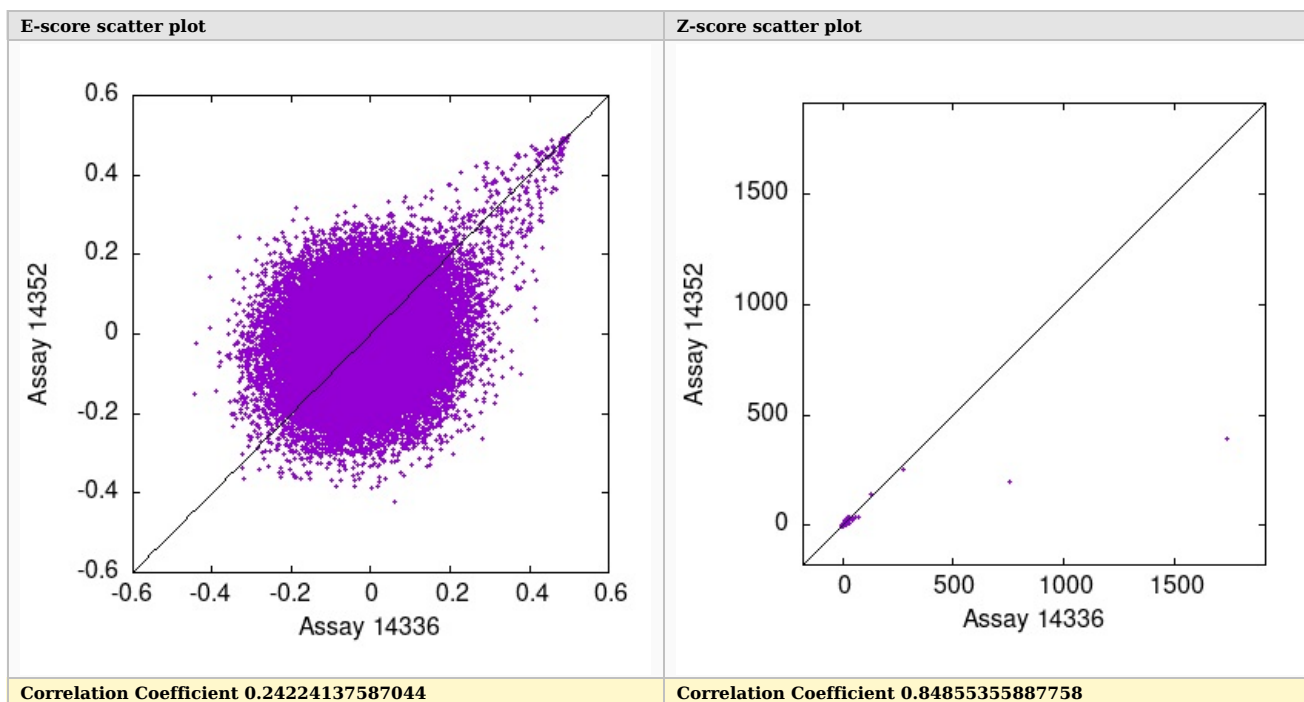


## QC report



## Top scoring motifs for Assay 14336

Protein ID: pTH15535.1 Gene: GABPA Domain: Ets 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
ACTTCCGG	0.49965	-ACTTCCGG--	ACTTCCGG	1,733.41939	-ACTTCCGG--
ACCGGAAG	0.49926	--CTTCCGGT-	ACCGGAAG	755.24893	--CTTCCGGT-
ACCGGAAA	0.49824	--TTTCCGGT-	ACCGGAAA	276.32107	--TTTCCGGT-
ATTTCCGG	0.49673	-ATTTCCGG--	ATTTCCGG	129.02993	-ATTTCCGG--
AACCGGAA	0.49591	---TTCCGGTT	AACTTCCG	72.34655	AACTTCCG---
CGGAAGTC	0.49555	GACTTCCG--	CCGGAAC	58.98398	-GTTTCCGG--
AACTTCCG	0.49511	AACTTCCG--	CCGGAAGC	58.75720	-GCTTCCGG--
CGGAAGC	0.49440	-GCTTCCGG--	CGGAAGTC	49.36761	GACTTCCG---
CGGAAAC	0.49426	-GTTTCCGG--	ACTTCCCG	48.22882	-ACTTCCCG--
ACTTCCGC	0.49405	-ACTTCCGC--	AACCGGAA	44.86769	---TTCCGGTT

## Top scoring motifs for Assay 14352

Protein ID: pTH15535.2 Gene: GABPA Domain: Ets 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
ACTTCCGG	0.49934	-ACTTCCGG--	ACTTCCGG	390.75416	-ACTTCCGG--
ACCGGAAG	0.49855	--CTTCCGGT-	ACCGGAAA	255.52405	--TTTCCGGT-
ACCGGAAA	0.49839	--TTTCCGGT-	ACCGGAAG	201.17996	--CTTCCGGT-
ATTTCCGG	0.49707	-ATTTCCGG--	ATTTCCGG	140.25732	-ATTTCCGG--
CCGGAAC	0.49506	-GTTTCCGG--	CCGGAAC	39.49614	-GTTTCCGG--
CGGAAGTC	0.49429	GACTTCCG--	CCGGAAGC	39.42211	-GCTTCCGG--
AACTTCCG	0.49382	AACTTCCG--	CTTCCGGC	39.24633	--CTTCCGGC
CCGGAAGC	0.49365	-GCTTCCGG--	AACTTCCG	38.14664	AACTTCCG--
CACTTCCG	0.49336	CACTTCCG--	CGGAAGTA	37.92895	TACTTCCG--
ACTTCCGC	0.49317	-ACTTCCGC--	CGGAAGTC	32.72673	GACTTCCG--