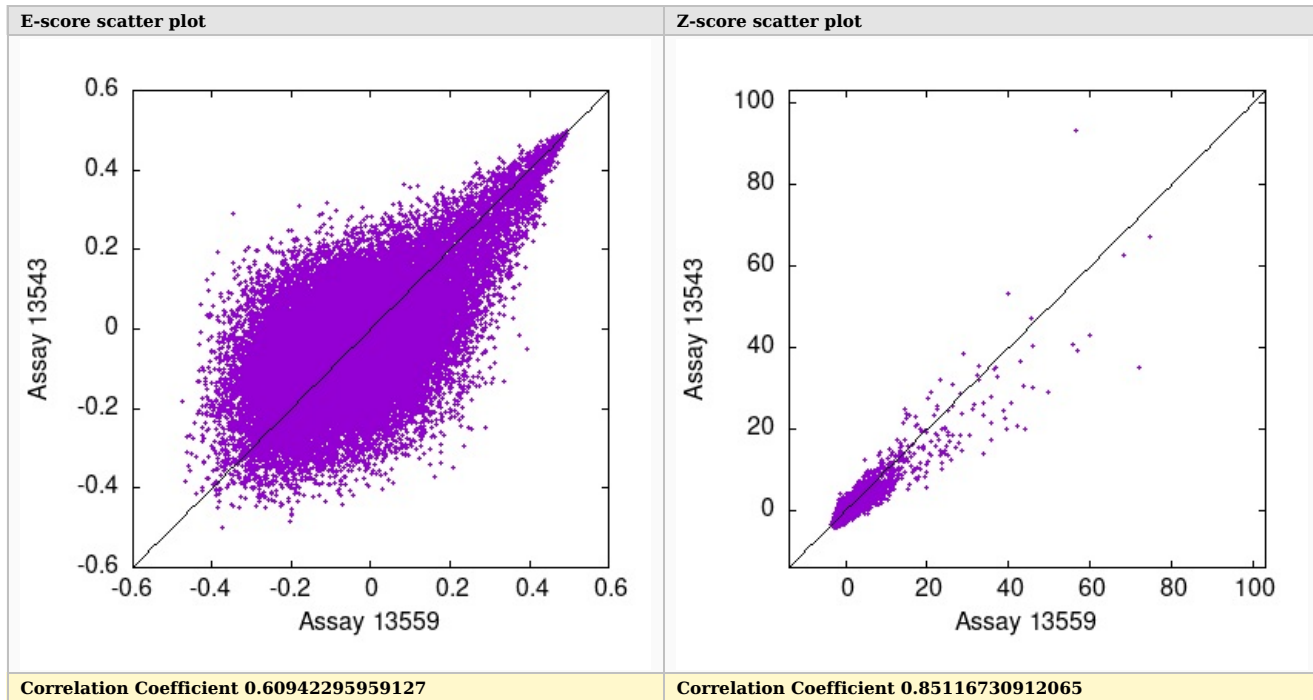




QC report





Top scoring motifs for Assay 13559

Protein ID: pTH14290.2 Gene: CGGBP1.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
CGCCGCCG	0.49670	CGCCGCCG--
GCCGCCGA	0.49533	-GCCGCCGA-
CGCCGCAG	0.49479	CGCCGCAG--
ACGGCGGC	0.49466	-GCCGCCGT-
ACCGCCGA	0.49418	-ACCGCCGA-
CGGCGGCA	0.49334	TGCCGCCG--
CCGCCGAA	0.49265	--CCGCCGAA
GCCGCGGC	0.49139	-GCCGCGGC-
CACCGCCG	0.49131	CACCGCGC--
GCCGCAGA	0.49074	-GCCGCAGA-



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CGCCGCCG	74.59760	CGCCGCCG-	
ACGGCGGC	72.24044	-GCCGCCGT	
GCCGCCGA	68.19641	-GCCGCCGA	
GCCGCGGC	60.08075	-GCCGCGGC	
CGCCGCAG	56.86047	CGCCGCAG-	
CGGCGGCA	56.56005	TGCCGCCG-	
ACCGCCGA	55.68139	-ACCGCCGA	
GCCGCGGA	49.64600	-GCCGCGGA	
CCGCGGCG	46.06611	CGCCCGCG-	
CTGCGGCA	46.00378	TGCCGCAG-	



Top scoring motifs for Assay 13543

Protein ID: pTH14290.1 Gene: CGGBP1.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
CGGCGGCA	0.49916	TGCCGCCG--
GCCGCCGA	0.49833	-GCCGCCGA-
CGCCGCCG	0.49770	CGCCGCCG--
GCCGCGGC	0.49630	-GCCGCGGC-
CCGCCGAA	0.49504	--CCGCCGAA
ACGGCGGC	0.49318	-GCCGCGGT-
CCGCGGCG	0.49303	-GCCGCGCG-
ACCGCCGA	0.49302	-ACCGCCGA-
CGCGGCGG	0.49246	CGCGGCGG--
CGCCGCAG	0.49240	CGCCGCAG--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CGGCGGCA	93.36270	TGCCGCCG--	
CGCCGCCG	67.19254	CGCCGCCG--	
GCCGCCGA	62.90803	-GCCGCCGA-	
GCCGCGCG	53.13536	-GCCGCGCG-	
CCGCCGAA	47.25810	--CCGCCGAA	
GCCGCGGC	43.04293	-GCCGCGGC-	
ACCGCCGA	41.02491	-ACCGCCGA-	
CCGCGGCG	40.47387	CGCCGCGG--	
CGCCGCAG	39.52276	CGCCGCAG--	
CGCCGCGG	38.59859	--CCGCGGCG	