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Data Article

Gene datasets associated with mouse cleft palate

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ABSTRACT

This article presents data on genes associated with cleft palate (CP), retrieved through both a full-text systematic review and a mouse genome informatics (MGI) database search. In order to group CP-associated genes according to function, pathway, biological process, and cellular component, the genes were analyzed using category enrichment bioinformatics tools, the Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene Ontology (GO). This approach provides invaluable opportunities for the identification of candidate pathways and genes in CP research.

Specifications Table

Subject area	*Biology*
More specific subject area	*Craniofacial development*
Type of data	*Table*
How data was acquired	*Systematic review and MGI database search, KEGG and GO analyses*

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Data format	*Analyzed*
Experimental factors	*Only genetic factors were considered in the bioinformatics analyses*
Experimental features	*Systematic review and MGI database search, KEGG and GO analyses*
Data source location	*N/A*
Data accessibility	*Data provided with this article*

Value of the Data

- The data presented here provide accurate gene datasets associated with mouse CP that are useful to determine the molecular mechanism(s) of CP.
- The KEGG data highlight biological terms enriched with CP-associated genes for further investigation of the cause(s) of CP.
- The GO annotation highlights functions enriched with CP-associated genes to be considered in CP pathology.

1. Data

The information in the list of CP-associated genes was obtained through a systematic review and a MGI database full-text review search. The CP phenotype has been reported in 301 mutant mice: CP caused by 195 single-gene mutations (Supplementary Table 1) and 27 spontaneous (unknown) mutations/deletions (Table 1), 9 chemical-induced cases of CP (Table 2), and 70 compound mutations (Table 3). For the bioinformatics analyses, phenotypic markers and genes with unknown genomic location were excluded from gene set enrichment analyses. Pairs of genes in compound mutant mice (140 genes in 70 mouse lines) were incorporated into further analyses. In total, 255 protein-coding genes (Supplementary Table 1 and 2-4 overlapped genes were excluded) were subjected to gene set enrichment analysis for further analyses.

1.1. Gene set enrichment analysis of mouse CP-associated genes

The KEGG represents one of the best-annotated canonical pathway databases, established by collecting information from the literature and organizing it in a pathway map, ontology, and membership [1]. To analyze the biological functions of CP-associated genes, we performed category enrichment analysis for a variety of functional relations using the KEGG. Among the KEGG pathways, 46 were statistically enriched with CP-associated genes (Table 4).

1.2. Functional categories of mouse CP-associated genes

The GO is a comprehensive ontology database for annotation of gene features through numerous hierarchical terms in three main domains: Biological Process (BP), Molecular Function (MF), and Cellular Component (CC) [2]. The most specific GO terms enriched in BP (Table 5), MF (Table 6) and CC terms (Table 7) are useful for the interpretation of genes of interest.

2. Experimental design, materials and methods

2.1. Experimental design

To generate an accurate database for mouse genetic information related to CP, current genetic information was collected through both a systematic review and search in the genetic database MGI. CP-associated genes were analyzed with the bioinformatics tools KEGG and GO.

Table 1
Spontaneous, unknown loci, and region deletions in mice with cleft palate.

No.	Allele symbol or mouse line	Allele name (chromosome #)	References	Note
1	**Abn**	Abnormal (unknown)	[108]	Anatomical abnormality.
2	**Acan (aka cmd-Bc)**	Aggrecan (Chr 7)	[5-7]	7-bp deletion of exon 5 or a complete loss of exons 2 to 18 of the aggrecan gene. Mouse strain is cmd.
3	**A/ line inbred**	(unknown)	[8-10]	A/Wysn mice exhibit CP with a higher frequency than WT mice. There is a mutation in the Wnt9b region.
4	**Am**	Amputated (Chr 8)	[11]	Radiation-induced mutation. Homo mutant mice exhibit CP with 100% penetrance.
5	**Br**	Brachyrrhine (Chr 17)	[109]	Cleft upper lip and short palate, maybe CP or soft palate cleft.
6	**CL/Fr**	(unknown)	[12,13]	15–40% of the mice exhibit CP. Frequency depends on the colony.
7	**Csp1**	Cleft secondary palate 1 (unknown)	[14]	ENU-induced mutagenesis. 9% of the null mice exhibit CP after 4 generations of backcrossing to the B6 strain (100% penetrance of CP in the first generation).
8	**Csp2 (aka line 110)**	Cleft secondary palate 2 (unknown)	[15]	ENU-induced mutagenesis. 4/30 (13%) penetrance.
9	**Cycsp (aka line 286)**	Curly tail and cleft secondary palate (Chr 3)	[15]	ENU-induced mutagenesis. 9/42 (21%) penetrance.
10	**Del(8–17)**	Deletion, Chr 5, 128–131 Mb (Chr 5)	[16]	Conserved synteny of the human 8q24 CL/P risk interval region. 4/121 of the homo mice exhibit CP, and 4/121 homo mice exhibit CL.
11	**Del(16Dgcr2-Hira)1Rak (aka LgDel)**	Deletion, Chr 16, Raju Kucherlapati 1 (Chr 16)	[17]	22q11 deletion syndrome mouse model. Mouse strain is LgDel.
12	**Eh**	hairy ears (Chr 15)	[18]	Mice with Eh/Eh, radiation-induced mutation in Chr15, exhibit CP with 100% penetrance.
13	**Far**	First arch (Chr 2)	[19]	Null mice exhibit secondary palate cleft (lip and primary palate are intact), absence of maxillary process, etc. Spontaneous mutation.
14	**Hpmd (aka line 171a)**	Hypoplastic mandible (unknown)	[15]	ENU-induced CP. 7/77 affected, but no detailed information is available.
15	**Knyn (aka 12WT-49)**	Kanyon (Chr 7)	[20]	ENU-induced midfacial cleft.
16	**Oca2 (aka P)**	Oculocutaneous albinism II; pink-eyed dilution cleft plate (Chr 7)	[21,22,110]	Spontaneous mutation of p-deletion homozygotes exhibit CP.
17	**Oel**	Open eyelids with cleft palate (unknown)	[111]	In abstract, it was described that mice with homo mutation exhibit CP.
18	**Pad**	Paddle (unknown)	[23,112]	Homo mutant mice exhibit CP.
19	**Pcp**	polydactyly with cleft palate (unknown)	[113]	Polydactyly with cleft palate
20	**Ptd**	Palate-tail-digits abnormality (Chr X)	[24]	60% of mutated hemi male and homo female mice exhibit CP.
21	**Sho**	Shorthead (unknown)	[25,26]	Null mice exhibit CP.
22	**Sme**	Small ear (unknown)	[114]	Radiation-induced.
23	**Srn**	Siren (unknown)	[27]	Mutant mice exhibit several abnormalities; CP with 21% penetrance, micrognathia with 39%, microstomia with 34%, microglossia with 26%. Mutant mice without CP have a narrow palate or high arched palate. No full text and image are available.
24	**Srt (aka line104)**	Shorty (Chr 17)	[15]	ENU-induced mutagenesis. 7/39 (18%) penetrance.

Table 1 (*continued*)

No.	Allele symbol or mouse line	Allele name (chromosome #)	References	Note
25	**Tbx10^{Dc} (aka Dc)**	T-box 10; Dancer (Chr 19)	[28-30]	Homo mutant mice exhibit CP and CL. Insertion of p23 gene into the intron 1 of Tbx10 causes gain of function of Tbx10 gene. Mouse strain is Dancer.
26	**Ur**	Urogenital (unknown)	[31,32]	Null mice exhibit CP.
27	**Zeb1 (aka Tw)**	Zinc finger E-box binding homeobox 1; twirler (Chr 18)	[33-35]	All homo mice exhibit CP with or without CL. A point mutation in the noncoding region of Zeb1. Mouse strain is Twirler.

CP, cleft palate; CL, cleft lip; Hemi, hemizygous; Het, heterozygous; Homo, homozygous; WT, wild-type.

Table 2
Chemically-induced mutations causing cleft palate in mice.

No.	Gene symbol	Gene name	References	Note
1	**Abcb1a (aka Mdr1a, mdr-3, Pgp)**	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	[36]	Spontaneous mutation in Abcb1a gene in the CF-1 mouse line can induce CP by L-652,280, the 8,9 Z photoisomer of the naturally occurring avermectin B1a.
2	**Aecp**	Vitamin A enhanced cleft palate	[37]	Vitamin A-induced CP, no genetic mutation.
3	**Cp2**	Cleft palate 2	[38]	Cortisone-induced CP.
4	**Ahr**	Aryl-hydrocarbon receptor	[39]	CP is induced by TCDD treatment in null mice with 72% penetrance (9% for non-treatment).
5	**Dxcp1**	Dexamethasone induced cleft palate 1	[40]	Dexamethasone induces CP. 29% of the mice with H-2a/b antigen exhibit CP, and 11% of the mice with H-2b/b antigen exhibit CP.
6	**Dxcp2**	Dexamethasone induced cleft palate 2	[40]	Glucocorticoid-induced CP.
7	**Dxcp3**	Dexamethasone induced cleft palate 3	[40]	Glucocorticoid-induced CP.
8	**Lgl**	Legless	[41]	CP was induced in null mice with retinoic acid treatment. Null mice without treatment and WT/het with treatment exhibit no CP.
9	**Papss2 (aka Sk2, Atpsk2)**	3'-Phosphoadenosine 5'-Phosphosulfate synthase 2	[42]	Cortisone-induced CP (95% in bm/bm mice and 20% in C57B6 mice) in homo mutant mice.

Table 3
Compound mutant mice with cleft palate.

No.	Gene symbol	Gene name	References	Note
1	**Adamts9 & Adamts20**	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9/a disintegrin-like and metallo-peptidase (reprolysin type) with thrombospondin type 1 motif, 20	[43]	Adamts9$^{+/-}$;bt/bt (mutation in Adamts20) mice exhibit CP with 100% penetrance.
2	**Adamts20 & Vcan**	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20/versican	[43]	bt/vt/;Vcan$^{hdf/+}$ mice exhibit CP with 65% penetrance.
3	**Akap8 (aka AKAP95) & Fign**	A kinase (PRKA) anchor protein 8 & fidgetin	[44]	20% of Akap8$^{+/-}$;Fign$^{-/-}$ mice exhibit CP. 2% of Akap8$^{-/-}$;Fign$^{+/-}$ mice exhibit CP.
4	**Alx1 (aka Cart1) & Alx4**	ALX homeobox1 & aristaless-like homeobox 4	[45]	Alx1$^{-/-}$;Alx4$^{-/-}$ DKO and Alx1$^{+/-}$;Alx4$^{-/-}$ mice exhibit midfacial cleft and CP with 100% penetrance. Alx1$^{-/-}$;Alx4$^{+/-}$ mice exhibit CP and midfacial cleft.
5	**Alx3 & Alx4**	Aristaless-like homeobox 3 & aristaless-like homeobox 4	[46]	Alx3$^{-/-}$;Alx4$^{+/-}$, Alx3$^{+/-}$;Alx4$^{-/-}$, Al3$^{-/-}$;Alx4$^{-/-}$ mice exhibit CP and midfacial cleft.
6	**Arid5b & Zfp950 (aka** BC055757**, Zfp826)**	AT rich interactive domain 5B (MRF1-like) & zinc finger protein 950	[47]	Arid5b$^{-/-}$;BC055757$^{-/-}$ DKO mice exhibit CP.
7	**Axin1 & Ctnnb1**	Axin 1 & beta catenin	[48]	Axin1$^{\Delta C6/\Delta C6}$;Ctnnb1$^{+/-}$ mice exhibit CP. Axin1$^{\Delta C6/\Delta C6}$ or other KO models show no CP.
8	**Bmp2 & Bmp4**	Bone morphogenetic protein 2 & bone morphogenetic protein 4	[49]	Wnt1-Cre;Bmp2$^{F/F}$;Bmp4$^{F/+}$ or Bmp4$^{F/F}$ (CKO or het) mice exhibit CP. No image is available, only table.
9	**Bmp4 & Bmp7**	Bone morphogenetic protein 4 & bone morphogenetic protein 7	[49]	Wnt1-Cre;Bmp4$^{F/F}$;Bmp7$^{F/F}$ double CKO mice exhibit CP. No image is available, only table.
10	**Bmp2 & Bmp4 & Bmp7**	Bone morphogenetic protein 2, 4, & 7	[49]	Wnt1-Cre;Bmp2$^{F/F}$;Bmp4$^{F/F}$;Bmp7$^{F/F}$ triple CKO mice exhibit CP. No image is available, only table. Combination of null/het, except triple het, exhibit CP. No image is available, only table.
11	**Boc & Cdo1**	Biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein & cysteine dioxygenase 1, cytosolic	[50]	Boc$^{-/-}$;Cdo1$^{-/-}$ mice exhibit CP (> 60 %), CL, a single nose, or other midfacial defects in various %. Boc$^{+/-}$;Cdo1$^{-/-}$ mice exhibit similar but low %.
12	**deltaH19 & Igf2r**	H19, imprinted maternally expressed transcript & Insulin like growth factor 2 receptor	[51]	5/10 double mutant (Igf2r$^{m-/+}$;ΔH19$^{m-/+}$ or Igf2r$^{m-/+}$;ΔH19$^{m-/-}$) mice exhibit CP.
13	**Disp1 & Shh**	Dispatched RND transporter family member 1 & sonic hedgehog	[52,53]	Disp1$^{\Delta 2/\Delta 2C}$;Shh-Cre$^{/+}$ or Disp1$^{C829F/\Delta 2C}$;Shh-Cre$^{/+}$ mice exhibit a loss of facial midline structure. Similar with Dips1 $^{\Delta 2/\Delta 2}$;Shh$^{+/-}$ or Dips1$^{C829F/\Delta 2}$;Shh$^{+/-}$mice, but partially rescued.
14	**Dlx1 & Dlx2**	Distal-less homeobox 1 & distal-less homeobox 2	[54]	Dlx1$^{-/-}$; Dlx2$^{-/-}$ DKO mice exhibit CP with 100% penetrance.
15	**Dlx5 & Dlx6**	Distal-less homeobox 5 & distal-less homeobox 6	[55]	Dlx5$^{-/-}$;Dlx6$^{-/-}$ DKO mice show severe bone malformations.
16	**Dlx5 & Dlx6 & Mef2c**	Distal-less homeobox 5 & 6 & myocyte enhancer factor 2c	[56]	Dlx5/6$^{+/-}$;Mef2c$^{+/-}$ triple het mice have a shot palate or soft palate cleft.
17	**Dph1 & Ovca2**	Diphthamide biosynthesis 1 & candidate tumor suppressor in ovarian cancer 2	[57]	Dph1 & Ovca2 DKO mice exhibit CP with 100% penetrance.

18	**Ednrb & Spry2**	Endothelin receptor type B & Sprouty homolog 2	[58]	Ednrb$^{+/-}$;Spry2$^{+/-}$ and Ednrb$^{-/-}$;Spry2$^{Tg/+}$ mice. Rescue models of Ednrb null mice.
19	**Ephb2 (aka Nuk) & Ephb3 (aka Sek4)**	Ehp receptor B2 & Eph receptor B3	[59]	10/22 Ephb2$^{-/-}$;Ephb3$^{-/-}$ DKO mice, 3/14 Ephb2$^{+/-}$;Ephb3$^{-/-}$ (het & null) mice, 1/10 Ephb2$^{-/-}$;Ephb3$^{+/-}$ (null & het) mice exhibit CP.
20	**Eya1 & Sumo1**	Eyes absent homolog 1 & SMT3 suppressor of mif two 3 homolog 1	[60]	36% of Eya1$^{+/-}$;Sumo1$^{+/-}$ double het mice exhibit CP.
21	**Fzd2 & Fzd7 & Vangl2**	Frizzled class receptor 2 & frizzled class receptor 7 & Vang-like 2 (van gogh, *Drosophila*)	[61]	Less than 10% of Fzd2$^{+/-}$;Fzd7$^{-/-}$ mice exhibit CP. About 50% of Fzd2$^{+/-}$;Fzd7$^{-/-}$;Vangl2$^{LP/+}$ mice exhibit CP; the frequency of CP is increased in case of haploinsufficiency of the Vangl2 gene.
22	**Gad1 & Gad2**	Glutamate decarboxylase 1 & glutamic acid decarboxylase 2	[62]	Gad1$^{-/-}$;Gad2$^{-/-}$ DKO mice exhibit CP.
23	**Gas1 & Shh**	Growth arrest specific 1 & sonic hedgehog	[63]	Gas1$^{-/-}$;Shh$^{+/-}$ mice exhibit complete CP with 100% penetrance.
24	**Gli2 & Gli3**	Gli-Kruppel family member GLI2 & Gli-Kruppel family member GLI3	[64]	Wnt1-Cre;Gli2;Gli3 double CKO mice exhibit CP.
25	**Hhat & Ptch1**	Hedgehog acyltransferase & patched 1	[65]	Hhat$^{creface/creface}$;Ptch1$^{wiggable/wiggable}$ DKO mice exhibit primary palate cleft and CL.
26	**Inhba & Inhbb**	Inhibin, beta A & inhibin, beta B	[66]	33% of Inhba$^{-/-}$;Inhbb$^{-/-}$ DKO mice exhibit CP. No image available, only text.
27	**Insig1 & Insig2**	Inulin induced gene, 1 and inulin induced gene, 2	[67]	52% of Insig1$^{-/-}$; Insig2$^{-/-}$ DKO mice exhibit CP, and 48% exhibit midfacial cleft.
28	**Irf6 & Sfn**	Interferon regulatory factor 6 & stratifin	[68]	Irf6$^{+/R84C}$;Sfn$^{+/Er}$ double het mice exhibit CP because of intraoral fusion; palatal shelves and the tongue and mandible as seen in Irf6$^{R84C/R84C}$.
29	**Itga5 & Itgav**	Integrin alpha 5 & integrin alpha V	[69]	Wnt1-Cre;Itga5;Itgav double CKO exhibit CP.
30	**Itgb6 & Itgb8**	Integrin beta 6 & integrin beta 8	[70]	2/3 DKO exhibit CP.
31	**Kat6a & Tbx1**	K (lysine) acetyltransferase 6A & T-box 1	[71]	Some Kat6a$^{+/-}$;Tbx1$^{+/-}$ double het mice exhibit CP and other DiGeorge syndrome-like phenotype.
32	**Kif3a & Gli2**	Kinesin family member 3A & GLI-Kruppel family member GLI2	[64]	CP and cleft face.
33	**Kdf1 & Sfn**	Keratinocyte differentiation factor 1 & stratifin	[72]	Kdf1$^{+/-}$;Sfn$^{+/Er}$ double het mice exhibit CP, as seen in Kdf1 null.
34	**Lbr & Tm7sf2**	Lamin B receptor & Transmembrane 7 superfamily member 2	[73]	Lbr$^{-/-}$;Tm7sf2$^{+/-}$ (Dhcr14$^{\Delta 4-7}$) mice. 1/4 null (a total of 4 mice survive at birth) mice exhibit CP. Image is not available, only text.
35	**Lhx6 & Lhx8**	LIM homeobox protein 6 & LIM homeobox protein 8	[74]	All Lhx6$^{-/-}$;Lhx8$^{+/LacZ}$, LhX6$^{+/-}$;Lhx8$^{Lacz/LacZ}$ and Lhx6$^{-/-}$; Lhx8$^{LacZ/Lacz}$ (combination of het & KO and DKO) mutant mice exhibit CP with 100% penetrance. Lhx6 single null mice do not have CP and can survive at least 2 weeks.
36	**Mapk1 & Mapk3 (aka Erk1)**	Mitogen-activated protein 1 & mitogen-activated protein 3	[75]	Wnt1-Cre;Mapk1$^{F/F}$; Mapk3$^{-/+}$ and Wnt1-Cre;Mapk1$^{F/F}$;Mapk3$^{-/-}$ (DKO) mice exhibit more severe CP than Wnt1-Cre;Mapk1 single CKO mice.
37	**Mdm2 & Mdm4**	Transformed mouse 3T3 cell double minute 2 & transformed mouse 3T3 cell double minute 4	[76]	Mdm2$^{+/-}$;Mdm4$^{+/-}$ double het mice exhibit CP with 10-20% penetrance with exencephaly or other neural tube defects. Image is not available, only text.
38	**Mmp14 (aka Mt1-mmp) & Mmp16 (aka Mt3-mmp)**	Matrix metallopeptidase 14 (membrane type 1-Mmp) & matrix metallopeptidase 16 (membrane type 3-Mmp)	[77]	Mmp14$^{-/-}$; Mmp16$^{-/-}$ DKO mice exhibit CP with 80% penetrance.
39	**Msc (aka MyoR) & Tcf21 (aka Capsulin)**	Musculin & transcription factor 21	[78]	Msc$^{-/-}$;Tcf21$^{-/-}$ DKO mice exhibit CP, but not single KO mice.

Table 3 (*continued*)

No.	Gene symbol	Gene name	References	Note
40	**Nog & Chrd**	Noggin & chordin	[79]	Wnt1-Cre;$Nog^{Lacz/F}$;$Chrd^{-/-}$ double CKO mice exhibit CP, similar to Wnt1-Cre;$Nog^{Lacz/F}$ CKO.
41	**Msx1 & Dlx5**	msh homeobox 1& distal-less homeobox 5	[80,81]	$Msx1^{-/-}$;$Dlx5^{-/-}$ DKO mice can rescue Msx1's CP to mild clefting, which can be seen in Dlx5 null mice.
42	**Osr2 & Pax9**	Odd-skipped related 2 & paired box 9	[82]	$Osr2^{-/-}$;$Pax9^{+/-}$ mice exhibit CP.
43	**Pax9 & Msx1**	paired box 9 & msh homeobox 1	[83]	All $Pax9^{-/-}$;$Msx1^{+/+}$, $Pax9^{-/-}$;$Msx1^{+/-}$, and $Pax9^{-/-}$;$Msx1^{-/-}$ mice exhibit CP because of the absent palatal process of premaxilla.
44	**Pbx1 & Pbx2**	Pre B cell leukemia homeobox 1 & pre B cell leukemia homeobox 2	[84]	$Pbx1^{-/-}$;$Pbx2^{+/-}$ mice exhibit CP and unilateral or bilateral CL. $Pbx1^{F/F}$;$Pbx2^{+/-}$;Crect-$Cre^{/+}$ mice exhibit CP and bilateral CL. $Pbx1^{F/F}$;$Pbx2^{+}$/-;Foxg1-$Cre^{/+}$ (KI) mice exhibit CP and bilateral CL, absence of premaxilla.
45	**Pbx1 & Pbx3**	Pre B cell leukemia homeobox 1 & pre B cell leukemia homeobox 3	[84]	$Pbx1^{-/-}$;$Pbx3^{+/-}$ mice exhibit CP and unilateral or bilateral CL. $Pbx1^{F/F}$;$Pbx3^{F/+}$;Foxg1-$Cre^{/+}$ (KI) mice exhibit CP and CL.
46	**Pbx1 & Wnt9b**	Pre B cell leukemia homeobox 1 & wingless-type MMTV integration site family, member 9B	[84]	$Pbx1^{+/-}$;$Wnt9b^{-/-}$ mice exhibit CL, increased incidence of CL compared with Wnt9b null only. $Pbx1^{F/+}$;$Wnt9b^{-/-}$;Foxg1-$Cre^{/+}$(KI) mice exhibit bilateral CL and CP.
47	**Pcgf2 & Bmi1**	Polycomb group ring finger 2 & BMI1 polycomb ring finger oncogene	[85]	$Pcgf2^{+}$/-;$Bmi1^{-/-}$ or $Pcgf2^{-/-}$;$Bmi1^{+/-}$ mice exhibit CP. No image, only text (with 6/6 penetrance). Combination of null & null is lethal at E9.5.
48	**Pdgfra & Arid5b**	Platelet-derived growth factor receptor, alpha polypeptide & AT rich interactive domain 5B (MRF1-like)	[47]	$Pdgfra^{+/-}$;$Ard5b^{-/-}$ mice exhibit CP.
49	**Pdgfra & Plekha1**	Platelet-derived growth factor receptor, alpha polypeptide & pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	[47]	$Pdgfra^{+/-}$;$Plekha1^{-/-}$ mice exhibit CP or midfacial cleft (2/7).
50	**Pdgfra & Pdgfrb**	Platelet-derived growth factor receptor, alpha polypeptide & platelet-derived growth factor receptor, beta polypeptide	[63]	Wnt1-Cre;$Pdgfra^{F/F}$;$Pdgfrb^{F/F}$ mice exhibit CP. No image is available, only text.
51	**Phc1 & Phc2**	Polyhomeotic -like 1 & polyhomeotic -like 2	[86]	$Phc1^{-/-}$;$Phc2^{+/-}$ or $Phc1^{+/-}$;$Phc2^{-/-}$ mice exhibit CP.
52	**Prrx1 & Prrx2**	Paired related homeobox 1 & paired related homeobox 2	[87]	$Prrx1^{-/-}$;$Prrx2^{-/-}$ mice exhibit CP and cleft mandible. $Prrx1^{-/-}$; $Prrx2^{+/-}$ mice exhibit CP and abnormal mandible.
53	**Ptprf & Ptprs**	Protein tyrosine phosphatase, receptor type, F & protein tyrosine phosphatase, receptor type, S	[88,89]	38% $Ptprf^{-/-}$; $Ptprs^{-/-}$ DKO mice exhibit CP and microglossia (aglossia).
54	**Pygo1 & Pygo2**	Pygopus 1 & pygopus 2	[90,91]	A low % of $Pygo1^{-/-}$;$Pylg2^{-/-}$ DKO mice exhibit CP, but both single KO mice show no CP.
55	**Rspo2 & Lrp6**	R-spondin 2 & low density lipoprotein receptor-related protein 6	[92]	$Rspo2^{-/-}$;$Lrp6^{+/-}$ mice exhibit CP. DKO mice die, double het mice are normal. No image is available, only text.
56	**Shh & Six3**	Sonic hedgehog & sine oculis-related homeobox 3	[93]	$Shh^{+/-}$;$Six3^{+/Ki(V250A)}$ double het mice exhibit CP in some parts, not consistent from the anterior to the posterior (see Fig. 2).

57	**Six1 & Eya1**	Sine oculis-related homeobox 1 & EYA transcriptional coactivator and phosphatase 1	[94]	$Six1^{-/-}$;$Eya1^{-/-}$ DKO mice exhibit CP.
58	**Six1 & Six4**	Sine oculis-related homeobox 1 & sine oculis-related homeobox 4	[95]	$Six1^{-/-}$;$Six4^{-/-}$ DKO mice lack the palatal process of maxilla & palatine bone and have a short maxilla. $Six1^{-/-}$;$Six4^{-/-}$ DKO mice also lack Meckel's cartilage and have a short mandible. No information and image about CP.
59	**Smad4 & Irf6**	SMAD family member 4 & interferon regulatory factor 6	[96]	K14-Cre;$Smad4^{F/F}$;$Irf6^{R84C/+}$ compound mutant mice exhibit submucous CP. K14-Cre;$Smad4^{F/F}$ mice show no CP.
60	**Smad4 & Map3K7 (aka Tak1)**	SMAD family member 4 & mitogen-activated protein kinase kinase kinase 7	[97]	K14-Cre;Smad4;Tak1 DCKO exhibit submucous CP.
61	**Smad4 & Trim 33**	SMAD family member 4 & tripartite motif-containing 33	[98]	K14-Cre;Smad4;Trim33 DCKO exhibit submucous CP.
62	**Snai1 (aka Sna, Sna1, Snail, Snail1) & Snai2 (aka Slug, Slugh, Snail2)**	Snail family zinc finger 1& Snail family zinc finger 2	[99]	$Snai1^{-/+}$;$Snai2^{-/-}$ or Wnt1-Cre;$Snai1^{F/-}$;$Snai2^{-/-}$ mice exhibit CP.
63	**Sox5 & Sox6**	SRY (sex determining region Y)-box 5 & SRY (sex determining region Y)-box 6	[100]	$Sox5^{-/-}$;$Sox6^{-/-}$ DKO mice exhibit CP.
64	**Spry1 & Spry2**	Sprouty homolog 1 & sprouty homolog 2	[101]	$Spry1^{-/-}$;$Spry2^{-/-}$ DKO mice exhibit CP.
65	**Tbx2 &Tbx3**	T-box 2 & T-box 3	[102]	38% of $Tbx2^{Cre/+}$;$Tbx3^{Cre/+}$ (double het) in the NMRI background and 86% of $Tbx2^{Cre/+}$;$Tbx3^{Cre/+}$ in the FvB/N background exhibit CP.
66	**Tgfb1 & Tgfb3**	Transforming growth factor, beta 1 & transforming growth factor, beta 3	[103]	$Tgfb1^{-/-}$;$Tgfb3^{-/-}$ DKO mice exhibit CP with 100% penetrance.
67	**Trp63 &Irf6**	Transformation related protein 63 & interferon regulatory factor 6	[104]	89% of $Trp63^{+/-}$;$Irf6^{R84C/+}$ double het mice exhibit CP.
68	**Vax1 & Vax2**	Ventral anterior homeobox 1 & ventral anterior homeobox 2	[105]	$Vax1^{-/-}$;$Vax2^{-/-}$ DKO mice exhibit CP.
69	**Wnt5a & Ror2**	Wingless-type MMTV integration site family, member 5A & receptor tyrosine kinase-like orphan receptor 2	[106]	$Wnt5a^{+/-}$;$Ror2^{+/-}$ double het mice exhibit CP.
70	**Zeb1 & Zeb2**	Zinc finger E-box binding homeobox 1 & Zinc finger E-box binding homeobox 2	[107]	$Zeb1^{-/-}$;$Zeb2^{+/-}$ compound mutant mice exhibit midfacial cleft. They die at E13.5.

CL, cleft lip; CKO, conditional knockout; CP, cleft palate; DKO, double knockout; Het, heterozygous; KI, knock-in; KO, knockout.

Table 4
KEGG pathways enriched with a statistically significant number of genes involved in cleft palate.

KEGG pathway	Cleft palate genes in pathway
MAPK signaling pathway	*Fgf8 Chuk Map3k7 Rac1 Pdgfrb Tgfbr1 Fgfr1 Egfr Cacna1s Sos1 Flna Grb2 Tgfb1 Fgf18 Crk Tgfbr2 Tgfb2 Fgf10 Fgf9*
TGF-beta signaling pathway	*Smad4 Bmp2 Inhbb Bmpr1a Chrd Pitx2 Tgfb1 Acvr2a Tgfbr2 Acvr1 Fst Tgfb2 Crebbp Tgfbr1*
WNT signaling pathway	*Axin1 Smad4 Prickle1 Map3k7 Rac1 Crebbp Gsk3b Ctnnbip1*
Neurotrophin signaling pathway	*Grb2 Crk Sos1 Rac1 Ptpn11 Gsk3b Gab1*
ErbB signaling pathway	*Grb2 Crk Egfr Sos1 Gsk3b Gab1*
Hedgehog signaling pathway	*Bmp2 Gli3 Gli2 Gsk3b Smo*
T cell receptor signaling pathway	*Grb2 Chuk Map3k7 Dlg1 Sos1 Gsk3b*
B cell receptor signaling pathway	*Grb2 Chuk Sos1 Rac1 Gsk3b*
Insulin signaling pathway	*Grb2 Crk Ptprf Sos1 Gsk3b*
GnRH signaling pathway	*Grb2 Mmp14 Egfr Cacna1s Sos1*
Chemokine signaling pathway	*Grb2 Chuk Crk Sos1 Rac1 Gsk3b*
JAK-STAT signaling pathway	*Grb2 Spry1 Sos1 Ptpn11 Crebbp*
Calcium signaling pathway	*Ednra Egfr Cacna1s Pdgfrb*
Focal adhesion	*Itgb1 Itgb6 Pdgfc Ilk Vegfa Rac1 Pdgfrb Col11a1 Egfr Sos1 Flna Gsk3b Grb2 Crk Itgav Col2a1*
Regulation of actin cytoskeleton	*Fgf8 Fgfr1 Itgb1 Egfr Itgb6 Pdgfc Sos1 Fgf18 Crk Itgav Fgf10 Rac1 Pdgfrb Fgf9*
Adherens junction	*Snai1 Smad4 Fgfr1 Egfr Map3k7 Tgfbr2 Ptprf Rac1 Tgfbr1 Crebbp*
ECM-receptor interaction	*Itgb1 Col11a1 Itgb6 Itgav Col2a1 Hspg2*
Gap junction	*Grb2 Egfr Pdgfc Sos1 Pdgfrb*
Cell adhesion molecules	*Vcan Itgb1 Itgav Ptprf*
Cytokine-cytokine receptor interaction	*Bmp2 Egfr Inhbb Bmpr1a Pdgfc Tgfb1 Acvr2a Tgfbr2 Acvr1 Vegfa Tgfb2 Pdgfrb Tgfbr1*
Natural killer cell mediated cytotoxicity	*Grb2 Sos1 Rac1 Ptpn11*
Pathways in cancer	*Fgf8 Bmp2 Itgb1 Smo Axin1 Chuk Mdm2 Vegfa Rac1 Pdgfrb Crebbp Tgfbr1 Smad4 Fgfr1 Egfr Sos1 Gli2 Gsk3b Grb2 Tgfb1 Fgf18 Gli3 Crk Tgfbr2 Itgav Tgfb2 Fgf10 Fgf9*
Chronic myeloid leukemia	*Smad4 Sos1 Grb2 Tgfb1 Crk Chuk Tgfbr2 Mdm2 Tgfb2 Ptpn11 Tgfbr1*
Prostate cancer	*Fgfr1 Egfr Pdgfc Sos1 Gsk3b Grb2 Chuk Mdm2 Pdgfrb Crebbp*
Renal cell carcinoma	*Sos1 Gab1 Grb2 Tgfb1 Crk Tgfb2 Vegfa Rac1 Ptpn11 Crebbp*
Pancreatic cancer	*Smad4 Egfr Tgfb1 Chuk Tgfbr2 Tgfb2 Vegfa Rac1 Tgfbr1*
Melanoma	*Fgf8 Fgfr1 Egfr Pdgfc Fgf18 Mdm2 Fgf10 Fgf9 Pdgfrb*
Colorectal cancer	*Smad4 Gsk3b Axin1 Tgfb1 Tgfbr2 Tgfb2 Rac1 Tgfbr1*
Endometrial cancer	*Grb2 Axin1 Egfr Ilk Sos1 Gsk3b*
Basal cell carcinoma	*Axin1 Bmp2 Gli3 Gli2 Gsk3b Smo*
Glioma	*Grb2 Egfr Mdm2 Sos1 Pdgfrb*
Small cell lung cancer	*Chuk Itgb1 Itgav Apaf1*
Osteoclast differentiation	*Grb2 Tgfb1 Chuk Map3k7 Tgfbr2 Tgfb2 Rac1 Tgfbr1*
Axon guidance	*Itgb1 Ephb2 Efna5 Gsk3b Nrp1 Ephb3 Efnb1 Rac1*
Cell cycle	*Smad4 Tgfb1 Mdm2 Tgfb2 Cdkn1c Crebbp Gsk3b*
Metabolic pathways	*Papss2 Sc5d Gad2 Inpp5e Glce Tm7sf2 Dhcr7 Piga Sgpl1 Cdo1*
Hypertrophic cardiomyopathy (HCM)	*Tgfb1 Itgb1 Itgb6 Itgav Tgfb2 Cacna1s*
Dilated cardiomyopathy	*Tgfb1 Itgb1 Itgb6 Itgav Tgfb2 Cacna1s*
Arrhythmogenic right ventricular Cardiomyopathy (ARVC)	*Itgb1 Itgb6 Itgav Cacna1s*
Bacterial invasion of epithelial cells	*Itgb1 Crk Ilk Rac1 Gab1*
Chagas disease (American trypanosomiasis)	*Tgfb1 Chuk Tgfbr2 Tgfb2 Tgfbr1*
Leishmaniasis	*Tgfb1 Itgb1 Map3k7 Tgfb2*
Toxoplasmosis	*Tgfb1 Chuk Itgb1 Map3k7 Tgfb2*
Endocytosis	*Tgfb1 Egfr Mdm2 Tgfbr2 Tgfb2 Tgfbr1*
Hepatitis C	*Grb2 Chuk Egfr Sos1 Gsk3b*
Amoebiasis	*Tgfb1 Col11a1 Col2a1 Tgfb2*

Table 5
GO biological process terms enriched with a statistically significant number of genes involved in cleft palate.

GO biological process	Cleft palate genes in biological process category
Cellular macromolecule metabolic process	*Ldb1 Shox2 Csrnp1 Map3k7 Efna5 Apaf1 Chd7 Alx3 Tshz1 Satb2 Tgfb1 Tgfbr2 Mdm4 Ptprs Ryk Ctnnbip1 Pax3 Prickle1 Pbx3 Dlx5 Foxe1 Six3 Axin1 Foxd3 Trp63 Msx2 Tfap2a Egfr Tbx10 Flna Grb2 Itgav Acan Tbx22 Fgf9 Bmp2 Ephb2 Pkdcc Dlg1 Pitx2 Jmjd6 Recql4 Cdkn1c Akap8 Alx1 Hoxa2 Msc Gli2 Dicer1 Sim2 Prdm16 Bnc2 Hand2 Tcof1 Pbx1 Vegfa Rac1 Igf2 Crebbp Snai1 Fgfr1 Pygo2 Bmi1 Six1 Eya4 Gab1 Prrx2 Mnt Hic1 Tcf21 Dlx6 Meox2 Tiparp Sox11 Foxc2 Nrp1 Tgfb2 Fbxo11 Pds5a Fgf8 Cask Ift88 Spry1 Sox6 Rad23b Whsc1 Foxf2 Six4 Smo Acvr2a Ptprf Mdm2 Acvr1 Vax2 Tgfbr1 Col11a1 Edn1 Chrd Hs2st1 Gli3 Dph1 Fst Sox9 Alx4 Ptpn11 Rax Pdgfc Lhx8 Ednra Ephb3 Ilk Impad1 Ctgf Zeb2 Pcgf2 Gsc Bmpr1a Pygo1 Gsk3b Glce Twist1 Itgb1 Ahr Pitx1 Pbx2 Chuk Piga Pdgfrb Sp8 Smad4 Ski Col2a1 Fgf10*
Regulation of cellular metabolic process	*Eya4 Ldb1 Shox2 Csrnp1 Insig2 Gab1 Map3k7 Prrx2 Mnt Hic1 Tcf21 Meox2 Dlx6 Efna5 Chd7 Alx3 Tshz1 Satb2 Sox11 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Mdm4 Pds5a Ctnnbip1 Fgf8 Pax3 Insig1 Prickle1 Ift88 Cask Inhbb Whsc1 Rad23b Sox6 Spry1 Pbx3 Dlx5 Foxe1 Foxf2 Smo Six4 Six3 Axin1 Acvr2a Foxd3 Acvr1 Mdm2 Vax2 Tgfbr1 Trp63 Msx2 Tfap2a Egfr Tbx10 Flna Chrd Edn1 Grb2 Gli3 Crk Itgav Sox9 Fst Tbx22 Alx4 Ptpn11 Fgf9 Rax Bmp2 Dlg1 Pdgfc Lhx8 Ednra Pitx2 Jmjd6 Ephb3 Ilk Ctgf Cdkn1c Pcgf2 Zeb2 Alx1 Hoxa2 Msc Gsc Bmpr1a Pygo1 Gli2 Gsk3b Dicer1 Sim2 Twist1 Prdm16 Itgb1 Ahr Pitx1 Pbx2 Bnc2 Hand2 Pbx1 Vegfa Pdgfrb Rac1 Igf2 Sp8 Crebbp Snai1 Smad4 Fgfr1 Pygo2 Ski Bmi1 Fgf10 Six1*
Regulation of primary metabolic process	*Eya4 Ldb1 Shox2 Csrnp1 Insig2 Gab1 Map3k7 Prrx2 Mnt Hic1 Tcf21 Meox2 Dlx6 Efna5 Chd7 Alx3 Tshz1 Satb2 Sox11 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Mdm4 Pds5a Ctnnbip1 Fgf8 Pax3 Insig1 Prickle1 Ift88 Cask Inhbb Whsc1 Rad23b Sox6 Spry1 Pbx3 Dlx5 Foxe1 Foxf2 Smo Six4 Six3 Axin1 Acvr2a Foxd3 Acvr1 Mdm2 Vax2 Tgfbr1 Trp63 Msx2 Tfap2a Egfr Tbx10 Flna Chrd Edn1 Gli3 Crk Itgav Sox9 Fst Tbx22 Alx4 Ptpn11 Fgf9 Rax Bmp2 Dlg1 Pdgfc Lhx8 Ednra Pitx2 Jmjd6 Ephb3 Ilk Ctgf Cdkn1c Pcgf2 Zeb2 Alx1 Hoxa2 Msc Gsc Bmpr1a Pygo1 Gli2 Gsk3b Dicer1 Sim2 Twist1 Prdm16 Itgb1 Ahr Pitx1 Pbx2 Bnc2 Hand2 Pbx1 Dhcr7 Vegfa Pdgfrb Rac1 Igf2 Sp8 Crebbp Snai1 Smad4 Fgfr1 Pygo2 Ski Bmi1 Fgf10 Six1*
Cell differentiation	*Vcan Ldb1 Shox2 Hspg2 Tcf21 Tiparp Dlx6 Efna5 Chd7 Satb2 Sox11 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Ryk Ctnnbip1 Fgf8 Pax3 Insig1 Prickle1 Ift88 Inhbb Sox6 Spry1 Pbx3 Dlx5 Smo Six4 Six3 Axin1 Acvr2a Foxd3 Acvr1 Ptprf Vax2 Efnb1 Tgfbr1 Trp63 Msx2 Col11a1 Tfap2a Egfr Flna Chrd Edn1 Clptm1 Grb2 Fgf18 Gli3 Acan Itgav Sox9 Fst Ptpn11 Fgf9 Bmp2 Ephb2 Pkdcc Lhx8 Ednra Pitx2 Jmjd6 Ephb3 Ilk Impad1 Ctgf Cdkn1c Zeb2 Alx1 Hoxa2 Plekha1 Bmpr1a Oca2 Gli2 Gsk3b Dicer1 Sim2 Boc Twist1 Prdm16 Itgb1 Ahr Pitx1 Gabrb3 Inpp5e Hand2 Adamts9 Pbx1 Dhcr7 Chuk Vegfa Sgpl1 Pdgfrb Rac1 Igf2 Crebbp Snai1 Smad4 Fgfr1 Cacna1s Ski Jag2 Bmi1 Col2a1 Fgf10 Six1*
Anatomical structure formation involved in morphogenesis	*Eya4 Ldb1 Shox2 Csrnp1 Insig2 Map3k7 Prrx2 Hspg2 Tcf21 Ofd1 Tiparp Meox2 Dlx6 Efna5 Apaf1 Chd7 Tshz1 Sox11 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Ryk Ctnnbip1 Fgf8 Mmp14 Pax3 Insig1 Prickle1 Ift88 Whsc1 Spry1 Dlx5 Foxe1 Foxf2 Smo Six4 Six3 Axin1 Foxd3 Acvr1 Ptprf Vax2 Efnb1 Tgfbr1 Trp63 Msx2 Col11a1 Tfap2a Egfr Flna Chrd Edn1 Hs2st1 Grb2 Fgf18 Gli3 Itgav Ift140 Sox9 Fst Br Alx4 Schip1 Ptpn11 Fgf9 Bmp2 Ephb2 Dlg1 Ednra Pitx2 Jmjd6 Ephb3 Ilk Impad1 Ctgf Zeb2 Alx1 Hoxa2 Gsc Plekha1 Bmpr1a Gli2 Gsk3b Dicer1 Boc Twist1 Itgb1 Ahr Zfp640 Hand2 Pbx1 Vegfa Sgpl1 Pdgfrb Rac1 Snai1 Smad4 Fgfr1 Luzp1 Cacna1s Ski Col2a1 Fgf10 Six1*
Positive regulation of cellular process	*Ldb1 Shox2 Csrnp1 Gab1 Map3k7 Prrx2 Hic1 Tcf21 Dlx6 Efna5 Apaf1 Sos1 Satb2 Sox11 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Mdm4 Disp1 Ryk Ctnnbip1 Fgf8 Mmp14 Pax3 Prickle1 Ift88 Cask Inhbb Sox6 Dlx5 Foxe1 Foxf2 Smo Six4 Six3 Axin1 Acvr2a Foxd3 Acvr1 Mdm2 Ptprf Efnb1 Tgfbr1 Trp63 Msx2 Tfap2a Egfr Flna Chrd Edn1 Grb2 Fgf18 Gli3 Itgav Sox9 Alx4 Ptpn11 Fgf9 Bmp2 Ephb2 Pkdcc Dlg1 Pdgfc Ednra Pitx2 Ephb3 Ilk Ctgf Recql4 Cdkn1c Zeb2 Alx1 Hoxa2 Bmpr1a Pygo1 Gli2 Gsk3b Dicer1 Boc Twist1 Prdm16 Itgb1 Ahr Pitx1 Igf2r Zfp640 Inpp5e Pbx2 Hand2 Adamts9 Pbx1 Chuk Vegfa Pdgfrb Rac1 Igf2 Crebbp Snai1 Smad4 Fgfr1 Ski Bmi1 Fgf10 Six1*
Regulation of macromolecule biosynthetic process	*Eya4 Ldb1 Shox2 Csrnp1 Map3k7 Prrx2 Mnt Hic1 Tcf21 Meox2 Dlx6 Chd7 Alx3 Tshz1 Satb2 Sox11 Foxc2 Tgfb1 Tgfb2 Mdm4 Pds5a Ctnnbip1 Fgf8 Pax3 Prickle1 Cask Inhbb Whsc1 Sox6 Pbx3 Dlx5 Foxe1 Foxf2 Smo Six4 Six3 Axin1 Acvr2a Foxd3 Acvr1 Mdm2 Vax2 Tgfbr1 Trp63 Msx2 Tfap2a Egfr Tbx10 Flna Chrd Edn1 Gli3 Itgav Sox9 Fst Tbx22 Alx4 Fgf9 Rax Bmp2 Pdgfc Lhx8 Pitx2 Jmjd6 Ilk Ctgf Cdkn1c Pcgf2 Zeb2 Alx1 Hoxa2 Msc Gsc Bmpr1a Pygo1 Gli2 Gsk3b Dicer1 Sim2 Twist1 Prdm16 Ahr Pitx1 Pbx2 Bnc2 Hand2 Pbx1 Vegfa Pdgfrb Rac1 Igf2 Sp8 Crebbp Snai1 Smad4 Fgfr1 Ski Bmi1 Fgf10 Six1*

Table 5 (*continued*)

GO biological process	Cleft palate genes in biological process category
Chordate embryonic development	*Bmp2 Shox2 Dlg1 Gab1 Ednra Pitx2 Map3k7 Prrx2 Hspg2 Pcgf2 Zeb2 Hoxa2 Alx1 Meox2 Gsc Bmpr1a Apaf1 Chd7 Gli2 Alx3 Satb2 Sox11 Foxc2 Tgfbr2 Tgfb2 Twist1 Fgf8 Pax3 Itgb1 Prickle1 Ift88 Sox6 Hand2 Smo Six4 Axin1 Acvr2a Foxd3 Pbx1 Acvr1 Vegfa Pdgfrb Tgfbr1 Snai1 Smad4 Col11a1 Egfr Tfap2a Fgfr1 Luzp1 Pygo2 Edn1 Grb2 Ski Gli3 Jag2 Itgav Bmi1 Col2a1 Br Alx4 Fgf9 Six1*
Tissue morphogenesis	*Bmp2 Shox2 Dlg1 Ednra Pitx2 Map3k7 Ilk Zeb2 Tcf21 Alx1 Bmpr1a Apaf1 Gli2 Sox11 Dicer1 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Twist1 Ctnnbip1 Fgf8 Pax3 Prickle1 Ahr Foxe1 Foxf2 Hand2 Smo Six4 Axin1 Pbx1 Chuk Acvr1 Vegfa Rac1 Trp63 Msx2 Snai1 Smad4 Col11a1 Egfr Tfap2a Fgfr1 Luzp1 Chrd Edn1 Hs2st1 Grb2 Ski Gli3 Jag2 Sox9 Fst Br Fgf10 Six1*
Epithelium development	*Bmp2 Dlg1 Ednra Pitx2 Map3k7 Ilk Zeb2 Tcf21 Alx1 Dlx6 Bmpr1a Apaf1 Gli2 Sox11 Dicer1 Nrp1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Twist1 Ctnnbip1 Fgf8 Pax3 Prickle1 Ahr Ift88 Dlx5 Foxf2 Hand2 Smo Six4 Pbx1 Chuk Acvr1 Vegfa Rac1 Tgfbr1 Trp63 Msx2 Smad4 Egfr Tfap2a Fgfr1 Luzp1 Pygo2 Edn1 Hs2st1 Grb2 Ski Gli3 Jag2 Sox9 Br Fgf10 Six1*
Pattern specification process	*Bmp2 Ldb1 Ednra Pitx2 Pcgf2 Zeb2 Hoxa2 Ofd1 Alx1 Meox2 Gsc Bmpr1a Gli2 Alx3 Tshz1 Satb2 Nrp1 Foxc2 Sim2 Tgfbr2 Ctnnbip1 Disp1 Fgf8 Pax3 Ahr Ift88 Spry1 Pbx2 Hand2 Six3 Smo Axin1 Acvr2a Pbx1 Acvr1 Vegfa Vax2 Efnb1 Sp8 Tgfbr1 Trp63 Msx2 Snai1 Smad4 Tfap2a Fgfr1 Chrd Edn1 Ski Gli3 Bmi1 Fst Alx4 Fgf10 Six1 Rax*
Sensory organ development	*Eya4 Bmp2 Ephb2 Dlg1 Insig2 Jmjd6 Pitx2 Prrx2 Hoxa2 Dlx6 Gsc Chd7 Gli2 Tshz1 Sox11 Dicer1 Foxc2 Tgfb1 Tgfbr2 Tgfb2 Twist1 Prdm16 Fgf8 Insig1 Ahr Inhbb Gabrb3 Dlx5 Foxf2 Hand2 Six4 Six3 Vegfa Vax2 Pdgfrb Rac1 Tgfbr1 Col11a1 Tfap2a Fgfr1 Cacna1s Pygo2 Edn1 Ski Gli3 Jag2 Col2a1 Sox9 Fgf10 Fgf9 Six1 Rax*
Tube development	*Bmp2 Pkdcc Dlg1 Ednra Jmjd6 Pitx2 Map3k7 Ilk Ctgf Zeb2 Tcf21 Alx1 Bmpr1a Apaf1 Chd7 Gli2 Sox11 Dicer1 Nrp1 Foxc2 Sim2 Tgfb1 Tgfbr2 Twist1 Ctnnbip1 Fgf8 Pax3 Mmp14 Prickle1 Ahr Ift88 Spry1 Hand2 Smo Six4 Pbx1 Dhcr7 Acvr1 Vegfa Trp63 Msx2 Smad4 Tfap2a Fgfr1 Luzp1 Edn1 Hs2st1 Fgf18 Ski Gli3 Sox9 Br Fgf10 Fgf9 Six1*
Embryonic organ morphogenesis	*Eya4 Shox2 Dlg1 Insig2 Pitx2 Prrx2 Hspg2 Pcgf2 Tcf21 Alx1 Hoxa2 Dlx6 Gsc Chd7 Gli2 Alx3 Tshz1 Satb2 Sox11 Foxc2 Tgfbr2 Tgfb2 Twist1 Fgf8 Insig1 Dlx5 Foxe1 Foxf2 Six4 Axin1 Vax2 Rac1 Tgfbr1 Col11a1 Tfap2a Fgfr1 Edn1 Gli3 Bmi1 Col2a1 Sox9 Alx4 Fgf10 Fgf9 Six1*
Skeletal system morphogenesis	*Shox2 Csrnp1 Dlg1 Insig2 Impad1 Ctgf Prrx2 Recql4 Hspg2 Pcgf2 Hoxa2 Alx1 Tiparp Gsc Plekha1 Alx3 Satb2 Sox11 Foxc2 Tgfbr2 Tgfb2 Twist1 Ryk Insig1 Dlx5 Zfp640 Six4 Axin1 Sgpl1 Pdgfrb Tgfbr1 Msx2 Tfap2a Col11a1 Fgf18 Ski Gli3 Acan Bmi1 Col2a1 Sox9 Br Alx4 Schip1 Six1*
Palate development	*Pkdcc Csrnp1 Dlg1 Insig2 Ephb3 Tcf21 Alx1 Tiparp Meox2 Dlx6 Msc Plekha1 Bmpr1a Chd7 Tshz1 Satb2 Sox11 Tgfbr2 Prdm16 Insig1 Dlx5 Foxe1 Zfp640 Hand2 Foxf2 Sgpl1 Tgfbr1 Snai1 Smad4 Tfap2a Pygo2 Ski Gli3 Col2a1 Alx4 Schip1*

2.2. Systematic review

The PRISMA (Preferred Reporting Items for Systematic reviews and Meta-Analyses) guideline and corresponding checklist were followed for this systematic review, as described previously [3]. The online databases searched included Medline (Ovid), PubMed (National Library of Medicine), and EMBASE (Ovid). In addition, relevant citations were searched in Scopus (Elsevier) to retrieve any exceptional studies missed by the database searches. The bibliographies of highly pertinent articles were further examined to avoid any errors introduced with the systematic review. Articles included in the systematic review met the following eligibility criteria: 1) described causative genes of mouse CP; 2) were published as original articles (not as review articles, editorials, or comments); 3) were written in English; 4) were published between the year 1980 and 2016; and 5) specified a CP type. Some articles were excluded from the systematic review because of one or more of the following reasons: 1) gene mutations were not described in the original articles; 2) CP was not described; 3) CP was caused by environmental factors; and 4) the articles failed to fit in any of the previous criteria but did not have useful CP genes or related information.

Table 6
GO Molecular Function terms enriched with a statistically significant number of genes involved in cleft palate.

GO molecular function	Cleft palate genes in molecular function category
Ion binding	*Eya4 Map3k7 Hic1 Tiparp Apaf1 Chd7 Tshz1 Nrp1 Tgfbr2 Mdm4 Ryk Mmp14 Prickle1 Cask Whsc1 Acvr2a Phc2 Acvr1 Mdm2 Ptprf Tgfbr1 Trp63 Egfr Chrd Gli3 Acan Fst Mmp16 Fgf9 Ephb2 Pkdcc Gad2 Lhx8 Jmjd6 Ephb3 Ilk Impad1 Recql4 Ctgf Zeb2 Pcgf2 Cdo1 Akap8 Plekha1 Bmpr1a Gli2 Pygo1 Dicer1 Gsk3b Prdm16 Papss2 Zfp640 Igf2r Bnc2 Adamts9 Chuk Vegfa Sgpl1 Pdgfrb Rac1 Sp8 Crebbp Snai1 Fgfr1 Pygo2 Ski Jag2 Bmi1 Fgf10*
Identical protein binding	*Bmp2 Ldb1 Inhbb Pdgfc Hand2 Axin1 Jmjd6 Pitx2 Acvr1 Mdm2 Vegfa Trp63 Smad4 Egfr Fgfr1 Bmpr1a Apaf1 Flna Grb2 Tgfb1 Col2a1 Tgfb2 Twist1 Schip1 Kcnj2*
Protein domain specific binding	*Bmp2 Ldb1 Itgb1 Cask Dlg1 Dlx5 Hand2 Axin1 Acvr2a Ilk Prrx2 Trp63 Plekha1 Lbr Sos1 Grb2 Ski Crk Bmi1 Twist1 Alx4 Ptpn11 Ctnnbip1*
Regulatory region nucleic acid binding	*Ldb1 Shox2 Ahr Sox6 Dlx5 Hand2 Foxd3 Pitx2 Vax2 Crebbp Trp63 Msx2 Tcf21 Smad4 Tfap2a Dlx6 Gli2 Sox11 Foxc2 Sox9 Twist1 Six1*
Chromatin binding	*Pax3 Ldb1 Whsc1 Pbx2 Pitx2 Vax2 Pcgf2 Mnt Trp63 Crebbp Akap8 Smad4 Tfap2a Chd7 Gli2 Satb2 Foxc2 Ski Gli3 Bmi1 Sox9 Six1*
Protein heterodimerization activity	*Bmp2 Itgb1 Ahr Gad2 Sox6 Hand2 Pbx1 Chuk Vegfa Tgfbr1 Alx1 Egfr Sos1 Sim2 Tgfb1 Itgav Tgfb2 Alx4 Twist1*
Transcription factor binding	*Ldb1 Prickle1 Ahr Insig2 Pbx2 Foxf2 Hand2 Pitx2 Pbx1 Crebbp Msx2 Tcf21 Tfap2a Flna Gsk3b Ski Twist1*
Protein complex binding	*Mmp14 Itgb1 Itgb6 Cask Gabrb3 Acvr2a Ilk Acvr1 Ptprf Ctgf Igf2 Tgfbr1 Egfr Fgfr1 Gsk3b Fst Ptpn11*
Transcription regulatory region sequence-specific DNA binding	*Msx2 Smad4 Ldb1 Dlx6 Tfap2a Shox2 Dlx5 Hand2 Sox11 Pitx2 Sox9 Vax2 Crebbp*
Glycosaminoglycan binding	*Fgfr1 Chrd Nrp1 Tgfbr2 Acan Ptprf Vegfa Ctgf Fgf9 Fgf10*
Growth factor activity	*Fgf8 Bmp2 Inhbb Pdgfc Tgfb1 Fgf18 Jag2 Vegfa Tgfb2 Ctgf Fgf10 Fgf9 Igf2*
Growth factor binding	*Fgfr1 Egfr Igf2r Nrp1 Acvr2a Tgfbr2 Acvr1 Col2a1 Ctgf Pdgfrb Tgfbr1*
SMAD binding	*Smad4 Bmp2 Bmpr1a Axin1 Ski Tgfbr2 Acvr1 Prdm16 Zeb2 Crebbp Tgfbr1*
RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	*Foxc2 Tcf21 Pitx2 Tfap2a Sox9 Twist1 Hand2 Sox11 Trp63*
Receptor signaling protein activity	*Smad4 Egfr Acvr2a Map3k7 Chuk Tgfbr2 Acvr1 Tgfb2*
Transmembrane receptor protein tyrosine kinase activity	*Nrp1 Ephb3 Fgfr1 Ephb2 Egfr Pdgfrb Ryk*
Transforming growth factor beta-activated receptor activity	*Acvr2a Acvr1 Tgfbr2 Bmpr1a Tgfbr1*

Table 7
GO cellular component terms enriched with a statistically significant number of genes involved in cleft palate.

GO cellular component	Cleft palate genes in cellular component category
Cytoplasm	*Eya4 Slc32a1 Insig2 Gab1 Tm7sf2 Map3k7 Hic1 Ofd1 Meox2 Apaf1 Satb2 Sox11 Nrp1 Tgfb1 H19 Tgfbr2 Tgfb2 Fbxo11 Ctnnbip1 Ryk Mmp14 Insig1 Prickle1 Ift88 Cask Inhbb Rad23b Spry1 Dlx5 Smo Six4 Axin1 Acvr2a Mdm2 Ptprf Vax2 Efnb1 Trp63 Msx2 Tfap2a Egfr Flna Edn1 Hs2st1 Krt5 Grb2 Gli3 Crk Ift140 Fst Dph1 Schip1 Ptpn11 Fgf9 Bmp2 Pkdcc Gad2 Dlg1 Pdgfc Pitx2 Ilk Impad1 Ctgf Recql4 Cdkn1c Zeb2 Cdo1 Akap8 Ovca2 Plekha1 Lbr Oca2 Gli2 Gsk3b Dicer1 Glce Itgb1 Ahr Pitx1 Igf2r Inpp5e Bnc2 Tcof1 Pbx1 Dhcr7 Chuk Piga Vegfa Sgpl1 Pdgfrb Rac1 Crebbp Snai1 Smad4 Fgfr1 Cacna1s Ski Jag2 Bmi1 Col2a1*
Plasma membrane part	*Fgf8 Slc32a1 Itgb1 Ephb2 Itgb6 Cask Dlg1 Ednra Axin1 Acvr2a Chuk Ephb3 Acvr1 Pdgfrb Rac1 Tgfbr1 Egfr Efna5 Plekha1 Cacna1s Clptm1 Grb2 Boc Jag2 Itgav Tgfbr2*

Table 7 (*continued*)

GO cellular component	Cleft palate genes in cellular component category
Transcription factor complex	*Pax3 Ldb1 Ahr Pitx1 Sox6 Pbx3 Pbx2 Foxf2 Hand2 Pbx1 Foxd3 Pitx2 Crebbp Msx2 Alx1 Smad4 Tfap2a Gsc Satb2 Ski Sox9 Alx4 Six1*
Cell surface	*Fgf8 Bmp2 Itgb1 Egfr Efna5 Igf2r Clptm1 Nrp1 Acvr2a Tgfb1 Boc Tgfbr2 Itgav Vegfa Tgfb2 Fgf10*
Dendrite	*Slc32a1 Cask Bmpr1a Dlg1 Sos1 Gsk3b Smo Dicer1 Axin1 Ilk Trp63 Kcnj2*
Neuronal cell body	*Ephb2 Bmpr1a Sos1 Gsk3b Smo Nrp1 Tgfb1 Boc Ilk Ptprf Tgfb2 Kcnj2*
Axon	*Slc32a1 Gad2 Dlg1 Gabrb3 Smo Dicer1 Nrp1 Tgfb1 Boc Ilk Tgfb2*
Basement membrane	*Itgb1 Cask Acan Vegfa Tgfb2 Col2a1 Hspg2 Fgf9*
Receptor complex	*Itgb1 Itgb6 Ahr Chuk Tgfbr2 Itgav Acvr1 Tgfbr1*
Growth cone	*Nrp1 Boc Ptprf Gsk3b Smo Dicer1*

2.3. Gene set enrichment analysis

Gene set enrichment analysis was conducted using the KEGG database (http://www.genome.jp/kegg), as described previously [4]. Significantly enriched categories were filtered to have a false discovery rate-adjusted p-value < 0.05 and at least four genes from the list of input genes. Reported enriched categories are “child” terms in the gene ontology hierarchy without any further statistically significant descendants. The GO database resource (http://www.geneontology.org) was used to identify functional categories of genes enriched with a statistically significant number of CP-associated genes from our curated list [2].

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Transparency document. Supporting information

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.03.010.

Appendix A. Supporting information

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References

[1] H. Ogata, S. Goto, K. Sato, W. Fujibuchi, H. Bono, M. Kanehisa, KEGG: kyoto encyclopedia of genes and genomes, Nucleic Acids Res 27 (1) (1999) 29–34 (PubMed PMID: 9847135; PubMed Central PMCID: PMCPMC148090).

[2] B. Zhang, S. Kirov, J. Snoddy, WebGestalt: an integrated system for exploring gene sets in various biological contexts (Web Server issue), Nucleic Acids Res. 33 (2005) W741–W748. http://dx.doi.org/10.1093/nar/gki475, (PubMed PMID: 15980575; PubMed Central PMCID: PMCPMC1160236).

[3] D. Sangani, A. Suzuki, H. VonVille, J.E. Hixson, J. Iwata, Gene mutations associated with temporomandibular joint disorders: a systematic review, OAlib 2 (6) (2015), http://dx.doi.org/10.4236/oalib.1101583, (PubMed PMID: 27695703; PubMed Central PMCID: PMCPMC5045035).

[4] R.C. Pelikan, J. Iwata, A. Suzuki, Y. Chai, J.G. Hacia, Identification of candidate downstream targets of TGFbeta signaling during palate development by genome-wide transcript profiling, J. Cell Biochem. 114 (4) (2013) 796–807. http://dx.doi.org/10.1002/jcb.24417, (PubMed PMID: 23060211; PubMed Central PMCID: PMCPMC3777336).
[5] E. Rittenhouse, L.C. Dunn, J. Cookingham, C. Calo, M. Spiegelman, G.B. Dooher, et al., Cartilage matrix deficiency (cmd): a new autosomal recessive lethal mutation in the mouse, J. Embryol. Exp. Morphol. 43 (1978) 71–84 (PubMed PMID: 632744).
[6] H. Watanabe, K. Kimata, S. Line, D. Strong, L.Y. Gao, C.A. Kozak, et al., Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrecan gene, Nat. Genet. 7 (2) (1994) 154–157. http://dx.doi.org/10.1038/ng0694-154, (PubMed PMID: 7920633).
[7] R.C. Krueger Jr, K. Kurima, N.B. Schwartz, Completion of the mouse aggrecan gene structure and identification of the defect in the cmd-Bc mouse as a near complete deletion of the murine aggrecan gene, Mamm. Genome: Off. J. Int. Mamm. Genome Soc. 10 (12) (1999) 1119–1125. http://dx.doi.org/10.1007/s003359901176, (PubMed PMID: 10594233).
[8] H. Kalter, The history of the A family of inbred mice and the biology of its congenital malformations, Teratology 20 (2) (1979) 213–232. http://dx.doi.org/10.1002/tera.1420200206, (PubMed PMID: 392800).
[9] D.M. Juriloff, Differences in frequency of cleft lip among the A strains of mice, Teratology 25 (3) (1982) 361–368. http://dx.doi.org/10.1002/tera.1420250313, (PubMed PMID: 7202260).
[10] D.M. Juriloff, M.J. Harris, S.L. Dewell, C.J. Brown, D.L. Mager, L. Gagnier, et al., Investigations of the genomic region that contains the clf1 mutation, a causal gene in multifactorial cleft lip and palate in mice, Birth Defects Res. Part A, Clin. Mol. Teratol. 73 (2) (2005) 103–113. http://dx.doi.org/10.1002/bdra.20106, (PubMed PMID: 15690355).
[11] O.P. Flint, Cell behaviour and cleft palate in the mutant mouse, amputated, J. Embryol. Exp. Morphol. 58 (1980) 131–142 (PubMed PMID: 7441149).
[12] S. Bornstein, D.G. Trasler, F.C. Fraser, Effect of the uterine environment on the frequency of spontaneous cleft lip in CL/FR mice, Teratology 3 (4) (1970) 295–298. http://dx.doi.org/10.1002/tera.1420030403, (PubMed PMID: 5538410).
[13] G. Millicovsky, L.J. Ambrose, M.C. Johnston, Developmental alterations associated with spontaneous cleft lip and palate in CL/Fr mice, Am. J. Anat. 164 (1) (1982) 29–44. http://dx.doi.org/10.1002/aja.1001640104, (PubMed PMID: 7102571).
[14] B.C. Bjork, A. Turbe-Doan, M. Prysak, B.J. Herron, D.R. Beier, Prdm16 is required for normal palatogenesis in mice, Human molecular genetics. 19 (5) (2010) 774–789. http://dx.doi.org/10.1093/hmg/ddp543, PubMed PMID: 20007998; PubMed Central PMCID: PMC2816611.
[15] B.J. Herron, W. Lu, C. Rao, S. Liu, H. Peters, R.T. Bronson, et al., Efficient generation and mapping of recessive developmental mutations using ENU mutagenesis, Nature genetics. 30 (2) (2002) 185–189. http://dx.doi.org/10.1038/ng812, PubMed PMID: 11818962.
[16] V.V. Uslu, M. Petretich, S. Ruf, K. Langenfeld, N.A. Fonseca, J.C. Marioni, et al., Long-range enhancers regulating Myc expression are required for normal facial morphogenesis, Nat. Genet. 46 (7) (2014) 753–758. http://dx.doi.org/10.1038/ng.2971, (PubMed PMID: 24859337).
[17] B.A. Karpinski, T.M. Maynard, M.S. Fralish, S. Nuwayhid, I.E. Zohn, S.A. Moody, et al., Dysphagia and disrupted cranial nerve development in a mouse model of DiGeorge (22q11) deletion syndrome, Dis. Model. Mech. 7 (2) (2014) 245–257. http://dx.doi.org/10.1242/dmm.012484, (PubMed PMID: 24357327; PubMed Central PMCID: PMC3917245).
[18] K. Katayama, A. Furuno, K. Akiyama, T. Tsuji, T. Kunieda, Characterization of chromosomal inversion of the mouse hairy ears (Eh) mutation associated with cleft palate, Mamm. Genome: Off. J. Int. Mamm. Genome Soc. 18 (4) (2007) 246–254. http://dx.doi.org/10.1007/s00335-007-9015-7, (PubMed PMID: 17520166).
[19] M.J. McLeod, M.J. Harris, G.F. Chernoff, J.R. Miller, First arch malformation: a new craniofacial mutant in the mouse, J. Hered. 71 (5) (1980) 331–335 (PubMed PMID: 7440954).
[20] G. Caruana, P.G. Farlie, A.H. Hart, S. Bagheri-Fam, M.J. Wallace, M.S. Dobbie, et al., Genome-wide ENU mutagenesis in combination with high density SNP analysis and exome sequencing provides rapid identification of novel mouse models of developmental disease, PloS One. 8 (3) (2013) e55429. http://dx.doi.org/10.1371/journal.pone.0055429, (PubMed PMID: 23469164; PubMed Central PMCID: PMC3585849).
[21] C.T. Culiat, L. Stubbs, R.D. Nicholls, C.S. Montgomery, L.B. Russell, D.K. Johnson, et al., Concordance between isolated cleft palate in mice and alterations within a region including the gene encoding the beta 3 subunit of the type A gamma-aminobutyric acid receptor, Proceedings of the National Academy of Sciences of the United States of America 90 (11) (1993) 5105–5109, PubMed PMID: 8389469; PubMed Central PMCID: PMC46663.
[22] L.B. Russell, C.S. Montgomery, N.L. Cacheiro, D.K. Johnson, Complementation analyses for 45 mutations encompassing the pink-eyed dilution (p) locus of the mouse, Genetics 141 (4) (1995) 1547–1562, PubMed PMID: 8601493; PubMed Central PMCID: PMC1206886.
[23] L. Johnston, D.J. Nash, Sagittal growth trends of the development of cleft palate in mice homozygous for the "paddle" gene, J. Craniofacial Genet. Dev. Biol. 2 (4) (1982) 265–276 (PubMed PMID: 7183705).
[24] J. Barra, An X-linked recessive mutation producing cleft palate, crooked tail, and polydactyly in mice, J. Hered. 81 (5) (1990) 388–392 (PubMed PMID: 2230077).
[25] N. Fitch, Development of cleft palate in mice homozygous for the shorthead mutation, J. Morphol. 109 (1961) 151–157. http://dx.doi.org/10.1002/jmor.1051090204, (PubMed PMID: 13893330).
[26] N. Fitch, A mutation in mice producing dwarfism, brachycephaly, cleft palate and micromelia, J. Morphol. 109 (1961) 141–149. http://dx.doi.org/10.1002/jmor.1051090203, (PubMed PMID: 13893329).
[27] B.Y. Orr, S.Y. Long, A.J. Steffek, Craniofacial, caudal, and visceral anomalies associated with mutant sirenomelic mice, Teratology 26 (3) (1982) 311–317. http://dx.doi.org/10.1002/tera.1420260313, (PubMed PMID: 6891838).
[28] J.O. Bush, Y. Lan, R. Jiang, The cleft lip and palate defects in Dancer mutant mice result from gain of function of the Tbx10 gene, Proc. Natl. Acad. Sci. USA 101 (18) (2004) 7022–7027. http://dx.doi.org/10.1073/pnas.0401025101, (PubMed PMID: 15118109; PubMed Central PMCID: PMC406459).
[29] M.S. Deol, P.W. Lane, A new gene affecting the morphogenesis of the vestibular part of the inner ear in the mouse, J. Embryol. Exp. Morphol. 16 (3) (1966) 543–558 (Epub 1966/12/01. PubMed PMID: 5297683).
[30] D.G. Trasler, S. Leong, Mitotic index in mouse embryos with 6-aminonicotinamide-induced and inherited cleft lip, Teratology 25 (2) (1982) 259–265. http://dx.doi.org/10.1002/tera.1420250215, (PubMed PMID: 7101202).

[31] L.C. Dunn, S. Gluecksohn-Schoenheimer, A new complex of hereditary abnormalities in the house mouse, J. Exp. Zool. 104 (1) (1947) 25–51 (PubMed PMID: 20285006).
[32] N. Fitch, An embryological analysis of two mutants in the house mouse, both producing cleft palate, J. Exp. Zool. 136 (2) (1957) 329–361 (PubMed PMID: 13525591).
[33] S.G. Gong, N.J. White, A.Y. Sakasegawa, The Twirler mouse, a model for the study of cleft lip and palate, Archives of oral biology 45 (1) (2000) 87–94, PubMed PMID: 10669096.
[34] K. Kurima, R. Hertzano, O. Gavrilova, K. Monahan, K.B. Shpargel, G. Nadaraja, et al., A noncoding point mutation of Zeb1 causes multiple developmental malformations and obesity in Twirler mice, PLoS Genet. 7 (9) (2011) e1002307. http://dx.doi.org/10.1371/journal.pgen.1002307, (PubMed PMID: 21980308; PubMed Central PMCID: PMC3183090).
[35] M.F. Lyon, Twirler: a mutant affecting the inner ear of the house mouse, J. Embryol. Exp. Morphol. 6 (1) (1958) 105–116 (PubMed PMID: 13539273).
[36] G.R. Lankas, L.D. Wise, M.E. Cartwright, T. Pippert, D.R. Umbenhauer, Placental P-glycoprotein deficiency enhances susceptibility to chemically induced birth defects in mice, Reprod. Toxicol. 12 (4) (1998) 457–463 (PubMed PMID: 9717696).
[37] M.L. Tyan, D.B. Tyan, Vitamin A-enhanced cleft palate susceptibility gene maps between C4 and B144 within the H-2 complex, Proc. Soc. Exp. Biol. Med. Soc. Exp. Biol. Med. 202 (4) (1993) 482–486 (PubMed PMID: 8456115).
[38] M. Vekemans, B.A. Taylor, F.C. Fraser, The susceptibility to cortisone-induced cleft palate of recombinant inbred strains of mice: lack of association with the H-2 haplotype, Genet. Res. 38 (3) (1981) 327–331 (PubMed PMID: 7333460).
[39] J.M. Peters, M.G. Narotsky, G. Elizondo, P.M. Fernandez-Salguero, F.J. Gonzalez, B.D. Abbott, Amelioration of TCDD-induced teratogenesis in aryl hydrocarbon receptor (AhR)-null mice, Toxicol. Sci.: Off. J. Soc. Toxicol. 47 (1) (1999) 86–92 (PubMed PMID: 10048156).
[40] J.J. Bonner, M.L. Tyan, Backcross test demonstrates the linkage of glucocorticoid-induced cleft palate susceptibility to H-2, Teratology 26 (2) (1982) 213–216. http://dx.doi.org/10.1002/tera.1420260214 (PubMed PMID: 7157197).
[41] G. Singh, D.M. Supp, C. Schreiner, J. McNeish, H.J. Merker, N.G. Copeland, et al., legless insertional mutation: morphological, molecular, and genetic characterization, Genes Dev. 5 (12A) (1991) 2245–2255 (PubMed PMID: 1748282).
[42] R.M. Pratt, D.S. Salomon, V.M. Diewert, R.P. Erickson, R. Burns, K.S. Brown, Cortisone-induced cleft palate in the brachymorphic mouse, Teratog., Carcinog., Mutagen. 1 (1) (1980) 15–23 (PubMed PMID: 6119797).
[43] H. Enomoto, C.M. Nelson, R.P. Somerville, K. Mielke, L.J. Dixon, K. Powell, et al., Cooperation of two ADAMTS metalloproteases in closure of the mouse palate identifies a requirement for versican proteolysis in regulating palatal mesenchyme proliferation, Development. 137 (23) (2010) 4029–4038. http://dx.doi.org/10.1242/dev.050591, PubMed PMID: 21041365; PubMed Central PMCID: PMC2976286.
[44] Y. Yang, C.L. Mahaffey, N. Berube, W.N. Frankel, Interaction between fidgetin and protein kinase A-anchoring protein AKAP95 is critical for palatogenesis in the mouse, The Journal of biological chemistry. 281 (31) (2006) 22352–22359. http://dx.doi.org/10.1074/jbc.M603626200, PubMed PMID: 16751186.
[45] S. Qu, S.C. Tucker, Q. Zhao, B. deCrombrugghe, R. Wisdom, Physical and genetic interactions between Alx4 and Cart1, Development 126 (2) (1999) 359–369 (PubMed PMID: 9847249).
[46] A. Beverdam, A. Brouwer, M. Reijnen, J. Korving, F. Meijlink, Severe nasal clefting and abnormal embryonic apoptosis in Alx3/Alx4 double mutant mice, Development. 128 (20) (2001) 3975–3986 (PubMed PMID: 11641221).
[47] J. Schmahl, C.S. Raymond, P. Soriano, PDGF signaling specificity is mediated through multiple immediate early genes, Nature genetics. 39 (1) (2007) 52–60. http://dx.doi.org/10.1038/ng1922, PubMed PMID: 17143286.
[48] I.V. Chia, M.J. Kim, K. Itoh, S.Y. Sokol, F. Costantini, Both the RGS domain and the six C-terminal amino acids of mouse Axin are required for normal embryogenesis, Genetics 181 (4) (2009) 1359–1368. http://dx.doi.org/10.1534/genetics.109.101055, (PubMed PMID: 19204372; PubMed Central PMCID: PMC2666505).
[49] M. Bonilla-Claudio, J. Wang, Y. Bai, E. Klysik, J. Selever, J.F. Martin, Bmp signaling regulates a dose-dependent transcriptional program to control facial skeletal development, Development 139 (4) (2012) 709–719. http://dx.doi.org/10.1242/dev.073197, (PubMed PMID: 22219353; PubMed Central PMCID: PMC3265059).
[50] W. Zhang, M. Hong, G.U. Bae, J.S. Kang, R.S. Krauss, Boc modifies the holoprosencephaly spectrum of Cdo mutant mice, Dis. Model. Mech. 4 (3) (2011) 368–380. http://dx.doi.org/10.1242/dmm.005744, (PubMed PMID: 21183473; PubMed Central PMCID: PMC3097458).
[51] J. Eggenschwiler, T. Ludwig, P. Fisher, P.A. Leighton, S.M. Tilghman, A. Efstratiadis, Mouse mutant embryos overexpressing IGF-II exhibit phenotypic features of the Beckwith-Wiedemann and Simpson-Golabi-Behmel syndromes, Genes Dev. 11 (23) (1997) 3128–3142 (PubMed PMID: 9389646; PubMed Central PMCID: PMC316748).
[52] H. Tian, J. Jeong, B.D. Harfe, C.J. Tabin, A.P. McMahon, Mouse Disp1 is required in sonic hedgehog-expressing cells for paracrine activity of the cholesterol-modified ligand, Development 132 (1) (2005) 133–142. http://dx.doi.org/10.1242/dev.01563, (PubMed PMID: 15576405).
[53] H. Tian, T. Tenzen, A.P. McMahon, Dose dependency of Disp1 and genetic interaction between Disp1 and other hedgehog signaling components in the mouse, Development 131 (16) (2004) 4021–4033. http://dx.doi.org/10.1242/dev.01257, (PubMed PMID: 15269168).
[54] M. Qiu, A. Bulfone, I. Ghattas, J.J. Meneses, L. Christensen, P.T. Sharpe, et al., Role of the Dlx homeobox genes in proximodistal patterning of the branchial arches: mutations of Dlx-1, Dlx-2, and Dlx-1 and -2 alter morphogenesis of proximal skeletal and soft tissue structures derived from the first and second arches, Developmental biology. 185 (2) (1997) 165–184. http://dx.doi.org/10.1006/dbio.1997.8556, PubMed PMID: 9187081.
[55] A. Beverdam, G.R. Merlo, L. Paleari, S. Mantero, F. Genova, O. Barbieri, et al., Jaw transformation with gain of symmetry after Dlx5/Dlx6 inactivation: mirror of the past? Genesis 34 (4) (2002) 221–227. http://dx.doi.org/10.1002/gene.10156, (PubMed PMID: 12434331).
[56] M.P. Verzi, P. Agarwal, C. Brown, D.J. McCulley, J.J. Schwarz, B.L. Black, The transcription factor MEF2C is required for craniofacial development, Developmental cell. 12 (4) (2007) 645–652. http://dx.doi.org/10.1016/j.devcel.2007.03.007, PubMed PMID: 17420000; PubMed Central PMCID: PMC1920108.
[57] C.M. Chen, R.R. Behringer, Ovca1 regulates cell proliferation, embryonic development, and tumorigenesis, Genes & development. 18 (3) (2004) 320–332. http://dx.doi.org/10.1101/gad.1162204, PubMed PMID: 14744934; PubMed Central PMCID: PMC338284.

[58] I.C. Welsh, A. Hagge-Greenberg, T.P. O'Brien, A dosage-dependent role for Spry2 in growth and patterning during palate development, Mechanisms of development. 124 (9-10) (2007) 746–761. http://dx.doi.org/10.1016/j.mod.2007.06.007, PubMed PMID: 17693063; PubMed Central PMCID: PMC2043129.
[59] D. Orioli, M. Henkemeyer, G. Lemke, R. Klein, T. Pawson, Sek4 and Nuk receptors cooperate in guidance of commissural axons and in palate formation, EMBO J. 15 (22) (1996) 6035–6049 (PubMed PMID: 8947026; PubMed Central PMCID: PMC452425).
[60] F.S. Alkuraya, I. Saadi, J.J. Lund, A. Turbe-Doan, C.C. Morton, R.L. Maas, SUMO1 haploinsufficiency leads to cleft lip and palate, Science. 313 (5794) (2006) 1751. http://dx.doi.org/10.1126/science.1128406, PubMed PMID: 16990542.
[61] H. Yu, X. Ye, N. Guo, J. Nathans, Frizzled 2 and frizzled 7 function redundantly in convergent extension and closure of the ventricular septum and palate: evidence for a network of interacting genes, Development 139 (23) (2012) 4383–4394. http://dx.doi.org/10.1242/dev.083352 (PubMed PMID: 23095888; PubMed Central PMCID: PMC3509732).
[62] F. Ji, N. Kanbara, K. Obata, GABA and histogenesis in fetal and neonatal mouse brain lacking both the isoforms of glutamic acid decarboxylase, Neurosci. Res. 33 (3) (1999) 187–194 (PubMed PMID: 10211762).
[63] M. Seppala, M.J. Depew, D.C. Martinelli, C.M. Fan, P.T. Sharpe, M.T. Cobourne, Gas1 is a modifier for holoprosencephaly and genetically interacts with sonic hedgehog, The Journal of clinical investigation. 117 (6) (2007) 1575–1584. http://dx.doi.org/10.1172/JCI32032, PubMed PMID: 17525797; PubMed Central PMCID: PMC1868789.
[64] C.F. Chang, Y.T. Chang, G. Millington, S.A. Brugmann, Craniofacial Ciliopathies Reveal Specific Requirements for GLI Proteins during Development of the Facial Midline, PLoS genetics. 12 (11) (2016) e1006351. http://dx.doi.org/10.1371/journal.pgen.1006351, PubMed PMID: 27802276; PubMed Central PMCID: PMC5089743.
[65] H. Kurosaka, A. Iulianella, T. Williams, P.A. Trainor, Disrupting hedgehog and WNT signaling interactions promotes cleft lip pathogenesis, J. Clin. Investig. 124 (4) (2014) 1660–1671. http://dx.doi.org/10.1172/JCI72688, (PubMed PMID: 24590292; PubMed Central PMCID: PMC3973078).
[66] M.M. Matzuk, T.R. Kumar, A. Vassalli, J.R. Bickenbach, D.R. Roop, R. Jaenisch, et al., Functional analysis of activins during mammalian development, Nature. 374 (6520) (1995) 354–356. http://dx.doi.org/10.1038/374354a0, PubMed PMID: 7885473.
[67] L.J. Engelking, B.M. Evers, J.A. Richardson, J.L. Goldstein, M.S. Brown, G. Liang, Severe facial clefting in Insig-deficient mouse embryos caused by sterol accumulation and reversed by lovastatin, J. Clin. Investig. 116 (9) (2006) 2356–2365. http://dx.doi.org/10.1172/JCI28988, (PubMed PMID: 16955138; PubMed Central PMCID: PMC1555642).
[68] R.J. Richardson, J. Dixon, S. Malhotra, M.J. Hardman, L. Knowles, R.P. Boot-Handford, et al., Irf6 is a key determinant of the keratinocyte proliferation-differentiation switch, Nature genetics. 38 (11) (2006) 1329–1334, Epub 2006/10/17. doi: ng1894 [pii]10.1038/ng1894. PubMed PMID: 17041603.
[69] C.J. Turner, K. Badu-Nkansah, D. Crowley, A. van der Flier, R.O. Hynes, alpha5 and alphav integrins cooperate to regulate vascular smooth muscle and neural crest functions in vivo, Development 142 (4) (2015) 797–808. http://dx.doi.org/10.1242/dev.117572, (PubMed PMID: 25670798).
[70] P. Aluwihare, Z. Mu, Z. Zhao, D. Yu, P.H. Weinreb, G.S. Horan, et al., Mice that lack activity of alphavbeta6- and alphavbeta8-integrins reproduce the abnormalities of Tgfb1- and Tgfb3-null mice, J. cell Sci. 122 (Pt 2) (2009) 227–232. http://dx.doi.org/10.1242/jcs.035246, (PubMed PMID: 19118215; PubMed Central PMCID: PMC2714418).
[71] A.K. Voss, H.K. Vanyai, C. Collin, M.P. Dixon, T.J. McLennan, B.N. Sheikh, et al., MOZ regulates the Tbx1 locus, and Moz mutation partially phenocopies DiGeorge syndrome, Developmental cell. 23 (3) (2012) 652–663. http://dx.doi.org/10.1016/j.devcel.2012.07.010, PubMed PMID: 22921202; PubMed Central PMCID: PMC3442180.
[72] S. Lee, Y. Kong, S.D. Weatherbee, Forward genetics identifies Kdf1/1810019J16Rik as an essential regulator of the proliferation-differentiation decision in epidermal progenitor cells, Developmental biology. 383 (2) (2013) 201–213. http://dx.doi.org/10.1016/j.ydbio.2013.09.022, PubMed PMID: 24075906; PubMed Central PMCID: PMC3841015.
[73] C.A. Wassif, K.E. Brownson, A.L. Sterner, A. Forlino, P.M. Zerfas, W.K. Wilson, et al., HEM dysplasia and ichthyosis are likely laminopathies and not due to 3beta-hydroxysterol Delta14-reductase deficiency, Hum. Mol. Genet. 16 (10) (2007) 1176–1187. http://dx.doi.org/10.1093/hmg/ddm065, (PubMed PMID: 17403717).
[74] M. Denaxa, P.T. Sharpe, V. Pachnis, The LIM homeodomain transcription factors Lhx6 and Lhx7 are key regulators of mammalian dentition, Dev. Biol. 333 (2) (2009) 324–336. http://dx.doi.org/10.1016/j.ydbio.2009.07.001, (PubMed PMID: 19591819; PubMed Central PMCID: PMC2738952).
[75] J. Newbern, J. Zhong, R.S. Wickramasinghe, X. Li, Y. Wu, I. Samuels, et al., Mouse and human phenotypes indicate a critical conserved role for ERK2 signaling in neural crest development, Proceedings of the National Academy of Sciences of the United States of America. 105 (44) (2008) 17115–17120. http://dx.doi.org/10.1073/pnas.0805239105, PubMed PMID: 18952847; PubMed Central PMCID: PMC2579387.
[76] T. Terzian, Y. Wang, C.S. Van Pelt, N.F. Box, E.L. Travis, G. Lozano, Haploinsufficiency of Mdm2 and Mdm4 in tumorigenesis and development, Mol. Cell. Biol. 27 (15) (2007) 5479–5485. http://dx.doi.org/10.1128/MCB.00555-06, (PubMed PMID: 17526734; PubMed Central PMCID: PMC1952101).
[77] J. Shi, M.Y. Son, S. Yamada, L. Szabova, S. Kahan, K. Chrysovergis, et al., Membrane-type MMPs enable extracellular matrix permissiveness and mesenchymal cell proliferation during embryogenesis, Dev. Biol. 313 (1) (2008) 196–209. http://dx.doi.org/10.1016/j.ydbio.2007.10.017, (PubMed PMID: 18022611; PubMed Central PMCID: PMC2262846).
[78] J.R. Lu, R. Bassel-Duby, A. Hawkins, P. Chang, R. Valdez, H. Wu, et al., Control of facial muscle development by MyoR and capsulin, Science 298 (5602) (2002) 2378–2381. http://dx.doi.org/10.1126/science.1078273, (PubMed PMID: 12493912).
[79] M. Matsui, J. Klingensmith, Multiple tissue-specific requirements for the BMP antagonist Noggin in development of the mammalian craniofacial skeleton, Developmental biology. 392 (2) (2014) 168–181. http://dx.doi.org/10.1016/j.ydbio.2014.06.006, PubMed PMID: 24949938; PubMed Central PMCID: PMC4399715.
[80] G. Levi, S. Mantero, O. Barbieri, D. Cantatore, L. Paleari, A. Beverdam, et al., Msx1 and Dlx5 act independently in development of craniofacial skeleton, but converge on the regulation of Bmp signaling in palate formation, Mech. Dev. 123 (1) (2006) 3–16. http://dx.doi.org/10.1016/j.mod.2005.10.007, (PubMed PMID: 16330189).
[81] J. Han, J. Mayo, X. Xu, J. Li, P. Bringas Jr, R.L. Maas, et al., Indirect modulation of Shh signaling by Dlx5 affects the oral-nasal patterning of palate and rescues cleft palate in Msx1-null mice, Development 136 (24) (2009) 4225–4233. http://dx.doi.org/10.1242/dev.036723, (PubMed PMID: 19934017; PubMed Central PMCID: PMC2781056).

[82] J. Zhou, Y. Gao, Z. Zhang, Y. Zhang, K.M. Maltby, Z. Liu, et al., Osr2 acts downstream of Pax9 and interacts with both Msx1 and Pax9 to pattern the tooth developmental field, Developmental biology. 353 (2) (2011) 344–353. http://dx.doi.org/10.1016/j.ydbio.2011.03.012, PubMed PMID: 21420399; PubMed Central PMCID: PMC3081931.
[83] M. Nakatomi, X.P. Wang, D. Key, J.J. Lund, A. Turbe-Doan, R. Kist, et al., Genetic interactions between Pax9 and Msx1 regulate lip development and several stages of tooth morphogenesis, Dev. Biol. 340 (2) (2010) 438–449. http://dx.doi.org/10.1016/j.ydbio.2010.01.031, (PubMed PMID: 20123092).
[84] E. Ferretti, B. Li, R. Zewdu, V. Wells, J.M. Hebert, C. Karner, et al., A conserved Pbx-Wnt-p63-Irf6 regulatory module controls face morphogenesis by promoting epithelial apoptosis, Developmental cell. 21 (4) (2011) 627–641. http://dx.doi.org/10.1016/j.devcel.2011.08.005, PubMed PMID: 21982646; PubMed Central PMCID: PMC3199312.
[85] T. Akasaka, M. van Lohuizen, N. van der Lugt, Y. Mizutani-Koseki, M. Kanno, M. Taniguchi, et al., Mice doubly deficient for the Polycomb Group genes Mel18 and Bmi1 reveal synergy and requirement for maintenance but not initiation of Hox gene expression, Development 128 (9) (2001) 1587–1597 (PubMed PMID: 11290297).
[86] A.M. Richarte, H.B. Mead, M.D. Tallquist, Cooperation between the PDGF receptors in cardiac neural crest cell migration, Dev. Biol. 306 (2) (2007) 785–796. http://dx.doi.org/10.1016/j.ydbio.2007.04.023, (PubMed PMID: 17499702; PubMed Central PMCID: PMC2040169).
[87] K. Isono, Y. Fujimura, J. Shinga, M. Yamaki, O.W. J, Y. Takihara, et al., Mammalian polyhomeotic homologues Phc2 and Phc1 act in synergy to mediate polycomb repression of Hox genes, Mol. Cell. Biol. 25 (15) (2005) 6694–6706. http://dx.doi.org/10.1128/MCB.25.15.6694-6706.2005, (PubMed PMID: 16024804; PubMed Central PMCID: PMC1190356).
[88] D. ten Berge, A. Brouwer, J. Korving, J.F. Martin, F. Meijlink, Prx1 and Prx2 in skeletogenesis: roles in the craniofacial region, inner ear and limbs, Development 125 (19) (1998) 3831–3842 (PubMed PMID: 9729491).
[89] M.F. Lu, H.T. Cheng, M.J. Kern, S.S. Potter, B. Tran, T.G. Diekwisch, et al., prx-1 functions cooperatively with another paired-related homeobox gene, prx-2, to maintain cell fates within the craniofacial mesenchyme, Development. 126 (3) (1999) 495–504, PubMed PMID: 9876178.
[90] N. Uetani, K. Bertozzi, M.J. Chagnon, W. Hendriks, M.L. Tremblay, M. Bouchard, Maturation of ureter-bladder connection in mice is controlled by LAR family receptor protein tyrosine phosphatases, J. Clin. Investig. 119 (4) (2009) 924–935. http://dx.doi.org/10.1172/JCI37196, (PubMed PMID: 19273906; PubMed Central PMCID: PMC2662538).
[91] K. Stewart, N. Uetani, W. Hendriks, M.L. Tremblay, M. Bouchard, Inactivation of LAR family phosphatase genes Ptprs and Ptprf causes craniofacial malformations resembling Pierre-Robin sequence, Development 140 (16) (2013) 3413–3422. http://dx.doi.org/10.1242/dev.094532, (PubMed PMID: 23863482).
[92] K.R. Schwab, L.T. Patterson, H.A. Hartman, N. Song, R.A. Lang, X. Lin, et al., Pygo1 and Pygo2 roles in Wnt signaling in mammalian kidney development, BMC Biol. 5 (2007) 15. http://dx.doi.org/10.1186/1741-7007-5-15, (PubMed PMID: 17425782; PubMed Central PMCID: PMC1858683).
[93] Y.R. Jin, T.J. Turcotte, A.L. Crocker, X.H. Han, J.K. Yoon, The canonical Wnt signaling activator, R-spondin2, regulates craniofacial patterning and morphogenesis within the branchial arch through ectodermal-mesenchymal interaction, Dev. Biol. 352 (1) (2011) 1–-13. http://dx.doi.org/10.1016/j.ydbio.2011.01.004, (PubMed PMID: 21237142; PubMed Central PMCID: PMC3089906).
[94] X. Geng, C. Speirs, O. Lagutin, A. Inbal, W. Liu, L. Solnica-Krezel, et al., Haploinsufficiency of Six3 fails to activate Sonic hedgehog expression in the ventral forebrain and causes holoprosencephaly, Dev. Cell 15 (2) (2008) 236–247. http://dx.doi.org/10.1016/j.devcel.2008.07.003, (PubMed PMID: 18694563; PubMed Central PMCID: PMC2597207).
[95] C. Guo, Y. Sun, B. Zhou, R.M. Adam, X. Li, W.T. Pu, et al., A Tbx1-Six1/Eya1-Fgf8 genetic pathway controls mammalian cardiovascular and craniofacial morphogenesis, J. Clin. Investig. 121 (4) (2011) 1585–1595. http://dx.doi.org/10.1172/JCI44630, (PubMed PMID: 21364285; PubMed Central PMCID: PMC3069777).
[96] R. Grifone, J. Demignon, C. Houbron, E. Souil, C. Niro, M.J. Seller, et al., Six1 and Six4 homeoproteins are required for Pax3 and Mrf expression during myogenesis in the mouse embryo, Development 132 (9) (2005) 2235–2249. http://dx.doi.org/10.1242/dev.01773, (PubMed PMID: 15788460).
[97] J. Iwata, A. Suzuki, R.C. Pelikan, T.V. Ho, P.A. Sanchez-Lara, M. Urata, et al., Smad4-Irf6 genetic interaction and TGFbeta-mediated IRF6 signaling cascade are crucial for palatal fusion in mice, Development 140 (6) (2013) 1220–1230 (Epub 2013/02/15. doi: dev.089615 [pii] 10.1242/dev.089615. PubMed PMID: 23406900; PubMed Central PMCID: PMC3585659).
[98] J. Lane, K. Yumoto, M. Azhar, J. Ninomiya-Tsuji, M. Inagaki, Y. Hu, et al., Tak1, Smad4 and Trim33 redundantly mediate TGF-beta3 signaling during palate development, Developmental biology. 398 (2) (2015) 231–241. http://dx.doi.org/10.1016/j.ydbio.2014.12.006, PubMed PMID: 25523394; PubMed Central PMCID: PMC4314443.
[99] S.A. Murray, K.F. Oram, T. Gridley, Multiple functions of Snail family genes during palate development in mice, Development 134 (9) (2007) 1789–1797. http://dx.doi.org/10.1242/dev.02837, PubMed PMID: 17376812.
[100] P. Smits, P. Li, J. Mandel, Z. Zhang, J.M. Deng, R.R. Behringer, et al., The transcription factors L-Sox5 and Sox6 are essential for cartilage formation, Developmental cell. 1 (2) (2001) 277–290, PubMed PMID: 11702786.
[101] A.D. Economou, A. Ohazama, T. Porntaveetus, P.T. Sharpe, S. Kondo, M.A. Basson, et al., Periodic stripe formation by a Turing mechanism operating at growth zones in the mammalian palate, Nat. Genet. 44 (3) (2012) 348–351. http://dx.doi.org/10.1038/ng.1090, (PubMed PMID: 22344222; PubMed Central PMCID: PMC3303118).
[102] S. Zirzow, T.H. Ludtke, J.F. Brons, M. Petry, V.M. Christoffels, A. Kispert, Expression and requirement of T-box transcription factors Tbx2 and Tbx3 during secondary palate development in the mouse, Developmental biology. 336 (2) (2009) 145–155. http://dx.doi.org/10.1016/j.ydbio.2009.09.020, PubMed PMID: 19769959.
[103] Z. Mu, Z. Yang, D. Yu, Z. Zhao, J.S. Munger, TGFbeta1 and TGFbeta3 are partially redundant effectors in brain vascular morphogenesis, Mech. Dev. 125 (5-6) (2008) 508–516. http://dx.doi.org/10.1016/j.mod.2008.01.003, (PubMed PMID: 18343643).
[104] H.A. Thomason, H. Zhou, E.N. Kouwenhoven, G.P. Dotto, G. Restivo, B.C. Nguyen, et al., Cooperation between the transcription factors p63 and IRF6 is essential to prevent cleft palate in mice, J. Clin. Investig. 120 (5) (2010) 1561–1569. http://dx.doi.org/10.1172/JCI40266, (PubMed PMID: 20424327; PubMed Central PMCID: PMC2860913).
[105] S.H. Mui, J.W. Kim, G. Lemke, S. Bertuzzi, Vax genes ventralize the embryonic eye, Genes Dev. 19 (10) (2005) 1249–1259. http://dx.doi.org/10.1101/gad.1276605, (PubMed PMID: 15905411; PubMed Central PMCID: PMC1132010).

[106] F. He, W. Xiong, X. Yu, R. Espinoza-Lewis, C. Liu, S. Gu, et al., Wnt5a regulates directional cell migration and cell proliferation via Ror2-mediated noncanonical pathway in mammalian palate development, Development. 135 (23) (2008) 3871–3879. http://dx.doi.org/10.1242/dev.025767, PubMed PMID: 18948417; PubMed Central PMCID: PMC3010758.
[107] T. Miyoshi, M. Maruhashi, T. Van De Putte, H. Kondoh, D. Huylebroeck, Y. Higashi, Complementary expression pattern of Zfhx1 genes Sip1 and deltaEF1 in the mouse embryo and their genetic interaction revealed by compound mutants, Dev. Dyn.: Off. Publ. Am. Assoc. Anat. 235 (7) (2006) 1941–1952. http://dx.doi.org/10.1002/dvdy.20799, (PubMed PMID: 16598713).
[108] D. Bennett, Anatomical abnormality, Mouse News Lett. 43 (1970) 57.
[109] A.G. Searle, Brachyrrhine, BR, Mouse News Lett. 35 (1966) 27.
[110] R.J.S. Phillips, p < 11 > , a pink-eyed allele, Mouse News Lett. 48 (1973) 30.
[111] S. Gluecksohn-Waelsch, Open eyelids (oel), Mouse News Lett. 25 (1961) 12.
[112] D.J. Nash, pad-paddle (provisional), Mouse News Lett. 40 (1969) 20.
[113] L. Pick, S. Schiffer, Polydactyly with cleft palate-pcp, Mouse News Lett. 65 (1981) 7.
[114] C. Rasberry, B.M. Cattanach, Small ear, a new dominant mutation, Mouse News Lett. 80 (1988) 158–159.