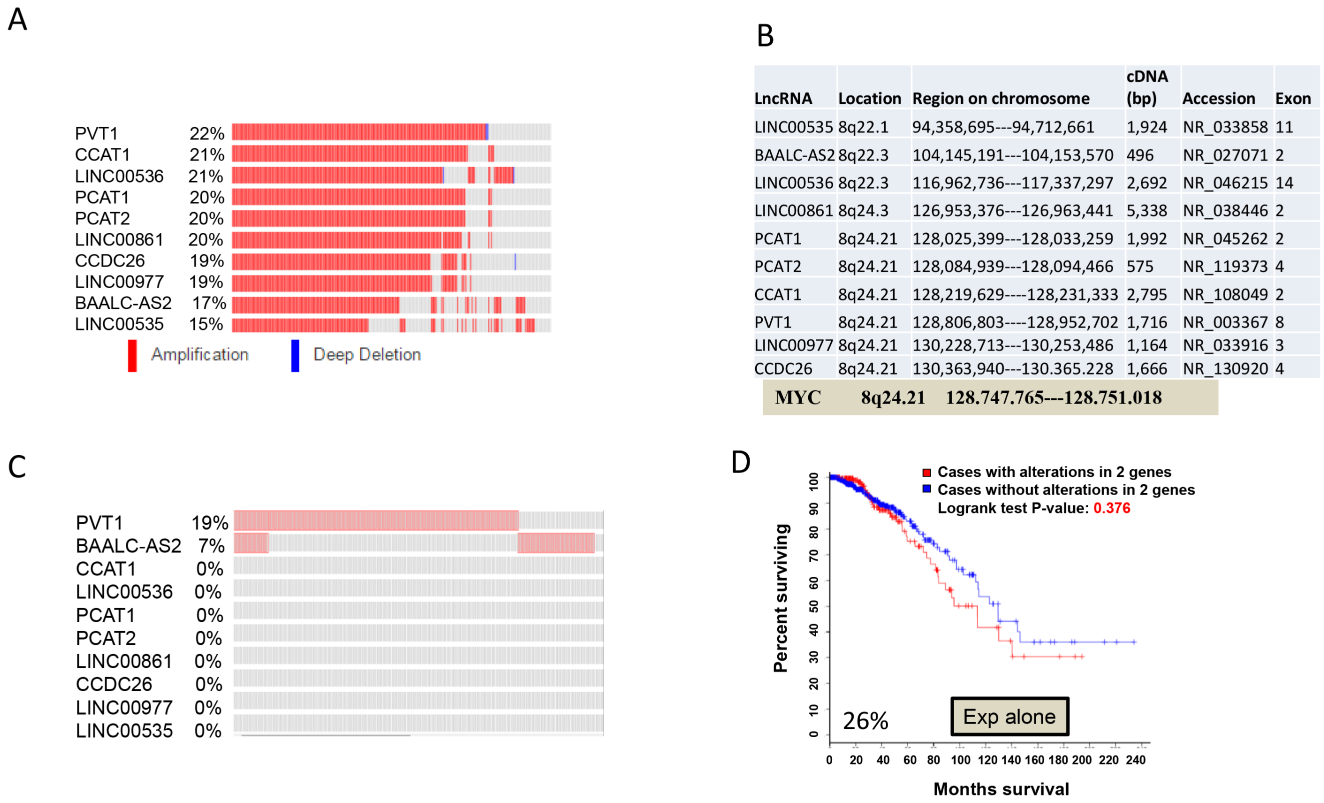
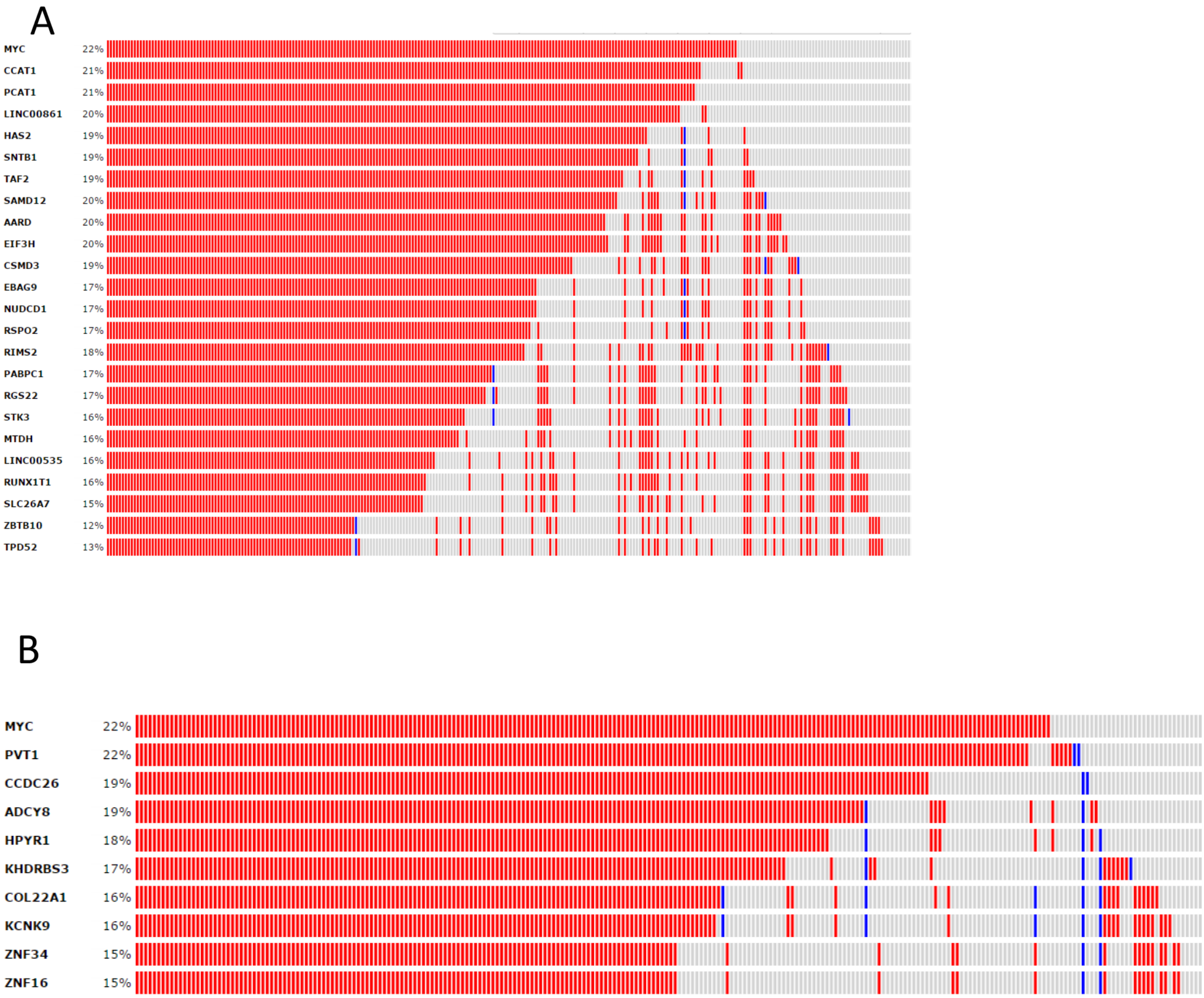
SUPPLEMENTARY FIGURES AND TABLES

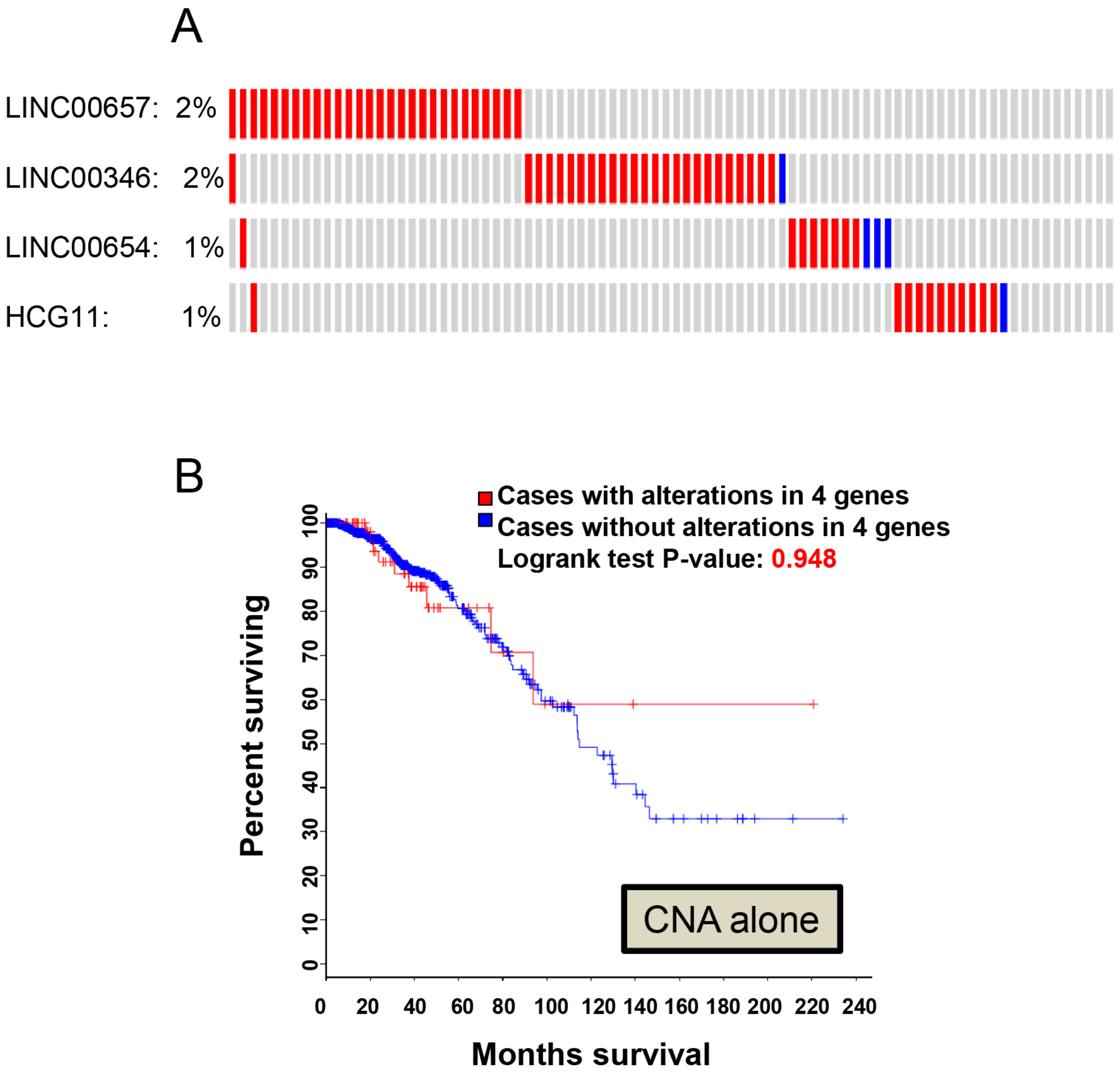


LncRNA	Location	Region on chromosome	cDNA (bp)	Accession	Exon
LINC00535	8q22.1	94,358,695---94,712,661	1,924	NR_033858	11
BAALC-AS2	8q22.3	104,145,191---104,153,570	496	NR_027071	2
LINC00536	8q22.3	116,962,736---117,337,297	2,692	NR_046215	14
LINC00861	8q24.3	126,953,376---126,963,441	5,338	NR_038446	2
PCAT1	8q24.21	128,025,399---128,033,259	1,992	NR_045262	2
PCAT2	8q24.21	128,084,939---128,094,466	575	NR_119373	4
CCAT1	8q24.21	128,219,629----128,231,333	2,795	NR_108049	2
PVT1	8q24.21	128,806,803----128,952,702	1,716	NR_003367	8
LINC00977	8q24.21	130,228,713---130,253,486	1,164	NR_033916	3
CCDC26	8q24.21	130,363,940---130.365.228	1,666	NR_130920	4
MYC	**8q24.21**	**128.747.765---128.751.018**			

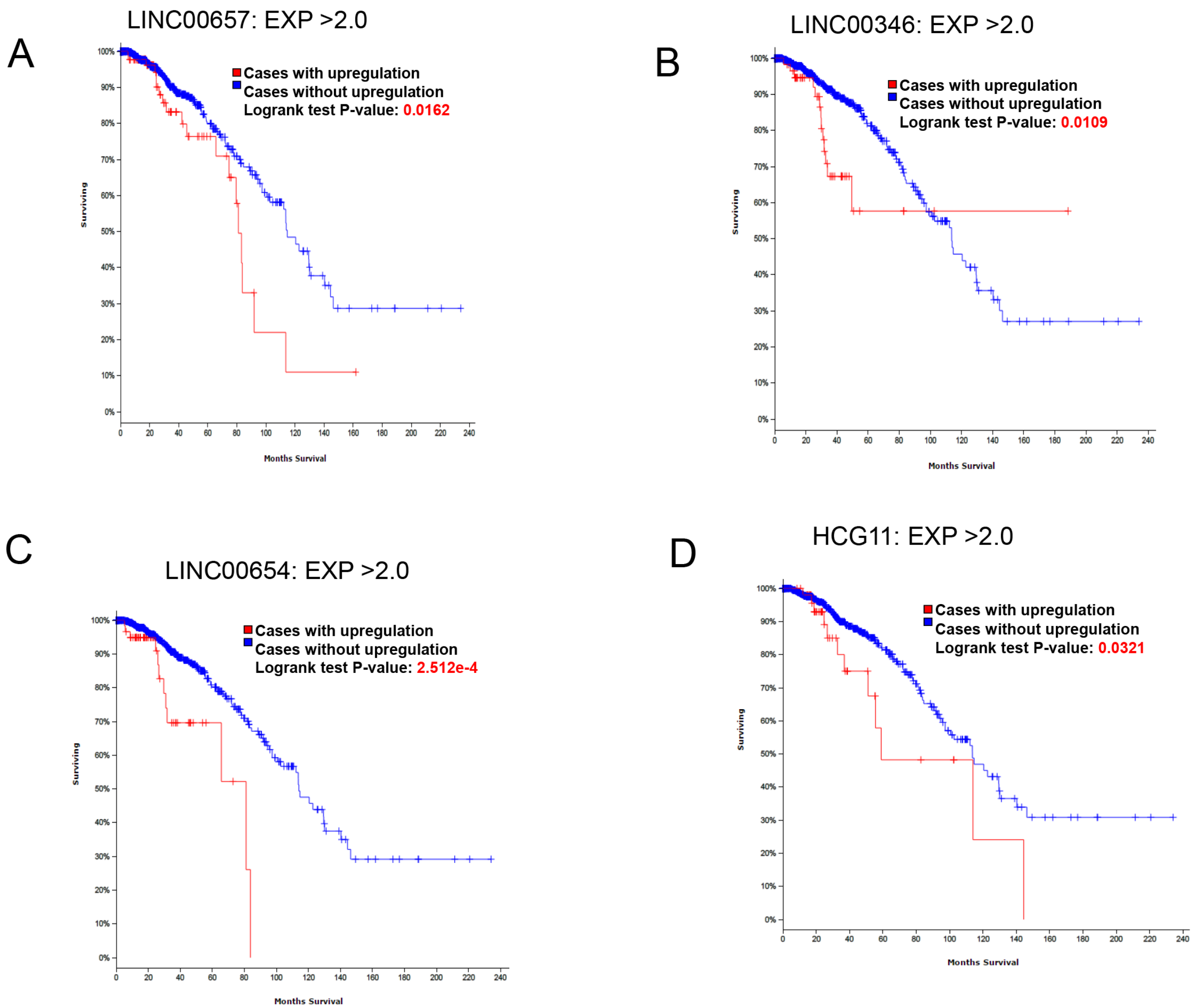
Supplementary Figure S1: Alterations in copy number and RNA expression for lncRNAs associated with poor OS. A. Relative alteration frequency of copy number for 10 lncRNAs. **B.** Listed 10 lncRNAs with location, cDNA size and accession numbers. **C.** Only 2 lncRNAs (PVT1 and BAALC-AS2) revealed alterations of RNA expression. **D.** Association between expression of PVT1 and BAALC-AS2 and OS is not significant.



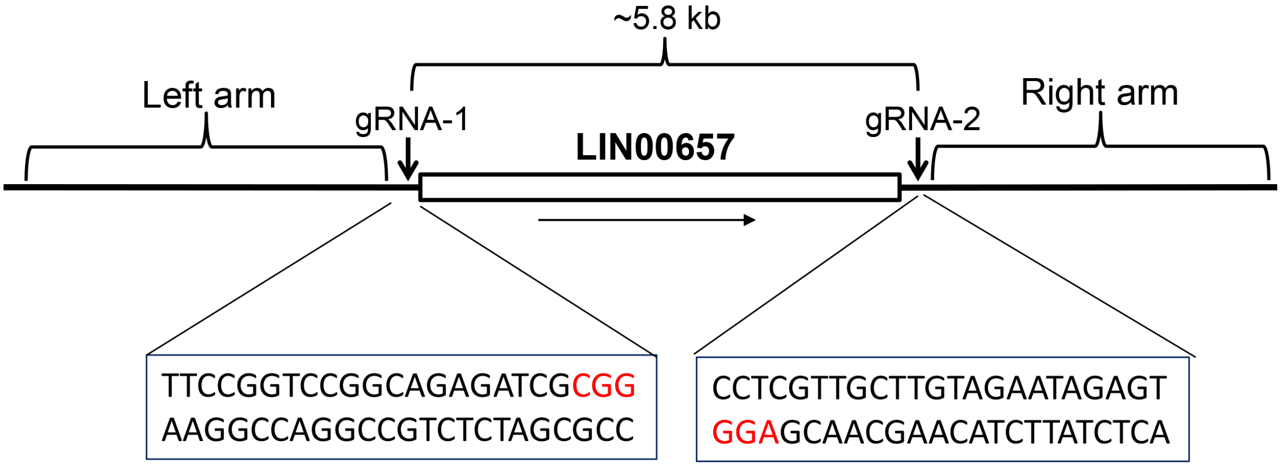
Supplementary Figure S2: Alterations in copy-number of lincRNAs related to Myc. A. Relative alteration frequency of copy number toward right side of Myc. **B.** Relative alteration frequency of copy number toward left side of Myc.



Supplementary Figure S3: Alterations in copy number of lncRNA signature 2. A. Relative frequency of CNA for 4 lncRNAs. **B.** Association between CNA and OS is not significant.

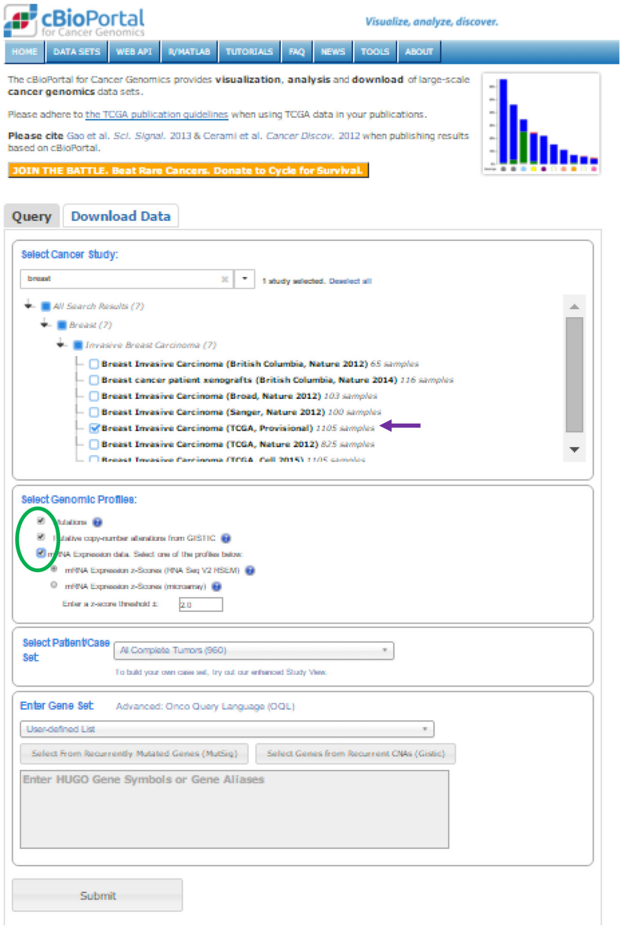


Supplementary Figure S4: Association of 4 individual lncRNAs with OS.



Supplementary Figure S5: A strategy for generation of LIN00657 knockout by CRISPR/Cas9. Two gRNA sequences are shown in bottom; PAM motifs are shown in red.

Primary search with default setting



The cBioPortal for Cancer Genomics provides **visualization**, **analysis** and **download** of large-scale **cancer genomics** data sets.

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Select Cancer Study: breast — 1 study selected. Deselect all

- *All Search Results (7)*
  - *Breast (7)*
    - *Invasive Breast Carcinoma (7)*
      - ☐ **Breast Invasive Carcinoma (British Columbia, Nature 2012)** *65 samples*
      - ☐ **Breast cancer patient xenografts (British Columbia, Nature 2014)** *116 samples*
      - ☐ **Breast Invasive Carcinoma (Broad, Nature 2012)** *103 samples*
      - ☐ **Breast Invasive Carcinoma (Sanger, Nature 2012)** *100 samples*
      - ☑ **Breast Invasive Carcinoma (TCGA, Provisional)** *1105 samples* ←
      - ☐ **Breast Invasive Carcinoma (TCGA, Nature 2012)** *825 samples*
      - ☐ **Breast Invasive Carcinoma (TCGA, Cell 2015)** *1105 samples*

Select Genomic Profiles:

☑ Mutations
☑ Putative copy-number alterations from GISTIC
☑ mRNA Expression data. Select one of the profiles below:
● mRNA Expression z-Scores (RNA Seq V2 RSEM)
○ mRNA Expression z-Scores (microarray)
Enter a z-score threshold ±: 2.0

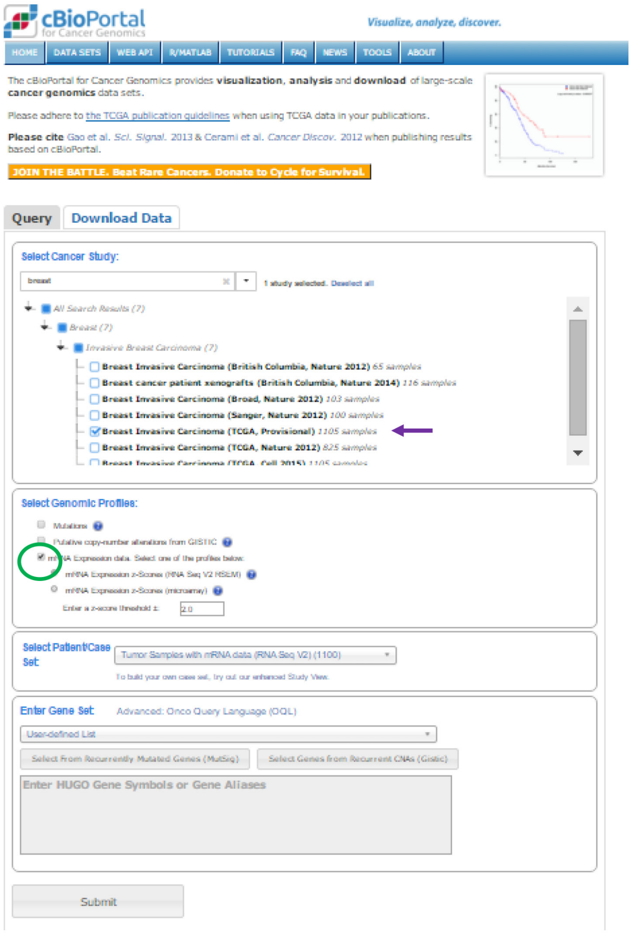
Select Patient/Case Set: All Complete Tumors (960)

To build your own case set, try out our enhanced Study View.

Enter Gene Set: User-defined List

Enter HUGO Gene Symbols or Gene Aliases

Search with expression (RNA-seq)



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      - ☐ **Breast Invasive Carcinoma (British Columbia, Nature 2012)** *65 samples*
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      - ☐ **Breast Invasive Carcinoma (TCGA, Nature 2012)** *825 samples*
      - ☐ **Breast Invasive Carcinoma (TCGA, Cell 2015)** *1105 samples*

Select Genomic Profiles:

☐ Mutations
☐ Putative copy-number alterations from GISTIC
☑ mRNA Expression data. Select one of the profiles below:
● mRNA Expression z-Scores (RNA Seq V2 RSEM)
○ mRNA Expression z-Scores (microarray)
Enter a z-score threshold ±: 2.0

Select Patient/Case Set: Tumor Samples with mRNA data (RNA Seq V2) (1100)

To build your own case set, try out our enhanced Study View.

Enter Gene Set: User-defined List

Enter HUGO Gene Symbols or Gene Aliases

Supplementary Figure S6: Datamining with primary search with default setting and search for expression only (RNA-seq).

Supplementary Table S1: lncRNAs used for primary search

See Supplementary File 1

Supplementary Table S1a: Primers used in this study

For detection	
LINC00657-RT-5.1	AAAGAGGTTGCCGACGTATG
LINC00657-RT-3.1	CAGGTCTTCCAGCTCCATGT
LINC00657-RT-5.2	GCAGGAGAATCGCTTGAACT
LINC00657-RT-3.2	ATTCCCAAATGCAACCACTC
For dual gRNA	
LINC00657-T1A	TTCCGGTCCGGCAGAGATCG
LINC00657-T2A	ACTCTATTCTACAAGCAACG
For donor vector	
LINC00657-right-Sal1-5.1	TCTTATCATGTCTGGTCGACTCCTTCATGCTTGGGCTCTG
LINC00657-right-Sal1-3.1	TTGATATCACCGGTGTCGACGCTGTGTGTCAGGCATTACG
LINC00657-left-Spe-5.1	CGACGGCCAGTGAAACTAGTCCCTGGCATAAGTCCCTATC
LINC00657-left-Spe-3.1	CCTGTACAGGTACCACTAGTGACTTGGCAGTTCTCTGCGC

Supplementary Table S2: Alterations of lncRNAs and their frequeny

See Supplementary File 2

Supplementary Table S3: Distribution of lncRNAs aroung 8q24

See Supplementary File 3

Supplementary Table S4: Cases with recurrence in red

See Supplementary File 4

Supplementary Table S5: LncRNAs associated with disease free survival

See Supplementary File 5

Supplementary Table S6: Alterations of lncRNAs associated with ER, PR and HER-2

See Supplementary File 6