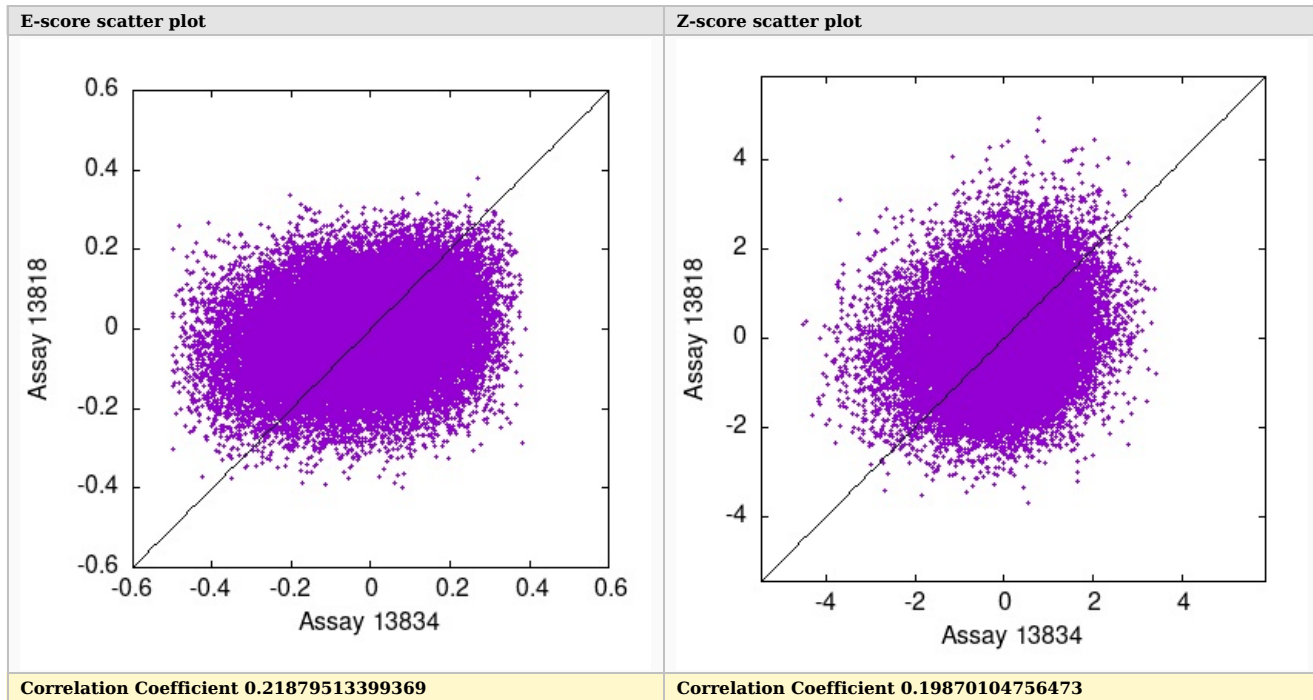


QC report





Top scoring motifs for Assay 13834

Protein ID: pTH13912.2 Gene: ARID2 Domain: ARID Flag: Reject

Array: 1M-HK

8 mer E-scores for probeset 'all'

8 mer Z-scores for probeset 'all'

Forward:			Reverse:		
					
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TATTAATA	0.38926	TATTAATA-----	ACTGTCTA	3.40787	ACTGTCTA----
GATCTAGA	0.38146	----GATCTAGA-	CTAAGTAA	3.36730	-CTAAGTAA---
ATCTAGAT	0.38034	-----ATCTAGAT	AGTATACT	3.30650	----AGTATACT
ACTAATTA	0.37815	---TAATTAGT--	ATAATGTA	3.23431	--TACATTAT--
GTACATTA	0.37708	---TAATGTAC--	ACTAATTA	3.23200	ACTAATTA----
AATATGAA	0.37691	--AATATGAA---	TTTCATGAA	3.20394	-TTTCATGAA---
ATAATGTA	0.37642	--ATAATGTA---	ATATTAAG	3.18300	-CTTAATAT---
ACACAATA	0.37467	---TATTGTGT--	GTTCAGTA	3.18009	GTTCAGTA----
TATAACGA	0.37425	-TATAACGA----	CTGTAACA	3.14260	--CTGTAACA---
AACAATAA	0.37311	--TTATTGTT---	ATCGCGAT	3.12209	-ATCGCGAT---



Top scoring motifs for Assay 13818

Protein ID: pTH13912.1 Gene: ARID2 Domain: ARID Flag: Reject

Array: 1M-ME

8 mer E-scores for probeset 'all'

8 mer Z-scores for probeset 'all'

Forward:			Reverse:		
					
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AATTTGTA	0.38117	--AATTTGTA-	ATACAAAA	4.93299	---TTTTGTAT-
AAGACTGA	0.34052	AAGACTGA---	AAGACTGA	4.67662	----TCAGTCTT
ATACAAAA	0.33557	---TTTTGTAT	AATTTGTA	4.46812	--AATTTGTA--
AACCTCGG	0.33499	CCGAGGTT---	AAACATAG	4.43085	---CTATGTTT-
GACTTATA	0.32929	--GACTTATA-	ACGATCGT	4.41897	-ACGATCGT---
AAACATAG	0.31838	---AAACATAG	CTTCATGC	4.33704	---CTTCATGC-
GCAAGCGA	0.31221	-TCGCTTGC--	AGTGTCGG	4.27600	--AGTGTCGG--
ATAATGCA	0.31002	-TGCATTAT--	AATTAGTA	4.26733	--AATTAGTA--
ATAAAGC	0.30790	---GCTTTTAT	GAAATTAA	4.26315	TTAATTTT----
CTTCATGC	0.30553	---CTTCATGC	ATAATGCA	4.22846	--ATAATGCA--