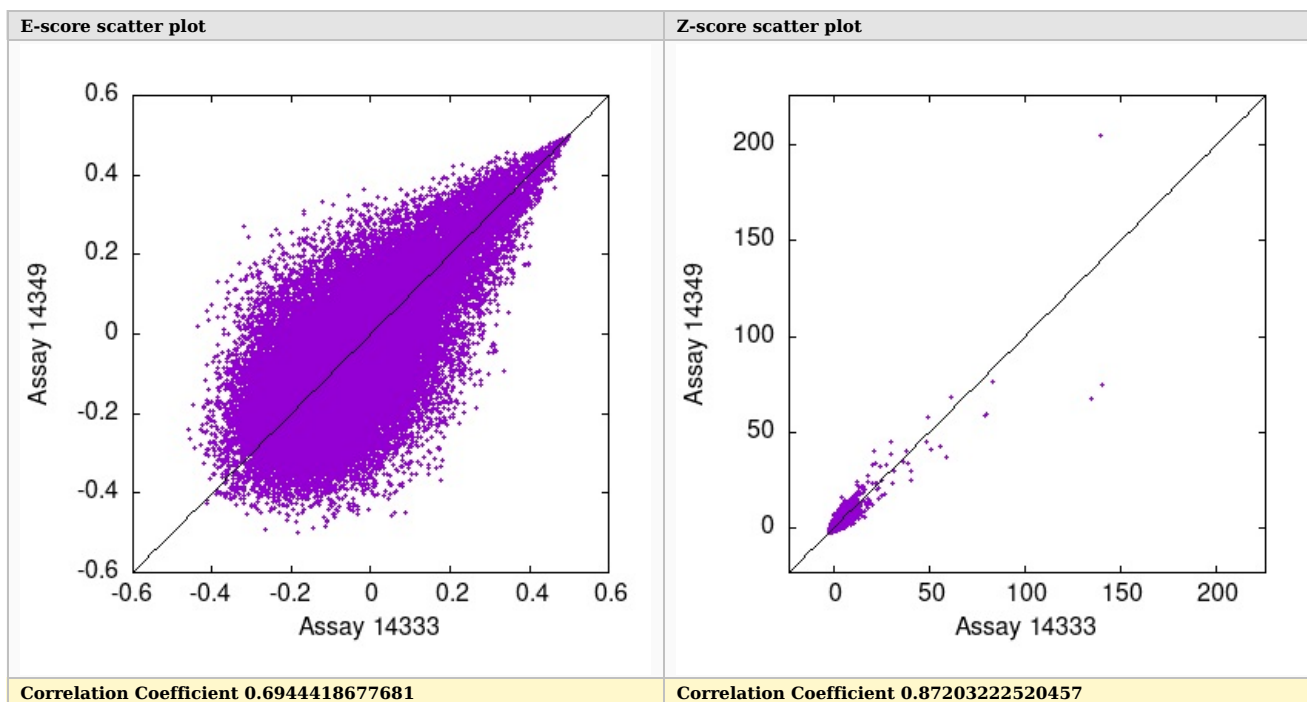


## QC report



Correlation Coefficient 0.6944418677681

Correlation Coefficient 0.87203222520457

### Top scoring motifs for Assay 14333

Protein ID: pTH15532.1 Gene: LEF1 Domain: HMG\_box Flag: Pass matched\_pair Array: 1M-ME

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CTTTGATC	0.49813	-GATCAAG-	AGATCAAA	140.57156	AGATCAAA--
AGATCAAA	0.49809	AGATCAAA--	CTTTGATC	139.90488	-GATCAAG-
CATCAAG	0.49723	-CATCAAG-	CATCAAG	134.65813	-CATCAAG-
CTTCAAG	0.49585	-CTTCAAG-	CTTCAAG	82.95967	-CTTCAAG-
ATCAAGA	0.49561	--ATCAAGA	ATCAAGA	80.25107	--ATCAAGA
ACATCAAA	0.49550	ACATCAAA--	ATCAAGC	79.05008	--ATCAAGC
ACTTCAAA	0.49478	ACTTCAAA--	ACATCAAA	61.43737	ACATCAAA--
ATCAAGC	0.49476	--ATCAAGC	ACTTCAAA	59.17107	ACTTCAAA--
ATCAAGG	0.49335	--ATCAAGG	GATCAAAC	55.58047	-GATCAAC-
GATCAAC	0.49182	-GATCAAC-	ATCAACG	51.16477	--ATCAACG

### Top scoring motifs for Assay 14349

Protein ID: pTH15532.2 Gene: LEF1 Domain: HMG\_box Flag: Pass matched\_pair Array: 1M-HK

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CTTTGATC	0.49909	-CTTTGATC-	CTTTGATC	205.02798	-CTTTGATC-
ACATCAAA	0.49597	--TTTGATGT	CTTCAAG	76.15573	-CTTTGAAG-
AGATCAAA	0.49558	--TTTGATCT	AGATCAAA	74.56111	--TTTGATCT
CATCAAG	0.49533	-CTTTGATG-	ACATCAAA	68.01338	--TTTGATGT
ATCAAGA	0.49512	TCTTTGAT--	CATCAAG	67.32372	-CTTTGATG-
ATCAAGG	0.49416	CCTTTGAT--	ATCAAGA	59.39198	TCTTTGAT--
CTTCAAG	0.49390	-CTTTGAAG-	ATCAAGC	59.06268	GCTTTGAT--
ATCAAGC	0.49346	GCTTTGAT--	ATCAAGG	58.23706	CCTTTGAT--
TGATCAAA	0.49274	--TTTGATCA	CTTTGAA	44.71681	CCTTTGAA--
ACTTTGAT	0.49225	ACTTTGAT--	TGATCAAA	44.62768	--TTTGATCA