

Article

Impact of Tumour Hypoxia on Evofosfamide Sensitivity in Head and Neck Squamous Cell Carcinoma Patient-Derived Xenograft Models

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Supplement:

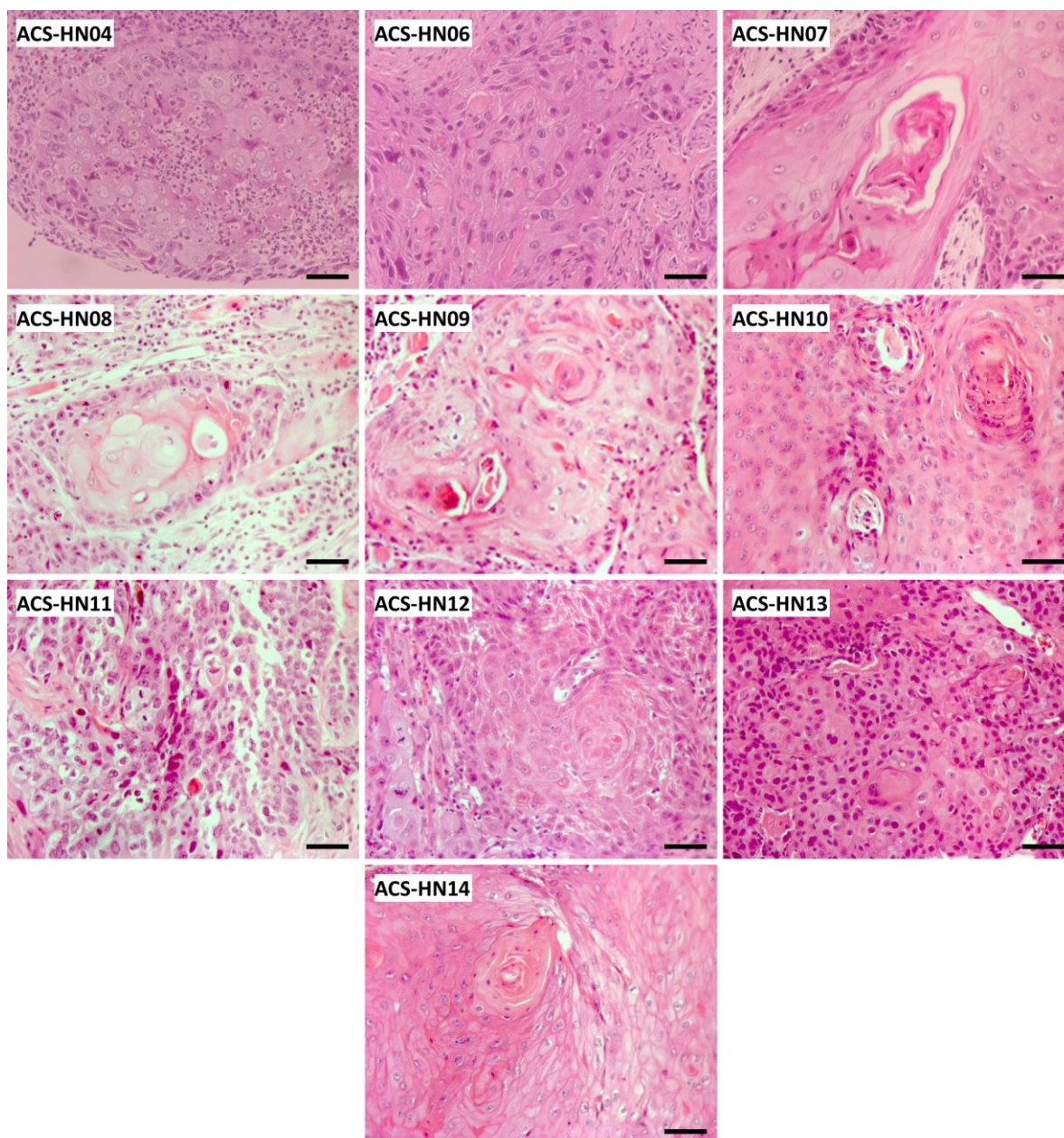


Figure S1. Histopathology of ten PDX models at P0. Scale bar = 50 μm.

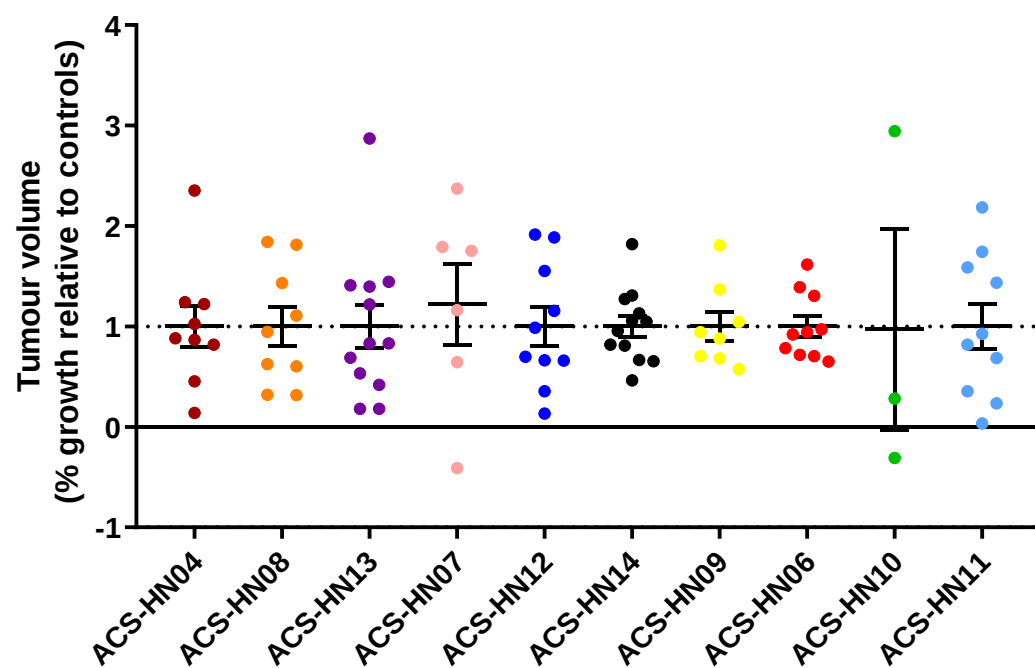


Figure S2. Tumour growth in control mice relative to the average control value at the end of treatment (or endpoint if earlier). Data represents individual values and the mean $\pm$ SEM.

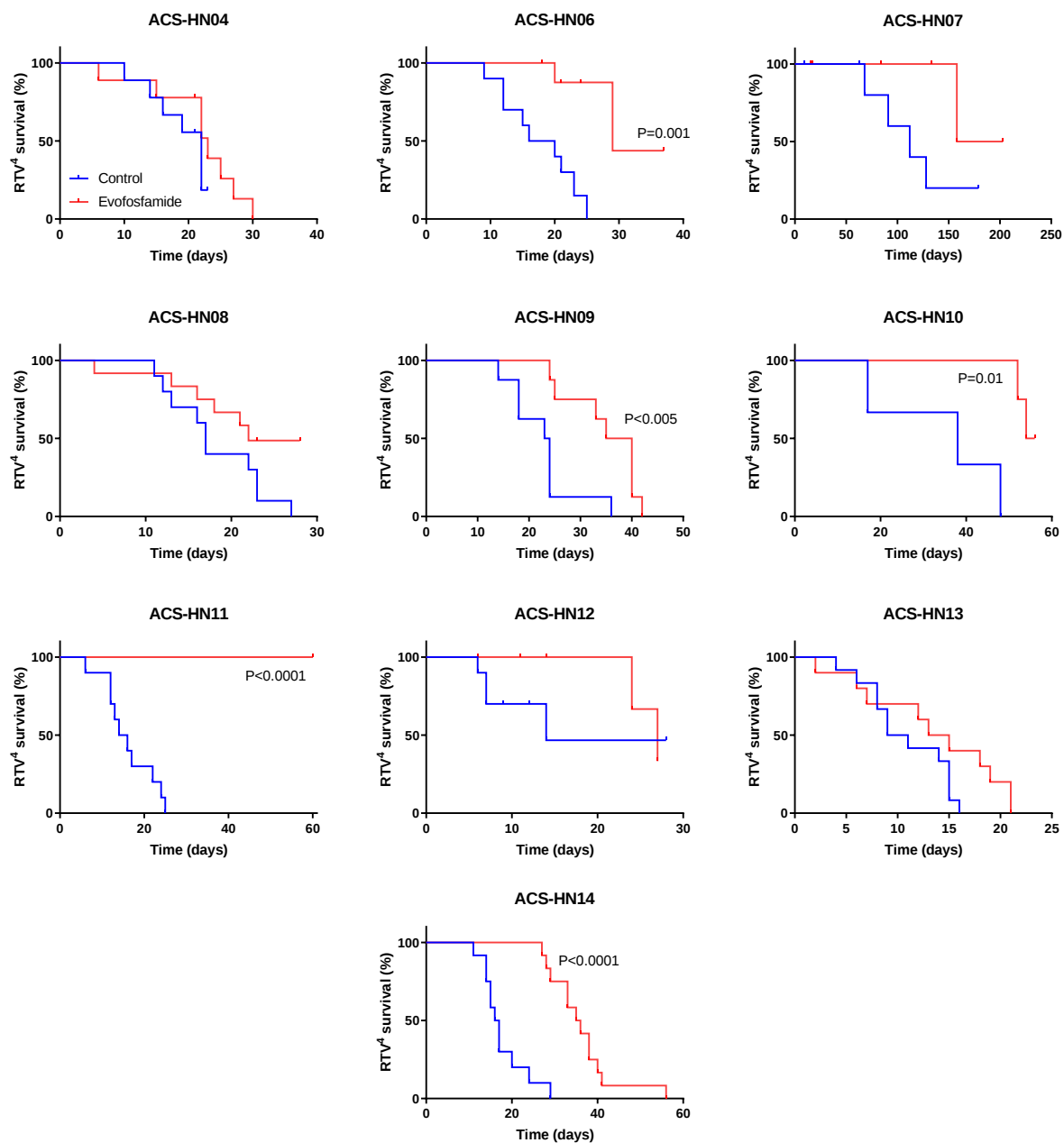


Figure S3. Antitumour efficacy of evofosfamide in ten HNSCC PDX models determined as the time taken for tumours to quadruple in size (RTV⁴, relative tumour volume $\times$ 4). NOD scid mice with P3 PDX tumours were treated with 50 mg/kg evofosfamide by IP injection qd $\times$ 5 for three weeks or control vehicle. Plots for ACS-HN06, ACS-HN07 and ACS-HN08 reproduced with permission from [49] © (2018) American Society for Clinical Investigation.

Table S1. Oligonucleotide probes for NanoString gene analysis.

Gene	Accession	Probes
<i>RPS13</i>	NM_001017.2	GAATCAGACGGAATTTAGCATCCTTATCCTTTCTGTTCTCTCAAGATGCCCTCAAGACCTAAGCGACAGCGTGACCTTGTTCACGAAAGCCATGACCTCCGATCACTCTCGCTTGGTCTTATAATATCGAGCCAAACGGTGAATCCGGCTCTCTATTA
<i>RPLP0</i>	NM_001002.3	CTGCATCTGCTTGGAGCCACATTGTCTGCTCCCAATGAAACATTTTCGCATCCTCTTCTTTCTTGGTGTGAGAAGATGCTCCGAAAGCCATGACCTCCGATCACTCCACCACAGCCTTCCCGCGAAGGGACATGCGGATCTG
<i>OAZ1</i>	NM_004152.2	AATAAGTTAGCTGAAAGATTGTGATCCCTCTGACTATTCCTCGCCACCCACAATTCTGCGGTTAGCAGGAAGGTTAGGGAACCGAAAGCCATGACCTCCGATCACTCTGTCTGGACGTTAGTTCCTCTGTTACATTCAGCCGATCATCGGAGTAG
<i>ADM</i>	NM_001124.1	TGCACACAAACACACTCACATTCCACGCGCGAACAACATTACACCTCGCCTGTTGAGATTATTGAGCTTCATCATGACCAGAAGCGAAAGCCATGACCTCCGATCACTCACTCGGTGTTCTTCTTCCACACAGGAGTAATCAGTCTTTCTTTTCA
<i>ALDOA</i>	NM_184041.2	CACCACACCACTGTACGAGGGAAGAAAGAGCGCGGGCAAGCCAGCAAAGACGCCTATCTCCAGTTTGATCGGGAAACTCGAAAGCCATGACCTCCGATCACTCTTATTGGCAGTGTCCGGAAGGGTGATGGACTTAGCATTCACAGACGA
<i>ANKRD37</i>	NM_181726.2	TCCAGGCTTCCAACTTTGTGCGCTTGIGTAGTGGCGAACCTAATCCTCGCTACATTCCTATTGTTTTCCGAAAGCCATGACCTCCGATCACTCTATTACATAAATCAATTTGGGCATCACTGGCTACAAGCAGGCTTAGGCAC
<i>BNIP3</i>	NM_004052.3	CTGCGGGATGTGCTTCAGCTGCGGGCGGTGGGAAAGCCAATTTGGTTTTACTCCCTCGATTATGCGGAGTCGAAAGCCATGACCTCCGATCACTCAGAGGGCACTGCGGCGATCGGAGTCCGCGCCGGG
<i>BNIP3L</i>	NM_004331.2	GGATGGTACGTGTTCCAGCCCCCATTTTCCCATTTGCCATTATCATTGCCTTTCGGGTTATATCTATCATTTACTTGACACCCTCGAAAGCCATGACCTCCGATCACTCTGTGCATCCAAAAGAATCTTCCATGTCTCCATTGTGGATGGAGGATGA
<i>EGLN3</i>	NM_022073.3	ATGAATGATTCCCTCTGGAATATCCGACAGGATCCACCATGTAGCTTCAACAGCCACTTTTTTCCAAATTTTGAAGAGCCCGAAAGCCATGACCTCCGATCACTCGATCTGACCAGAAGAACAGGAGTCTGTCAAAAATGGGCTCCACATCTGCT
<i>FAM162A</i>	NM_014367.3	AAGCGACCTGACCATATGAGGATCTTTTCTGCCAATCCGTAGGTTTGTGCACCGTGTGGACGGCAACTCAGAGATAACGCATATCGAAAGCCATGACCTCCGATCACTCCATCAAGCATCTCCAACGAGACAGTCTCTGGGATTTCATCTCTCTTTTG
<i>KCTD11</i>	NM_001002914.2	TCTGAAGGGATGGCCTCCGAGACCCCGGCAGATCCCTGGAGTTTATGTATTGCCAACGAGTTTGTCTTTTCGAAAGCCATGACCTCCGATCACTCAACCAGCAGGTGACGGTGGCGAGCACAGGGCCGAC
<i>LOX</i>	NM_002317.4	TACGGTGAAATTGTGCAGCCTGAGGCATACGCATGATGTCTGTGTAGCAGATAAGGTTGTTATTGTGGAGGATGTTACTACACGAAAGCCATGACCTCCGATCACTCAGAACACCAGGCACTGATTTATCCATTGGGAGTTTGTCTTGCCTCTCAA
<i>NDRG1</i>	NM_001135242.1	ACACAACAACAAGGAATCCCTTACATCGAGTAACCCCAATTCCACCCCACTGTTGAGATTATTGAGCTTCATCATGACCAGAAGCGAAAGCCATGACCTCCGATCACTCTCTGGAACCAAGCTGGGATCCACAGAAATCACAAGTGCATGGATCTCA
<i>P4HA1</i>	NM_000917.3	CAGAGACTTTATCTATGGTAGAAATCTCGCTTCATCCAGTTGCCTTAGGCAAAGACGCCTATCTTCCAGTTGATCGGGAAACTCGAAAGCCATGACCTCCGATCACTCCTATCCAGGTCTCCCTGCTGATATACCGCATAGCTCAAATAATCTAGAA
<i>P4HA2</i>	NM_004199.2	GTTAACCTGTGATATGCTGCATCCGACGATTTACTCGGGCCACAACAGGCGAACCTAATCTCTCGCTACATTCCTATTGTTTTCGAAAGCCATGACCTCCGATCACTCTGCTCCCACTCCATAATTGCAACCTGTAACAATCTGCAGTCTTACT
<i>PKD1</i>	NM_002610.3	TCAGGTCTCCTTGGAAAGTATTGTGCGTAAAGACGTGATATGGGCAATCCACCAATTGGTTTTACTCCCTCGATTATGCGGAGTCGAAAGCCATGACCTCCGATCACTCCTAATGTAGATAACTGCATCTGTCCGTAACCTCTAGGGAATACAGCT
<i>PFKFB3</i>	NM_004566.3	CATCGAAAACCGCAATTTGTCCCTCTCTTTCGCCAGGTAGCTTTTGACACTTCGGGTTATATCTATCATTTACTTGACACCCTCGAAAGCCATGACCTCCGATCACTCTTTGGCAAAATGAAGGATCATGTGTCTCTCTCTAGTAGTATTGGTGG
<i>SLC2A1</i>	NM_006516.2	TGAGTGGTTGGTAGGAAGAGATGGGAAGGGGCAATCCTAATGGAGCCTCAACAGCCACTTTTTTCCAAATTTTGAAGAGCCCGAAAGCCATGACCTCCGATCACTCTCCCTGCACTCCAGTGCTCCCACTGGTCTCAGGTAAGAAAGATTAATT
<i>MKI67</i>	NM_002417.2	CTGATGGCATTAGATTCTGACGCTAAGAGTTCTCCCTCTACATCTGCACCGTGTGGACGGCAACTCAGAGATAACGCATATCGAAAGCCATGACCTCCGATCACTCGTCTTCTCTTCACTACTGATGGTTTAGGCGTGTGCATGGCTTTGCTG
<i>POR</i>	NM_000941.2	TGCTGAAAAGAGATACTTCTTCGGCCACCGCTCGGACACGGTGGAGCCTGGAGTTTATGTATTGCCAACGAGTTTGTCTTTTCGAAAGCCATGACCTCCGATCACTCCAGTAGGTTAGGAGACCCACGATGAGCGAAAACAGAATCATGTCCGTCA
<i>SLFN11</i>	NM_001104587.1	AATGCCTCTCTTGTAGTCCATGGAACGCACAGAGGTCTCAGATCTACGGTACAGATAAGGTGTATGTGGAGGATGTTACTACACGAAAGCCATGACCTCCGATCACTCAAGGTCTTCTTCCAAGATTTTGGCTTCTTTTGGTCTTCAGGAAACAG