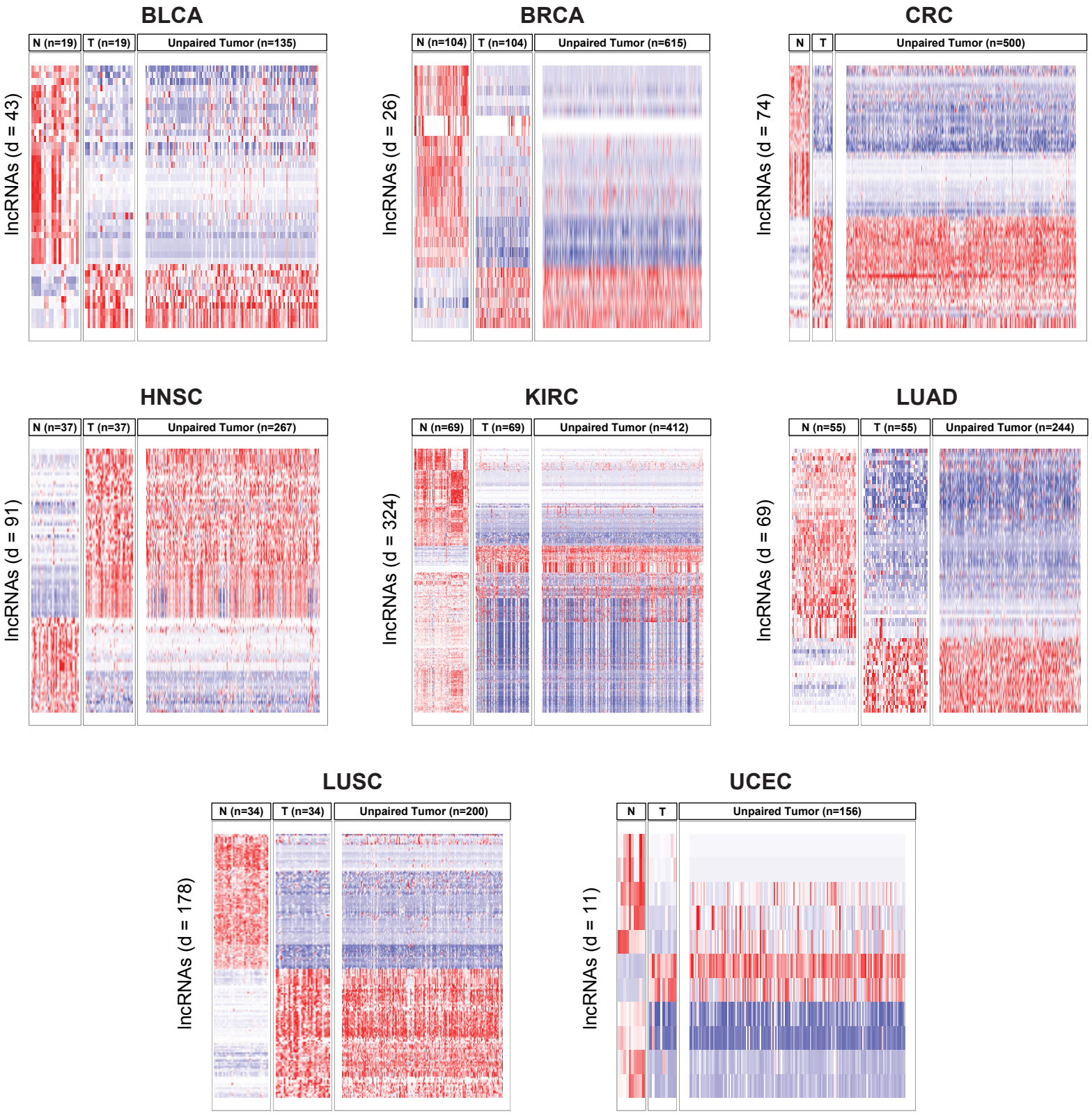
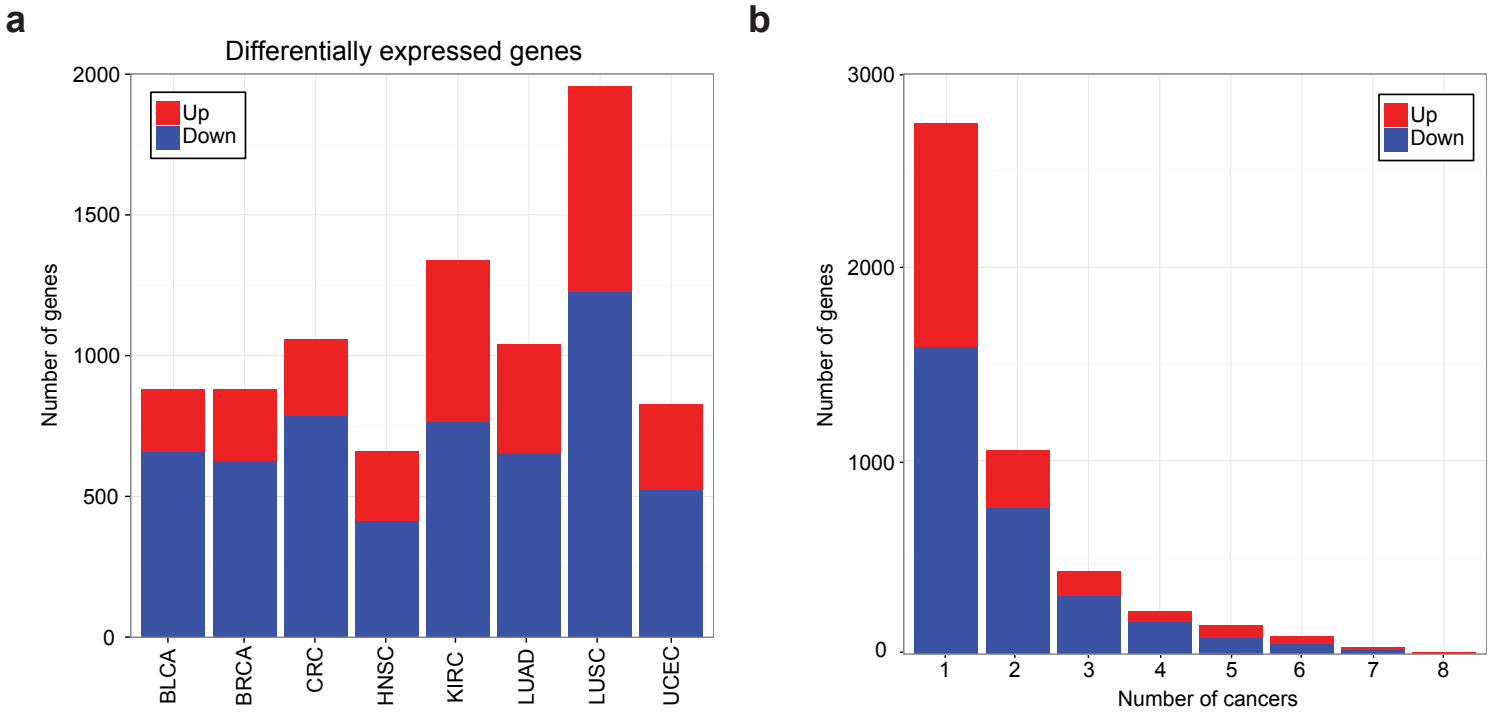
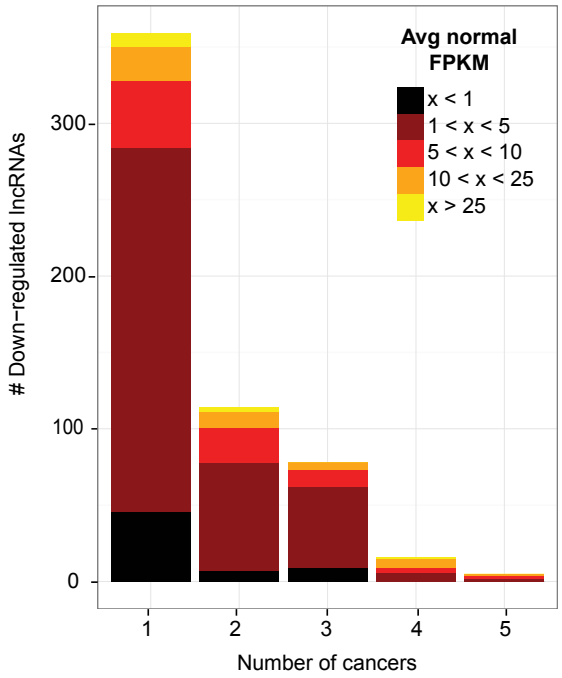
Supplementary Figure 1 | Differentially expressed lncRNAs. Heatmaps of differentially expressed lncRNAs for each cancer type (red = high expression, blue = low expression), separated into normal samples (N), tumor samples with a matched normal (T), and unpaired tumor samples. Sample sizes are also reported, space permitting.



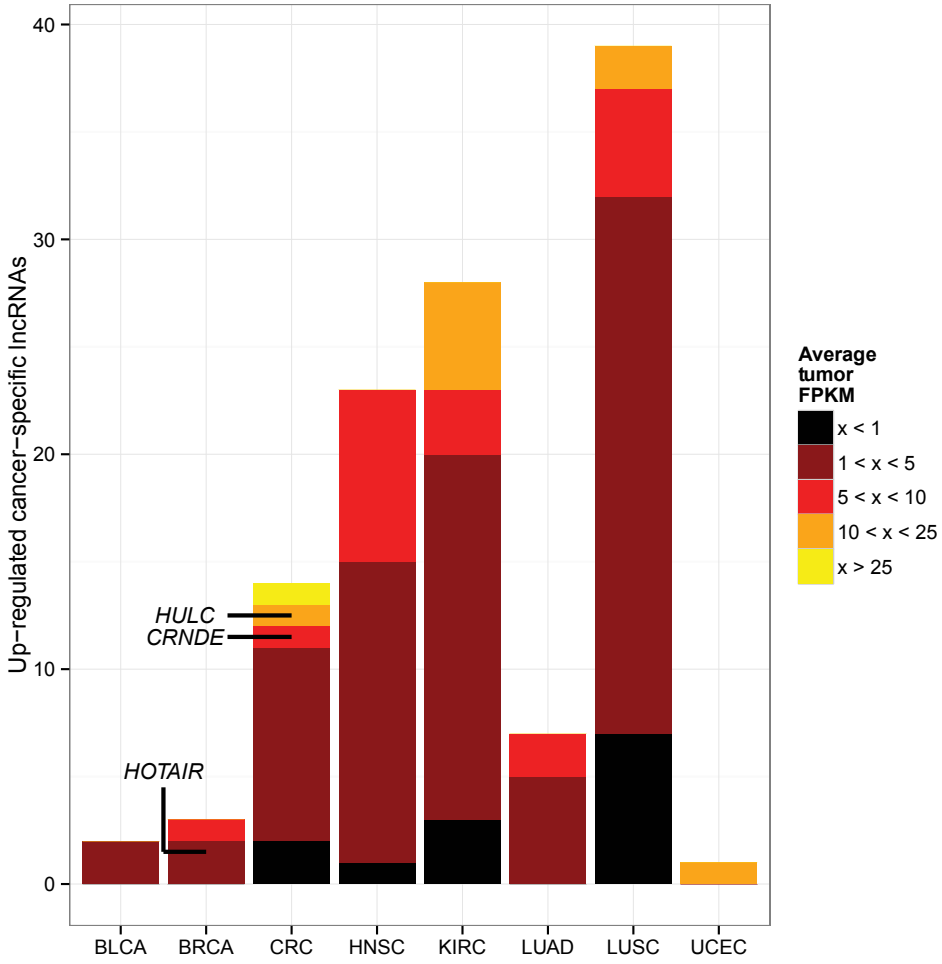
Supplementary Figure 2 | Differentially expressed protein coding genes across eight cancer types. **(a)** Number of up-regulated (red) and down-regulated (blue) coding genes that are differentially expressed within each cancer type. **(b)** Number of cancer types that each coding gene is differentially expressed in.



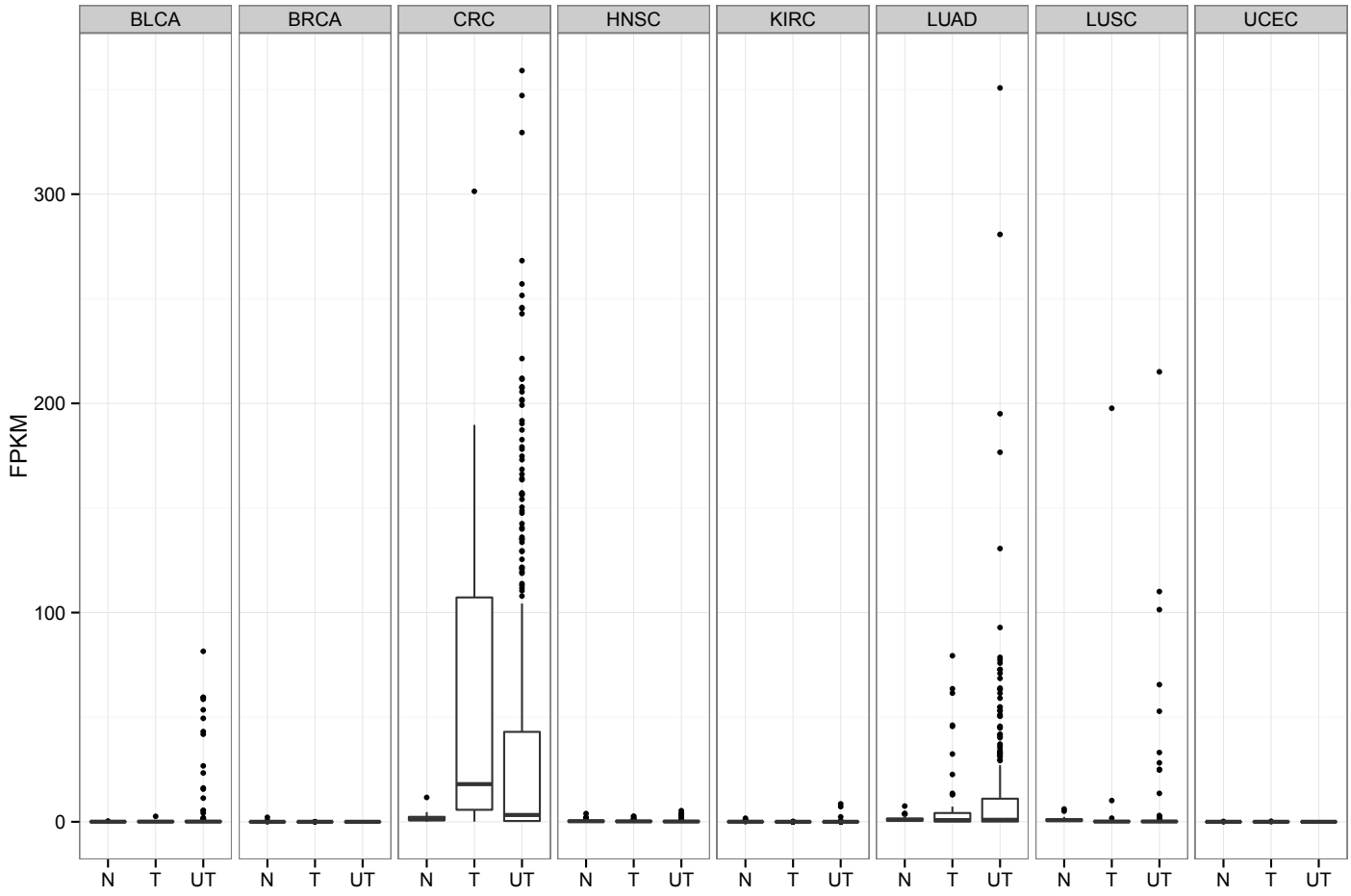
Supplementary Figure 3 | Average expression levels of down-regulated lncRNAs. Average expression (FPKM) of normal tissue samples for down-regulated lncRNAs. For lncRNAs differentially expressed in multiple cancers, each lncRNA-cancer pair is counted separately.



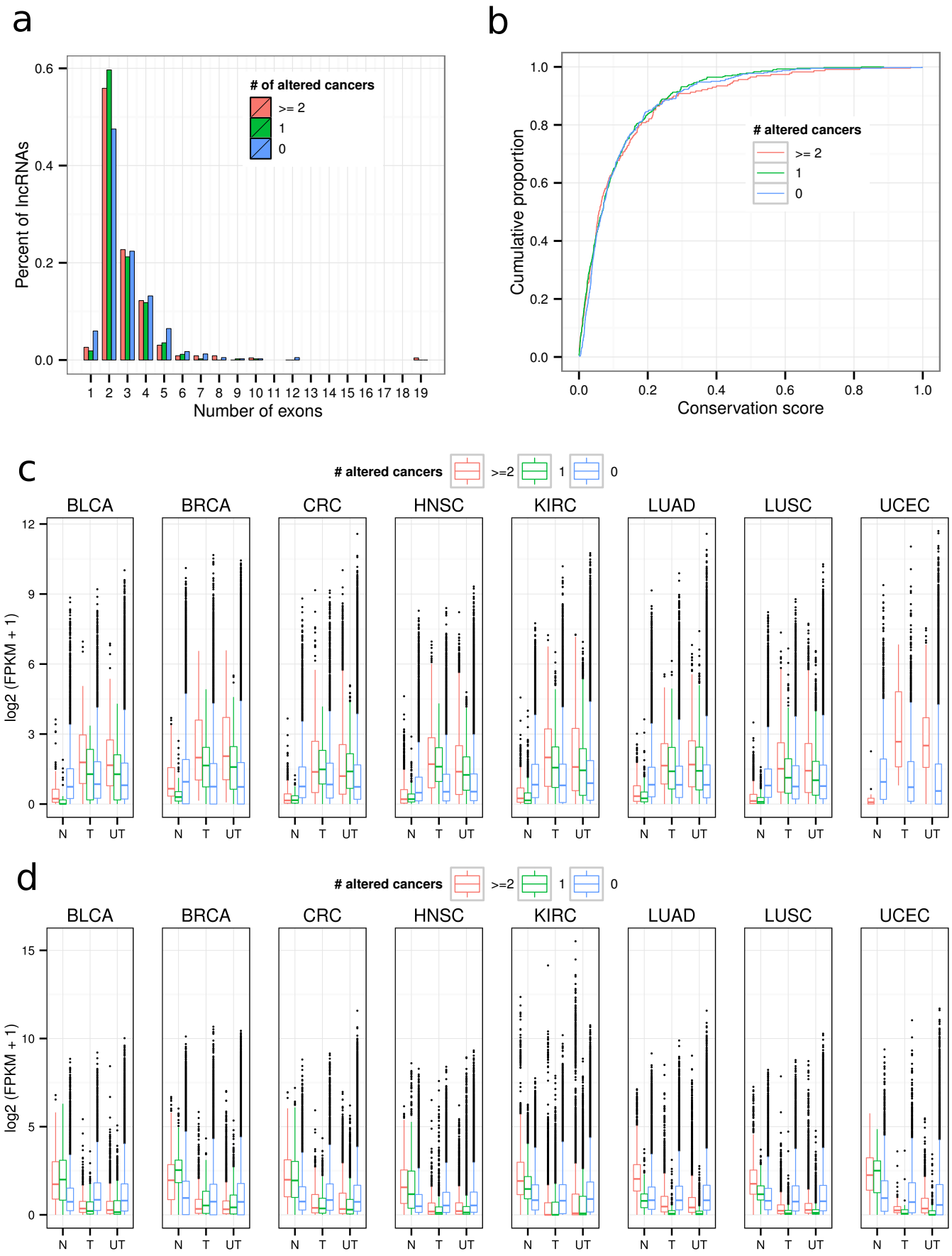
Supplementary Figure 4 | Average tumor expression levels of up-regulated cancer-specific lncRNAs. Three well-characterized lncRNAs (*HOTAIR*, *HULC*, and *CRNDE*) are highlighted, showing that other previously uncharacterized lncRNAs have higher expression levels and may be useful as tissue-specific biomarkers.



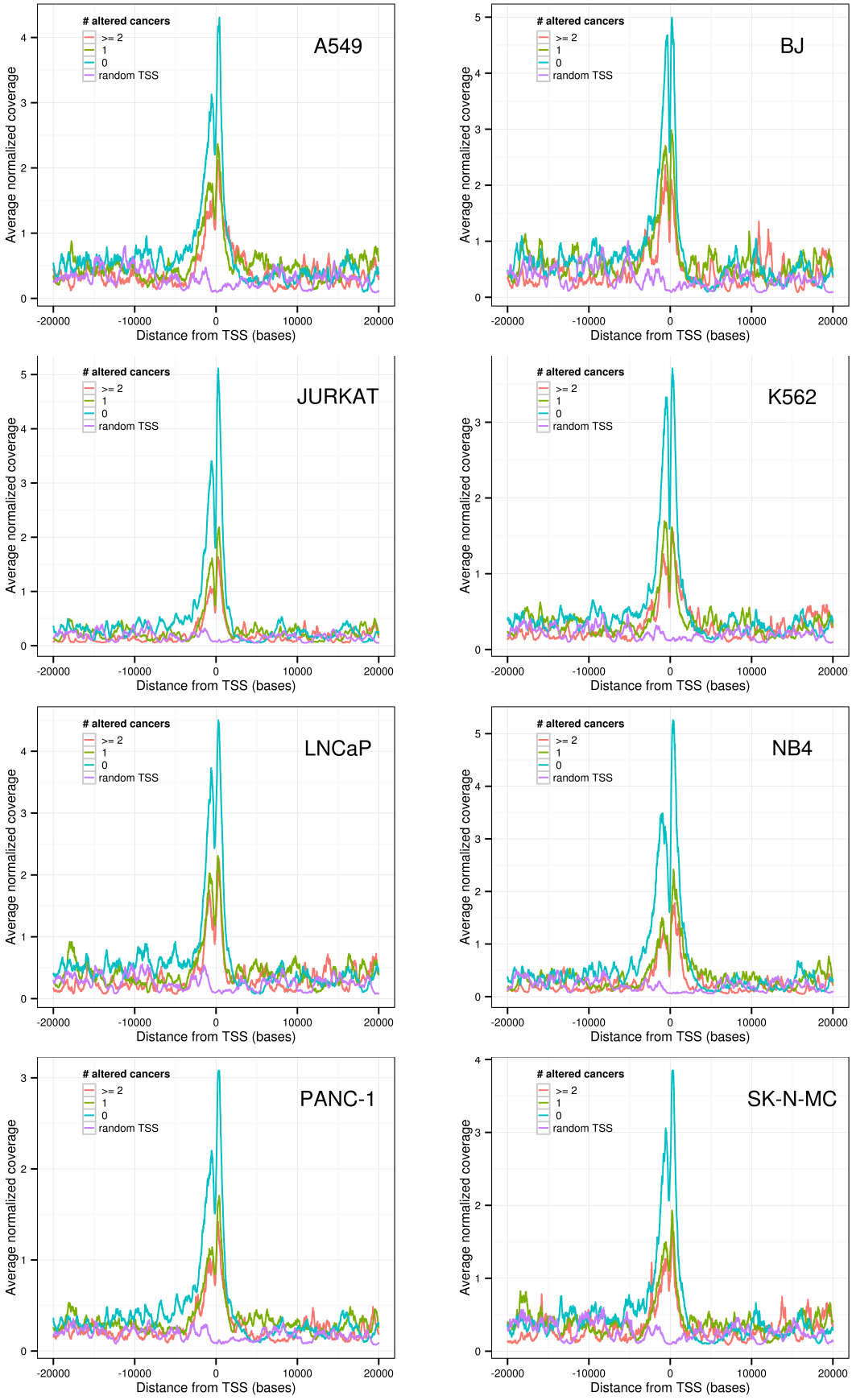
Supplementary Figure 5 | Expression levels of a cancer-specific lncRNA. Boxplots showing expression levels (FPKM) of *TCONS_00011854* for normal samples (N), tumor samples with a matched normal (T), and unpaired tumor samples (UT) across all eight cancer types. This lncRNA is differentially expressed in colorectal cancer (CRC) only.



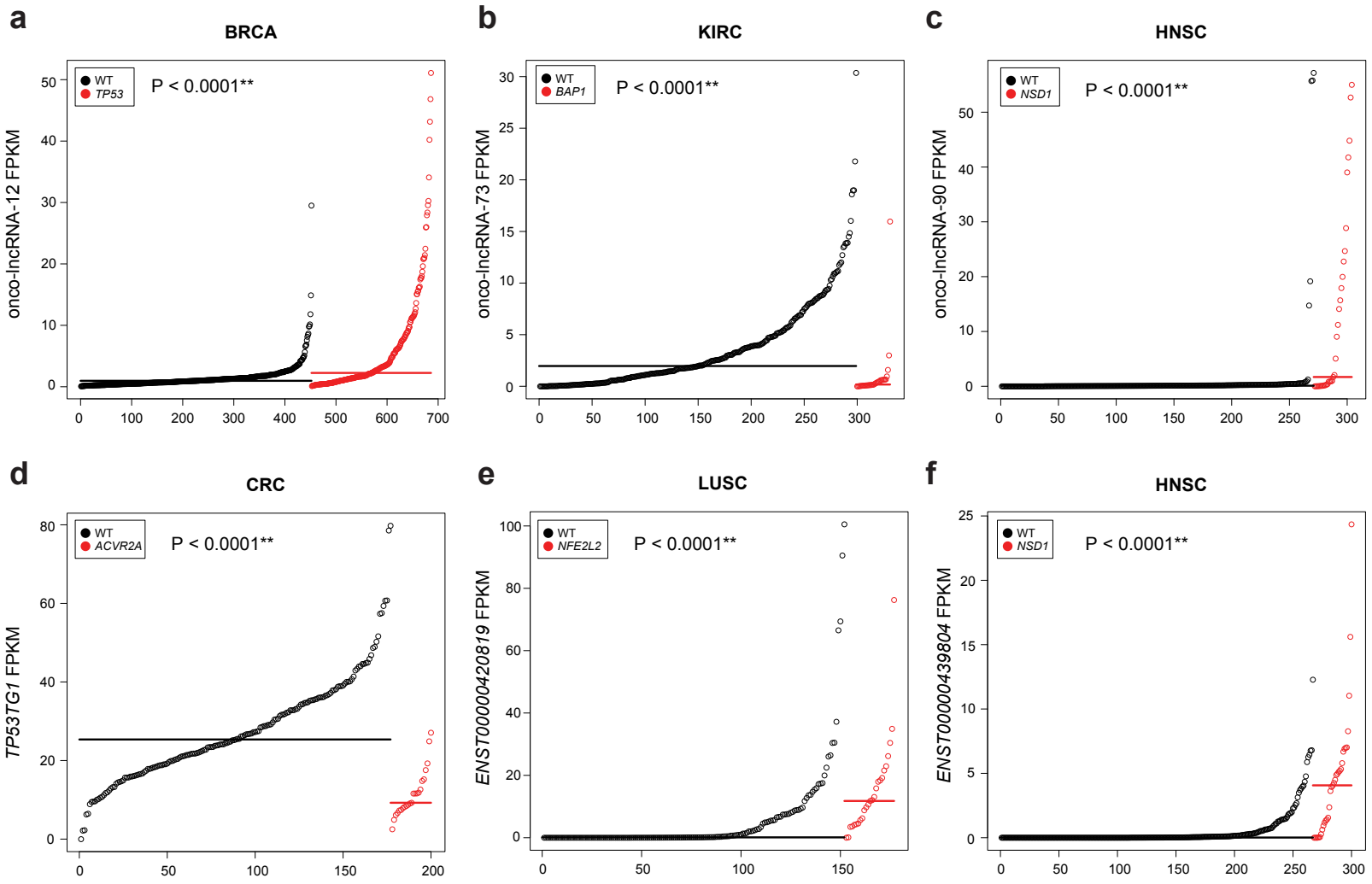
Supplementary Figure 6 | Characterization of lncRNAs with enriched expression. LncRNAs are grouped by the number of cancer types in which the lncRNA is altered, where the “>=2” class refers to the onco-lncRNAs.(a) Number of exons; (b) Sequence conservation; (c,d) Expression of lncRNAs in normal (N), matched tumor (T), and unmatched tumor (UT) samples in cancers where lncRNAs are up-regulated (c) and down-regulated (d).



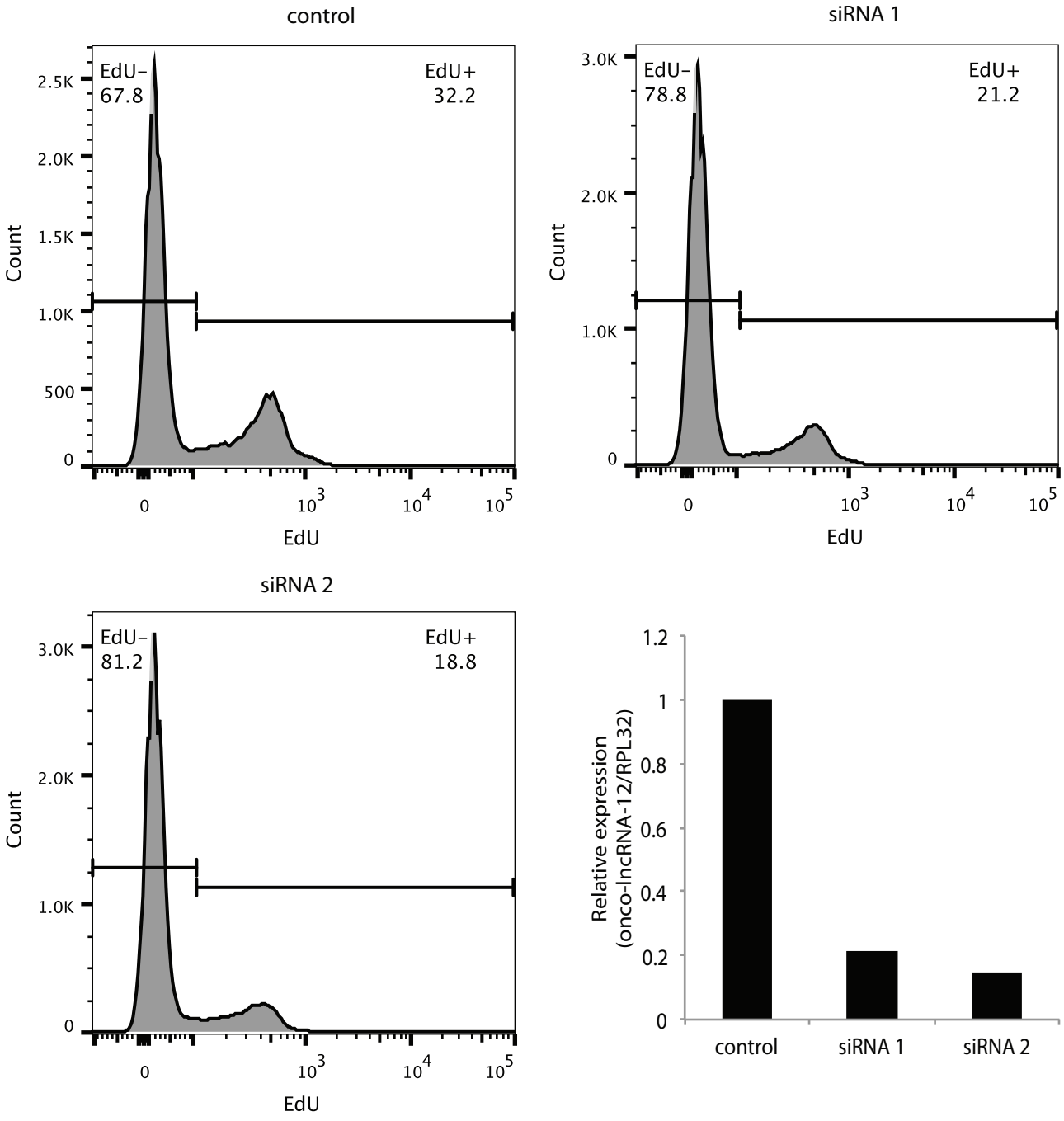
Supplementary Figure 7 | H3K4me3 Chip-Seq coverage near transcript start sites (TSS) of lncRNAs with enriched expression. LncRNAs are grouped by the number of cancer types in which the lncRNA is altered, where the ">=2" class refers to the onco-lncRNAs. Average normalized coverage is calculated as the total number of reads per million mapped averaged across lncRNAs within each group.



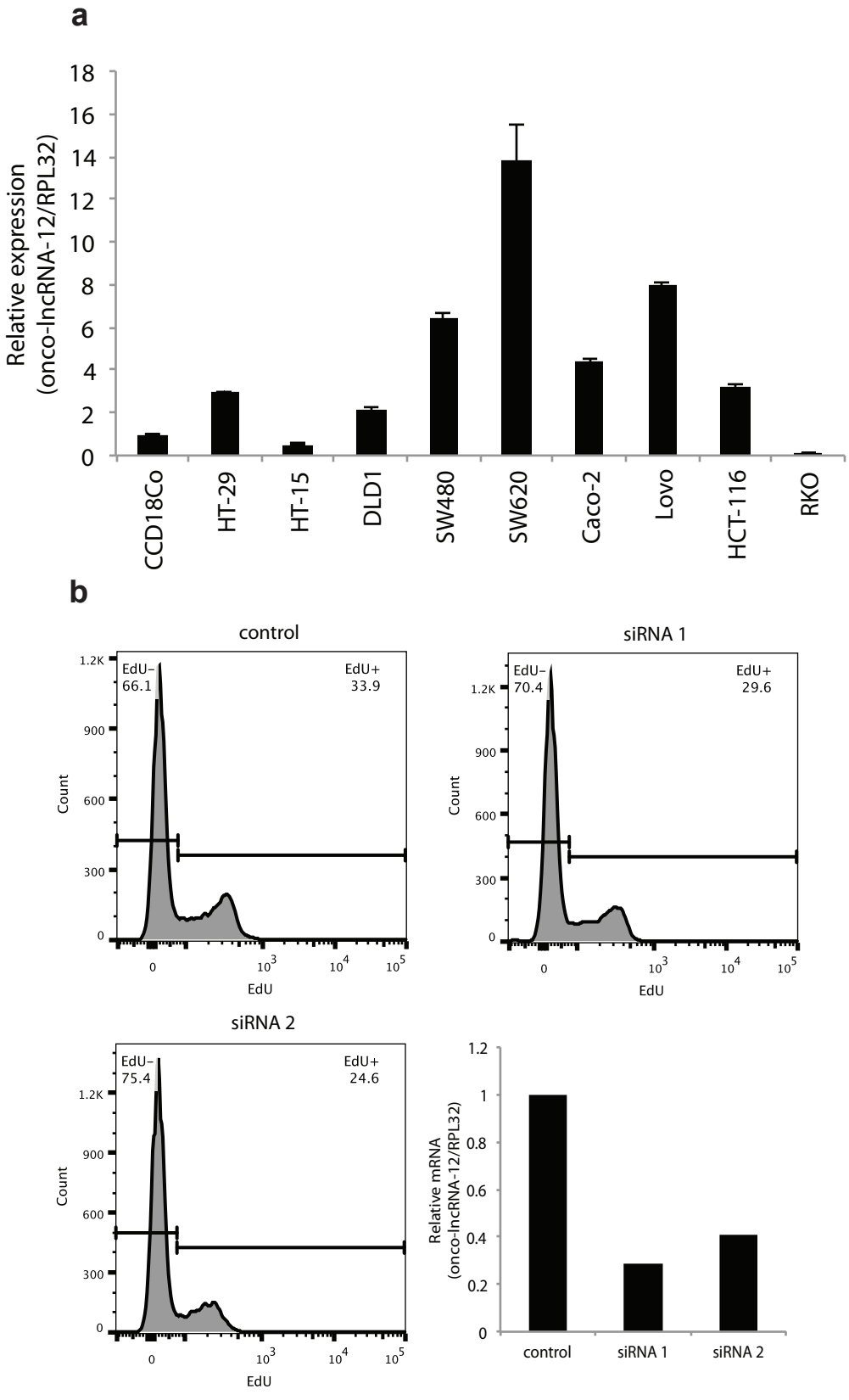
Supplementary Figure 8 | Association between onco-lncRNA expression and mutational status. Red points correspond to mutated samples and black points correspond to wild type (WT) samples. Samples are ordered by expression (FPKM) within each group. Black and red horizontal lines display the median expression across each group. P-values for each mutational association are also reported (** FDR < 0.01). **(a)** Onco-lncRNA-12 and *TP53* in BRCA, **(b)** onco-lncRNA-73 and *BAP1* in KIRC, **(c)** onco-lncRNA-90 and *NSD1* in HNSC, **(d)** *TP53TG1* and *ACVR2A* in CRC, **(e)** *ENST00000420819* and *NFE2L2* in LUSC, and **(f)** *ENST00000439804* and *NSD1* in HNSC.



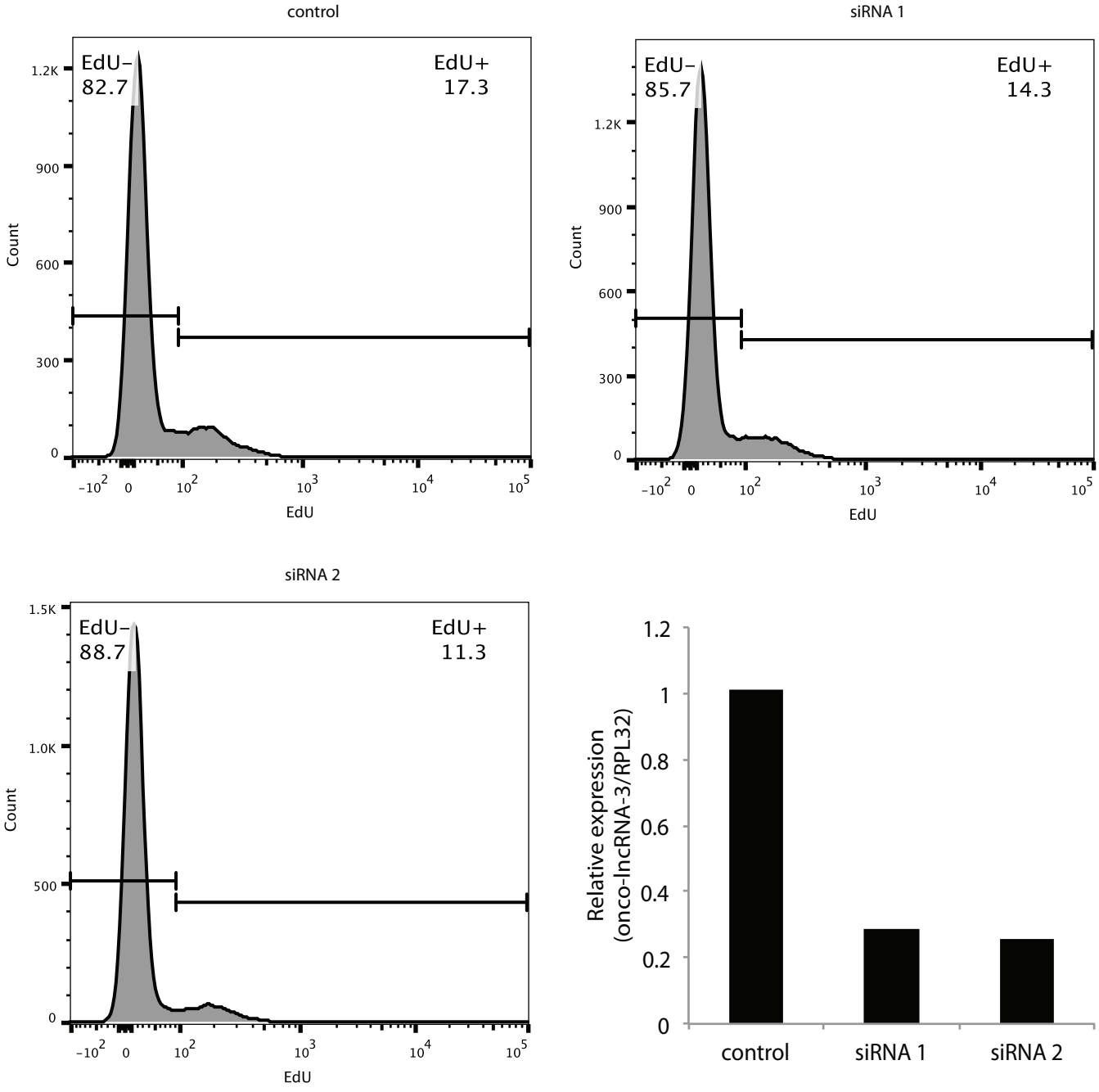
Supplementary Figure 9 | S-phase cell cycle alteration with altered *onco-lncRNA-12* expression in a lung cancer cell line. EdU incorporation was measured after 72 hour *onco-lncRNA-12* or control knock-down in the A549 lung cancer cell line. X-axis shows EdU fluorescence and Y-axis is cell count. Significance for both siRNAs is $p<0.0002$ by a two-tailed Student's *t*-test. Knockdown efficiency was measured by qPCR relative to control knockdown. *n* of at least 2 biological replicates in at least two independent experiments. Graphs are representative of results.



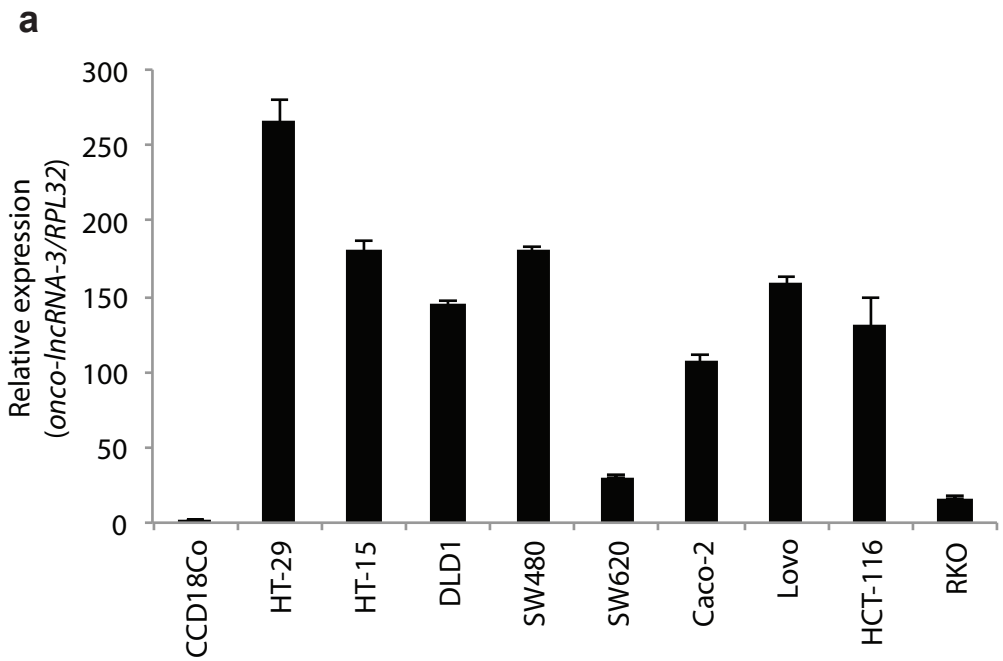
Supplementary Figure 10 | S-phase cell cycle alteration with altered *onco-lncRNA-12* expression in a colon cancer cell line. (a) qPCR validation of *onco-lncRNA-12* across a panel of colon cancer cell lines (n = 9) relative to a control cell line, CCD-18Co, and normalized to the housekeeping gene *RPL32*. All error bars are mean +/- standard error across *n* = 3 biological replicates. **(b)** EdU incorporation was measured after 72 hour *onco-lncRNA-12* or control knockdown in the SW620 colon cancer cell line. X-axis shows EdU fluorescence and Y-axis is cell count. Significance for siRNA 1 compared to control is p=0.009 and p=0.03 for siRNA 2 compared to control by a two-tailed Student's *t*-test. Knockdown efficiency was measured by qPCR relative to control knockdown. *n* of at least 2 biological replicates in at least two independent experiments. Graphs are representative of results.

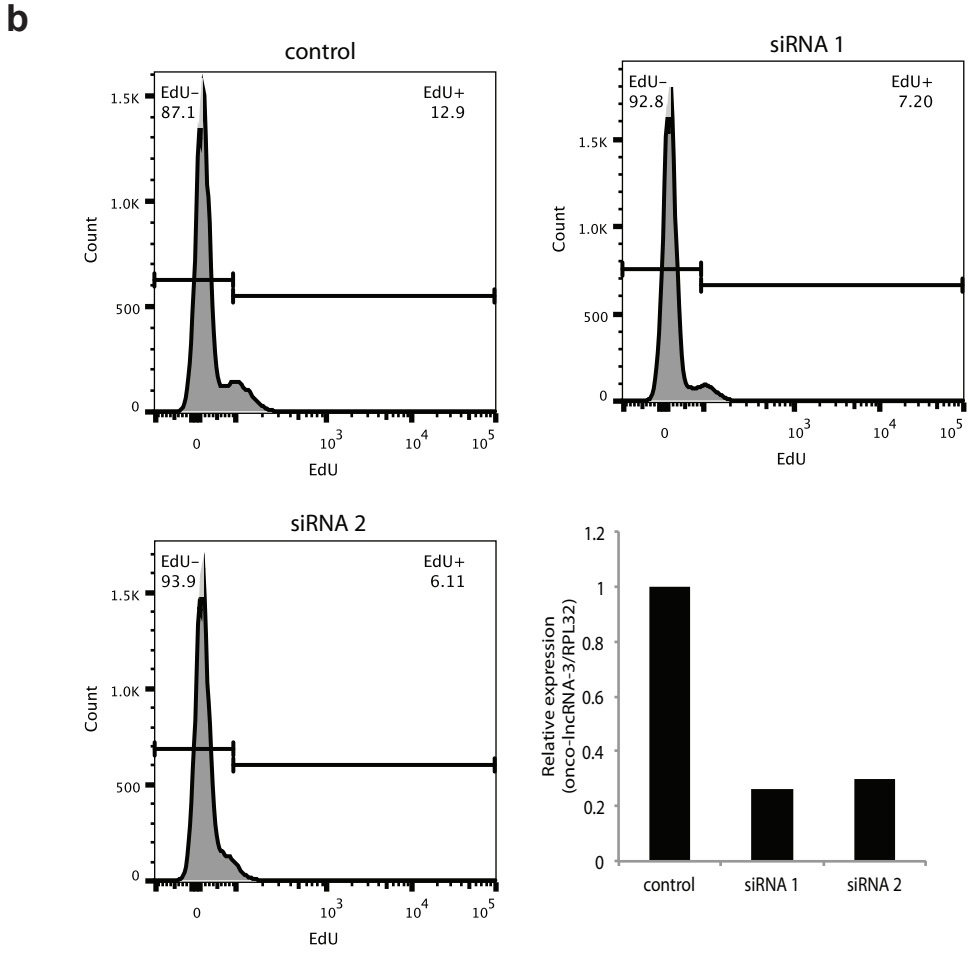


Supplementary Figure 11 | S-phase cell cycle alteration with altered *onco-lncRNA-3* expression in a lung cancer cell line. EdU incorporation was measured after 72 hour *onco-lncRNA-3* or control knockdown in the H322M lung cancer cell line. X-axis shows EdU fluorescence and Y-axis is cell count. Significance for siRNA 1 compared to control is p=0.04 and p=0.02 for siRNA 2 compared to control by a two-tailed Student's *t*-test. Knockdown efficiency was measured by qPCR relative to control knockdown. *n* of at least 2 biological replicates in at least two independent experiments. Graphs shown are representatives.

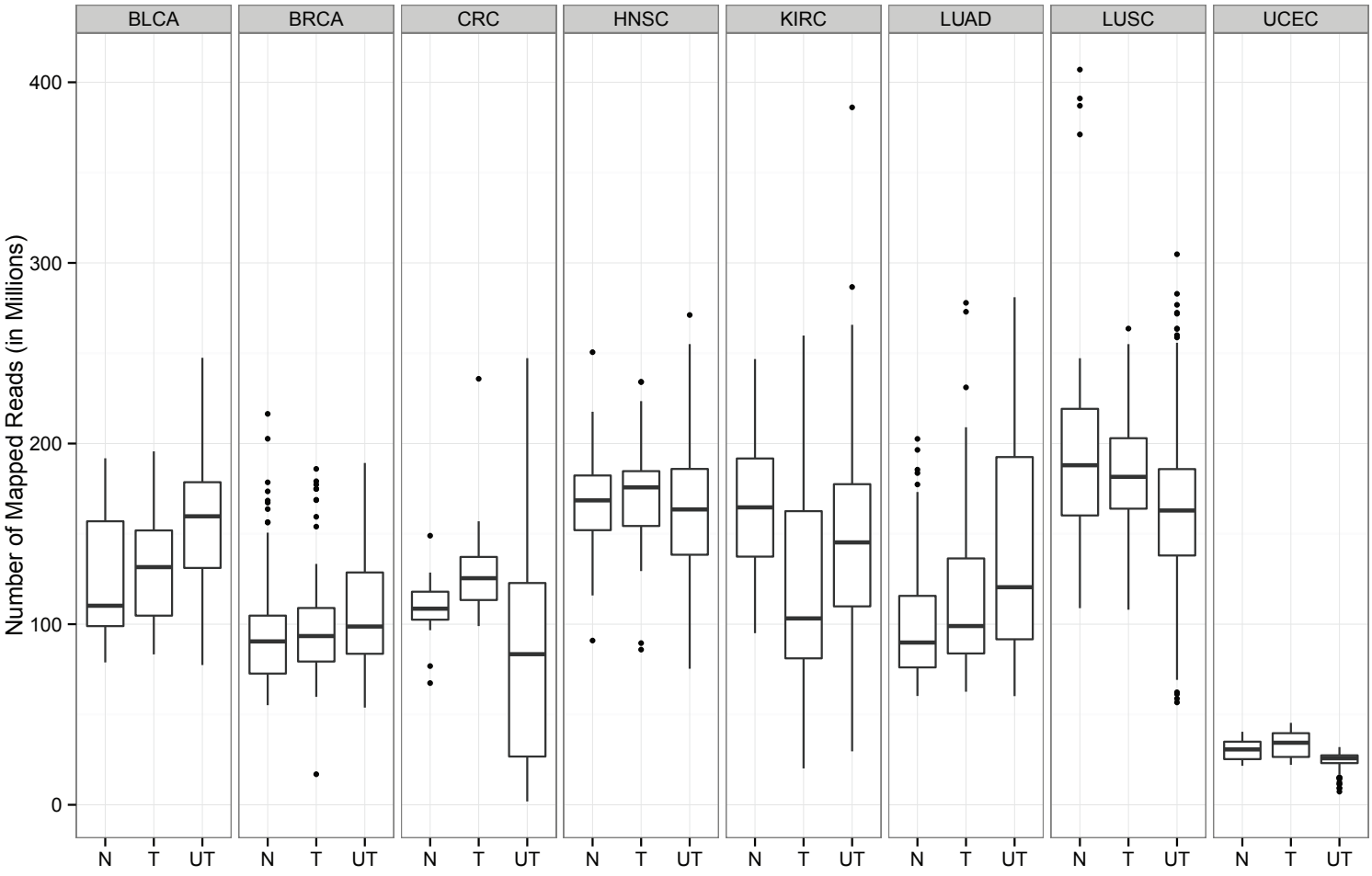


Supplementary Figure 12 | S-phase cell cycle alteration with altered *onco-lncRNA-3* expression in a colon cancer cell line. (a) qPCR validation of *onco-lncRNA-3* expression across a panel of colon cancer cell lines (n = 9) relative to a control cell line, CCD-18Co, and normalized to the housekeeping gene *RPL32*. All error bars are mean +/- standard error across *n* = 3 biological replicates. **(b)** EdU incorporation was measured after 72 hour *onco-lncRNA-3* or control knockdown in the HT29 colon cancer cell line. X-axis shows EdU fluorescence and Y-axis is cell count. Significance for siRNA 1 compared to control is p=0.009 and p=0.03 for siRNA 2 compared to control by a two-tailed Student's *t*-test. Knockdown efficiency was measured by qPCR relative to control knockdown. *n* of at least 2 biological replicates in at least two independent experiments. Graphs shown are representative of results.

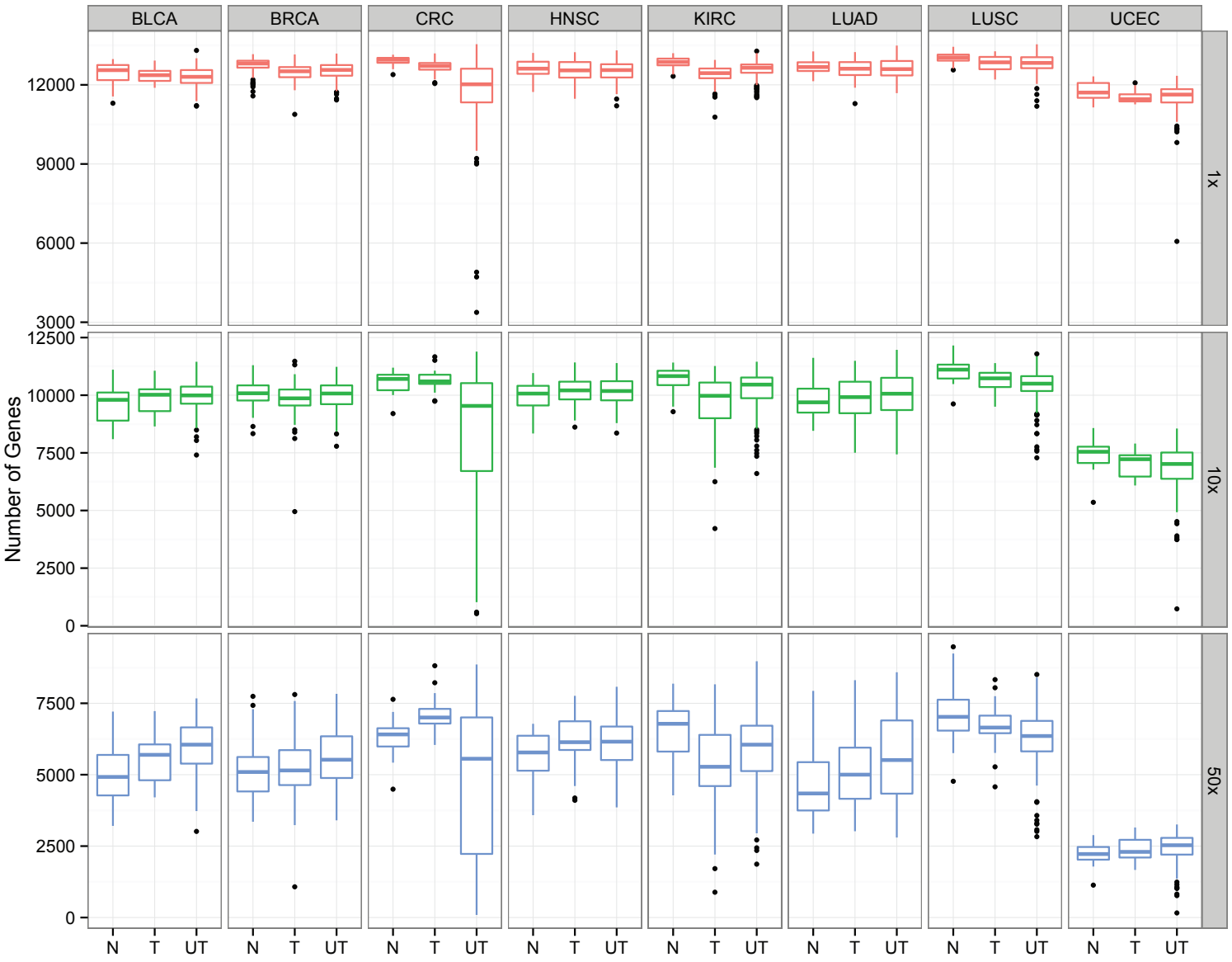




Supplementary Figure 13 | Number of mapped reads across eight cancer types. Boxplots showing the number of mapped reads for normal samples (N), tumor samples with a matched normal (T), and unpaired tumor samples (UT) across all eight cancer types. UCEC samples and approximately half of the CRC tumor samples were sequenced as single-end reads on Illumina GAIIx while the other samples, including all of the matched tumor and adjacent normal CRC pairs, were sequenced as paired-end reads on Illumina HiSeq.



Supplementary Figure 14 | Number of protein coding genes at 1x, 10x, and 50x coverage. Boxplots showing the number of protein coding genes meeting the specified coverage threshold for normal samples (N), tumor samples with a matched normal (T), and unpaired tumor samples (UT) across all eight cancer types.



Supplementary Figure 15 | Number of lncRNAs at 1x, 10x, and 50x coverage. Boxplots showing the number of lncRNAs meeting the specified coverage threshold for normal samples (N), tumor samples with a matched normal (T), and unpaired tumor samples (UT) across all eight cancer types.