

Use case 1: miRNA-target-protein analysis

a) Compare Normal/Tumor miRNA-target interactions:

1. User can select one or more miRNA
2. User can select one or more gene Target
3. User can select one or more TCGA tissue
4. User can select Normal, Tumor or Normal & Tumor

The screenshot shows the 'miRNA-target-protein analysis' interface. On the left, there are four numbered selection steps: 1. Select miRNA(s) (hsa-miR-150, hsa-miR-1182), 2. Select Target(s) (BTLA, TFDP2), 3. Select TCGA Tissue(s) (CESC - Cervical squamous cell carcinoma & endocervical adenocarcinoma, COAD - Colon adenocarcinoma), and 4. Select Tissue Type (Normal, Tumor, Normal & Tumor). The main table displays results for two miRNAs across two tissues. The table has columns for miRNA, Gene, and p-values for CESC (Normal and Tumor) and COAD (Normal and Tumor). The results are as follows:

miRNA	Gene	CESC NORMAL mirna/gene p-value	CESC TUMOR mirna/gene p-value	COAD NORMAL mirna/gene p-value	COAD TUMOR mirna/gene p-value
hsa-miR-1182	TFDP2	1	0.4233136	1	0.2136576
hsa-miR-150	BTLA	0.9494265	2.314461e-35	0.0006205503	5.843321e-34

Figure 1

b) Details for a specific tumor type:

1. User can select one or more miRNA
2. User can select one or more gene Target
3. User can select only one TCGA tissue
4. User can select to show all interaction or only interactions where protein expression value is given
5. User can click on the value in the last column (number of ceRNA competitors) in order to visualize all ceRNA interactions that involve the selected miRNA and gene. (see use case 2a)

The screenshot shows the 'miRNA-target-protein analysis' interface with detailed results for BRCA tissue. The left sidebar shows: 1. Select miRNA(s) (hsa-miR-150), 2. Select Target(s) (empty), 3. Select TCGA Tissue (BRCA - Breast invasive carcinoma), and 4. Select what kind of miRNA-target to show (Show all interactions). The main table displays results for hsa-miR-150 across various genes in BRCA tissue. The table has columns for miRNA, Gene, BRCA protein antigen, BRCA mirna/gene correlation, BRCA mirna/gene p-value, BRCA gene/protein correlation, BRCA gene/protein p-value, Interaction Type, and Number of ceRNA interactions. The results are as follows:

miRNA	Gene	BRCA protein antigen	BRCA mirna/gene correlation	BRCA mirna/gene p-value	BRCA gene/protein correlation	BRCA gene/protein p-value	Interaction Type	Number of ceRNA interactions
hsa-miR-150	A1CF		+	0.5065593			No Interaction*	0
hsa-miR-150	ABCB7		-	0.4074191			Degradation	77
hsa-miR-150	ABCG8		-	0.6896325			Degradation	33
hsa-miR-150	ABHD15		+	0.6244975			No Interaction*	0
hsa-miR-150	ABHD18		+	0.01335916			No Interaction*	0
hsa-miR-150	ABHD2		-	0.243445			Degradation	78
hsa-miR-150	ACOT9		+	0.01059544			No Interaction*	0

Figure 2

Use case 2: ceRNA interactions analysis

a) Compare among different tissues:

1. User can select one or more ceRNA (mRNA)
2. User can select one or more ceRNA (mRNA, lncRNA, pseudogene)
3. User can select one or more TCGA tissue
4. User can click on the p-value of a ceRNA interaction in order to visualize the list of shared miRNA (see use case 2b)

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Show 10 entries Search:

1. Select ceRNA(s) A (mRNA)
AGO2

2. Select ceRNA(s) B (mRNA/lncRNA/pseudogene)

3. Select TCGA Tissue(s)
CESC - Cervical squamous cell carcinoma & endocervical adenocarcinoma
BLCA - Bladder urothelial carcinoma

Show/Update Results

ceRNA A	ceRNA B	ceRNA B Biotype	BLCA ceRNA p-value	CESC ceRNA p-value
All	All	All	All	All
AGO2	C1orf112	protein_coding		0.40108
AGO2	NFYA	protein_coding		0.40842
AGO2	M6PR	protein_coding	0.4829	0.45297
AGO2	CYP26B1	protein_coding	0.49897	0.24009
AGO2	CDC27	protein_coding	0.49259	0.24349
AGO2	MYCBP2	protein_coding	0.3241	
AGO2	PHTF2	protein_coding		0.3705

Figure 3

b) Details for a specific tumor type

1. User can select one or more ceRNA (mRNA)
2. User can select one or more ceRNA (mRNA, lncRNA, pseudogene)
3. User can select only one TCGA tissue
4. User can click on the value of last column ("number of tissue having this ceRNA") in order to visualize the same ceRNA interaction in other tissues (see use case 2a)
5. User can click on a miRNA of the "list of miRNA" in order to visualize all the miRNA target and interaction type for the selected miRNA (see use case 1b)

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Show 10 entries Search:

1. Select ceRNA(s) A (mRNA)
CD44

2. Select ceRNA(s) B (mRNA/lncRNA/pseudogene)

3. Select TCGA Tissue
BRCA - Breast invasive carcinoma

Show/Update Results

ceRNA A	ceRNA B	ceRNA B Biotype	BRCA ceRNA p-value	BRCA ceRNA mscor	Number of shared miRNAs	List of shared miRNAs	Number of tissues with ceRNA interaction
All	All	All	All	All	All	All	All
CD44	AC016831.7	lincRNA	0.4762	0.00102374651715176	2	hsa-miR-192 / hsa-miR-373	2
CD44	ACVR2B	protein_coding	0.4947	0.0000653792891735228	1	hsa-miR-192	2
CD44	ADRBK2	protein_coding	0.47573	0.000412211840947252	1	hsa-miR-192	3
CD44	AFF4	protein_coding	0.48161	0.000292413015386975	1	hsa-miR-211	3
CD44	AGAP1	protein_coding	0.41117	0.00429092234167147	2	hsa-miR-143 / hsa-miR-211	2

Figure 4