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HOX gene cluster (de)regulation in brain: from neurodevelopment to malignant glial tumours

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1 **Abstract:**

2 HOX genes encode a family of evolutionarily conserved homeodomain transcription factors that are
3 crucial both during development and adult life. In humans, 39 HOX genes are arranged in four clusters
4 (HOXA, B, C, and D) in chromosomes 7, 17, 12 and 2, respectively. During embryonic development,
5 particular epigenetic states accompany their expression along the anterior-posterior body axis. This
6 tightly regulated temporal-spatial expression pattern reflects their relative chromosomal localization,
7 and is critical for normal embryonic brain development, when HOX genes are mainly expressed in
8 the hindbrain and mostly absent in the forebrain region. Epigenetic marks, mostly polycomb-
9 associated, are dynamically regulated at HOX loci and regulatory regions to ensure the finely tuned
10 HOX activation and repression, highlighting a crucial epigenetic plasticity necessary for homeostatic
11 development. HOX genes are essentially absent in healthy adult brain, whereas they are detected in
12 malignant brain tumours, namely gliomas, where HOX genes display critical roles by regulating
13 several hallmarks of cancer. Here, we review the major mechanisms involved in HOX genes
14 (de)regulation in the brain, from embryonic to adult stages, in physiological and oncologic conditions.
15 We focus particularly on the emerging causes of HOX gene deregulation in glioma, as well as on
16 their functional and clinical implications.

17

18 **Keywords:** glioma; epigenetics; transcriptional regulation; neurodevelopment; homeobox

19

20 **Abbreviations:** 3C: chromosome conformation capture; 3D: 3-dimensional; 4C-seq: circularized
21 chromosome conformation capture with deep sequencing; 5C: chromosome conformation capture
22 carbon copy; AQB: AC1Q3QWB drug; CAM: chicken chorioallantoic membrane; CGGA: Chinese
23 Glioma Genome Atlas; ChIP: chromatin immunoprecipitation; CHROMO: chromatin organization
24 modifier; CNS: central nervous system; CNV: copy number variations; COMPASS: complex proteins
25 associated with Set1; DNA: deoxyribonucleic acid; ESCs: embryonic stem cells; GBM: glioblastoma;
26 G-CIMP: glioma CpG island methylator phenotype; GSCs: GBM stem cells; H2AK119ub:
27 ubiquitination of H2AK119 residues; H3K27ac: histone H3 lysine 27 acetylation; H3K27me3:
28 histone H3 lysine 27 trimethylation; H3K4me3: histone H3 lysine 4 trimethylation; Hi-C:
29 chromosome capture followed by high-throughput sequencing; HOX: homeobox; HUVEC: human
30 umbilical vein endothelial cells; LGG: low-grade gliomas; lncRNA: long non-coding RNA; miRNAs:
31 micro RNA; mRNA: messenger RNA; OS: overall survival; PARs: promoter-associated RNAs; PcG:
32 polycomb group; PCR: polymerase chain reaction; PDX: patient-derived xenograft; PRE: polycomb
33 responsive element; RA: retinoic acid; RNA: ribonucleic acid; SINE: short interspersed nuclear
34 elements; TAD: topological associating domain; TCGA: The Cancer Genome Atlas; TMZ:

- 1 temozolomide; TrxG: trithorax-group proteins; TSS: transcription start sites; WHO: World Health
- 2 Organization
- 3

1 **1. Introduction**

2 Genetic mutations in the fruit fly *Drosophila melanogaster* that resulted in homeotic transformations
3 of one body segment to another (e.g., antennae growing at the posterior part instead of at the head of
4 the fly) led to the identification of master transcriptional regulators named homeobox genes [1-5].
5 These genes are characterized by a consensus DNA sequence of 183 base pairs, the so-called
6 homeobox, that encodes the homeodomain, a 61-amino acid peptide motif with a distinctive helix-
7 loop-helix-turn-helix structure [6]. This homeodomain serves, among other functions, as a DNA
8 binding domain that preferentially recognizes a specific TA-rich core DNA sequence, such as TAAT
9 or TTAT [7-10]. Homeobox genes are of paramount importance for the developmental and post-
10 developmental regulation of morphogenesis, patterning and differentiation, independently of the
11 organ, limb or tissue where they are expressed [11-19].

12 HOX genes represent the main subset of the homeobox family. They display evolutionarily conserved
13 transcription factor functions common to all bilaterian animals [20], and are considered crucial for
14 the establishment of segmental identity along the anterior-posterior body axis of vertebrates. HOX
15 proteins also have non-transcriptional activities and are implicated in regulating various processes,
16 such as DNA replication and repair, mRNA translation, and protein degradation (reviewed by
17 Rezsóhazy et al. [21]). Structurally, they are divided into two exons and one intron, being the
18 homeobox sequence present in the second exon (Fig. 1A). In *D. melanogaster*, eight collinear HOX
19 genes, split into two clusters (the antennapedia and bithorax complexes), are responsible for
20 segmental patterning. In amniotes, there are 39 HOX genes distributed into four clusters (HOXA,
21 HOXB, HOXC, and HOXD) according to their chromosomal localization (7p15, 17q21.2, 12q13, and
22 2q31, respectively, in humans) [22]. Each cluster is divided into 13 paralogue groups (HOX1 at the
23 3' end to HOX13 at the 5' end of each cluster), with 9 to 11 genes assigned to each cluster, based on
24 their sequence homology and position within the cluster (Fig. 1B). It is thought that these four clusters
25 originated during vertebrate evolution due to two rounds of whole genome duplication that resulted
26 in paralogue clusters with partial redundant functions [20,23,24]. The temporal-spatial collinear
27 expression of HOX genes during embryogenesis [25,23] is one of the most organized and captivating
28 mechanisms of gene regulation, in which the expression pattern of each paralogue group directly
29 mirrors their collinear chromosomal organization. The first paralogues (HOX1 and HOX2) are the
30 first to be expressed (shortly after the establishment of the primitive streak), followed by the other
31 paralogues (from the 3' end to the 5' end in each cluster) in a time/developmental stage-dependent
32 manner. In addition to their temporally regulated expression, they are gradually expressed from more
33 anterior regions to more posterior regions of the embryo. This spatial collinearity (i.e., the relation
34 between the relative chromosomal position of a HOX gene and its spatial expression in the body) was

1 first described in *D. melanogaster* [4]. Since then, it has been observed throughout the animal
2 kingdom [26]. Nonetheless, temporal collinearity is reserved to bilaterians with intact chromosomal
3 organization of HOX in clusters [27,28]. Unsurprisingly, at least 15 genetic disorders were associated
4 with germline mutations in 10 out of 39 HOX genes in humans (as reviewed in Quinonez, Innis [29]).
5 In mouse, loss-of-function mutations of 26 out of 28 tested Hox genes resulted in a particular
6 phenotype/defect in the animal, which mirrors those observed in humans and may thus help clinicians
7 to better predict the effects of alterations in specific HOX genes in patients [29].

8 This review will critically summarize the major molecular mechanisms of transcriptional regulation
9 of HOX genes in the healthy brain, with a special focus on their dynamic epigenetic landscapes during
10 critical stages of neuro-development. In addition, it will discuss the most critical molecular alterations
11 and functional roles of HOX genes in brain tumours, as well as their recently highlighted clinical
12 relevance in patients.

13 **2. General principles of HOX regulation**

14 The collinear activation, in time and space, of HOX genes during vertebrate development relies on a
15 multi-scale regulation that involves the *cis*-regulatory landscape, the three-dimensional (3D)
16 chromatin configuration, the histone modification pattern and RNA-based regulation [27].

- 17 • Proximal and remote *cis*-regulatory regions

18 Early studies in transgenic mice showed that some individual Hox genes inserted at ectopic positions
19 in the genome can recapitulate their endogenous expression pattern, indicating that the necessary
20 regulatory sequences are in their vicinity [30,31]. Accordingly, multiple proximal *cis*-regulatory
21 sequences that can influence transcription of neighbouring genes were identified within Hox clusters
22 [32-34]. For instance, two retinoic acid (RA) response elements embedded in the Hoxb cluster control
23 expression of *Hoxb5* to *Hoxb9* in the developing neural tube [35]. Such proximal regulatory
24 sequences provide a frame for the evolutionary conserved temporal collinear activation of HOX
25 genes. However, novel HOX-associated patterning functions, which often use the collinear property
26 of only a subset of genes from the same cluster, emerged in vertebrate lineages. These novel functions
27 often rely on *cis*-regulatory sequences located outside the HOX cluster. For instance the development
28 of both proximal and distal limb segments, in the limb buds, relies on two subsequent waves of Hoxd
29 genes transcription, controlled by distinct remote *cis*-regulatory regions located on each side of the
30 gene cluster [36-38]. A similar long-range regulation is also documented at the other HOX clusters
31 to control the coordinated activation of HOX genes in specific developmental stages and tissues [41-
32 43]. These observations revealed the importance of the remote transcriptional control to the HOX-

1 mediated patterning of the developing vertebrate embryo. In addition, as the distant enhancers and
2 HOX promoters must physically interact, the 3D chromatin conformation has to be taken into account
3 to understand HOX regulation. Accordingly, a significant advance in our understanding of HOX
4 control came with the development of molecular tools to assess the 3D genome organization at high-
5 resolution.

6 • A 3D chromatin conformation-based regulation

7 The development of the Chromosome Conformation Capture (3C) methodology and its derivatives
8 (circularized chromosome conformation capture with deep sequencing, 4C-seq; chromosome
9 conformation capture carbon copy, 5C; and chromosome capture followed by high-throughput
10 sequencing, Hi-C) [44] allowed the analysis of the relationship between genome architecture and
11 gene expression control over time. Specifically, Hi-C approaches showed that chromosomes are
12 divided into mega base-scale regions, called Topological associating domains (TADs) in which
13 chromatin interactions are highly favoured [45,46]. These domains are relatively stable in the
14 different cell types, and are proposed to be structural features of the genome [45]. Strikingly, both
15 HOXA and HOXD clusters lie at the boundary between two TADs [45]. This topological organization
16 might separate these compact gene clusters in two independent functional units that will specify
17 contacts between remote enhancers and their cognate HOX target genes during development (Fig. 2).
18 This scheme explains the bi-modal regulation of the Hoxd cluster during limb development. Long-
19 range interactions between the 3' Hoxd genes and enhancers located in the telomeric gene desert
20 occur within the 3' (telomeric) TAD. Conversely, 5' genes segregate in the 5' (centromeric) TAD
21 where they contact enhancers in the centromeric gene desert. Interestingly, a subset of contacts
22 between Hox promoters and their distal enhancers occur by default within the TAD, regardless of the
23 enhancer activity and their expression status [39,41]. In parallel to the enhancer-promoter contacts
24 established concomitantly with gene activation [48,49], this pre-established configuration at a subset
25 of genes might prime them for rapid induction [32,50].

26 The molecular bases of TAD ontogeny at HOX cluster are not fully understood. A critical factor is
27 the chromatin barrier insulator CTCF (CCCTC-binding factor) that is often located at TAD
28 boundaries [45]. Specifically, deletion of CTCF binding sites within the Hoxa cluster can reposition
29 the TAD boundary and lead to misregulation of Hox genes expression [51,52]. However, other yet to
30 be identified actors might contribute to TAD boundary positioning [53]. These include the structural
31 protein cohesin that promotes DNA loop formation between distant regions [54], as well as genomic
32 features, such as the presence of short interspersed nuclear elements (SINE) [45]. Tissue-specific
33 transcription factors also could influence TAD boundary position. This hypothesis is supported by

1 the observation that this position can vary in a tissue-specific manner at the HOXA and HOXD
2 clusters (reviewed in [32]), with reallocation of some genes from one TAD to the other. Therefore,
3 there could be an interplay between intra-cluster TAD boundaries and tissue-specific transcriptional
4 machinery [32].

5 Unlike HOXA and HOXD, the HOXB and HOXC clusters are not associated with a TAD boundary
6 [45], suggesting that TADs are not required for long-range regulations within these clusters. Their
7 genomic organization might create a physical separation between the 3' and 5' parts of each cluster.
8 Indeed, due to its remote localization, *HOXB13* is isolated from *HOXB1-HOXB9*, while the HOXC
9 cluster does not contain paralogues for the groups 1-3 (Fig. 1B).

- 10 • HOX genes are *bona-fide* polycomb targets

11 HOX gene activation is associated with dynamic changes in their chromatin signature. Hence,
12 expression patterns induced by productive enhancer-promoter contacts are maintained and faithfully
13 transmitted to daughter cells. Besides the gain of the activating H3K27ac (acetylation of histone H3
14 lysine 27) mark within enhancers [55], the most drastic changes affect the distribution of the
15 repressive H3K27me3 and the permissive H3K4me3 marks within HOX clusters.

16 In embryonic stem cells (ESCs), which do not express HOX genes, whole HOX clusters are fully
17 decorated by H3K27me3, while at their promoter area this mark co-exists with H3K4me3,
18 constituting the so-called bivalent chromatin [56,57] (Fig. 3A). It has been suggested that bivalent
19 chromatin domains repress transcription of genes through H3K27me3, while keeping them 'poised'
20 for alternative fates, through resolution into either H3K4me3 or H3K27me3, upon stem cell
21 differentiation [56]. In the developing embryo, collinear activation of HOX genes is accompanied by
22 a progressive loss of H3K27me3 associated with H3K4me3 gain. Consequently, H3K27me3- and
23 H3K4me3-marked domains demarcate repressed and active HOX genes, respectively, along the
24 cluster (Fig. 3B). In differentiated cells and tissues where all HOX genes are repressed, such as the
25 forebrain, H3K27me3 coats the whole clusters [58,59,57] (Fig. 3C). This observation highlights the
26 importance of the polycomb (PcG) and trithorax (TrxG) groups of proteins that regulate H3K27me3
27 and H3K4me3 deposition, respectively, in the epigenetic regulation of HOX genes.

28 PcG-mediated silencing relies on two complexes that act sequentially: Polycomb Repressive complex
29 1 and 2 (PRC1 and PRC2). In the canonical model, PRC2 first deposits H3K27me3 at the targeted
30 chromatin. H3K27me3 then recruits PRC1 that induces a compacted chromatin state mainly through
31 ubiquitination of H2AK119 residues (H2AK119ub). This two-step model is supported by the finding
32 that while both complexes are required for proper HOX gene silencing [60,58,61], PRC1 deficiency

1 does not affect the PRC2-mediated H3K27me3 pattern [58]. Unlike in *Drosophila*, no polycomb
2 responsive element (PRE) has been formally described in vertebrates, questioning the mechanism for
3 PRC targeting at specific loci. The observation that PRC2 components can associate with long non-
4 coding RNAs (lncRNA) and promoter-associated RNAs (PARs) suggests the implication of RNA
5 transcripts in this process [62-64]. For instance, the lncRNA HOTAIR, which is produced in the 5'
6 part of the HOXC cluster, recruits PRC2 and acts in *trans* to silence the genes located in the 5' part
7 of the HOXD cluster in cultured cells [63,65]. Similarly, it has been suggested that Hoxa adjacent
8 lncRNA 1 (*Har11*), a lncRNA located approximately 50Kb downstream of the HOXA cluster,
9 represses this cluster in mouse ESCs by recruiting PRC2 to Hoxa promoters [66]. However,
10 functional studies in animals indicate that *Har11* is dispensable for normal development [67,68], and
11 brought conflicting results on *Hotair* [69-71], questioning the role of lncRNAs in the regulation of
12 HOX clusters *in vivo*. It has also been proposed that PRC2 recruitment could be responsive to
13 permissive chromatin signatures at promoters [72]. In agreement, studies in mammalian cells and
14 tissues showed that PRC2 is recruited by default at transcriptionally inactive CpG islands/promoters
15 [73,74].

16 TrxG proteins are the second main epigenetic regulator of HOX clusters. Specifically, deposition of
17 H3K4me3 at HOX clusters in mammals relies on the COMPASS-like complex that contains MLL1
18 and 2, the homologues of *Drosophila* Trx [75]. Interestingly, this complex also contains the
19 H3K27me3-demethylase KDM6A that removes H3K27me3 at HOX loci [76-78]. This suggests that
20 H3K4me3 deposition and H3K27me3 removal are coupled at HOX promoters. Like for PRC2, it has
21 been suggested that lncRNAs promote recruitment of the TrxG/MLL complex. For instance,
22 *HOTTIP*, located at the 5' tip of the HOXA locus, recruits in *cis* the WDR5/MLL proteins and
23 promotes H3K4me3 deposition [79]. Alternatively, as observed for other COMPASS-like complexes
24 [80], TrxG/MLL complexes could be recruited at promoters through association with the
25 transcriptional machinery.

- 26 • Active and repressed HOX genes are within distinct nuclear compartments in the nucleus

27 Altogether, a model emerges whereby H3K27me3 is deposited by default at transcriptionally inactive
28 HOX genes, a process that can be promoted by lncRNA activity. Upon enhancer-induced activation,
29 the transcriptional machinery would bring TrxG/MLL/KDM6A complexes to promoters to sustain
30 HOX gene transcriptional activity by inducing H3K4me3 deposition and H3K27me3 removal.
31 Interestingly, the dynamics of H3K27me3/H3K4me3 distribution along the different HOX clusters
32 impacts their 3D architecture. Indeed, 4C approaches showed the segregation of active and repressed
33 HOX genes within distinct nuclear compartments [55,59]. Specifically, H3K27me3-marked HOX

1 loci cluster together within inactive nuclear compartments, denoted polycomb bodies, where they can
2 contact, although at a lower frequency, other polycomb targets through intra- and inter-chromosomal
3 interactions [+ Pirotta & Li, 81,82]. Upon induction, HOX genes switch to more discrete H3K4me3-
4 associated compartments, thus modifying the cluster 3D organization [55,59]. This spatial separation
5 between the silent and expressed parts of HOX clusters might facilitate their finely tuned regulation.

6 • miRNA and post-transcriptional regulation

7 In addition to transcriptional regulation, HOX expression is also controlled at the post-transcriptional
8 level by the mean of several processes, including polycistronic transcription, RNA processing or
9 sequence-specific transcriptional control. These issues have been recently extensively reviewed
10 [Casaca et al., 2018]. Among those, one important mechanism is regulation via microRNA (miRNA)
11 repression. These short RNA species negatively regulate gene expression by binding target mRNA
12 in a sequence-specific manner, further leading to degradation *via* the RNA-induced silencing complex
13 (reviewed in Bartel, 2018). Several highly conserved miRNA families are embedded within HOX
14 clusters, including for instance the miR-10, miR-615 and miR-196 families. Interestingly, among the
15 predicted targets of these HOX-embedded miRNAs, many are protein-coding HOX mRNAs [Yekta
16 et al., 2008]. To which extent these miRNAs indeed contribute to control and coordinate HOX output
17 remain to be fully determined. Nonetheless, functional studies have highlighted that *miR-196* and
18 *miR-10* do contribute to HOX mRNA regulation in vertebrates [Mandsfield and McGlenn, 2012;
19 Casaca, 2018]. This is best illustrated by miR-196 that acts by delimiting *Hoxb8* activity in developing
20 hind limb and neural tissue [Hornstein, 2005; Asli and Kessel, 2010].

21 **3. Roles of HOX genes in the developing brain**

22 Most HOX genes are expressed in the developing vertebrate central nervous system (CNS) where
23 they have critical functions. They first play a central role in cell fate determination within hindbrain
24 and spinal cord segments, further contributing to the establishment of functional neuronal networks
25 [86; 98]. These structures are indeed key coordination centres of the CNS that, via dedicated neural
26 assemblies, regulate complex physiological processes, including breathing, locomotion, heartbeat,
27 and different sensory systems [107].

28 Following the onset of neural induction, the early vertebrate hindbrain is transiently segmented in
29 seven or eight cellular compartments, depending on the species, called rhombomeres (r1 to r8) (Fig.
30 1B). While no physical barrier exists between them, cells of each rhombomere remain well segregated
31 and do not mix with those of the other rhombomeres [83,84]. Each of these segments constitutes an
32 independent lineage-restricted unit that creates regional diversity along the anterior-posterior axis of

1 the developing hindbrain, thus acting as a template for the future adult brainstem structure and
2 function. Each rhombomere is the source of distinctive neural progenitors that ultimately generate
3 rhombomere-specific populations of neurons [85]. For instance, among motor neurons, trigeminal
4 neurons develop in r2/r3, while facial and vagal neurons form in r4 and r7/r8, respectively. Although
5 such a clear segmentation is not present in the spinal cord, neuronal regional diversity is also observed
6 along the anterior-posterior axis. Specifically, spinal motor neurons are organized into longitudinal
7 columns along the four main spinal cord units: cervical, thoracic, lumbar and sacral [86]. For instance,
8 phrenic motor neurons are generated at the anterior cervical level, while preganglionic and hypaxial
9 neurons form at the thoracic level (Fig. 1B).

10 Strikingly, specific combinations of Hox gene expression and/or expression levels define the regional
11 identity in hindbrain and spinal cord. Specifically, Hox1-Hox5 paralogue group genes display
12 rhombomere-specific nested expression patterns in hindbrain. Similarly, Hox4-Hox11 genes are
13 expressed in a nested fashion along the anterior-posterior spinal cord axis [87,88,86,89] (Fig. 1B).
14 Disturbance of these patterns in the mouse and other vertebrate models have revealed that HOX genes
15 play a key role in the segmentation and specification of several rhombomeres in hindbrain, and in the
16 maintenance of columnar identity in spinal cord [90-93,86].

17 The HOX combinatorial code in hindbrain and spinal cord is also involved in key steps of neural
18 development by acting as a determinant to control the formation of distinct neuronal subtypes within
19 the different segments. Specifically, studies conducted on motor neuron specification highlighted the
20 importance of HOX transcription factors in regulating the diversity and identity of motor neuron pools
21 in spinal cord, and in establishing the pattern and specificity of limb muscle innervation
22 [94,90,95,92,86,96]. In addition, studies conducted in Hox conditional mouse mutants support a role
23 for Hox genes in later stages of CNS development to generate neural circuit assemblies. For instance,
24 the formation of respiratory, somatosensory and auditory circuits is perturbed in the absence of
25 specific Hox genes [97-99].

26 Therefore, neuronal subtype specification and connectivity in hindbrain and spinal cord rely on HOX-
27 specific expression patterns and the associated regionalization along the anterior-posterior axis. These
28 expression patterns are set up sequentially during two phases of regulation in progenitors and post-
29 mitotic neurons, respectively. They involve a complex interplay between morphogen signals, cross-
30 regulatory interactions between Hox genes, and polycomb-associated epigenetic modifications. First,
31 in the neural tube, opposite gradients of RA and Fibroblast growth factor (FGF) signalling act in
32 concert to establish the initial Hox expression pattern in the early CNS [100,18]. RA primarily
33 promotes the expression of the Hox1-5 paralogue group of genes through activation and direct binding

1 of RA receptors (RARs) [101]. In spinal cord, FGF establishes the Hox4-Hox10 gene expression
2 patterns through the induction and subsequent binding of the homeodomain protein factors CDX
3 [102,103]. Studies in differentiating mouse neural progenitors showed that binding of RARs and CDX
4 to their cognate Hox target genes and their subsequent activation are associated with the rapid removal
5 of the repressive H3K27me3 mark [104]. This chromatin remodelling provides a template to transmit
6 these initial gene expression patterns to early post-mitotic neurons where they will be refined and
7 segmentally restricted. Although neural progenitors display a nested pattern of Hox expression, clear
8 Hox posterior boundaries will be indeed established at the time of differentiation and often maintained
9 up to late foetal stages in restricted neuronal subpopulations. This second regulatory phase relies on
10 direct self- and cross-regulatory interactions between HOX transcription factors and Hox genes,
11 associated with the combined action of other transcription factors [105,106]. For instance, a complex
12 interplay between the KROX20 transcription factor and the Hox1 and Hox2 paralogue groups ensures
13 that *Hoxb1* expression is restricted to r4 in the vertebrate hindbrain, where it will be then maintained
14 through an auto-regulatory loop [107,108]. EZH2, the enzymatic component of PRC2, is required to
15 maintain Hox expression patterns in the segmented hindbrain. Accordingly, its neural-specific
16 depletion in the mouse leads to migration and connectivity defects of pre-cerebellar pontine neurons
17 [109]. In the spinal cord, PRC2-mediated H3K27me3 pattern at Hox loci is determined during the
18 progenitor phase. However, Hox gene expression pattern is refined and maintained in post-mitotic
19 cells through a mechanism that seems to depend on PRC1, the other PRC complex. Specifically,
20 depletion of the PRC1 component BMI-1 affects *Hoxc9* expression and the spinal cord columnar
21 identity [110].

22 After neurulation, HOX expression patterns are maintained up to late foetal/early post-natal stages in
23 restricted neuronal subpopulation of the hindbrain, and in restricted domains of the spinal cord
24 [95,98,99, Gofflot and Lizen, 2018]. A handful of studies further report that HOX expression may
25 persist post-natally and in the adult brain. For instance, RT-PCR analyses in human adult brain extract
26 highlighted the expression of the 3' HOX genes (HOX1-HOX7 paralogues) [12]. A more systematic
27 analysis conducted in the adult mouse brain evidenced that the expression of genes belonging to
28 Hox2-Hox8 paralogue groups is maintained in the hindbrain derivatives. The same analysis also
29 support that some Hox transcripts are neo-expressed in specific brain regions at adulthood [Hutlet et
30 al., 2014]. These observations suggest that HOX transcripts could be functionally required in the brain
31 after birth, stressing the need to formally assess their function at adulthood. Indeed, several lines of
32 evidence mainly based on functional *in vivo* data obtained for the *Hoxa2* and *Hoxa5* loci suggest a
33 role in synapse formation and maturation [reviewed in Gofflot and Lizen, 2018]. Unlike in hindbrain
34 and spinal cord, HOX genes are not expressed in the developing forebrain, the most anterior part of

1 the developing CNS, and also in adult brain [111]. This repression is mediated by H3K27me3 [59],
2 and is critical for brain expansion. This evolutionary conserved feature of the CNS leads to a more
3 prominent anterior region (brain) compared with the posterior ones. A study conducted in *Drosophila*
4 and the mouse revealed that brain expansion is severely reduced following Hox ectopic expression,
5 or loss of PcG function [112]. Surprisingly, mutation of the *Abd-B* HOX gene rescues the reduced
6 brain proliferation observed in PRC2 mutants in *Drosophila*. This intriguing observation, which has
7 not yet been assessed in vertebrate brain, suggests that in the developing *Drosophila* brain, one of the
8 primary roles of PRC2 is to repress Hox genes [113]. From this analysis, it emerges a picture whereby
9 HOX genes repress the neural stem cell proliferation programme in the more posterior parts. PcG-
10 mediated repression of HOX genes prevent this anti-proliferative action in the forebrain, thus
11 promoting brain expansion [113]. Altogether, this observation stresses the importance of maintaining
12 HOX genes repressed in forebrain.

13 **4. HOX deregulation in brain gliomas**

14 HOX genes may present tumour suppressive or oncogenic functions, and their expression is
15 frequently altered in cancer, including leukaemia [114-118], breast [119-121], brain [122-127], lung
16 [128,129], colon [130], cervix [131], bladder [132,133], and kidney cancers [134]. In the context of
17 this review, we will focus on brain tumours, specifically high-grade gliomas.

18 **4.1. Malignant primary brain tumours**

19 Malignant primary brain tumours represent approximately 32% of all brain tumours and affect more
20 than 250 000 individuals each year worldwide (17th most common cancer type) [135]. Despite their
21 relatively low incidence compared with other primary cancers (e.g., lung, breast, prostate and
22 colorectal cancers) and metastatic brain tumours, they constitute a major source of morbidity and
23 mortality. They are the 12th most deadly cancer worldwide (almost 190 000 estimated deaths per year)
24 [135], and rank first in average of years of life lost among all tumour types [136].

25 Gliomas represent the majority of all malignant brain tumours (81%).

26 Until 2016, gliomas were traditionally classified based on histologic features as astrocytic,
27 oligodendroglial, oligoastrocytic (mixed), or ependymal tumours, as described in the 2007 World
28 Health Organization (WHO) classification guidelines [139]. In this classification, tumours were
29 named after the normal cells from which they resembled. However, this classification methodology
30 was prone to considerable inter-observer variability, particularly in the context of diffusely infiltrating
31 gliomas (e.g., differences in the classification of astrocytoma vs. oligodendroglioma vs.
32 oligoastrocytoma) [140-142]. Moreover, advances in (epi)genetics and transcriptomic analyses have

1 shed light on the biological and clinical variability observed within each histologically-defined
2 glioma entity [143,142]. These observations suggested that some of the molecular alterations
3 underlying this variability might in fact be used as biomarkers for more accurate glioma classification
4 [143], which contributed to the 2016 revision of the guidelines [141]. For example, according to the
5 most recent WHO classification of CNS tumours, gliomas can be isocitrate dehydrogenase (IDH)-
6 wildtype or IDH-mutant [142]. Gliomas are also stratified according to their malignancy grade, from
7 benign grade I to highly-malignant grade IV. Glioblastoma (GBM) is the most common and
8 malignant form of glioma [137], being almost universally fatal with very low 2- and 5-year survival
9 rates [138]. IDH-wildtype GBMs are the most common (90%), occur mainly in elderly patients
10 (median age at diagnosis: 62 years), are localized in the supratentorial region, and correspond to
11 primary GBM that develop *de novo* (i.e., with a short clinical history of less than 3 months before
12 diagnosis, and without a pre-existing lower-grade precursor lesion) [143,142]. They are associated
13 with copy number gains on chromosome 7 (where the HOXA cluster is located), chromosome 10
14 monosomy, *EGFR* amplification, and mutations in *PTEN*, *TERT*, *CDKN2A* and *CDKN2B* genes.
15 *TERT* promoter mutation is mutually exclusive with *ATRX* mutation, which are common in IDH-
16 mutant GBM [142]. IDH-mutant GBMs typically occur in younger adults (median age at diagnosis:
17 44 years), are preferentially localized in the frontal lobe, and include most of secondary GBMs (i.e.,
18 GBMs that develop from a pre-existing diffuse or anaplastic astrocytoma) [142,143]. These tumours
19 are characterized by copy number gains on chromosome 7, loss of heterozygosity of the 17p arm,
20 *TP53* and *ATRX* mutations, and the glioma CpG island methylator phenotype (G-CIMP) [142,143].

21 **4.2. Aberrant HOX gene expression in glioma**

22 Abdel-Fattah et al. [125] were the first to report the aberrant overexpression of 9 of the 39 HOX genes
23 (*HOXA6*, *A7*, *A9*, *A13*, *B13*, *D4*, *D9*, *D10*, and *D13*) in gliomas compared with normal human
24 astrocytes and temporal lobe cells (these may include astrocytes, microglia, and neurons; summarized
25 in Table 1). In 2008, Murat et al. [124] described the overexpression of several HOX genes (*HOXA2*,
26 *A3*, *A5*, *A7*, *A9*, *A10*, *C6*, *D4*, *D8*, and *D10*) in tumour samples compared with non-neoplastic brain
27 samples from patients with GBM. In 2009, Buccoliero et al. [144] analysed the expression of HOXD
28 genes in 14 paediatric grade I gliomas and 6 non-neoplastic human brain tissues, and described that
29 *HOXD1* and *HOXD12* were overexpressed in grade I gliomas compared to non-neoplastic tissues,
30 while *HOXD3*, *D8*, *D9*, and *D10* presented lower expression in grade I glioma (the last three were
31 exceptionally expressed in non-neoplastic tissues). On the other hand, *HOXD4*, *D11*, and *D13* were
32 not expressed in grade I glioma. Sun et al. [145] reported later that *HOXD10* was expressed in GBM.
33 In 2010, Costa et al. [122] showed widespread activation of HOX genes (*HOXA1*, *A2*, *A3*, *A4*, *A5*,
34 *A7*, *A9*, *A10*, *B7*, and *C6*) in a subset of GBM patients compared with less malignant gliomas or

1 normal brain tissues. Duan et al. [146] later corroborated these findings by describing that HOXA9,
2 A11, and A13 proteins, and *HOXA9*, *A10*, *A11*, and *A13* mRNA levels were strongly upregulated in
3 GBM compared with grade II/III gliomas. However, *HOXA11* expression was significantly
4 downregulated in recurrent GBMs compared with primary GBMs [147]. Several other studies also
5 reported the overexpression of specific HOX genes in GBM compared with non-neoplastic brain
6 samples: *HOXA1* [148], *HOXA9* [150], *HOXA13* [146], *HOXB3* [151], *HOXB7* [152], *HOXB9* [153],
7 *HOXC6* [154], *HOXC9* [155], *HOXC10* [156,157], *HOXD4* [158], and *HOXD9* [126]. Among these
8 genes, *HOXA1*, *HOXA9*, *HOXA13*, *HOXB9*, and *HOXC10* were expressed in a grade-dependent
9 manner [148,150,146,153,156]. *HOXB1* and *HOXD10* expression levels were shown to be lower in
10 glioma than in non-neoplastic samples [159,160], and *HOXB1* particularly low in GBM compared to
11 grade I and II gliomas. Moreover, Gaspar et al. [123] found that *HOXA2*, *A5*, *A7*, and *A9* were
12 overexpressed in short-term (<1 year) paediatric GBM survivors compared with long-term survivors.
13 Gallo et al. [161] identified a specific gene signature of patient-derived GBM stem cells (GSCs),
14 compared with normal human foetal neural stem cells and non-neoplastic brain cortical tissues, which
15 included 24 of the 39 HOX genes. In agreement, Li et al. [162] reported that *CD133* expression, a
16 marker of GBM stem cells, correlates with *HOXA5*, *A7*, *A10*, *C4*, and *C6* expression in GBM.

17 In summary, different studies reported that the expression of several HOX genes is consistently
18 altered in glioma. The few discrepancies among studies, in which a particular HOX gene was
19 described to be up- and down-regulated, might be explained by: i) the different methods used to
20 evaluate gene/protein expression; ii) the different processing and origin of patients' samples; iii) the
21 use of cell lines in some studies and tumour samples in others; and iv) the different types of samples
22 used to define the "non-tumour" condition. Some of these limitations could be mitigated by using
23 larger cohorts of equally processed and normalized samples (e.g. [163,164], n >500 glioma samples),
24 and by defining standard methodologies for assessing gene expression alterations in these tumours.

25 **4.3. HOX functional roles in GBM**

26 Considering the aberrant expression of HOX genes in GBM, it is reasonable to hypothesize that they
27 might be functionally relevant for the pathophysiology of these tumours. Various studies based on
28 genetic manipulations of these genes, employing silencing or overexpressing approaches, reported
29 that 18 of the 39 HOX genes, have important functional roles in glioma, including *HOXA5*, *A6*, *A7*,
30 *A9*, *A10*, *A11*, *A13*, *B1*, *B3*, *B7*, *B9*, *B13*, *C6*, *C9*, *C10*, *D4*, *D9*, and *D10*. Most of the described roles
31 are associated with oncogenic functions, although *HOXA11*, *HOXB1*, and *HOXD10* displaying
32 tumour suppressive functions in GBM (summarized in Fig. 4).

33 HOX genes act mostly as oncogenes in glioma:

1 The genetic manipulation of *HOXA5*, *A9*, *A10*, *A13*, *B3*, *B7*, *B9*, *C6*, *C9*, *C10*, and *D9* showed that
2 their expression increases the viability of GBM cell lines
3 [151,154,152,149,146,153,161,157,156,150,126,165,122], and five of them (*HOXA9*, *A13*, *C6*, *C10*,
4 and *D9*) also reduce cell death [122,146,156,150,126,151]. *HOXA7*, *A9*, *B7*, *B9*, *C9*, and *C10* also
5 increased GBM cell lines migration capacity [166,152,153,157,156,150,165], while *HOXA6*, *A13*,
6 *B3*, and *B13* promoted increased invasion [166,152,153,157,167,156,150,151,165,146].
7 Interestingly, *HOXC6*, *C10*, and *D9* also increased GBM cell lines colony formation capacity
8 [157,156,126,154], and *HOXA13*, *C6*, and *D9* prevented cell cycle arrest [146,126,154].

9 Additionally, *HOXA9* and *HOXB9* increased GBM stem cell capacity and increased expression of
10 stem cell markers (e.g., NESTIN) *in vitro* [153,150]. Similarly, *HOXD9* was highly expressed in the
11 “side population” of GBM cells, a population of cells identified by flow cytometry and associated
12 with cancer stem cell features, and in GSCs compared with normal astrocytes and neural
13 stem/progenitor cells [126]. Interestingly, *HOXC9* was one of the 16 genes upregulated in CD133⁺, a
14 glioma stem cell marker, but not in CD133⁻ GBM cell lines, compared in both cases with non-
15 neoplastic cells. Moreover, in this 16-gene list, *HOXC9* and *E2F2* were the only genes associated
16 with increased glioma malignancy [155].

17 In another *in vitro* study, *HOXC9* was shown to decrease Beclin1-mediated autophagy through
18 inhibition of *DAPK1* (death-associated protein kinase 1) [165]. Moreover, it has been reported that
19 *HOXA9* and *HOXC10* increase tumour angiogenesis *in vitro* and *in vivo* [150,168]. Indeed, *HOXC10*
20 overexpression enhances tube formation, migration, and proliferation of Human Umbilical Vein
21 Endothelial Cells (HUVEC, a specific type of endothelial cells) and neovascularization in the Chicken
22 Chorioallantoic Membrane (CAM) *in vivo* assay {Tan, 2018 #9161}.

23 Three genes from the HOXA cluster have also been reported to have an important role in resistance
24 to therapy. Specifically, *HOXA9* and *HOXA10* have been associated with decreased sensitivity to the
25 chemotherapy drug temozolomide (TMZ) in GBM patients, a finding that was further supported by a
26 causal relationship in cell lines [169,124,150], and *HOXA5* also decreased sensitivity to radiotherapy
27 *in vitro* and *in vivo* [149].

28 *In vivo*, three genes of the “nine paralogues”, *HOXA9*, *HOXB9*, and *HOXC9*, were shown to promote
29 oncogenesis, as shown by the increased tumour volumes in subcutaneous GBM mouse models
30 [153,150,165]. In clinically more relevant orthotopic models (i.e., based on intracranial implantation
31 of GBM cells in mice), *HOXA5*, *A9*, *A10*, *A13*, *C6*, and *C9* expression increased the GBM-associated
32 death rate [146,161,150,165,154,149]. Particularly interesting in these orthotopic models was *HOXA9*

1 and *HOXA5*, which increased the resistance to TMZ-based chemotherapy and radiotherapy,
2 respectively, as indicated by the lower overall survival (OS) of mice bearing tumours positive for
3 these HOX genes, as compared to negative tumours [150]. Interestingly, *HOXA9* overexpression in
4 non-neoplastic human astrocytes induced their transformation when intracranially implanted, as
5 shown by tumour formation and tumour-related death in 70% of the tested mice. Moreover,
6 histological examination of the tumours formed after intracranial injection showed the presence of
7 characteristic hallmarks of malignant gliomas. Remarkably, this tumorigenic capacity is not observed
8 when cells are implanted subcutaneously, which stresses the critical importance of the tumour
9 microenvironment.

10 Although most HOX genes display pro-tumour functions, a few exceptions have been reported.
11 HOXB1 has tumour suppressive functions in GBM, by decreasing cell viability and promoting
12 apoptosis *in vitro* [159]. HOXD10 decreases the invasive potential of GBM cell lines [170,171], and
13 HOXA11 increases the sensitivity of GBM cell lines to chemotherapy and radiotherapy [147].

14 The functional impact of approximately half of HOX genes in GBM has already been described,
15 particularly concerning the HOXA cluster. This stronger emphasis in HOXA genes could be partly
16 explained due to the fact that they are on chromosome 7, which is frequently amplified in GBM,
17 although HOXA gene copy number alterations have not been consistently associated with its
18 expression [122,150,149,161]. Future studies on the roles of the other HOX genes in glioma will be
19 critical to provide a more complete picture of their implication in these tumours. Additionally,
20 considering the enormous heterogeneity observed between different glioma tumours, studies in
21 glioma subtypes other than GBM will be of critical importance. Moreover, some of the previous
22 findings could be consolidated by using: i) more biologically relevant models based on gene silencing,
23 instead of overexpression approaches in which gene expression may reach unrealistic levels; ii) more
24 clinically relevant patient-derived primary cell cultures, as opposed to cell lines that have been
25 established and cultured for many years and that no longer faithfully reflect the original tumour; iii)
26 stem cell cultures in serum-free conditions (e.g., neurospheres) that could be particularly useful to
27 understand whether HOX roles are more relevant in the glioma stem-cell subpopulation or in more
28 differentiated cells; and iv) 3D cultures (e.g., organoids) that better mimic the tumour
29 microenvironment, endogenous cell organization, and organ structures, which could help might be
30 relevant to better understand the role of HOX genes in more complex contexts.

31 **4.4. Molecular bases of HOX gene deregulation in glioma**

32 It is now clear that in glioma, the HOX gene activation pattern does not follow the coordinated
33 collinear expression observed during normal embryonic development (described above). This process

1 is complex, which in addition to the deregulation of the main processes controlling HOX expression
2 in normal contexts (described above) also involves epigenetic alterations, gene copy number
3 variations, and direct activation by other transcriptional complexes.

4 Copy number variations (CNV) at HOX loci:

5 A pathognomonic characteristic of GBM IDH-wildtype is chromosome 7 trisomy (considered an
6 early event in gliomagenesis) and chromosome 10 monosomy. As the HOXA locus is on chromosome
7 7, chromosome 7 trisomy might increase HOXA gene expression in these patients. Indeed, a
8 correlation was observed between chromosome 7 gain and *HOXA1*, *HOXA4* [172], and *HOXA5* [149]
9 expression in GBM and IDH-wildtype patients. However, this is not true for all HOXA genes because
10 no correlation was observed between CNV and expression of *HOXA2* [172], *HOXA9* [150], *HOXA10*
11 [161], and *HOXA13* [172]. This issue has been less studied at the other HOX clusters. Nonetheless,
12 it was recently shown that overexpression of eight HOX genes distributed over the HOXB, C and D
13 clusters was CNV-independent in IDH-wildtype samples [172]. Altogether, these observations
14 support the hypothesis that CNV, if present, are not the main driving force of HOX gene
15 overexpression in aggressive glioma.

16 Protein- or miRNA-directed targeting of HOX genes: Several miRNAs have been shown to
17 negatively regulate HOX genes in GBM. For example, *HOXB1* is a target of hsa-miR-3175 [148],
18 and *HOXD10* is a target of hsa-miR-21 [162], hsa-miR-10b [134], and hsa-miR-23a [149,160] in
19 GBM. Moreover, hsa_circ_0074362 (circular RNA) was shown to act as a hsa-mir-1236-3p sponge
20 to promote *HOXB7* expression in GBM [141].

21 Protein-gene promoter interactions is another well-known mechanism governing HOX deregulation.
22 Gallo et al. [161] described that MLL protein, which contributes to HOXA gene regulation in
23 haematopoiesis and leukemic cells, directly interacts with the promoter of *HOXA10* in glioblastoma
24 stem cells. HOXA10 protein then interacts with the promoter region of *HOXA7* and *HOXC10*,
25 activating their transcription [161].

26 Epigenetic alterations

27 As depicted in section 2, Polycomb group proteins and the associated H3K27me3 mark are key
28 players in the control of HOX expression during normal development. A large number of studies have
29 highlighted that *bona-fide* polycomb target genes are also more likely to gain aberrant DNA
30 methylation in cancer cells [Ohm et al. 2007; Deneberg et al. 2011; 176]. Thus, not surprisingly,
31 aberrant DNA methylation is a well-documented signature at HOX loci in glioma.

32 This was first observed by Martinez et al. [174] who evaluated the DNA methylation profile of 1505
33 CpGs sites, covering 807 genes, in 87 GBM patient samples. They identified 25 genes that were

1 hypermethylated and 7 that were hypomethylated in at least 20% of samples. Among the 25
2 hypermethylated genes, 3 were HOXA genes: *HOXA11* (hypermethylated in 51% of GBM), *HOXA9*
3 (in 44%), and *HOXA5* (in 20%). Genome-wide analyses confirmed that the four HOX clusters tend
4 to be hypermethylated in GBM and IDH-wildtype glioma, when compared to non-tumour brain
5 samples (Kurscheid et al. [175]. This reminds the observation that hypermethylation of homeobox
6 gene promoters, including HOX genes, is emerging as a pan-cancer signature [176]. Interestingly, the
7 level of DNA methylation alteration can vary between genes and patients. In 2012, Di Vinci et al.
8 [177] analysed DNA methylation of *HOXA3*, *A7*, *A9*, and *A10* in 63 glioma and found patient-specific
9 DNA methylation patterns. This finding was validated by Pojo et al. [150] for *HOXA9*. *HOXA3* was
10 the gene with the highest DNA methylation levels in GBM, while *HOXA7*, *A9*, and *A10* presented
11 lower levels [177].

12 Gain of expression associated with gain of methylation at HOX loci is not in line with the canonical
13 inhibitory effect of DNA promoter methylation on gene transcription. Refined analyses that integrated
14 DNA methylation and strand-oriented expression patterns in glioma patient samples [172] provided
15 some explanations to this apparent paradox. Specifically, for several genes, ectopic expression was
16 associated with CpG islands/promoters that gained methylation at their borders, while their
17 transcription start sites (TSS) remained methylation-free. At other genes, extensive methylation of
18 their main CpG islands/promoter was associated with the use of an alternative promoter. For instance,
19 in IDH-wildtype glioma, *HOXC11* transcription initiated from an unmethylated alternative promoter
20 located 5 kb upstream the canonical, aberrantly methylated promoter [172]. This picture becomes
21 even more complex in the case of chromosome 7 gain. Kurscheid et al. [175] suggested that
22 hypermethylation of the HOXA cluster could compensate the CNV at this cluster in GBM cells with
23 low expression level (HOX-low), while key CpG sites located in the HOXA locus could escape this
24 hypermethylation phenotype in HOX-high GBM cells. Specifically, they showed that a CpG island
25 located at the *HOXA10* non-canonical promoter escape to hypermethylation in HOX-high GBM cells.

26 Court et al. [172] provided evidences that besides the DNA methylation gain, HOX clusters in IDH-
27 wildtype glioma samples are characterized also by dramatic reduction of H3K27me3. Given the
28 importance of this mark for HOX gene repression in normal brain [59] (as previously detailed in
29 section 2), its loss might be crucial for their aberrant expression in aggressive glioma. A study by
30 Costa et al. [122] suggests that alteration of the PI3K pathway could be involved in this process. They
31 showed that PTEN-dependent activation of the PI3K pathway resulted in AKT-mediated
32 phosphorylation of EZH2, the catalytic subunit of the PRC2 complex, that suppresses H3K27me3,
33 leading to derepression of previously silenced HOXA genes. Moreover, they demonstrated that this

1 process is reversible, because PI3K pathway pharmacological inhibition abolished HOXA gene
2 overexpression in GBM cells. Court et al. [172] also proposed that loss of H3K27me3 at HOX genes
3 is a consequence of genome-wide hypomethylation that characterizes cancer cells. In the mouse,
4 widespread DNA methylation depletion triggers H3K27me3 redistribution [179,180] that in turn
5 leads to dramatic loss of H3K27me3 and ectopic expression at a subset of polycomb target genes,
6 including Hox clusters [180].

7 Alterations in 3D chromatin structure and HOX deregulation in glioma

8 Recent studies revealed that alteration in 3D genome organisation is also a feature of glioma cells.
9 Flavahan et al. [178] showed in IDH-mutant glioma that hypermethylation of CTCF binding sites
10 leads to the decrease in the recruitment of CTCF insulator proteins. Therefore, the resulting loss of
11 insulation between TADs leads to aberrant gene activation, such as the oncogene PDGFRA [178].
12 The generation of 3D genome maps by *in situ* Hi-C in glioblastoma stem cells (GSCs) also stressed
13 that 3D structures are altered in these cells, and also between different GSCs lines, providing a layer
14 of glioblastoma inter-patient heterogeneity (Johnston et al. 2019). Whether this type of alteration also
15 contributes to HOX deregulation in glioma is not documented. However, given the importance of
16 remote regulatory regions and 3D structure in the control of HOX expression during normal
17 development, it is critical to further explore this issue.

18 In conclusion, HOX clusters display various molecular alterations in glioma cells. To which extent
19 and how each of these alterations contributes to HOX genes gain of expression remain to be
20 determined. Comprehensive studies in which CNVs, DNA methylation, histone modifications and
21 gene expression are analysed in an integrative manner at HOX clusters are now required to decipher
22 the interplay between these molecular signatures in glioma samples and to identify the causes of their
23 alterations. Interestingly, the finding that the HOXA cluster is over-activated in GBM concomitantly
24 with specific HOXB, C and D genes [125,124,122] suggests again that a complex and inter-dependent
25 mechanism of HOX gene regulation might exist in glioma.

26 **4.5. HOX target genes**

27 As HOX proteins are transcription factors and their targets might be the true biological effectors of
28 their functional roles, several authors have tried to identify these targets in GBM. Potential direct or
29 indirect targets of HOXA5, A9, A10, A11, A13, B9, C6, C9, C10, D9, and D10 were already
30 described, and direct targets were confirmed by chromatin immunoprecipitation (ChIP) for HOXA9,
31 A10, B9, C9, and C10. For the sake of comprehensiveness, a brief summary of some potential HOX

1 targets genes is presented in the following paragraphs (the complete list of potential targets can be
2 found in the original publications).

3 HOXA5

4 Cimino et al. [149] identified 692 differentially expressed genes (144 upregulated and 412
5 downregulated) upon HOXA5 expression in mouse GBM cell lines. By combining this information
6 with data on genes containing HOXA5 binding sequences found by ChIP-seq analysis in human
7 carcinoma cells, they identified 136 common genes (46 upregulated and 90 downregulated). Pathway
8 enrichment analysis of the 46 upregulated genes (e.g. *ASPM*, *AURKA*, *BLM*, *CCNB1*, *CDC25C*,
9 *CDKN3*, *CLSPN*, *FOXMI*, *INCENP*, *MDK*, and *PCNA*) showed that many were implicated in the cell
10 cycle and DNA damage pathways, fitting well with the findings from other studies implicating
11 HOXA5 as a pro-tumour factor.

12 HOXA9

13 Microarray analysis of GBM cell lines (U87, U251, and a primary GBM cell line) in which *HOXA9*
14 is overexpressed or silenced, identified more than 3000 deregulated transcripts in U87 and U251 cells,
15 and over 6000 transcripts in the primary GBM cell line [182,150]. Only 61 were altered (18
16 upregulated and 43 downregulated) in all three cell lines, indicating that gene regulation by HOXA9
17 in GBM follows a cell-specific pattern. Overexpression of *HOXA9* in normal human astrocytes led to
18 the differential expression of more than 500 transcripts, from which 256 were common to at least one
19 of the GBM cell lines (77 upregulated and 179 downregulated) [182,150]. Pathway and gene set
20 enrichment analyses showed that the HOXA9 differentially expressed genes were enriched, for
21 example, in inflammatory response, cell adhesion/migration, stem cells, DNA repair, and cycling
22 genes. Moreover, *HOXA9*-overexpressing cells showed deregulation of the mismatch repair (MMR)
23 and BCL2 DNA repair systems, as indicated by downregulation of PMS2 and MSH6, and
24 upregulation of BCL2 proteins. Later, Xavier-Magalhães et al. [183] identified *HOTAIR*, a lncRNA
25 located at the HOXC cluster with oncogenic functions in GBM, as a direct target (positive regulation)
26 of HOXA9 by ChIP-PCR. Interestingly, *HOTAIR*, the first described lncRNA to present trans-acting
27 functions, negatively regulates HOXD genes in physiological conditions [63]. Whether this
28 mechanism also occurs or is deregulated in glioma remains to be explored. Recently, Gonçalves et al.
29 [184] demonstrated that WNT6, a ligand and activator of the WNT pathway, which displays
30 oncogenic functions in GBM [185], is transcriptionally regulated by HOXA9, identifying a novel link
31 between HOX and WNT signalling.

32 HOXA10

1 Gallo et al. [161] identified, by ChIP-on-chip analysis, 261 direct HOXA10 targets in GBM stem
2 cells, and validated 7 of them by ChIP-quantitative PCR (*HOXA7*, *HOXC10*, *HOXC11*, *HOXC12*,
3 *HOXB13*, *CBX6*, *TERT*, *FGF17*, *JAG2*, and *NODAL*). Enrichment analysis identified significant
4 enrichment for genes involved in processes as growth factor activity, homeobox, CHROMO domain,
5 cytokine, and actin cytoskeleton organization. Additionally, Kim et al. [169] showed that, in GBM
6 cell lines, HOXA10 regulates, in a PI3K-independent manner, PTEN nuclear function (with a
7 different function than the tumour suppressive PTEN cytoplasmic function) through induction of
8 EGR1, which consequently upregulates RAD51 expression, impairing the homologous
9 recombination DNA repair system. In agreement, *HOXA10* silencing increased γ -H2AX, a marker of
10 DNA double strand breaks, in GBM cells [169].

11 HOXA11

12 Silencing of HOXA11, which presents tumour suppressive functions in GBM, led to more than two-
13 fold changes in the expression of 62 genes (11 upregulated and 51 downregulated) in GBM cells
14 [147]. This gene list was significantly enriched in genes implicated in the regulation of growth and
15 mitochondrion activity. Specifically, *TGFBR2*, *CRIMI*, *DPYSL2*, and *CRMP1* were downregulated
16 upon HOXA11 silencing, whereas *TXNIP*, *CD22*, *EPCAM*, *MMP3*, and *SLC16A6* were upregulated.

17 Duan et al. [146] analysed the gene expression profiling data from The Cancer Genome Atlas
18 (TCGA), Rembrandt and the Chinese Glioma Genome Atlas (CGGA) datasets to identify genes
19 showing high correlation (positive or negative) with HOXA13, in order to discover its potential
20 targets in GBM. Positively correlated genes belonged mainly to pathways related to cancer, focal
21 adhesion, WNT pathway, and cell cycle. On the other hand, negatively correlated genes were mostly
22 implicated in the MAPK, ERBB, VEGF, PPAR, and mTOR signalling pathways. *In vitro*, Duan et
23 al. [146] observed that HOXA13 silencing led to decreased levels of nuclear β -catenin and of
24 phosphorylated SMAD2 and SMAD3. Conversely, the level of phosphorylated β -catenin was
25 increased in the cytoplasm, which is indicative of WNT pathway inactivation. Similarly, Yan et al.
26 [154] suggested that the WNT pathway is regulated by HOXC6, through downregulation of WIF-1,
27 a WNT antagonist.

28 HOXB9

29 *TGF β 1* was identified as a direct target of HOXB9 by ChIP-PCR, leading to increased levels of
30 CD133, OCT4, NESTIN, BMI-1, and, similarly to HOXA13, phosphorylated SMAD2 [153].

31 HOXC9

1 HOXC9 has a role in the regulation of autophagy, and DAPK1 was identified as a direct target
2 (negative regulation) by ChIP-quantitative PCR and luciferase reporter assays [165]. HOXC9
3 silencing released DAPK1 transcriptional repression, resulting in activation of the DAPK1-Beclin1
4 pathway and autophagy induction in GBM cells. In agreement, the expression of autophagy protein
5 (i.e., ATG7, ATG5, ATG3, and LC3B) was induced by HOXC9 silencing, while no alterations were
6 found in apoptotic-related proteins (e.g., caspase 9/3 and BCL2) [165].

7 HOXC10

8 In the context of the growing interest in understanding the complex interactions between cancer and
9 immune cells, a recent study showed HOXC10 plays a role in tumour immune evasion [156]. Indeed,
10 HOXC10 silencing in GBM cell lines decreases the expression of proteins involved in tumour
11 immunosuppression (i.e., TGFB2, PDL2, CCL2, and TDO2). *PDL2* and *TDO2* were identified as
12 direct targets of HOXC10 in these cells by ChIP-quantitative PCR [156]. Moreover, Tan et al. [168]
13 reported a significant enrichment of HOXC10-correlated genes and angiogenic gene sets in GBM
14 patients. Mechanistically, they found that HOXC10 modulates GBM angiogenesis through direct
15 regulation of *VEGFA* (ChIP-quantitative PCR and luciferase reporter assays). Moreover, they showed
16 that PRMT5 and WDR5, which regulate histone post-translational modifications, are required for
17 HOXC10-mediated *VEGFA* upregulation [168]. Thus, although bevacizumab (anti-VEGFA
18 monoclonal antibody) does not significantly improve OS in patients with GBM [186,187], it
19 significantly decreased the growth of HOXC10-overexpressing intracranial tumours in mice and
20 efficiently impaired their angiogenic capacity [168]. This suggests that HOXC10 may be a clinically
21 useful biomarker of bevacizumab response in GBM.

22 HOXD9

23 Tabuse et al. [126] performed gene microarray analysis to identify potential HOXD9 target genes in
24 GBM cell lines. *HOXD9* silencing led to upregulation of some genes known to be relevant in cancer
25 (e.g., *TRAIL*, *ANGPTL4*, and *SEMA4D*), and downregulation of others (e.g., *BRCAL*, *TGFB1*, and
26 *BCL2*). Interestingly, *BCL2* was also positively associated with another group 9 paralogue, *HOXA9*,
27 in GBM [150].

28 HOXD10

29 Finally, it has been repeatedly reported that, in GBM cell lines, HOXD10 acts by negatively
30 regulating the metastatic-related protein RHOC [173,170,171] and matrix metalloproteinases, such
31 as MMP14 [160,145,171].

1 Overall, these findings suggest that although the transcriptional target genes of the different HOX
2 proteins mostly do not overlap, they frequently lead to transcriptional programmes that regulate
3 similar molecular processes/pathways (e.g., cell cycle, death, migration/invasion, and inflammation
4 are pathways commonly affected across studies testing different HOX genes), all of which are
5 particularly relevant in the context of cancer. Moreover, it is not surprising that many of the identified
6 targets might be cell type-dependent, as several factors are known to contribute to the diversity and
7 specificity of HOX protein activity, leading to highly dynamic, context-specific HOX transcriptional
8 activation, and to their functional diversification. Indeed, it was described that i) there are many
9 transcriptional partners – HOX cofactors and collaborators – that also present cell type-specific
10 expression patterns [188,189]; ii) the binding between HOX proteins and their cofactors might be
11 context-dependent [190], and different combinations may lead to distinct binding specificities,
12 contributing to the spatiotemporal specificity of HOX proteins; and iii) chromatin accessibility and
13 DNA shape, which may vary between cells, also showed to confer HOX specificity [191].
14 Bioinformatic studies are needed to cross the thousands of genes and dozens of pathways
15 differentially regulated by each of the 39 HOX proteins in glioma, to better integrate the data. More
16 studies are also needed to identify HOX targets in particular glioma cells of the various tumour niches
17 (e.g., in glioma stem cells versus more differentiated glioma cells; and proliferating versus invading
18 cells), which may be relevant for the design of new therapeutic interventions.

19 **4.6. Clinical implications of HOX genes**

20 In 2008, Murat et al. [124] suggested that a HOX-dominated gene signature, which included *HOXA2*,
21 *A3*, *A5*, *A7*, *A9*, *A10*, *C6*, *D4*, *D8*, and *D10*, was an independent predictive factor of therapy resistance
22 in GBM. In 2010, Costa et al. [122] showed that *HOXA1*, *A2*, *A3*, *A4*, *A5*, *A7*, *A9*, *B7*, and *C6* are
23 overexpressed in GBM compared with non-tumour brain samples, and found that *HOXA9* expression
24 was associated with poor prognosis, independently of other well-known prognostic factors [122].
25 Indeed, in patients with *MGMT* promoter methylation (associated with better prognosis), *HOXA9*
26 could still identify a subset of patients with poor prognosis [122]. Moreover, the combination of
27 *HOXA9* and *HOXA10* expression was also associated with shorter OS in paediatric patients with GBM
28 [123]. More recently, the prognostic value of *HOXA9* in GBM was consolidated in additional patient
29 cohorts [150]. Although the DNA methylation levels of *HOXA3*, *A9*, and *A10* positively correlate
30 with WHO grading, *HOXA9* and *HOXA10* DNA methylation has been associated with better
31 prognosis in patients with GBM [177]. Conversely, *HOXD8*, *D13*, and *C4* hypermethylation was
32 observed in short-term (<1 year OS) GBM survivors [192]. Additionally, *HOXA5*, *A10*, *A13*, *B9*, *C4*,
33 *C6*, *C9*, *C10*, and *D4* were individually associated with shorter OS in patients with GBM

1 [149,146,153,157,156,124,165,154,158,162]. Among them, *HOXB9* and *HOXD4* are also associated
2 with shorter OS in patients with glioma, grade II glioma (*HOXD4* only), and grade III glioma
3 [153,158]. In line with their tumour suppressive functions in GBM, *HOXA11* and *HOXB1* were
4 individually associated with longer OS in patients with GBM [159,147].

5 In the future, these very interesting results should be updated and put into perspective in the light of
6 the new 2016 WHO classification of gliomas that includes molecular features to differentiate glioma
7 subtypes. Moreover, the validation of the prognostic value of HOX genes in several independent,
8 large, and robust datasets, preferably using more robust multivariable statistical analysis, will be of
9 paramount importance to potentially bring HOX genes into the clinics.

10 Recently, drugs interfering with the PRC2 complex emerged as promising agents for cancer
11 treatment, as the FDA recently-approved drug Tazemetostat for epithelioid sarcoma. While the
12 overall benefit in other tumour types remains to be determined, it is important to consider that PRC2
13 inhibitors might lead to decreased H3K27me3 at HOX loci, potentially leading to their over-
14 activation. Nonetheless, Khan et al. [193] recently demonstrated that, in opposition to the classical
15 view that PRC2 is the major transcriptional repressive complex of HOX genes, the knockdown of
16 some PRC2 subunits, such as SUZ12, EZH2, or EED, in mouse F9 teratocarcinoma cells, globally
17 decreased H3K27me3 levels, but not in HOX clusters, where curiously H3K27me3 increased instead.
18 Indeed, although decreased enrichment of the PRC2 complexes was observed at HOX loci upon
19 SUZ12, EZH2, or EED silencing, the expression of HOX genes did not increase [193]. MTF2 was
20 pointed as the potential responsible molecule for H3K27me3 enrichment in HOX loci in the absence
21 of PRC2 [193]. Whether a similar effect and underlying mechanism is more generally observed in
22 cancer, including in GBM, remains to be investigated. Additionally, Li et al. [194] described that
23 AC1Q3QWB (AQB), a small-molecule compound, is a selective disruptor of *HOTAIR*-*EZH2*
24 interactions, blocking PRC2 recruitment to target genes, presenting a pre-clinical potential worth of
25 further evaluation for the treatment of GBM and breast cancers with high levels of *EZH2* and
26 *HOTAIR*. Indeed, AQB administration to orthotopic mice models of GBM and breast cancer
27 significantly decreased tumour aggressiveness. *In vitro* and *in vivo*, AQB treatment resulted in
28 increased *HOXD10* expression, among other PRC2 target genes. Further experiments in orthotopic
29 mice models of a breast cancer and a GBM patient-derived xenograft (PDX) demonstrated that the
30 combinatorial treatment of AQB with an indirect inhibitor of EZH2 (DZNep) significantly reduced
31 tumour growth and increased mice OS, respectively. However, besides the unknown role of *HOXD10*
32 in GBM, and whether it acts as a tumour suppressor or an oncogene, the complete transcriptional
33 profile of HOX genes before and after treatment with these PRC2-targeting compounds remains

1 unknown. Moreover, drugs like DZNep are now recognized as global histone methylation inhibitors,
2 rather than a H3K27-specific one [195]. These studies emphasize that, in the context of precision
3 medicine, the global identification of the transcriptional signatures of a specific cancer patient should
4 be considered to aim in the decision for particular targeted therapies, as the uninformed use of these
5 agents may lead to pro-tumour effects that will harm a subset of patients.

6 **5. Conclusions and future perspectives**

7 Deregulation of HOX genes is a common phenomenon in malignant primary brain tumours, and most
8 findings reported to date associate HOX gene overexpression with oncogenic functions in glioma.
9 These include critical cancer hallmarks, such as increased cell viability, invasion, migration,
10 angiogenesis, stem cell capacity, and therapy resistance, and decreased cell death/apoptosis
11 (summarized in Fig. 4). Of note, all these studies have not explored the potential role of HOX genes
12 in influencing interactions between cancer cells and those of the tumour microenvironment.
13 Interestingly, Bertolini et al (2019) reported that GBM neurospheres influence non-neoplastic cells
14 from their microenvironment by delivering HOXA7 and HOXA10 via large oncosomes. This large
15 oncosomes, which were abundantly found in the serum of patients with shorter OS, are able to
16 reprogram recipient cells to proliferate, grow as spheres and to migrate. It should also be interesting
17 to investigate how HOX genes may influence tumour immune responses, both in treatment-naïve
18 contexts and under treatment, particularly with immunotherapies. Interestingly, Pojo et al. [150]
19 showed that *HOXA9* downregulates genes involved in antigen processing/presentation in various
20 human GBM [150]. Moreover, Li et al. [156] found that HOXC10 positively regulates genes involved
21 in tumour immunosuppression in GBM, including *PDL2* and *TDO2*. Together with recent reports in
22 ovarian cancer linking HOXA9 to an M2 macrophage tumour-promoting phenotype and reduction of
23 CD8⁺ lymphocyte infiltration [196], these findings strengthen the idea that HOX genes may play an
24 important role in the regulation of the immune system in the tumour microenvironment.

25 Considering the critical functional roles and putative prognostic value of specific HOX genes in
26 cancer, including in malignant glioma, and their complex molecular interactions with upstream
27 regulators and downstream targets, it becomes clear that additional studies are necessary to better
28 understand how HOX operate in glioma, and whether they may be therapeutically explored in the
29 clinics. For example, future studies will be critical to identify the whole molecular networks
30 interacting with HOX genes in brain tumours, by generating genome-wide binding profiles to identify
31 their targets, their upstream binding factors (including lncRNA and miRNAs), and protein partners,
32 as well as HOX-specific DNA methylation studies to explore both transcription factor-related and –
33 independent HOX functions. These integrated approaches will broaden our understanding of HOX

1 roles in normal and abnormal development and malignant transformation, may allow the
2 identification of potentially targetable players suitable for therapeutic intervention, and/or to the
3 development of clinically useful diagnostic/prognostic tools in a paradigm of precision medicine. In
4 addition, it is still unclear whether HOX genes have causative roles in gliomagenesis, or whether their
5 alterations are a bystander consequence of malignant transformation, as well as whether HOX-
6 directed therapies may be useful for the treatment of glioma and other HOX-driven cancers (e.g.,
7 acute myeloid leukaemia). These open questions will continue to feed the researchers' interest for
8 many years.

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1 **Figure legends**

2 **Fig. 1**

3 **HOX expression patterns in the hindbrain and spinal cord**

4 **(a)** HOX genes are composed by only two exons and one intron. The homeobox sequence, which
5 encodes a 61-amino-acid peptide motif (the homeodomain) with a distinctive helix-loop-helix-turn-
6 helix structure, is within the second exon. **(b)** A colour code indicates the relative area of expression
7 of each HOX gene along the anterior-posterior axis in the developing CNS. The left panel illustrate
8 the rhombomere (r)-specific nested patterns of expression of the Hox1-Hox5 paralogues in the
9 hindbrain. Higher colour intensity indicates higher expression. Positions of motor neuron pools are
10 shown within their rhombomere(s) of origin (Trigem.: Trigeminal; Gl.: Glossopharyngeal). In the
11 spinal cord (right panel), the overlapping Hox4-Hox11 gene expression pattern is shown in relation
12 with the motor neuron columnar organization. MMC: Medial motor column; PMC: Phrenic motor
13 column; LMC: Lateral motor column; PGC: preganglionic motor column; HMC: hypaxial motor
14 column.

15

16 **Fig. 2**

17 **Topological architecture at the HOXD cluster.** The HOXD cluster is localized at the boundary of
18 two adjacent topological associated domains (TAD) that each includes an enhancer-enriched gene-
19 desert area. Consequently, the 3' and 5' HOXD genes are controlled by distinct sets of remote
20 enhancers during development. Cen., centromere; Tel., telomere.

21

22 **Fig. 3**

23 **H3K27me3- and H3K4me3-marked domains demarcate silent and expressed HOX genes**

24 Encode-derived ChIP-seq and RNA-seq data show H3K27me3 and H3K4me3 distribution and Hoxa
25 gene expression in mouse A) ES cells, B) embryonic kidney and C) forebrain. In ES cells and
26 forebrain, where all Hoxa genes are repressed, H3K27me3 covered the whole cluster. It may be
27 associated with H3K4me3 at promoter regions, constituting bivalent domains. In embryonic kidney,
28 two H3K4me3- and H3K27me3-marked domains delineate expressed and repressed genes along the
29 cluster.

30

31

32

1 **Fig. 4**

2 **Summary of the main functional roles of HOX genes in glioblastoma and their clinical**
3 **prognostic value.**

4 HOX genes display various critical functional roles in GBM (regulation of cell viability, invasion,
5 migration, apoptosis, cell cycle, colony formation, angiogenesis, resistance to temozolomide and to
6 radiotherapy, and stem cell capacity) that are globally associated with malignancy *in vitro* and *in vivo*.
7 Importantly, some HOX genes have prognostic value in GBM, with putative clinical relevance. Red
8 and blue colours in the heatmap indicate increased and decreased effects, respectively, upon
9 expression of the corresponding HOX gene. Grey colour indicates unknown effects. Empty cells
10 represent absence of the respective paralogue in that cluster. OS, overall survival; TMZ,
11 temozolomide.

12

Figure 1

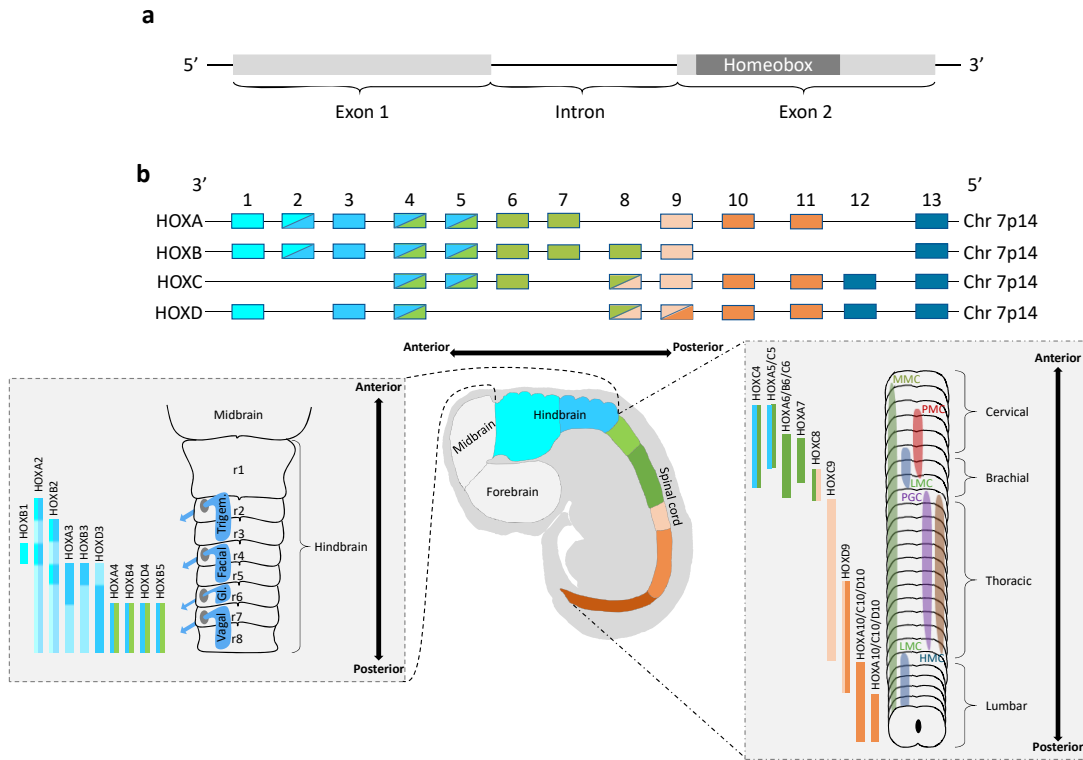


Figure 2

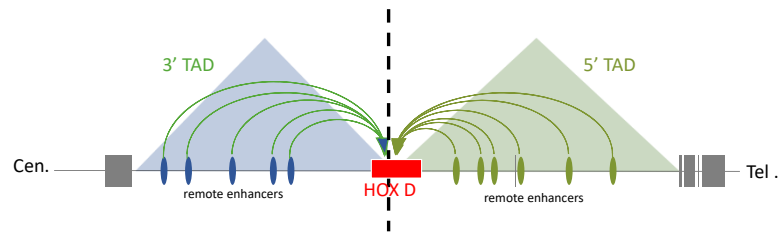


Figure 3

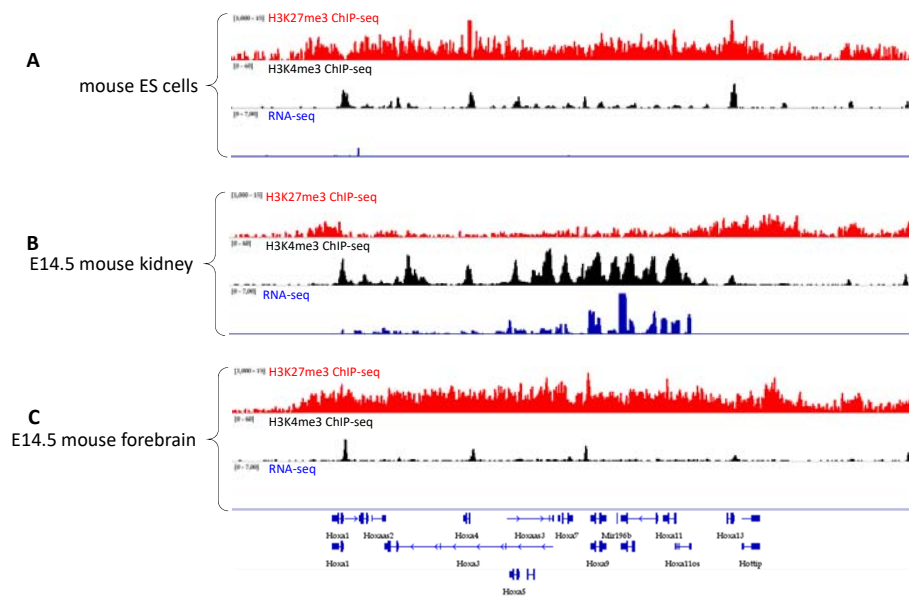


Figure 4

