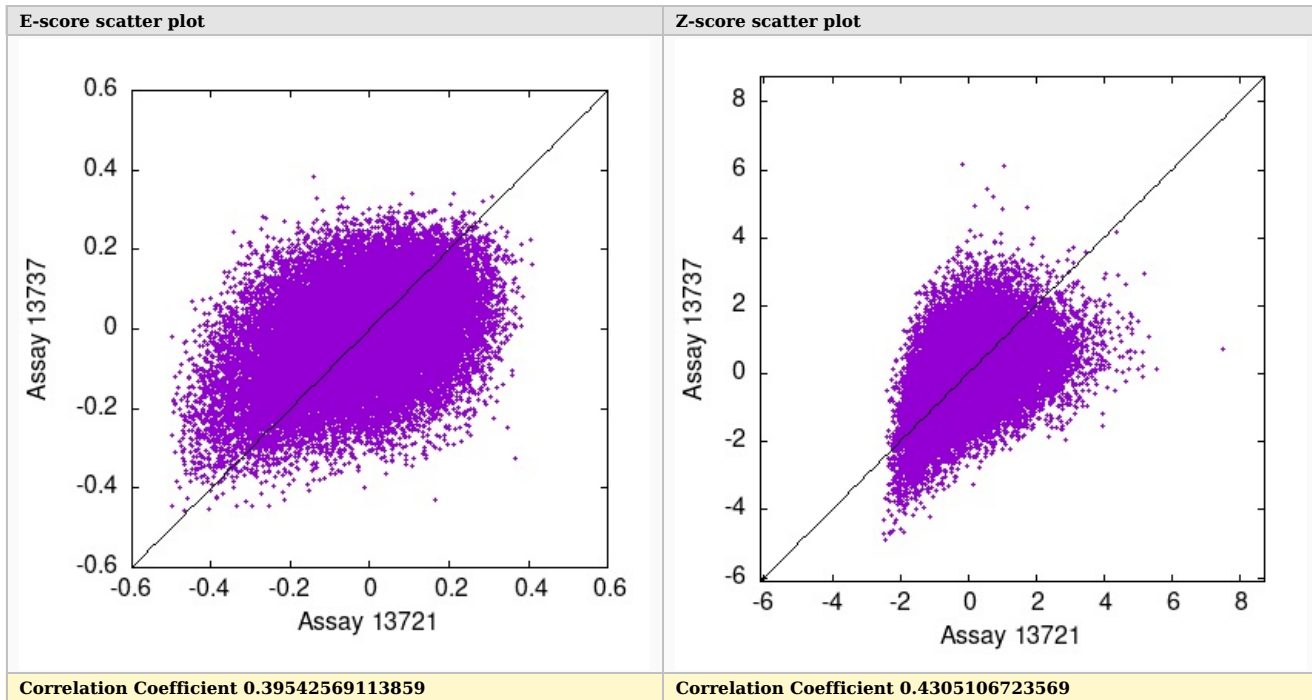


QC report



Top scoring motifs for Assay 13721

Protein ID: pTH14300.1 Gene: DR1.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
AGAATTCT	0.41021	--AGAATTCT--	AGAATTCT	7.50831	-AGAATTCT-
TAAATTTA	0.40568	-TAAATTTA--	ACATTATC	5.56728	GATAATGT--
TATATACA	0.38791	---TATATACA-	ATATTTTA	5.35578	--TAAATAT-
TGATATCA	0.38403	TGATATCA---	TAAATTTA	5.18569	-TAAATTTA-
GTTGCAAC	0.38391	--GTTGCAAC--	ATAATATA	5.17795	-ATAATATA-
AATTACGT	0.38304	---AATTACGT	ATATATTA	5.17795	--TAATATAT-
AACTGATA	0.37854	---AACTGATA-	ATTATATA	5.17795	-ATTATATA-
ATATTTTA	0.37666	--ATATTTTA--	ACAAACAT	5.01084	ACAAACAT--
ATATTTAC	0.37148	--ATATTTAC--	TCTATAGA	5.00425	-TCTATAGA-
AATTGTTA	0.36845	-AATTGTTA--	ATAACAAT	4.92264	-ATAACAAT-

Top scoring motifs for Assay 13737

Protein ID: pTH14300.2 Gene: DR1.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
AGTTTTTC	0.38469	-AGTTTTTC-	AGTTTTTC	6.15337	-AGTTTTTC--
CATTTGCA	0.33963	--CATTTGCA-	AGTCTACA	6.09858	--AGTCTACA-
AGTCTACA	0.33899	-AGTCTACA-	CAGCTAAC	5.43669	---GTTAGCTG
AACGTAAC	0.33135	--GTTACGTT	CATTTGCA	5.20628	--CATTTGCA-
ACAATGTC	0.33092	GACATTGT--	CGTATACG	4.94688	--CGTATACG-
AAAGTCAC	0.32857	GTGACTTT--	CGCAACAA	4.88908	--TTGTTGCG-
CGCAACAA	0.32287	--TTGTTGCG	ACAAATAG	4.82954	-CTATTTGT--
TAATAATA	0.31546	-TATTATTA-	ACAATGTC	4.19659	GACATTGT--
CGAGAGCC	0.31448	--GGCTCTCG	TTTCGAAA	4.14968	---TTTCGAAA
ACAAATAG	0.31252	--CTATTTGT	GTAAGTTA	4.10358	-TAACTTAC--