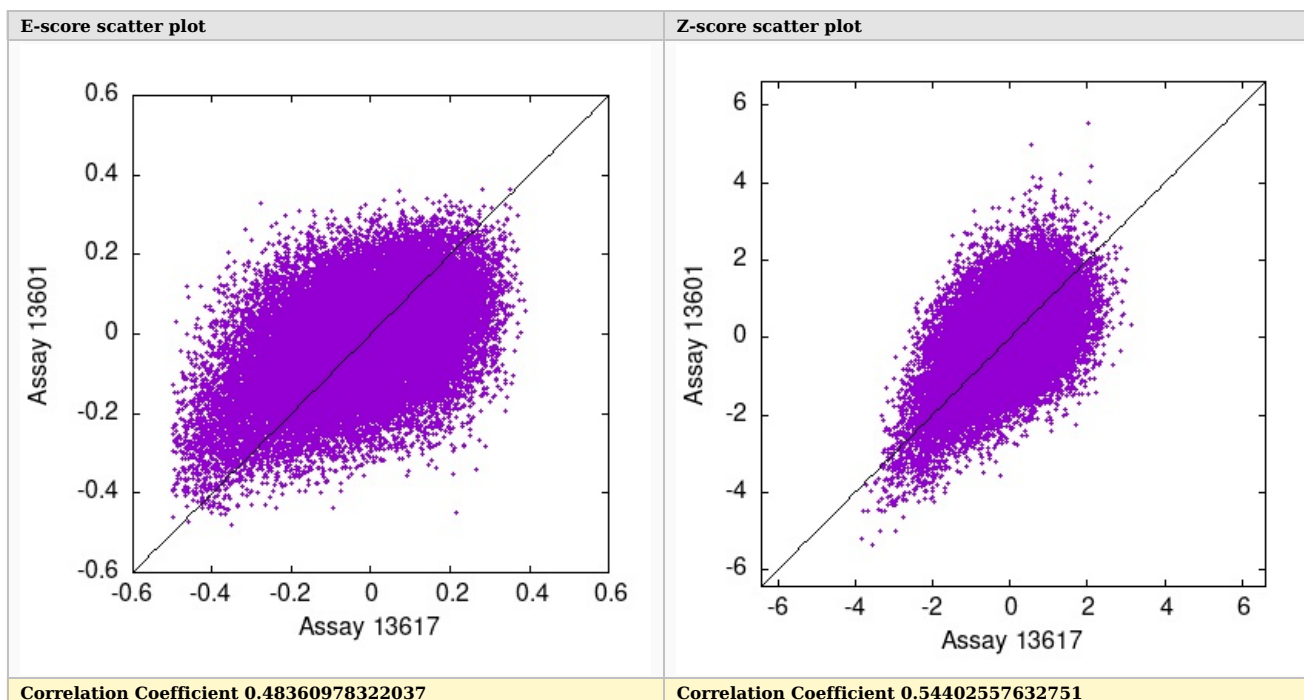


QC report



Top scoring motifs for Assay 13617

Protein ID: pTH14298.2 Gene: DACH2.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
GATATGTA	0.39117	GATATGTA---	ATCATACA	3.12503	ATCATACA--
ATTAATAA	0.38532	-ATTAATAA--	GAAATTTT	3.00935	GAAATTTT--
ACAAACAG	0.38018	-ACAAACAG--	ATAACGA	2.97313	-TCGTTTAT-
ATCATACA	0.37680	--TGTATGAT-	ACAAACAG	2.95469	ACAAACAG--
ACAAATCA	0.37457	-ACAAATCA--	GATATGTA	2.91639	GATATGTA--
AAACGTTT	0.37281	-AAACGTTT--	ATTATAAT	2.90411	ATTATAAT--
GTCTAGAC	0.37280	--GTCTAGAC-	ATTATTAA	2.89790	ATTATTAA--
TATTAATA	0.37216	TATTAATA--	AATATTAA	2.86220	AATATTAA--
ATTATTAA	0.37126	--TTAATAAT-	ATTGTTGC	2.85373	ATTGTTGC--
CGTTATAA	0.36921	---TTATAACG	GATTAATA	2.84843	--TATTAATC

Top scoring motifs for Assay 13601

Protein ID: pTH14298.1 Gene: DACH2.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
GTTATAAC	0.36254	--GTTATAAC-	GTTATAAC	5.52356	---GTTATAAC----
CTTGTAAC	0.36251	GTTACAAG---	TGTGCACA	4.96173	---TGTGCACA-----
TGTGCACA	0.35863	TGTGCACA---	CTTGTAAC	4.43213	---CTTGTAAC-----
AACAAAGC	0.34658	--AACAAAGC-	TGCATGCA	4.23014	-TGCATGCA-----
AACTTTGG	0.33983	---CCAAGTT-	AACAAAGC	4.13010	-GCTTTGTT-----
ACAGTTCT	0.33627	---ACAGTTCT	GATCGTTA	4.11350	-----TAACGATC-
CAGACAAC	0.33510	--CAGACAAC-	GTTGCAAC	4.01313	---GTTGCAAC-----
ATTCGTTA	0.33255	-TAACGAAT--	ACAGTTCT	3.92501	ACAGTTCT-----
CCAACAAC	0.33236	CCAACAAC---	AACTTTGG	3.89666	-----AACTTTGG
AAACCAAA	0.33150	-AAACCAAA--	CCAACAAC	3.85665	---CCAACAAC-----