Supplement 3.

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Figure 1. EV removes dependence between variability and overall mean expression. The EV measures is unbiased with respect to overall mean expression. We compare the distribution of EV conditional on mean expression for each tissue to the distribution of the coefficient of variation conditional on mean expression. The coefficient of variation shows high upward bias towards genes with low expression.



adipose_tissue



adrenal_cortex



airway_epithelial_cells 2 0 2 4 ထို | 5 10 15 20 0 mean expression ן. ק coef. of variation 0. 0.5



astrocytes





breast









breast_stroma



cd31+_cells



cd49a+_cells



cd4+_t_cells



cerebellum



cervix





chorion_villus_cells



colon



endometrium



fetal_cartilage



gingival_epithelium





hippocampus



kidney





myometrium





omental_adipose_tissue



ovary





pbmc



penis





pituitary





placenta



prostate_gland



rectum





rectum_mucosa





salivary_gland



sigmoid_colon



sinus_mucosa





skeletal_muscle





skin





stomach



thyroid





trigeminal_ganglia



u251_cells





urethra



vulva







Figure 2. EV is independent of the number of experiments per tissue in dataset. We show the distribution of EV per tissue and indicate the number of GEO experiments used to compile the set of microarrays for each tissue. The EV distribution is very similar across tissues regardless of the number of GEO experiments included in the dataset.