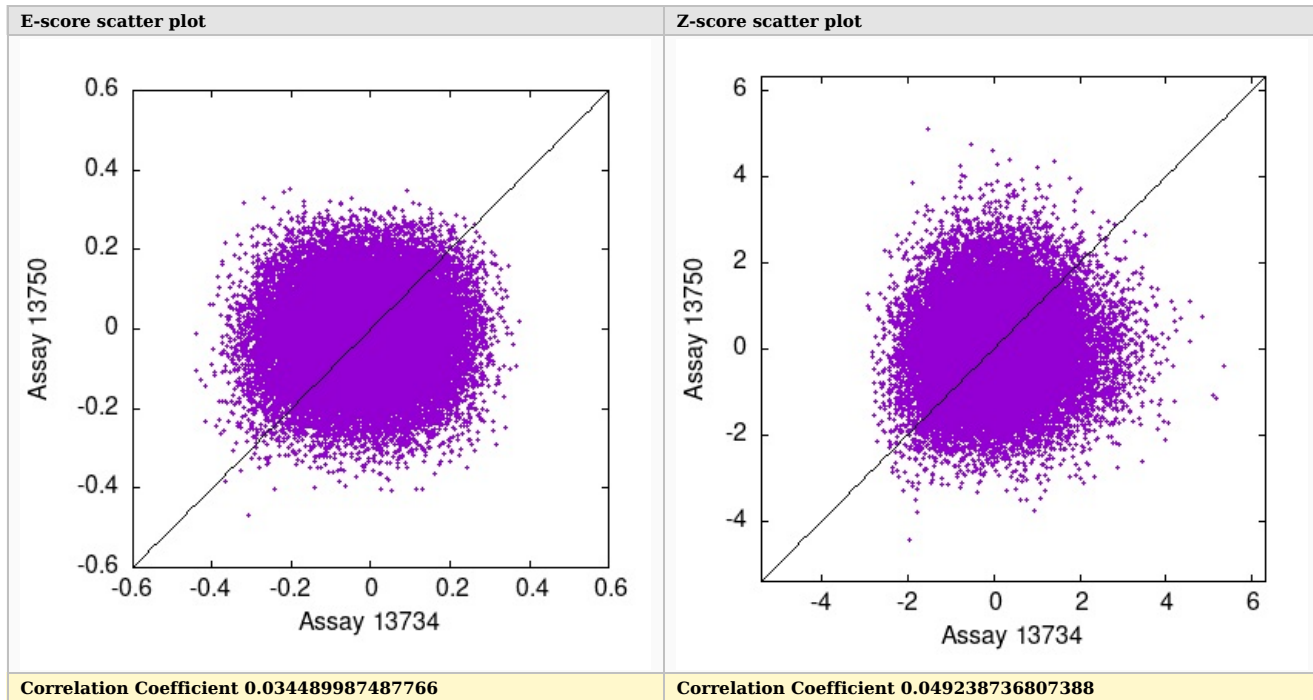


QC report



Top scoring motifs for Assay 13734

Protein ID: pTH14321.1 Gene: RAG1.DBD 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

TAACGAAA	0.37527	--TAACGAAA---
TACTTTAA	0.36656	----TTAAAGTA
ACTAAAAG	0.36105	----ACTAAAAG-
TATAAATA	0.35417	----TATAAATA-
TATACAGA	0.35063	--TCTGTATA---
CTTATTAC	0.34602	-CTTATTAC----
CACTAATA	0.34495	---CACTAATA--
GAGTGATA	0.34218	TATCACTC----
AAGCAGAA	0.34204	---AAGCAGAA--
TCAGTAAA	0.34055	--TCAGTAAA---

Top 10

Scores

Alignment

TAACGAAA	5.34366	-TAACGAAA--
AATTAGTA	5.19005	-AATTAGTA--
ACTAAAAG	5.08755	CTTTTAGT---
AACACGAG	4.84484	--AACACGAG-
ATAATGCA	4.57289	--ATAATGCA-
TATAAATA	4.57289	-TATAAATA--
CAAATACA	4.34095	---CAAATACA
TACAACTA	4.23599	-TACAACTA--
GAGTGATA	4.22085	-TATCACTC--
ACTTTAAT	4.20893	ACTTTAAT---

Top scoring motifs for Assay 13750

Protein ID: pTH14321.2 Gene: RAG1.DBD 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

CGGGGTGA	0.35404	-TCACCCCG----
CTGGGGTA	0.35006	----CTGGGGTA--
CGCCGGTA	0.34287	----CGCCGGTA--
CGACAGTA	0.33058	----CGACAGTA--
ACGCTGGA	0.32913	---ACGCTGGA---
GCGCAAC	0.32051	GTTGCGCC-----
GACAGTAC	0.32008	-----GACAGTAC-
AAACCCAG	0.31764	---AAACCCAG----
CGGATCCG	0.31712	-----CGGATCCG
CACAGCTA	0.31575	----CACAGCTA--

Top 10

Scores

Alignment

CGGGGTGA	5.09497	-CGGGGTGA----
CACGGAGA	4.76283	-CACGGAGA----
GTGCGATA	4.61680	-GTGCGATA----
GACAGTAC	4.38461	-----GACAGTAC
ATGGACAC	4.36560	--ATGGACAC---
TGGACACA	4.29517	---TGGACACA--
GCGTGGTA	4.23980	GCGTGGTA----
ATGAAAAG	4.20197	--ATGAAAAG----
CACGCAAG	4.01756	-----CACGCAAG
ATCATCCA	3.98587	---TGGATGAT--