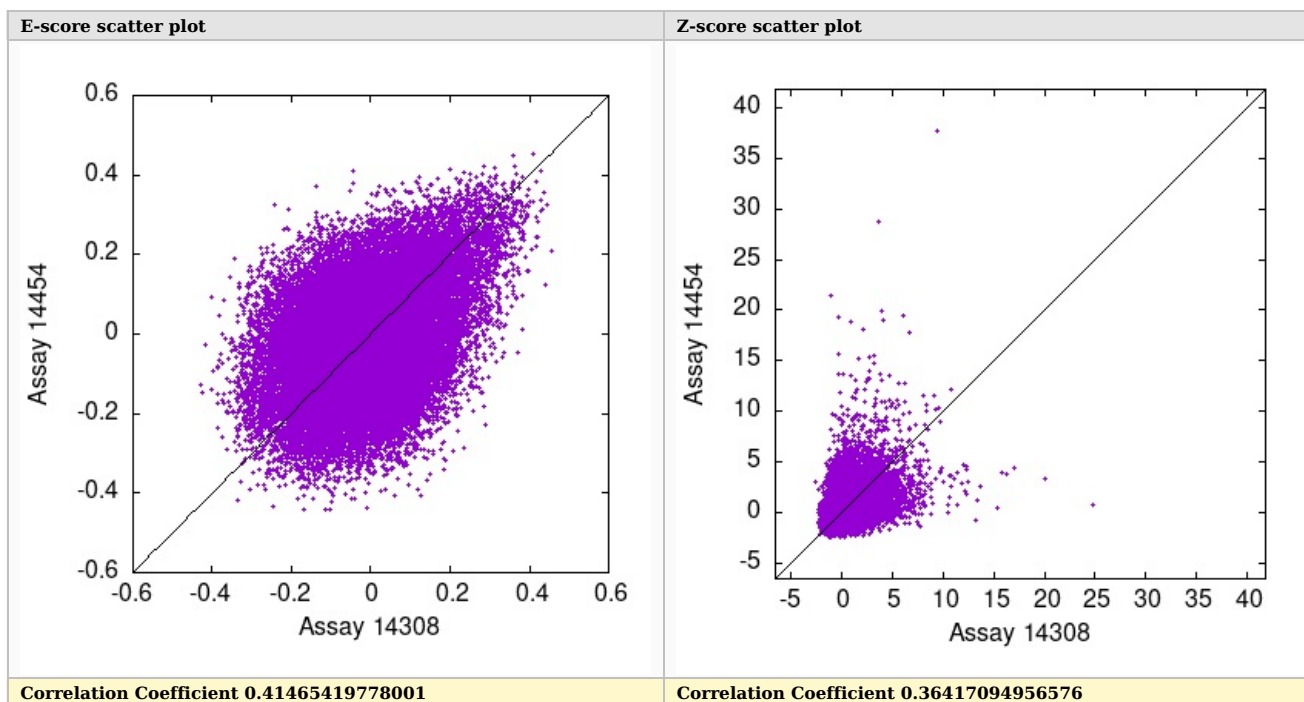




QC report



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--	



Top scoring motifs for Assay 14454

Protein ID: pTH14319.5 Gene: PURB.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
Top 10	Scores	Alignment
AACCCACC	0.45144	-AACCCACC-
CAACCCAC	0.44733	CAACCCAC--
AATCCACC	0.42350	--AATCCACC-
ACCAACCA	0.42241	--ACCAACCA
GACCAACC	0.41628	-GACCAACC-
AAACCGAC	0.41404	AAACCGAC--
ACCAACCT	0.40887	--ACCAACCT
ACCCACCA	0.40867	--ACCCACCA
AACCTTCC	0.40813	-AACCTTCC-
AGCCACAC	0.40442	-AGCCACAC-

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AACCCACC	37.79456	-AACCCACC--	
CAACCCAC	28.79666	CAACCCAC---	
ACCAACCT	21.39678	--ACCAACCT-	
AAACCGAC	19.86329	AAACCGAC---	
AATCCACC	19.44300	-AATCCACC--	
CCAACACG	19.25146	---CCAACACG	
AAGGTGGT	18.99940	---ACCACCTT	
ACCTACCC	18.86731	--ACCTACCC-	
ACGGTCGG	18.15799	---CCGACCGT	
AAACCCAC	17.75728	AAACCCAC---	