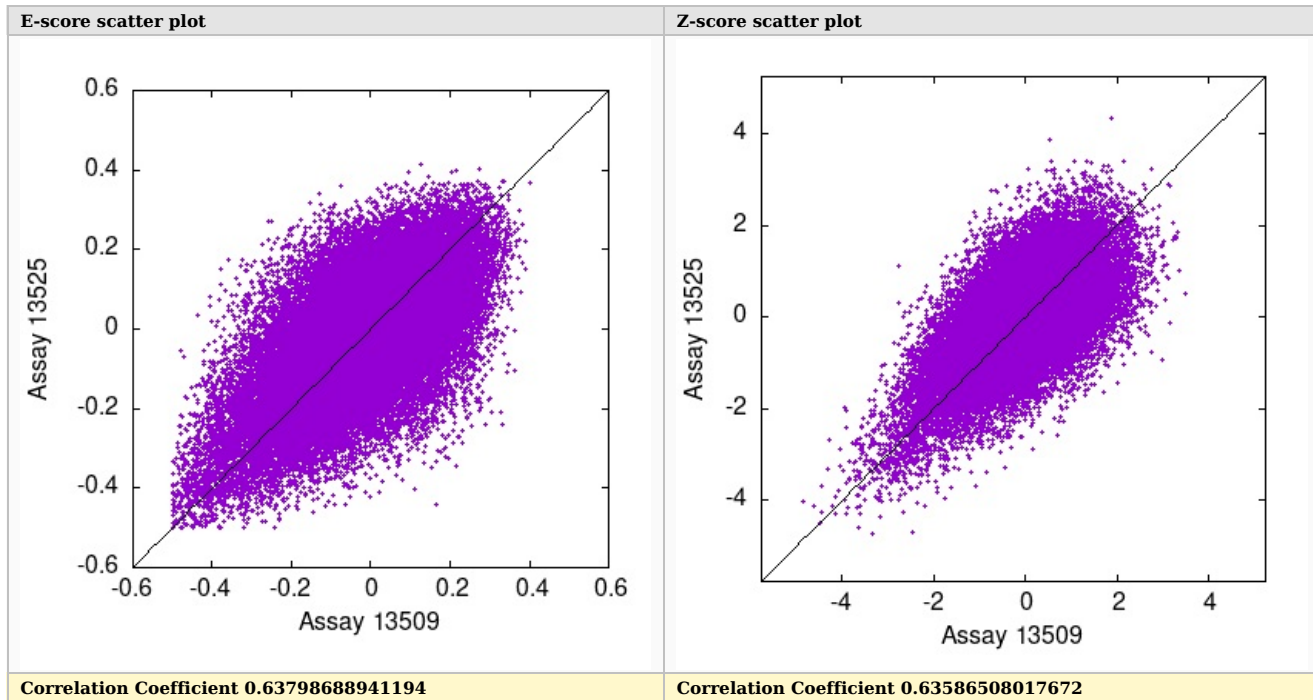


QC report



Top scoring motifs for Assay 13509

Protein ID: pTH14239.1 Gene: ADNP.DBD.1 Domain: Homeobox 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
ACAAACAT	0.40105	-ATGTTTGT--	AATTTATG	3.50058	--AATTTATG--
AATTTATG	0.38986	--AATTTATG-	CAAATTTG	3.36253	CAAATTTG----
AATTTGTA	0.38943	--AATTTGTA-	AACATTAA	3.31713	----TTAATGTT
AACATTAA	0.38340	TTAATGTT---	AATGCATT	3.30075	--AATGCATT--
CAAATTTG	0.38283	CAAATTTG---	AATTTGTA	3.28358	--AATTTGTA--
ATATATAA	0.37806	---ATATATAA	AATATTTT	3.25227	--AATATTTT--
AATTGTTA	0.37670	--AATTGTTA-	ACATGTAA	3.20706	-ACATGTAA---
ATAATGCA	0.37562	--ATAATGCA-	AACAAAAT	3.20424	--ATTTTGTT--
TATAATAA	0.37389	--TTATTATA-	AACTTTAT	3.14421	-AACTTTAT---
AACATGTT	0.37184	--AACATGTT-	AGAATTCT	3.14349	-AGAATTCT---

Top scoring motifs for Assay 13525

Protein ID: pTH14239.2 Gene: ADNP.DBD.1 Domain: Homeobox 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
GTCATGAC	0.41536	-----GTCATGAC	TACTAGTA	4.31890	TACTAGTA-----
TACTAGTA	0.40346	---TACTAGTA--	GTCATGAC	3.84475	----GTCATGAC-
ATGCGCAT	0.40033	---ATGCGCAT---	AACGTTTG	3.39400	--AACGTTTG---
AACGTTTG	0.39521	CAAACGTT-----	CGCAACAA	3.38606	-----TTGTTGCG-
GATGCATC	0.39308	---GATGCATC--	ATGTATGC	3.38206	---ATGTATGC--
CAACAATG	0.38459	---CAACAATG--	CAACAATG	3.37589	---CAACAATG---
ATAGTAAT	0.37179	--ATAGTAAT---	ATTATAAT	3.37101	-----ATTATAAT-
AACGTATT	0.37145	--AACGTATT---	AAATTACG	3.29589	---AAATTACG---
GACAAACA	0.36991	---GACAAACA---	ATATGCTG	3.27850	-----ATATGCTG
TATAACGA	0.36955	---TCGTATATA--	CGTATAAA	3.23410	-----TTTATACG-