

Additional File 4. Chi-Squared Enrichment Analysis Methodology

- 1) Construct a contingency table of genes for each tissue type
- 2) Conduct a chi-square test using the `chisq.test()` function in R
- 3) Extract the standardized residuals(`stdres`) whereby:

> standardized residuals, $(\text{observed} - \text{expected}) / \sqrt{V}$, where V is the
> residual cell variance (Agresti, 2007, section 2.4.5 for the case where
> x is a matrix, $n * p * (1 - p)$ otherwise).

Breast Tissue Essential Gene Enrichment Analysis
Contingency Table

	Hypervariable	Hypovariable	NV	
Essential	165	103	2095	2363
Non-Essential	1283	854	37452	39589
	1448	957	39547	41952

Chi-Squared Test Summary

X-Squared	Degrees of Freedom	P-Value
146.198632787005	2	1.79213309275818e-32

Standardized Residuals

	Hypervariable	Hypovariable	NV
Essential	9.679	6.964	-12.073
Non-Essential	-9.679	-6.964	12.073

Cerebellum Tissue Essential Gene Enrichment Analysis
Contingency Table

	Hypervariable	Hypovariable	NV	
Essential	160	76	2128	2364
Non-Essential	1480	761	37357	39598
	1640	837	39485	41962

Chi-Squared Test Summary

X-Squared	Degrees of Freedom	P-Value
75.557486782899	2	3.91651876644079e-17

Standardized Residuals

	Hypervariable	Hypovariable	NV
Essential	7.386	4.368	-8.665
Non-Essential	-7.386	-4.368	8.665

Frontal Cortex Tissue Essential Gene Enrichment Analysis
Contingency Table

	Hypervariable	Hypovariable	NV	
Essential	181	121	2062	2364
Non-Essential	1579	1133	36886	39598
	1760	1254	38948	41962

Chi-Squared Test Summary

X-Squared	Degrees of Freedom	P-Value
118.069557050356	2	2.29890723006322e-26

Standardized Residuals

	Hypervariable	Hypovariable	NV
Essential	8.645	6.261	-10.840
Non-Essential	-8.645	-6.261	10.840

Cerebellum Tissue Methylation Enrichment Analysis
Contingency Table

	High Methylation	Low Methylation	Medium Methylation	
Hypervariable	183	626	186	995
Hypovariable	38	472	32	542
NV	2377	6015	1394	9786
	2598	7113	1612	11323

Chi-Squared Test Summary

X-Squared	Degrees of Freedom	P-Value
170.654433820031	4	7.5684732413822e-36

Standardized Residuals

	High Methylation	Low Methylation	Medium Methylation
Hypervariable	-3.57596	0.06529	4.21279
Hypovariable	-9.04103	11.97954	-5.68945
NV	8.59096	-7.52068	0.06401

Frontal Cortex Tissue Methylation Enrichment Analysis
Contingency Table

	High Methylation	Low Methylation	Medium Methylation	
Hypervariable	178	627	276	1081
Hypovariable	60	662	72	794
NV	2397	5355	1762	9514
	2635	6644	2110	11389

Chi-Squared Test Summary

X-Squared	Degrees of Freedom	P-Value
280.693146499535	4	1.57958487900589e-59

Standardized Residuals

	High Methylation	Low Methylation	Medium Methylation
Hypervariable	-5.46631	-0.23494	6.23142
Hypovariable	-10.79327	14.83749	-7.11254
NV	11.73222	-10.00349	-0.04067