

Table S1. Real-time PCR primers for analysis of transcript levels

Gene	Oligo name	Sequence	Reference
<i>Hoxd1</i>	d1bUp	CCACAGCACTTTTCGAGTGGA	Morey et al., 2007
<i>Hoxd1</i>	Hoxd1r	ACTCTTTCTCTAGCTCTGTCAG	
<i>Hoxd3</i>	d3pA	GAACTCCAAGCAGAAGAACAG	Condie and Capecchi, 1993
<i>Hoxd3</i>	Hoxd3r	CAGATAGCGGTTGAAGTGAAC	
<i>Hoxd4</i>	Hoxd4f	GGAGAACGAGGGAGAACCA	
<i>Hoxd4</i>	Hoxd4r	TCTGCTGCTGCTATGACTGC	
<i>Hoxd8</i>	Hoxd8f	CACTTAAATCAGAGCTCGTCTCC	
<i>Hoxd8</i>	Hoxd8r	GACCTCGATTCTCCTCTTCCTGG	
<i>Hoxd10</i>	Hoxd10f	GTGCAGGAGAAGGAAAGCAAAG	Modified from Mizusawa et al., 2004
<i>Hoxd10</i>	Hoxd10r	TAACGCTCTTACTGATCTCTAGGC	
<i>Hoxd11</i>	Hoxd11f	TCCAGGCAAACGAGAGAAAC	
<i>Hoxd11</i>	Hoxd11r	TTGGCAAATAAGGTTTCTGGA	
<i>Hoxd12</i>	Hoxd12f	CAACTTGAACATGGCAGTGCAAG	
<i>Hoxd12</i>	Hoxd12r	CTGCTGCTTTGTGTAGGGTTTCC	
<i>Hoxd13</i>	Hoxd13f	AGTCCTGGACGCTAGCCAACG	
<i>Hoxd13</i>	Hoxd13r	GTAGACGCACATGTCCGGCTG	
<i>Actin</i>	Actinf	AGAGCTATGAGCTGCCTGACG	
<i>Actin</i>	Actinr	TGTGTTGGCATAGAGGTCTTTACG	
<i>Lnp</i>	LnpaUp	GTGGAAGGCTCAAGCTCAAC	
<i>Lnp</i>	LnpbLo	TGCTGGGCAATCTGAATATG	
<i>GAPDH</i>	GABDHf	ATCACCATCTTCCAGGAGCGAG	
<i>GAPDH</i>	GABDHr	GACCCTTTTGGCTCCACCCTTC	Modified from Boyer et al., 2006
<i>FgfR2b</i>	FGFR2f	CTGTTCAATGTGACGGAGATGG	
<i>FgfR2b</i>	FGFR2r	ACAGACGCGTTGTTAYCCTCAC	
<i>FgfR2c</i>	FGF2Cf	CACTCTGCATGGTTGACAGTTC	
<i>FgfR2c</i>	FGF2Cr	CACTCTGCATGGTTGACAGTTC	
<i>Fgf8</i>	FGF8f	AAAGTCACACAGCGACATGTGAGG	
<i>Fgf8</i>	FGF8r	TCTGTGAATACGCAGTCCTTGCCT	
<i>Fgf10</i>	FGF10f	AGCGGGACCAAGAATGAAGACTGT	
<i>Fgf10</i>	FGF10r	CCTGCCATTGTGCTGCCAGTAAA	
<i>Etv4</i>	Pea3f	ACCATGGAGAGCAGTGCCTTTACT	
<i>Etv4</i>	Pea3r	ATGCACATCCAGGGACATCTGAGT	

Table S2. Real-time PCR primers for ChIP analysis of promoter regions

Promoter/exon	Oligo name	Sequence	Reference
<i>Hoxd1</i>	Hoxd1promf	GAGTAACTTGACCTTCTCAGAG	
	Hoxd1promr	ATTGCGGGAGAAAGGCAGGGAAG	
<i>Hoxd10</i>	Hoxd10prof	TAGTAGATGTCGCTGTTGTCCG	
	Hoxd10pror	ACATGACAACCAAGCCAATGAGA	
<i>Olig2</i>	Olig2f	GCCTGACGCTACAGTGACAA	Boyer et al., 2006
	Olig2r	GGCTAATTCCGCTCAATGAA	Boyer et al., 2006
<i>Actin</i>	Actinf	CCTCGATGCTGACCCTCATCC	
	Actinr	GACACTGCCCCATTCAATGTCTC	

Table S3. Fosmid probes

		Whitehead (Sanger)				
	Region	name	Ensemble name	Coordinates		Size (bp)
				Start	End	
Hoxd	<i>GCR*</i>	WI1-2157A11	G135P63331H7	74242615	74282044	39,429
	<i>Lnp*</i>	WI1-482L15	G135P61870C5	74329582	74372986	43,404
	<i>Evx2-Hoxd13*</i>	WI1-469P2	G135P67444A12	74474157	74513003	38,846
	<i>Hoxd4-Hoxd1*</i>	WI1-121N10	G135P67844B8	74566983	74605438	38,455
	<i>Island III</i>	WI1-1404J11	G135P64810D7	74040543	74081331	40,788
Pax6	<i>Rcn**</i>	WI1-1767E4	G135P601417F11	105221381	105259938	38,557
	<i>Rpl10**</i>	WI1-1550J22	G135P601672D2	105387894	105425103	37,209

Names are Ensembl (r 45) (http://jun2007.archive.ensembl.org/Mus_musculus/index.html). Mouse genome assembly number: NCBI m37.

Asterisks indicate fosmids previously used in *Morey et al., 2007; Morey et al., 2009; **and Eskeland et al., 2010.

Table S4. Normalised interprobe distance for A1 & P1 and A2 & P2 cell lines

Cell line	<i>Hoxd3-Hoxd13</i> (93 kb)	<i>GCR-Lnp</i> (89 kb)	<i>Rcn-Rpl10</i> (166 kb)
	Normalized interprobe distance (d^2/r^2)		
A1	0.0056	0.0021	0.0039
P1	0.0084 ($P=0.0002$)	0.0024 ($P=0.05$)	0.0030 ($P=0.11$)
A2	0.0060	0.0025	0.0054
P2	0.0084 ($P=0.03$)	0.0027 ($P=0.90$)	0.0038 ($P=0.08$)
	Squared interprobe distance (d^2) (μm^2)		
A1	0.16	0.066	0.11
P1	0.25 ($P<0.0001$)	0.073 ($P=0.34$)	0.09 ($P=0.14$)
A2	0.20	0.09	0.18
P2	0.27 ($P=0.02$)	0.08 ($P=0.88$)	0.12 ($P=0.10$)

Statistical analysis of data for Fig. 4. Interprobe distances are median values; P -values from Mann-Whitney U tests.

Table S5. Interprobe distances for E11 limb bud sections

Limb region	<i>Hoxd3-Hoxd13</i> (93 kb)	<i>GCR-Lnp</i> (89 kb)	<i>Rcn-Rpl10</i> (166 kb)
	Interprobe distance (d^2) (μm^2)		
Distal posterior	0.178	0.076	0.080
Distal anterior	0.116 ($P=0.0008$)	0.076 ($P=0.93$)	0.081 ($P=0.10$)
Proximal posterior	0.153 ($P=0.02$)	0.076 ($P=0.46$)	0.090 ($P=0.06$)
Proximal anterior	0.098 ($P=0.0002$)	0.074 ($P=0.45$)	0.112 ($P=0.05$)
Flank	0.130 ($P=0.0002$)	0.078 ($P=0.49$)	0.112 ($P=0.17$)

Statistical analysis of data for Fig. 5. Interprobe distances are median values, P -values from Mann-Whitney U tests.

Table S6. Frequency of HoxD GCR and *Pax6* apposite probes separated by ≥ 600 nm for E11 limb bud sections

Limb region	<i>Hoxd3-Hoxd13</i> (93 kb)	GCR- <i>Lnp</i> (89 kb)	<i>Rcn-Rpl10</i> (166 kb)
	Frequency (%) ≥ 600 nm		
Distal posterior	27	5	4
Distal anterior	8 ($P=0.0001$)	4 ($P=1.00$)	12 ($P=0.02$)
Proximal posterior	7 ($P=0.0001$)	0 ($P=0.12$)	4 ($P=0.44$)
Proximal anterior	9 ($P=0.001$)	5 ($P=1.00$)	14 ($P=0.009$)
Flank	3.5 ($P=0.0001$)	0 ($P=0.12$)	4 ($P=0.44$)

Statistical analysis of data for Fig. S3. *P*-values from Fisher's exact tests.

Table S7. Interprobe distances for HoxD regulatory regions in E11 limb bud sections

Limb region	<i>Hoxd13</i> -GCR (231 kb)	Island III-GCR (201 kb)	<i>Hoxd13</i> -island III (432 kb)
	Interprobe distance (d^2) (μm^2)		
Distal posterior	0.076	0.084	0.072
Distal anterior	0.098 ($P=0.04$)	0.087 ($P=0.43$)	0.067 ($P=0.96$)
Proximal posterior	0.107 ($P=0.002$)	0.098 ($P=0.99$)	0.085 ($P=0.11$)
Proximal anterior	0.098 ($P=0.02$)	0.094 ($P=1.00$)	0.099 ($P=0.005$)
Flank	0.171 ($P=0.0001$)	0.098 ($P=0.77$)	0.081 ($P=0.04$)

Statistical analysis of data for Fig. 6B. Interprobe distances are median values; P -values from Mann-Whitney U tests.

Table S8. Colocalisation frequency of 5' HoxD and enhancer probes for E11 limb bud sections

Limb region	<i>Hoxd13</i> -GCR (231 kb)	Island III-GCR (201 kb)	<i>Hoxd13</i> -island III (432 kb)
	Colocalisation frequency (%)		
Distal posterior	30	13	19
Distal anterior	14 ($P=0.01$)	11 ($P=0.83$)	14 ($P=0.30$)
Proximal posterior	5 ($P<0.0001$)	11 ($P=0.839$)	16 ($P=0.61$)
Proximal anterior	8 ($P=0.0001$)	13 ($P=1.00$)	13 ($P=0.22$)
Flank	7 ($P<0.0001$)	12 ($P=1.00$)	10 ($v0.07$)

Statistical analysis of data for Fig. 6C. P -values from Fisher's Exact tests.