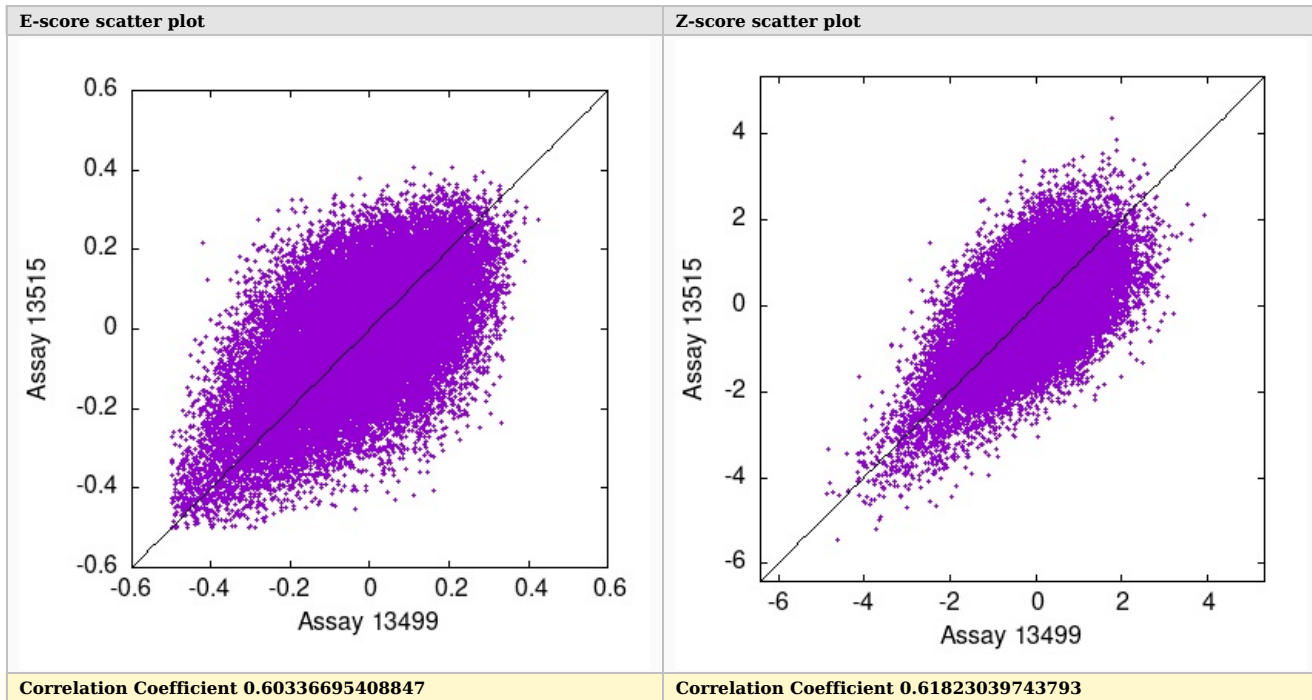


QC report



Top scoring motifs for Assay 13499

Protein ID: pTH13934.1 Gene: HLHA9.FL Domain: HLH 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
ACAACAAT	0.42379	-----ATTGTTGT--	TTTCGAAA	3.91971	--TTTCGAAA---
TTTCGAAA	0.39567	TTTCGAAA-----	AACGCGTT	3.65111	-AACGCGTT----
ATTTGTAC	0.39199	-----ATTTGTAC--	AATTGTTA	3.59535	--AATTGTTA---
CAACAATA	0.39149	-----TATTGTTG--	ACAACAAT	3.54209	---ATTGTTGT---
ATAATATA	0.39128	----TATATTAT----	TAAATTTA	3.41221	--TAAATTTA---
AATTGTTA	0.39113	-----AATTGTTA--	CGTTAACG	3.30314	-----CGTTAACG
AAATTTGT	0.37428	-----AAATTTGT--	ATTTACTA	3.20429	---ATTTACTA---
AAATTTGT	0.37070	-----AAATTTGT--	ATGATCAT	3.19706	---ATGATCAT---
CGTTAACG	0.36907	-----CGTTAACG	ACATATGT	3.11320	ACATATGT-----
AATTTGTA	0.36836	-----AATTTGTA--	AGCAATTG	3.09215	-CAATTGCT----

Top scoring motifs for Assay 13515

Protein ID: pTH13934.2 Gene: HLHA9.FL Domain: HLH 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
ATGCGCAT	0.40751	----ATGCGCAT	TGTTAACA	4.35698	--TGTTAACA----
CGATAACA	0.40549	---CGATAACA-	ATTGTTGC	3.87656	ATTGTTGC-----
TGTTAACA	0.39493	---TGTTAACA-	CAACGTTG	3.61733	-----CAACGTTG-
TATTAATA	0.38933	---TATTAATA-	AGTTAACT	3.55370	--AGTTAACT----
ATTGTTGC	0.38217	-ATTGTTGC---	CGATAACA	3.46063	---CGATAACA----
CGCGCGCG	0.38125	---CGCGCGCG-	TGTGTTAA	3.45116	TGTGTTAA-----
GTTTAAAC	0.37560	----GTTTAAAC	AAACGTTT	3.40775	-----AAACGTTT-
GCGCAAAA	0.37418	---GCGCAAAA-	ACAAACAG	3.39530	---ACAAACAG----
CAATGTCA	0.37105	CAATGTCA----	CAGTACTG	3.38004	---CAGTACTG----
GTTATAAC	0.36778	----GTTATAAC	AACGTTTG	3.37657	-----AACGTTTG