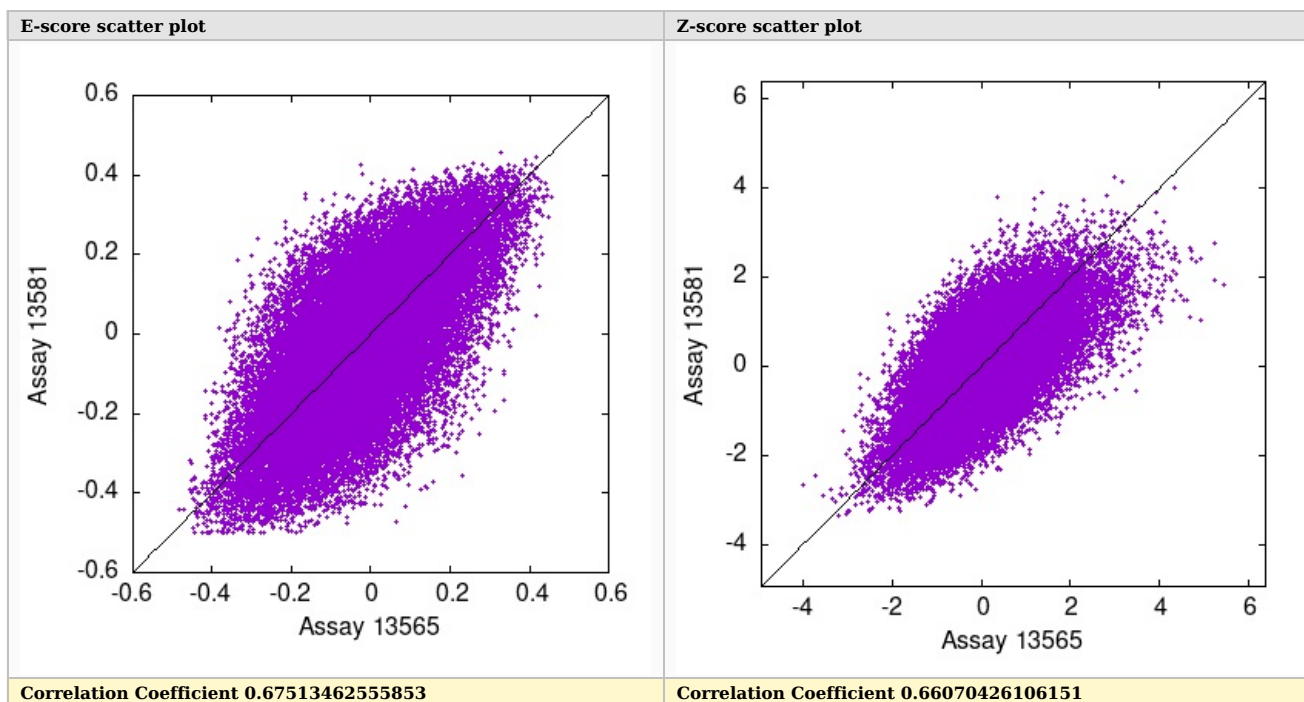


QC report





Top scoring motifs for Assay 13565

Protein ID: pTH13957.1 Gene: CHAMP1.DBD Domain: zf-C2H2 Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
ATAATATA	0.45767	---TATATTAT-	
ACTAATAA	0.44891	TTATTAGT----	
AACTAACG	0.44567	--CGTTAGTT---	
GTTAGTTA	0.44439	--GTTAGTTA--	
AACTAACT	0.44214	-AGTTAGTT---	
AAAGTAAT	0.43872	--ATTACTTT--	
GTTAACTA	0.43644	----TAGTTAAC	
ATTAGTTG	0.43482	--ATTAGTTG--	
AAGTAACA	0.43339	-TGTTACTT---	
AACTAATG	0.43212	-CATTAGTT---	



8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ACTAATAA	5.45107	TTATTAGT - - -
GTTAGTTA	5.26544	- - GTTAGTTA - -
ATAATATA	5.25693	- - - TATATTAT -
AACTAACG	4.94130	- CGTTAGTT - - -
ACTAACGG	4.92239	CCGTTAGT - - - -
ATATGTTA	4.85238	- - ATATGTTA - -
AAGTAATT	4.74237	- AATTACTT - - -
GTTAACCTA	4.73338	- - - - TAGTTAAC
AACTAACT	4.70248	- AGTTAGTT - - -
CGTTAGTC	4.68527	- CGTTAGTC - - -



Top scoring motifs for Assay 13581

Protein ID: pTH13957.2 Gene: CHAMP1.DBD Domain: zf-C2H2 Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AATAATAA	0.45602	--AATAATAA--
ACTAATTA	0.44618	---ACTAATTA---
ACTATAAT	0.43729	---ACTATAAT---
ATATTAAG	0.42970	---ATATTAAG---
ACTAACAT	0.42635	--ACTAACAT---
TAATAATA	0.42584	-TAATAATA---
ATATAACA	0.42535	-ATATAACA---
ATTATTTT	0.42493	GAAATAAT---
AGTAATTA	0.42441	--AGTAATTA---
AAATAATA	0.42221	-AAATAATA---

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AATAATAA	4.25128	--AATAATAA--
AGTAATTA	4.13176	--AGTAATTA---
ACTAATTA	4.00186	---ACTAATTA---
ACTATAAT	3.92271	---ACTATAAT---
ATATCACA	3.91826	---ATATCACA---
ATATAACA	3.82133	-ATATAACA---
ATTATTTT	3.78685	GAAATAAT---
ATATACAA	3.78323	--ATATACAA---
ATATTAAG	3.72001	---ATATTAAG---
ATTAATCA	3.63989	--ATTAATCA---