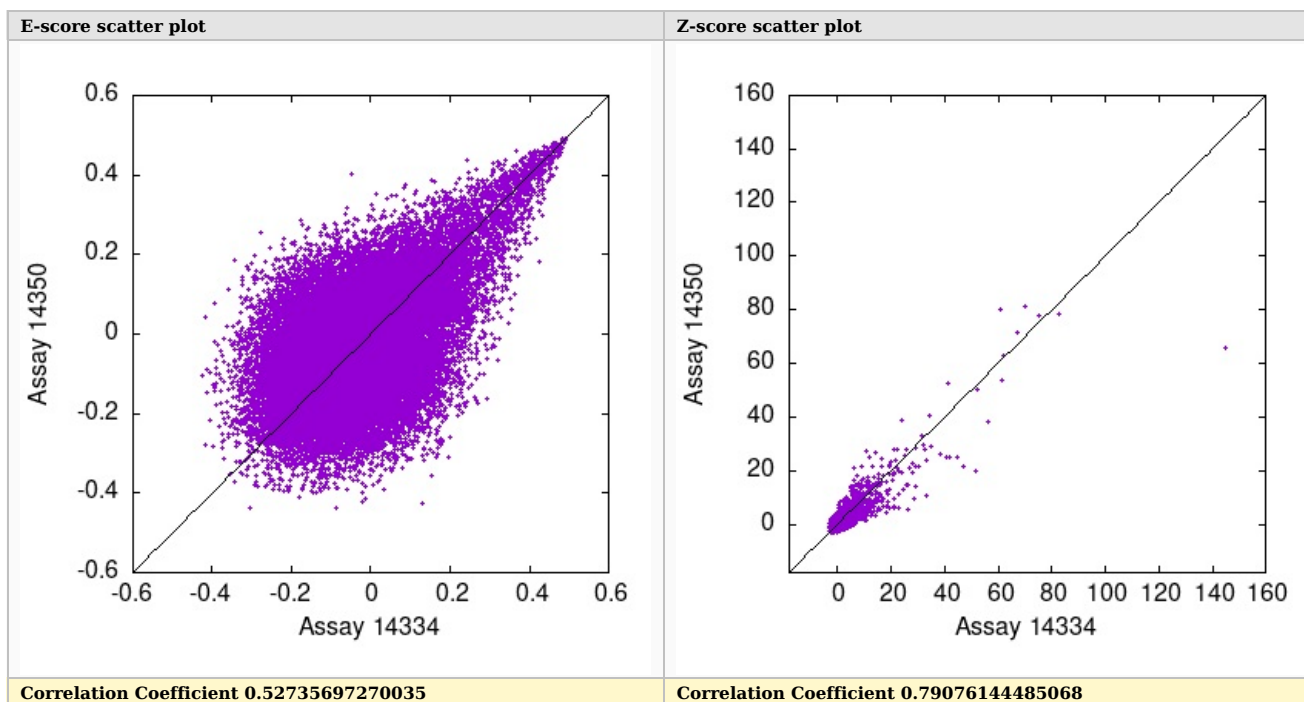




## QC report





### Top scoring motifs for Assay 14334

Protein ID: pTH15533.1 Gene: VDR Domain: zf-C4 Flag: Pass\_matched\_pair Array: 1M-ME

#### 8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
CGAGTTCA	0.49038	CGAGTTCA -
GAGTTCAC	0.49021	-GAGTTCAC
ATGAACTC	0.48720	-GAGTTCAT
CGGGTTCA	0.48709	CGGGTTCA -
AGAGTTCA	0.48548	AGAGTTCA -
ATGAACCC	0.48534	-GGGTTTCAT
TGAACCCA	0.48472	TGGGTTCA -
GAGTTCAA	0.48342	-GAGTTCAA
TGAACTCA	0.48305	TGAGTTCA -
AGGGTTCA	0.48275	AGGGTTCA -

#### 8 mer Z-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
CGAGTTCA	145.01235	CGAGTTCA-
GAGTTCAC	82.76054	-GAGTTCAC
CGGGTTCA	75.44957	-CGGGTTCA-
ATGAACTC	70.18169	-GAGTTTCAT
TGAACCCA	67.09064	TGGGTTCA-
AGAGTTCA	61.80059	AGAGTTCA-
AGGGTTCA	61.28421	AGGGTTCA-
TGAACTCA	60.57973	TGAGTTCA-
ATGAACCC	56.00507	-GGGTTTCAT
GGGTTCAC	52.44654	-GGGTTCAAC



### Top scoring motifs for Assay 14350

Protein ID: pTH15533.2 Gene: VDR Domain: zf-C4 Flag: Pass\_matched\_pair Array: 1M-HK

#### 8 mer E-scores for probeset 'all'

Forward:	Reverse:	
Top 10	Scores	Alignment
TGAACCCA	0.49242	-TGAACCCA
CGAGTTCA	0.49094	-TGAACCTG
GAGTTCAC	0.48944	GTGAACCT-
ATGAACCC	0.48800	ATGAACCC-
GAGTTCAA	0.48760	TTGAACCT-
AGGGTTCA	0.48689	-TGAACCCCT
CGGGTTCA	0.48620	-TGAACCCG
ATGAACTC	0.48608	ATGAACTC-
TGAACTCA	0.48582	-TGAACCTCA
GGGTTCAC	0.48248	GTGAACCC-

#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ATGAACTC	81.12825	ATGAACTC -
TGAACTCA	79.89877	-TGAACCTCA
GAGTTCAC	78.20904	GTGAACTC -
CGGGTTCA	77.71140	-TGAACCCG
TGAACCCA	71.43622	-TGAACCCA
CGAGTTCA	65.46401	-TGAACCTCG
AGAGTTCA	62.82718	-TGAACTCT
AGGGTTCA	53.84939	-TGAACCCCT
GAGTTCAA	52.66733	TTGAACTC -
GGGTTCAA	50.34642	TTGAACCC -