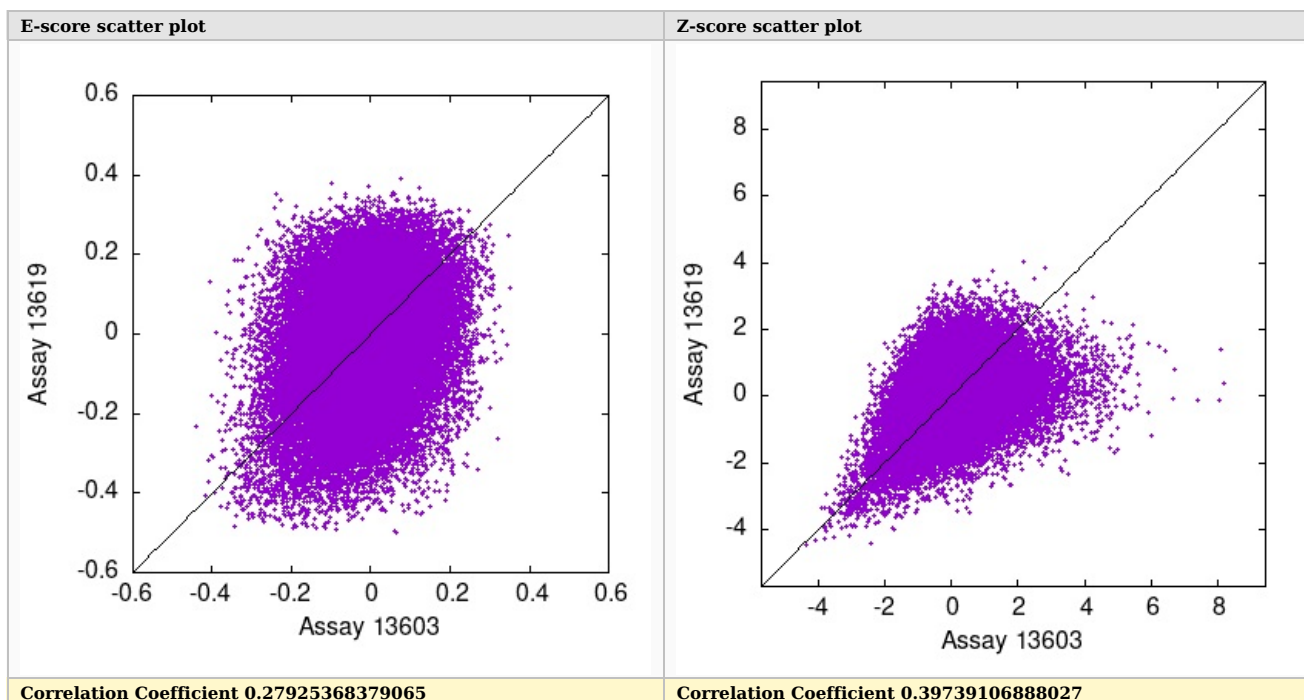


QC report



Top scoring motifs for Assay 13603

Protein ID: pTH14301.1 Gene: DRAP1.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:



Reverse:



8 mer Z-scores for probeset 'all'

Forward:



Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
GTTATCA	0.35041	--GTTATCA----	GTTATAAC	8.16776	---GTTATAAC-
GTTATAAC	0.34687	---GTTATAAC---	TGGTGTA	8.07930	----TTACACCA
GATCGTTA	0.34362	--GATCGTTA----	GATCGTTA	8.02816	---TAACGATC
TGTGCACA	0.33036	--TGTGCACA----	CCACGAAG	7.39545	---CCACGAAG-
ACAGTTCT	0.32715	ACAGTTCT-----	GGTTATCA	6.70610	----TGATAACC
AACGTGAT	0.32401	-----ATCACGTT	CCAACAAC	6.67535	--CCAACAAC-
GGCGGAGA	0.32102	-----TCTCGCCC	ATTGGTTC	6.42998	---GAACCAAT-
CCAACAAC	0.31624	---GTTGTTGG---	CAAATTTG	6.23487	--CAAATTTG-
GGAATGGA	0.31443	--GGAATGGA----	GTCAGGTA	6.01858	TACCTGAC----
CTTTAGCA	0.31391	--CTTTAGCA----	TGCCGACA	5.91224	-TGCCGACA---

Top scoring motifs for Assay 13619

Protein ID: pTH14301.2 Gene: DRAP1.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:



Reverse:



8 mer Z-scores for probeset 'all'

Forward:



Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
TACTAGTA	0.39065	TACTAGTA-----	ATTATAAT	4.04329	----ATTATAAT
GCTGAAAA	0.38072	--GCTGAAAA---	TACTAGTA	3.82709	---TACTAGTA-
CGCGCGCG	0.37016	--CGCGCGCG---	CGCGCGCG	3.76422	---CGCGCGCG-
GATATGTA	0.36811	----TACATATC-	AGAATTCT	3.53880	----AGAATTCT
CGAGCAAA	0.35790	--CGAGCAAA---	GTACATTA	3.50098	GTACATTA----
TATTAATA	0.35335	---TATTAATA--	TTTGCAAA	3.47404	---TTTGCAAA-
AATCATGA	0.35214	---AATCATGA--	ACAAACAG	3.46391	----ACAAACAG
CTGAACAA	0.35175	--CTGAACAA---	AATCAATT	3.43372	--AATCAATT-
TAATATAA	0.34903	--TAATATAA---	CGAGCAAA	3.41450	--CGAGCAAA-
GCATATGC	0.34586	-----GCATATGC	TATTAATA	3.40464	--TATTAATA-