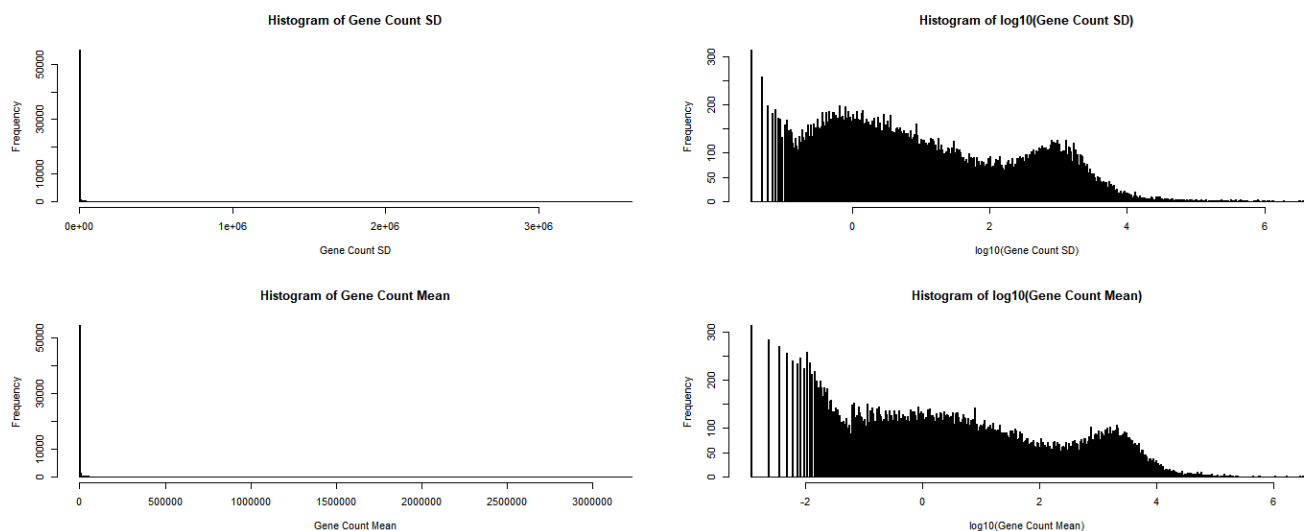


# Genome-wide differential expression in multiple myeloma patients with autologous stem cell transplant

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## Supplemental Material



**Figure S 1. Gene count statistics from filtered data.** Histograms depict the abnormal distribution of gene counts after filtering, where a minority of genes have a vastly higher count mean compared to the rest of the data.

Gene ID	Count Mean
ENSG00000211592	3227241
ENSG00000211896	2866435
ENSG00000211895	1720231
ENSG00000132465	1068318
ENSG00000243466	576198
ENSG00000166710	556507
ENSG00000156508	451604
ENSG00000211662	246893
ENSG00000239951	230213
ENSG00000241351	229240
Average of All Genes	1057

**Table S 1. Highest gene count means.** Average of count genes for all genes also included for comparison.

Gene ID	Count SD
ENSG00000211895	3608104
ENSG00000211896	3252802
ENSG00000211592	3129906
ENSG00000243466	1863934
ENSG00000211662	1319491
ENSG00000132465	1274457
ENSG00000211668	1183398
ENSG00000211660	1092188
ENSG00000211598	1008740
ENSG00000211897	1001512
Average of All Genes	1408

**Table S 2. Highest gene count standard deviations.** Average of standard deviations for all genes also included for comparison.