





QC report

Top scoring motifs for Assay 13761

Protein ID: pTH14337.1 Gene: SP110.DBD Domain: SAND Flag: Reject 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
ACCCGCCC	0.43979	-ACCCGCCC--	GTTGTTCA	6.05367	---TGAACAAC
CCCGCCCA	0.41640	--CCCGCCCA-	ACCCGCCC	5.97479	ACCCGCCC--
GCCCGCCC	0.40031	-GCCCGCCC--	ATATTGCA	5.75796	--TCGAATAT-
CCCGCCCG	0.38768	--CCCGCCCG-	CGCGCGCA	5.48461	-CGCGCGCA--
CGCCCGCC	0.38549	CGCCCGCC--	GTACTTTA	5.35921	--GTACTTTA-
CCCACCCA	0.38479	--CCCACCCA-	ATGCGCTA	5.28483	--TAGCGCAT-
GC GCGCGC	0.37059	-GCGCGCGC--	TATGTGAA	5.26847	-TATGTGAA--
CCACCGCC	0.36393	CCACCGCC--	GCGCGCGC	5.15071	GCGCGCGC--
CATCAAAG	0.36303	---CATCAAAG	CGCGCGCG	5.12389	-CGCGCGCG--
TATGTGAA	0.36141	--TTCACATA-	CCCGCCCG	5.09451	-CCCGCCCG--