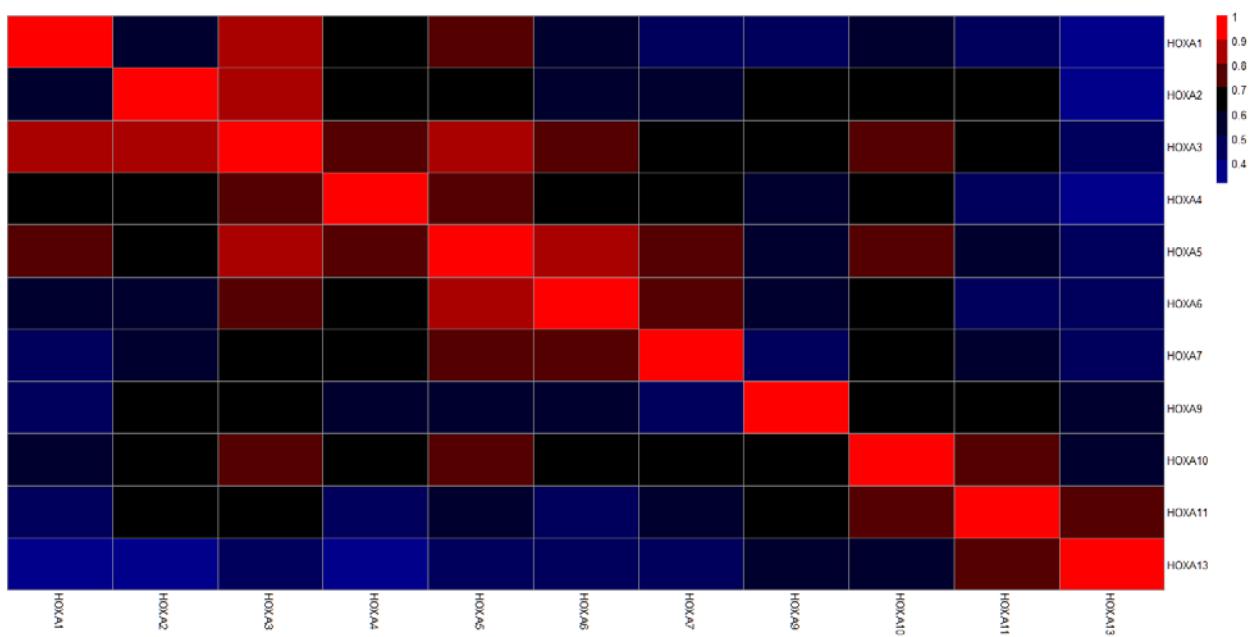
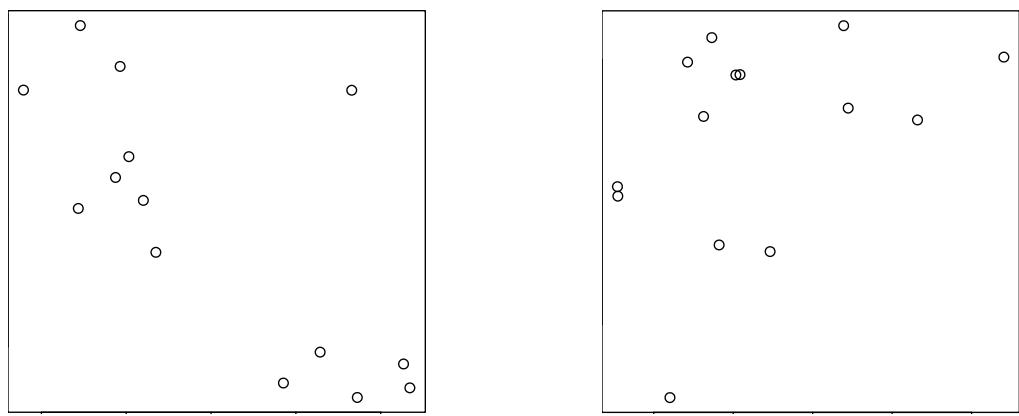


## SUPPLEMENTARY MATERIAL

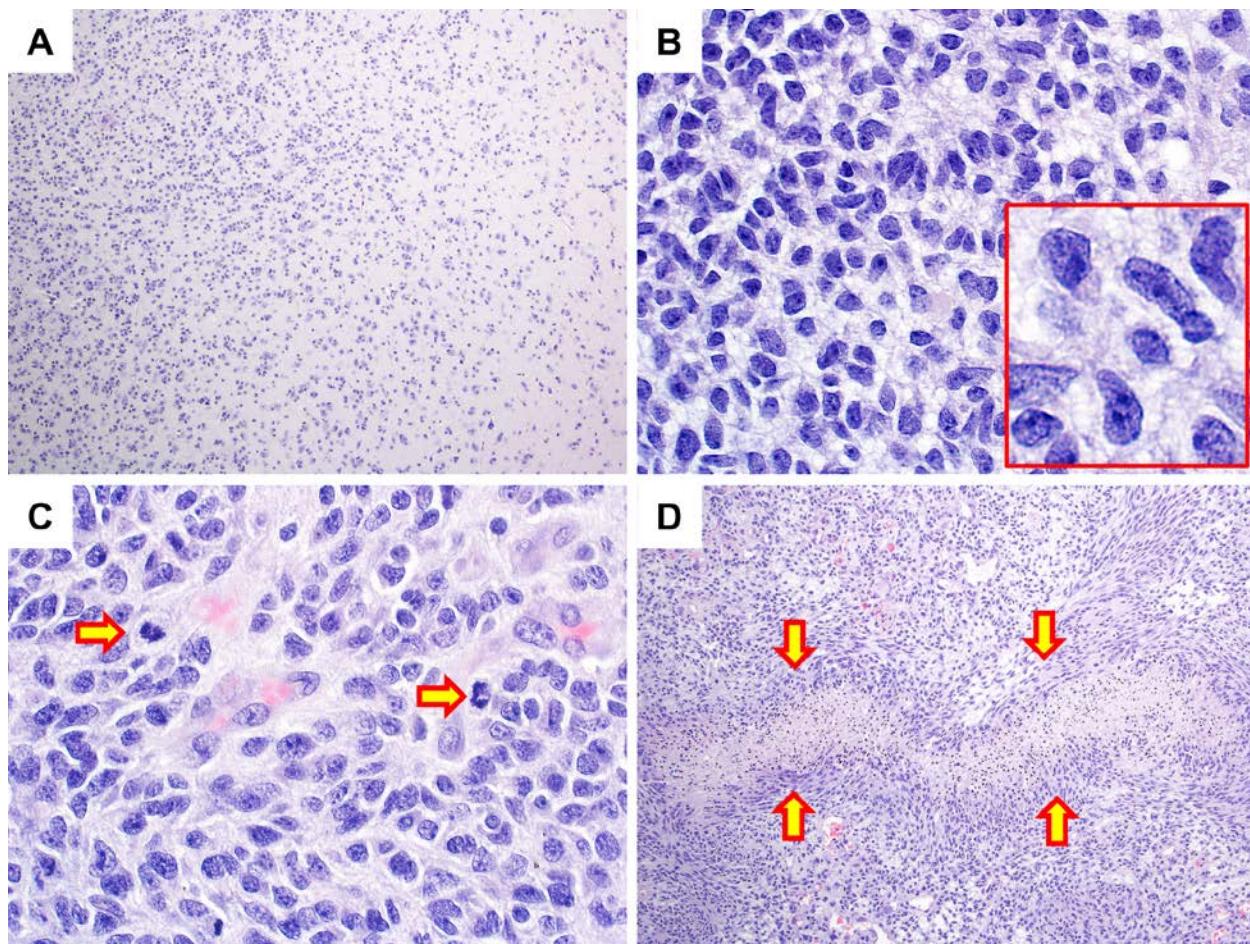
### SUPPLEMENTARY FIGURES



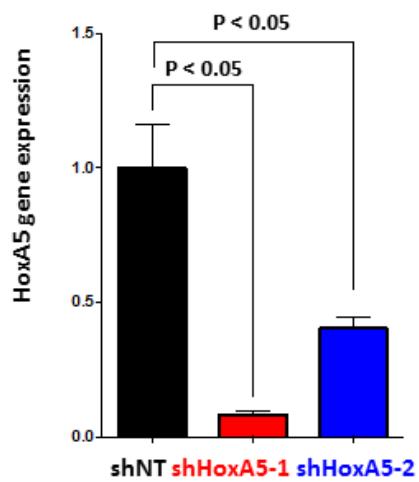
**Supplementary Figure 1.** Correlation of gene expression across HOXA gene cluster in TCGA glioblastoma dataset.



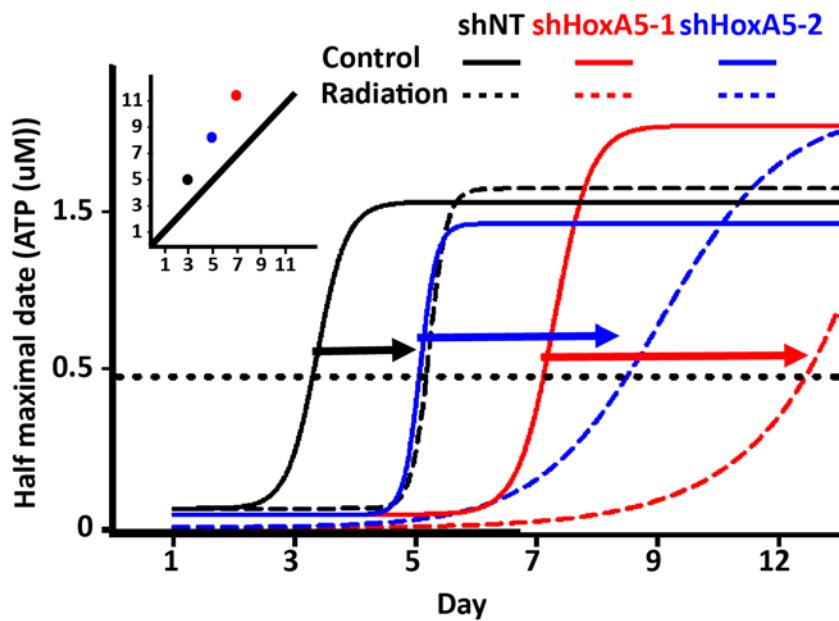
**Supplementary Figure 2.** C7orf13 and RNF32 expression in relation to promoter methylation in proneural glioblastoma.



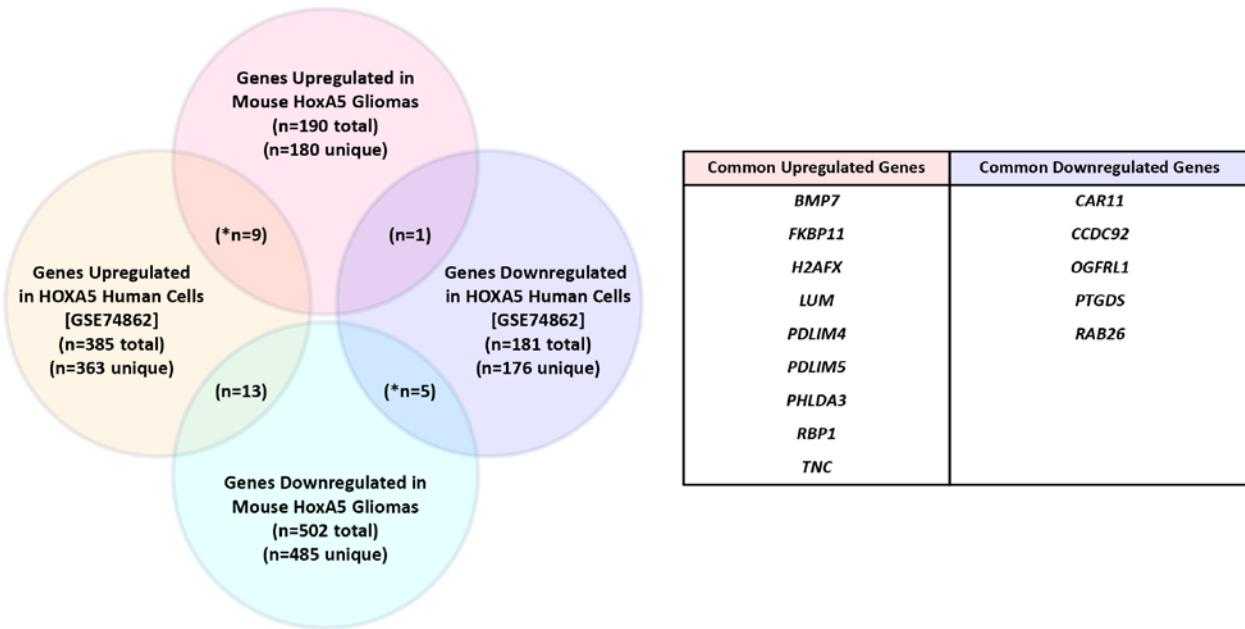
**Supplementary Figure 3.** Histopathology of HoxA5 RCAS generated glioblastoma in mice. (A) The glioma cells show diffuse infiltration throughout the cortex and white matter. (B) The neoplastic cells have an astrocytic morphology with enlarged, irregular, and hyperchromatic nuclei. High grade features are frequent, including (C) Mitotic figures (arrows) and (D) pseudopalisading necrosis (arrows).



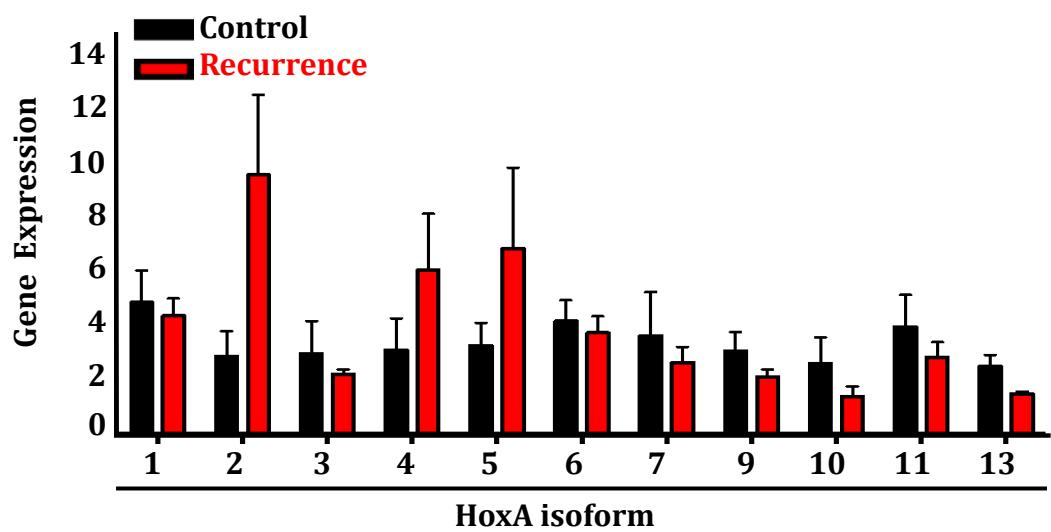
**Supplementary Figure 4.** Efficacy of HoxA5 shRNA knockdown in isolated PDGF-driven mouse glioblastoma cells *in vitro*.



**Supplementary Figure 5.** The half maximal date of proliferation of each tumor cell type was compared before and after radiation. The inset summarizes the half maximum of the proliferation. The half maximum of each shRNA treatment group without radiation is shown in the x-axis and that with radiation is shown in the y-axis.



**Supplementary Figure 6.** Venn diagram of overlapping and unique significantly expressed genes across HoxA5 overexpressing mouse glioblastoma and human carcinoma cells (GEO dataset GSE74862). Overlapping genes in the same direction are listed in the table to the right.



**Supplementary Figure 7.** HoxA relative gene expression in PDGF-driven mouse primary and post-radiation recurrent glioblastoma.

## SUPPLEMENTARY TABLES

**Supplementary Table 1.** HOXA genes ranked in association with survival in IDH wildtype glioblastoma

Symbol	DE.FC	DE.Qval	SA.Qval	hazard.score	rank
HOXA5	-2.122	0	0.003	20.121	1
HOXA3	-1.191	0.231	0.071	0.87	15
HOXA4	-2.55	0.519	0.227	0.467	25
HOXA1	-0.326	1	0.648	0	65
HOXA2	-1.288	1	0.3	0	65
HOXA6	-0.273	1	0.368	0	65
HOXA7	-1.078	1	0.465	0	65
HOXA9	-0.795	1	0.74	0	65
HOXA10	-1.133	1	0.686	0	65
HOXA11	-0.131	1	0.347	0	65
HOXA13	-0.804	1	0.44	0	65

SA.Qval: Gene survival association q-value

DE.Qval: gene differential expression q-values

DE.FC: gene differential expression fold changes

hazard score:  $-\log_{10}(\text{SA.Qval}) * -\log_{10}(\text{DE.Qval}) * \log_2(\text{DE.FC})$ .

**Supplementary Table 2.** RT-PCR primer sequences. (h=human target, m=mouse target).

Gene	Forward	Reverse
<b>mActin</b>	AGCAAGCAGGAGTACGATGAG	AAAACGCAGCTCAGTAACAGT
<b>mHoxA1</b>	TGGCCACGTATAATAACTCC	AAGTGGAACTCCTCTCCAG
<b>mHoxA2</b>	AGTATCCCTGGATGAAGGAG	AAGCTGAGTGGTGGTGTACG
<b>mHoxA3</b>	AACAAATCTTCCCTGGATG	CATAGGTAGCGGTTGAAGTG
<b>mHoxA4</b>	CCTGGATGAAGAAGATCCAC	TCTGAAACCAGATCTGACC
<b>mHoxA5</b>	CTCATTTCGCGGTCGCTATCC	ATCCATGCCATTGTAGCCGTA
<b>mHoxA6</b>	AGCAGCAGTACAAACCTGAC	AGTCCAATTCCCTCTCAAGC
<b>mHoxA7</b>	TCCTACGACCAAAACATCC	AATTCCCTCTCCAGTTCCAG
<b>mHoxA9</b>	TTGTCCCTGACTGACTATGC	AACTCCTCTCCAGTTCCAG
<b>mHoxA10</b>	CCCTTCAGAAAACAGTAAAGC	TTCACTTGTCTGTCCGTGAG
<b>mHoxA11</b>	GACCCGAGAGCAGCAG	GACGCTTCTCTTGTGATG
<b>mHoxA13</b>	AAATGTACTGCCCAAAGAG	GATATCCTCCTCCGTTGTC
<b>hACTIN</b>	AGAAAATCTGGCACACACC	AGAGGCGTACAGGGATAGCA
<b>hP53</b>	CCCAAGCAATGGATGATTGA	GGCATTCTGGGAGCTTCATCT
<b>hP21</b>	GGCAGACCAGCATGACAGATT	GCGGATTAGGGCTTCCTCT
<b>hPUMA</b>	GACCTCAACGCACAGTACGAG	AGGAGTCCCAGTATGAGATTGT
<b>hBAX</b>	CCCGAGAGGTCTTTCCGAG	CCAGCCCATGATGGTTCTGAT