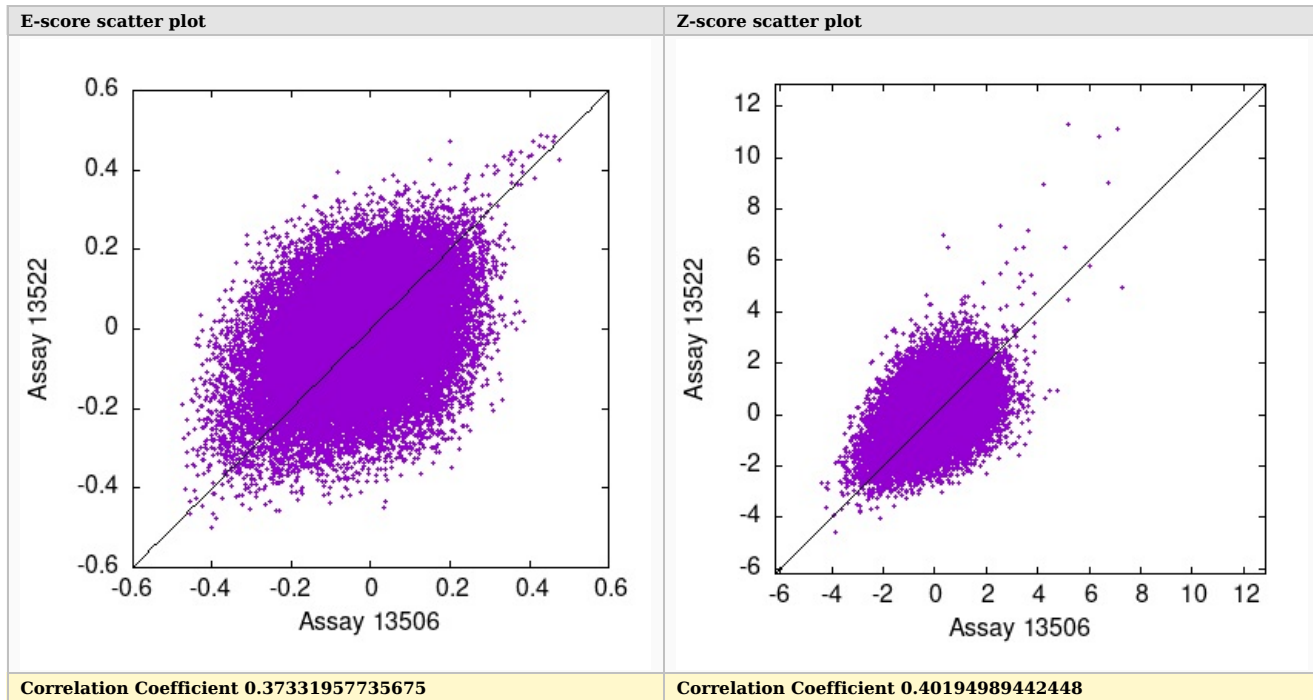


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CGGGGAGA	0.47691	-CGGGGAGA-	CGGGGAGA	7.28865	-CGGGGAGA----
ATCTCCCC	0.46349	--GGGGAGAT	ATCTCCCC	7.12798	--GGGGAGAT----
CTCTCCCC	0.46125	--GGGGAGAG	CTCTCCCC	6.72256	--GGGGAGAG----
AGGGGAGA	0.44648	-AGGGGAGA-	AGGGGAGA	6.36499	-AGGGGAGA----
CAGGGGAG	0.43560	CAGGGGAG--	CAGGGGAG	5.99341	CAGGGGAG-----
GGGGAGAA	0.43072	--GGGGAGAA	ACGGGGAG	5.16725	ACGGGGAG-----
TCTCCCCA	0.42627	-TGGGGAGA-	GGGGAGAA	5.15620	--GGGGAGAA----
ACGGGGAG	0.41342	ACGGGGAG--	TCTCCCCA	5.09054	-TGGGGAGA----
GGGGGAGA	0.40974	-GGGGGAGA-	TATGTACA	4.76964	-TATGTACA----
ACTCCCG	0.40469	-CGGGGAGT-	AGACGTCT	4.44325	-----AGACGTCT

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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GGGGAGAA	0.48689	--GGGGAGAA	GGGGAGAA	11.26646	--GGGGAGAA
AGGGGAGA	0.48540	-AGGGGAGA-	ATCTCCCC	11.10212	--GGGGAGAT
ATCTCCCC	0.48470	--GGGGAGAT	AGGGGAGA	10.82751	-AGGGGAGA-
CTCTCCCC	0.47306	--GGGGAGAG	CTCTCCCC	9.04326	--GGGGAGAG
GGGGGAGA	0.47196	-GGGGGAGA-	GGGGGAGA	8.94242	-GGGGGAGA-
AAAGGGAG	0.47193	AAAGGGAG--	ACTCCCC	7.31461	-GGGGGAGT-
TCTCCCCA	0.46022	-TGGGGAGA-	AAGGGGAG	7.16501	AAGGGGAG--
CAGGGGAG	0.45605	CAGGGGAG--	AAAGGGAG	6.95849	AAAGGGAG--
GGGGAGTA	0.44647	--GGGGAGTA	TCTCCCCA	6.53068	-TGGGGAGA-
AAGGGGAG	0.44495	AAGGGGAG--	ACTCCCG	6.49865	-CGGGGAGT-