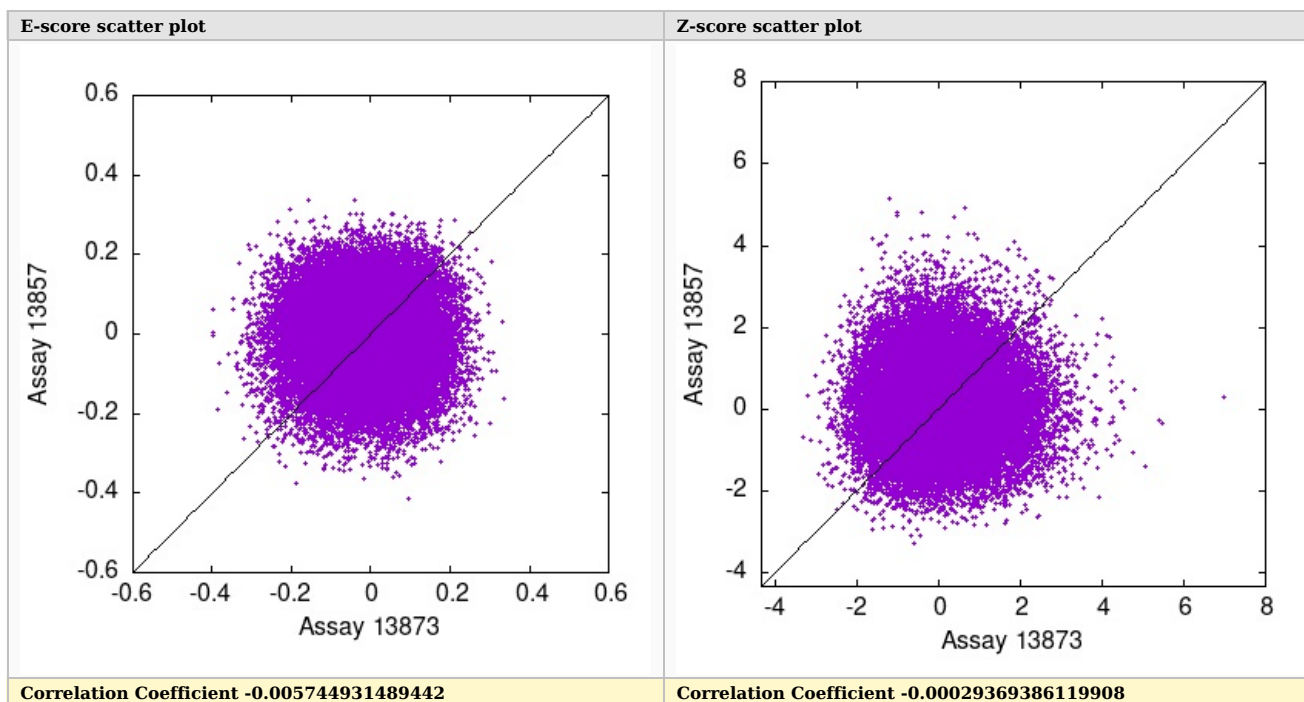


## QC report



### Top scoring motifs for Assay 13873

Protein ID: pTH14262.2 Gene: MBD4.DBD Domain: MBD Flag: Reject 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
AGACGTCT	0.33399	---AGACGTCT-	TTCTAGAA	6.98199	----TTCTAGAA----
CAAGCGAA	0.33377	-CAAGCGAA---	GTCTATTA	5.46783	----GTCTATTA----
ATTACGAA	0.31499	ATTACGAA----	AGACGTCT	5.39310	AGACGTCT-----
AACTGATC	0.30788	--AACTGATC--	AGGACTTC	5.08191	-GAAGTCCT-----
AGGACTTC	0.30424	-GAAGTCCT---	ATTGCAAT	4.81776	-----ATTGCAAT
GTCACCTA	0.30366	-TAAGTGAC---	ATTACGAA	4.75928	-----ATTACGAA
AACCGCTC	0.30111	--AACCGCTC--	ACGATTTG	4.52737	-----ACGATTTG--
TTCTAGAA	0.29869	--TTCTAGAA--	ACGCGACC	4.50891	---GGTCGCGT-----
AGCCAATC	0.29807	--AGCCAATC--	AAACATGG	4.49222	----CCATGTTT----
TCGTTCAA	0.29757	----TTGAACGA	CCACATAC	4.45342	----GTATGTGG----

### Top scoring motifs for Assay 13857

Protein ID: pTH14262.1 Gene: MBD4.DBD Domain: MBD Flag: Reject 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
TGCACTAA	0.33637	---TGCACTAA--	GCCCTAGC	5.14909	--GCCCTAGC----
CATCCAGG	0.33513	-----CATCCAGG	CTAAGCAA	4.91084	-----CTAAGCAA--
GCACTAAC	0.31227	-----GCACTAAC--	ACCTACGG	4.81712	-----ACCTACGG--
GGGCATCA	0.30243	TGATGCC-----	TAACGTTA	4.80622	-----TAACGTTA
ATATGAAC	0.30224	ATATGAAC-----	GCACTAAC	4.74408	--GCACTAAC----
CTCTAAGA	0.30131	-----CTCTAAGA	AGGGACGA	4.68990	AGGGACGA-----
TATATGAA	0.30114	---TATATGAA--	GGCGCGCC	4.29538	-GGCGCGCC-----
TAACGTTA	0.30014	---TAACGTTA--	GTAAGAAA	4.28374	--GTAAGAAA----
CTTGTTCA	0.29462	---TGAACAAG--	GTAACCAA	4.24938	-----GTAACCAA--
TGGGCCAA	0.29418	---TGGGCCAA--	CTCTAAGA	4.24475	---CTCTAAGA---