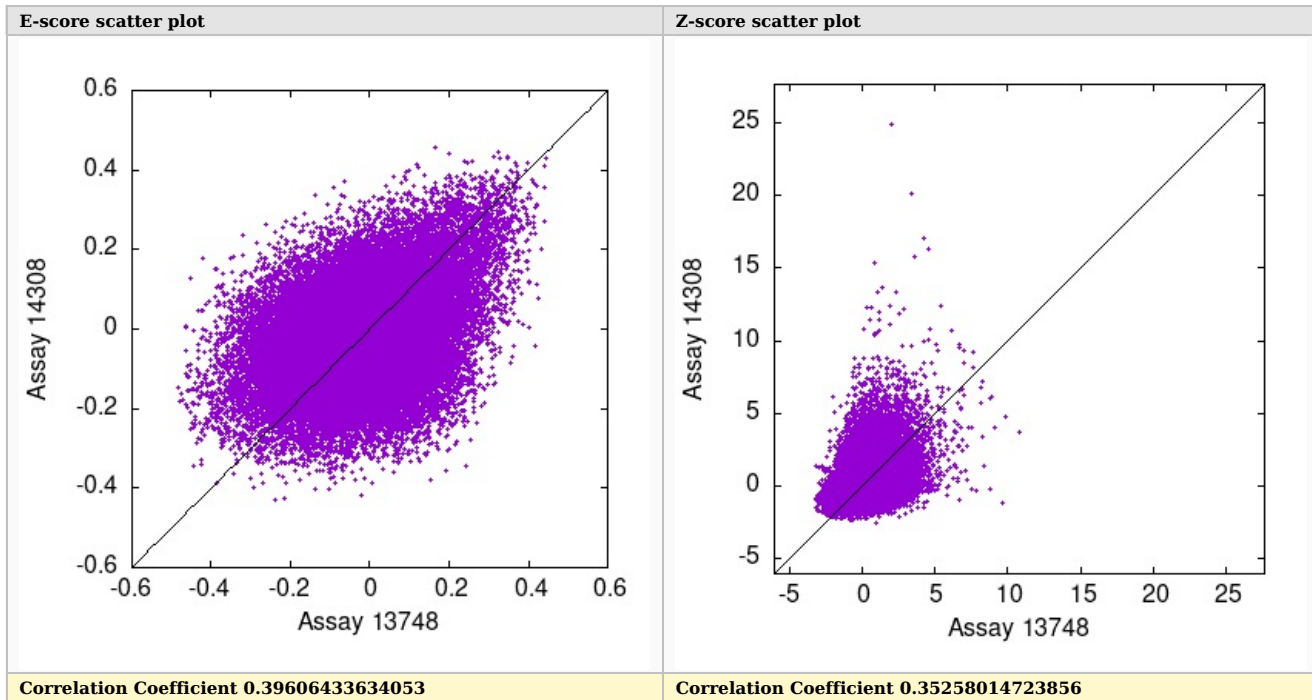




## QC report





### Top scoring motifs for Assay 13748

Protein ID: pTH14319.2 Gene: PURB.FL Domain: Unknown Flag: Unsure Array: 1M-HK

#### 8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ACCCACCA	0.44384	--ACCCACCA
AACCCACA	0.44165	--AACCCACA-
CAACCCAC	0.44001	-CAACCCAC--
AACCCACC	0.43994	--AACCCACC-
AAACCGAC	0.43176	-AAACCGAC--
ACAACCCA	0.42523	ACAACCCA--
ACCCTCAA	0.42291	--ACCCTCAA
GACCGACA	0.42050	--GACCGACA-
GACCAACC	0.41992	--GACCAACC-
ACCCACTA	0.41951	---ACCCACTA



#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
CAACCCAC	10.81382	-CAACCCAC--
ACCAACAT	9.84610	---ACCAACAT
ACCAACCT	9.59111	---ACCAACCT
AAACCGAC	9.07453	-AAACCGAC--
ATTGTTGG	8.93709	-CCAACAAT--
TACCAACA	8.82472	--TACCAACA-
AATCCACC	8.77324	-AATCCACC--
CCAACCGA	8.36612	CCAACCGA---
CAACCAAC	8.26340	-CAACCAAC--
ACCCACTA	8.23112	---ACCCACTA



### Top scoring motifs for Assay 14308

Protein ID: pTH14319.3 Gene: PURB.FL Domain: Unknown Flag: Pass\_matched\_pair Array: 1M-ME

#### 8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GTGGGTGA	0.45685	--GTGGGTGA
AGTGGGTG	0.44434	--AGTGGGTG-
GTGGGTAA	0.44008	--GTGGGTAA
GGTGGGAA	0.43513	-GGTGGGAA-
CACCCACA	0.43287	-TGTGGGTG-
ACACCCAC	0.42911	--GTGGGTGT
ACCCACCA	0.42782	TGGTGGGT--
AGGTGGGA	0.42775	AGGTGGGA--
AGCCCAAC	0.42102	-GGTGGGCT-
GAGGGTAA	0.42101	--GAGGGTAA

#### 8 mer Z-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GTGGGTGA	24.82892	--GTGGGTGA-
AGTGGGTG	20.11566	-AGTGGGTG--
GGTGGGAA	17.10084	--GGTGGGAA--
AAGTGGGT	16.27579	AAGTGGGT---
CACCCACA	15.81220	-TGTGGGTG--
GTGGGTAA	15.35330	--GTGGGTAA-
GGTAGGGA	13.69125	-GGTAGGGA--
TCCCGCCA	13.35153	---TGGCGGGA
AGGTGGAG	13.30178	-AGGTGGAG--
CCAACACA	12.39753	-TGTGTTGG--