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Supplemental Information

Comprehensive Characterization of Somatic Mutations Impacting lncRNA Expression for Pan-Cancer

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Supplementary Information

Supplementary Figure Legends

Supplementary Fig. 1 (A) Bar chart showing the number of MutLncs across cancer types. (B) Bar chart showing unmixed and mixed MutLncs, including TF, gene, microRNA, methylation-related MutLncs.

Supplementary Fig. 2 (A) Examples of two MutLncs in which expression features are correlated to mutations. Expression profile, bar chart and genome mutation status are shown. (B) Examples of three MutLncs showing expression features, especially in correlation with synonymous and non-synonymous mutations.

Supplementary Fig. 3 (A) Degree distribution of co-occurrence networks across cancer types. Degrees are shown along the X axis and number of nodes along the Y axis. (B) Bar chart showing the number of MutLncs participating in the co-occurrence network. (C) Co-occurrence matrix showing the probability of co-occurrence between each pair of MutLncs for eight cancer types. The darker color represents more significant co-occurrence in a specific cancer.

Supplementary Fig. 4 (A) Bar chart of KEGG pathways enriched for MutLncs in BLCA and HNSC, ranked by −log10(P). (B) Density distribution of Pearson correlation coefficients for MutLncs and the corresponding genes of enrichment analysis in STAD. (C) Distribution of common GO terms of MutLncs identified over 3 cancer types.

Supplementary Fig. 5 (A) Density distribution of Pearson correlation coefficients for MutLncs and corresponding methylations across cancer types. (B) Density distribution of Pearson correlation coefficients for MutLncs and corresponding microRNAs across cancer types. (C) Density distribution of Pearson correlation coefficients for MutLncs and corresponding genes across cancer types. (D) Density distribution of Pearson correlation coefficients for

MutLncs and corresponding TFs across cancer types. (E) Enrichment GO terms of TF, gene, microRNA, and methylation-related MutLncs across different cancer types. (F) Pie chart of the number of MutLncs with mixed or unmixed effects in KICH.

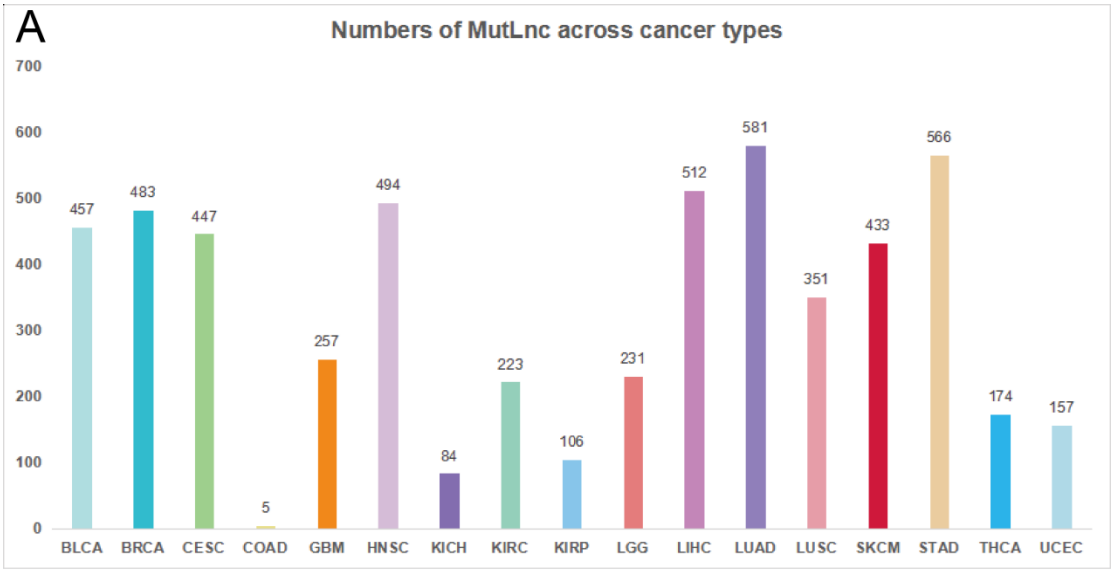
Supplementary Fig. 6 (A) Mutation type and (B) base of ENSG00000256769.

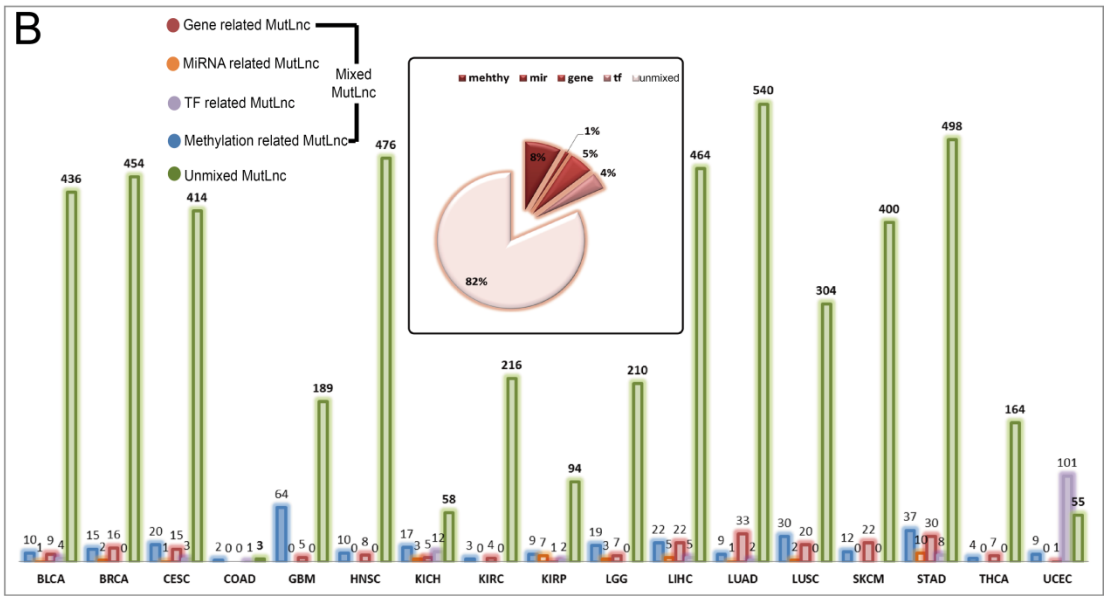
Supplementary Fig. 7 (A) The size of circles represented the number of lncRNA, TF and mutation in cancers. (B) The percent of TF-related mutations in all mutations in cancers. (C) The radar chart showed the number of mutations in top TFs.

Supplementary Fig. 8 (A) The possible mechanism of somatic mutation resulting in tumor development. (B) The possible mechanism of somatic mutation resulting in drug resistant.

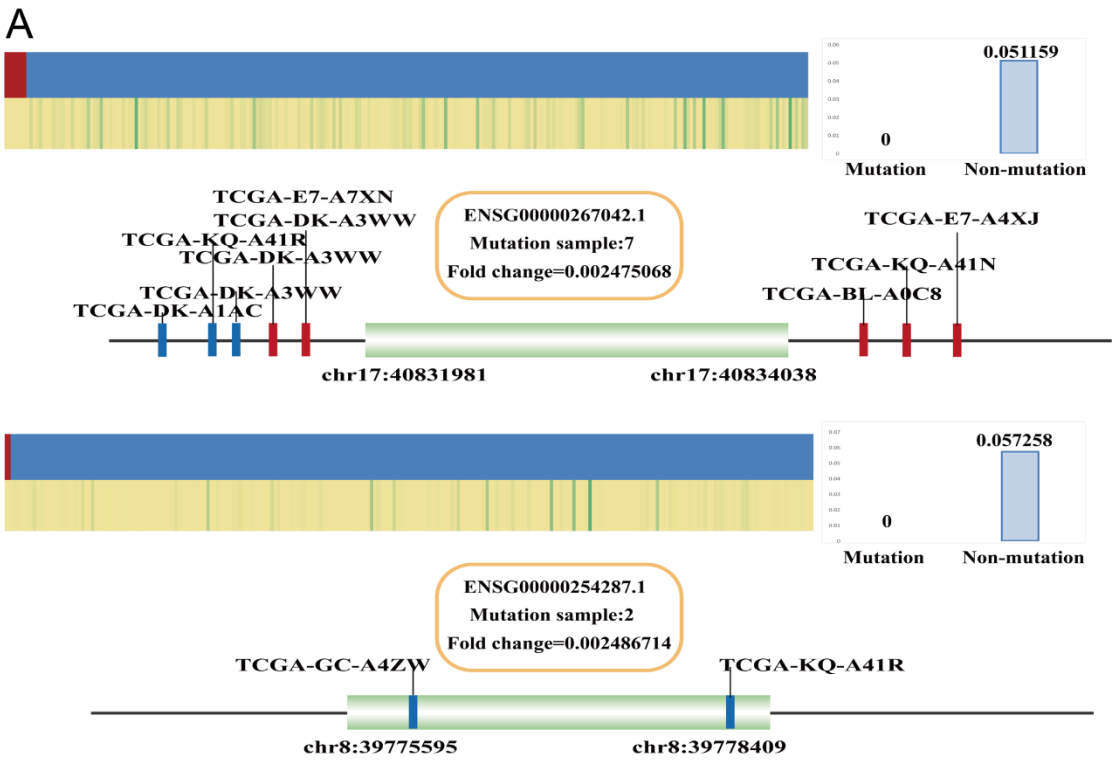
Supplementary Fig. 9 The basic principle to identify MutLncs correlated to mutations across 17 cancer types. Step 1. Somatic mutation, lncRNA expression, somatic mutation and lncRNA annotation data were collected from TCGA, TANRIC and Genecode V19. Step 2. MutLncs were identified in each cancer type by integrating multiple data sets. Step 3. The effect process by which the mutations influence lncRNA expression were evaluated by considering the effects of methylations, genes, TFs and microRNAs.

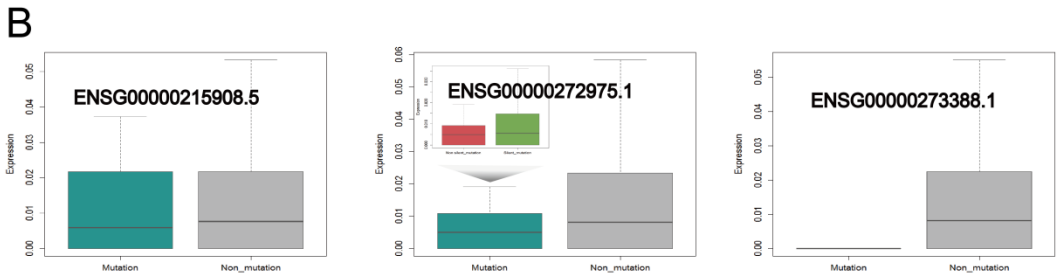
Supplementary Fig. 10 (A) Computed flow considering methylation participation in the effect process underlying the effects of somatic mutations on lncRNA expression. (B) Fisher test to identify co-occurrence MutLnc pairs (C) and cancer similarity.



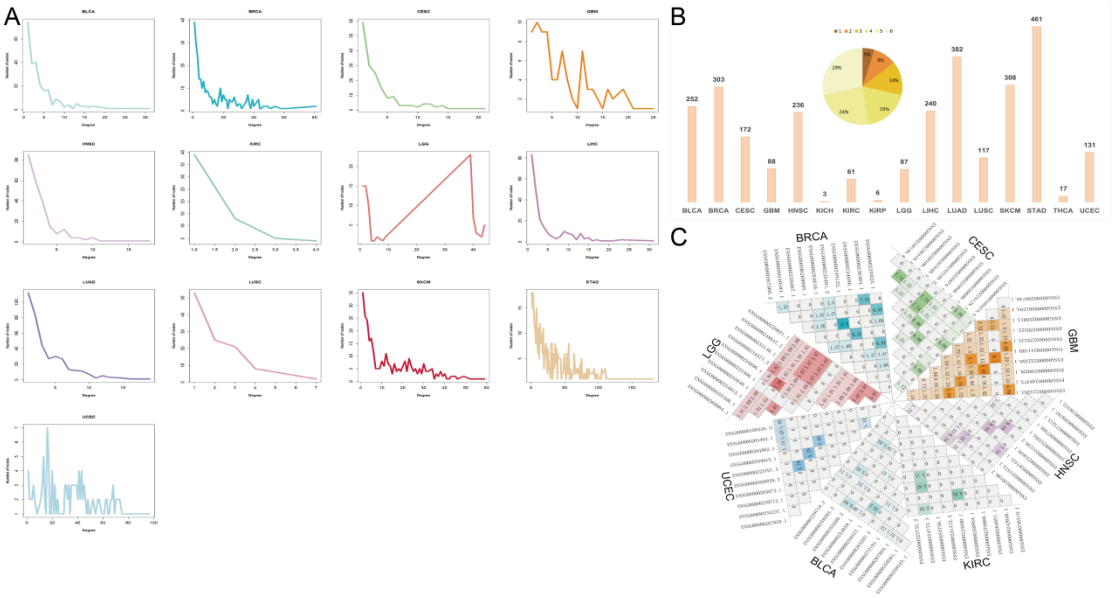


Supplementary Fig. 1

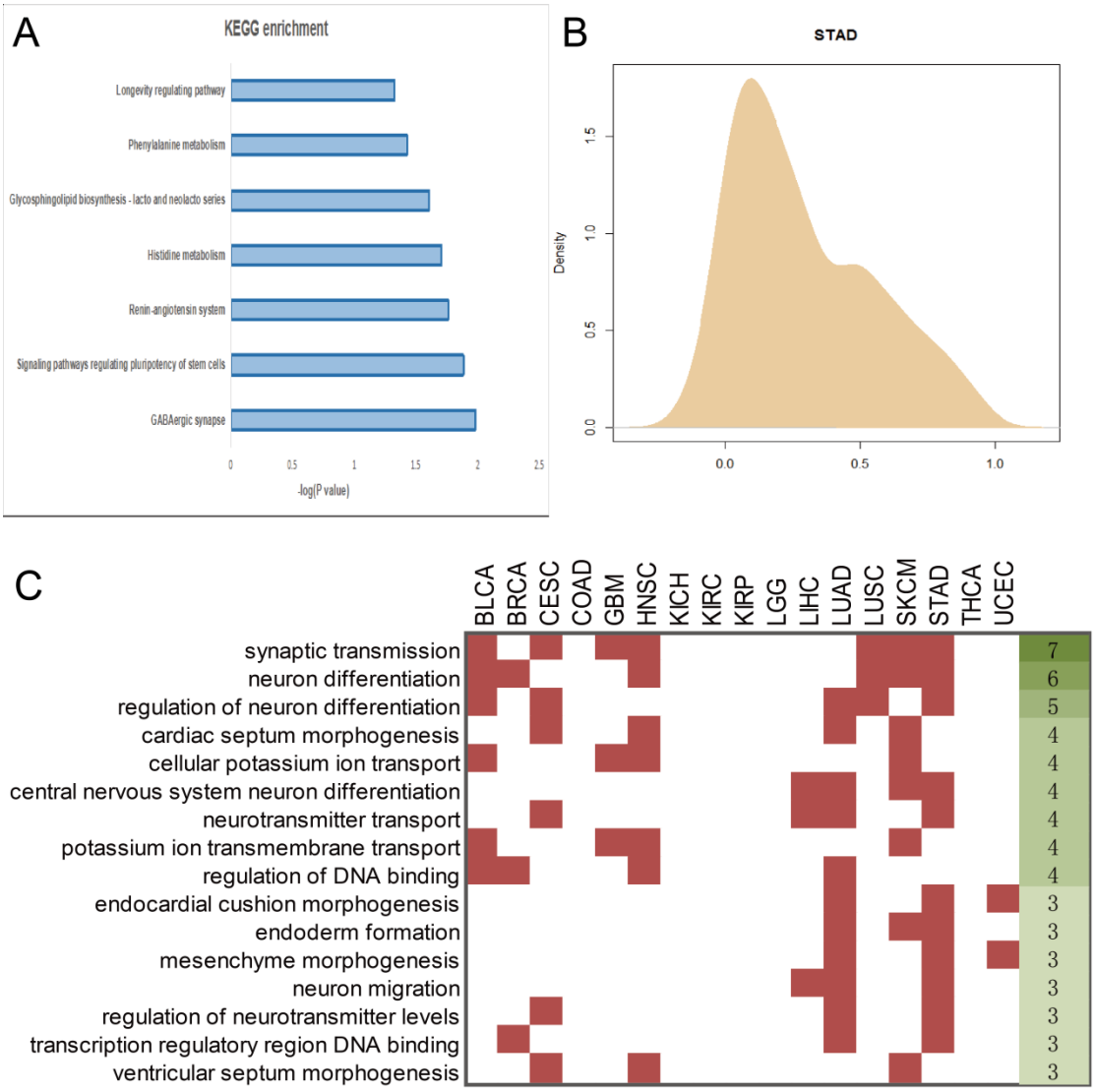




Supplementary Fig. 2



Supplementary Fig. 3



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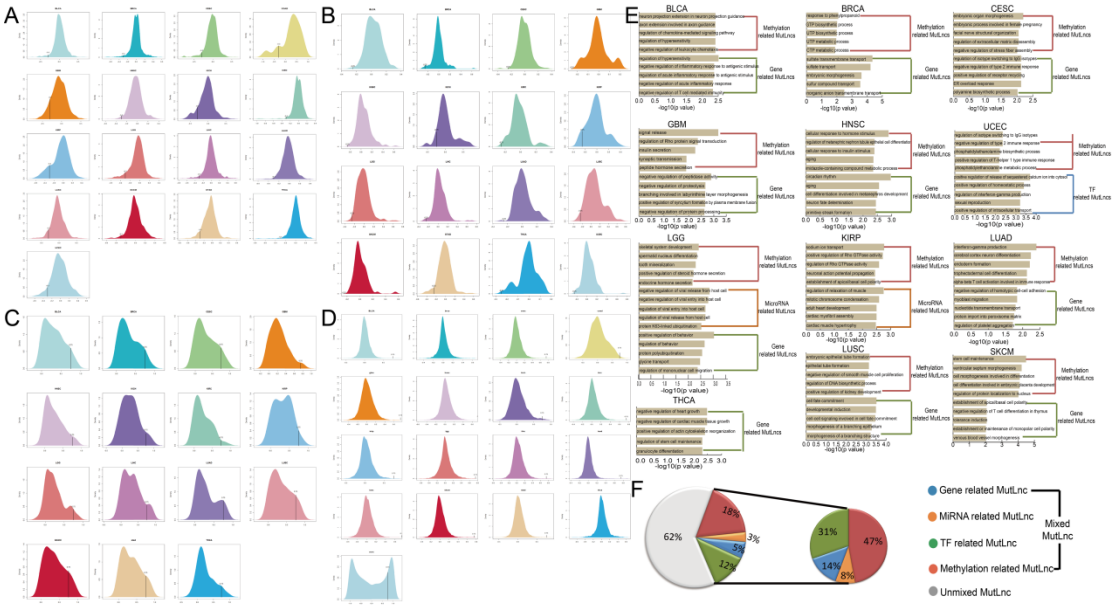
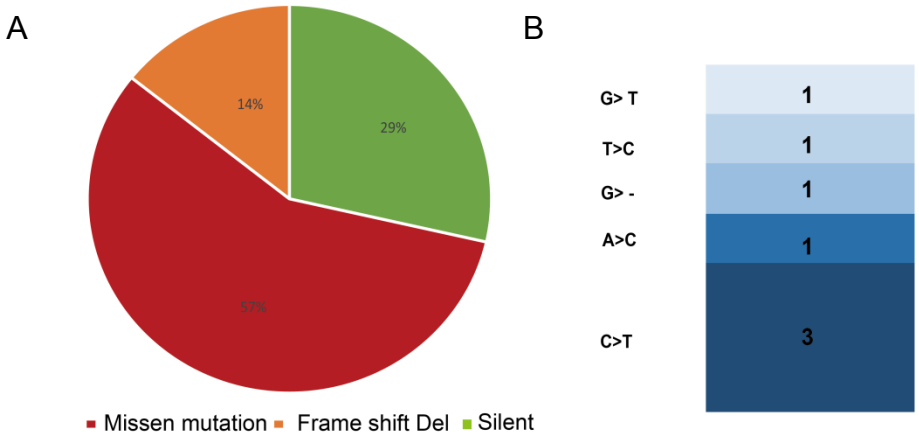
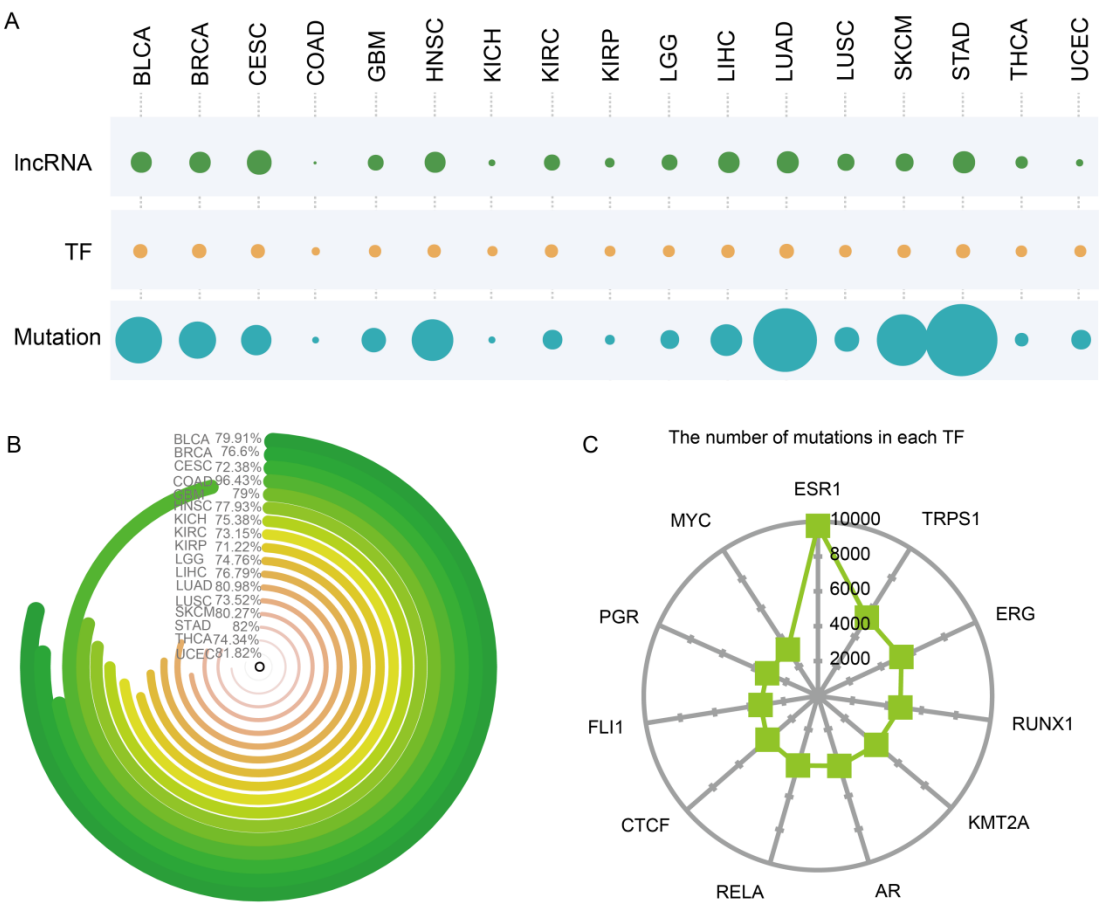


Supplementary Fig. 5



Supplementary Fig. 6



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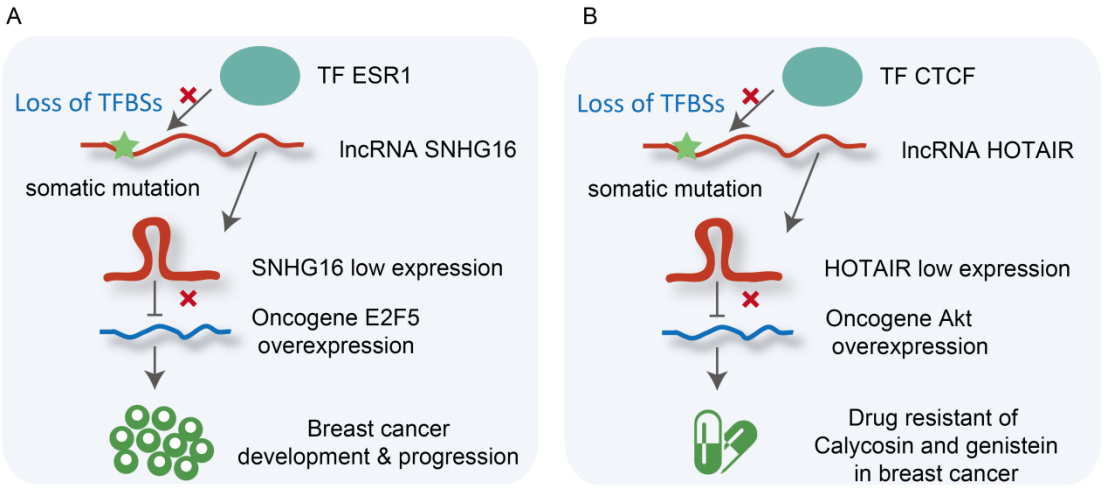

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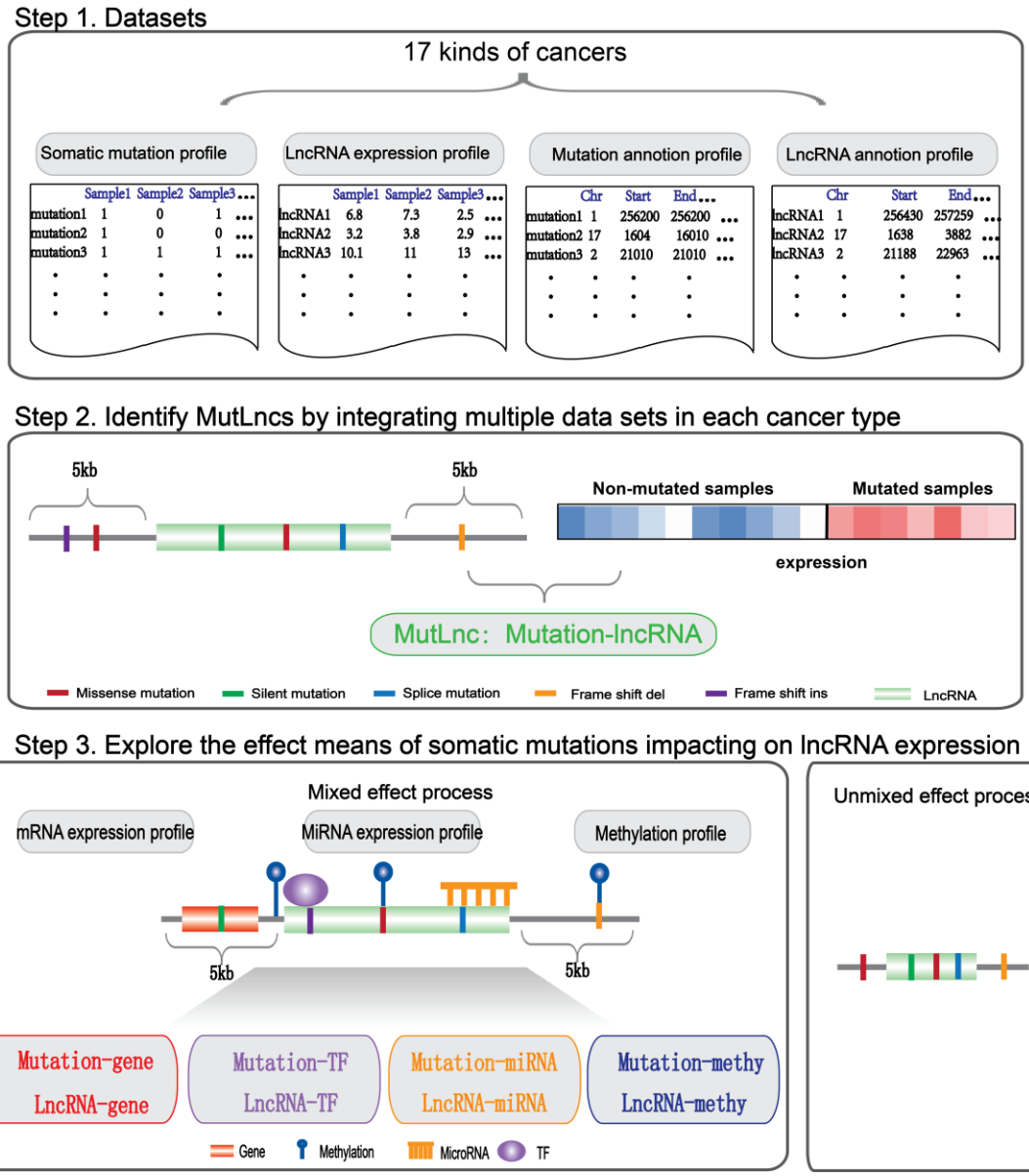
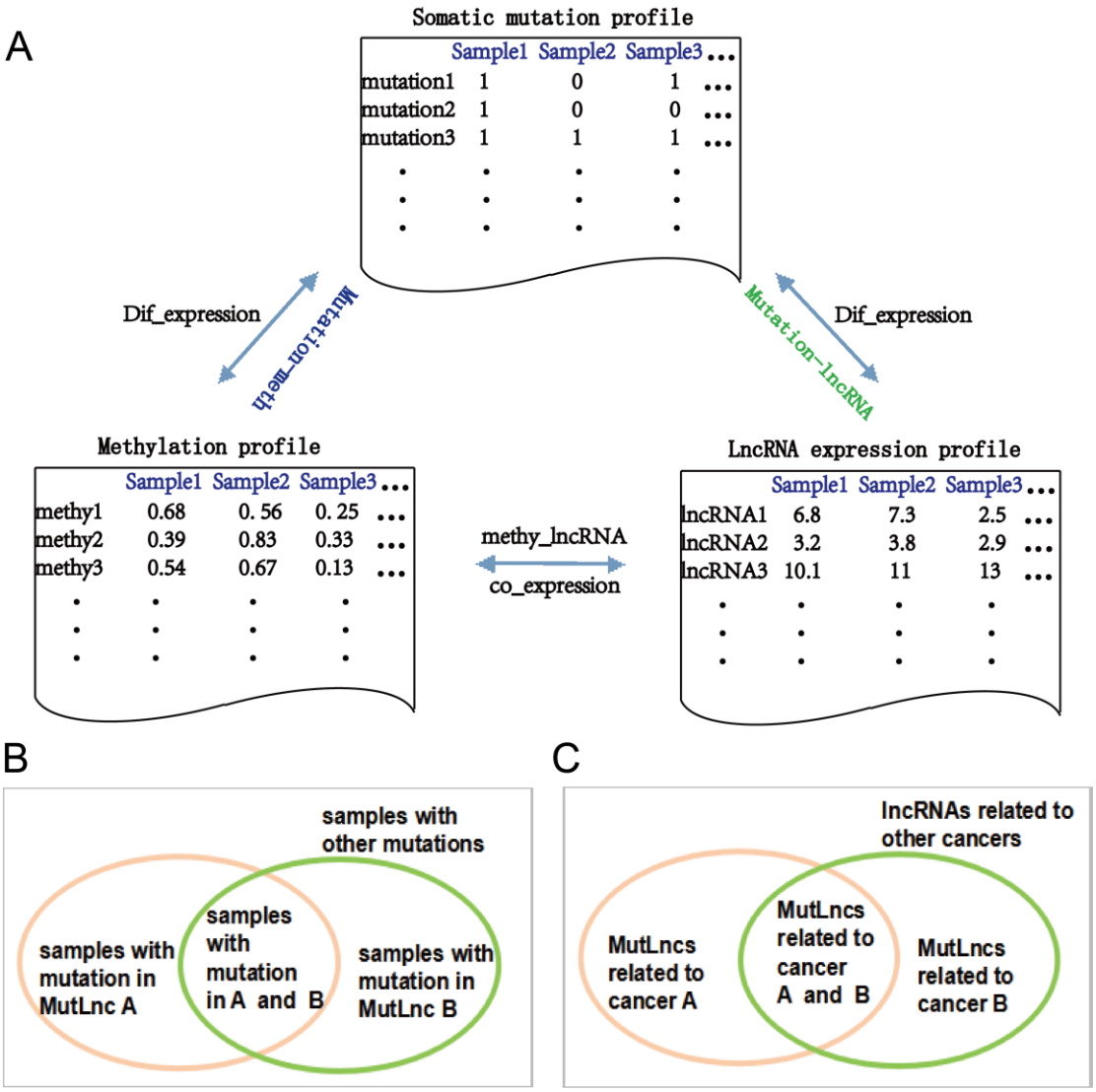


Supplementary Fig. 9



Supplementary Fig. 10