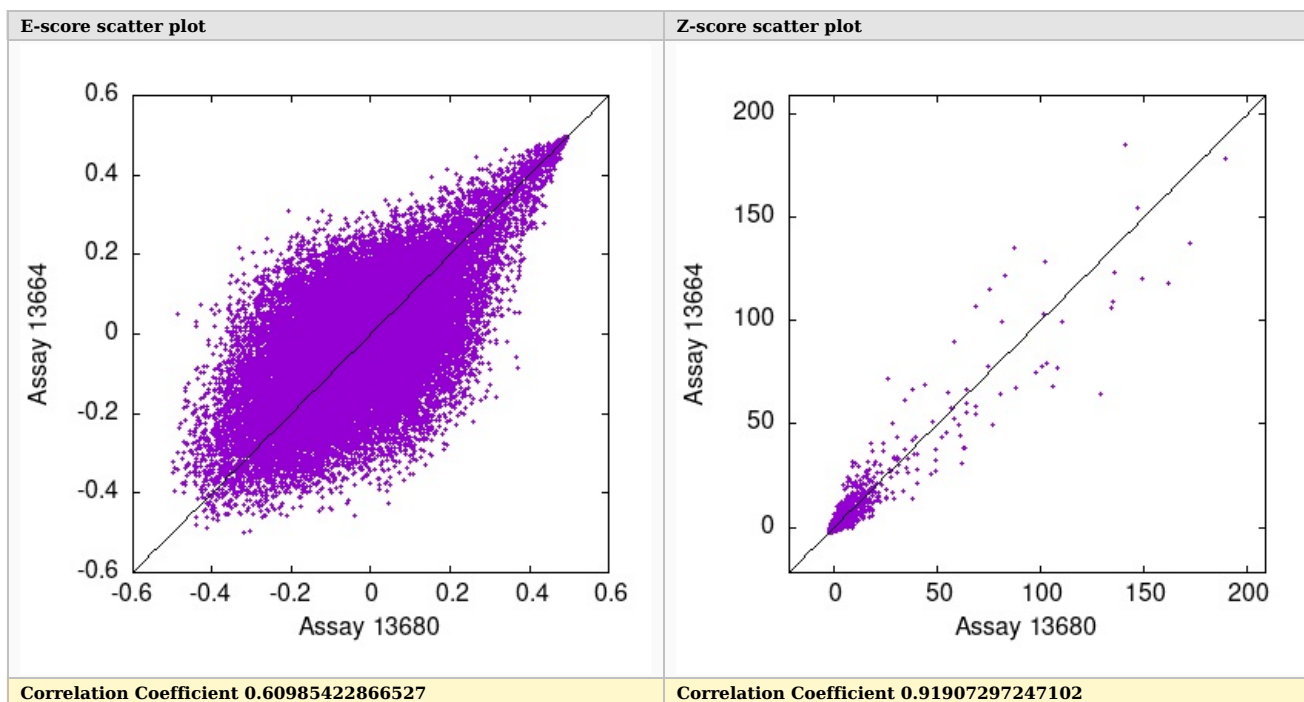


QC report



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'

Forward:

Reverse:



Top 10

Scores

Alignment

GCGCTAA	0.49586	-GCGCTAA-
ATTGCGCC	0.49567	-GCGCAAT-
AGCGCTAA	0.49567	-AGCGCTAA-
GCGCAAAA	0.49527	-GCGCAAAA-
CGGCGCAA	0.49494	CGGCGCAA--
GCGCTAAC	0.49453	--GCGCTAAC
GCGCAAAA	0.49434	--GCGCAAAA
AGCGCAAA	0.49339	-AGCGCAAA-
ATTAGCGC	0.49323	-GCGCTAAT
TAGCGCTA	0.49298	TAGCGCTA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GCGCTAA	189.54975	-GCGCTAA-
ATTGCGCC	172.48681	-GCGCAAT-
AGCGCTAA	161.60280	-AGCGCTAA-
CGGCGCAA	149.14762	CGGCGCAA--
GCGCAAAA	146.67734	-GCGCAAAA-
TAGCGCTA	140.87145	TAGCGCTA--
AGCGCAAA	135.36138	-AGCGCAAA-
GCGCAAAA	135.22420	--GCGCAAAA
GCGCAAAC	133.89748	--GCGCAAAC
ATTAGCGC	129.19198	-GCGCTAAT

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'

Forward:

Reverse:



Top 10

Scores

Alignment

GCGCTAA	0.49653	-GCGCTAA-
GCGCAAAA	0.49633	-GCGCAAAA-
TAGCGCTA	0.49612	TAGCGCTA--
AGCGCTAA	0.49584	-AGCGCTAA-
GCGCTAAC	0.49444	--GCGCTAAC
TTGCGCAA	0.49435	TTGCGCAA--
CGGCGCTA	0.49380	CGGCGCTA--
GCGCAAAC	0.49377	--GCGCAAAC
TGCGCAAA	0.49373	-TGCGCAAA-
CTTTGCGC	0.49366	--GCGCAAAG

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAGCGCTA	185.11795	TAGCGCTA--
GCGCTAA	178.62337	-GCGCTAA-
GCGCAAAA	154.52119	-GCGCAAAA-
ATTGCGCC	137.58601	-GCGCAAT-
ATTTGCGC	135.39991	--GCGCAAT
TTGCGCAA	128.60180	TTGCGCAA--
AGCGCAAA	123.35616	-AGCGCAAA-
GCGCTAAC	122.11518	--GCGCTAAC
CGGCGCAA	119.99053	CGGCGCAA--
AGCGCTAA	117.88525	-AGCGCTAA-