

List id.	Reference	List size	Data analysis method(s)
<i>Schizophrenia</i>			
Arion	Arion et al. [1]	110 genes	HM($p < 0.05$, $ FC > 0.263$)
Barnes	Barnes et al. [2]	1998 probe sets	DQC, t -test($p < 0.05$)
Glatt	Glatt et al. [3]	177 probe sets	t -test($p < 0.05$)
Maycox	Maycox et al. [4]	1846 probe sets	DQC, t -test($p < 0.05$)
Mistry	Mistry et al. [5]	136 probe sets	MTA, CFC, t -test(FDR < 0.1)
PS	Pérez-Santiago et al. [6]	160 probe sets	MTA, CFC, t -test(80% CF NFP < 10)
<i>Bipolar disorder</i>			
Nakatani	Nakatani et al. [7]	108 genes	HM($p < 0.05$, $ FC > 1.5$)
Ryan	Ryan et al. [8]	81 genes	DQC, ANCOVA($p < 0.05$)
Seifu_A	Seifuddin et al. [9]	171 genes	MTA, CFC, HM($p < 0.05$, $ FC > 1.07$)
Seifu_F	Seifuddin et al. [9]	141 genes	MTA, CFC, HM($p < 0.05$, $ FC > 1.07$)
Seifu_H	Seifuddin et al. [9]	100 genes	MTA, CFC, HM($p < 0.05$, $ FC > 1.07$)
<i>Parkinson's disease</i>			
Simunovic	Simunovic et al. [10]	1044 probe sets	SAM, t -test, ANOVA
Zhang_B	Zhang et al. [11]	100 probe sets	HM($p < 0.05$, FC > 1.58 or < -2.09)
Zhang_P	Zhang et al. [11]	100 probe sets	HM($p < 0.05$, FC > 1.33 or < -1.61)
Zhang_S	Zhang et al. [11]	100 probe sets	HM($p < 0.05$, FC > 1.50 or < -1.95)

Abbreviations: CFC, confounding factor control; CF, confidence; DQC, data quality control; FC, fold-change; MTA, meta-analysis; NFP, number of false positives.

References

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