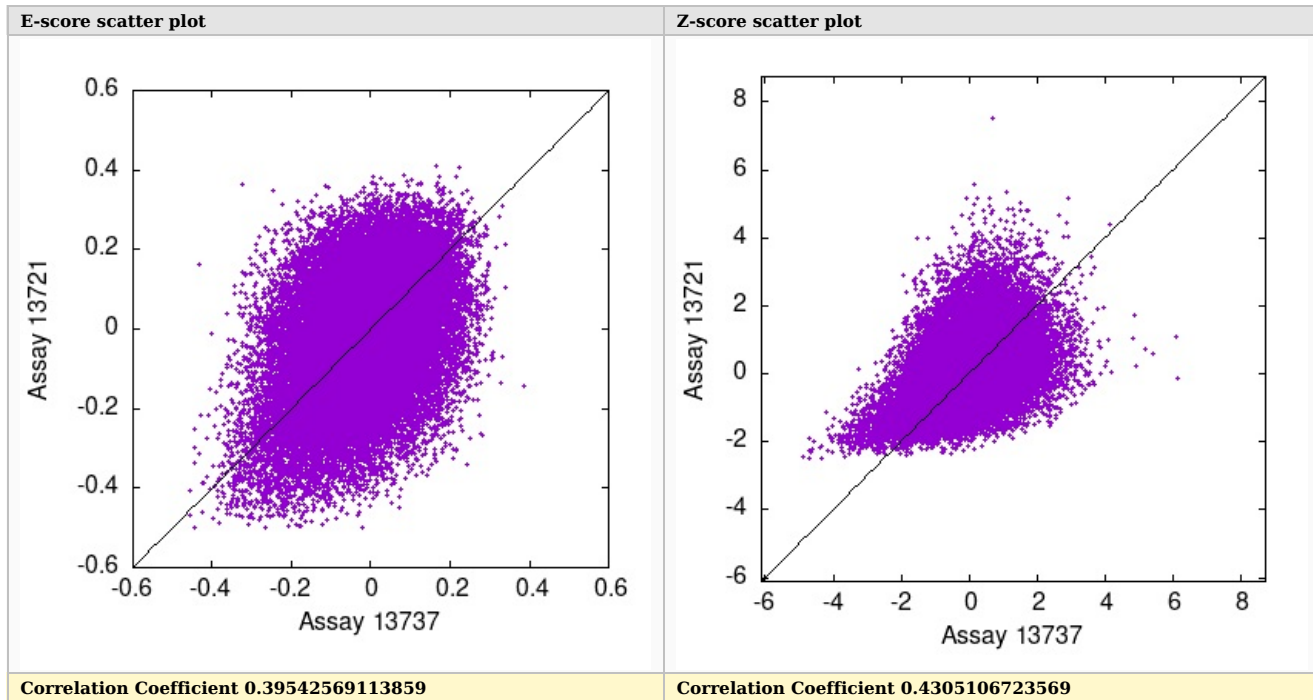


QC report



Top scoring motifs for Assay 13737

Protein ID: pTH14300.2 Gene: DR1.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGTTTTTC	0.38469	-AGTTTTTC-
CATTGCA	0.33963	--CATTGCA
AGCTACA	0.33899	-AGCTACA-
AACGTAAC	0.33135	--GTTACGTT
ACAATGTC	0.33092	GACATTGT--
AAAGTCAC	0.32857	GTGACTTT--
CGCAACAA	0.32287	--TTGTTGCG
TAATAATA	0.31546	-TATTATTA-
CGAGAGCC	0.31448	--GGCTCTCG
ACAAATAG	0.31252	--CTATTGT

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGTTTTTC	6.15337	-AGTTTTTC--
AGTCTACA	6.09858	--AGTCTACA-
CAGCTAAC	5.43669	--GTTAGCTG
CATTGCA	5.20628	--CATTGCA-
CGTATACG	4.94688	--CGTATACG-
CGCAACAA	4.88908	--TTGTTGCG-
ACAAATAG	4.82954	-CTATTGT--
ACAATGTC	4.19659	GACATTGT---
TTTCGAAA	4.14968	---TTTCGAAA
GTAAGTTA	4.10358	-TAACTTAC--

Top scoring motifs for Assay 13721

Protein ID: pTH14300.1 Gene: DR1.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGAATTCT	0.41021	--AGAATTCT--
TAAATTTA	0.40568	-TAAATTTA--
TATATACA	0.38791	---TATATACA-
TGATATCA	0.38403	TGATATCA----
GTTGCAAC	0.38391	--GTTGCAAC--
AATTACGT	0.38304	---AATTACGT
AACTGATA	0.37854	---AACTGATA-
ATATTTTA	0.37666	--ATATTTTA--
ATATTTAC	0.37148	--ATATTTAC--
AATTGTGA	0.36845	-AATTGTGA---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGAATTCT	7.50831	-AGAATTCT-
ACATTATC	5.56728	GATAATGT--
ATATTTTA	5.35578	--TAAAATAT
TAAATTTA	5.18569	-TAAATTTA-
ATAATATA	5.17795	-ATAATATA-
ATATATTA	5.17795	--TAATATAT
ATTATATA	5.17795	-ATTATATA-
ACAAACAT	5.01084	ACAAACAT--
TCTATAGA	5.00425	-TCTATAGA-
ATAACAAT	4.92264	-ATAACAAT-