

COMT Expression Correlations in Four Brain Areas

James L. Dannemiller
Rice University

April 29, 2018

April 29, 2018

Gene Network

Spring, 2018

COMT catalyzes degradation of catecholamines including dopamine, norepinephrine and epinephrine.

(pre post recovery missing stats v1.Rnw): Program to generate tables pre- and post- preprocessing of the data on number of rows with missing observations on various variables. Additionally, some chromosomes were initially listed as 'Un' for unknown.

Table 1: Total numbers of probes (Row 1), original number of probes with chromosome names identified (Row 2), number of probes with chromosome names identified after processing (Row 3).

	prefrontal	cerebellum	temporal	pons
Number of probes	20000	20000	20000	20000
Original	17945	17953	17957	17973
Processed	19921	19922	19922	19928

Table 2: Total numbers of probes (Row 1), original number of probes with known transcription start positions (Row 2), number of probes with known transcription start positions after processing (Row 3).

	prefrontal	cerebellum	temporal	pons
Number of probes	20000	20000	20000	20000
Original	17945	17953	17957	17973
Processed	19917	19917	19919	19923

Table 3: Total numbers of probes (Row 1), original number of probes with LOCxx gene symbols (Row 2), number of probes with LOCxx gene symbols after processing (Row 3).

	prefrontal	cerebellum	temporal	pons
Number of probes	20000	20000	20000	20000
Original	452	461	461	462
Processed	147	156	145	144

Table 4: Total numbers of probes (Row 1), original number of probes with LOCxx gene symbols (Row 2), number of probes with LOCxx gene symbols after processing (Row 3).

Measure	prefrontal	cerebellum	temporal	pons
Number of probes	20000	20000	20000	20000
Original	452	461	461	462
Processed	147	156	145	144