

Interpretation for ALL dataset SRP056295 (Pabst, Blood, 2016)

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We look forward to make the quantitative summary for some critical values and parameters, which are summarized as in the following table

A summarized report about preprocessing process before we start to study the impact of classification methods on RNAseq count data.

recountID	No.runs	No.features	No.samples after prerocessing	No.genes after preprocessing	unique samples	pheno Table dimensions	No. of classes
"SRP042620"	167	58037	162	55506	167	162 X 22	5
"SRP057196"	461	58037	461	16941	461	461 X 26	9
"SRP003611"	52	58037	0	51239	8	0 X 17	
"SRP061240"	384	58037	186	7056	192	186 X 19	3
"SRP062966"	117	58037	117	45247	117	117 X 25	2
"SRP066834"	729	58037	729	15741	729	729 X 23	3
"SRP056295"	520	58037	259	43780	263	259 X 17	2
"SRP039694"	15	58037	0	46858	0	0 X 25	0