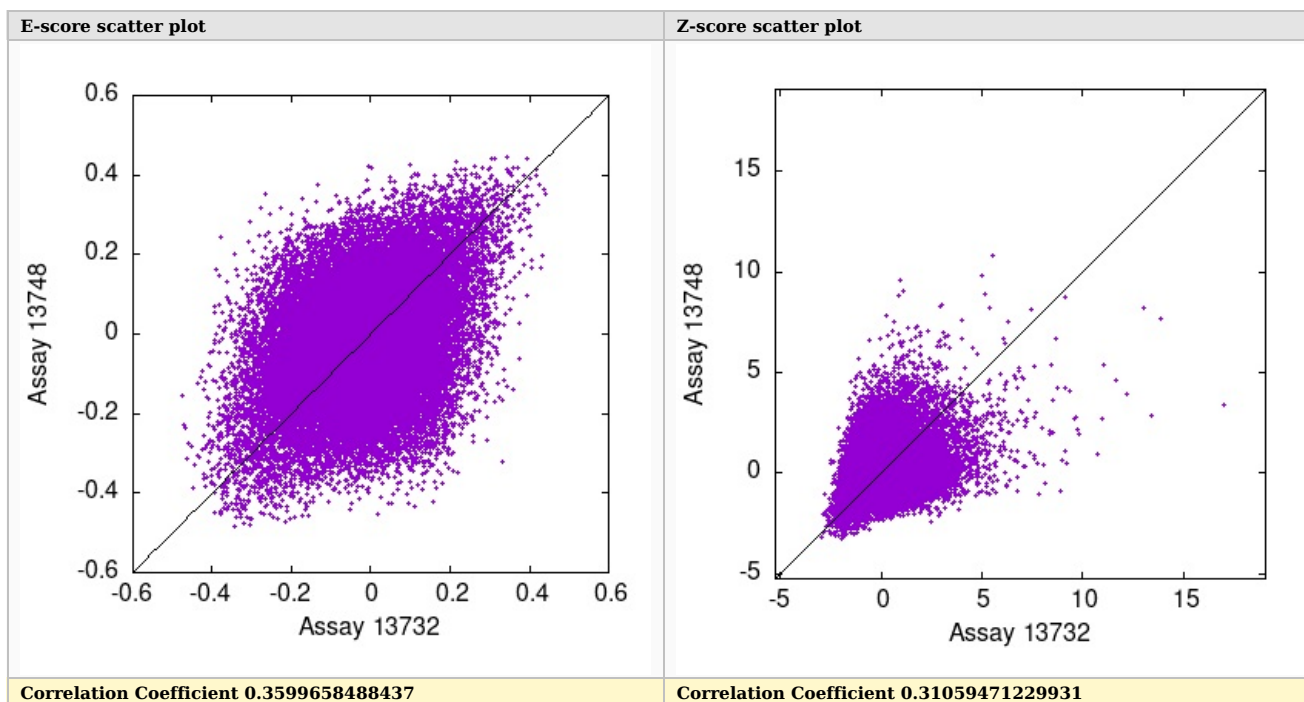




QC report





Top scoring motifs for Assay 13732

Protein ID: pTH14319.1 Gene: PURB.FL Domain: Unknown Flag: Unsure Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AACCAACT	0.43998	- - AACCAACT
CCAACACA	0.43600	CCAACACA - -
GTGGGTAA	0.43286	- TTACCCAC -
GTGGGTGA	0.42922	- TCACCCAC -
AAACCAAC	0.42558	- AAACCAAC -
AGTGGGTG	0.41991	- - CACCCACT
AACCAACA	0.41733	- - AACCAACA
AAACCCAC	0.41660	- AAACCCAC -
AACACACA	0.40589	- - AACACACA
ACACCCAC	0.40478	- ACACCCAC -



8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AGTGGGTG	17.05951	--CACCCACT--
AACCAACT	13.91154	--AACCAACT--
GTTGGAAA	13.39048	-TTTCCAAC--
AAACCCAC	13.06679	-AAACCCAC--
AACCAACA	12.21802	--AACCAACA--
AAACCAAC	11.66808	-AAACCAAC--
CCAACACA	11.02444	----CCAACACA
ACACAACC	10.93924	-ACACAACC--
TGGGTAAA	10.72670	TTTACCCA--
ACACCCAC	9.82966	-ACACCCAC--



Top scoring motifs for Assay 13748

Protein ID: pTH14319.2 Gene: PURB.FL Domain: Unknown Flag: Unsure Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ACCCACCA	0.44384	--ACCCACCA
AACCCACA	0.44165	--AACCCACA-
CAACCCAC	0.44001	--CAACCCAC--
AACCCACC	0.43994	--AACCCACC-
AAACCGAC	0.43176	-AAACCGAC--
ACAACCCA	0.42523	ACAACCCA---
ACCCTCAA	0.42291	---ACCCTCAA
GACCGACA	0.42050	--GACCGACA-
GACCAACC	0.41992	--GACCAACC-
ACCCACTA	0.41951	---ACCCACTA

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
CAACCCAC	10.81382	-CAACCCAC--
ACCAACAT	9.84610	---ACCAACAT
ACCAACCT	9.59111	---ACCAACCT
AAACCGAC	9.07453	-AAACCGAC--
ATTGTTGG	8.93709	-CCAACAAT--
TACCAACA	8.82472	--TACCAACA-
AATCCACC	8.77324	-AATCCACC--
CCAACCGA	8.36612	CCAACCGA---
CAACCAAC	8.26340	-CAACCAAC--
ACCCACTA	8.23112	---ACCCACTA