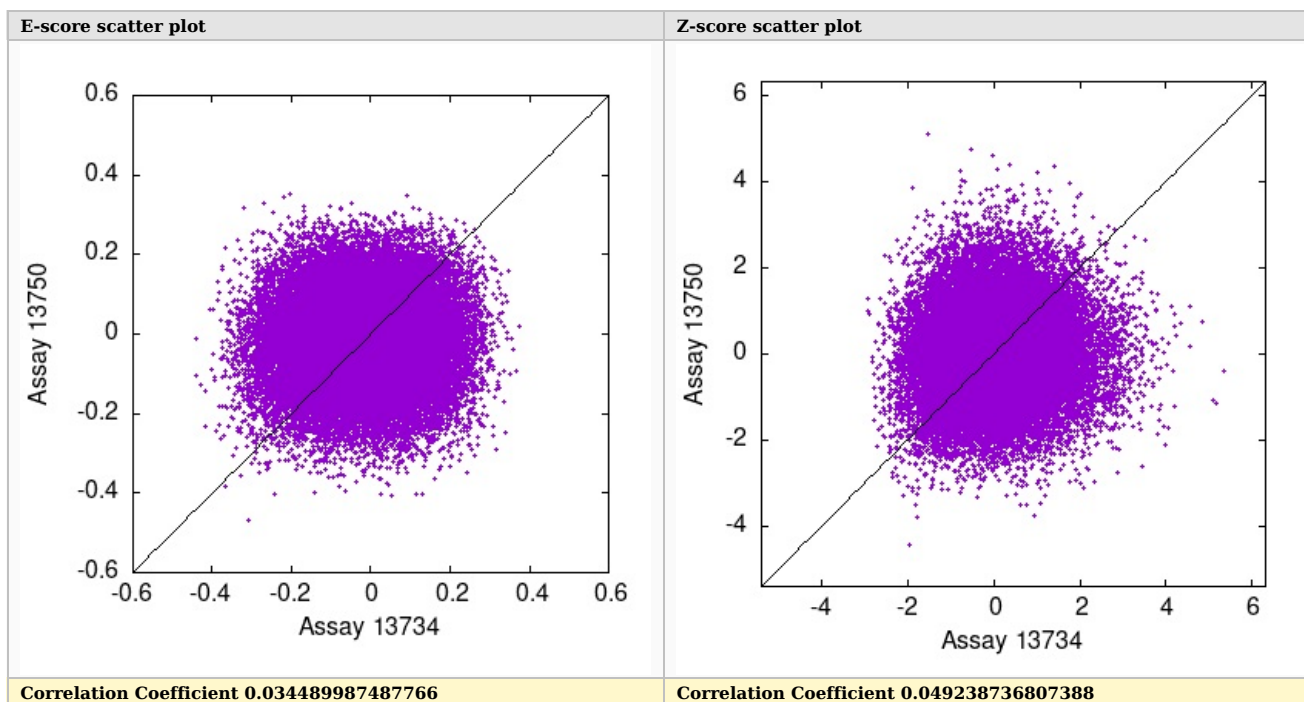


## QC report



### 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	Top 10	Scores	Alignment
TAACGAAA	0.37527	--TAACGAAA---	TAACGAAA	5.34366	-TAACGAAA--
TACTTTAA	0.36656	----TTAAAGTA	AATTAGTA	5.19005	-AATTAGTA--
ACTAAAAG	0.36105	----ACTAAAAG-	ACTAAAAG	5.08755	CTTTTAGT---
TATAAATA	0.35417	----TATAAATA-	AACACGAG	4.84484	--AACACGAG-
TATACAGA	0.35063	--TCTGTATA---	ATAATGCA	4.57289	--ATAATGCA-
CTTATTAC	0.34602	-CTTATTAC----	TATAAATA	4.57289	-TATAAATA-
CACTAATA	0.34495	---CACTAATA--	CAAATACA	4.34095	---CAAATACA
GAGTGATA	0.34218	TATCACTC----	TACAACCTA	4.23599	-TACAACCTA--
AAGCAGAA	0.34204	---AAGCAGAA--	GAGTGATA	4.22085	-TATCACTC--
TCAGTAAA	0.34055	--TCAGTAAA---	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	Top 10	Scores	Alignment
CGGGGTGA	0.35404	-TCACCCCG----	CGGGGTGA	5.09497	-CGGGGTGA----
CTGGGGTA	0.35006	----CTGGGGTA--	CACGGAGA	4.76283	-CACGGAGA----
CGCCGGTA	0.34287	----CGCCGGTA--	GTGCGATA	4.61680	-GTGCGATA----
CGACAGTA	0.33058	----CGACAGTA--	GACAGTAC	4.38461	-----GACAGTAC
ACGCTGGA	0.32913	---ACGCTGGA---	ATGGACAC	4.36560	--ATGGACAC---
GCGCAAC	0.32051	GTTGCGCC-----	TGGACACA	4.29517	---TGGACACA--
GACAGTAC	0.32008	-----GACAGTAC-	GCGTGGTA	4.23980	GCGTGGTA----
AAACCCAG	0.31764	---AAACCCAG----	ATGAAAAG	4.20197	--ATGAAAAG----
CGGATCCG	0.31712	-----CGGATCCG	CACGCAAG	4.01756	-----CACGCAAG
CACAGCTA	0.31575	----CACAGCTA--	ATCATCCA	3.98587	---TGGATGAT--