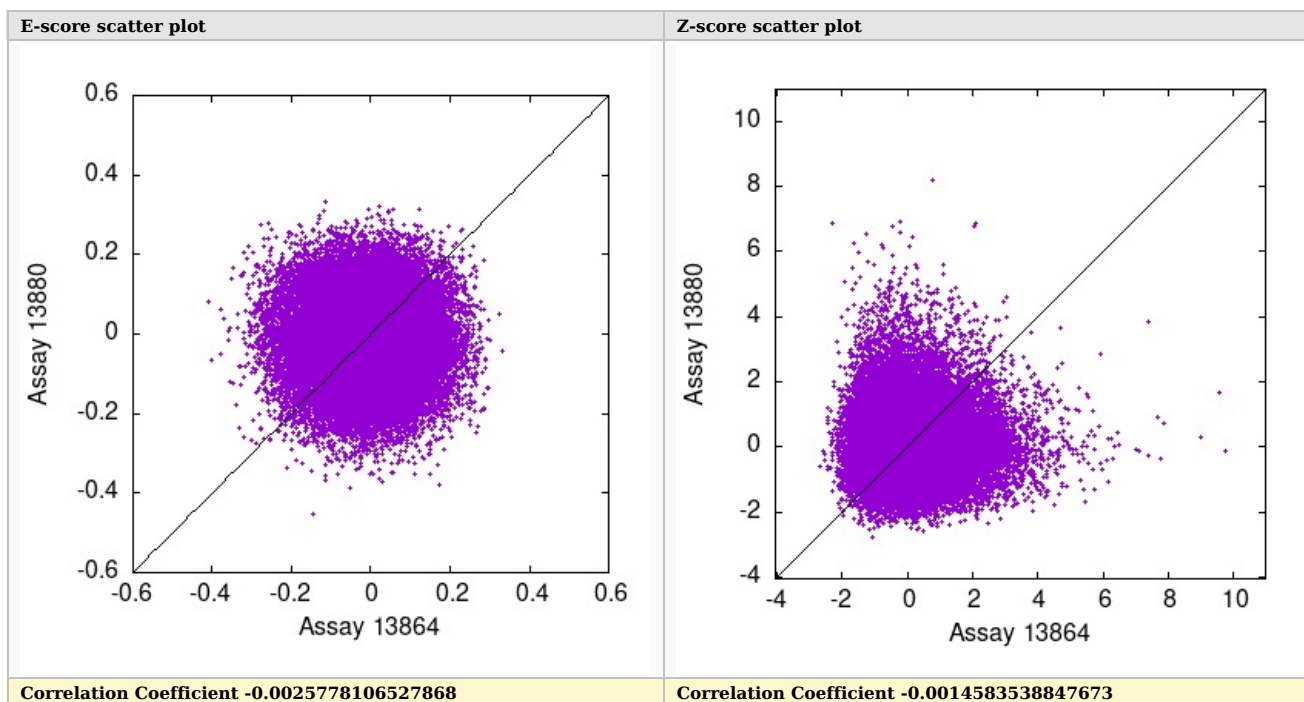


QC report



Top scoring motifs for Assay 13864

Protein ID: pTH14273.1 Gene: MYPOP Domain: Myb_DNA-binding

Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

8 mer Z-scores for probeset 'all'

Forward:			Reverse:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATGATCAC	0.33019	--ATGATCAC--	TGCAACAA	9.72062	---TGCAACAA--
AGTCGACA	0.32474	---TGTCGACT--	AGTCGACA	9.56863	--AGTCGACA---
CCCACGCA	0.29938	---CCCACGCA---	GTTGCAAC	8.99189	---GTTGCAAC--
AATATTGA	0.29684	-AATATTGA---	ATGATCAC	7.84439	---GTGATCAT--
AGCTACAT	0.29663	--ATGTAGCT--	ATCCGGCA	7.74905	--ATCCGGCA---
CAAGTCAG	0.29318	-----CTGACTTG	TAAGTGGA	7.64873	TAAGTGGA-----
TAAGTGGA	0.29170	-TAAGTGGA---	AATGATCG	7.37609	-----CGATCATT
CATGATTA	0.28908	TAATCATG----	AACTACTT	7.37156	-AAGTAGTT-----
CGCTTTGA	0.28775	-CGCTTTGA----	GAACGTAC	7.11358	-GAACGTAC-----
ATTGCTGA	0.28746	-ATTGCTGA----	GGTGCTGA	6.98435	----TCAGCACC-

Top scoring motifs for Assay 13880

Protein ID: pTH14273.2 Gene: MYPOP Domain: Myb_DNA-binding

Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

8 mer Z-scores for probeset 'all'

Forward:			Reverse:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TGAAGCAA	0.33108	-----TGAAGCAA	GAGGTGGA	8.17220	-GAGGTGGA-
GAGGTGGA	0.32092	TCCACCTC-----	ACTTTGCC	6.91866	GGCAAAGT--
ATGTGGAG	0.31478	---ATGTGGAG---	CATGCATG	6.85302	-CATGCATG-
GCGACCGA	0.31243	-GCGACCGA----	CCTGATTC	6.84627	-CCTGATTC-
ATCAGTTA	0.31211	--TAAGTGAT---	TTCTAGAA	6.78838	-TTCTAGAA-
AAGTACTT	0.30921	---AAGTACTT---	AGGACACA	6.75197	--AGGACACA
CACAGCCG	0.30788	-----CGGCTGTG-	GCTCCCCC	6.55713	GGGGGAGC--
AGCCGATC	0.30448	---AGCCGATC---	AAAGCTAC	6.51863	-AAAGCTAC-
ATCACAGG	0.30305	---CCTGTGAT----	AATTAGGC	6.42793	-AATTAGGC-
AACTGATG	0.29745	---AACTGATG---	GAAGAGAC	6.24370	-GAAGAGAC-