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Mammalian SP/KLF transcription factors: Bring in the family

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Abstract

The advent of the genome projects has provided new avenues to explore the question of how DNA sequence information is used appropriately by mammalian cells. Regulation of transcription is not the only, but is certainly a very important, mechanism involved in this process. We can now identify all the genes encoding transcription factors belonging to a certain class and study their biological functions in unprecedented detail through the use of an array of biomolecular tools. It is important to use rigorous and uniform definitions for the classification of transcription factors, because this helps us to comprehend the functions of transcription factor families in biological networks. Here, we propose an unambiguous nomenclature for the members of the Specificity Protein/Krüppel-like Factor (SP/KLF) transcription factor family.

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GC and GT boxes (5′-GGGGCGGGG-3′ and 5-GGTGTGGGG-3′) are recurring motifs in promoters and more distal regulatory elements of mammalian genes. A protein interacting with these motifs was first identified in the 21-bp repeats of the SV40 early promoter [1] and termed SP1, for Specificity Protein 1. Molecular cloning revealed that the DNA binding domain of SP1 is composed of three abutting zinc fingers of the classical Cys_2–His_2 type [2]. Closely related, but distinct, factors were later identified and called SP2, SP3, and SP4 [3,4]. The linkage of each factor to a *HOX* gene cluster further emphasized their evolutionary relationships (Supplemental Fig. 1; [5]), as did the discovery of SP-related factors in *Drosophila* [6,7]. SP-related factors are also found in relatively simple multicellular organisms such as the nematode *Caenorhabditis elegans* but not in unicellular organisms such as baker's yeast, *Saccharomyces cerevisiae*.

The *SP1–4* genes are closely linked to the genes encoding the other SP factors (*SP5–9*), usually in pairwise combinations (Supplemental Fig. 1; [8,9]). A characteristic hallmark of SP factors is the presence of the Buttonhead (BTD) box CXCPXC, just N-terminal to the zinc fingers (Fig. 1; [10]). The function of the BTD box is unknown, but the fact that it is also present in *Drosophila* and *C. elegans* SP factors suggests an important physiological role. Another feature of most SP factors is the presence of a conserved amino acid stretch, the so-called SP box, located close to the N-terminus (Supplemental Fig. 2; [10]).

The first mammalian Krüppel-like factor was cloned from erythroid cells and therefore called erythroid Krüppel-like factor or EKLF (KLF1; [11]). This was soon followed by the discovery of a number of related factors, and the KLF nomenclature was first introduced by Turner and Crossley following a proposal from the HUGO Gene Nomenclature Committee [12]. The absence of the BTD box is the most distinguishing feature between the SP and the KLF sub-

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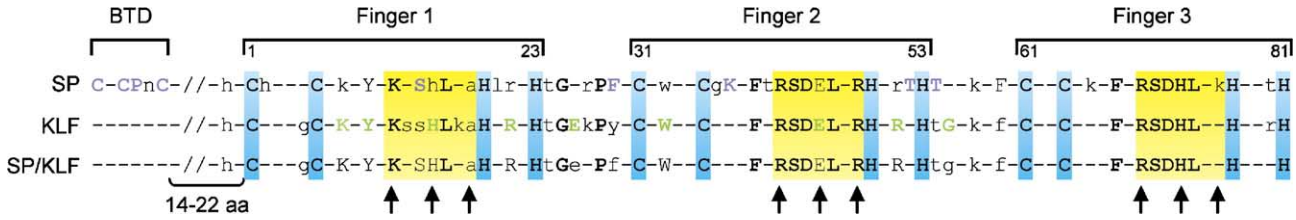

Fig. 1. Characteristic hallmarks of SP/KLF family members. Consensus sequences for the zinc finger domains of all the SP and KLF factors in human (25 factors), *Drosophila* (9 factors), and *C. elegans* (6 factors) are shown for the SP factors, the KLF factors, and the entire family. All the DNA binding domains are 81 aa in length, with the exception of those of Ce-Y40B1A.4 (Finger 1: CXXC instead of CXXXXC), Ce-T22C8.5 (Finger 3: HXXXXH instead of HXXXH), and D-BTD (Finger 2: CXXC instead of CXXXXC). The highly conserved BTD box N-terminal to the zinc fingers is a unique feature of the SP factors. Bold capital letters indicate residues that are 100% conserved between all family members (black), between all KLF factors (green), or between all SP factors (purple). Capital letters indicate >90% conservation, lowercase letters >75% conservation. Blue bars indicate the cysteine and histidine residues involved in zinc coordination, yellow boxes residues thought to contact DNA. The arrows point at the residues that probably determine the recognition specificity of the fingers through specific contacts with DNA bases.

families (Fig. 1). Based on this criterion, KLFs are also found in *Drosophila* and *C. elegans*. Outside the zinc finger domain, there is usually very little homology between SP/KLFs. This makes the analysis of functional domains particularly challenging.

Three fingers keep the family together

The array of three zinc fingers is the most outstanding feature of the SP/KLF family members. Without exception, the finger domain of mammalian SP/KLFs consists of 81 amino acids (Fig. 1). This strongly suggests that the fingers act as a single unit, with heavy constraints not only on the amino acids of the Cys_2–His_2 units, but also on those of the interfinger domains. Indeed, the interfinger domains are highly conserved (Fig. 1). By comparison to the crystal structure of the Zif268–DNA complex [13], it can be inferred that the SP/KLF finger domain interacts with the G-rich strand of the 9-bp recognition sequence in a 3′-to-5′ fashion, e.g., finger 3 with the first three nucleotides, finger 2 with the three nucleotides in the middle, and finger 1 with the most 3′ nucleotides. The residues thought to make contact with the DNA and conferring specific base recognition are among the most conserved parts of the finger domain (Fig. 1).

Don't call me names

The discovery of novel genes and their corresponding proteins is one of the most exciting aspects of molecular biology. Naturally, investigators have been clever in creating names for their newly found factors, loosely guided by field-specific gentlemen's agreements on nomenclature. Owing to the complexity of the genomes of higher vertebrates, many genes have been discovered a number of times and given different names. These names are often based on the experimental systems used, resulting in a sometimes confusing array of different names for a single factor. The mammalian SP/KLF family has also suffered from inadequate nomenclature (Table 1). With such highly conserved factors, one might draw inspiration from invertebrate model organisms such as *Drosophila* to resolve this issue. However, the orthologous relationships between mammalian and *Drosophila* factors are not easily established, even when functional assays are used. For instance, transgenic rescue of the *Drosophila* btd mutant by mouse Sp1 and Sp8 is incomplete. Yet, Sp8 was dubbed the mouse Btd orthologue because it rescued the phenotype slightly better [14]. However, phylogenetic analysis does not support the notion that Sp8 is the mouse Btd homologue. By this analysis SP8 is rather more closely related to D-SP1 than to BTD (Fig. 2). *Drosophila* appears to have only four SP factors, as opposed to nine in mammals. The orthologous relationships between mammalian and *Drosophila* SP factors are therefore not easily described on a one-to-one basis. Thus, for reasons of clarity, a straightforward nomenclature for the mouse and human SP/KLF factors, independent of the nomenclature used for invertebrate genes, is highly desirable. Transgenic rescue experiments, such as those described by [14], can then be judged on their own merits in the context of the orthologous relationships between the factors.

An unambiguous nomenclature for mouse and human SP/KLF transcription factors

The availability of near-complete genome sequences of mouse and human greatly facilitates the unambiguous assignment of names to all the members of the SP/KLF family. We propose to base the subgroup of mammalian SP factors on the presence of the BTD domain just N-terminal to the zinc fingers. The remaining factors are placed in the KLF subgroup, characterized by the presence of the highly conserved 81-amino-acid DNA binding domain. This subdivision is supported by phylogenetic analysis based on the BTD/zinc finger domains (Fig. 2). The proposed

Table 1

Unified Nomenclature	Synonyms	Accession #	aa	Ch.	Knockout phenotype	References
H SP1		NM_138473.2	785	12q13.13	Early embryonic lethal (E10)	[16]
M Sp1		NM_013672.1	784	15F3		
H SP2		NM_003110.3	606	17q21.32		
M Sp2		NM_030220.2	606	11D		
H SP3	SPR-2	NM_003111.1	781	2q31.1	Perinatal lethal. Impaired hematopoiesis tooth and bone development	[17–19]
M Sp3		BC079874.1	783	2C3		
H SP4	HF1B, SPR-1	NM_003112.1	784	7p15	Mild growth retardaton, impaired sexual behaviour, sudden cardiac death	[20–22]
M Sp4	HF1-b	NM_009239.1	782	12		
H SP5		NM_001003845.1	398	2q31.1	No overt phenotype	[10]
M Sp5		NM_022435.2	398	2C3		
H SP6	KLF14	NM_199262.2	376	17q21.31/32		
M Sp6	Epiprofin	NM_031183.1	367	11D		
H SP7	OSX, osterix	NM_152860.1	431	12q13.13	No bone formation	[23]
M Sp7	Osx, osterix	NM_130458.1	428	15F3		
H SP8		NM_182700.2	508	7p21.2	Brain malformations, posterior axial skeleton truncations, and shortened limbs. Perinatal lethality	[14,24]
M Sp8*	mBtd	NM_177082.3	504*	12F2		
H SP9		(hCT1831218)	484**	2q31		
M SP9		AY591908	484	2C3		
H KLF1	EKLF	NM_006563.1	362	19p13	Severe anemia. Embryonic lethal (E14)	[25,26]
M Klf1	EKLF	NM_010635.1	376	8C3		
H KLF2	LKLF	NM_016270.1	355	19p13.1	Disturbed tunica media formation and blood vessel stabilization. Impaired fetal liver erythropoiesis. Embryonic lethal (E12E14). Required for lung development and survival of resting T-cells.	[27–30]
M Klf2	LKLF	NM_008452.1	354	8C1		
H KLF3	BKLF	NM_016531.2	345	4p14	Progressive myeloproliferative disorder	[31]
M Klf3	9930027G08Rik, BKLF, Bklf, Tef2	NM_008453.1	344	5C3.3		
H KLF4	GKLF, EZF	NM_004235.1	470	9q31	Perinatal lethality due to loss of barrier function of the skin. Required for terminal differentiation of goblet cells in the colon	[32,33]
M Klf4	GKLF, EZF	NM_010637.1	474	4B3		
H KLF5	CKLF, IKLF, BTEB2	NM_001730.2	457	13q21.33	KO: early embryonic lethal. HZ: diminished levels of arterial-wall thickening, angiogenesis, cardiac hypertrophy and interstitial fibrosis.	[34]
M Klf5	CKLF, IKLF, BTEB2	NM_009769.1	446	14E2.1		
H KLF6	COPEB, GBF, ZF9, BCD1, CPBP, PAC1, ST12	NM_001300.2	283	10p15		
M Klf6	BCD1, Zf9, CPBP, FM2, FM6, Ierepo1, Ierepo3	NM_011803.1	284	13A1		
H KLF7	UKLF	NM_003709.1	302	2q32		
M Klf7	9830124P08Rik	NM_033563.1	301	1C1-C3		
H KLF8	BKLF3, DXS741, ZNF741	NM_007250.2	359	Xp11.21		
M Klf8	A830097P10Rik, BKLF3, ZNF74	NM_173780	355	XF3		
H KLF9	BTEB, BTEB1	NM_001206.1	244	9q13	Mild behavioral defects. Subfertility, uterine hypoplasia, and partial progesterone resistance	[35,36]
M Klf9	BTEB-1, bteb1	NM_010638.1	244	19C1		
H KLF10	EGRA, TIEG, TIEG1	NM_005655.1	480	8q22.2		
M Klf10	Tieg Tieg1 mGIF, Egral, EGRα, Gdnfif	NM_013692	479	1C5		
H KLF11	FKLF, FKLF1, TIEG2	NM_003597.2	512	2p25.1	No overt phenotype	[37]
M Klf11	D12Ertd427e, Tieg2b, Tieg3***	NM_178357***	502	12		

(continued on next page)

Table 1 (*continued*)

Unified Nomenclature	Synonyms	Accession #	aa	Ch.	Knockout phenotype	References
H KLF12	AP2REP, AP-2rep, HSPC122	NM_007249.3	402	13q22.1		
M Klf12	AP-2rep, 2700063E05Rik, B130052C06Rik	NM_010636.1	402	14E2.2		
H KLF13	BTEB3, FKLF2, NSLP1, FKLF-2, RFLAT1, RFLAT-1	NM_015995.1	289	15q13.2		
M Klf13	NSLP1, FKLF-2, RFLAT1, RFLAT-1	NM_021366.1	289	7C		
H KLF14	BTEB5	NM_138693.1	323	7q32.2		
M Klf14	BTEB5	XM_145243	325	6A3		
H KLF15	KKLF	NM_014079.2	416	3q21.3		
M Klf15	CKLF, KKLF, 1810013I09Rik	NM_023184.2	415	6D2		
H KLF16	DRRF, BTEB4, NSLP2	NM_031918.1	252	19p13.3		
M Klf16	DRRF, BTEB4	NM_078477.1	251	10C1		

Numbers of amino acids (aa) are given for the longest known isoform.

* Deduced from Ensembl mouse genome database through comparison with human SP8 NM_182700.2.

** Deduced from Ensembl human genome database through comparison with mouse Sp9 AY591908.

*** The currently assigned mouse orthologue of human TIEG2 is based on AJ275989.1. However, AJ275989.1 aligns poorly with the mouse genome and appears to represent the human TIEG2 sequence. NM_178357 (Tieg3) aligns with the human and mouse genomes as would be expected for the mouse Tieg2 orthologue.

unambiguous nomenclature for all human and mouse SP/KLF factors known to date is listed in Table 1, which also lists characteristic features of each factor.

Twenty-five and counting

Several groups have taken bioinformatics approaches to find all the members of the SP/KLF family in the human and mouse genomes [9,15]. The discovery of SP8 was based on the prediction that there should be an *SP* gene accompanying the *SP4* gene on human chromosome 7p15/mouse chromosome 12. Indeed, this turned out to be the case [9]. Yet, a new member, SP9, was recently described by the group of Belmonte [8], bringing the total count to 25. Despite the fact that SP9 bears all the distinctive hallmarks of an SP factor (Figs. 1 and 2, Supplemental Fig. 1), the gene encoding SP9 had escaped annotation in the genome databases. Thus, while exploration of the biological role of 25 factors already presents a formidable challenge to the scientific community, the mammalian genome might have more surprises in stock. The definition of SP/KLF factors proposed here provides a warm welcome to new additions to the family and a framework to position their biological functions in the context of the family.

Note added in proof

During the review process of the manuscript, additional knockout phenotypes of Sp4 and KLF5 were reported. Sp4 appears to be essential for hippocampal integrity and may modulate behavioural processes relevant to psychiatric processes [38]. KLF5 is an essential component in the network controlling adipocyte differentiation [39].

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Appendix A. Supplementary data

Supplementary data for this article may be found on ScienceDirect.

References

[1] W.S. Dynan, R. Tjian, The promoter-specific transcription factor Sp1 binds to upstream sequences in the SV40 early promoter, Cell 35 (1983) 79–87.

[2] J.T. Kadonaga, K.R. Carner, F.R. Masiarz, R. Tjian, Isolation of cDNA encoding transcription factor Sp1 and functional analysis of the DNA binding domain, Cell 51 (1987) 1079–1090.

[3] C. Kingsley, A. Winoto, Cloning of GT box-binding proteins: a novel Sp1 multigene family regulating T-cell receptor gene expression, Mol. Cell. Biol. 12 (1992) 4251–4261.

[4] G. Hagen, S. Muller, M. Beato, G. Suske, Cloning by recognition site

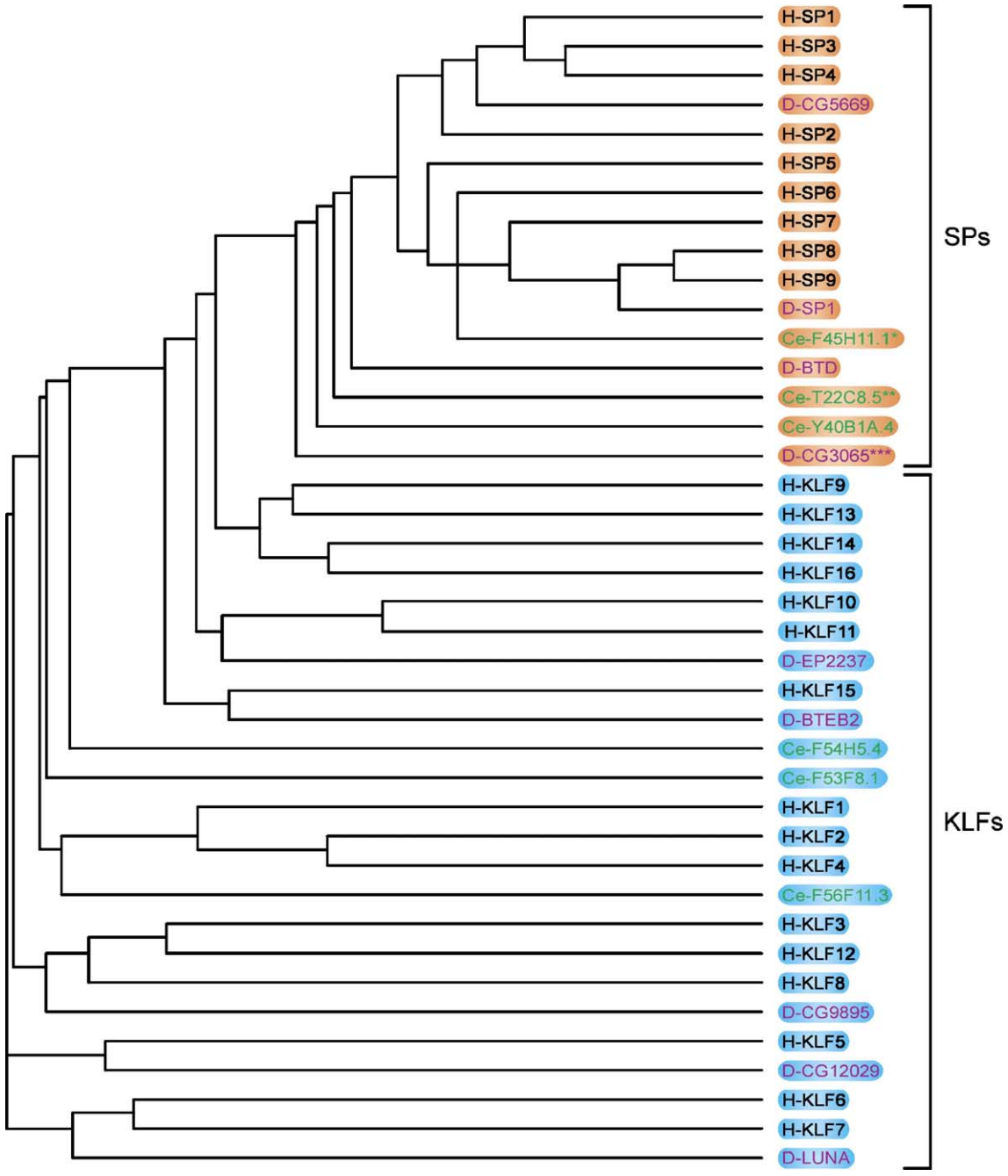

Fig. 2. Relationships between the SP factors and KLFs of human, *Drosophila,* and *C. elegans*. Of each factor, the 110-aa domain containing the BTD/zinc finger motifs was used for the multiple alignment with ClustalW (http://www.ebi.ac.uk/clustalw/). This alignment was used to construct the cladogram. *The current sequence of *C. elegans* F45H11.1 contains only the BTD motif and the first finger. **One amino acid was removed from finger 3 of Ce-T22C8.5 (HXXXH instead of HXXXXH), because the extra amino acid is not handled appropriately in the multiple alignment generated with ClustalW. ***The sequence of D-CG3065 was deduced from the *Drosophila* genome sequence; the current annotation does not contain the complete BTD/zinc finger motif.

screening of two novel GT box binding proteins: a family of Sp1 related genes, Nucleic Acids Res. 20 (1992) 5519–5525.

[5] S. Scohy, P. Van Vooren, C. Szpirer, J. Szpirer, Assignment of Sp genes to rat chromosome bands 7q36 (Sp1), 10q31 → q32.1 (Sp2), 3q24 → q31 (Sp3) and 6q33 (Sp4) and of the SP2 gene to human chromosome bands 17q21.3 → q22 by in situ hybridization, Cytogenet. Cell Genet. 81 (1998) 273–274.

[6] E.A. Wimmer, H. Jackle, C. Pfeifle, S.M. Cohen, A Drosophila homologue of human Sp1 is a head-specific segmentation gene, Nature 366 (1993) 690–694.

[7] E.A. Wimmer, G. Frommer, B.A. Purnell, H. Jackle, buttonhead and D-Sp1: a novel Drosophila gene pair, Mech. Dev. 59 (1996) 53–62.

[8] Y. Kawakami, C.R. Esteban, T. Matsui, J. Rodriguez-Leon, S. Kato, J.C. Belmonte, Sp8 and Sp9, two closely related buttonhead-like transcription factors, regulate Fgf8 expression and limb outgrowth in vertebrate embryos, Development 131 (2004) 4763–4774.

[9] P. Bouwman, S. Philipsen, Regulation of the activity of Sp1-related transcription factors, Mol. Cell. Endocrinol. 195 (2002) 27–38.

[10] S.M. Harrison, D. Houzelstein, S.L. Dunwoodie, R.S. Beddington,

Sp5, a new member of the Sp1 family, is dynamically expressed during development and genetically interacts with Brachyury, Dev. Biol. 227 (2000) 358–372.
[11] I.J. Miller, J.J. Bieker, A novel, erythroid cell-specific murine transcription factor that binds to the CACCC element and is related to the Kruppel family of nuclear proteins, Mol. Cell. Biol. 13 (1993) 2776–2786.
[12] J. Turner, M. Crossley, Mammalian Kruppel-like transcription factors: more than just a pretty finger, Trends Biochem. Sci. 24 (1999) 236–240.
[13] N.P. Pavletich, C.O. Pabo, Zinc finger-DNA recognition: crystal structure of a Zif268–DNA complex at 2.1 A, Science 252 (1991) 809–817.
[14] D. Treichel, F. Schock, H. Jackle, P. Gruss, A. Mansouri, mBtd is required to maintain signaling during murine limb development, Genes Dev. 17 (2003) 2630–2635.
[15] T. Ravasi, T. Huber, M. Zavolan, A. Forrest, T. Gaasterland, S. Grimmond, et al., Systematic characterization of the zinc-finger-containing proteins in the mouse transcriptome, Genome Res. 13 (2003) 1430–1442.
[16] M. Marin, A. Karis, P. Visser, F. Grosveld, S. Philipsen, Transcription factor Sp1 is essential for early embryonic development but dispensable for cell growth and differentiation, Cell 89 (1997) 619–628.
[17] P.F. Van Loo, P. Bouwman, K.W. Ling, S. Middendorp, G. Suske, F. Grosveld, et al., Impaired hematopoiesis in mice lacking the transcription factor Sp3, Blood 102 (2003) 858–866.
[18] H. Gollner, C. Dani, B. Phillips, S. Philipsen, G. Suske, Impaired ossification in mice lacking the transcription factor Sp3, Mech. Dev. 106 (2001) 77–83.
[19] P. Bouwman, H. Gollner, H.P. Elsasser, G. Eckhoff, A. Karis, F. Grosveld, et al., Transcription factor Sp3 is essential for post-natal survival and late tooth development, EMBO J. 19 (2000) 655–661.
[20] V.T. Nguyen-Tran, S.W. Kubalak, S. Minamisawa, C. Fiset, K.C. Wollert, A.B. Brown, et al., A novel genetic pathway for sudden cardiac death via defects in the transition between ventricular and conduction system cell lineages, Cell 102 (2000) 671–682.
[21] H. Gollner, P. Bouwman, M. Mangold, A. Karis, H. Braun, I. Rohner, et al., Complex phenotype of mice homozygous for a null mutation in the Sp4 transcription factor gene, Genes Cells 6 (2001) 689–697.
[22] D.M. Supp, D.P. Witte, W.W. Branford, E.P. Smith, S.S. Potter, Sp4, a member of the Sp1-family of zinc finger transcription factors, is required for normal murine growth, viability, and male fertility, Dev. Biol. 176 (1996) 284–299.
[23] K. Nakashima, X. Zhou, G. Kunkel, Z. Zhang, J.M. Deng, R.R. Behringer, et al., The novel zinc finger-containing transcription factor osterix is required for osteoblast differentiation and bone formation, Cell 108 (2002) 17–29.
[24] S.M. Bell, C.M. Schreiner, R.R. Waclaw, K. Campbell, S.S. Potter, W.J. Scott, Sp8 is crucial for limb outgrowth and neuropore closure, Proc. Natl. Acad. Sci. USA 100 (2003) 12195–12200.
[25] A.C. Perkins, A.H. Sharpe, S.H. Orkin, Lethal beta-thalassaemia in mice lacking the erythroid CACCC-transcription factor EKLF, Nature 375 (1995) 318–322.
[26] B. Nuez, D. Michalovich, A. Bygrave, R. Ploemacher, F. Grosveld, Defective haematopoiesis in fetal liver resulting from inactivation of the EKLF gene, Nature 375 (1995) 316–318.
[27] C.T. Kuo, M.L. Veselits, J.M. Leiden, LKLF: a transcriptional regulator of single-positive T cell quiescence and survival, Science 277 (1997) 1986–1990.
[28] C.T. Kuo, M.L. Veselits, K.P. Barton, M.M. Lu, C. Clendenin, J.M. Leiden, The LKLF transcription factor is required for normal tunica media formation and blood vessel stabilization during murine embryogenesis, Genes Dev. 11 (1997) 2996–3006.
[29] M.A. Wani, R.T. Means Jr., J.B. Lingrel, Loss of LKLF function results in embryonic lethality in mice, Transgenic Res. 7 (1998) 229–238.
[30] M.A. Wani, S.E. Wert, J.B. Lingrel, Lung Kruppel-like factor, a zinc finger transcription factor, is essential for normal lung development, J. Biol. Chem. 274 (1999) 21180–21185.
[31] A.C. Perkins, H. Yang, P.M. Crossley, Y. Fujiwara, S.H. Orkin, Deficiency of the CACC-element binding protein, BKLF, leads to a progressive myeloproliferative disease and impaired expression of SHP-1, Blood 90 (Suppl. 1) (1997) 575a.
[32] J.P. Katz, N. Perreault, B.G. Goldstein, C.S. Lee, P.A. Labosky, V.W. Yang, et al., The zinc-finger transcription factor Klf4 is required for terminal differentiation of goblet cells in the colon, Development 129 (2002) 2619–2628.
[33] J.A. Segre, C. Bauer, E. Fuchs, Klf4 is a transcription factor required for establishing the barrier function of the skin, Nat. Genet. 22 (1999) 356–360.
[34] T. Shindo, I. Manabe, Y. Fukushima, K. Tobe, K. Aizawa, S. Miyamoto, et al., Kruppel-like zinc-finger transcription factor KLF5/BTEB2 is a target for angiotensin II signaling and an essential regulator of cardiovascular remodeling, Nat. Med. 8 (2002) 856–863.
[35] M. Morita, A. Kobayashi, T. Yamashita, T. Shimanuki, O. Nakajima, S. Takahashi, et al., Functional analysis of basic transcription element binding protein by gene targeting technology, Mol. Cell. Biol. 23 (2003) 2489–2500.
[36] R.C. Simmen, R.R. Eason, J.R. McQuown, A.L. Linz, T.J. Kang, L. Chatman Jr., et al., Subfertility, uterine hypoplasia, and partial progesterone resistance in mice lacking the Kruppel-like factor 9/basic transcription element-binding protein-1 (Bteb1) gene, J. Biol. Chem. 279 (2004) 29286–29294.
[37] C.Z. Song, G. Gavriilidis, H. Asano, G. Stamatoyannopoulos, Functional study of transcription factor KLF11 by targeted gene inactivation, Blood Cells Mol. Dis. 34 (2005) 53–59.
[38] X. Zhou, J.M. Long, M.A. Geyer, E. Masliah, J.R. Kelsoe, A. Wynshaw-Boris, K.R. Chien, Reduced expression of the SP4 gene in mice causes deficits in sensorimotor gating and memory associated with hippocampal vacuolization, Mol. Psychiatry, advance online publication 23 November 2004.
[39] Y. Oishi, I. Manabe, K. Tobe, K. Tsushima, T. Shindo, K. Fujiu, G. Nishimura, K. Maemura, T. Yamauchi, N. Kubota, R. Suzuki, T. Kitamura, S. Akira, T. Kadowaki, R. Nagai, Krppel-like transcription factor KLF5 is a key regulator of adipocyte differentiation, Cell Metab. 1 (2005) 27–39.