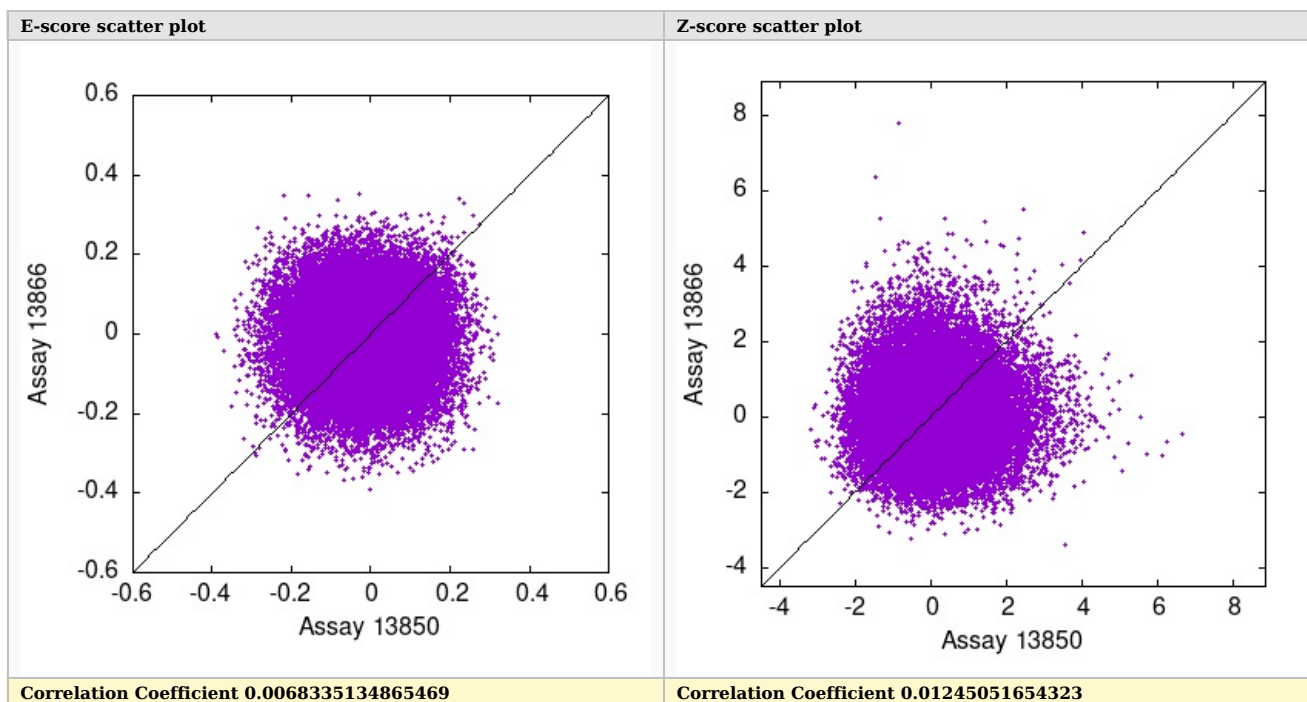


QC report



Top scoring motifs for Assay 13850

Protein ID: pTH14250.1 Gene: ZHX2.DBD.2 Domain: Homeobox Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment	Top 10	Scores	Alignment
GGCGCGCA	0.32024	GGCGCGCA----	GTTCAGA	6.66517	---GTTCAGA--
GTTCAGA	0.31960	---GTTCAGA	GTAAGTGA	6.27342	-----GTAAGTGA
CAGGTTTC	0.31352	--CAGGTTTC--	GGCGCGCA	6.14099	-----TGCGCGCC
ATACATAC	0.30940	-GTATGTAT---	CTCATTCC	5.71459	-----CTCATTCC-
CAGTCTGA	0.30811	--CAGTCTGA--	CAGTCTGA	5.57350	CAGTCTGA-----
GTAAGTGA	0.30376	-TCACTTAC---	CAGGTTTC	5.31678	-----CAGGTTTC-
CAGGTATA	0.29936	--CAGGTATA--	ACAGCAGT	5.25207	---ACTGCTGT--
ATGGAGAC	0.29921	---ATGGAGAC-	CTGATGTC	5.08286	-----CTGATGTC-
CCGGGAGA	0.29868	--CCGGGAGA--	AAACGTAA	5.00995	-----TTACGTTT
ACTCACTC	0.29846	--GAGTGAGT--	ACTCACTC	4.98949	--GAGTGAGT---

Top scoring motifs for Assay 13866

Protein ID: pTH14250.2 Gene: ZHX2.DBD.2 Domain: Homeobox Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATTACGAA	0.35283	-ATTACGAA----	ATTACGAA	7.76292	ATTACGAA-----
AACTGATC	0.34920	---AACTGATC---	AACTGATC	6.36475	--AACTGATC---
GACGCTCC	0.34778	-----GGAGCGTC	CTAGTTC	5.47718	-GAACGTAG----
CAGTGATC	0.34145	---CAGTGATC---	CCTACCGA	5.24245	CCTACCGA-----
CCGTTGAC	0.33744	GTCACCG-----	AGGTTCG	5.23561	-----CGAACCT-
CTGGAATC	0.32882	-----CTGGAATC-	GGTAATCA	5.15544	-----TGATTACC
GAGGCTCC	0.30456	-----GGAGCCTC	AAGGGCGC	4.87657	--AAGGGCGC---
ATGATCCG	0.30345	-----ATGATCCG-	CTAGCTAG	4.83759	CTAGCTAG-----
CTCAGTTC	0.30235	--GAACGTAG----	GAGGCTCC	4.83096	-----GGAGCCTC
CCTACCGA	0.30228	-CCTACCGA-----	CAGTGATC	4.73585	--CAGTGATC---