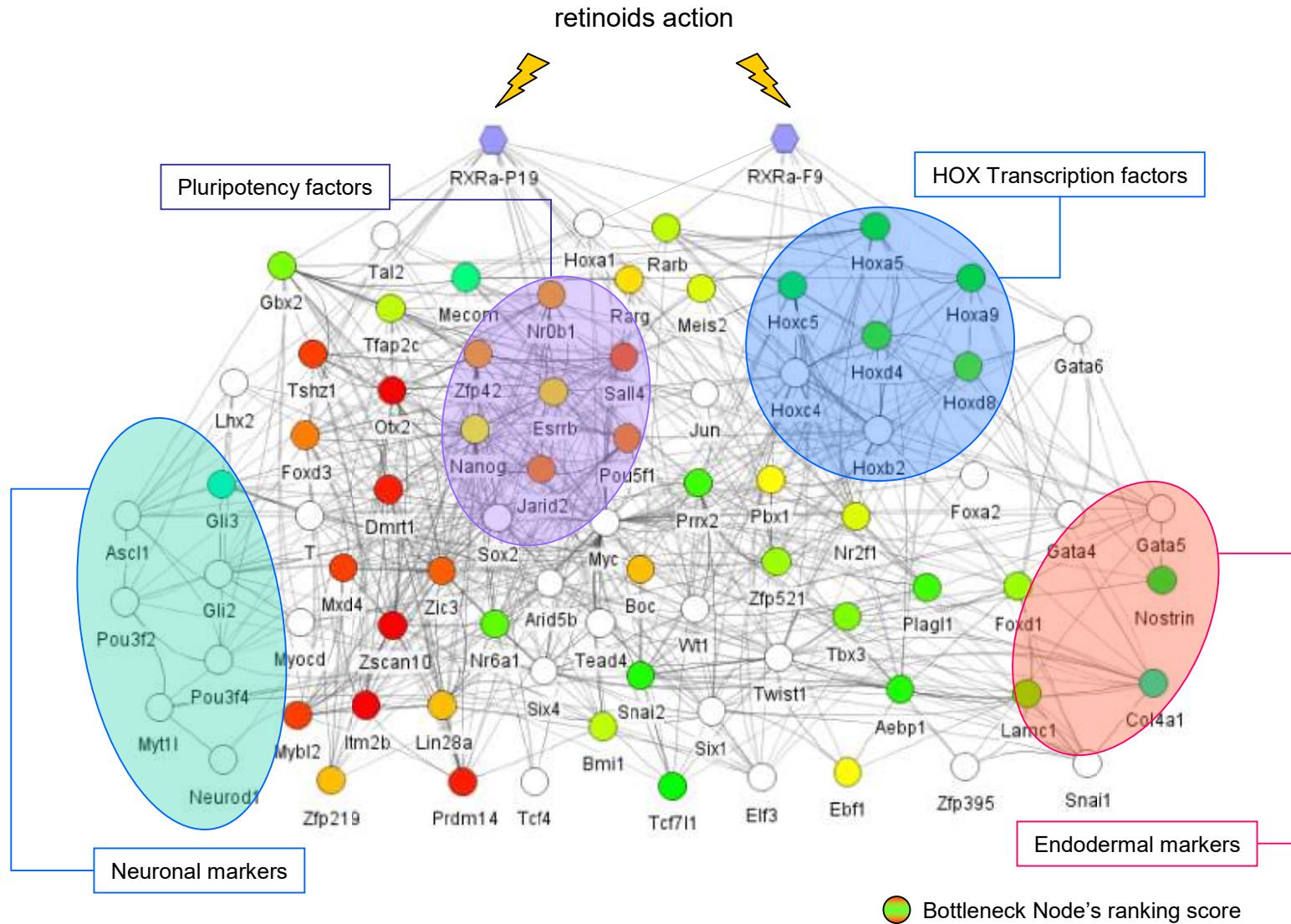


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

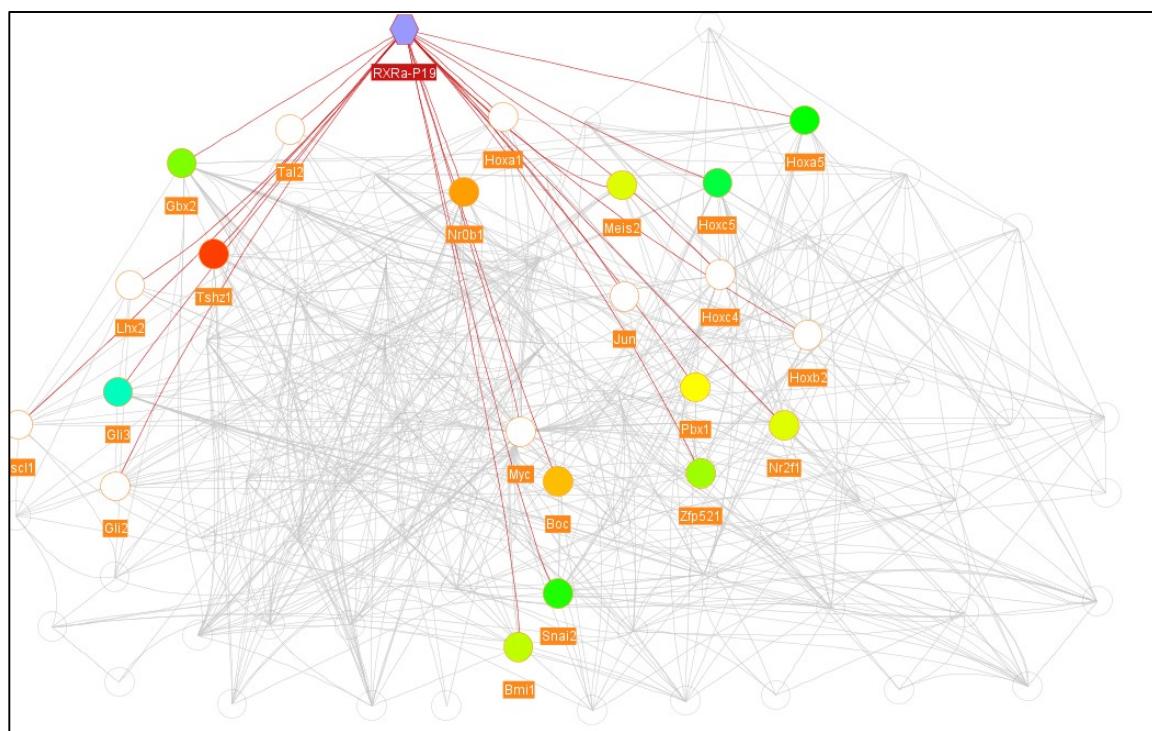


The reduced GRN comprising 80 nodes and 626 edges was reconstructed by applying topological ranking to identify key connector nodes (bottleneck node's ranking score; displayed as heatmap). Four major sub-networks associated with cell pluripotency, HOX factors and neuronal or endodermal cell fate markers are highlighted. A detailed view of the connectivity between these major sub-networks is provided below.

**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

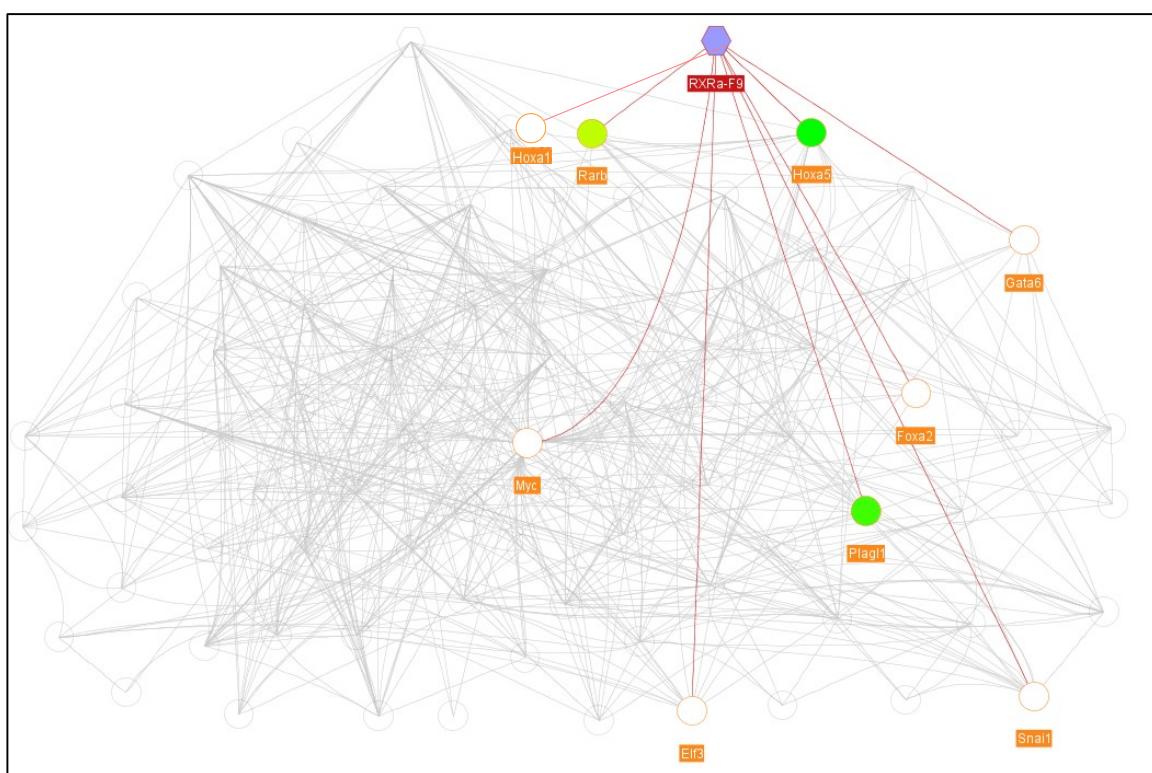
A

**RXR $\alpha$ -P19**



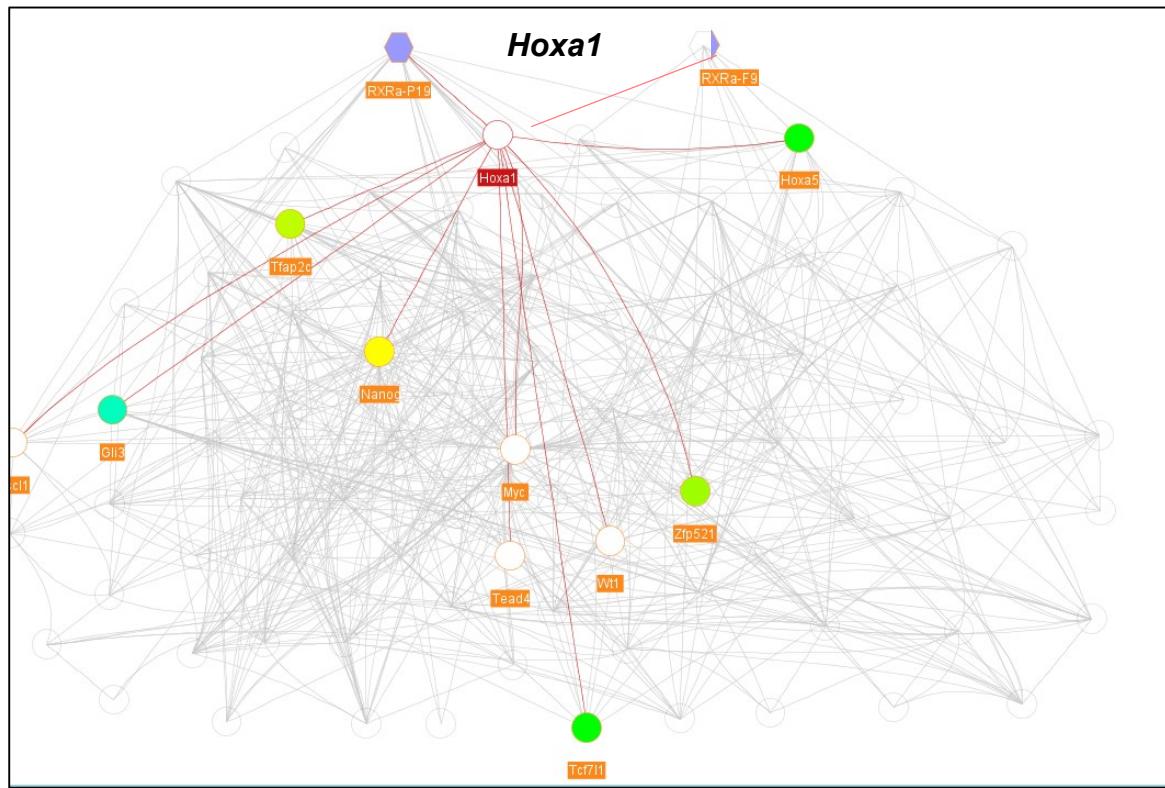
B

**RXR $\alpha$ -F9**

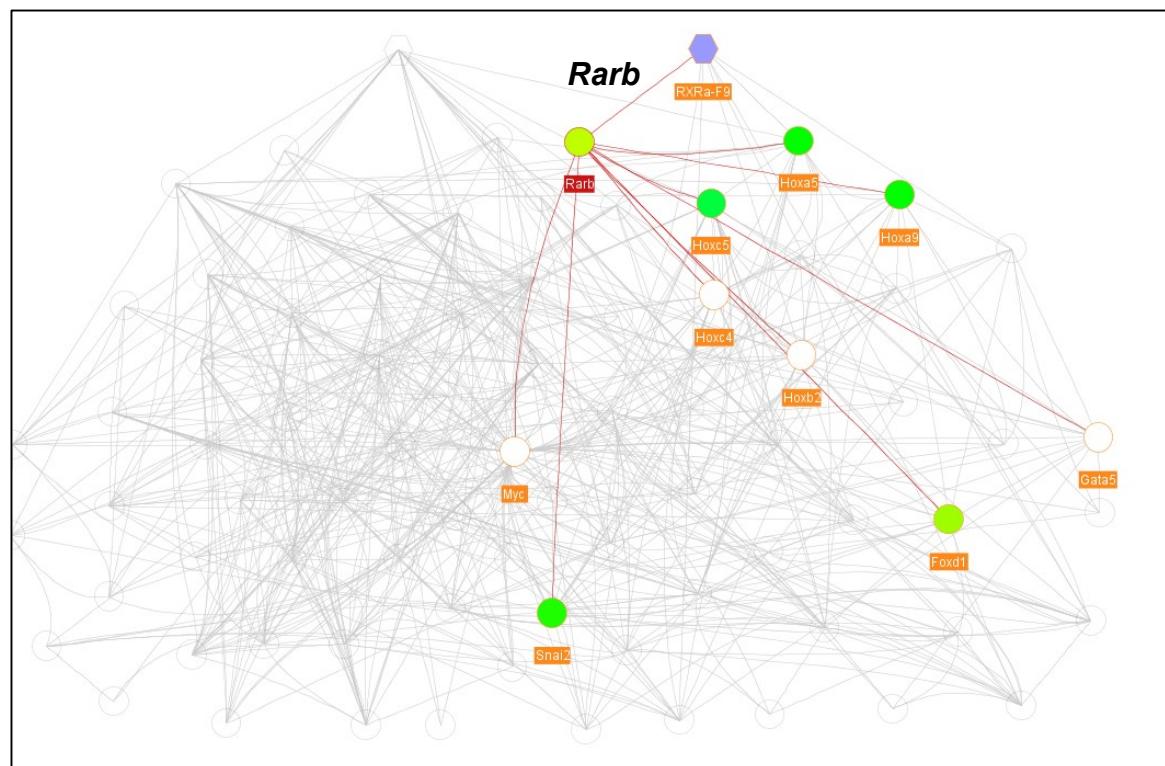


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

C

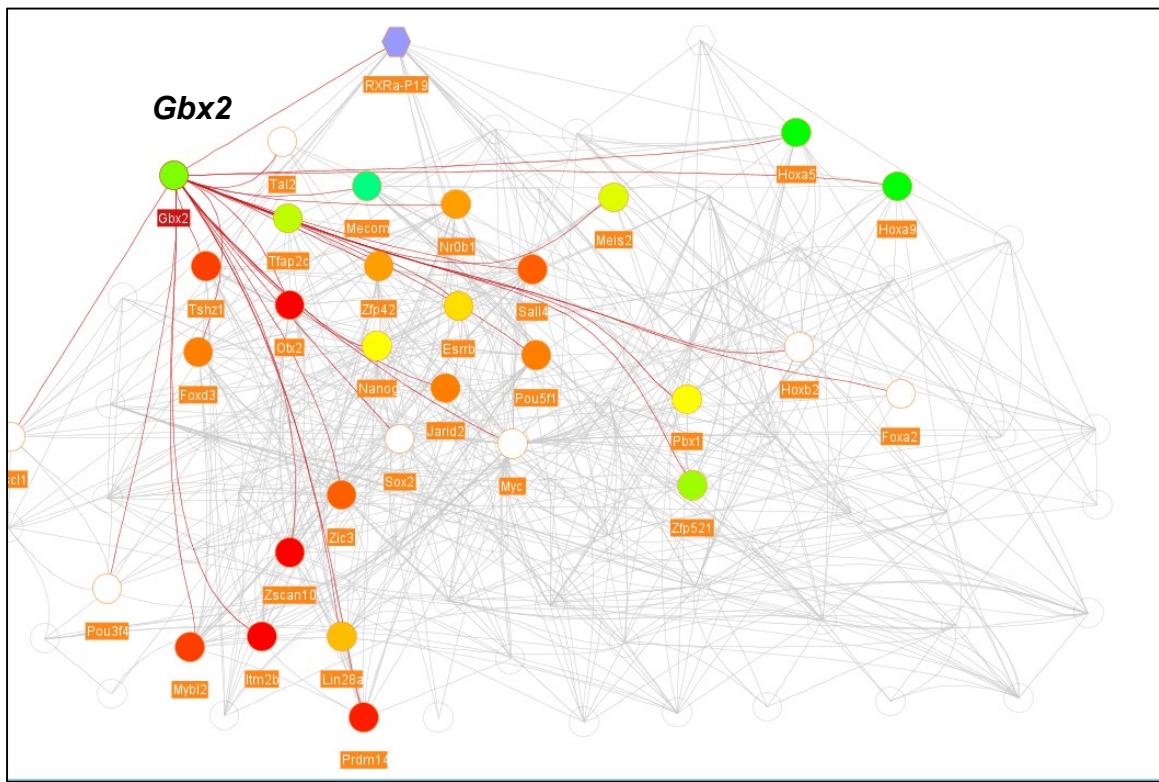


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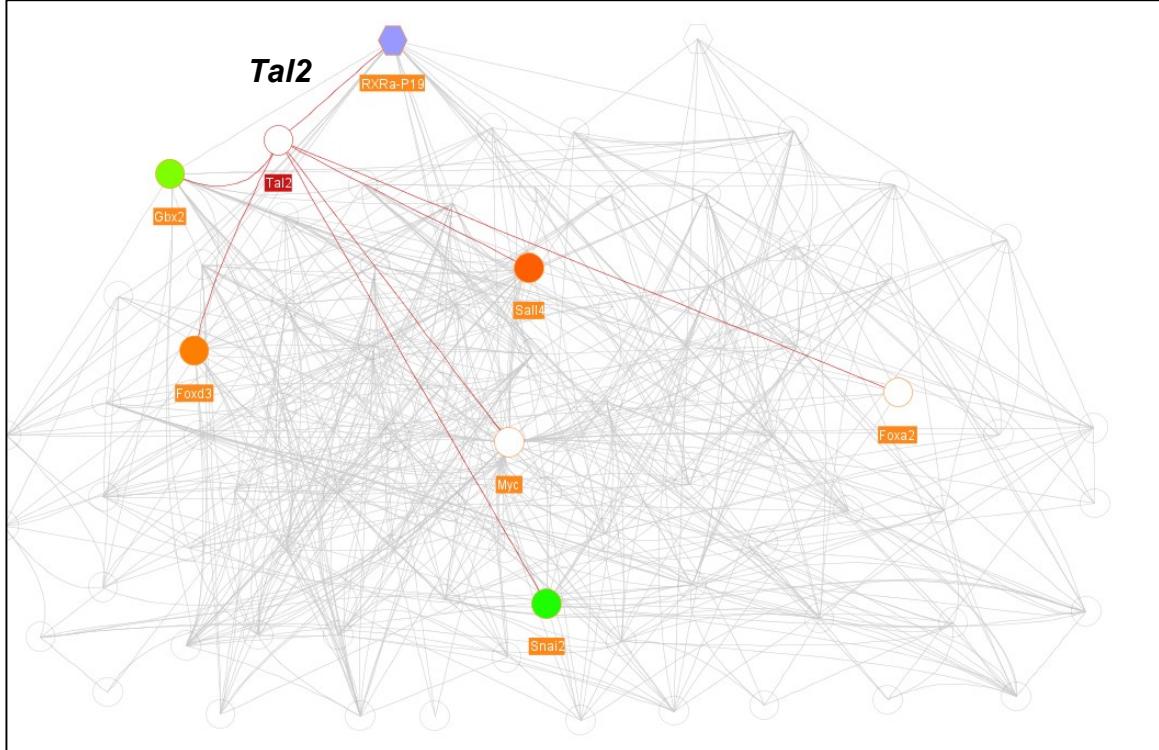


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

E

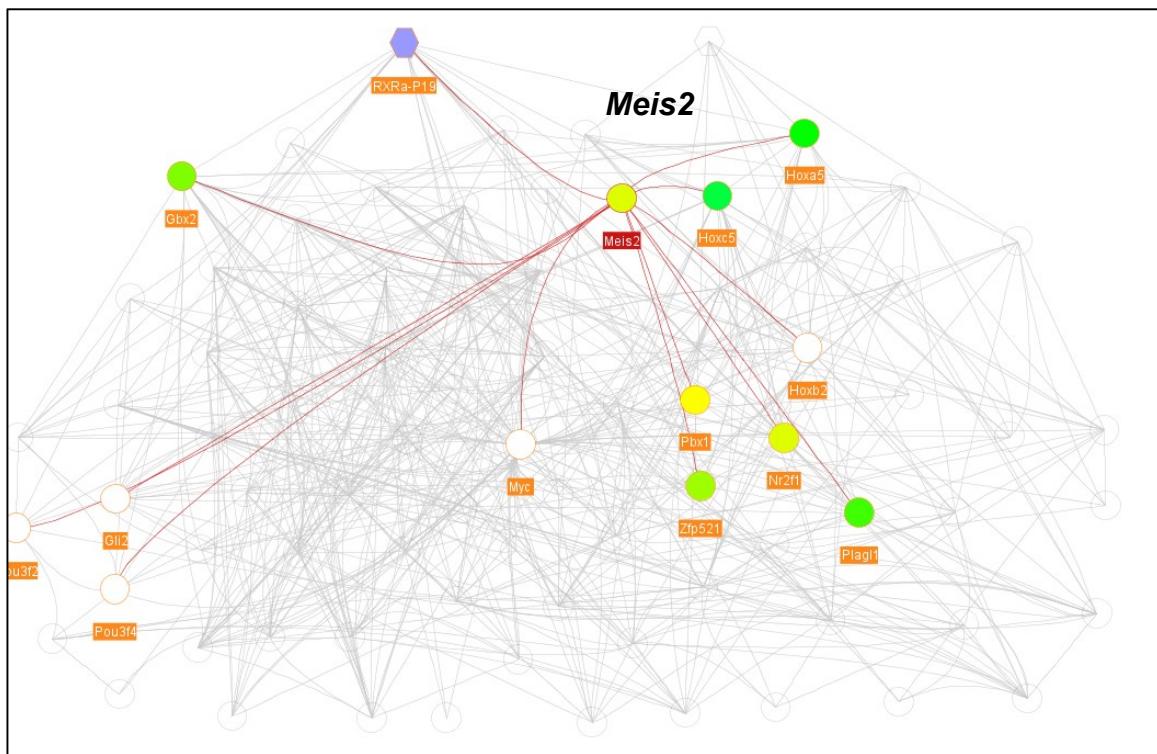


F

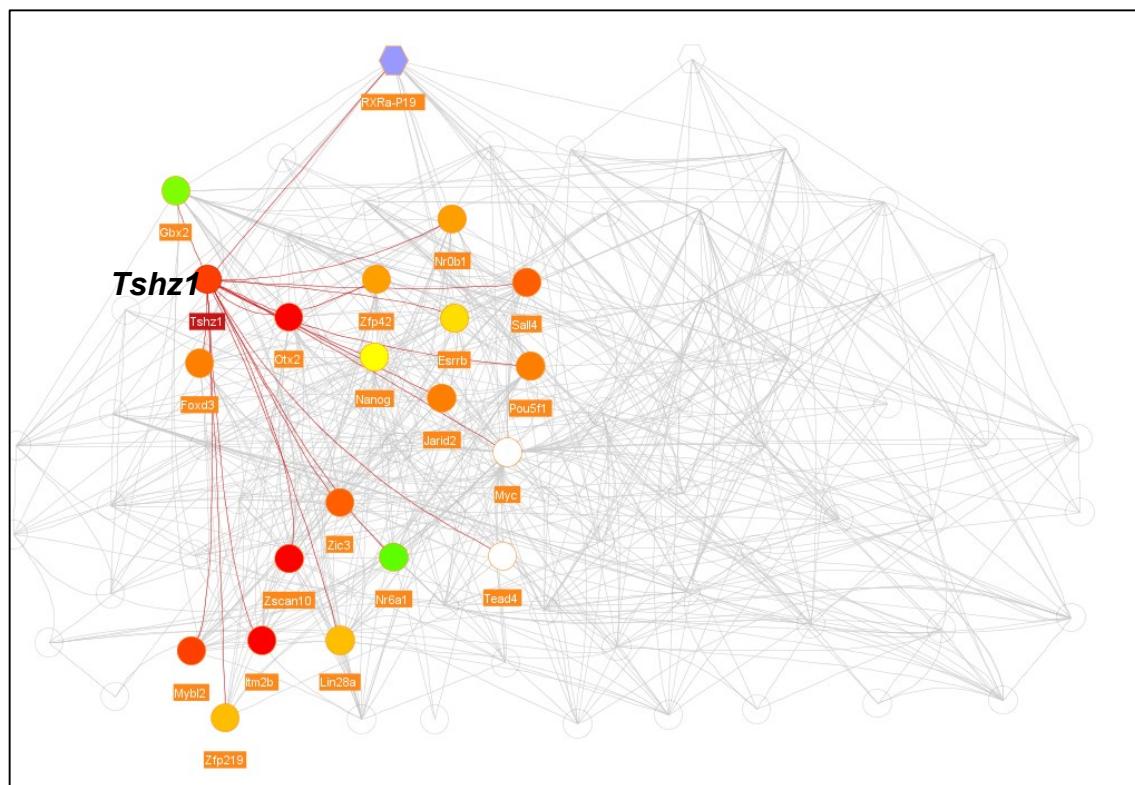


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

**G**

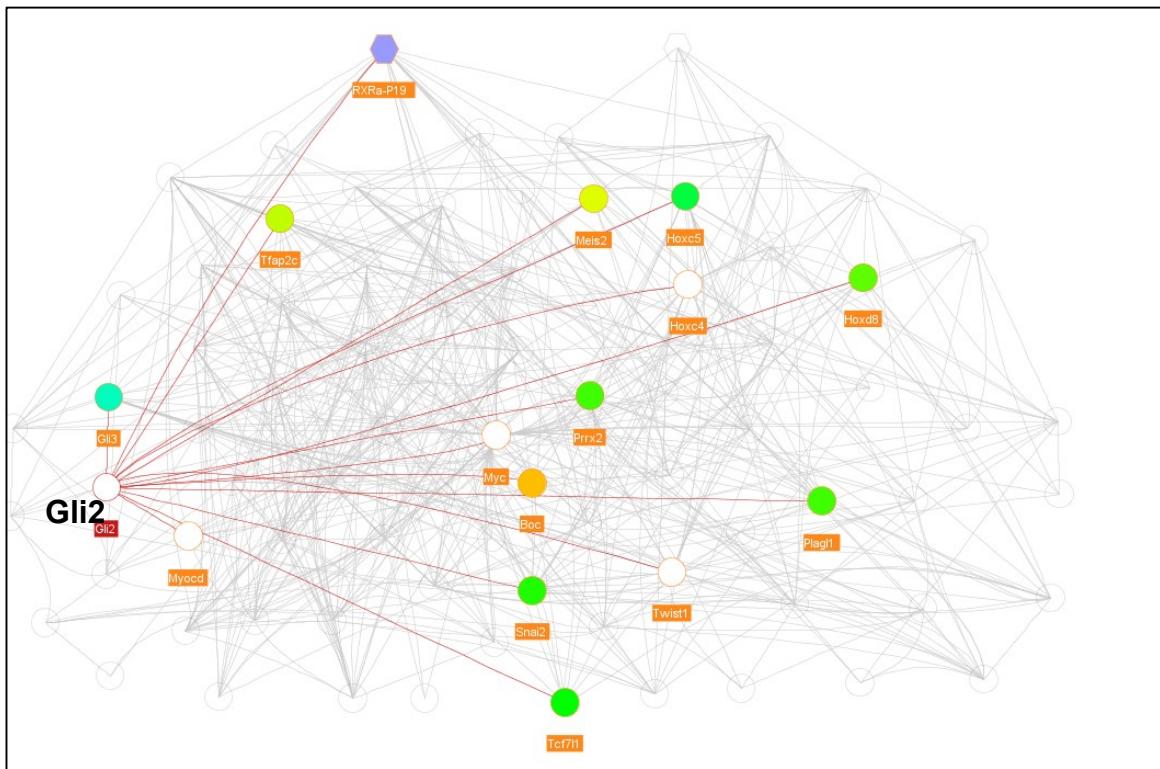


**H**

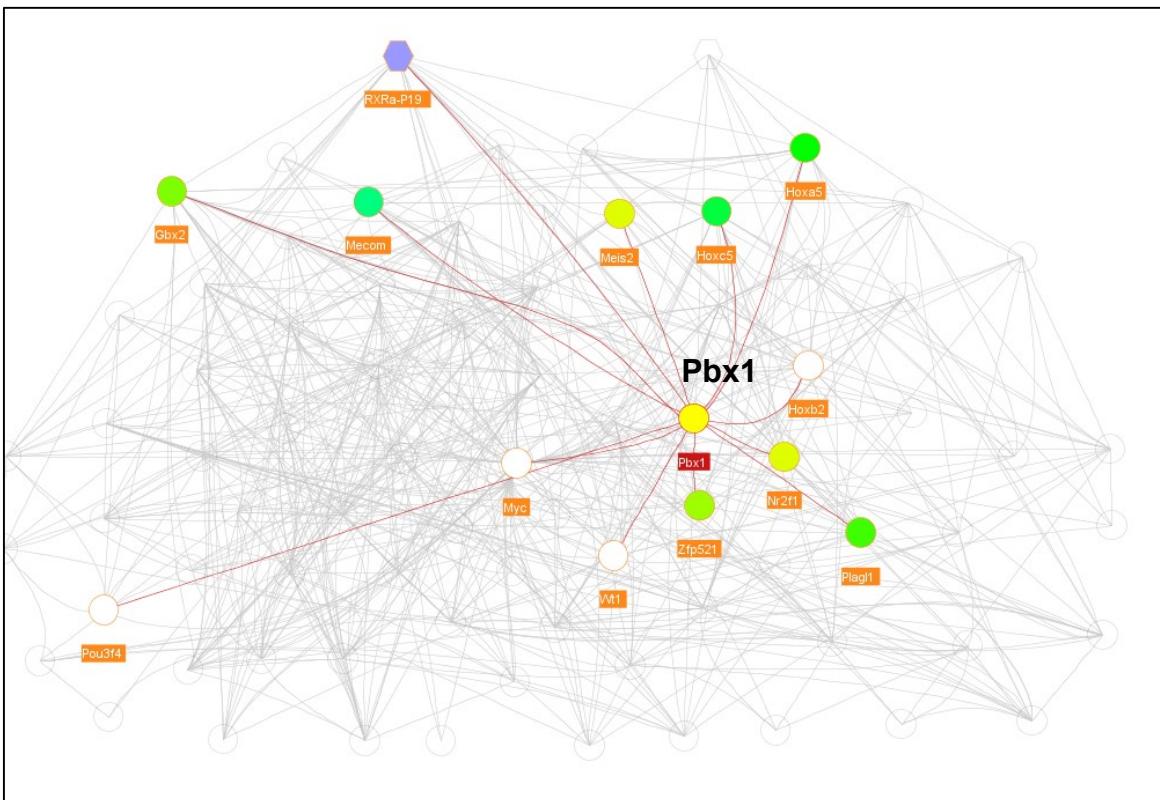


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

I

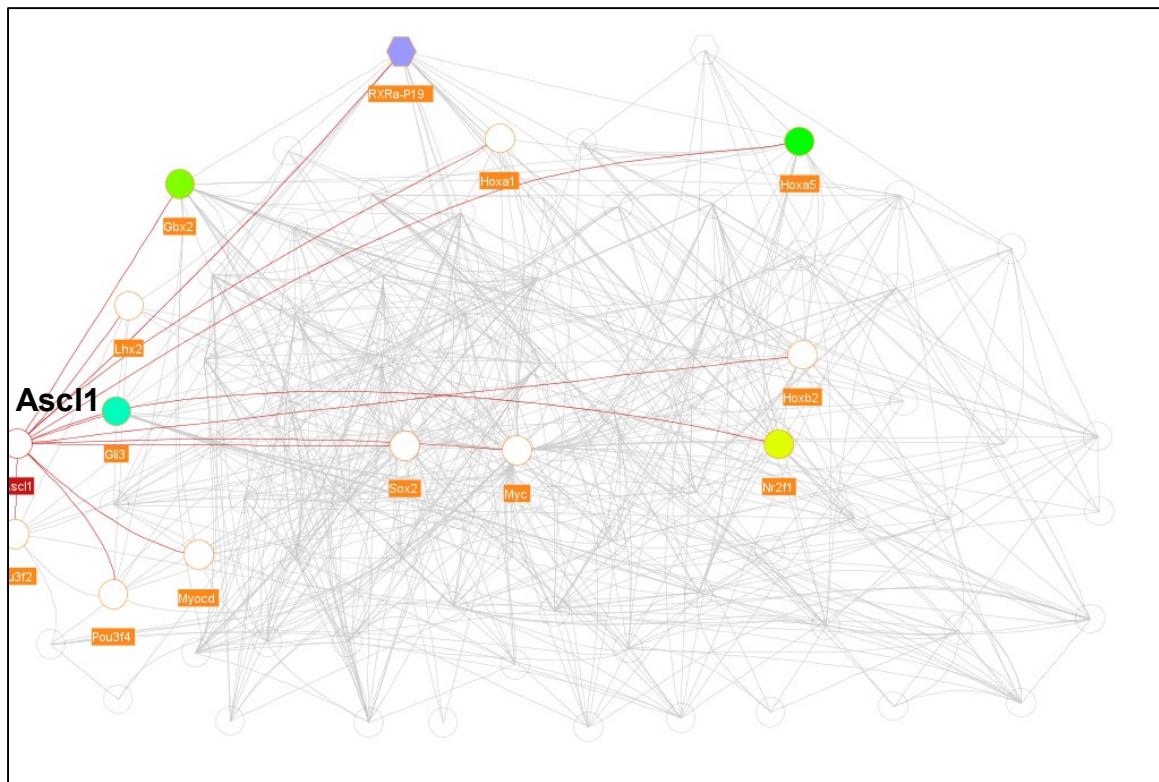


J

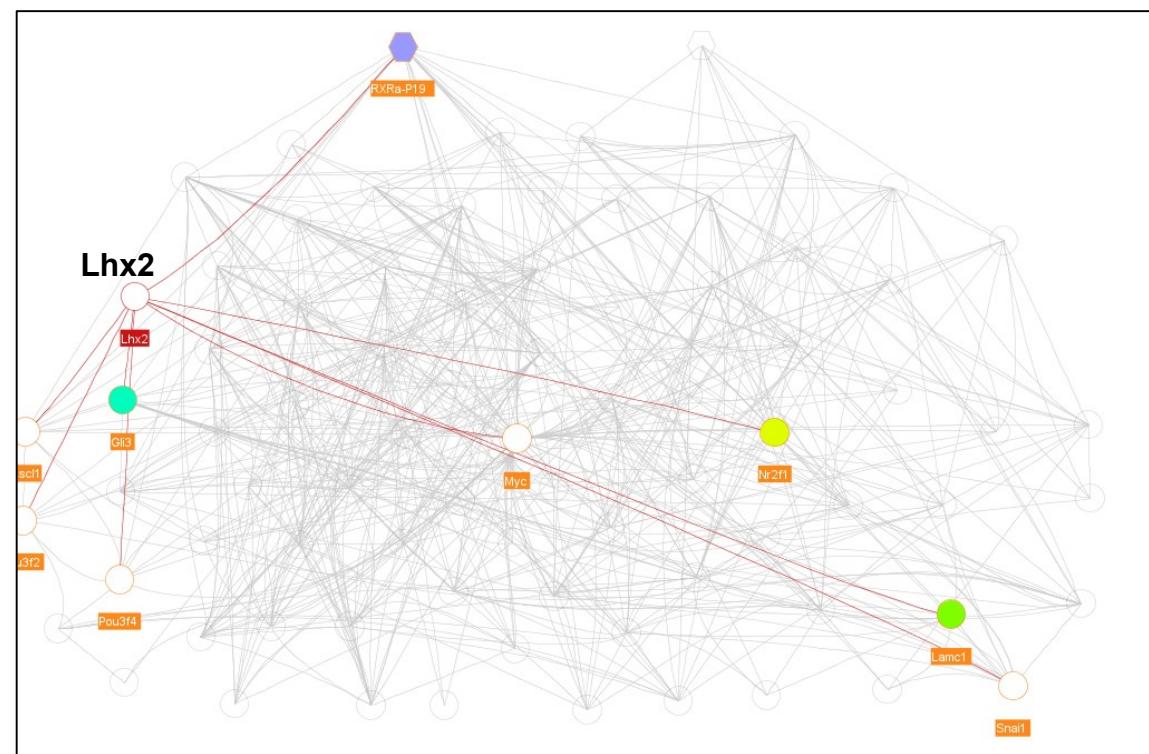


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

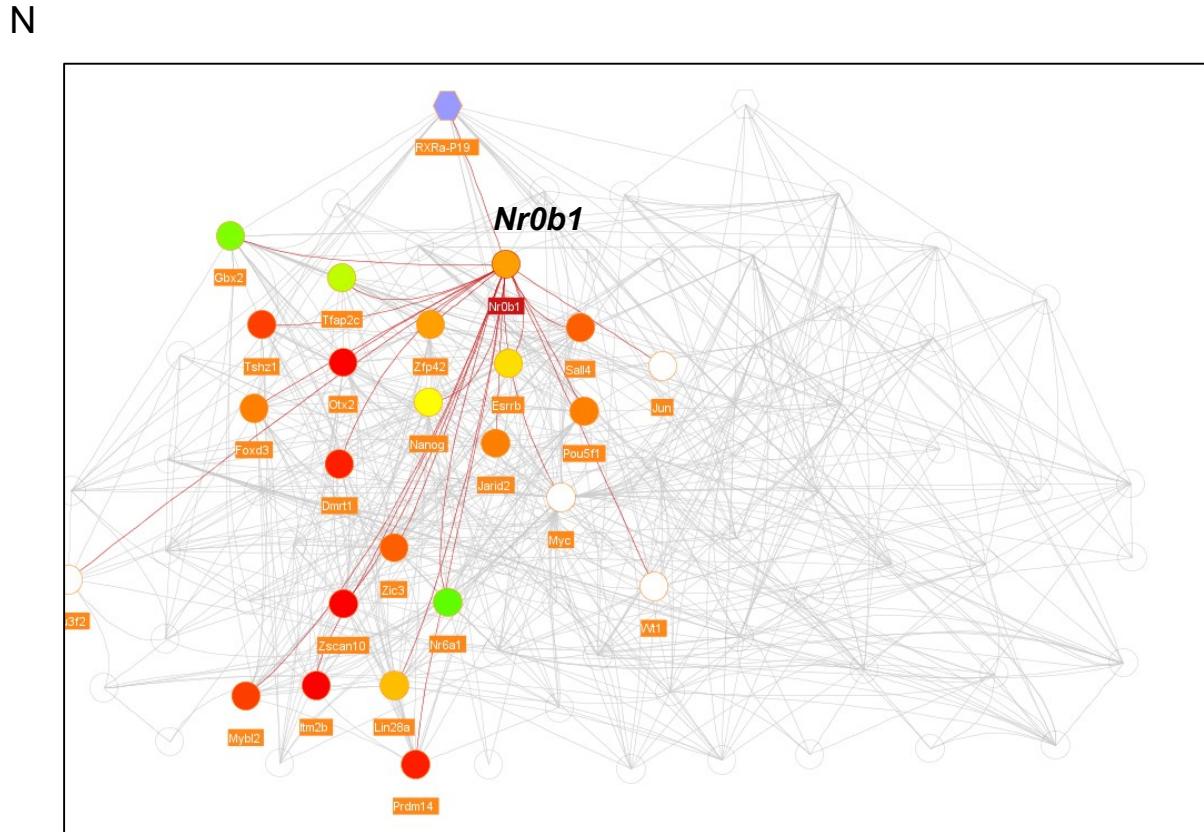
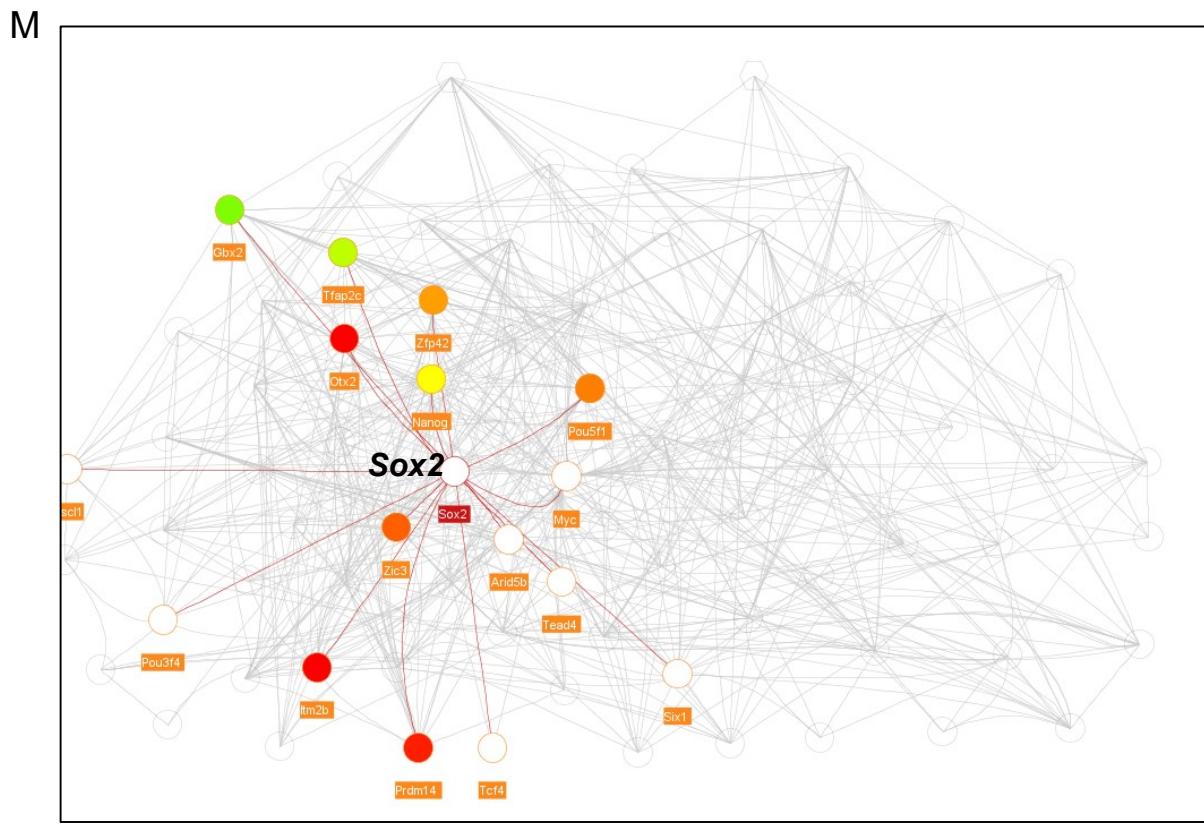
K



L

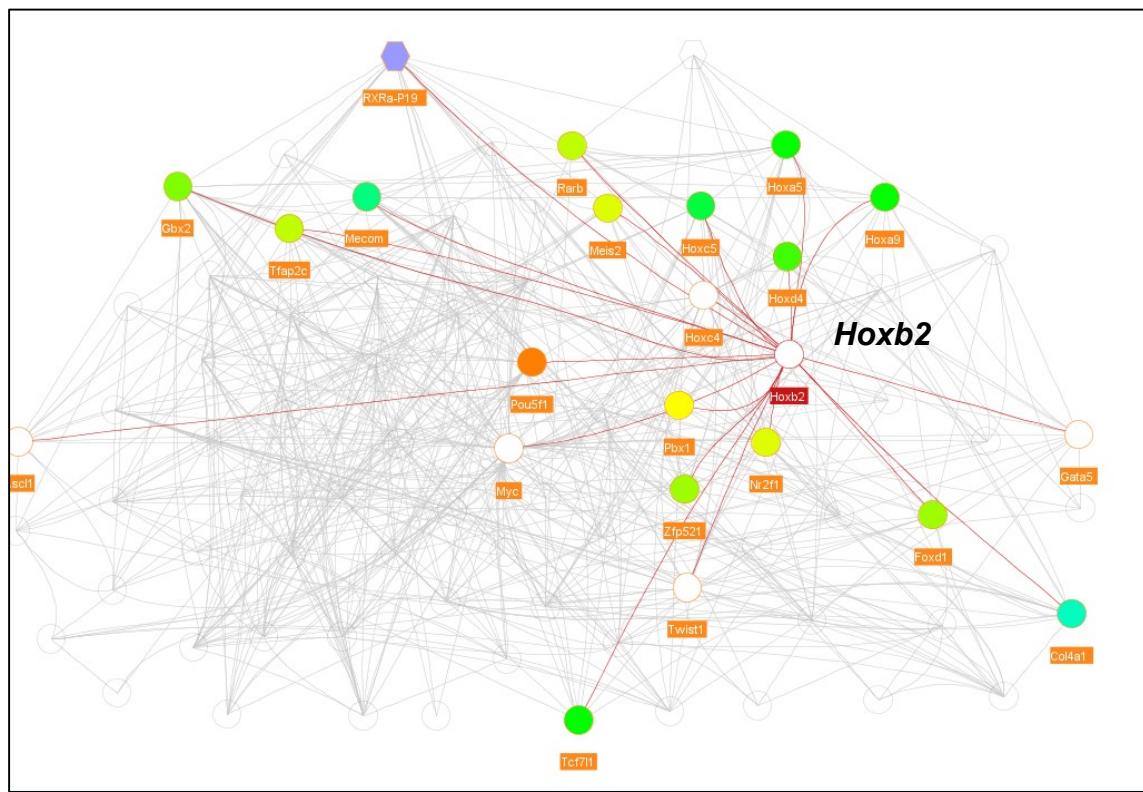


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

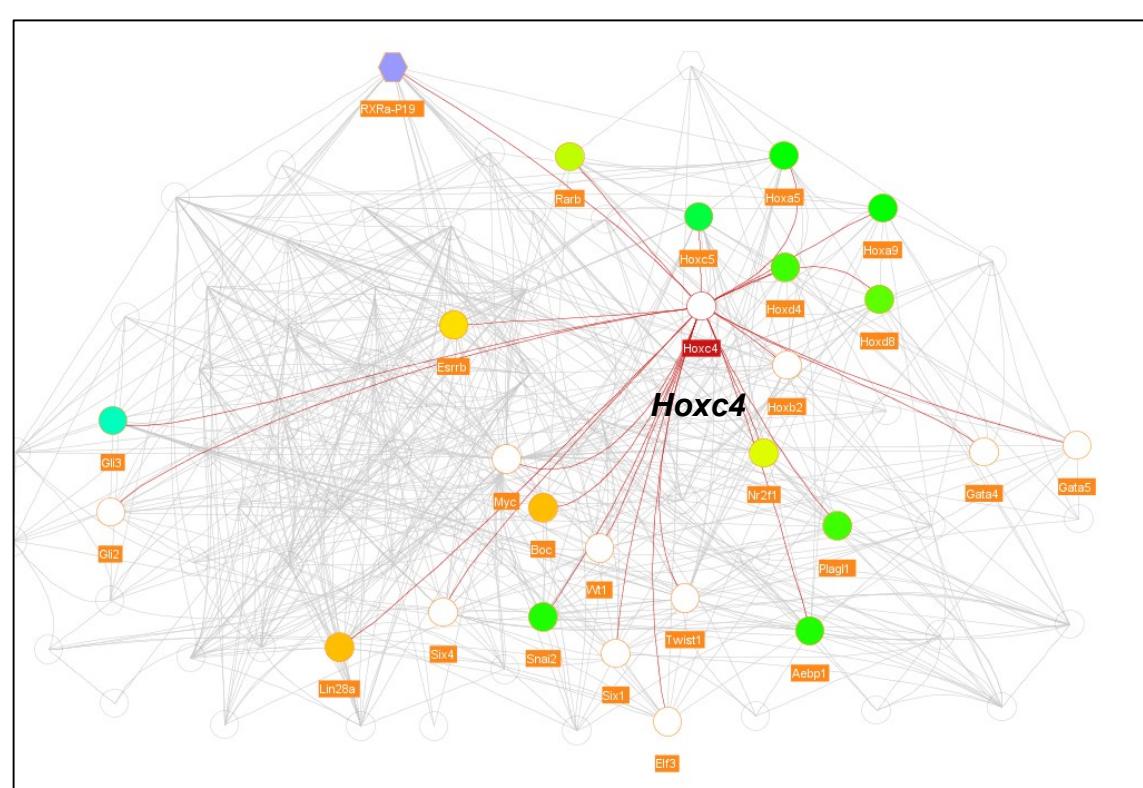


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

0

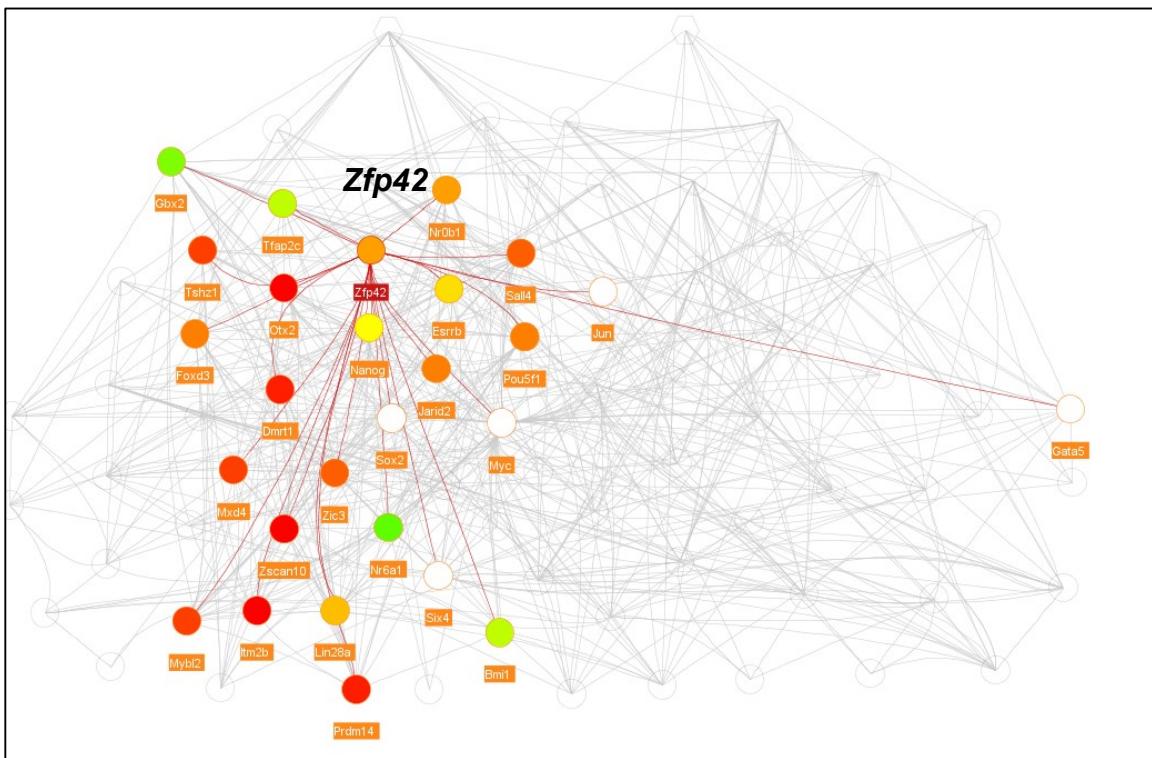


P

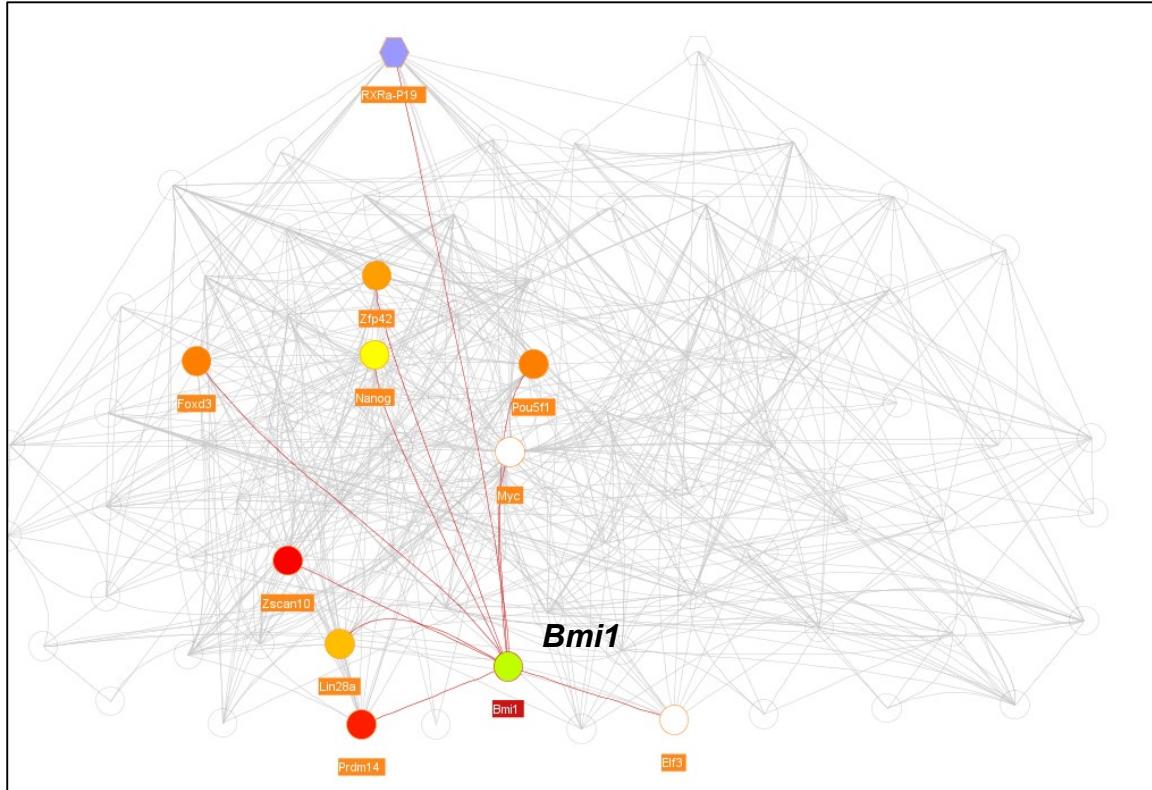


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

Q

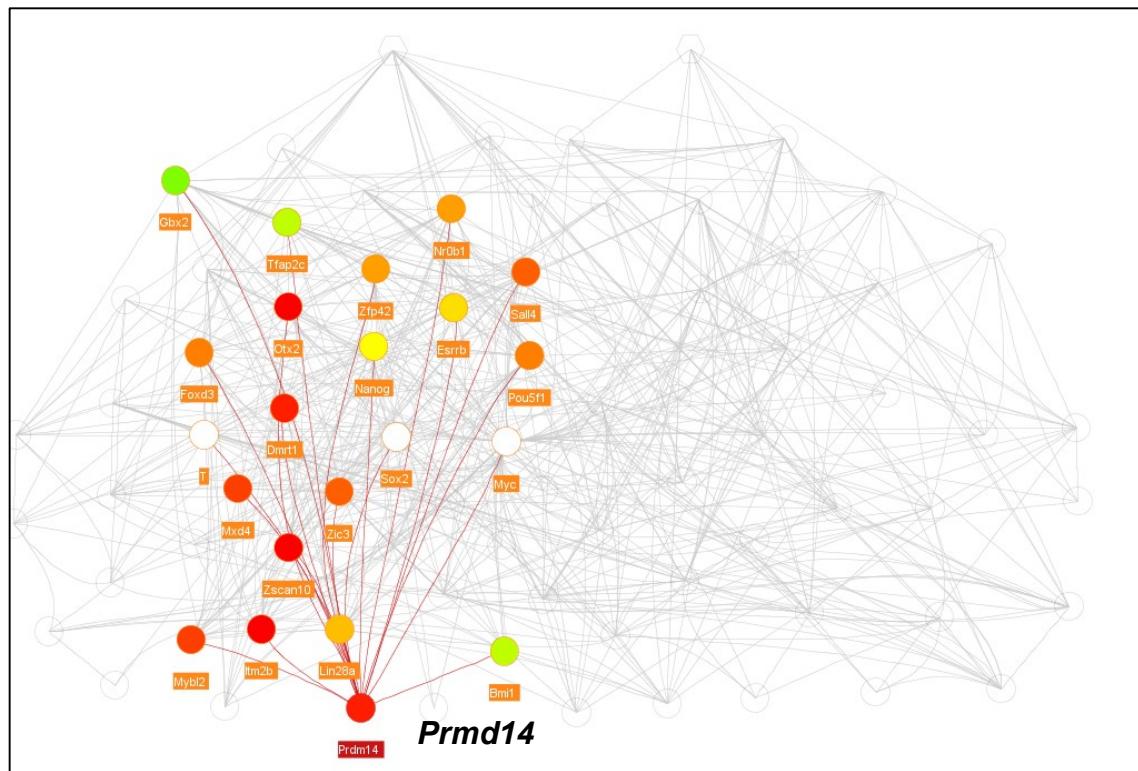


R

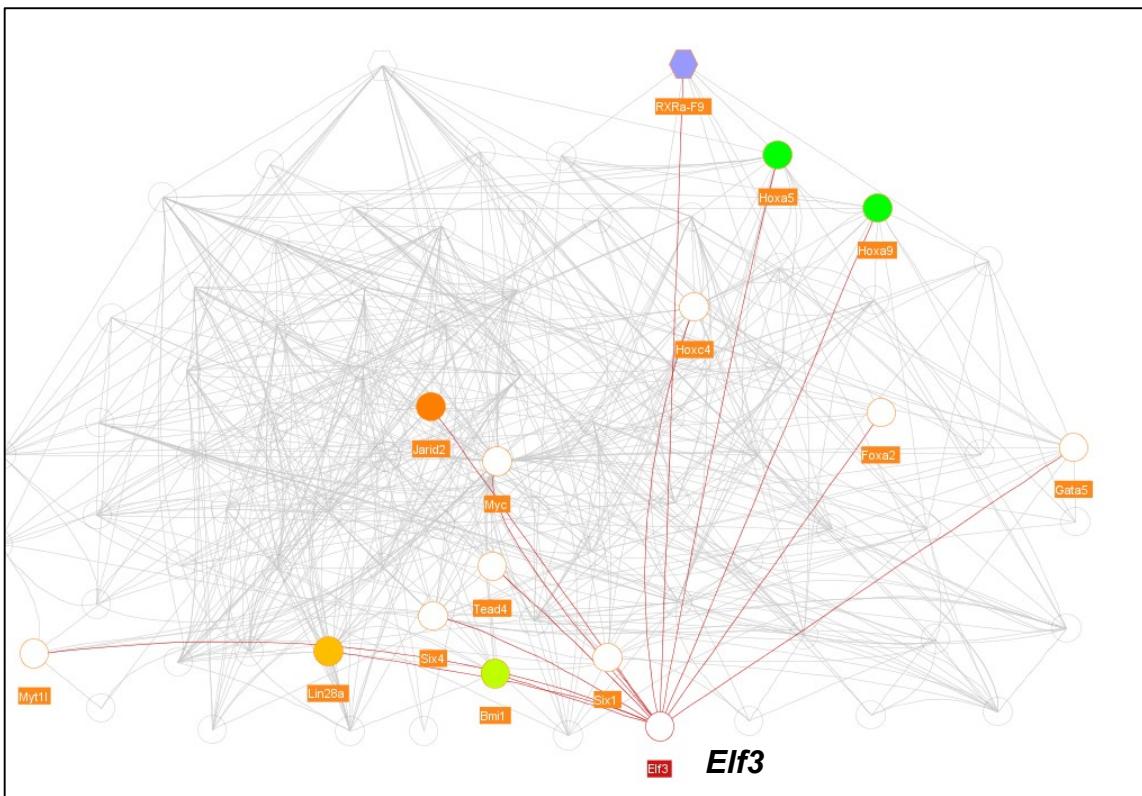


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

S

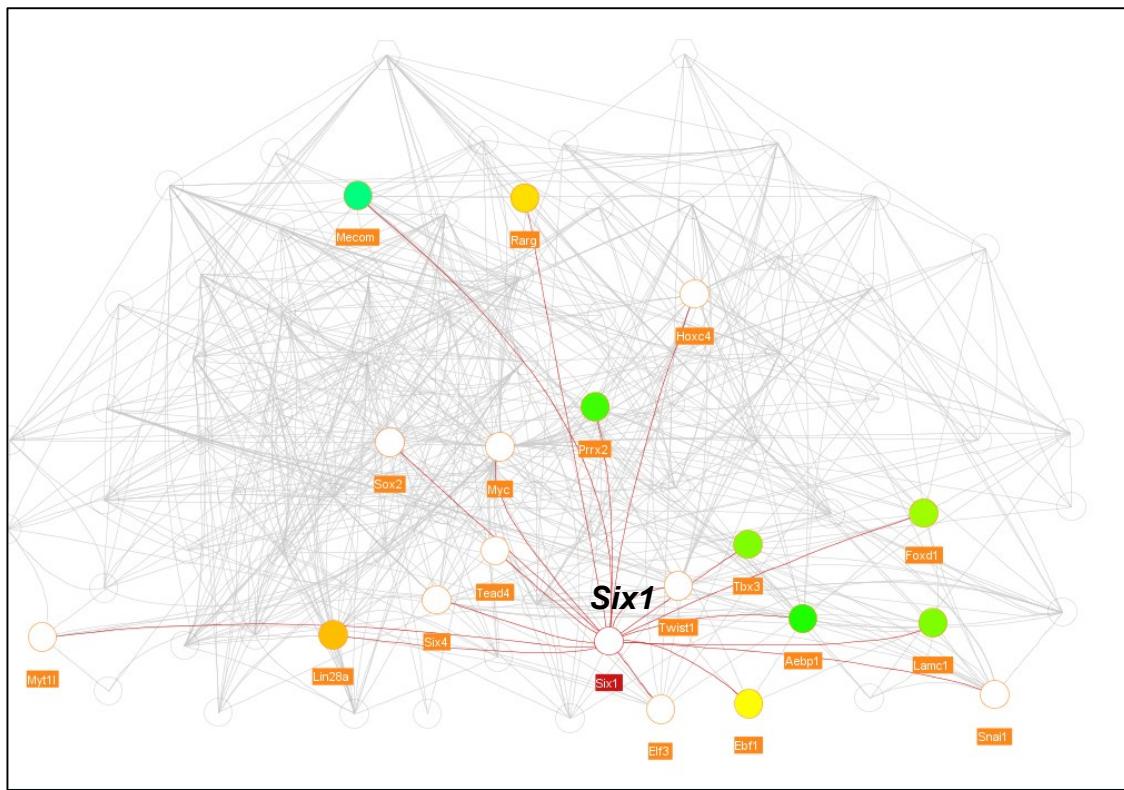


T

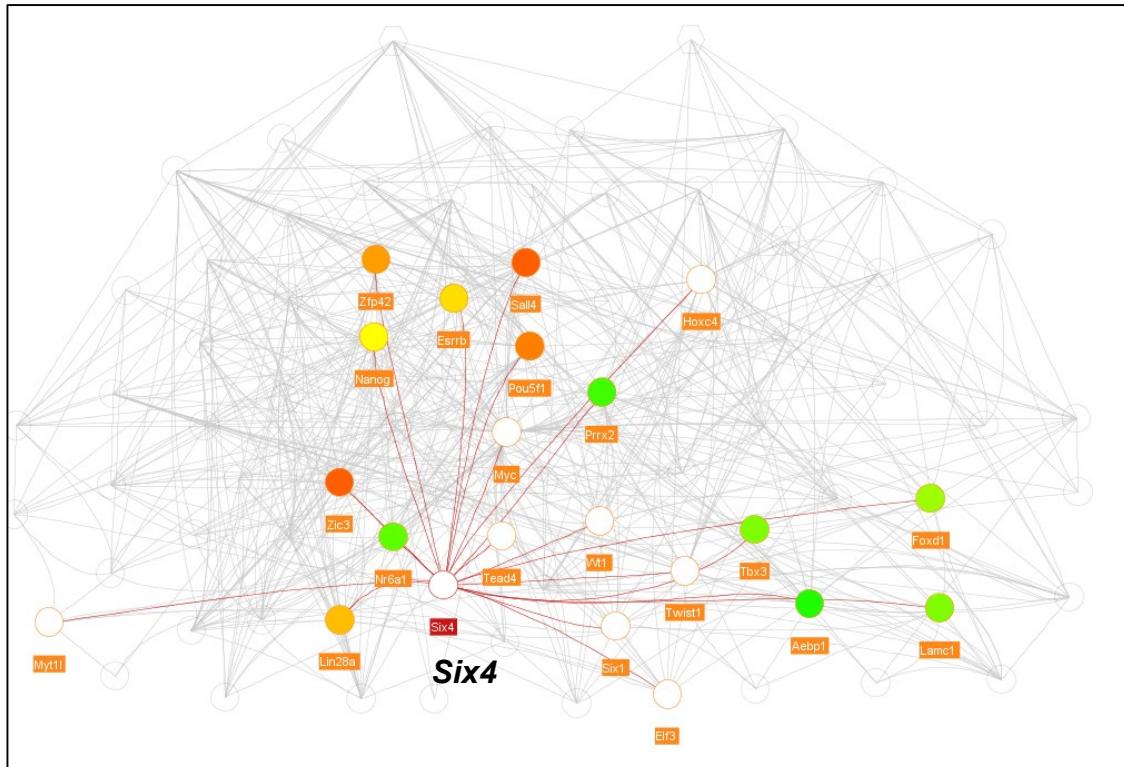


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

U

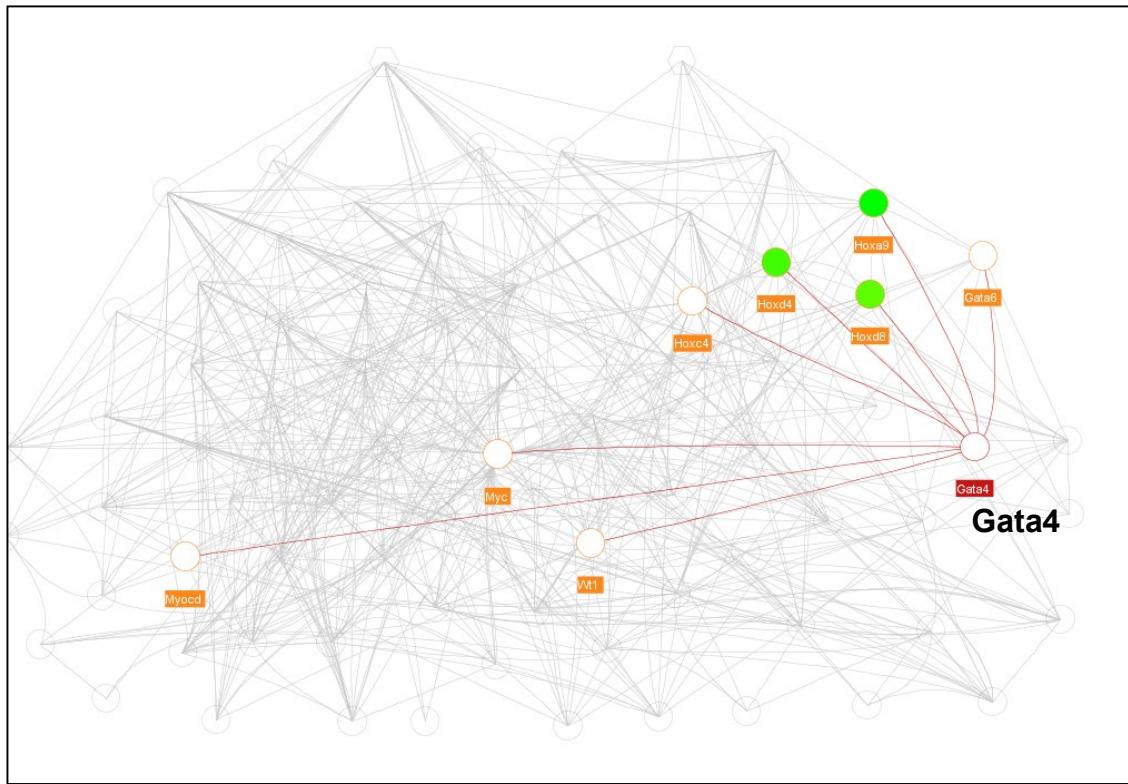


V

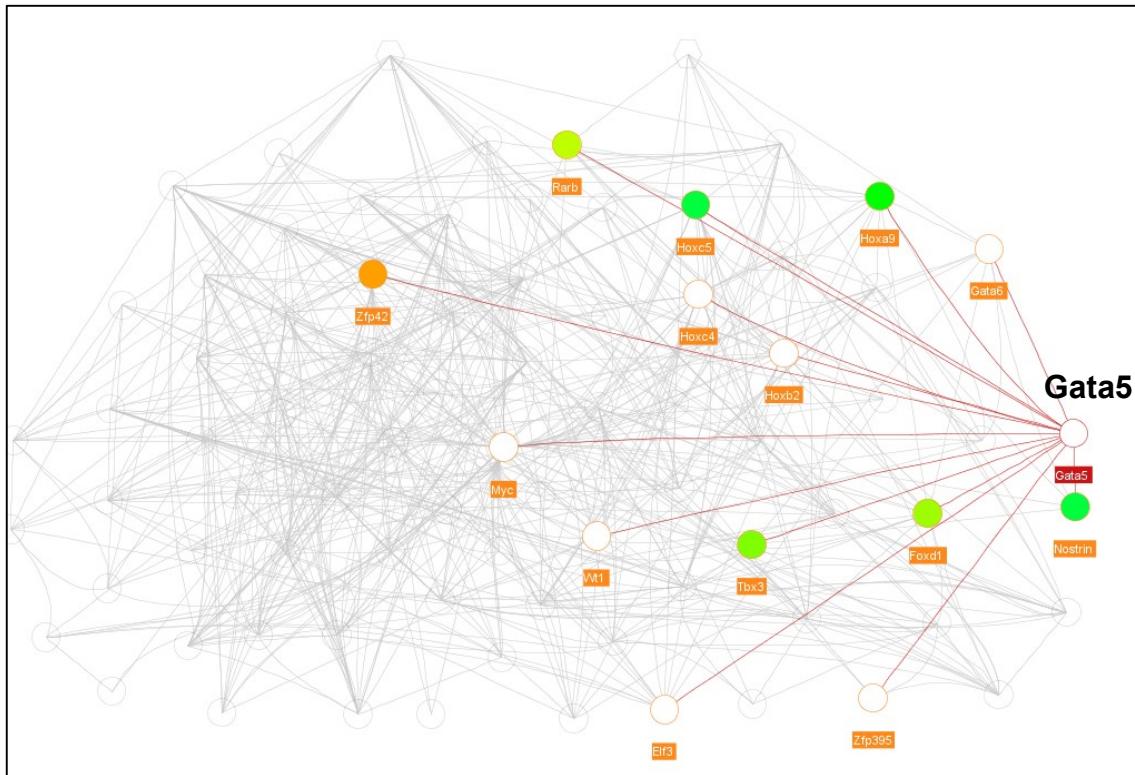


**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.**

W



X



**Supplemental Figure S17. Gene regulatory wiring reconstructed from the reduced Gene regulatory network governing the RA-driven cell-fate decisions in F9 and P19 cells.** (A to X) Illustration of connectivity of RXR $\alpha$  (A, B) and downstream key regulatory genes (C, *Hoxa1*; D, *Rarb*; E, *Gbx2*; F, *Tal2*; G, *Meis2*; H, *Tshz1*; I, *Gli2*; J, *Pbx1*; K, *Ascl1*; L, *Lhx2*; M, *Sox2*; N, *Nr0b1*; O, *Hoxb2*; P, *Hoxc4*; Q, *Zfp42*; R, *Bmil*; S, *Prmd14*; T, *Elf3*; U, *Six1*; V, *Six4*; W, *Gata4*; X, *Gata5*) with the neuronal, endodermal and common programs. Note that early RA-induced factors like RAR $\beta$  and HOXA1 are each interconnected with nodes projecting to endodermal and neuronal factors revealing their impact on the development of both the endodermal and the neuronal lineages (**Supplemental Fig. S17C, D**).

In the neuronal lineage, the early-induced transcription factors GBX2<sup>1</sup> and TAL2 are depicted by edges linking these factors specifically to the RXR $\alpha$ /RAR node of P19 cells. Further downstream, GBX2 is connected to pluripotency factors (SOX2, NANOG, SALL4 or POU5F1/OCT4), which correlates with its repressive activity depicted as part of the co-expression path 10 derived from DREM (**Figure 4D**); it is also linked to the neuronal fate determination factors POU3F4/BRN4 and ASCL1, as well as to the PBX-related homeobox factor MEIS2/STRA10<sup>2</sup>. Notably, an essential role of MEIS2 in neurogenesis has been recently reported<sup>3</sup>, in addition to its implication in cell cycle regulation<sup>4</sup> and cell fate specification<sup>5,6</sup>. The broad functionality of MEIS2 is also apparent from the number of its interactions in the reduced GRN (**Supplemental Fig. S17G**), which includes multiple HOX factors, PBX1 or the zinc finger protein 521(ZFP521) - all of which are expressed in both P19 and F9 cells - and with other neurogenesis-related TFs like GLI2, BRN2 or BRN4. GBX2 is also connected to TSHZ1, a homeodomain factor previously shown to regulate the development and maturation of the olfactory bulb<sup>7</sup>, and which we describe here as a new potential factor that promotes neuronal commitment (**Figure 6**). Indeed, TSHZ1 is connected to pluripotency regulators (SALL4, POU5F1, NANOG, NR0B1), but also to ZIC3 – a factor that plays a critical role in forebrain development<sup>8</sup> - and to the neural crest marker FOXD3<sup>9</sup>. With longer exposure to RA, P19 cells gain in expression of additional neuronal factors, among them ASCL1/MASH1, a factor that is essential for neuronal differentiation of P19 cells<sup>10,11</sup>. Importantly, ASCL1 is connected to several other neuronal-specific factors, such as GLI3, POU3F2/BRN2 or POU3F4/BRN4, as well as to LHX2, a transcriptional factor previously shown to play an essential role for retinal gliogenesis<sup>12</sup>. Note that we demonstrated that LHX2 is able to promote neuronal differentiation (**Figure 6**), which is in keeping with its connection to the downstream acting neuronal factors ASCL1, GLI3, POU3F2/BRN2 and POU3F4/BRN4 (**Supplemental Fig. S17L**). Among the factors involved in endodermal specification is ZFP42/REX1, which is expressed selectively in undifferentiated F9 cells. Notably, RA represses its expression in mouse stem cells<sup>13,14</sup> and its ablation impaired RA-induced primitive endodermal differentiation<sup>15</sup>. Furthermore, previous studies demonstrated that ZFP42/REX1 is regulated by NANOG and SOX2<sup>16,17</sup>. Notably, this described regulatory relationship with the self-renewal components NANOG, SOX2, KLF4 and OCT4 is recapitulated in the reduced GRN, as is its direct role in endodermal differentiation through interaction with BMI1 and the transcription factor PRDM14 (**Supplemental Fig. S17Q**). In fact, the Polycomb factor BMI1 is known to facilitate primitive endoderm formation through GATA6 stabilisation<sup>18</sup>, while PRDM14 is involved in the maintenance of the pluripotency and inhibits ES cells from adopting endodermal fates<sup>19</sup>. Another F9 cell-specific endodermal differentiation-related factor is the Ets domain TF ELF3<sup>20</sup>, which is a direct RA target gene that is also connected to the Homeobox TFs SIX1 and SIX4 (**Supplemental Fig. S17Q**); the latter are involved in pharyngeal endoderm formation<sup>21</sup>. Finally, the GRN contains the nodes GATA4 and GATA6, which are critical for endodermal differentiation<sup>22,23</sup>.

In summary, the reconstructed gene regulatory network properly reconstitutes a scenario in which cascades of TF-driven common regulatory programs - preferentially active during the first hours of treatment – in concert with temporally evolving, similarly TF-driven endodermal and neuronal programs are responsible for the acquisition of these two cell fates in distinct germ layers, such that cell fate specification is pre-defined by a given cellular context even when the same trigger is used for program initiation.

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