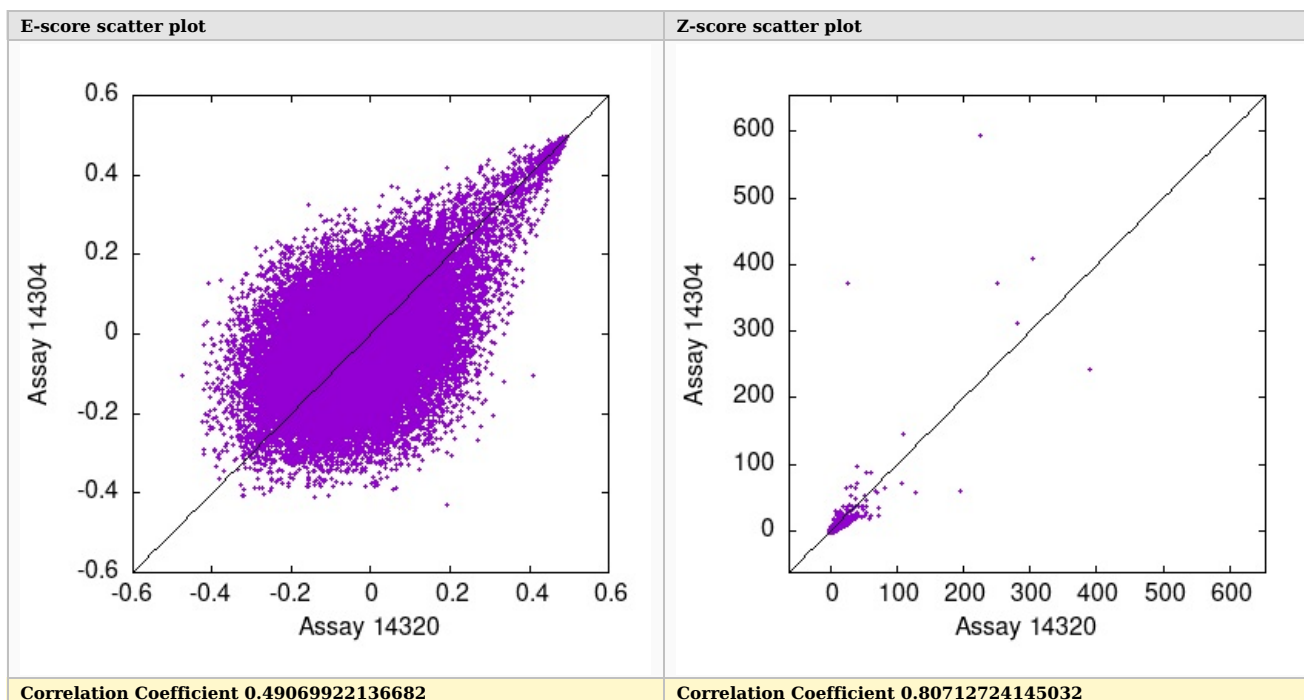


## QC report



Correlation Coefficient 0.49069922136682

Correlation Coefficient 0.80712724145032

### Top scoring motifs for Assay 14320

Protein ID: pTH15525.2 Gene: ZSCAN4 Domain: zf-C2H2 Flag: Pass\_matched\_pair 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
GCACACAC	0.49608	--GCACACAC	GCACACAC	389.98717	--GCACACAC
GGTGTGCA	0.49345	-TGCACACC-	TGCACACA	304.26484	--TGCACACA-
TGCACACA	0.49316	-TGCACACA-	GGTGTGCA	280.64290	-TGCACACC-
GCACACAA	0.49214	--GCACACAA	TGTGCACA	250.55986	-TGTGCACA-
GTGCACAC	0.49187	GTGCACAC--	GTGCACAC	225.01627	GTGCACAC--
TGTGCACA	0.49155	-TGTGCACA-	GCACACAA	193.81548	--GCACACAA
ATGCACAC	0.49091	ATGCACAC--	ATGTGCAC	127.88415	GTGCACAT--
ATGTGCAC	0.48961	GTGCACAT--	ATGCACAC	109.43534	ATGCACAC--
GCACACCC	0.48959	--GCACACCC	GCACATAA	105.87750	--GCACATAA
GCACATAA	0.48803	--GCACATAA	GCACACCA	80.03703	--GCACACCA

### Top scoring motifs for Assay 14304

Protein ID: pTH15525.1 Gene: ZSCAN4 Domain: zf-C2H2 Flag: Pass\_matched\_pair 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
GTGCACAC	0.49674	GTGCACAC--	GTGCACAC	594.35652	-GTGCACAC--
GCACACAC	0.49612	--GCACACAC	TGCACACA	410.10621	--TGCACACA-
TGCACACA	0.49554	-TGCACACA-	TGTGCACA	372.12273	TGTGCACA--
TGTGCACA	0.49552	-TGTGCACA-	ACACACAC	371.27702	-ACACACAC--
ACACACAC	0.49493	--ACACACAC	GGTGTGCA	311.04799	--TGCACACC-
GGTGTGCA	0.49412	-TGCACACC-	GCACACAC	243.11594	-GCACACAC--
ATGCACAC	0.49098	ATGCACAC--	ATGCACAC	145.40070	-ATGCACAC--
GCACACCC	0.49080	--GCACACCC	GTACACAC	96.78226	-GTACACAC--
CACACACA	0.49025	-CACACACA-	AGTGTGCA	87.11524	--TGCACACT-
GCACACAA	0.48982	--GCACACAA	GCACACCC	86.61443	--GCACACCC