Supplementary

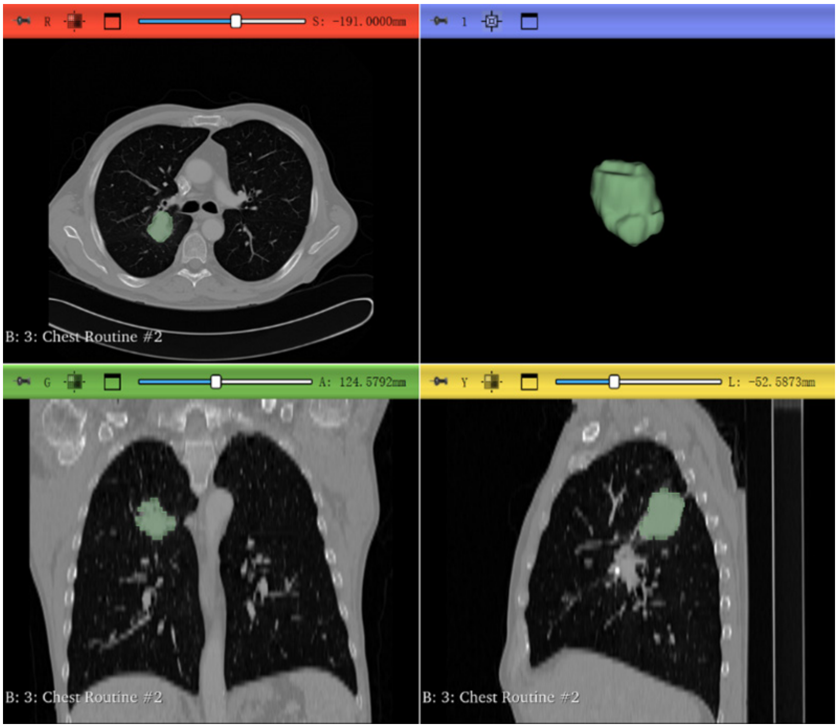

Figure S1 A snapshot of the three-dimensional-slicer software.

Table S1 Hypoxia genes downloaded from the MSigDB

ADM, ADORA2B, AK4, AKAP12, ALDOA, ALDOB, ALDOC, AMPD3, ANGPTL4, ANKZF1, ANXA2, ATF3, ATP7A, B3GALT6, B4GALNT2, BCAN, BCL2, BGN, BHLHE40, BNIP3L, BRS3, BTG1, CA12, CASP6, CAV1, CCNG2, NOCT, CDKN1A, CDKN1B, CDKN1C, CHST2, CHST3, CITED2, COL5A1, CP, CSRP2, CCN2, CXCR4, ACKR3, CCN1, DCN, DDIT3, DDIT4, DPYSL4, DTNA, DUSP1, EDN2, EFNA1, EFNA3, EGFR, ENO1, ENO2, ENO3, ERO1A, ERRFI1, ETS1, EXT1, F3, FAM162A, FBP1, FOS, FOSL2, FOXO3, GAA, GALK1, GAPDH, GAPDHS, GBE1, GCK, GCNT2, GLRX, GPC1, GPC3, GPC4, GPI, GRHPR, GYS1, HAS1, HDLBP, HEXA, HK1, HK2, HMOX1, HOXB9, HS3ST1, HSPA5, IDS, IER3, IGFBP1, IGFBP3, IL6, ILVBL, INHA, IRS2, ISG20, JMJD6, JUN, KDELR3, KDM3A, KIF5A, KLF6, KLF7, KLHL24, LALBA, LARGE1, LDHA, LDHC, LOX, LXN, MAFF, MAP3K1, MIF, MT1E, MT2A, MXI1, MYH9, NAGK, NCAN, NDRG1, NDST1, NDST2, NEDD4L, NFIL3, NR3C1, P4HA1, P4HA2, PAM, PCK1, PDGFB, PDK1, PDK3, PFKFB3, PFKL, PFKP, PGAM2, PGF, PGK1, PGM1, PGM2, PHKG1, PIM1, PKLR, PKP1, PLAC8, PLAUR, PLIN2, PNRC1, PPARGC1A, PPFIA4, PPP1R15A, PPP1R3C, PRDX5, PRKCA, CAVIN3, CAVIN1, PYGM, RBPJ, RORA, RRAGD, S100A4, SAP30, SCARB1, SDC2, SDC3, SDC4, SELENBP1, SERPINE1, SIAH2, SLC25A1, SLC2A1, SLC2A3, SLC2A5, SLC37A4, SLC6A6, SRPX, STBD1, STC1, STC2, SULT2B1, TES, TGFB3, TGFBI, TGM2, TIPARP, TKTL1, TMEM45A, TNFAIP3, TPBG, TPD52, TPI1, TPST2, UGP2, VEGFA, VHL, VLDLR, CCN5, WSB1, XPNPEP1, ZFP36, ZNF292

https://dx.doi.org/10.21037/tlcr-24-982

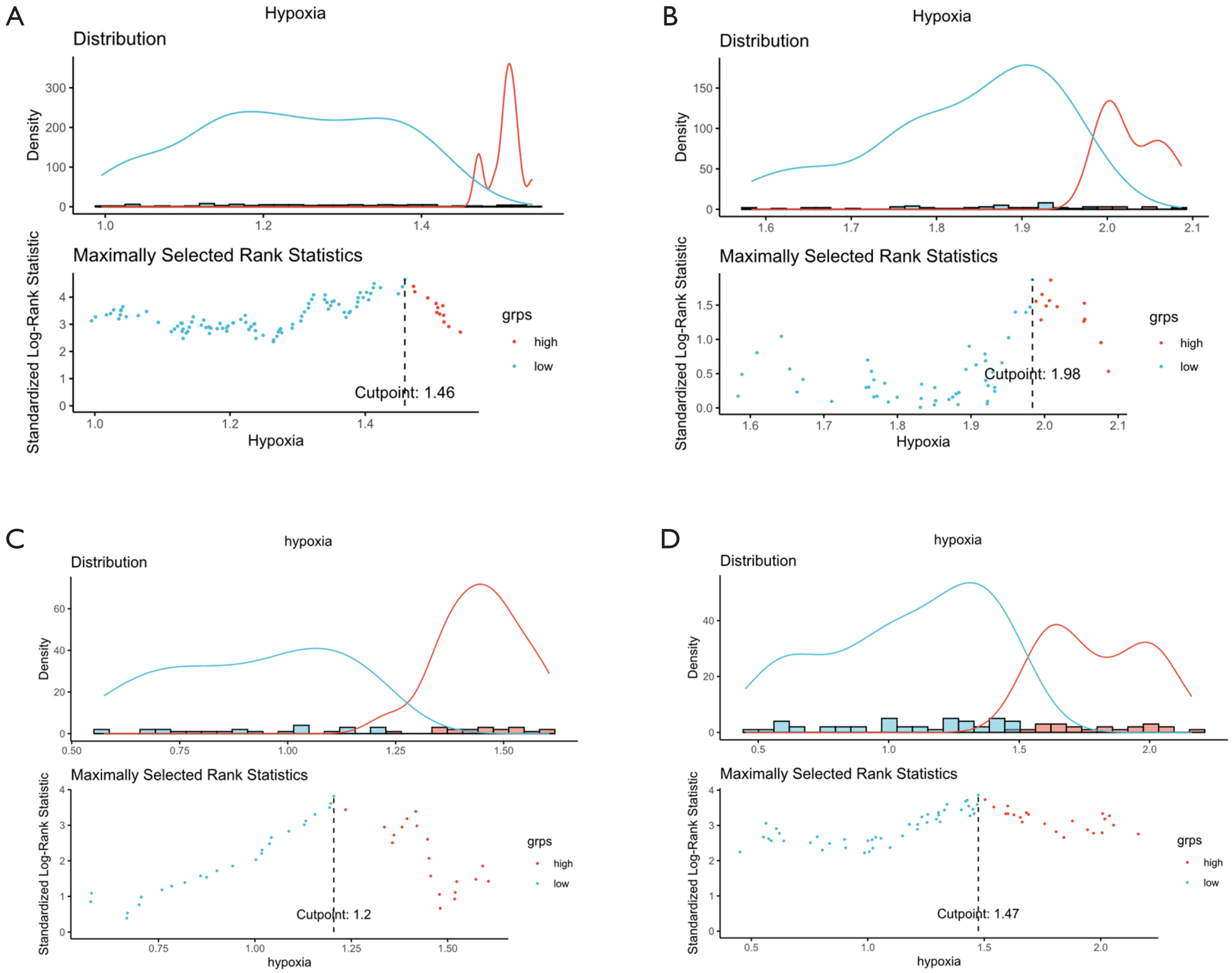

Figure S2 Survival cut-off calculation of the hypoxia scores. The cut-off values of the hypoxia scores of the radiogenomic (A), TCGA (B), GSE87340 (C), and GSE19188 (D) cohorts, respectively. X-axis: hypoxic score. Grps, groups.

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