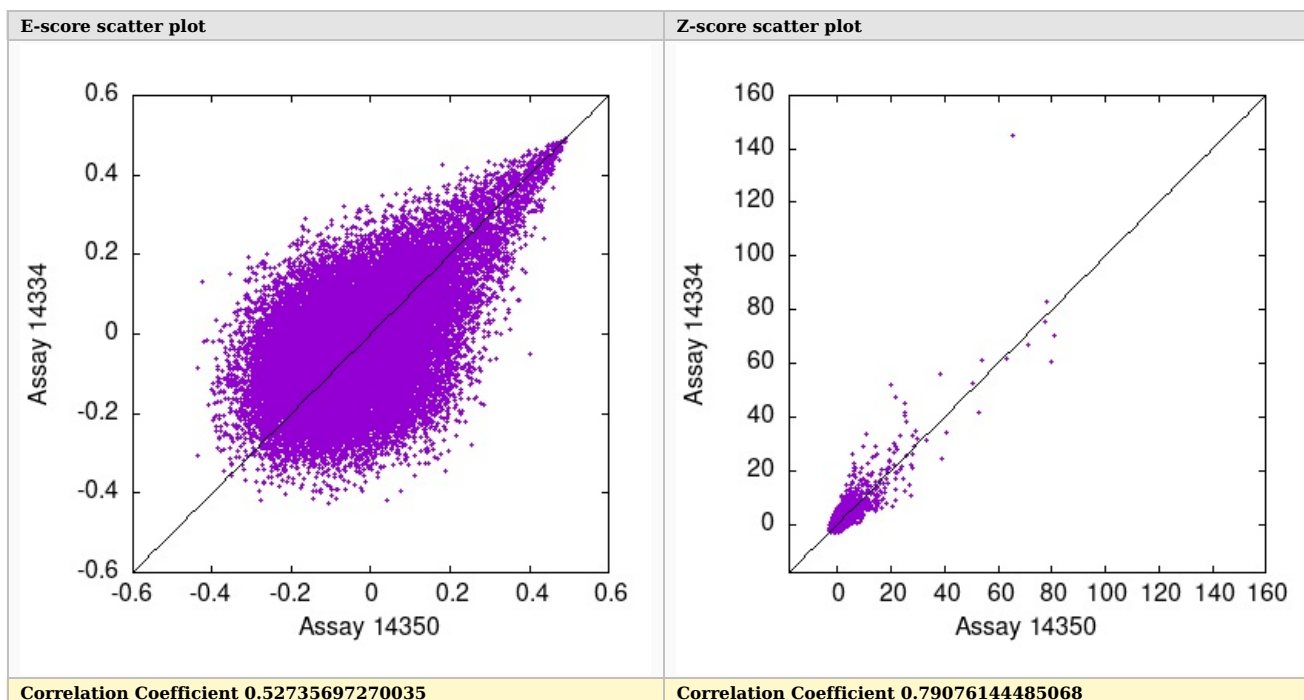




QC report





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	-TGAACTCG
GAGTTTCA	0.48944	GTGAATCT-
ATGAACCC	0.48800	ATGAACCC-
GAGTTCAA	0.48760	TTGAATCT-
AGGGTTCA	0.48689	-TGAACCCCT
CGGGTTCA	0.48620	-TGAACCCG
ATGAATCT	0.48608	ATGAATCT-
TGAATCTA	0.48582	-TGAATCTA
GGGTTTCA	0.48248	GTGAACCC-



8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ATGAATCT	81.12825	ATGAATCT -
TGAATCTA	79.89877	-TGAATCTA
GAGTTTCA	78.20904	GTGAATCT -
CGGGTTCA	77.71140	-TGAACCCG
TGAACCCA	71.43622	-TGAACCCA
CGAGTTCA	65.46401	-TGAATCTG
AGAGTTCA	62.82718	-TGAATCTT
AGGGTTCA	53.84939	-TGAACCTT
GAGTTCAA	52.66733	TTGAATCT -
GGGTTCAA	50.34642	TTGAACCC -



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 -
GAGTTTCA	0.49021	-GAGTTTCA
ATGAATCT	0.48720	-GAGTTTCA
CGGGTTCA	0.48709	CGGGTTCA -
AGAGTTCA	0.48548	AGAGTTCA -
ATGAACCC	0.48534	-GGGTTTCA
TGAACCCA	0.48472	TGGGTTCA -
GAGTTCAA	0.48342	-GAGTTCAA
TGAATCTA	0.48305	TGAGTTCA -
AGGGTTCA	0.48275	AGGGTTCA -

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CGAGTTCA	145.01235	CGAGTTCA-	
GAGTTTCA	82.76054	-GAGTTTCA	
CGGGTTCA	75.44957	CGGGTTCA-	
ATGAATCT	70.18169	-GAGTTTCAT	
TGAACCCA	67.09064	TGGGTTCA-	
AGAGTTCA	61.80059	AGAGTTTCA-	
AGGGTTCA	61.28421	AGGGTTCA-	
TGAATCTA	60.57973	TGAGTTCA-	
ATGAACCC	56.00507	-GGGTTTCAT	
GGGTTCAA	52.44654	-GGGTTCAA	