

**Table S1.** Demographics and clinical characteristics of 277 controls and 277 patients with lung adenocarcinoma.

Variable	Control (n=277) n (%)	LUAD (n=277) n (%)	p value
Age			
Mean $\pm$ SD	64.53 $\pm$ 4.17	65.90 $\pm$ 13.64	p=0.176
Gender			
Male	126 (45.5%)	126 (45.5%)	p=1.000
Female	151 (54.5%)	151 (54.5%)	
Cigarette smoking status			
Never-smoker	215 (77.6%)	178 (64.3%)	p=0.001
Ever-smoker	62 (22.4%)	99 (35.7%)	
EGFR mutation status			
Wild type		111 (40.1%)	
Mutation		166 (59.9%)	
stage			
I+II		72 (26.0%)	
III+IV		205 (74.0%)	
Tumor T status			
T1+T2		167 (60.3%)	
T3+T4		110 (39.7%)	
Lymph node status			
Negative		83 (30.0%)	
Positive		194 (70.0%)	
Distant metastases			
Negative		132 (47.7%)	
Positive		145 (52.3%)	
Cell differentiation			
Well		27 (9.7%)	
Moderate		217 (78.3%)	
Poor		33 (11.9%)	

Abbreviation: LUAD, lung adenocarcinoma.

**Table S2.** The context sequences of the four *visfatin* SNPs in this study.

Variable	TaqMan Assay ID	Context Sequence
<i>visfatin</i> (rs11977021)	C__11405260_10	ATACTCCAATCTGACCTGATTTGAC[C/T]TCAG TAAAAAACAACACTGGTGAAGTAG
<i>visfatin</i> (rs61330082)	C__88870749_10	ATCATGGAAGTGGAAGGTATCACCA[G/A]GCA CTCACCAATGTAGTAAATACTA
<i>visfatin</i> (rs2110385)	C__16125685_10	ATAAGACTGGTTTTCTTGAGGAAGC[G/T]GAAC ATGAAAGGCTATATGTCTGAT
<i>visfatin</i> (rs4730153)	C__2673294_10	CCTTTAATCATATCTCATGTTTACT[A/G]TACCA AACCATCAACATCACAGAGA

**Table S3.** Clinicopathologic characteristics of lung adenocarcinoma patients stratified by EGFR status and genotypes at *visfatin* rs2110385.

Variable	ALL (N=277)			EGFR wild type (N=111)			EGFR mutation (N=166)		
	GG (n=228)	GT+TT (n=49)	<i>p</i> value	GG (n=93)	GT+TT (n=18)	<i>p</i> value	GG (n =135)	GT+TT (n=31)	<i>p</i> value
Stages									
I+II	58 (25.4%)	14 (28.6%)	<i>p</i> =0.650	22 (23.7%)	4 (22.2%)	<i>p</i> =0.895	36 (26.7%)	10 (32.3%)	<i>p</i> =0.530
III+IV	170 (74.6%)	35 (71.4%)		71 (76.3%)	14 (77.8%)		99 (73.3%)	21 (67.7%)	
Tumor T status									
T1+T2	138 (60.5%)	29 (59.2%)	<i>p</i> =0.862	52 (55.9%)	8 (44.4%)	<i>p</i> =0.371	86 (63.7%)	21 (67.7%)	<i>p</i> =0.672
T3+T4	90 (39.5%)	20 (40.8%)		41 (44.1%)	10 (55.6%)		49 (36.3%)	10 (32.3%)	
Lymph node status									
Negative	69 (30.3%)	14 (28.6%)	<i>p</i> =0.815	25 (26.9%)	4 (22.2%)	<i>p</i> =0.680	44 (32.6%)	10 (32.3%)	<i>p</i> =0.971
Positive	159 (69.7%)	35 (71.4%)		68 (73.1%)	14 (77.8%)		91 (67.4%)	21 (67.7%)	
Distant metastases									
Negative	110 (48.2%)	22 (44.9%)	<i>p</i> =0.670	45 (48.4%)	9 (50.0%)	<i>p</i> =0.900	65 (48.1%)	13 (41.9%)	<i>p</i> =0.532
Positive	118 (51.8%)	27 (55.1%)		48 (51.6%)	9 (50.0%)		70 (51.9%)	18 (58.1%)	
Cell differentiation									
Well/ Moderate	200 (87.7%)	44 (89.8%)	<i>p</i> =0.684	73 (78.5%)	15 (83.3%)	<i>p</i> =0.643	127 (94.1%)	29 (93.5%)	<i>p</i> =0.912
Poor	28 (12.3%)	5 (10.2%)		20 (21.5%)	3 (16.7%)		8 (5.9%)	2 (6.5%)	

Abbreviation: EGFR, epidermal growth factor receptor.

**Table S4.** Clinicopathologic characteristics of lung adenocarcinoma patients stratified by EGFR status and genotypes at Visfatin rs4730153.

Variable	ALL (N=277)			EGFR wild type (N=111)			EGFR mutation (N=166)		
	GG (n=230)	GA+AA (n=47)	<i>p</i> value	GG (n =93)	GA+AA (n =18)	<i>p</i> value	GG (n =137)	GA+AA (n =29)	<i>p</i> value
Stages									
I+II	61 (26.5%)	11 (23.4%)	<i>p</i> =0.657	22 (23.7%)	4 (22.2%)	<i>p</i> =0.895	39 (28.5%)	7 (24.1%)	<i>p</i> =0.636
III+IV	169 (73.5%)	36 (76.6%)		71 (76.3%)	14 (77.8%)		98 (71.5%)	22 (75.9%)	
Tumor T status									
T1+T2	141 (61.3%)	26 (55.3%)	<i>p</i> =0.445	52 (55.9%)	8 (44.4%)	<i>p</i> =0.371	89 (65.0%)	18 (62.1%)	<i>p</i> =0.767
T3+T4	89 (38.7%)	21 (44.7%)		41 (44.1%)	10 (55.6%)		48 (35.0%)	11 (37.9%)	
Lymph node status									
Negative	72 (31.3%)	11 (23.4%)	<i>p</i> =0.281	25 (26.9%)	4 (22.2%)	<i>p</i> =0.680	47 (34.3%)	7 (24.1%)	<i>p</i> =0.288
Positive	158 (68.7%)	36 (76.6%)		68 (73.1%)	14 (77.8%)		90 (65.7%)	22 (75.9%)	
Distant metastases									
Negative	113 (49.1%)	19 (40.4%)	<i>p</i> =0.276	45 (48.4%)	9 (50.0%)	<i>p</i> =0.900	68 (49.6%)	10 (34.5%)	<i>p</i> =0.137
Positive	117 (50.9%)	28 (59.6%)		48 (51.6%)	9 (50.0%)		69 (50.4%)	19 (65.5%)	
Cell differentiation									
Well/ Moderate	203 (88.3%)	41 (87.2%)	<i>p</i> =0.843	73 (78.5%)	15 (83.3%)	<i>p</i> =0.643	130 (94.9%)	26 (89.7%)	<i>p</i> =0.282
Poor	27 (11.7%)	6 (12.8%)		20 (21.5%)	3 (16.7%)		7 (5.1%)	3 (10.3%)	

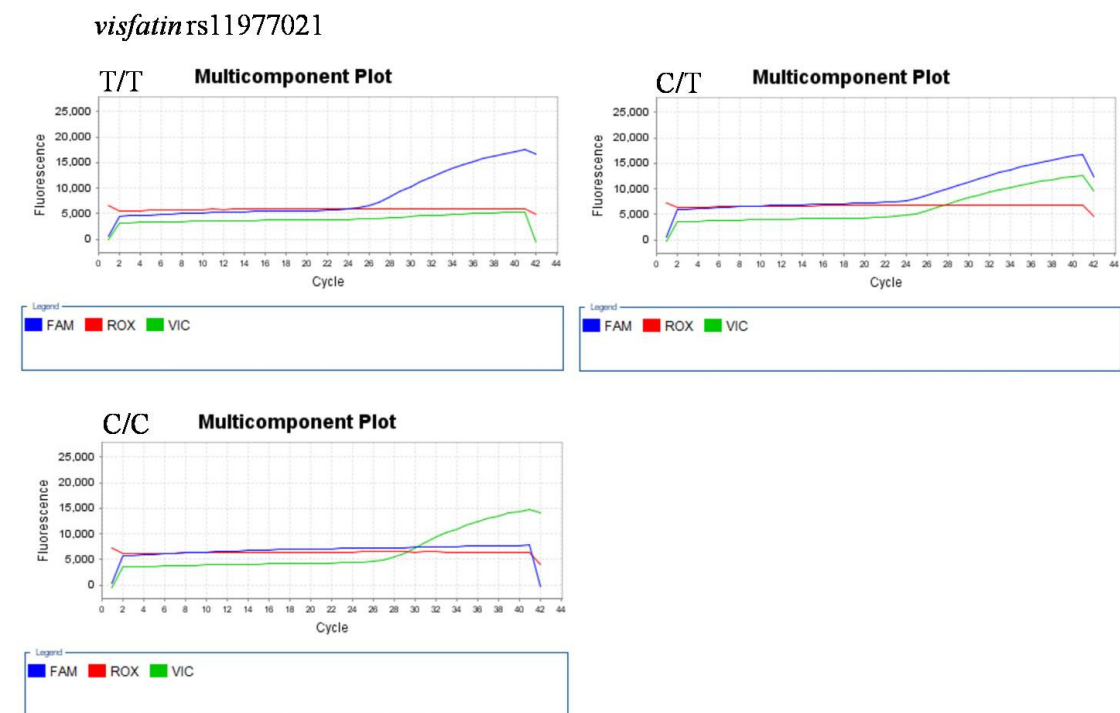
Abbreviation: EGFR, epidermal growth factor receptor.

**Table S5.** ALFA allele frequencies of Visfatin SNPs

Visfatin SNPs	rs11977021		rs61330082		rs2110385		rs4730153	
Population	Ref Allele	Alt Allele	Ref Allele	Alt Allele	Ref Allele	Alt Allele	Ref Allele	Alt Allele
<b>Total</b>	C=0.751497	T=0.248503	G=0.78939	A=0.21061	T=0.63197	A=0.00000, G=0.36803	A=0.49024	G=0.50976
<b>Asian</b>	C=0.4625	T=0.5375	G=0.507	A=0.493	T=0.2	A=0.0, G=0.8	A=0.105	G=0.895
<b>South Asian</b>	C=0.716	T=0.284	G=0.717	A=0.283	T=0.82	A=0.00, G=0.18	A=0.37	G=0.63
<b>European</b>	C=0.755595	T=0.244405	G=0.75706	A=0.24294	T=0.5107	A=0.0000, G=0.4893	A=0.42751	G=0.57249
<b>Latin American 1</b>	C=0.7428	T=0.2572	G=0.671	A=0.329	T=1.00	A=0.00, G=0.00	A=0.435	G=0.565
<b>Latin American 2</b>	C=0.6862	T=0.3138	G=0.677	A=0.323	T=1.00	A=0.00, G=0.00	A=0.299	G=0.701
<b>African</b>	C=0.8940	T=0.1060	G=0.8920	A=0.1080	T=0.8547	A=0.0000, G=0.1453	A=0.7868	G=0.2132
<b>Other</b>	C=0.7309	T=0.2691	G=0.773	A=0.227	T=0.614	A=0.000, G=0.386	A=0.4687	G=0.5313

The **Allele Frequency Aggregator (ALFA)** analysis of the aggregate allele frequency of *visfatin* SNPs using the database of Genotypes and Phenotypes (dbGaP). Release Version: 20201027095038.

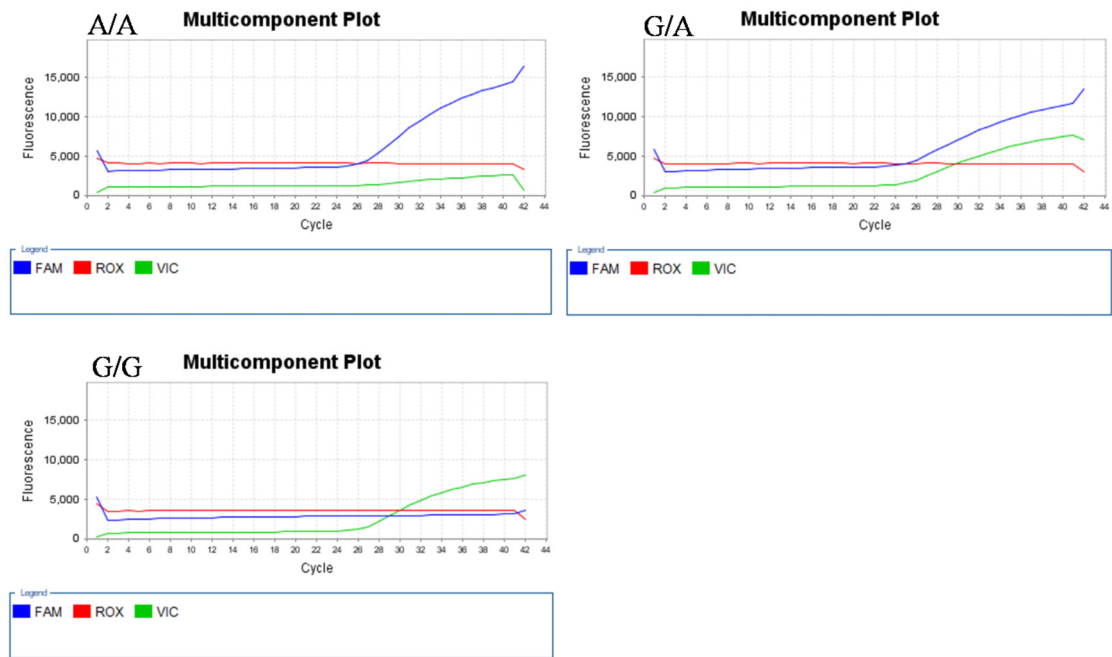
**Figure S1**



**Figure S1:** Representative TaqMan assay for *visfatin* rs11977021 genotyping.

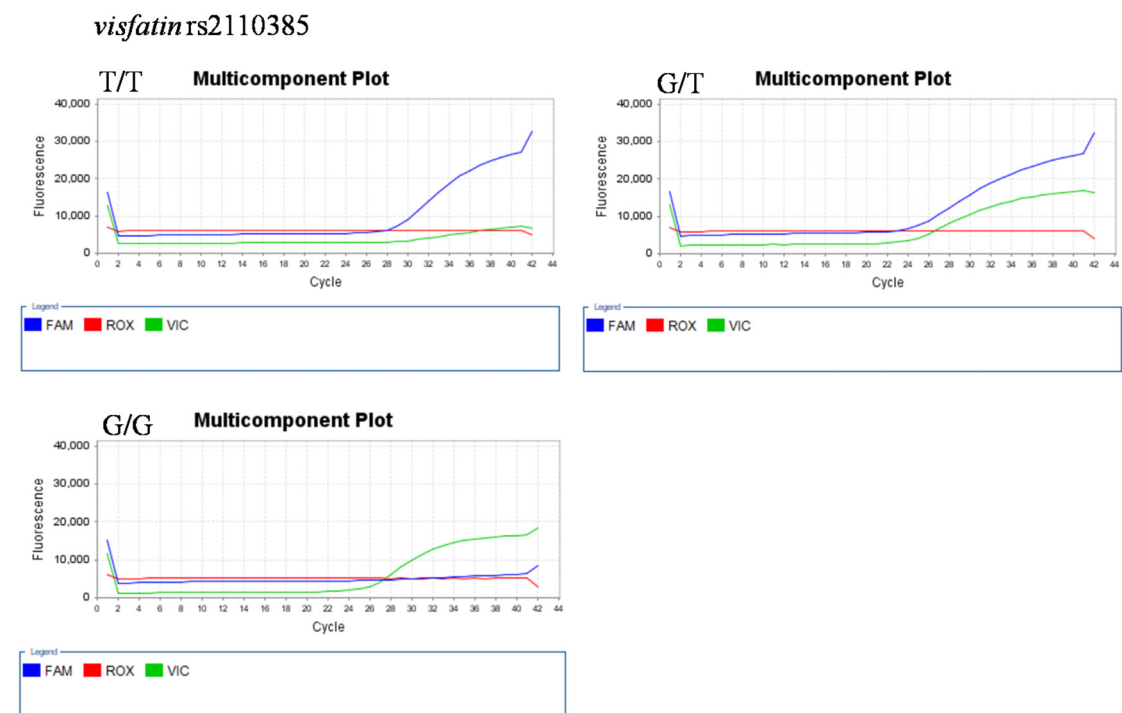
**Figure S2**

*visfatin* rs61330082



**Figure S2:** Representative TaqMan assay for *visfatin* rs61330082 genotyping.

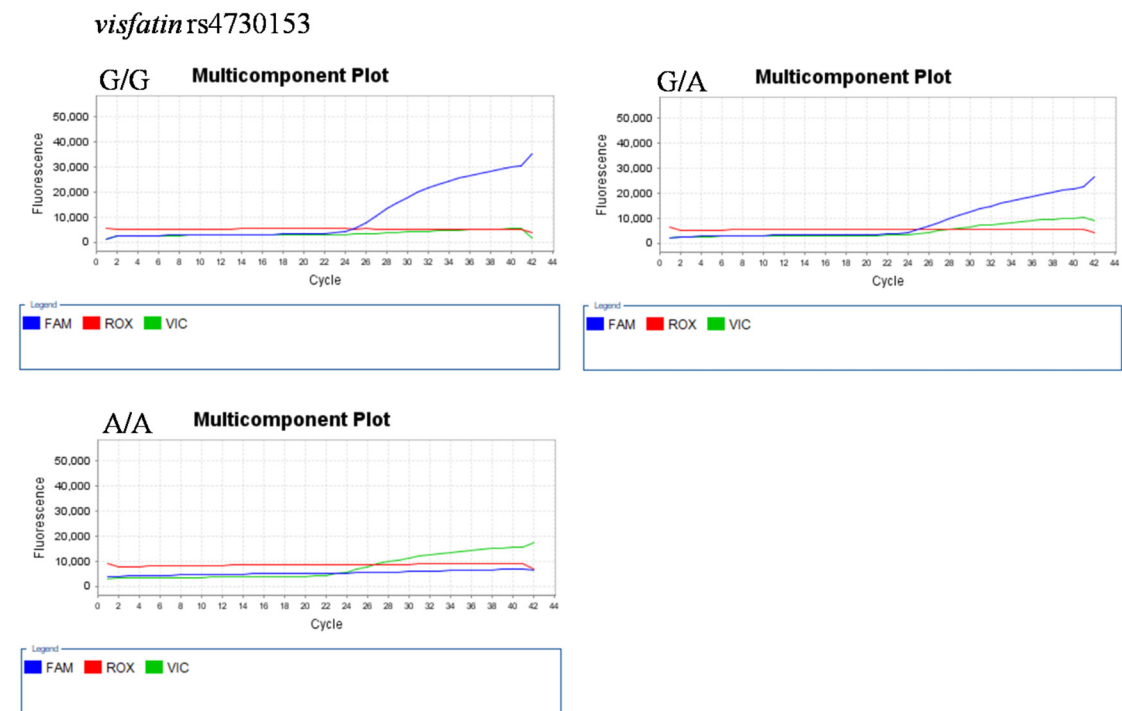
**Figure S3**



**Figure S3:** Representative TaqMan assay for *visfatin* rs2110385 genotyping.



**Figure S4**



**Figure S4:** Representative TaqMan assay for *visfatin* rs4730153 genotyping.