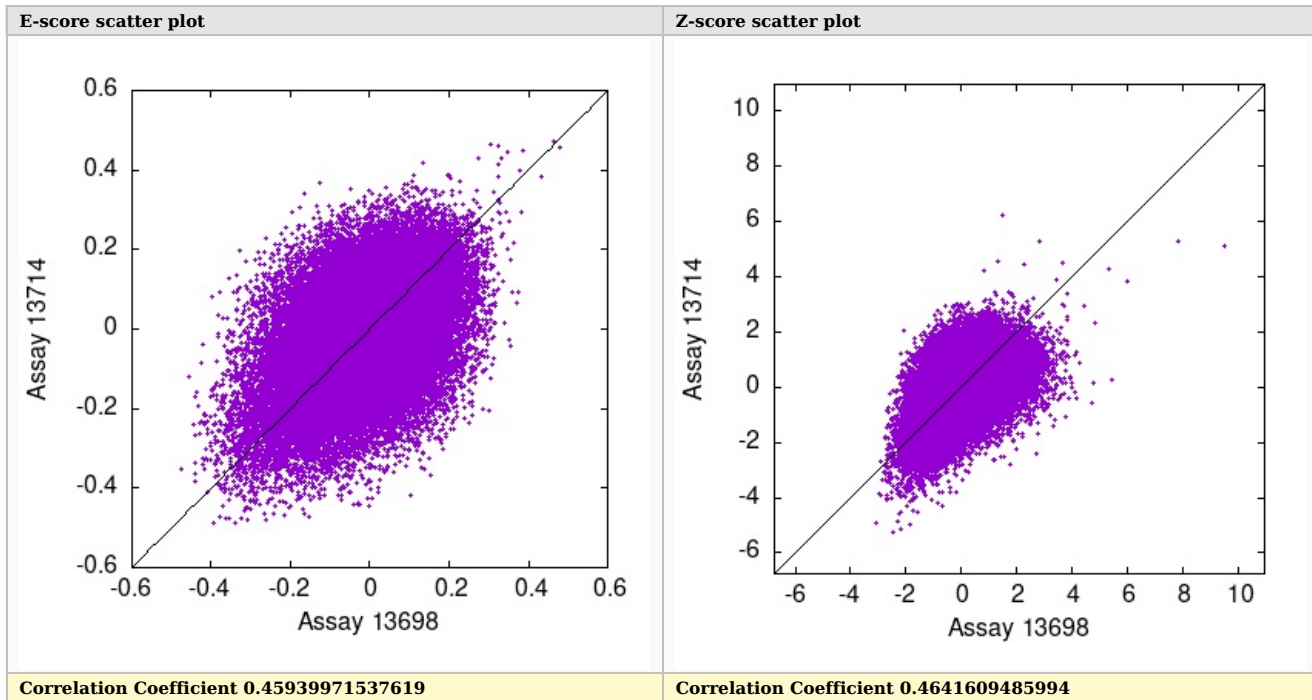


QC report



Top scoring motifs for Assay 13698

Protein ID: pTH14210.1 Gene: JRK.DBD Domain: CENP-B_N 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
ATCCGGAA	0.47778	---ATCCGGAA--	ATCCGGAA	9.49685	-----ATCCGGAA--
TATCCGGA	0.46404	--TATCCGGA--	TATCCGGA	7.84255	-----TATCCGGA--
ATTCCGGA	0.43337	---TCCGGAAT	ATTCCGGA	6.03276	-----TCCGGAAT
TAACCGGA	0.38804	--TAACCGGA--	TATAAATA	5.45596	-----TATAAATA--
AATCCGGA	0.38396	--AATCCGGA--	TAACCGGA	5.31828	-----TAACCGGA--
CCGGATAA	0.38008	--TTATCCGG--	AATCCGGA	4.85837	-----AATCCGGA--
TATACAGA	0.37557	--TATACAGA--	TATACAGA	4.77276	-----TATACAGA--
TATAAATA	0.37071	--TATAAATA--	ACAAATGG	4.71254	-----ACAAATGG--
GTACTTTA	0.36481	--GTACTTTA--	ATAATGTA	4.46040	TACATTAT-----
CGGATACA	0.36007	TGTATCCG----	TATATGGA	4.29098	-----TATATGGA--

Top scoring motifs for Assay 13714

Protein ID: pTH14210.2 Gene: JRK.DBD Domain: CENP-B_N 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
TATCCGGA	0.47249	TATCCGGA--	TTCCGGAA	6.24708	-TTCCGGAA-
AACCGGAA	0.46408	-AACCGGAA-	AACCGGAA	5.27728	-AACCGGAA-
TTCCGGAA	0.45914	-TTCCGGAA-	TATCCGGA	5.26893	TATCCGGA--
ATCCGGAA	0.45839	-ATCCGGAA-	ATCCGGAA	5.10310	-ATCCGGAA-
TAACCGGA	0.44737	TAACCGGA--	ATCCGGAT	4.56572	-ATCCGGAT-
CATCCGGA	0.44384	CATCCGGA--	CATCCGGA	4.51451	CATCCGGA--
ATCCGGAT	0.42865	-ATCCGGAT-	TCCGGAAA	4.43473	--TCCGGAAA
ATCCGGAC	0.42777	-ATCCGGAC-	TAACCGGA	4.29781	TAACCGGA--
CTTCCGGA	0.41662	--TCCGGAAG	CTTCCGGA	4.25531	--TCCGGAAG
TCCGGAAA	0.41412	--TCCGGAAA	ATCCGGAC	3.90314	-ATCCGGAC-