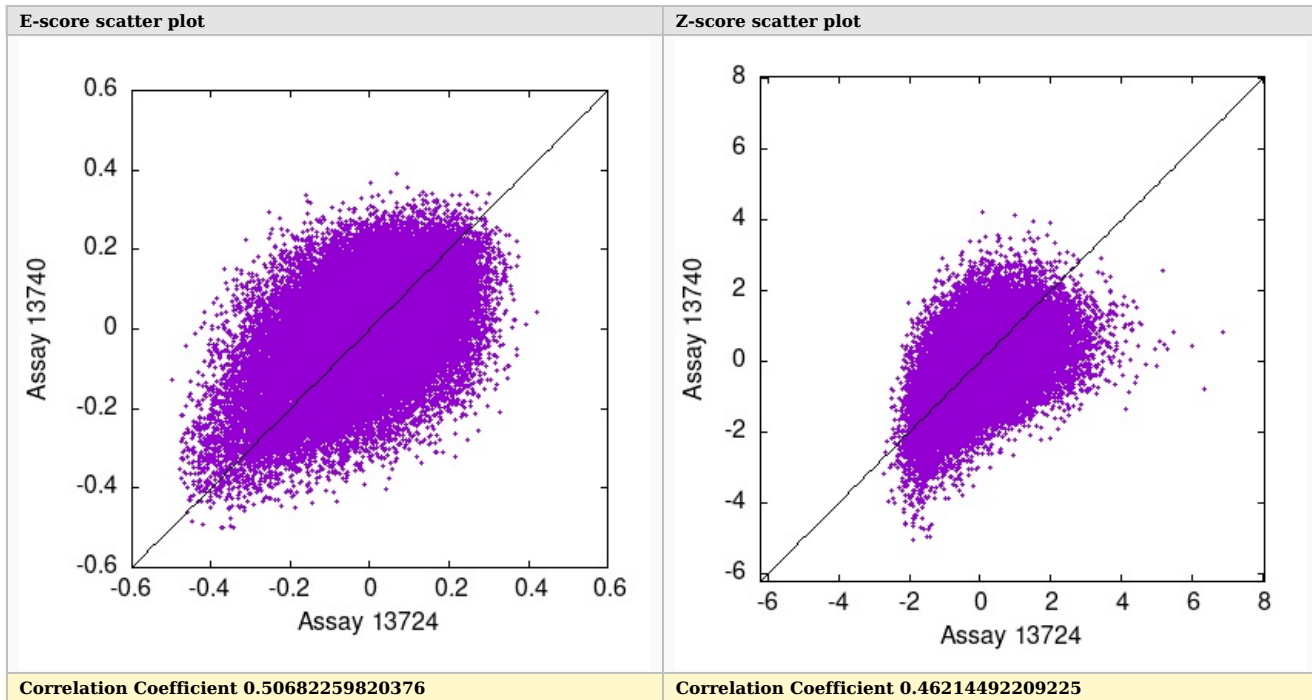


QC report



Top scoring motifs for Assay 13724

Protein ID: pTH14306.1 Gene: KCNIP3.FL Domain: Unknown Flag: Reject 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
AACATGTT	0.42106	-AACATGTT-----	AACATGTT	6.86255	AACATGTT--
TGTATACA	0.39366	-TGTATACA-----	ATGTACAT	6.33825	--ATGTACAT-
ACATACAA	0.37437	--ACATACAA-----	TGTATACA	6.02036	--TGTATACA
ATGTACAT	0.37275	--ATGTACAT-----	ACATACAA	5.46788	--ACATACAA-
TAACGAAA	0.37235	--TAACGAAA-----	ACAACCTTA	5.30603	-ACAACCTTA-
AGCAATTG	0.36981	-----CAATTGCT	TAACAGTA	5.23242	-TAACAGTA-
GTACTTTA	0.36974	TAAAGTAC-----	GTACTTTA	5.15337	--TAAAGTAC
ATCGATGC	0.36520	--GCATCGAT-----	TATATTAA	5.06944	--TATATTAA
AGTCATGA	0.36495	--AGTCATGA-----	AGCAATTG	5.01858	-AGCAATTG-
ACAACCTTA	0.36461	--ACAACCTTA-----	ATATATTA	4.95609	-ATATATTA-

Top scoring motifs for Assay 13740

Protein ID: pTH14306.2 Gene: KCNIP3.FL Domain: Unknown Flag: Reject 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
GCTGTGAA	0.39042	-GCTGTGAA-----	GCTGTGAA	4.20587	GCTGTGAA-----
CGACTGAA	0.36959	-----CGACTGAA-	AAGCTTTC	4.15935	-----GAAAGCTT-
AAGCTTTC	0.35785	-----GAAAGCTT	ACTAAAAT	3.97814	-----ACTAAAAT----
CGCTAAAA	0.34571	--CGCTAAAA-----	AACCAATC	3.92308	-----AACCAATC
ATGTGACA	0.34560	--ATGTGACA-----	AAACAGTT	3.67088	-----AAGTGTTC
TCAATTGA	0.34499	TCAATTGA-----	CTGAACGA	3.58133	---CTGAACGA---
ATACAAAT	0.34234	--ATTTGTAT-----	GTATACGA	3.56617	--GTATACGA---
CAATGTCA	0.34168	-----TGACATTG-	ATGAAGTA	3.51980	---ATGAAGTA---
AATCTGGC	0.33848	-AATCTGGC-----	TGTGACAA	3.50740	---TGTGACAA---
GTATACGA	0.33839	GTATACGA-----	CAATGTCA	3.47309	-----CAATGTCA-