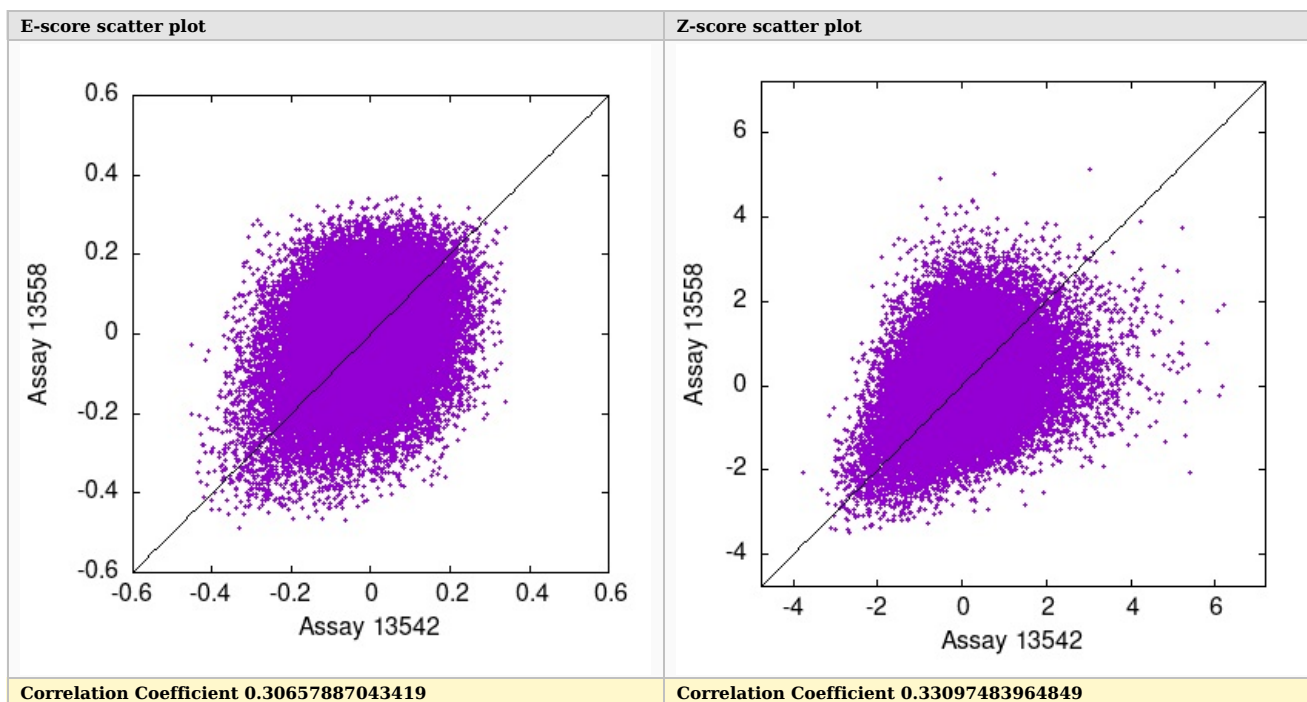


QC report



Top scoring motifs for Assay 13542

Protein ID: pTH14289.1 Gene: CENPX.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
CCAACAAA	0.34087	---CCAACAAA--	CTGCTAAC	6.19841	-CTGCTAAC---
TGGCGAAA	0.33796	----TGGCGAAA-	GTGGTAGA	6.17779	GTGGTAGA----
TATACAAA	0.33656	----TATACAAA-	GTGCGCAC	6.08312	-GTGCGCAC---
CCAGTTAC	0.32978	---GTAACCTGG--	TATACAAA	6.07695	-TATACAAA---
CTGCTAAC	0.32876	CTGCTAAC-----	AAACGTAC	5.80845	-AAACGTAC---
GTGCGCAC	0.32741	---GTGCGCAC--	TGGAGTAA	5.61789	-TGGAGTAA---
ACCGTTTA	0.32381	----TAACCGGT-	CTGACCTA	5.38968	CTGACCTA----
ATAACCAA	0.32300	---ATAACCAA--	CGACATGA	5.37617	----CGACATGA
ACGTGACC	0.32267	-ACGTGACC----	TGGGTCAA	5.31198	-TGGGTCAA---
AACCTTAT	0.32057	-----AACCTTAT	TGGCGAAA	5.29720	-TGGCGAAA---

Top scoring motifs for Assay 13558

Protein ID: pTH14289.2 Gene: CENPX.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
CAGTGAC	0.34617	GTGCACTG----	ACAGTTAC	5.10239	GTAACGTG----
GCTTATAA	0.34244	----GCTTATAA	AAACGTTT	5.00556	--AAACGTTT--
TACACACA	0.34080	---TACACACA-	ACTACCAT	4.88543	--ATGGTAGT--
CGACTCAA	0.34012	--CGACTCAA--	ATTTGTGC	4.38658	--ATTTGTGC--
AAACGTTT	0.33649	----AAACGTTT	CACAGTTA	4.34110	-TAACTGTG---
ACTCATGA	0.33277	----ACTCATGA	CTCAAACA	4.23592	-TGTTTGAG---
ATATAGCA	0.32883	----ATATAGCA	GCTTATAA	4.22779	--TTATAAGC--
AATCTTGA	0.32662	----AATCTTGA	ACTCATGA	4.21373	TCATGAGT----
GAAATTGC	0.32468	----GAAATTGC	TTGCGCAA	4.18961	----TTGCGCAA
ATTTGTGC	0.32220	--GCACAAAT--	CGACTCAA	4.11180	----TTGAGTCG