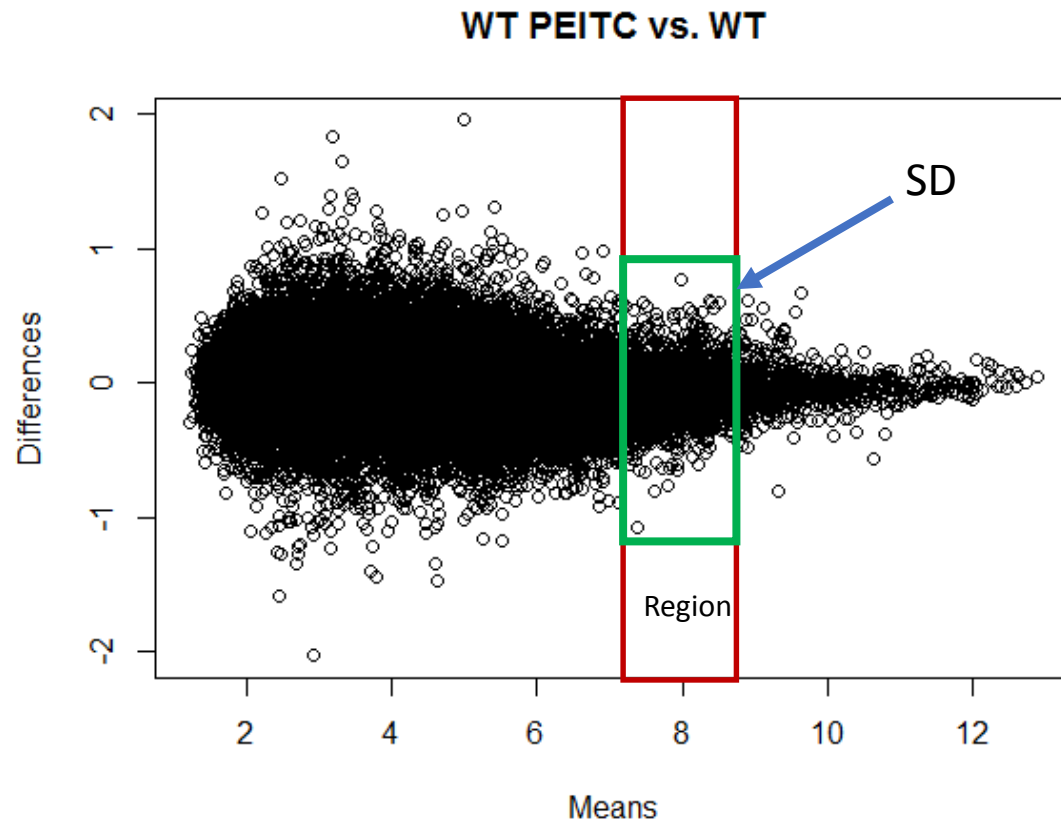


Regularization using difference vs. mean



For each gene and some small epsilon (e.g. = 0.1),
define a region on X-axis as:

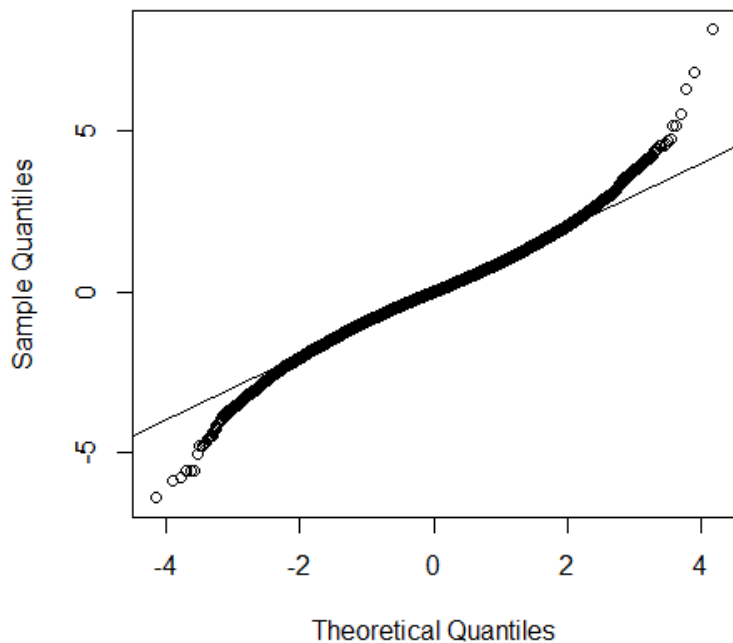
Region = **mean** of the 2 treatments \pm epsilon

Estimate SD of **differences** for **all data** inside that region

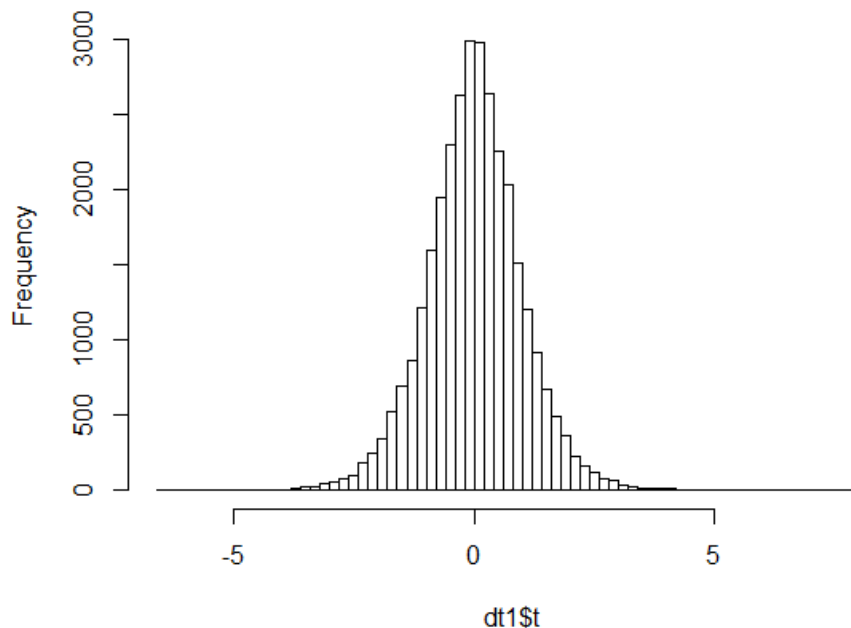
Divide each difference by the estimate of standard
deviation (SD) obtained as above to get test statistics (t)

Assuming the test statistic is normally distributed
(CHECK!), calculate p-values

Normal Q-Q Plot



Histogram of dt1\$t



Note that genes with higher means have smaller SD (red), and the opposite (green)

Need to work out correct distribution for the test statistics t (lighter tails than normal)

PROBEID	ENTREZID	SYMBOL	GENENAME	WT_PEITC	WT	Diff(PEITC vs. WT)	Mean(WT PEITC, WT)	sd	t	p
16827764	16	AARS	alanyl-tRNA synthetase	8.1256	8.5622	-0.4366	8.3439	0.1524	-2.7413	0.0061
17121606	81926	ABHD17A_2	abhydrolase domain containing 17A	6.9121	7.4355	-0.5235	7.1738	0.2098	-2.3831	0.0172
16952244	30	ACAA1	acetyl-CoA acyltransferase 1	5.4676	4.8771	0.5905	5.1723	0.2737	2.1221	0.0338
16712035	414149	ACBD7	acyl-CoA binding domain containing 7	3.9408	5.2832	-1.3424	4.6120	0.2682	-4.8133	0.0000
16867648	125981	ACER1	alkaline ceramidase 1	3.8314	3.2007	0.6307	3.5160	0.2866	2.1631	0.0305
16786248	641371	ACOT1	acyl-CoA thioesterase 1	3.5997	2.5222	1.0774	3.0610	0.2953	3.5651	0.0004
16931838	49	ACR	acrosin	4.3923	3.7247	0.6676	4.0585	0.2972	2.2076	0.0273
16982047	2180	ACSL1	acyl-CoA synthetase long chain family member 1	6.8194	7.3782	-0.5588	7.0988	0.2006	-2.6637	0.0077
16754729	79611	ACSS3	acyl-CoA synthetase short chain family member 3	3.6325	4.3010	-0.6685	3.9668	0.2930	-2.1758	0.0296
16948278	86	ACTL6A	actin like 6A	7.6968	8.0884	-0.3915	7.8926	0.1841	-2.0262	0.0427