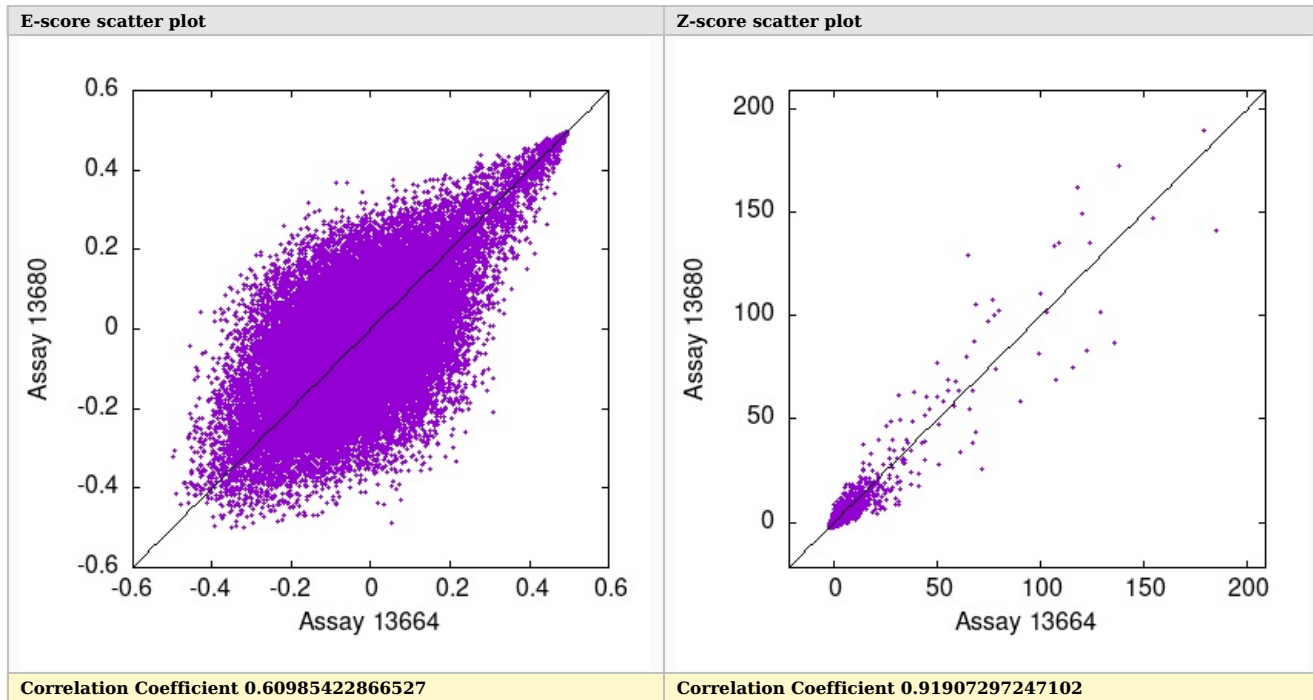


QC report



Top scoring motifs for Assay 13664

Protein ID: pTH14274.1 Gene: MYPOP.DBD Domain: Myb_DNA-binding 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
GCGCTAA	0.49653	-GGCGCTAA-	TAGCGCTA	185.11795	TAGCGCTA--
GCGCAAA	0.49633	-GGCGCAAA-	GCGGCTAA	178.62337	-GGCGCTAA-
TAGCGCTA	0.49612	TAGCGCTA--	GCGGCAAA	154.52119	-GGCGCAAA-
AGCGCTAA	0.49584	-AGCGCTAA-	ATTGCGCC	137.58601	-GGCGCAAT-
GCGCTAAC	0.49444	--GCGCTAAC	ATTTGCGC	135.39991	--GCGCAAT
TTGCGCAA	0.49435	TTGCGCAA--	TTGCGCAA	128.60180	TTGCGCAA--
CGGCGCTA	0.49380	CGGCGCTA--	AGCGCAAA	123.35616	-AGCGCAAA-
GCGCAAAC	0.49377	--GCGCAAAC	GCGCTAAC	122.11518	--GCGCTAAC
TGCGCAAA	0.49373	-TGCGCAAA-	CGGCGCAA	119.99053	CGGCGCAA--
CTTTGCGC	0.49366	--GCGCAAG	AGCGCTAA	117.88525	-AGCGCTAA-

Top scoring motifs for Assay 13680

Protein ID: pTH14274.2 Gene: MYPOP.DBD Domain: Myb_DNA-binding 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
GCGCTAA	0.49586	-GGCGCTAA-	GCGCTAA	189.54975	-GGCGCTAA-
ATTGCGCC	0.49567	-GGCGCAAT-	ATTGCGCC	172.48681	-GGCGCAAT-
AGCGCTAA	0.49567	-AGCGCTAA-	AGCGCTAA	161.60280	-AGCGCTAA-
GCGCAAA	0.49527	-GGCGCAAA-	CGGCGCAA	149.14762	CGGCGCAA--
CGGCGCAA	0.49494	CGGCGCAA--	GCGGCAAA	146.67734	-GGCGCAAA-
GCGTAAC	0.49453	--GCGTAAC	TAGCGCTA	140.87145	TAGCGCTA--
GCGCAAAA	0.49434	--GCGCAAAA	AGCGCAAA	135.36138	-AGCGCAAA-
AGCGCAAA	0.49339	-AGCGCAAA-	GCGCAAAA	135.22420	--GCGCAAAA
ATTAGCGC	0.49323	--GCGCTAAT	GCGCAAAC	133.89748	--GCGCAAAC
TAGCGCTA	0.49298	TAGCGCTA--	ATTAGCGC	129.19198	--GCGCTAAT