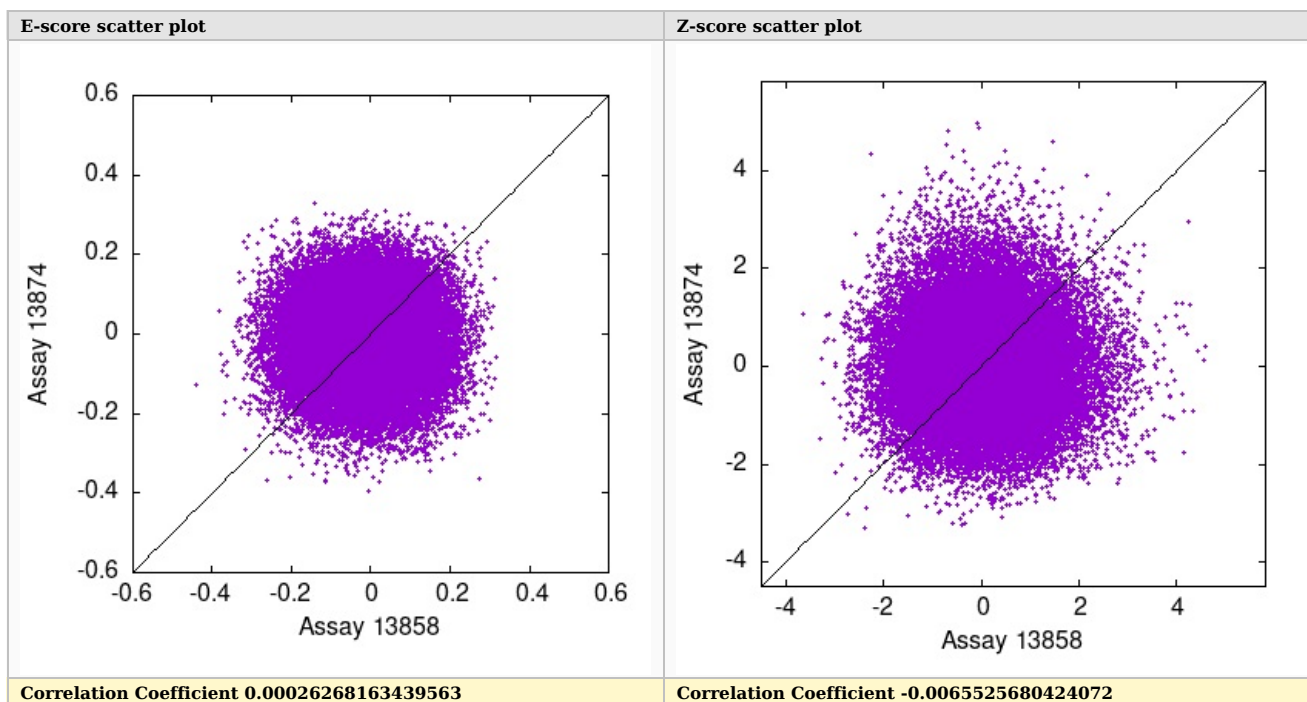


QC report



Top scoring motifs for Assay 13858

Protein ID: pTH14263.1 Gene: MBD6.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
CTCTAAGA	0.31690	--TCTTAGAG--	AGAGATGA	4.60171	----TCATCTCT--
CGGAAACA	0.31344	---CGGAAACA	CAAGGTGG	4.55760	---CCACCTTG--
CCCCGCAC	0.31336	GTGCGGGG---	CCCCGCAC	4.44410	--CCCCGCAC--
AGTGGATG	0.30694	-AGTGGATG--	CAGCCGAA	4.33637	--CAGCCGAA--
TGCGGAAA	0.30453	-TGCAGAAA--	AGTTCACG	4.27375	----CGTGAAC--
ATTATGTA	0.30370	-TACATAAT--	AATGCCGA	4.23661	----TCGGCATT--
GCTTGCAC	0.30183	--GTGCAAGC--	ACCTGACT	4.22367	----ACCTGACT--
CGATCGGC	0.30055	--GCCGATCG--	GCGCTCCA	4.16294	----GCGCTCCA--
TCTTAAGA	0.30032	-TCTTAAGA--	AGCGACGC	4.13506	-AGCGACGC----
CCGATCGC	0.29847	---CCGATCGC	CTGGGCCA	4.13466	TGGCCAG-----

Top scoring motifs for Assay 13874

Protein ID: pTH14263.2 Gene: MBD6.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
CGCATCAA	0.32892	--CGCATCAA--	ACCATGGT	4.96302	ACCATGGT-----
ACATAAGT	0.31095	---ACATAAGT--	CTTGCGCC	4.86984	--CTTGCGCC----
CTCCAAGA	0.30977	-CTCCAAGA----	CTATCTAC	4.80673	--CTATCTAC----
CGCATTTA	0.30222	--CGCATTTA--	GCCCCACC	4.58838	--GCCCCACC----
ACCAAGAA	0.30196	--ACCAAGAA--	CTAGCTAG	4.54766	--CTAGCTAG----
AGTCCCGA	0.30094	-AGTCCCGA----	CTCCAAGA	4.42079	-----CTCCAAGA
CGTCGCAG	0.30076	CGTCGCAG-----	CCCGCTCC	4.39328	--CCCGCTCC----
AAAATTGC	0.29889	-----AAAATTGC	CACCCCAA	4.35031	-----CACCCCAA--
CTTGCGCC	0.29851	GGCGCAAG-----	CGCATCAA	4.27238	-----CGCATCAA--
TCCAAGAA	0.29426	--TCCAAGAA--	ACCATACC	4.17131	--ACCATACC----