



Supplementary Materials

Genetic Variation in the Vascular Endothelial Growth Factor (VEGFA) Gene at rs13207351 Is Associated with Worse Overall Survival of Patients with Head and Neck Cancer

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Table S1. Hazard ratios and 95% CIs estimated by univariate Cox regression analysis under additive genetic models for all examined variants in NPC and non-NPC patients (with tumors located in the larynx).

Variant	NPC Patients			non-NPC Patients		
	Event/Total	HR (95% CI)	p-Value	Event/Total	HR (95% CI)	p-Value
NBS1 rs1805794 (p.E185Q)			0.605			0.730
C	3/15	0.58 (0.17-2.00)	0.387	10/21	1.33 (0.65-2.73)	0.433
G	13/44	1.10 (0.52-2.32)	0.806	30/60	1.10 (0.67-1.82)	0.703
GC	15/63	Reference	--	31/67	Reference	--
EDNRA rs5333 (p.H323H)			0.809			0.728
C	0/5	--	--	4/6	1.33 (0.48-3.73)	0.585
CT	11/46	0.78 (0.38-1.63)	0.515	26/58	0.89 (0.54-1.45)	0.640
T	21/70	Reference	--	41/83	Reference	--
EDNRA rs5334 (p.E335E)			0.855			0.728
A	0/4	--	--	4/6	1.33 (0.48-3.73)	0.585
AG	11/46	0.81 (0.39-1.69)	0.575	26/58	0.89 (0.54-1.45)	0.640
G	21/70	Reference	--	41/83	Reference	--
FAS rs1800682 (-670)			0.602			0.295
A	9/28	1.22 (0.55-2.68)	0.621	19/40	1.30 (0.74-2.29)	0.366
AG	20/79	Reference	--	32/74	Reference	--
G	2/14	0.56 (0.13-2.40)	0.434	20/34	1.54 (0.88-2.70)	0.128
FAS rs2234768 (-690)						0.171
C	--	--	--	1/1	3.97 (0.54-29.19)	0.175
CT	8/20	2.22 (0.98-5.00)	0.056	9/27	0.64 (0.32-1.29)	0.215
T	23/101	Reference	--	61/120	Reference	--
VEGFA rs699947 (-2578)			0.136			0.890
A	3/18	1.04 (0.27-3.91)	0.959	11/20	1.19 (0.58-2.42)	0.636
AC	18/51	2.17 (0.94-4.99)	0.069	35/72	1.08 (0.65-1.80)	0.774
C	8/48	Reference	--	25/56	Reference	--
VEGFA rs144854329			0.182			0.890
het del18bp	21/61	2.03 (0.61-6.81)	0.251	35/72	0.91 (0.46-1.79)	0.780
hom del18bp	7/41	1.00 (0.26-3.86)	0.998	25/56	0.84 (0.41-1.72)	0.636
reference	3/18	Reference	--	11/20	Reference	--
VEGFA rs35864111			0.182			0.890

het ins1bp	21/61	2.03 (0.61-6.81)	0.251	35/72	0.91 (0.46-1.79)	0.780
hom ins1bp	7/41	1.00 (0.26-3.86)	0.998	25/56	0.84 (0.41-1.72)	0.636
reference	3/18	Reference	--	11/20	Reference	--
VEGFA rs833061 (-1498)			0.731			0.134
C	5/22	1.57 (0.48-5.15)	0.458	12/31	1.20 (0.57-2.54)	0.635
CT	11/47	1.38 (0.51-3.73)	0.526	43/74	1.74 (0.98-3.08)	0.060
T	6/34	Reference	--	16/43	Reference	--
VEGFA rs1570360 (-1154)			0.570			0.865
A	5/26	0.79 (0.26-2.36)	0.672	29/60	0.90 (0.53-1.54)	0.703
G	15/55	1.32 (0.58-3.03)	0.512	17/35	1.05 (0.57-1.95)	0.874
GA	9/39	Reference	--	25/53	Reference	--
VEGFA rs13207351 (-1190)			0.294			0.012
A	14/54	1.85 (0.71-4.82)	0.207	40/68	2.21 (1.23-3.96)	0.008
AG	9/27	2.23 (0.79-6.28)	0.127	15/34	1.19 (0.59-2.41)	0.624
G	9/39	Reference	--	16/46	Reference	--
VEGFA rs3025039 (+936)			0.826			0.504
C	21/83	Reference	--	48/103	Reference	--
CT	8/30	1.19 (0.53-2.70)	0.670	17/34	1.18 (0.68-2.05)	0.559
T	1/4	0.67 (0.09-4.96)	0.691	6/10	1.61 (0.69-3.77)	0.272

HR, hazard ratio; CI, confidence interval.

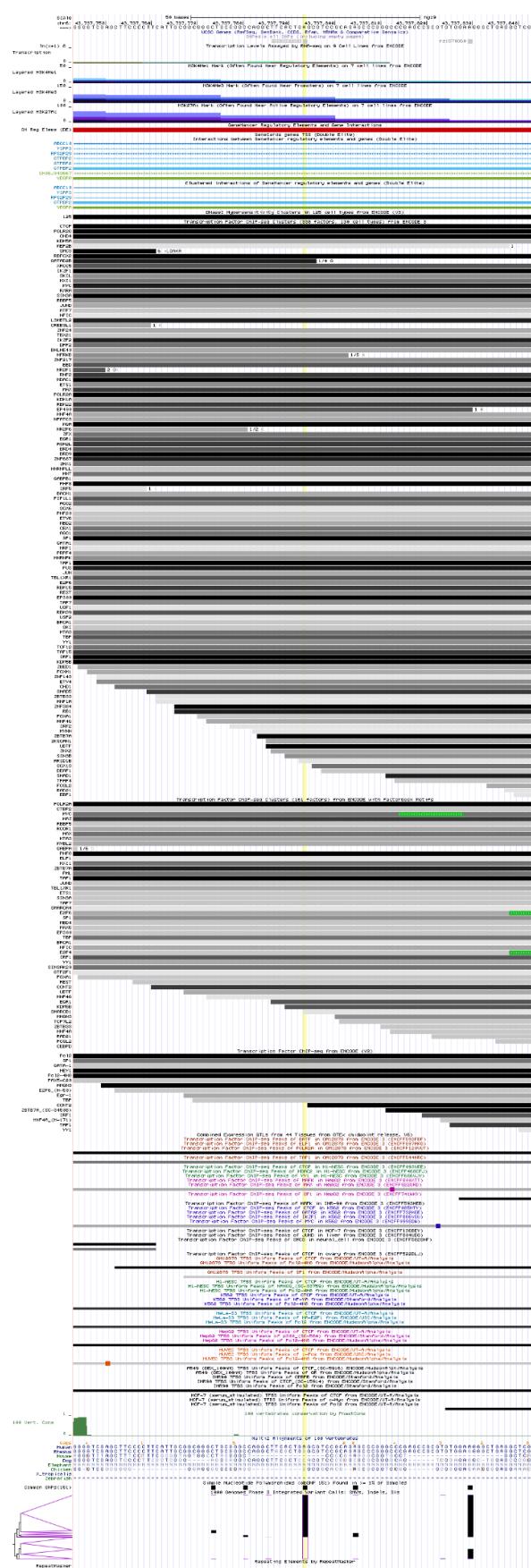


Figure S1. Analysis of regulatory element markers as well as transcription factor binding sites in loci associated with VEGFA rs13207351 from the UCSC Genome Browser (<http://genome.ucsc.edu>, accessed on 15 February 2021) and ENCODE (https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr6%3A43737744%2D43737844&hgsid=1030849587_t7VZPWaPfjsrlzTTaw-dln7DOIgoT, accessed on 15 February 2021).

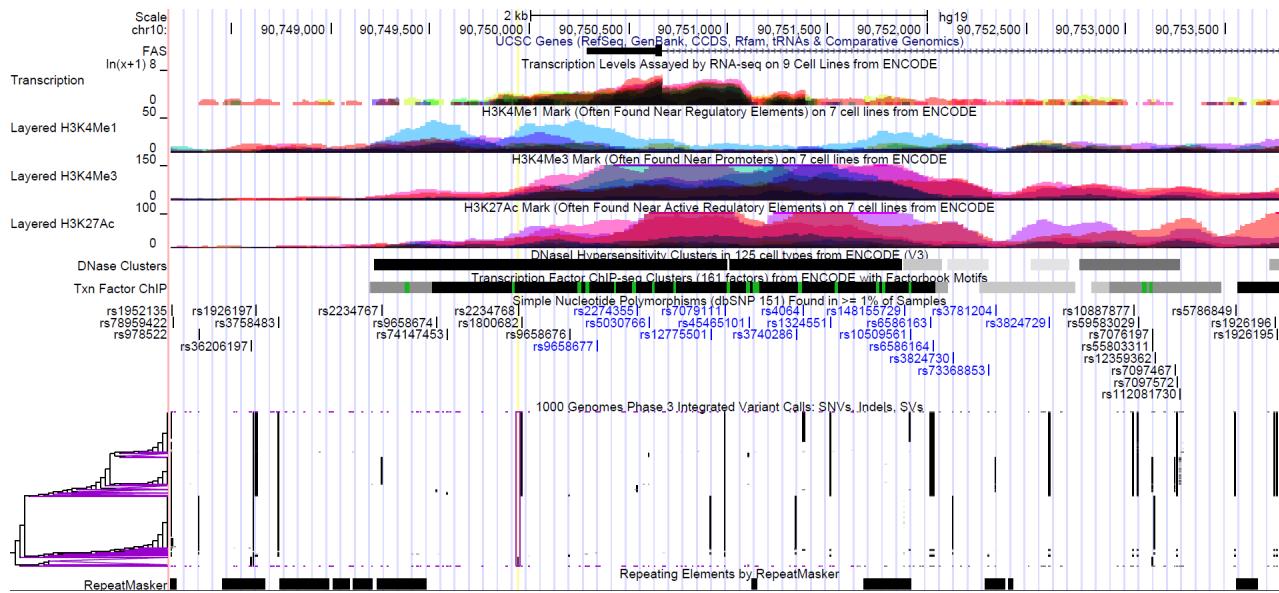


Figure S2. Analysis of regulatory element markers as well as transcription factor binding sites in genomic loci associated with *FAS* rs2234768 from the UCSC Genome Browser (<http://genome.ucsc.edu>) and ENCODE (https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr10%3A90748194%2D90753813&hgsid=1030946669_QZu9OaqVBNAI1d5rluV4CLcRdd5q, accessed on 15 February 2021).