SUPPLEMENTARY INFORMATION

Title: HERG1A potassium channel is the predominant isoform in head and neck squamous cell carcinomas: evidence for regulation by epigenetic mechanisms

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Table S1. Correlation between HERG1A (NT) and HERG1 pan (CT) immunostaining (N=123)

Characteristic	No.	HERG1A protein expression	
		Negative	Positive
HERG1 protein expression			
Negative	15	8	7
Positive	108	3	105

† Kendall's Tau = 0.580; *P* <0.001

Table S2. Associations between HERG1A protein expression and clinicopathological findings, site, relapse and disease outcome

Characteristic	No.	HERG1A protein expression (%)	*P*
- pT classification			
T1-T2	35	29 (83)	0.203[#]
T3	45	42 (93)	
T4	45	42 (93)	
- pN classification			
N0	40	32 (80)	0.018[†]
N1-3	85	81 (95)	
- Disease stage			
I-II	15	9 (60)	<0.001[#]
III	24	22 (92)	
IV	86	82 (95)	
- Pathological grade			
Well differentiated	35	28 (80)	0.048[#]
Moderately differentiated	56	53 (95)	
Poorly differentiated	34	32 (94)	
- Site			
Pharynx	61	58 (95)	0.128[†]
Larynx	64	55 (86)	
- Tumour Recurrence‡			
No	35	29 (80)	0.028[†]
Yes	75	72 (96)	
- Distant Metastasis			
No	60	52 (87)	0.038[†]
Yes	50	49 (98)	
- Disease status			
Alive without disease	29	24 (83)	0.045[†]
Dead of index cancer	70	67 (96)	
Died of other causes	14	13 (85)	
Total Cases	125	113 (90)	

[#] Chi-square and [†] Fisher's exact tests.

‡ 15 patients who died from causes not related to the index tumour before 36 months of follow-up were excluded from the recurrence analysis.

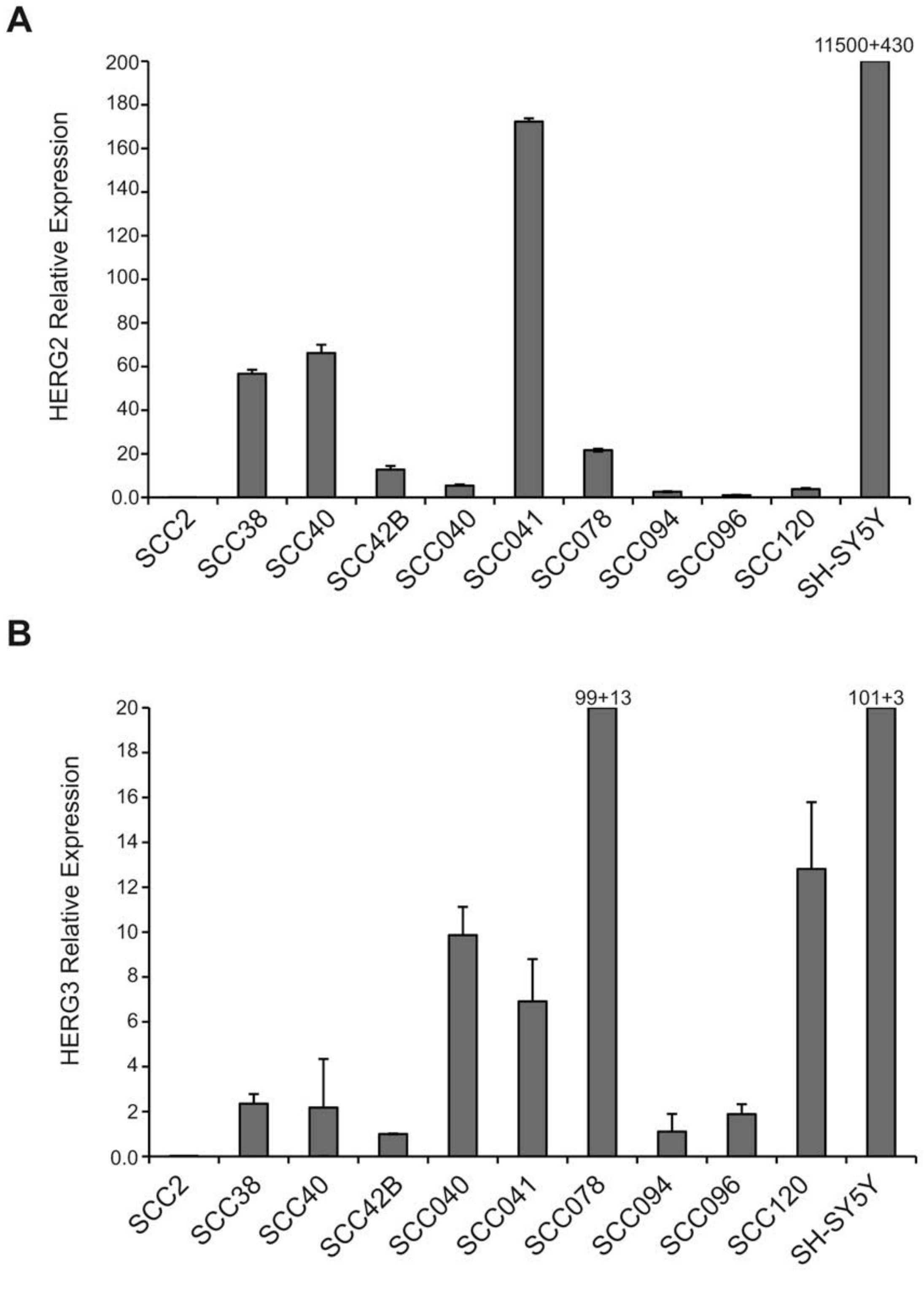
Table S3. Primers used in real-time RT-PCR and qChIP *

GENE	FORWARD (5’ -> 3’)	REVERSE (5’ -> 3’)
HERG1A	ACCGTGAGATCATAGCACCTAA	ACAGGACCTGGGTGACCTTCT
HERG1B #	ACAGGACCTGGGTGACCTTCT	ACGTCGGCGCCCAGGGACA
HERG2	GGCCTTGGTTCCTATAGCCT	TCCAGGGGATGTAGAGGTGA
HERG3	CGGACCTCTTGACCATTCCT	ATTGTCTTCGCTGGCATGTC
Kv 1.3	GCCAGTTCCCGTGATTGTTT	CGTTTTGAAAGGGGTCTGGG
KCa 3.1	GTTCGTGGCCAAGCTTTACA	GCATTAACAGCCTGCCTCTC
Kv3.4	CGCTCTTCGAGGATCCCTACT	TGGTGATGGAGACCAGGATGA
HERG2 (KCNH6)*	ACGCTGCTGAGCCCG	CCTGCCCGGAGCCACA
HERG3 (KCNH7)*	GCGGGTGTCTAGAAGTGGTG	CTCTTTGTGGCAGAGCATCC
Kv 1.3 (KCNA3)*	GCAGCCTGACTCCCCGT	GCCCTCATGTTGTACCTCGG
KCa 3.1 (KCNN4)*	TGTTTGGGTGTGGCTCTTTG	GTCCACACACAGGCACAAAT
Kv 3.4 (KCNC4)*	TGCCTCCTCTTCGTCTCCTC	CTCCAAACACCCTTCCCGAG
HERG1 (KCNH2)*	CCCGCAGTCCAGTCTTGG	CAGCACTAGGCTTCGGGTG
	Probe 6-FAM-CGCCCGTGCTCGGCTTGG-TAMRA	

Primer sequences taken from Pillozi *et al.* [13].

Figure Legends

Figure S1. Analysis of HERG2 and HERG3 mRNA levels by real-time RT-PCR in HNSCC-derived cell lines. Data are expressed as the fold change in HERG2 or HERG3 levels in the HNSCC-derived cell lines normalised to L19 mRNA levels. The graphs represent the means + SD of at least two independent experiments performed in quadruplicate. SH-SY5Y cells served as a positive control.


A
HERG2 Relative Expression
0.0
20
40
60
80
100
120
140
160
180
200
11500+430
SCC2
SCC38
SCC40
SCC42B
SCC040
SCC041
SCC078
SCC094
SCC096
SCC120
SH-SY5Y
B
HERG3 Relative Expression
0.0
2
4
6
8
10
12
14
16
18
20
99+13
101+3
SCC2
SCC38
SCC40
SCC42B
SCC040
SCC041
SCC078
SCC094
SCC096
SCC120
SH-SY5Y