558485 | 0,367495 | 0,407401 | No | No | - |
| SAMD11 | List_1 | cg06531475 | 0,408476338 | 0,359276554 | 0,05 | 0,180444384 | 0,380042 | 0,420152 | No | No | - |
| SAMD11 | List_1 | cg05527507 | 0,371538733 | 0,302086783 | 0,07 | 0,289882266 | 0,389513 | 0,429716 | No | No | - |
| ITGA11 | List_3 | cg26217827 | 0,753100814 | 0,702906286 | 0,05 | 0,098161224 | 0,447136 | 0,487513 | No | No | - |
| SKI | List_  | cg12580943 | 0,406229153 | 0,371280077 | 0,03 | 0,126526867 | 0,470157 | 0,510339 | No | No | - |
|       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|
|       |       | List_ |       |       |       |       |       |
|       |       | 1     |       |       |       |       |       |
|       |       | cg20929545 | 0,845081943 | 0,84798478 | 0,00 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 1     |       |       |       |       |       |
|       |       | cg18437077 | 0,186368161 | 0,187926203 | 0,00 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 2     |       |       |       |       |       |
|       |       | cg09557034 | 0,406291947 | 0,350981476 | 0,06 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 3     |       |       |       |       |       |
|       |       | cg12681370 | 0,320011323 | 0,290717118 | 0,03 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 1     |       |       |       |       |       |
|       |       | cg15321108 | 0,101309763 | 0,096079549 | 0,01 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 3     |       |       |       |       |       |
|       |       | cg12529671 | 0,751832014 | 0,815446149 | -0,06 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 1     |       |       |       |       |       |
|       |       | cg14324200 | 0,301379616 | 0,242303319 | 0,06 |       |       |
|       |       |       |       |       |       |       |       |
|       |       | List_ |       |       |       |       |       |
|       |       | 3     |       |       |       |       |       |
|       |       | cg11401394 | 0,555186425 | 0,578771979 | -0,02 |       |       |
| Gene_Symbol | Expression HCC to Normal | p-value |
|-------------|--------------------------|---------|
| ALDH4A1     | Down                     | ≤0.001  |
| ANO10       | Up                       | ≤0.001  |
| ATG4B       | Up                       | ≤0.001  |
| ATP11A      | Up                       | ≤0.05   |
| ATP6V0A1    | Up                       | ≤0.001  |
| ATP6V1C1    | Up                       | ≤0.001  |
| B3GNT9      | Down                     | ≤0.01   |
| BLOC1S1     | Up                       | ≤0.05   |
| BMP8A       | Up                       | ≤0.001  |
| C1QTNF4     | n.s.                     | -       |
| C9orf3      | n.s.                     | -       |
| CAMTA1      | Down                     | ≤0.001  |
| CBFA2T3     | Down                     | ≤0.001  |
| CCDC40      | Up                       | ≤0.001  |
| CCDC57      | n.s.                     | -       |
| CCDC84      | Up                       | ≤0.001  |
| CCR5        | Down                     | ≤0.05   |
| CHERP       | n.s.                     | -       |
| CHST11      | n.s.                     | -       |
| CLEC14A     | Up                       | ≤0.01   |
| CMYA5       | Down                     | ≤0.001  |
| CNKR1       | Down                     | ≤0.001  |
| COPA        | Up                       | ≤0.001  |
| CREBBP      | Down                     | ≤0.05   |
| CRHBP       | Down                     | ≤0.001  |
| CRYBB3      | n.s.                     | -       |
| CUL3        | Down                     | ≤0.001  |
| CYP1A2      | Down                     | ≤0.001  |
| DDX51       | Up                       | ≤0.001  |
| DNAH17      | Up                       | ≤0.001  |
| DNASE1L2    | Up                       | ≤0.001  |
| DNHD1       | Up                       | ≤0.001  |
| EGFLAM      | Up                       | ≤0.01   |
| EXOC2       | Up                       | ≤0.01   |
| FAM189A1    | Down                     | ≤0.01   |
| FAM20B      | Up                       | ≤0.001  |
| FBRSL1      | Up                       | ≤0.001  |
| FGFR4       | Up                       | ≤0.001  |
| FNDC1       | n.s.                     | -       |
| GALK2       | n.s.                     | -       |
| GAS7        | n.s.                     | -       |
| GLTSCR1     | Up                       | ≤0.001  |
| HIPK1       | n.s.                     | -       |
| Gene       | Expression | p-Value |
|------------|------------|---------|
| HK3        | Down       | ≤0.001  |
| HLA-DPB2   | Down       | ≤0.01   |
| IRX3       | Up         | ≤0.001  |
| ITGA11     | Up         | ≤0.001  |
| ITGAM      | n.s.       | -       |
| ITGB3      | Down       | ≤0.001  |
| KAT2A      | Up         | ≤0.001  |
| KCNK7      | Up         | ≤0.01   |
| KCNS2      | n.s.       | -       |
| KIAA1875   | Up         | ≤0.001  |
| KLHL5      | n.s.       | -       |
| KREMEN2    | Up         | ≤0.001  |
| KRTCAP3    | Down       | ≤0.001  |
| LHX3       | n.s.       | -       |
| LITAF      | n.s.       | -       |
| LPP        | Down       | ≤0.01   |
| LZTS1      | Up         | ≤0.001  |
| MAP4       | Up         | ≤0.001  |
| MAST2      | Up         | ≤0.001  |
| MATN2      | Down       | ≤0.01   |
| MCM6       | Up         | ≤0.001  |
| MICA       | Up         | ≤0.001  |
| MYH14      | Up         | ≤0.001  |
| NAA30      | Down       | ≤0.001  |
| NID1       | Down       | ≤0.001  |
| NRP2       | Down       | ≤0.001  |
| NSD1       | Up         | ≤0.001  |
| PALM3      | Down       | ≤0.001  |
| PAQR6      | Up         | ≤0.001  |
| PCNX       | Down       | ≤0.001  |
| PDE4DIP    | n.s.       | -       |
| PIAS1      | n.s.       | -       |
| PIK3CG     | Down       | ≤0.01   |
| PPAP2B     | Down       | ≤0.001  |
| PPM1D      | n.s.       | -       |
| PPP2R5C    | Down       | ≤0.01   |
| PRMT7      | Up         | ≤0.01   |
| PRR5       | Down       | ≤0.001  |
| PTRRC      | Down       | ≤0.001  |
| PTPRJ      | Up         | ≤0.01   |
| PURA       | Down       | ≤0.001  |
| REEP3      | Down       | ≤0.001  |
| RGS10      | Up         | ≤0.01   |
| RNF220     | Up         | ≤0.001  |
| RWDD1      | n.s.       | -       |
| SAMD11     | Down       | ≤0.001  |
| SATB2      | Up         | ≤0.001  |
| Gene   | Regulation | p-value | | Gene   | Regulation | p-value | |
|--------|------------|---------| | |--------|------------|---------| |
| SCAMP1 | n.s.       |         | | SIPA1L1| n.s.       |         | |
| SIPA1L1| n.s.       |         | | SLC25A27| n.s.       |         | |
| SKI    | Down       | ≤0.05   | | SMARCC1| Up         | ≤0.001  | |
| SORBS1 | Down       | ≤0.001  | | SORBS1 | Down       | ≤0.001  | |
| SPG11  | Down       | ≤0.05   | | SPN    | Down       | ≤0.001  | |
| STRN4  | Up         | ≤0.001  | | STX1A  | Up         | ≤0.001  | |
| STX3   | Up         | ≤0.05   | | SWAP70 | Up         | ≤0.001  | |
| THRSP  | Down       | ≤0.001  | | THSD7A | Up         | ≤0.01   | |
| TIGD1  | Up         | ≤0.001  | | TMEM18 | n.s.       |         | |
| TNS1   | Down       | ≤0.001  | | TSC2   | Up         | ≤0.001  | |
| TSC2   | Up         | ≤0.001  | | UCN    | Up         | ≤0.001  | |
| UGT2B15| Down       | ≤0.001  | | USP34  | n.s.       |         | |
| USP34  | n.s.       |         | | WDR82  | n.s.       |         | |
| WNT7A  | Down       | ≤0.001  | | ZDDHC7 | n.s.       |         | |
| ZIC5   | Up         | ≤0.001  | | ZMIZ2  | Up         | ≤0.001  | |
| ZMIZ2  | Up         | ≤0.001  | | ZNF212 | Up         | ≤0.001  | |
| ZNF212 | Up         | ≤0.001  | | ZNF366 | n.s.       |         | |
| ZNF366 | n.s.       |         | | ZNF540 | n.s.       |         | |
| ZNF540 | n.s.       |         | | ZNF876P| Up         | ≤0.01   | |
| ZNF876P| Up         | ≤0.01   | | ZYG11A | n.s.       |         | |
| ZYG11A | n.s.       |         | |
| Gene_Symbol | Logrank p-value | Hazard Ratio (high) | p(HR) | n(high) | n(low) |
|-------------|----------------|---------------------|-------|---------|--------|
| ALDH4A1     | 0.56           | 0.9                 | 0.55  | 182     | 182    |
| ANO10       | 0.004          | 1.7                 | 0.0043| 181     | 181    |
| ATG4B       | 0.003          | 1.7                 | 0.0033| 182     | 182    |
| ATP11A      | 0.031          | 1.5                 | 0.031 | 182     | 182    |
| ATP6V0A1    | 0.034          | 1.5                 | 0.035 | 182     | 182    |
| ATP6V1C1    | 0.73           | 1.1                 | 0.73  | 182     | 182    |
| B3GNT9      | 0.047          | 1.1                 | 0.048 | 182     | 182    |
| BLOC1S1     | 0.74           | 1.1                 | 0.75  | 182     | 182    |
| BMP8A       | 0.045          | 1.4                 | 0.046 | 172     | 173    |
| C1QTNF4     | 0.51           | 1.1                 | 0.5   | 165     | 177    |
| C9orf3      | 0.5            | 0.89                | 0.5   | 182     | 182    |
| CAMTA1      | 0.012          | 1.6                 | 0.013 | 182     | 182    |
| CBFA2T3     | 0.095          | 0.74                | 0.095 | 182     | 182    |
| CCDC40      | 0.23           | 1.2                 | 0.23  | 181     | 181    |
| CCDC57      | 0.44           | 0.87                | 0.44  | 182     | 182    |
| CCDC84      | 0.34           | 1.2                 | 0.34  | 182     | 182    |
| CCR5        | 0.022          | 0.67                | 0.023 | 182     | 182    |
| CHERP       | 0.85           | 1.0                 | 0.84  | 182     | 182    |
| CHST11      | 0.4            | 1.2                 | 0.4   | 181     | 180    |
| CLEC14A     | 0.15           | 0.77                | 0.15  | 181     | 181    |
| CMYA5       | 0.9            | 0.98                | 0.9   | 182     | 182    |
| CNKSR1      | 0.78           | 1.1                 | 0.77  | 180     | 174    |
| COPA        | 0.025          | 1.5                 | 0.026 | 182     | 182    |
| CREBBP      | 0.8            | 0.96                | 0.8   | 182     | 182    |
| CRHBP       | 0.12           | 0.76                | 0.12  | 182     | 182    |
| CRYBB3      | 0.51           | 1.1                 | 0.51  | 178     | 179    |
| CUL3        | 0.096          | 1.3                 | 0.098 | 182     | 182    |
| CYP1A2      | 0.93           | 0.98                | 0.93  | 182     | 182    |
| DDX51       | 0.12           | 1.3                 | 0.13  | 182     | 182    |
| DNAH17      | 0.086          | 1.4                 | 0.087 | 179     | 175    |
| DNASE1L2    | 0.45           | 0.87                | 0.45  | 176     | 180    |
| DNHD1       | 0.92           | 0.98                | 0.93  | 182     | 182    |
| EGFLAM      | 0.48           | 0.88                | 0.48  | 181     | 179    |
| EXOC2       | 0.13           | 1.3                 | 0.13  | 182     | 182    |
| FAM189A1    | 0.54           | 1.1                 | 0.54  | 152     | 178    |
| FAM20B      | 0.21           | 1.3                 | 0.21  | 181     | 181    |
| FBRS1L1     | 0.067          | 1.4                 | 0.068 | 182     | 182    |
| FGFR4       | 0.059          | 1.4                 | 0.061 | 182     | 182    |
| FNDC1       | 0.25           | 1.2                 | 0.25  | 182     | 182    |
| GALK2       | 0.78           | 0.95                | 0.78  | 182     | 182    |
| GAS7        | 0.23           | 1.2                 | 0.23  | 180     | 181    |
| GLTSCR1     | 0.39           | 1.2                 | 0.39  | 181     | 180    |
| HIPK1       | 0.26           | 1.2                 | 0.25  | 182     | 182    |
| HK3         | 0.88           | 1.0                 | 0.88  | 180     | 181    |
| Gene        | Start | End  | Start | End  | Start | End  |
|-------------|-------|------|-------|------|-------|------|
| HLA-DPB2    | 0.17  | 0.78 | 0.17  | 179  | 181  |      |
| IRX3        | 0.96  | 1.0  | 0.96  | 182  | 182  |      |
| ITGA11      | 0.22  | 1.2  | 0.22  | 180  | 181  |      |
| ITGAM       | 0.61  | 1.1  | 0.61  | 182  | 182  |      |
| ITGB3       | 0.93  | 1.0  | 0.94  | 182  | 182  |      |
| KAT2A       | 0.24  | 1.2  | 0.24  | 182  | 182  |      |
| KCNK7       | 0.19  | 1.3  | 0.19  | 176  | 179  |      |
| KCNS2       | N/A   | N/A  | N/A   | N/A  | N/A  |      |
| KIAA1875    | 0.39  | 1.2  | 0.39  | 174  | 180  |      |
| KLHL5       | 0.079 | 1.4  | 0.079 | 182  | 182  |      |
| KREMEN2     | 0.18  | 1.3  | 0.18  | 179  | 157  |      |
| KRTCAP3     | 0.15  | 0.77 | 0.15  | 182  | 182  |      |
| LHX3        | 0.46  | 0.87 | 0.46  | 172  | 174  |      |
| LITAF       | 0.12  | 1.3  | 0.12  | 182  | 182  |      |
| LPP         | 0.038 | 1.5  | 0.038 | 182  | 182  |      |
| LZTS1       | 0.65  | 1.1  | 0.64  | 181  | 181  |      |
| MAP4        | 0.0069| 1.6  | 0.0074| 182  | 182  |      |
| MAST2       | 0.0039| 1.7  | 0.0043| 182  | 182  |      |
| MATN2       | 0.55  | 0.9  | 0.55  | 182  | 182  |      |
| MCM6        | 0.0041| 0.7  | 0.0045| 181  | 181  |      |
| MICA        | 0.15  | 1.3  | 0.15  | 182  | 182  |      |
| MYH14       | 0.24  | 1.2  | 0.24  | 182  | 182  |      |
| NAA30       | 0.22  | 1.2  | 0.23  | 180  | 181  |      |
| NID1        | 0.0052| 1.6  | 0.0057| 182  | 182  |      |
| NRP2        | 0.41  | 1.2  | 0.41  | 182  | 182  |      |
| NSD1        | 0.48  | 1.1  | 0.48  | 181  | 180  |      |
| PALM3       | 0.42  | 0.87 | 0.42  | 182  | 182  |      |
| PAQR6       | 0.99  | 1.0  | 0.99  | 182  | 182  |      |
| PCNX        | 0.79  | 0.96 | 0.8   | 181  | 181  |      |
| PDE4DIP     | 0.28  | 1.2  | 0.28  | 182  | 182  |      |
| PIAS1       | 0.067 | 1.4  | 0.069 | 182  | 182  |      |
| PIK3CG      | 0.89  | 0.98 | 0.9   | 181  | 170  |      |
| PPAP2B      | 0.16  | 0.78 | 0.16  | 182  | 182  |      |
| PPM1D       | 0.018 | 1.5  | 0.018 | 182  | 182  |      |
| PPP2R5C     | 0.12  | 1.3  | 0.12  | 182  | 182  |      |
| PRMT7       | 0.81  | 1.0  | 0.81  | 182  | 182  |      |
| PRR5        | 0.67  | 1.1  | 0.67  | 182  | 182  |      |
| PTPRC       | 0.93  | 0.99 | 0.94  | 182  | 182  |      |
| PTPRJ       | 0.88  | 1.0  | 0.87  | 182  | 182  |      |
| PURA        | 0.99  | 1.0  | 1     | 181  | 180  |      |
| REEP3       | 0.025 | 1.5  | 0.025 | 182  | 182  |      |
| RGS10       | 0.062 | 1.4  | 0.063 | 182  | 182  |      |
| RNF220      | 0.02  | 1.5  | 0.021 | 182  | 182  |      |
| RWDD1       | 0.02  | 1.5  | 0.021 | 181  | 181  |      |
| SAMD11      | 0.74  | 0.94 | 0.74  | 182  | 182  |      |
| SATB2       | 0.99  | 1.0  | 0.99  | 180  | 181  |      |
| SCAMP1      | 0.35  | 1.2  | 0.35  | 182  | 182  |      |
| Gene      | Fold Change | Log2 Fold Change | Dysregulated | Tissue 1 | Tissue 2 |
|-----------|-------------|------------------|--------------|----------|----------|
| SIPA1L1   | 0.96        | 1.0              | 0.96         | 182      | 182      |
| SKI       | 0.55        | 1.1              | 0.54         | 182      | 182      |
| SLC25A27  | 0.75        | 1.1              | 0.75         | 181      | 181      |
| SMARCC1   | 0.011       | 1.6              | 0.012        | 182      | 182      |
| SORBS1    | 0.29        | 1.2              | 0.29         | 182      | 182      |
| SPG11     | 0.44        | 1.1              | 0.44         | 181      | 181      |
| SPN       | 0.22        | 0.81             | 0.22         | 182      | 182      |
| STRN4     | 0.0072      | 1.6              | 0.0078       | 182      | 182      |
| STX1A     | 0.0018      | 1.7              | 0.002        | 181      | 181      |
| STX3      | 0.00097     | 1.8              | 0.0011       | 182      | 182      |
| SWAP70    | 0.026       | 1.5              | 0.027        | 182      | 182      |
| THRSP     | 0.064       | 0.72             | 0.066        | 182      | 182      |
| THSD7A    | 0.18        | 1.3              | 0.19         | 178      | 177      |
| TIGD1     | 0.096       | 1.3              | 0.1          | 182      | 182      |
| TMEM18    | 0.027       | 1.5              | 0.028        | 182      | 182      |
| TNS1      | 0.12        | 1.3              | 0.12         | 182      | 182      |
| TSC2      | 0.71        | 1.1              | 0.7          | 182      | 182      |
| UCN       | 0.039       | 1.4              | 0.039        | 181      | 181      |
| UGT2B15   | 0.18        | 0.79             | 0.19         | 182      | 182      |
| USP34     | 0.028       | 1.5              | 0.029        | 182      | 182      |
| WDR82     | 0.074       | 1.4              | 0.074        | 182      | 182      |
| WNT7A     | N/A         | N/A              | N/A          | N/A      | N/A      |
| ZDHHC7    | 0.0048      | 1.7              | 0.0053       | 181      | 181      |
| ZIC5      | 0.21        | 1.2              | 0.21         | 181      | 181      |
| ZMIZ2     | 0.11        | 1.3              | 0.12         | 182      | 182      |
| ZNF212    | 0.037       | 1.5              | 0.037        | 182      | 182      |
| ZNF366    | 0.096       | 0.74             | 0.099        | 179      | 181      |
| ZNF540    | 0.18        | 0.79             | 0.18         | 178      | 180      |
| ZNF876P   | 0.9         | 0.98             | 0.89         | 178      | 168      |
| ZYG11A    | 0.34        | 1.2              | 0.34         | 179      | 178      |
ANO10 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `ANO10` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

|     | coef  | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|-----|-------|-------|----------|---------|---------|-------|-------|--------|
| ANO10 |  0.321 | 1.378 | 0.133    | 1.062   | 1.788   | 2.414 | 0.016 | *      |
| Age  |  0.011 | 1.011 | 0.008    | 0.995   | 1.028   | 1.367 | 0.172 |
| Gendermale | -0.112 | 0.894 | 0.226    | 0.573   | 1.393   | -0.496 | 0.620 |
| RaceBlack |  0.655 | 1.924 | 0.495    | 0.729   | 5.080   | 1.321 | 0.186 |
| RaceWhite | -0.025 | 0.976 | 0.239    | 0.611   | 1.558   | -0.104 | 0.917 |
| Stage2 |  0.205 | 1.227 | 0.266    | 0.728   | 2.068   | 0.769 | 0.442 |
| Stage3 |  0.910 | 2.483 | 0.236    | 1.563   | 3.946   | 1.393 | 0.000 ***|
| Stage4 |  1.480 | 4.392 | 0.622    | 1.297   | 14.876  | 2.378 | 0.017 *   |
| Purity |  0.706 | 2.027 | 0.457    | 0.827   | 4.966   | 1.545 | 0.122 |

Rsquare = 0.101 (max possible = 9.66e-01)
Likelihood ratio test p = 1.3e-04
Wald test p = 8.29e-05
Score (logrank) test p = 3.03e-05

ATG4B in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `ATG4B` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

|     | coef  | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|-----|-------|-------|----------|---------|---------|-------|-------|--------|
| ATG4B |  0.350 | 1.419 | 0.191    | 0.976   | 2.063   | 1.833 | 0.067 |
| Age  |  0.011 | 1.011 | 0.008    | 0.995   | 1.028   | 1.396 | 0.250 |
| Gendermale | -0.021 | 0.979 | 0.236    | 0.616   | 1.555   | -0.091 | 0.928 |
| RaceBlack |  0.838 | 2.312 | 0.492    | 0.881   | 6.067   | 1.702 | 0.089 |
| RaceWhite |  0.016 | 1.016 | 0.237    | 0.639   | 1.615   | 0.067 | 0.947 |
| Stage2 |  0.301 | 1.351 | 0.262    | 0.809   | 2.257   | 1.150 | 0.250 |
| Stage3 |  0.916 | 2.500 | 0.234    | 1.579   | 3.958   | 3.909 | 0.000 ***|
| Stage4 |  1.648 | 5.194 | 0.622    | 1.297   | 14.876  | 2.378 | 0.017 *   |
| Purity |  0.512 | 1.669 | 0.458    | 0.681   | 4.092   | 1.119 | 0.263 |

Rsquare = 0.095 (max possible = 9.66e-01)
Likelihood ratio test p = 3.22e-04
Wald test p = 2.08e-04
Score (logrank) test p = 7.18e-05

ATP11A in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `ATP11A` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

|     | coef  | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|-----|-------|-------|----------|---------|---------|-------|-------|--------|
| ATP11A |  0.215 | 1.240 | 0.108    | 1.004   | 1.532   | 1.999 | 0.046 * |
| Age  |  0.015 | 1.015 | 0.008    | 0.998   | 1.031   | 1.754 | 0.080 |
| Gendermale | -0.061 | 0.941 | 0.230    | 0.599   | 1.477   | -0.265 | 0.791 |
| RaceBlack |  0.852 | 2.344 | 0.491    | 0.895   | 6.141   | 1.734 | 0.083 |
| RaceWhite | -0.026 | 0.974 | 0.238    | 0.612   | 1.552   | -0.109 | 0.913 |
| Stage2 |  0.294 | 1.342 | 0.262    | 0.804   | 2.242   | 1.125 | 0.261 |
| Stage3 |  0.910 | 2.484 | 0.236    | 1.566   | 3.942   | 3.863 | 0.000 ***|
| Stage4 |  1.814 | 6.134 | 0.630    | 1.784   | 21.089  | 2.879 | 0.004 ** |
| Purity |  0.523 | 1.686 | 0.463    | 0.680   | 4.181   | 1.128 | 0.259 |

Rsquare = 0.096 (max possible = 9.66e-01)
Likelihood ratio test p = 2.6e-04
Wald test p = 1.54e-04
Score (logrank) test p = 5.69e-05

ATP6V0A1 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `ATP6V0A1` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

|     | coef  | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|-----|-------|-------|----------|---------|---------|-------|-------|--------|
| ATP6V0A1 |  0.198 | 1.219 | 0.157    | 0.896   | 1.657   | 1.262 | 0.020 |

Rsquare = 0.096 (max possible = 9.66e-01)
Likelihood ratio test p = 2.6e-04
Wald test p = 1.54e-04
Score (logrank) test p = 5.69e-05
### B3GNT9 in LIHC (n=371):
**Model:** Surv(OS, EVENT) ~ `B3GNT9` + Age + Gender + Race + Stage + Purity

| coef   | HR   | se(coef) | 95%CI_l | 95%CI_u | z     | p    | signif |
|--------|------|----------|---------|---------|-------|------|--------|
| B3GNT9 | 0.261| 1.299    | 0.110   | 1.047   | 1.611 | 2.381| 0.017  |
| Age    | 0.013| 1.013    | 0.008   | 0.997   | 1.029 | 1.566| 0.117  |
| Gendermale | -0.060 | 0.942 | 0.228 | 0.603 | 1.472 | -0.263 | 0.792 |
| RaceBlack | 0.870 | 2.387 | 0.489 | 0.916 | 6.220 | 1.781 | 0.075 |
| RaceWhite | -0.025 | 0.975 | 0.037 | 0.613 | 1.550 | -0.106 | 0.916 |
| Stage2 | 0.314 | 1.368 | 0.262 | 0.819 | 2.288 | 1.196 | 0.232 |
| Stage3 | 0.887 | 2.427 | 0.237 | 1.524 | 3.865 | 3.733 | 0.000 *** |
| Stage4 | 1.550 | 4.711 | 0.620 | 1.398 | 15.869 | 2.501 | 0.012 * |
| Purity | 0.929 | 2.532 | 0.483 | 0.983 | 6.522 | 1.924 | 0.054 |

Rsquare = 0.089 (max possible = 9.66e-01)  
Likelihood ratio test p = 6.55e-04  
Wald test p = 4.13e-04  
Score (logrank) test p = 1.49e-04

### BMP8A in LIHC (n=371):
**Model:** Surv(OS, EVENT) ~ `BMP8A` + Age + Gender + Race + Stage + Purity

| coef   | HR   | se(coef) | 95%CI_l | 95%CI_u | z     | p    | signif |
|--------|------|----------|---------|---------|-------|------|--------|
| BMP8A  | -0.015 | 0.985 | 0.179 | 0.693 | 1.399 | -0.086 | 0.932 |
| Age    | 0.011 | 1.011 | 0.008 | 0.995 | 1.027 | 1.330 | 0.184 |
| Gendermale | -0.145 | 0.865 | 0.232 | 0.549 | 1.364 | -0.623 | 0.533 |
| RaceBlack | 0.891 | 2.439 | 0.489 | 0.935 | 6.359 | 1.823 | 0.068 |
| RaceWhite | 0.004 | 1.004 | 0.237 | 0.630 | 1.598 | 0.015 | 0.988 |
| Stage2 | 0.315 | 1.370 | 0.261 | 0.820 | 2.288 | 1.203 | 0.229 |
| Stage3 | 0.952 | 2.591 | 0.237 | 1.629 | 4.122 | 4.022 | 0.000 *** |
| Stage4 | 1.593 | 4.921 | 0.619 | 1.463 | 16.553 | 2.575 | 0.010 * |
| Purity | 0.576 | 1.753 | 0.458 | 0.725 | 4.365 | 1.258 | 0.208 |

Rsquare = 0.085 (max possible = 9.66e-01)  
Likelihood ratio test p = 1.2e-03  
Wald test p = 7.25e-04  
Score (logrank) test p = 2.74e-04

### CAMTA1 in LIHC (n=371):
**Model:** Surv(OS, EVENT) ~ `CAMTA1` + Age + Gender + Race + Stage + Purity

| coef   | HR   | se(coef) | 95%CI_l | 95%CI_u | z     | p    | signif |
|--------|------|----------|---------|---------|-------|------|--------|
| CAMTA1 | 0.274 | 1.316 | 0.160 | 0.962 | 1.799 | 1.716 | 0.086 |
| Age    | 0.013 | 1.013 | 0.008 | 0.997 | 1.030 | 1.562 | 0.118 |
| Gendermale | -0.153 | 0.858 | 0.225 | 0.553 | 1.334 | -0.679 | 0.497 |
| RaceBlack | 0.741 | 2.098 | 0.495 | 0.795 | 5.357 | 1.497 | 0.135 |
| RaceWhite | -0.028 | 0.972 | 0.028 | 0.610 | 1.549 | -0.120 | 0.905 |
### CCR5 in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `CCR5` + Age + Gender + Race + Stage + Purity

310 patients with 106 dying (61 missing obs.)

| coef    | HR (se(coef)) | 95% CI_l  | 95% CI_u | z     | p   | signif |
|----------|---------------|-----------|-----------|-------|-----|--------|
| CCR5     | 0.069 (1.071) | 0.143     | 0.809     | 1.419 | 0.481| 0.630  |
| Age      | 0.011 (1.011) | 0.008     | 0.995     | 1.027 | 1.343| 0.179  |
| Gendermale| -0.124 (0.884) | 0.228     | 0.566     | 1.381 | -0.543| 0.587  |
| RaceBlack| 0.875 (2.392) | 0.491     | 0.914     | 6.261 | 1.776| 0.076  |
| RaceWhite| 0.002 (1.002) | 0.237     | 0.630     | 1.594 | 0.008| 0.994  |
| Stage2   | 0.318 (1.374) | 0.261     | 0.824     | 2.293 | 1.217| 0.223  |
| Stage3   | 0.956 (2.600) | 0.235     | 1.640     | 4.123 | 4.063| 0.000  |
| Stage4   | 1.614 (5.025) | 0.621     | 1.489     | 16.959| 2.601| 0.009  |
| Purity    | 0.690 (1.993) | 0.517     | 0.724     | 5.488 | 1.334| 0.182  |

Rsquare = 0.085 (max possible = 9.66e-01)
Likelihood ratio test p = 1.11e-03
Wald test p = 6.66e-04
Score (logrank) test p = 2.51e-05

### COPA in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `COPA` + Age + Gender + Race + Stage + Purity

310 patients with 106 dying (61 missing obs.)

| coef    | HR (se(coef)) | 95% CI_l  | 95% CI_u | z     | p   | signif |
|----------|---------------|-----------|-----------|-------|-----|--------|
| COPA     | 0.312 (1.367) | 0.125     | 1.069     | 1.747 | 2.495| 0.013  *
| Age      | 0.014 (1.014) | 0.008     | 0.997     | 1.030 | 1.646| 0.100  |
| Gendermale| -0.072 (0.930) | 0.228     | 0.595     | 1.455 | -0.317| 0.751  |
| RaceBlack| 0.867 (2.379) | 0.495     | 0.902     | 6.272 | 1.752| 0.080  |
| RaceWhite| 0.079 (1.082) | 0.238     | 0.679     | 1.725 | 0.331| 0.741  |
| Stage2   | 0.225 (1.252) | 0.264     | 0.746     | 2.101 | 0.850| 0.395  |
| Stage3   | 0.927 (2.528) | 0.234     | 1.597     | 4.000 | 3.961| 0.000  ***
| Stage4   | 1.838 (6.285) | 0.628     | 1.835     | 21.520| 2.927| 0.003  **
| Purity    | 0.460 (1.585) | 0.461     | 0.642     | 3.913 | 0.998| 0.318  |

Rsquare = 0.104 (max possible = 9.66e-01)
Likelihood ratio test p = 9.02e-05
Wald test p = 6.52e-05
Score (logrank) test p = 2.4e-05

### LPP in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `LPP` + Age + Gender + Race + Stage + Purity

310 patients with 106 dying (61 missing obs.)

| coef    | HR (se(coef)) | 95% CI_l  | 95% CI_u | z     | p   | signif |
|----------|---------------|-----------|-----------|-------|-----|--------|
| LPP      | 0.157 (1.170) | 0.184     | 0.816     | 1.679 | 0.855| 0.392  |
| Age      | 0.012 (1.012) | 0.008     | 0.996     | 1.028 | 1.457| 0.145  |
| Gendermale| -0.122 (0.885) | 0.226     | 0.568     | 1.379 | -0.541| 0.589  |
| RaceBlack| 0.882 (2.416) | 0.490     | 0.926     | 6.308 | 1.802| 0.072  |
| RaceWhite| -0.037 (0.963) | 0.242     | 0.600     | 1.548 | -0.154| 0.878  |
| Stage2   | 0.303 (1.353) | 0.261     | 0.811     | 2.259 | 1.157| 0.247  |
| Stage3   | 0.921 (2.512) | 0.238     | 1.577     | 4.002 | 3.877| 0.000  ***
| Stage4   | 1.652 (5.219) | 0.623     | 1.539     | 17.693| 2.653| 0.008  **
| Purity    | 0.590 (1.804) | 0.457     | 0.736     | 4.422 | 1.290| 0.197  |

Rsquare = 0.087 (max possible = 9.66e-01)
MAP4 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `MAP4` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

| coef    | HR  | se(coef) | 95%CI_l | 95%CI_u | z     | p    | signif |
|---------|-----|----------|---------|---------|-------|------|--------|
| MAP4    | 0.354 | 1.425    | 0.169   | 1.023   | 1.985 | 2.094 | 0.036  |      * |
| Age     | 0.012 | 1.012    | 0.008   | 0.996   | 1.028 | 1.455 | 0.146  |      |
| Gendermale | -0.127 | 0.881    | 0.227   | 0.565   | 1.373 | -0.561 | 0.575  |      |
| RaceBlack | 0.899 | 2.457    | 0.488   | 0.943   | 6.397 | 1.841 | 0.066  |      |
| RaceWhite | 0.030 | 1.031    | 0.238   | 0.647   | 1.642 | 0.127 | 0.899  |      |
| Stage2  | 0.225 | 1.252    | 0.265   | 0.745   | 2.104 | 0.850 | 0.396  |      |
| Stage3  | 0.834 | 2.303    | 0.240   | 1.438   | 3.688 | 3.474 | 0.001  |      **|
| Stage4  | 1.494 | 4.453    | 0.620   | 1.320   | 15.025| 2.407 | 0.016  |      * |
| Purity  | 0.664 | 1.942    | 0.459   | 0.790   | 4.774 | 1.447 | 0.148  |      |

Rsquare = 0.097 (max possible = 0.66e-01)
Likelihood ratio test p = 2.21e-04
Wald test p = 1.49e-04
Score (logrank) test p = 4.71e-05

MST2 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `MST2` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

| coef    | HR  | se(coef) | 95%CI_l | 95%CI_u | z     | p    | signif |
|---------|-----|----------|---------|---------|-------|------|--------|
| MST2    | 0.433 | 1.542    | 0.138   | 1.176   | 2.021 | 3.134 | 0.002  |      **|
| Age     | 0.012 | 1.012    | 0.008   | 0.999   | 1.029 | 1.499 | 0.134  |      |
| Gendermale | 0.005 | 1.005    | 0.232   | 0.637   | 1.584 | 0.021 | 0.983  |      |
| RaceBlack | 0.944 | 2.570    | 0.492   | 0.980   | 6.743 | 1.918 | 0.055  |      |
| RaceWhite | 0.067 | 1.070    | 0.238   | 0.671   | 1.705 | 0.284 | 0.776  |      |
| Stage2  | 0.157 | 1.170    | 0.267   | 0.693   | 1.976 | 0.588 | 0.556  |      |
| Stage3  | 0.839 | 2.314    | 0.238   | 1.452   | 3.687 | 3.530 | 0.000  |      ***|
| Stage4  | 1.674 | 5.333    | 0.622   | 1.576   | 18.046| 2.692 | 0.007  |      **|
| Purity  | 0.440 | 1.553    | 0.454   | 0.638   | 3.779 | 0.969 | 0.332  |      |

Rsquare = 0.113 (max possible = 0.66e-01)
Likelihood ratio test p = 2.42e-05
Wald test p = 1.2e-05
Score (logrank) test p = 4.08e-06

MCM6 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `MCM6` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

| coef    | HR  | se(coef) | 95%CI_l | 95%CI_u | z     | p    | signif |
|---------|-----|----------|---------|---------|-------|------|--------|
| MCM6    | 0.417 | 1.517    | 0.105   | 1.234   | 1.864 | 3.964 | 0.000  |      ***|
| Age     | 0.016 | 1.016    | 0.008   | 0.999   | 1.033 | 1.850 | 0.064  |      |
| Gendermale | 0.061 | 1.063    | 0.236   | 0.669   | 1.690 | 0.259 | 0.796  |      |
| RaceBlack | 0.643 | 1.902    | 0.509   | 0.701   | 5.161 | 1.263 | 0.207  |      |
| RaceWhite | 0.125 | 1.134    | 0.244   | 0.703   | 1.828 | 0.515 | 0.607  |      |
| Stage2  | 0.131 | 1.140    | 0.270   | 0.672   | 1.934 | 0.485 | 0.628  |      |
| Stage3  | 0.759 | 2.136    | 0.241   | 1.333   | 3.424 | 3.153 | 0.002  |      **|
| Stage4  | 1.918 | 6.805    | 0.629   | 1.982   | 23.367| 3.047 | 0.002  |      **|
| Purity  | 0.324 | 1.383    | 0.459   | 0.563   | 3.399 | 0.707 | 0.480  |      |

Rsquare = 0.13 (max possible = 0.66e-01)
Likelihood ratio test p = 2.14e-06
Wald test p = 1.59e-06
Score (logrank) test p = 4.46e-07

NID1 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `NID1` + Age + Gender + Race + Stage + Purity

Likelihood ratio test p = 9.16e-04
Wald test p = 5.39e-04
Score (logrank) test p = 2.05e-04
# REEP3 in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `REEP3` + Age + Gender + Race + Stage + Purity

| coef   | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|--------|-------|----------|---------|---------|-------|-------|--------|
| NID1   | 0.246 | 1.279    | 0.094   | 1.063   | 1.539 | 2.608 | 0.009  ** |
| Age    | 0.017 | 1.017    | 0.009   | 1.000   | 1.034 | 1.944 | 0.052  |
| Gendermale | -0.022 | 0.978    | 0.234   | 0.619   | 1.546 | -0.095 | 0.925  |
| RaceBlack | 0.890 | 2.434    | 0.491   | 0.931   | 6.367 | 1.814 | 0.070  |
| RaceWhite | -0.020 | 0.981    | 0.238   | 0.615   | 1.564 | -0.082 | 0.934  |
| Stage2 | 0.312 | 1.366    | 0.263   | 0.816   | 2.286 | 1.185 | 0.236  |
| Stage3 | 0.930 | 2.536    | 0.235   | 1.601   | 4.016 | 3.966 | 0.000  *** |
| Stage4 | 1.920 | 6.823    | 0.634   | 23.658  | 3.027 | 0.027 | 0.354  |
| Purity | 0.422 | 1.525    | 0.455   | 0.625   | 3.722 | 0.927 | 0.354  |

Rsquare = 0.105 (max possible = 9.66e-01)

Likelihood ratio test p = 7.52e-05
Wald test p = 5.37e-05
Score (logrank) test p = 1.78e-05

# RNF220 in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `RNF220` + Age + Gender + Race + Stage + Purity

| coef   | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|--------|-------|----------|---------|---------|-------|-------|--------|
| RNF220 | 0.592 | 1.808    | 0.147   | 0.942   | 1.679 | 1.554 | 0.120  |
| Age    | 0.011 | 1.013    | 0.008   | 0.997   | 1.030 | 1.584 | 0.113  |
| Gendermale | -0.111 | 0.895    | 0.227   | 0.573   | 1.397 | -0.489 | 0.625  |
| RaceBlack | 0.943 | 2.568    | 0.491   | 0.982   | 6.717 | 1.923 | 0.055  |
| RaceWhite | -0.063 | 0.939    | 0.242   | 0.585   | 1.508 | -0.260 | 0.795  |
| Stage2 | 0.286 | 1.332    | 0.262   | 0.797   | 2.224 | 1.095 | 0.274  |
| Stage3 | 0.894 | 2.445    | 0.239   | 1.532   | 3.902 | 3.748 | 0.000  *** |
| Stage4 | 1.657 | 5.244    | 0.620   | 1.555   | 17.689 | 2.671 | 0.008  ** |
| Purity | 0.537 | 1.711    | 0.460   | 0.694   | 4.216 | 1.166 | 0.244  |

Rsquare = 0.092 (max possible = 9.66e-01)

Likelihood ratio test p = 4.78e-04
Wald test p = 2.38e-04
Score (logrank) test p = 8.85e-05

# SMARCC1 in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `SMARCC1` + Age + Gender + Race + Stage + Purity

| coef   | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p     | signif |
|--------|-------|----------|---------|---------|-------|-------|--------|
| SMARCC1 | 0.408 | 1.503    | 0.143   | 1.136   | 1.989 | 2.853 | 0.004  ** |
| Age    | 0.015 | 1.016    | 0.008   | 0.999   | 1.032 | 1.874 | 0.061  |
Gender: male
-
0.085
0.918
0.228
1.435
-0.374
0.709

Race: Black
0.759
2.137
0.501
0.801
5.701
1.517
0.129

Race: White
0.075
1.078
0.238
0.676
1.721
0.316
0.752

Stage: 2
0.230
1.258
0.264
0.749
2.112
0.869
0.385

Stage: 3
1.744
5.718
0.623
1.686
19.387
2.799
0.005

Stage: 4
1.744
5.718
0.623
1.686
19.387
2.799
0.005

Purity
0.449
1.567
0.461
0.635
3.865
0.975
0.330

Rsquare = 0.109 (max possible = 9.66e-01)

Likelihood ratio test p = 4.44e-05
Wald test p = 3.11e-05
Score (logrank) test p = 1.06e-05

STRN4 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `STRN4` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

| Coef  | HR  | SE(coef) | 95%CI_l | 95%CI_u | z     | p    | Signif |
|-------|-----|----------|---------|---------|-------|------|--------|
| STRN4 | 0.360 | 1.433 | 0.154 | 1.059 | 1.939 | 2.330 | 0.020 | *      |
| Age   | 0.013 | 1.013 | 0.008 | 0.997 | 1.030 | 1.587 | 0.112 |
| Gender: male | -0.002 | 0.998 | 0.235 | 0.630 | 1.583 | -0.007 | 0.994 |
| Race: Black | 0.791 | 2.206 | 0.493 | 0.839 | 5.797 | 1.604 | 0.109 |
| Race: White | 0.019 | 1.019 | 0.237 | 0.640 | 1.622 | 0.080 | 0.936 |
| Stage: 2 | 0.248 | 1.282 | 0.264 | 0.763 | 2.151 | 0.939 | 0.348 |
| Stage: 3 | 0.915 | 2.497 | 0.234 | 1.578 | 3.951 | 3.909 | 0.000 | ***   |
| Stage: 4 | 1.675 | 5.339 | 0.622 | 1.723 | 19.387 | 2.799 | 0.005 | **    |
| Purity | 0.561 | 1.753 | 0.455 | 0.719 | 4.275 | 1.234 | 0.217 |

Rsquare = 0.1 (max possible = 9.66e-01)

Likelihood ratio test p = 1.46e-04
Wald test p = 1.11e-04
Score (logrank) test p = 3.93e-06

STX1A in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `STX1A` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

| Coef  | HR  | SE(coef) | 95%CI_l | 95%CI_u | z     | p    | Signif |
|-------|-----|----------|---------|---------|-------|------|--------|
| STX1A | 0.385 | 1.470 | 0.121 | 1.159 | 1.865 | 3.177 | 0.001 | **    |
| Age   | 0.010 | 1.010 | 0.008 | 0.994 | 1.026 | 1.236 | 0.217 |
| Gender: male | -0.116 | 0.891 | 0.225 | 0.573 | 1.384 | -0.014 | 0.907 |
| Race: Black | 0.938 | 2.555 | 0.490 | 0.977 | 6.678 | 1.913 | 0.056 |
| Race: White | -0.030 | 0.971 | 0.240 | 0.606 | 1.554 | -0.124 | 0.901 |
| Stage: 2 | 0.288 | 1.333 | 0.261 | 0.799 | 2.225 | 1.100 | 0.271 |
| Stage: 3 | 0.865 | 2.374 | 0.238 | 1.490 | 3.781 | 3.640 | 0.000 | ***   |
| Stage: 4 | 1.763 | 5.830 | 0.622 | 1.724 | 19.712 | 2.837 | 0.005 | **    |
| Purity | 0.585 | 1.795 | 0.468 | 0.717 | 4.497 | 1.249 | 0.212 |

Rsquare = 0.108 (max possible = 9.66e-01)

Likelihood ratio test p = 4.71e-05
Wald test p = 1.65e-05
Score (logrank) test p = 3.93e-05

STX3 in LIHC (n=371):
Model: Surv(OS, EVENT) ~ `STX3` + Age + Gender + Race + Stage + Purity
310 patients with 106 dying (61 missing obs.)

| Coef  | HR  | SE(coef) | 95%CI_l | 95%CI_u | z     | p    | Signif |
|-------|-----|----------|---------|---------|-------|------|--------|
| STX3  | 0.320 | 1.377 | 0.101 | 1.130 | 1.677 | 3.176 | 0.001 | **    |
| Age   | 0.012 | 1.013 | 0.008 | 0.996 | 1.029 | 1.501 | 0.133 |
| Gender: male | -0.002 | 0.998 | 0.232 | 0.633 | 1.575 | -0.007 | 0.994 |
| Race: Black | 0.978 | 2.659 | 0.492 | 1.014 | 6.972 | 1.988 | 0.047 | *      |
| Race: White | 0.011 | 1.011 | 0.240 | 0.631 | 1.619 | 0.045 | 0.964 |
| Stage: 2 | 0.262 | 1.300 | 0.263 | 0.776 | 2.177 | 0.998 | 0.318 |
| Stage: 3 | 0.844 | 2.325 | 0.239 | 1.456 | 3.711 | 3.536 | 0.000 | ***   |
### SWAP70 in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `SWAP70` + Age + Gender + Race + Stage + Purity

310 patients with 106 dying (61 missing obs.)

| coef    | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p      | signif |
|---------|-------|----------|---------|---------|-------|--------|--------|
| SWAP70  | 0.282 | 1.326    | 0.119   | 1.049   | 1.675 | 2.360  | 0.018  |
| Age     | 0.013 | 1.013    | 0.008   | 0.997   | 1.030 | 1.610  | 0.107  |
| Gendermale | -0.032 | 0.969 | 0.231   | 0.616   | 1.525 | -0.137 | 0.891  |
| RaceBlack | 0.859 | 2.361    | 0.491   | 0.902   | 6.184 | 1.749  | 0.080  |
| RaceWhite | -0.025 | 0.976 | 0.237   | 0.613   | 1.553 | -0.104 | 0.917  |
| Stage2  | 0.260 | 1.297    | 0.263   | 0.775   | 2.171 | 0.990  | 0.322  |
| Stage3  | 0.933 | 2.542    | 0.235   | 1.603   | 4.030 | 3.968  | 0.000  |
| Stage4  | 1.602 | 4.962    | 0.620   | 1.471   | 16.741| 2.581  | 0.010  |
| Purity  | 0.722 | 2.059    | 0.464   | 0.830   | 5.108 | 1.558  | 0.119  |

Rsquare = 0.113 (max possible = 9.66e-01)
Likelihood ratio test p = 2.57e-05
Wald test p = 1.26e-05
Score (logrank) test p = 3.84e-06

### UCN in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `UCN` + Age + Gender + Race + Stage + Purity

310 patients with 106 dying (61 missing obs.)

| coef    | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p      | signif |
|---------|-------|----------|---------|---------|-------|--------|--------|
| UCN     | 0.123 | 1.131    | 0.148   | 0.846   | 1.513 | 0.833  | 0.405  |
| Age     | 0.010 | 1.010    | 0.008   | 0.994   | 1.026 | 1.226  | 0.220  |
| Gendermale | -0.165 | 0.848 | 0.226   | 0.544   | 1.321 | -0.728 | 0.467  |
| RaceBlack | 0.849 | 2.337    | 0.491   | 0.892   | 6.123 | 1.728  | 0.084  |
| RaceWhite | -0.008 | 0.992 | 0.237   | 0.624   | 1.578 | -0.032 | 0.974  |
| Stage2  | 0.300 | 1.350    | 0.262   | 0.808   | 2.256 | 1.145  | 0.252  |
| Stage3  | 0.932 | 2.540    | 0.236   | 1.600   | 4.031 | 3.956  | 0.000  |
| Stage4  | 1.643 | 5.173    | 0.622   | 1.529   | 17.498| 2.643  | 0.008  |
| Purity  | 0.534 | 1.706    | 0.460   | 0.692   | 4.205 | 1.160  | 0.246  |

Rsquare = 0.101 (max possible = 9.66e-01)
Likelihood ratio test p = 1.35e-04
Wald test p = 7.97e-05
Score (logrank) test p = 2.97e-05

### ZNF212 in LIHC (n=371):

Model: Surv(OS, EVENT) ~ `ZNF212` + Age + Gender + Race + Stage + Purity

310 patients with 106 dying (61 missing obs.)

| coef    | HR    | se(coef) | 95%CI_l | 95%CI_u | z     | p      | signif |
|---------|-------|----------|---------|---------|-------|--------|--------|
| ZNF212  | 0.228 | 1.255    | 0.201   | 0.847   | 1.860 | 1.135  | 0.257  |
| Age     | 0.011 | 1.011    | 0.008   | 0.995   | 1.027 | 1.330  | 0.183  |
| Gendermale | -0.129 | 0.879 | 0.226   | 0.564   | 1.370 | -0.569 | 0.570  |
| RaceBlack | 0.850 | 2.341    | 0.492   | 0.892   | 6.142 | 1.728  | 0.084  |
| RaceWhite | 0.034 | 1.035    | 0.238   | 0.649   | 1.650 | 0.143  | 0.886  |
| Stage2  | 0.312 | 1.366    | 0.262   | 0.818   | 2.281 | 1.192  | 0.233  |
| Stage3  | 0.915 | 2.496    | 0.236   | 1.571   | 3.964 | 3.875  | 0.000  |
| Stage4  | 1.665 | 5.286    | 0.623   | 1.560   | 17.912| 2.674  | 0.007  |
| Purity  | 0.453 | 1.574    | 0.470   | 0.627   | 3.951 | 0.965  | 0.334  |

Rsquare = 0.088 (max possible = 9.66e-01)
Likelihood ratio test $p = 7.32 \times 10^{-4}$
Wald test $p = 4.4 \times 10^{-4}$
Score (logrank) test $p = 1.63 \times 10^{-4}$
**Supplemental Table 13: Clinico-pathological data of patients (validation cohort Mainz)**

| Characteristic                     | low (≤ 0.162516) | high (> 0.162516) | p-value<sup>2</sup> |
|------------------------------------|------------------|-------------------|---------------------|
| Median age in years (range)        | N = 372 (71%)<sup>1</sup> | N = 149 (29%)<sup>1</sup> | 0.5                 |
| Gender                             |                  |                   | 0.9                 |
| Male                               | 294 (79%)        | 116 (78%)         |                     |
| Female                             | 78 (21%)         | 33 (22%)          |                     |
| Etiology of liver disease          |                  |                   |                     |
| Alcohol abuse                      | 104 (28%)        | 51 (34%)          | 0.2                 |
| HCV                                | 80 (22%)         | 24 (16%)          | 0.2                 |
| HBV                                | 71 (19%)         | 24 (16%)          | 0.5                 |
| NASH                               | 34 (9.1%)        | 7 (4.7%)          | 0.13                |
| Hemochromatosis                    | 19 (5.1%)        | 5 (3.4%)          | 0.5                 |
| BCLC                               |                  |                   | >0.9                |
| A                                  | 66 (18%)         | 24 (16%)          |                     |
| B                                  | 242 (65%)        | 97 (65%)          |                     |
| C                                  | 43 (12%)         | 18 (12%)          |                     |
| D                                  | 21 (5.6%)        | 10 (6.7%)         |                     |
| ECOG PST                           |                  |                   | 0.3                 |
| 0-1                                | 359 (97%)        | 142 (96%)         |                     |
| 2                                  | 4 (1.1%)         | 4 (2.7%)          |                     |
| 3                                  | 4 (1.1%)         | 0 (0%)            |                     |
| 4                                  | 3 (0.8%)         | 2 (1.4%)          |                     |
| Liver cirrhosis                    |                  |                   | 0.5                 |
| Absent                             | 133 (36%)        | 59 (40%)          |                     |
| Present                            | 239 (64%)        | 90 (60%)          |                     |
| Child-Pugh-Score                   |                  |                   | 0.7                 |
| A                                  | 140 (54%)        | 48 (50%)          |                     |
| B                                  | 97 (38%)         | 38 (40%)          |                     |
| C                                  | 21 (8.1%)        | 10 (10%)          |                     |
| Portal vein thrombosis (PVT)       | 46 (12%)         | 18 (12%)          | >0.9                |
| Vascular invasion                  |                  |                   | >0.9                |
| Absent                             | 239 (64%)        | 94 (63%)          |                     |
| Micro                              | 75 (20%)         | 32 (21%)          |                     |
| Macro                              | 58 (16%)         | 23 (15%)          |                     |

<sup>1</sup> Statistics presented: median (IQR); n (%)

<sup>2</sup> Statistical tests performed: Wilcoxon rank-sum test; chi-square test of independence; Fisher's exact test
Supplemental Table 14: Large and small liver cell changes

| Patient | Pathology number | Large cell change_grade | Small cell change_grade |
|---------|------------------|-------------------------|-------------------------|
| 1       | 05-28637         | 2                       | 1                       |
| 2       | 07-07906         | 3                       | 2                       |
| 3       | 08-24098         | 3                       | 3                       |
| 4       | 08-32197         | 1                       | 1                       |
| 5       | 08-40746         | 3                       | 2                       |
| 6       | 09-27796         | 3                       | 1                       |
| 7       | 09-09377         | 4                       | 2                       |
| 8       | 11-44812         | 3                       | 2                       |

Criteria

| Grade | Description |
|-------|-------------|
| grade 1 | 1~5%         |
| grade 2 | 6~25%        |
| grade 3 | 26~50%       |
| grade 4 | 51~100%      |