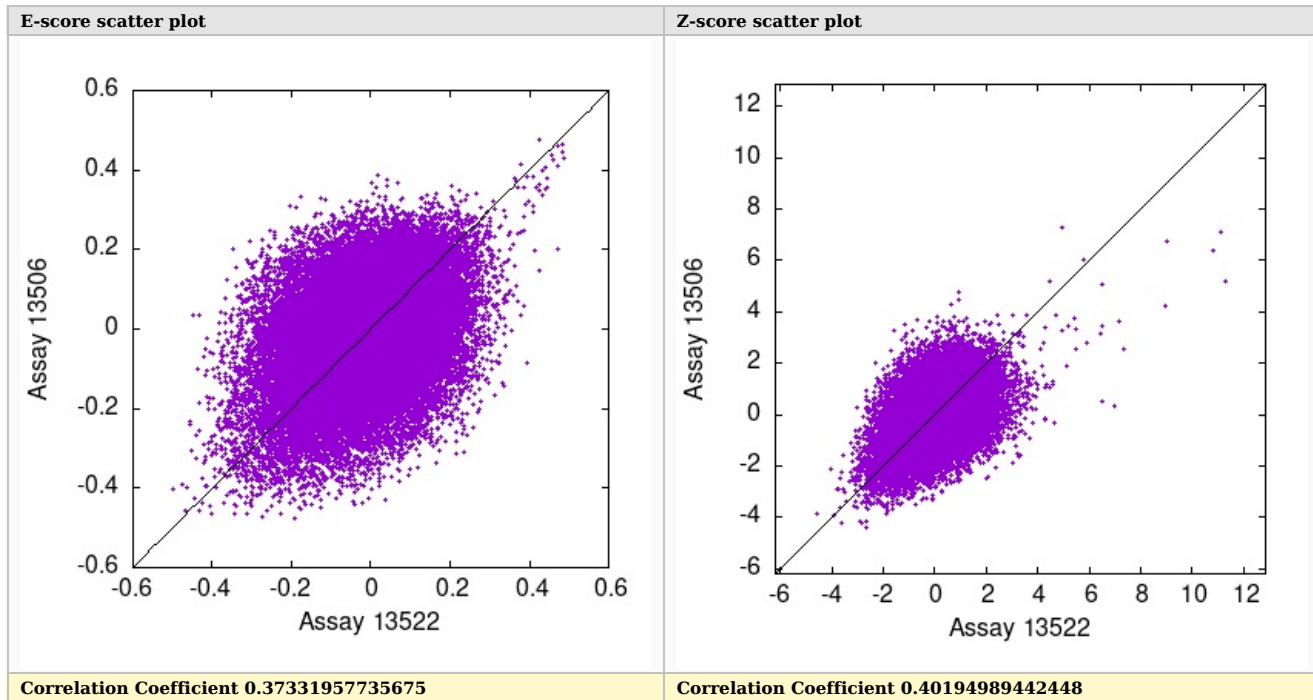


QC report



Top scoring motifs for Assay 13522

Protein ID: pTH13951.2 Gene: AKAP8L.DBD Domain: zf-C2H2 Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GGGGAGAA	0.48689	--GGGGAGAA
AGGGGAGA	0.48540	--AGGGGAGA-
ATCTCCCC	0.48470	--GGGGAGAT
CTCTCCCC	0.47306	--GGGGAGAG
GGGGGAGA	0.47196	--GGGGGAGA-
AAAGGGAG	0.47193	AAAGGGAG--
TCTCCCCA	0.46022	-TGGGGAGA-
CAGGGGAG	0.45605	CAGGGGAG--
GGGGAGTA	0.44647	--GGGGAGTA
AAGGGGAG	0.44495	AAGGGGAG--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GGGGAGAA	11.26646	--GGGGAGAA
ATCTCCCC	11.10212	--GGGGAGAT
AGGGGAGA	10.82751	--AGGGGAGA-
CTCTCCCC	9.04326	--GGGGAGAG
GGGGGAGA	8.94242	--GGGGGAGA-
ACTCCCCC	7.31461	-GGGGAGT-
AAGGGGAG	7.16501	AAGGGGAG--
AAAGGGAG	6.95849	AAAGGGAG--
TCTCCCCA	6.53068	-TGGGGAGA-
ACTCCCCG	6.49865	-CGGGGAGT-

Top scoring motifs for Assay 13506

Protein ID: pTH13951.1 Gene: AKAP8L.DBD Domain: zf-C2H2 Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CGGGGAGA	0.47691	-CGGGGAGA----
ATCTCCCC	0.46349	--GGGGAGAT----
CTCTCCCC	0.46125	--GGGGAGAG----
AGGGGAGA	0.44648	-AGGGGAGA----
CAGGGGAG	0.43560	CAGGGGAG-----
GGGGAGAA	0.43072	--GGGGAGAA----
TCTCCCCA	0.42627	-TGGGGAGA----
ACGGGGAG	0.41342	ACGGGGAG-----
GGGGGAGA	0.40974	-GGGGGAGA----
ACTCCCCG	0.40469	-CGGGGAGT-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CGGGGAGA	7.28865	-CGGGGAGA----
ATCTCCCC	7.12798	--GGGGAGAT----
CTCTCCCC	6.72256	--GGGGAGAG----
AGGGGAGA	6.36499	-AGGGGAGA----
CAGGGGAG	5.99341	CAGGGGAG-----
ACGGGGAG	5.16725	ACGGGGAG-----
GGGGAGAA	5.15620	--GGGGAGAA----
TCTCCCCA	5.09054	-TGGGGAGA----
TATGTACA	4.76964	-TATGTACA-----
AGACGTCT	4.44325	-----AGACGTCT