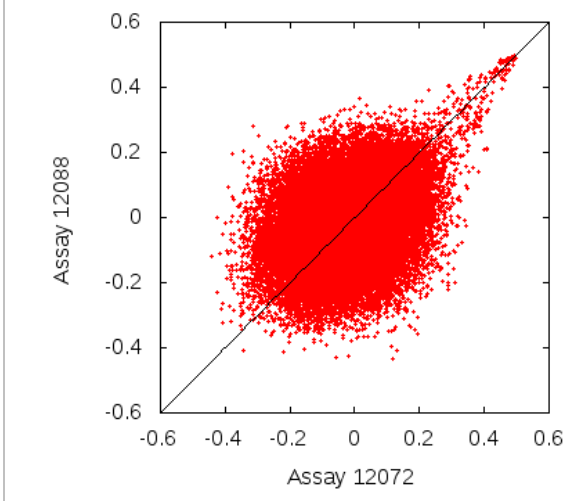
PBM database

QC report

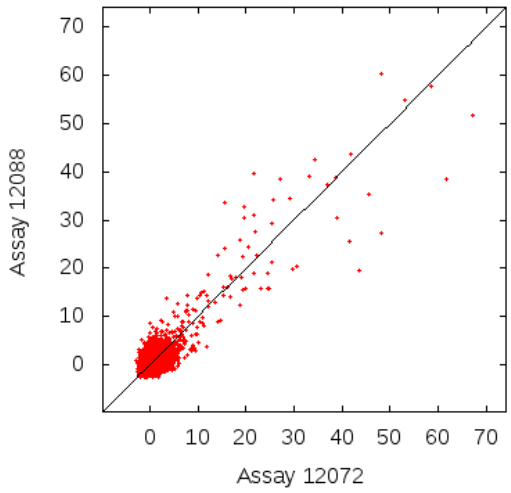
Go to PBM assays | Back to Main menu

E-score scatter plot



Correlation Coefficient 0.335379732266

Z-score scatter plot



Correlation Coefficient 0.699069521154

Top scoring motifs for Assay 12072
Protein ID: pEX0562.1 **Gene:** Zld **Domain:** Unknown **Flag:** Unknown **Array:** 1M-ME

8mer E-scores for probeset 'all' (export E-scores)

Forward: **Reverse:**

Top 10	Scores	Alignment
ACTACCTG	0.49558	ACTACCTG--
CTACCTGC	0.49506	-CTACCTGC-
CTACCTGA	0.49504	-CTACCTGA-
CAGGTAGC	0.49464	GCTACCTG--
CAGGTAGA	0.49303	TCTACCTG--
CGCAGGTA	0.49183	--TACCTGCG
ACAGGTAG	0.49114	-CTACCTGT-
AGCAGGTA	0.49060	--TACCTGCT
GCAGGTAC	0.49052	-GTACCTGC-
TACCTGCA	0.48999	--TACCTGCA

8mer Z-scores for probeset 'all' (export Z-scores)

Forward: **Reverse:**

Top 10	Scores	Alignment
CTACCTGA	67.12072	-CTACCTGA-
ACTACCTG	61.74712	ACTACCTG--
CTACCTGC	58.68029	-CTACCTGC-
CAGGTAGC	53.00260	GCTACCTG--
CGCAGGTA	48.18641	--TACCTGCG
CAGGTAGA	48.04194	TCTACCTG--
GCAGGTAC	45.47330	-GTACCTGC-
GTCAGGTA	43.43051	--TACCTGAC
ACAGGTAG	41.78974	-CTACCTGT-
CTCAGGTA	41.53711	--TACCTGAG

Top scoring motifs for Assay 12088
Protein ID: pEX0562.2 **Gene:** Zld **Domain:** Unknown **Flag:** Unknown **Array:** 1M-HK

8mer E-scores for probeset 'all' (export E-scores)

Forward: **Reverse:**

Top 10	Scores	Alignment
CTACCTGC	0.49657	-CTACCTGC-
CAGGTAGC	0.49595	GCTACCTG--
CAGGTAGA	0.49528	TCTACCTG--
CTACCTGA	0.49478	-CTACCTGA-
AGCAGGTA	0.49322	--TACCTGCT
CAGGTACC	0.49166	GGTACCTG--
ACAGGTAG	0.49153	-CTACCTGT-
GGCAGGTA	0.49100	--TACCTGCC
CAGGTAGG	0.49075	CCTACCTG--
GCAGGTAC	0.49061	-GTACCTGC-

8mer Z-scores for probeset 'all' (export Z-scores)

Forward: **Reverse:**

Top 10	Scores	Alignment
CAGGTAGA	60.34693	TCTACCTG--
CTACCTGC	57.73100	-CTACCTGC-
CAGGTAGC	54.79160	GCTACCTG--
CTACCTGA	51.65945	-CTACCTGA-
ACAGGTAG	43.79361	-CTACCTGT-
AGCAGGTA	42.40232	--TACCTGCT
GGCAGGTA	39.58105	--TACCTGCC
GCAGGTAA	38.98803	-TTACCTGC-
CAGGTAGG	38.81356	CCTACCTG--
ACTACCTG	38.55292	ACTACCTG--

Flag Assays

Assay	QC flag	Author	Comments	Actions
12072	Pass_matched_pair	ally		Save Assay 12072
12088	Pass_matched_pair	ally		Save Assay 12088

Save Both ☑ Save As Pair