

# Results File Format

**Column 1:** ID for the molecule measured (transcript IDs in this example). Column name must be 'Molecule'. This is REQUIRED.

**Column 2:** Other OPTIONAL Identifiers.

**Optional Columns:** Various analysis results. Columns are flexible to the analysis conducted.

**Pvalue:** p-value of the test. Column name must be 'Pvalue'.  
**PvalueAdj:** adjusted p-value for the test. Column name must be 'PvalueAdj'.

Molecule	Gene	NCases	NControls	baseMean	log2FoldChange	lfcSE	stat	Pvalue	PvalueAdj
NM_000014	A2M	100	100	1889.680119	-0.46319172	0.52404	-0.4848	0.80035	0.984757
NM_000015	NAT2	98	99	3490.874312	3.979896417	0.82957	7.2215	3.43E-05	0.000385
NM_000016	ACADM	99	98	1207.657311	-2.11547061	0.90685	-2.8381	0.07604	0.477411
NM_000017	ACADS	95	94	128.6574772	-5.80762897	0.82892	-7.4583	2.06E-10	2.23E-09
NM_000018	ACADVL	100	100	4203.536292	-0.97538594	0.51438	-0.8381	0.83524	0.874757

Data starts on line 2

Each column contains data for 1 molecule. Missing values are allowed ('NA' or leave empty).

**Column 3 and 4:** Number of cases ('NCases') and controls ('NControls') for each molecule. Use these columns for analyses where this varies by molecule. OPTIONAL

**Note:** The results file is formatted as a tab-separated file.