

Retinal patterning by Pax6-dependent cell adhesion molecules

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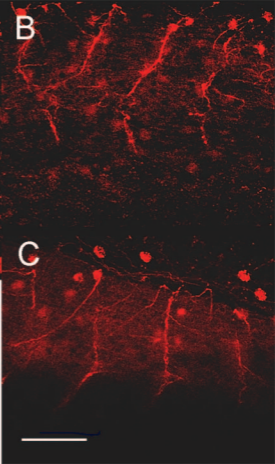
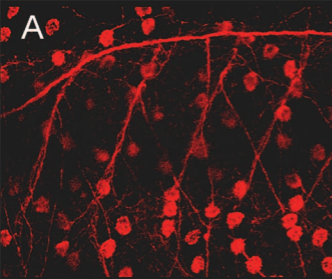
Additional Supporting Information may be found in the online version of this article.

Description

Supporting Information Figure 1.

Supporting Information Figure 2.

Supporting Information Table 1.



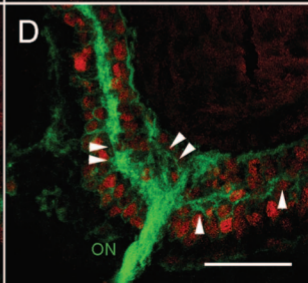
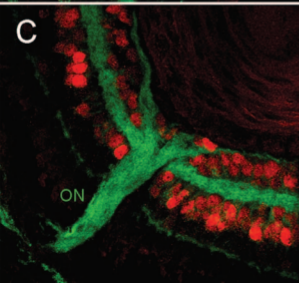
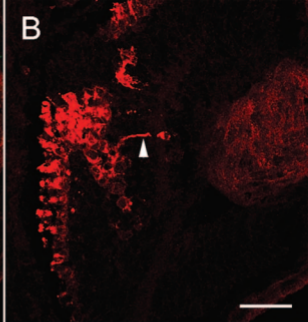
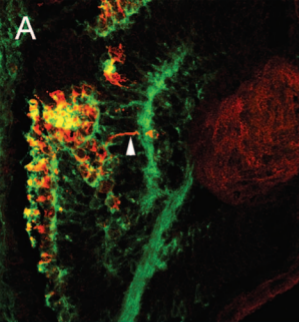


Table SIII. Target explorer analysis of known functional Pax6 binding sites

Ref	Site	Sequence	Assay		Target Explorer		
			Binding	Best hit sequence*	Pos	Dir	Score
A	L1170	CTAGATGTTATTTACTAATGGTGCACCAT	YES	TTATTTACTAATGGTGC	8	F	3.97
	L1 Hox-mut	CTAGATGTTATTTACccATGGTGCACCAT	YES	TTATTTACCCATGGTGC	8	F	6.92
	L1 Pax-mut	CTAGATGTTAagaACTAATGGTGCAC	NO	No hit			-
B	L1 HPD	ATGGTGCAGCCATTAGTGAATAACATCTAG	YES	GCAGCCATTAGTGAATAA	6	R	3.97
	L1 H-	ATGGTGCAGCCATcgGTGAATAACATCTAG	YES	GCAGCCATcgGTGAATAA	6	R	4.71
	L1 PD-	ATGtTcgtGCCATTAGTGAATAACATCTAG	NO	No hit			-
	L1 HPD-	ATGtTcgtGCCATcgGTGAATAACATCTAG	NO	No hit			-
C	NCAM	TGCTCCTCGGTCCATTGCTCC	YES	TGCTCCTCGGTCCATTGC	1	F	1.54
	PBS+ NCAM PBS-	aagcttTCGGTCCATctcgag	NO	AAGCTTTCGGTCCATCTC	1	F	1.79
D	Consensus	tagaagcaGATTTTCACGCTTGATTTCTtacaatat	YES	ATTTTCACGCTTGATTTCC	10	F	14.68
	Er81 BS	tagaagcaGCTTCTCCCGCTTGCTTTCTtacaata	YES	CTTCTCCCGCTTGCTTTC	10	F	6.24
	Er81 Mut	tagaagcaGCTTCTCTCGAGTGCTTTCTtacaata	NO	No hit			-
E F	H2B-2.2	TCAATACGCAACGCCGCGAAGACGGACC	YES	GCAACGCCGCGAAGACGG	8	R	3.24
	H2A-2.1	CAACTATTTCTTCAAGCGTGTCAACAAA	NO	TTCTTCAAGCGTGTCAAC	8	R	0.37
	CD19-1	CAGACACCCATGGTTGAGTGCCCTCCAG	YES	ACACCCATGGTTGAGTGC	4	F	3.48
	Cd19-2	GAATGGGGCACTGAGGCGTGACCACCGC	YES	GCACTGAGGCGTGACCAC	8	R	9.09
	lε	GCTGAGGGCACTGAGGCAGAGCGGCCCC	~yes	GCACTGAGGCAGAGCGGC	8	R	0.29
	H2A/e5	TTGTGACGCAGCGGAGCGGAACGGTGCT	YES	GCAGCGGAGCGGAACGGT	8	R	7.68
	H2A-17C	TTGTGACGCAGCGGTGCGTGACGACTGT	YES	GCAGCGGTGCGTGACGAC	8	R	8.72
G	P6CON	GGATGCAATTTACGCATGAGTGCTCGAGGGATCCACGTCGA	YES	AATTTACGCATGAGTGC	7	F	15.4
	Mab2122-1	CCCCAAAAGGAAAGTGAAGGATGTAATTAATGCC	YES	CAAAAGGAAAGTGAAGGA	4	R	2.62
	Mab2122-2	CCCGGAGAGCAGCGAAGTACAGCTCAGGCCG	NO	No hit			-
	Mab2122-3	TCCGGGTTTTCTCTCCTCTGGGTTGCGTT	NO	GTTTTCTCTCTCTCTGG	6	F	1.61
	Mab2122-4	GCTCCTTGATGGTGTATTAACGAAGTGGCAGCTCCT	NO	No hit			-
	Mab2122-5	ATCCGTCTCATCATACTTGAGTTAATGAGGCA	YES	CTCATCATACTTGAGTTAAT	7	F	4.3
	Tgfb2-6	GATAGATGGCTTTGATGCGTAAACTTGAGAG	YES	GCTTTGATGCGTAAACT	9	R	11.17
	Tgfb2-7	TCCTGACCACAACCTCTAGTGACTACTCCA	NO	No hit			-
	Tgfb2-8	TTAGCCACATCATTCACTCATCACACAACTC	YES	TCATTTCACTCATCACACA	10	F	2.56

Tgfb2-9	AGCCCTGAAGACATGCCTTCCAATCTGAGAC	NO	GAAGACATGCCTTCCAAT	7	R	0.87
Tgfb2-10	ACTGCTGACCTAACTCTTGAGTTCTCCGGGAT	NO	GACCTAACTCTTGAGTTC	7	F	5.5
Tgfb2-11	TGTCACACAGTATCATAACTTGACATTTTCTACTTCAACTTGCTCA	YES	No hit			-

*Analyzed by Target Explorer (Sosinsky et al., 2003, ref. in article) using our weight matrix based on Pax-binding motifs (Epstein et al., 1994, ref in article).

Italic : false positive or false negative motifs.

References: A) Chalepakis et al., 1994, cited in article; B) Meech et al., 1999, cited in article; C) Holst et al., 1997, cited in article;

D) Tuoc TC, Stoykova A. 2008. Er81 is a downstream target of Pax6 in cortical progenitors. *BMC Dev Biol* **8**: 23;

E) Czerny T, Busslinger M. 1995. DNA-binding and transactivation properties of Pax-6: three amino acids in the paired domain are responsible for the different sequence recognition of Pax-6 and BSAP (Pax-5). *Mol Cell Biol* **15**: 2858-2871.

F) Czerny T, Schaffner G, Busslinger M. 1993. DNA sequence recognition by Pax proteins: bipartite structure of the paired domain and its binding site. *Genes Dev* **7**: 2048-2061.

G) Wolf LV, Yang Y, Wang J, Xie Q, Braunger B, Tamm ER, Zavadil J, Cvekl A. 2009. Identification of Pax6-dependent gene regulatory networks in the mouse lens. *PLOS one* **4**: e4190.