

miRNA Expression and Integration with Gene Expression

This tutorial outlines how to analyze miRNA expression data in Partek Genomics Suite and outlines how miRNA expression data can be integrated with mRNA expression data from gene expression microarrays.

This tutorial illustrates how to:

- [Analyze differentially expressed miRNAs](#)
- [Integrate miRNA and Gene Expression data](#)

*Note: the workflow described below is enabled in Partek Genomics Suite version 7.0 software. Please fill out the form on [Our support page](#) to request this version or use the **Help > Check for Updates** command to check whether you have the latest released version. The screenshots shown within this tutorial may vary across platforms and across different versions of Partek Genomics Suite.*

Description of the data set

The data set for this tutorial includes miRNA from 3 human brain samples and 3 heart samples quantified using the Affymetrix GeneChip miRNA 1.0 array. The same sample set was also processed on GeneChip Human Gene 1.0 ST arrays for mRNA expression.

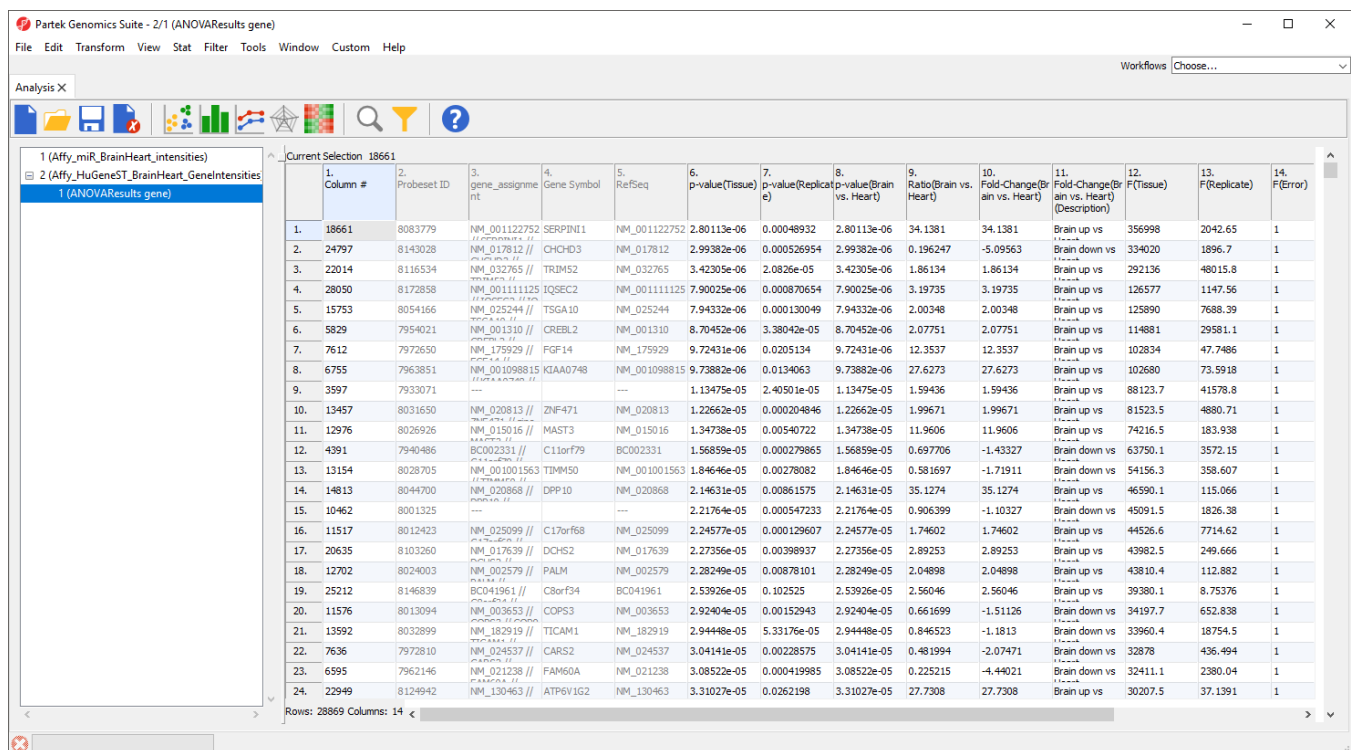
For this tutorial, the gene expression and miRNA expression studies have been analyzed and stored in Partek Genomics Suite project (ppj) format as *miRNA AmRNA integration*. The project contains two Partek format files: *Affy_miR_BrainHeart_intensities.fmt* with the miRNA data and *Affy_HuGeneST_BrainHeart_GeneIntensities.fmt* with the analyzed mRNA data. There is also an ANOVA results spreadsheet open as a child spreadsheet of *Affy_HuGeneST_BrainHeart_GeneIntensities.fmt*.

- Download the [miRNA Expression and Integration with Gene Expression data set](#) and save it in an easily accessible location on your computer

We can now open the project in Partek Genomics Suite.

- Select **File**
- Select **Import**
- Select **Ziped Project...**
- Select the **miRNA_tutorial_data.zip** zipped folder

The project files will open in the *Analysis* tab (Figure 1).



The screenshot displays the Partek Genomics Suite interface, specifically the 'Analysis' tab. The main window shows a table with 14 columns and 28669 rows. The columns are labeled as follows: 1. Column #, 2. Probeset ID, 3. gene_assignment, 4. Gene Symbol, 5. RefSeq, 6. p-value(Tissue), 7. p-value(Replicate), 8. p-value(Brain vs. Heart), 9. Ratio(Brain vs. Heart), 10. Fold-Change(Brain vs. Heart), 11. Fold-Change(Brain vs. Heart) (Description), 12. F(Tissue), 13. F(Replicate), and 14. F(Error). The table contains data for various genes, including SERPINE1, CHCHD3, TRIM52, IQSEC2, TSGA10, CREBL2, FGF14, KIAA0748, ZNF471, MAST3, C11orf79, TBMH50, DPP10, C11orf68, DCHS2, PALM, C8orf34, COPS3, TICAM1, CARIS2, FAM60A, and ATP6V1G2. The status bar at the bottom indicates 'Rows: 28669 Columns: 14'.

1. Column #	2. Probeset ID	3. gene_assignment	4. Gene Symbol	5. RefSeq	6. p-value(Tissue)	7. p-value(Replicate)	8. p-value(Brain vs. Heart)	9. Ratio(Brain vs. Heart)	10. Fold-Change(Brain vs. Heart)	11. Fold-Change(Brain vs. Heart) (Description)	12. F(Tissue)	13. F(Replicate)	14. F(Error)
1.	18661	8083779	NM_001122752	SERPINE1	NM_001122752	2.80113e-06	0.00048932	2.80113e-06	34.1381	Brain up vs	356998	2042.65	1
2.	24797	8143028	NM_017812	CHCHD3	NM_017812	2.99382e-06	0.000526954	2.99382e-06	0.196247	Brain down vs	334020	1896.7	1
3.	22014	8116534	NM_032765	TRIM52	NM_032765	3.42305e-06	2.0826e-05	3.42305e-06	1.86134	Brain up vs	292136	48015.8	1
4.	28050	8172858	NM_001111125	IQSEC2	NM_001111125	7.90025e-06	0.000870654	7.90025e-06	3.19735	Brain up vs	126577	1147.56	1
5.	15753	8054166	NM_025244	TSGA10	NM_025244	7.94332e-06	0.000130049	7.94332e-06	2.00348	Brain up vs	125890	7688.39	1
6.	5829	7954021	NM_001310	CREBL2	NM_001310	8.70452e-06	3.38042e-05	8.70452e-06	2.07751	Brain up vs	114881	29581.1	1
7.	7612	7972650	NM_175929	FGF14	NM_175929	9.72431e-06	0.0205134	9.72431e-06	12.3537	Brain up vs	102834	47.7486	1
8.	6755	7963851	NM_001098815	KIAA0748	NM_001098815	9.73882e-06	0.0134063	9.73882e-06	27.6273	Brain up vs	102680	73.5918	1
9.	3597	7933071	---	---	---	1.13475e-05	2.40501e-05	1.13475e-05	1.59436	Brain up vs	88123.7	41578.8	1
10.	13457	8031650	NM_020813	ZNF471	NM_020813	1.22662e-05	0.000204846	1.22662e-05	1.99671	Brain up vs	81523.5	4880.71	1
11.	12976	8026926	NM_015016	MAST3	NM_015016	1.34738e-05	0.00540722	1.34738e-05	11.9606	Brain up vs	74216.5	183.938	1
12.	4391	7940486	BC002331	C11orf79	BC002331	1.56859e-05	0.000279865	1.56859e-05	0.697706	Brain down vs	63750.1	3572.15	1
13.	13154	8028705	NM_001001563	TBMH50	NM_001001563	1.84646e-05	0.00278082	1.84646e-05	0.581697	Brain down vs	54156.3	358.607	1
14.	14813	8044700	NM_020868	DPP10	NM_020868	2.14631e-05	0.00861575	2.14631e-05	35.1274	Brain up vs	46590.1	115.066	1
15.	10462	8001325	---	---	---	2.21764e-05	0.000547233	2.21764e-05	0.906399	Brain down vs	45091.5	1826.38	1
16.	11517	8012423	NM_025099	C11orf68	NM_025099	2.24577e-05	0.000129607	2.24577e-05	1.74602	Brain up vs	44526.6	7714.62	1
17.	20635	8103260	NM_017639	DCHS2	NM_017639	2.27356e-05	0.00398937	2.27356e-05	2.89253	Brain up vs	43982.5	249.666	1
18.	12702	8024003	NM_002579	PALM	NM_002579	2.28249e-05	0.00878101	2.28249e-05	2.04898	Brain up vs	43810.4	112.882	1
19.	25212	8146839	BC041961	C8orf34	BC041961	2.53926e-05	0.102525	2.53926e-05	2.56046	Brain up vs	39380.1	8.75376	1
20.	11576	8013094	NM_003653	COPS3	NM_003653	2.92404e-05	0.00152943	2.92404e-05	0.661699	Brain down vs	34197.7	652.838	1
21.	13592	8032899	NM_182919	TICAM1	NM_182919	2.94448e-05	5.33176e-05	2.94448e-05	0.846523	Brain down vs	33960.4	18754.5	1
22.	7636	7972810	NM_024537	CARIS2	NM_024537	3.04141e-05	0.00228575	3.04141e-05	0.481994	Brain down vs	32878	436.494	1
23.	6595	7962146	NM_021238	FAM60A	NM_021238	3.08522e-05	0.000419985	3.08522e-05	0.225215	Brain down vs	32411.1	2380.04	1
24.	22949	8124942	NM_130463	ATP6V1G2	NM_130463	3.31027e-05	0.0262198	3.31027e-05	27.7308	Brain up vs	30207.5	37.1391	1

Figure 1. The miRNA tutorial data set

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating:  Results:  36 rates