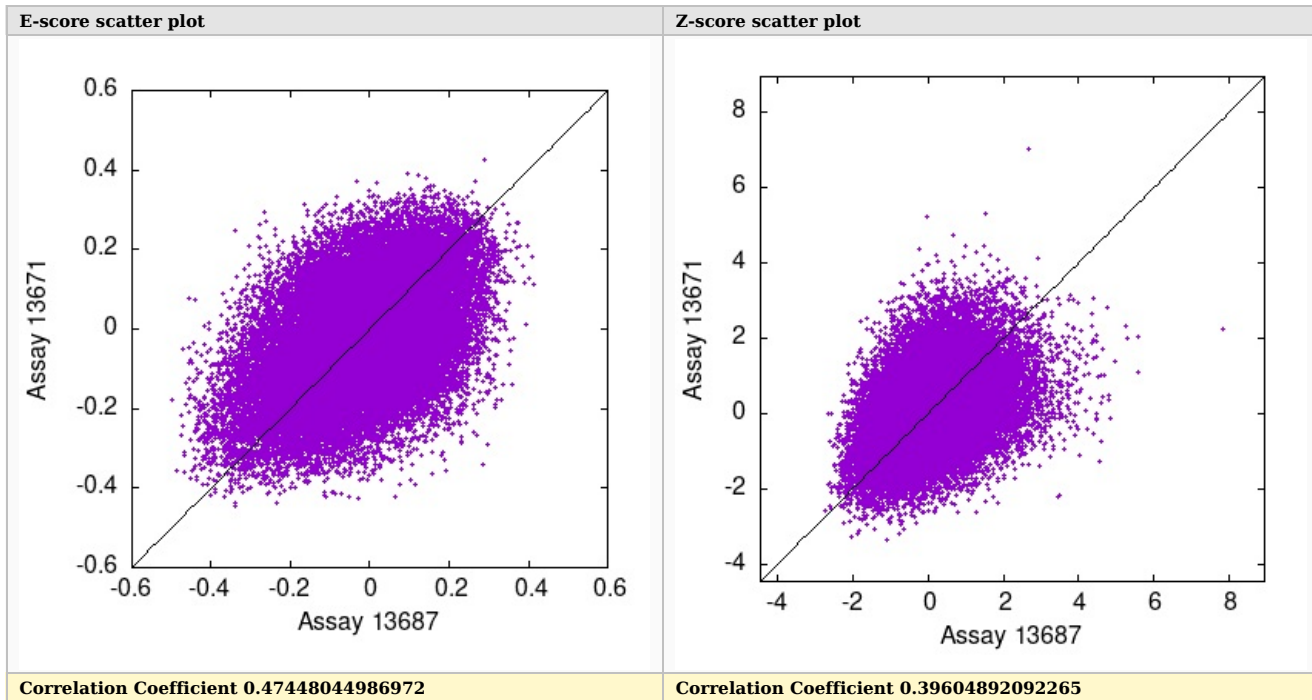


QC report



Top scoring motifs for Assay 13687

Protein ID: pTH14287.2 Gene: CENPS.FL Domain: Unknown 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
AGATATCT	0.41488	--AGATATCT---	TGTTAACA	7.82011	--TGTTAACA--
TGTTAACA	0.40809	--TGTTAACA---	ATATAAAC	5.58579	--ATATAAAC---
TACCGATA	0.40074	-----TACCGATA	ATTTAAAT	5.57230	--ATTTAAAT---
TCTCGAGA	0.39819	--TCTCGAGA---	GTGTACAC	5.29108	--GTGTACAC---
TATATTGA	0.39440	TATATTGA-----	TAAGTTAA	5.24216	-----TTAACTTA
GTTATAAC	0.39189	--GTTATAAC---	TATTTGCA	4.98228	--TATTTGCA--
ATATAAAC	0.38696	--ATATAAAC---	ATCTAGAT	4.86168	--ATCTAGAT---
AACAACAA	0.37950	--TTGTTGTT---	AATATAGA	4.78978	AATATAGA----
TACACACA	0.37413	TGTGTGTA-----	CATATAAG	4.78948	CATATAAG----
ATGTTAAC	0.37229	--ATGTTAAC---	AGTATACT	4.77710	--AGTATACT--

Top scoring motifs for Assay 13671

Protein ID: pTH14287.1 Gene: CENPS.FL Domain: Unknown 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
TAAATTTA	0.42398	--TAAATTTA	TAAATTTA	7.01123	--TAAATTTA
CAGAAACA	0.39108	--CAGAAACA	CAAACTTA	5.29229	--CAAACTTA
ATTGTACC	0.38729	GGTACAAT--	AGTTTTTG	5.20864	--CAAAAACT--
GTATAATA	0.37862	--GTATAATA-	CATAATAC	4.73742	--CATAATAC
AATTCGAA	0.37281	--TTCGAATT-	ACATGGAT	4.46173	--ACATGGAT
TAATAAGA	0.37145	--TAATAAGA	TAACAGTA	4.45973	--TAACAGTA-
AGTTTTTG	0.36687	--CAAAAACT	CAGAAACA	4.37108	--CAGAAACA-
TACAATCA	0.36077	--TACAATCA	AAAAATAA	4.26333	--AAAAATAA
CATAATAC	0.35955	--GTATTATG-	ATTGTACC	4.21875	GGTACAAT--
TAACAGTA	0.35655	--TACTGTTA	ATAATGCA	4.18978	--ATAATGCA