Supplementary Figures

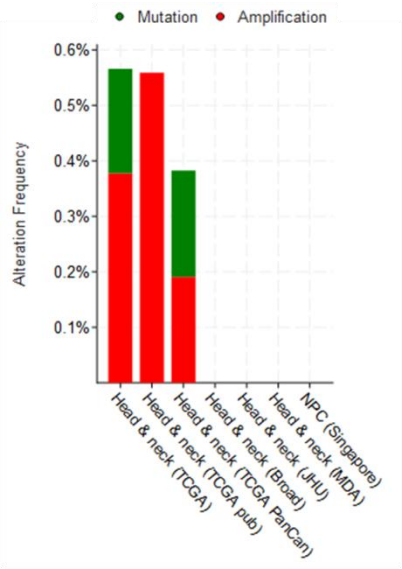

Figure S1. Genomic analysis of the *IDH2* gene in HNSCC and NPC (data from the cBioPortal database).

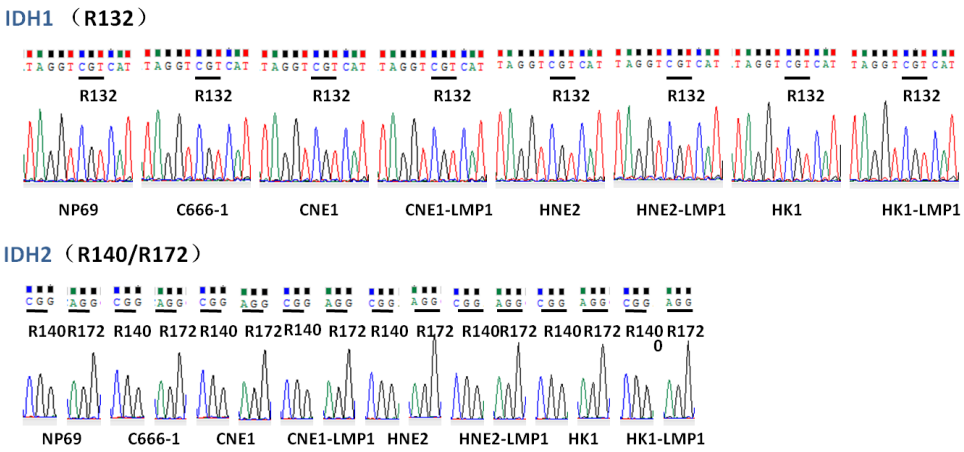

Figure S2. The cDNA region contains the hotspot site of IDH1 (R132) and IDH2 (R140 and R172) was sequenced using the Sanger sequencing method in immortalized human nasopharyngeal epithelial cells (NP69) and NPC cells (C666-1, CNE1, HNE2 and HK1).

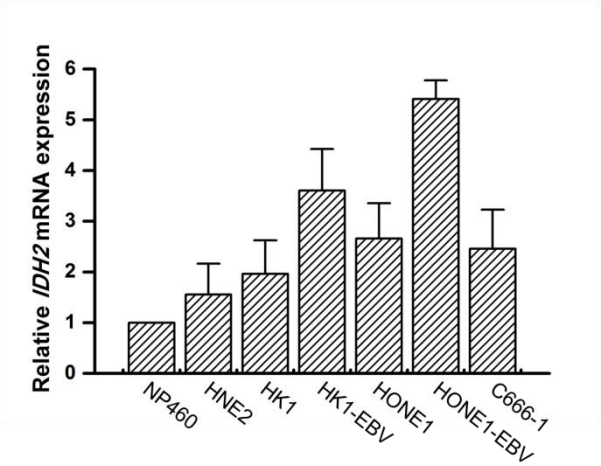

Figure S3. IDH2 expression in NPC cell lines (HNE2, HK1, HK1-EBV, C666-1, HONE1, HONE1-EBV) and immortalized nasopharyngeal epithelial cell line (NP460) was measured by RT-PCR.

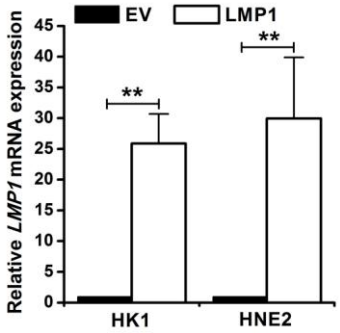

Figure S4. *LMP1* mRNA expression was measured by RT-PCR.

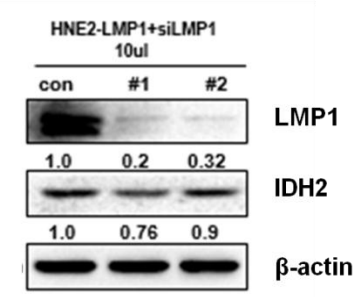

Figure S5. LMP1 and IDH2 protein expression was detected by Western blot analysis and β-actin served as a loading control.

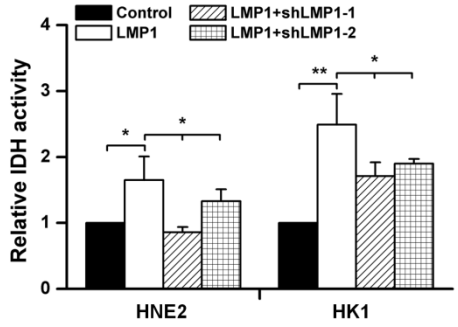

Figure S6. IDH2 activity was measured in groups as indicated.

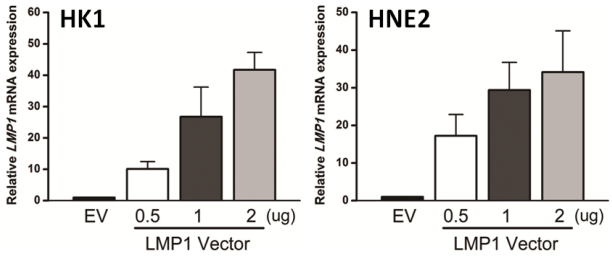

Figure S7. HK1 and HNE2 cells were transiently transfected with 0.5, 1 and 2 ug LMP1 vector. *LMP1* mRNA expression was measured by RT-PCR.

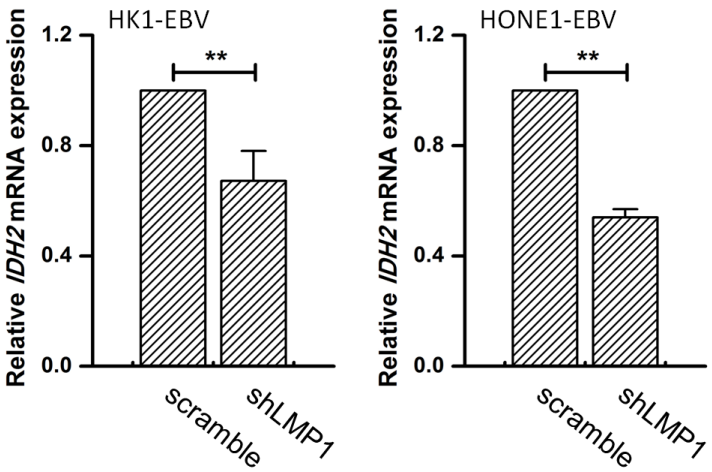

Figure S8. Knockdown of LMP1 in HK1-EBV and HONE1-EBV cell lines decreased IDH2 expression. *IDH2* mRNA expression was determined by RT-PCR (columns = mean; bars = S.D.; N = 3; **, $p < 0.01$).

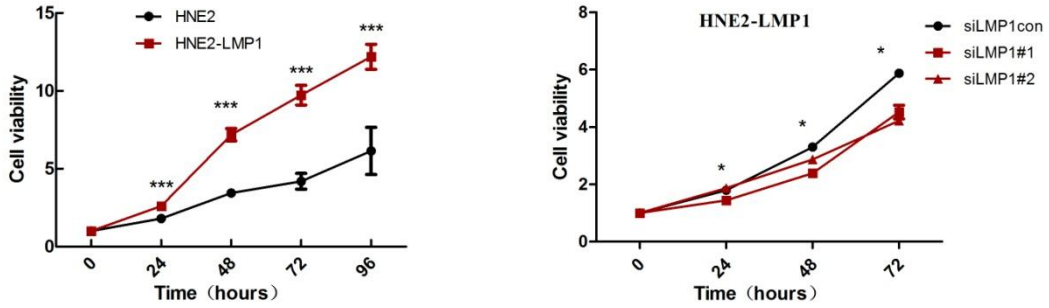

Figure S9. Viability was measured by MTS in NPC cells transfected with empty- or LMP1-expressing vector *(left)*, and in cells transfected with control or LMP1 siRNAs *(right)*.

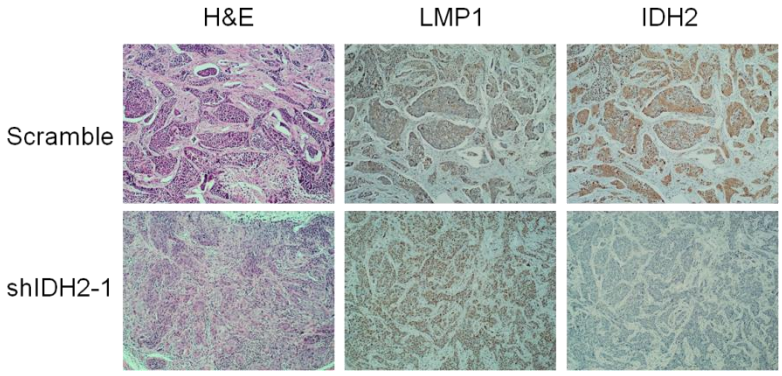

Figure S10. Representative images of H&E staining and LMP1/IDH2 staining by using immunohistochemistry in xenograft tumor sections (100×).

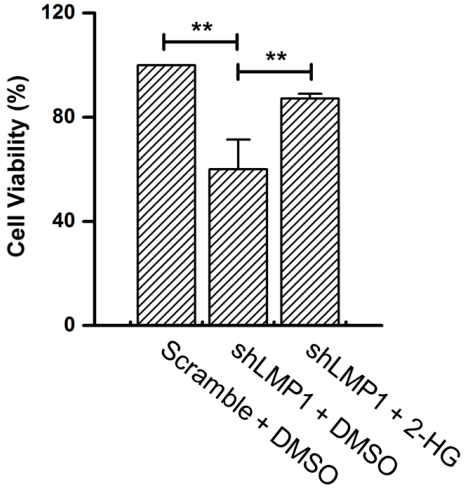

Figure S11. Scramble or LMP1 shRNA was transfected into HK1-EBV cells. Cells tranfected with LMP1 shRNA were also treated with DMSO/1 mM octyl-2-HG. Cell viability was measured by MTS (columns = mean; bars = S.D.; N = 3; **, $p < 0.01$).

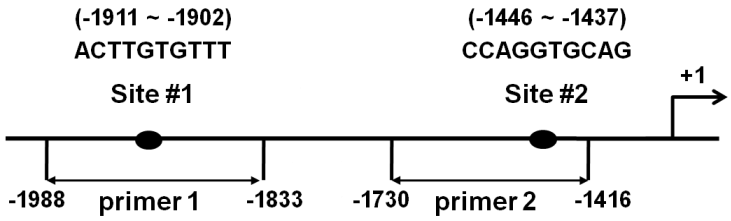

Figure S12. Schematic diagram of c-Myc-binding sites in 2000 bp of the human *IDH2* promoter and primers in the ChIP assay.

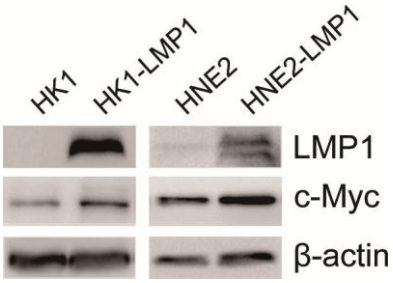

Figure S13. c-Myc protein expression was detected by Western blot analysis in the same blot with Figure 2D. β-actin served as a loading control.

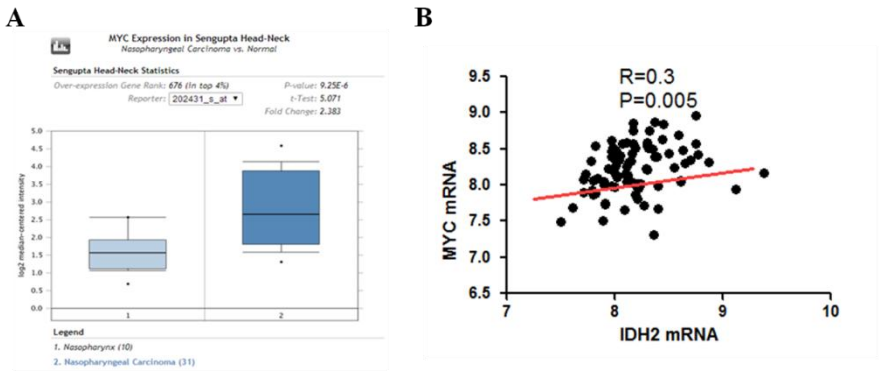

Figure S14. A, c-Myc expression in NPC tissues (N = 31) and nasopharynx tissues (N = 10) from the Oncomine database. B, correlation between *c-Myc* and *IDH2* mRNA expression levels as analyzed in head and neck cancer from the SurvExpress database.

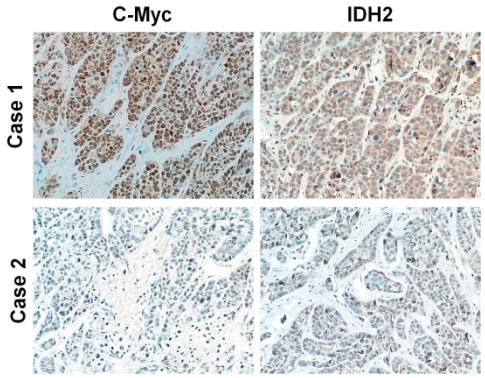

Figure S15. Representative IHC photos for the expression of c-Myc and IDH2 in NPC tissues (200×).

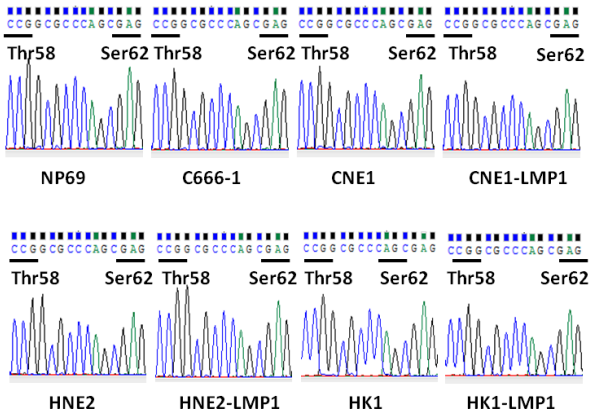

Figure S16. The cDNA region containing the hotspot sites of c-Myc (Thr58 and Ser62) was sequenced by the Sanger sequencing method in immortalized human nasopharyngeal epithelial cells (NP69) and NPC cells (C666-1, CNE1, HNE2 and HK1).

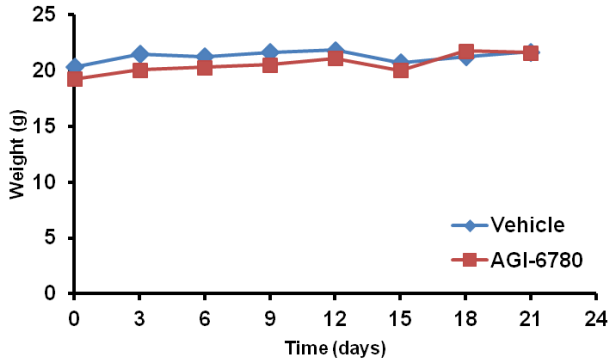

Figure S17. The weight curve of nude mice treated with corn oil (vehicle) or AGI-6780 (150 mg/kg; N = 5).