

琉球大学学術リポジトリ

SIW/SNF遺伝子異常の食道扁平上皮がん発がんの早期における誘発

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Table 3. The association between SWI/SNF alterations and clinicopathological characteristics.

Characteristics	Categories	SWI/SNF mutation			<i>ACTL6B</i> methylation		
		(+)	(-)	<i>P</i> value	(+)	(-)	<i>P</i> value
Total		8	84		18	34	
Clinical T stage				0.71			1
	T1 and T2	2	33		6	12	
	T3 and T4	6	51		12	22	
Clinical N stage				1			0.41
	N0	2	20		3	3	
	N1, N2, and N3	6	64		15	31	
Clinical M stage				0.38			0.73
	M0	5	66		13	27	
	M1	3	18		5	7	

Table S1. Primers used for Sanger sequencing.

Gene	Target variation	Forward primer (5' -> 3')	Reverse primer (5' -> 3')	Amplified region	Amplicon length (bp)
<i>ARID1A</i>	c.2017C>T	GTGAGCACATCAGGGATTTCCA	AGTCACCTTTCCCTCTCCCTAA	chr1:27087407-27087629	223
<i>ARID1A</i>	c.5013_5034delGGTAATGATGTCCCTCAAGTCT	TGGTGGATAGACGACATGGAG	GAAGATCCCAAACCCTCTC	chr1:27102036-27102243	208
<i>ARID2</i>	c.1925G>T	AATTCCTACTTGGGATTTTCAGTC	GAAGATTGGTTGGCAACAGG	chr12:46243756-46243885	130
<i>ARID2</i>	c.28C>A	TCTGGTAGGAAGCGCTGG	TTCTGCCTCTCACCTCTGCTG	chr12:46123541-46123723	183
<i>ARID2</i>	c.994C>T	ACGATATTGAAGGACAGCGG	GGTACAGTCACATGCTTACCTCAG	chr12:46230587-46230793	207
<i>ATRX</i>	c.277G>A	GGGTATTGTTCCAGTTGTCAG	GACGCATCTTCATTTACAGTTTC	chrX:76952112-76952250	139
<i>ATRX</i>	c.319G>C	GGGTATTGTTCCAGTTGTCAG	GCCATGTTTGGTCGTTTG	chrX:76951953-76952250	298
<i>ATRX</i>	c.5394A>C	GGATCCATTAAGGAGTTCAGG	CTACTGAAAGAGCGGGAAAG	chrX:76874158-76874411	254
<i>PBRM1</i>	c.239A>G	GCCTGTCACTTGGAAATGTTG	CTGGAAGTCAGCAGTCAGCAA	chr3:52702547-52702764	218
<i>PBRM1</i>	c.3778G>C	TTGTGAGAGCCGCTACAATG	CTATCAGTTAATGGAAGTGCTC	chr3:52598016-52598173	158
<i>PBRM1</i>	c.3883G>C	TGCTTTCCGGCTTATTCTGGAG	AAGCTGAGGTAGAGAAGGAGGTT	chr3:52597350-52597573	224
<i>PBRM1</i>	c.4129G>A	GTGGGGACAGAATGGAGAAA	TACTGGTTGGGTGCCATTTG	chr3:52595639-52595834	196
<i>PHF10</i>	c.1018T>A	ACAGCTCCTCTGGCAATGTATC	TATTTACGGGAGAGGCTGGTC	chr6:170110275-170110486	212
<i>SMARCA1</i>	c.2689G>T	CACAGGGTTTCACAACTGG	AAACATCTCTGAACAAAGGTAC	chrX:128602660-128602887	228
<i>SMARCA4</i>	c.1481C>G	CCTGCAGGAATACCTCAATAGC	TAGAAGAGCGCACGTCAAG	chr19:11105497-11105711	215
<i>SMARCA4</i>	c.254C>T	CACATGCTGACCCTGCCTT	GGACTCTGGAGTATGACAAACACA	chr19:11095911-11096131	221
<i>SMARCA4</i>	c.2644G>A	AGATTCTCCCCATGTGCC	AAGGGTGCCTTAAACCACTG	chr19:11132335-11132624	290
<i>SMARCA4</i>	c.3619G>A	TTATGACCTCCTGGGCTCCTTTG	CTGGTCCACGTTGAGCTTGATC	chr19:11143917-11144097	181
<i>SMARCA1</i>	c.1129G>C	GAAGGGCAGGGTGTCTATTT	TACTCAAGCATCCCACCACA	chr2:217288310-217288527	218
<i>SMARCC1</i>	c.3095G>A	AAATCTCCCTCCACAGGTCA	CTTACACATGCCGTTAGGTGC	chr3:47632146-47632343	198

Table S2. Primers used for DNA methylation analysis and expression analysis.

Gene	Type	Forward primer sequence	Reverse primer sequence	Annealing temperature (°C)
<i>ACTL6B</i>	M	TTTTCGGTCGGTTATTGTTTC	CTACGCTACTAACGACCCG	58
<i>ACTL6B</i>	U	TTGTTTTGGTTGGTTATTGTTTT	CTACTACTAACAACCCATAA	58
<i>ACTL6B</i>	RT	CTCCACATCGACACCAATG	TTGGCTCAGACTTGACGTG	62
<i>GAPDH</i>	RT	AGGTGAAGGTCGGAGTCAACG	AGGGGTCATTGATGGCAACA	54

M, primers specific to methylated DNA; U, primers specific to unmethylated DNA; and RT, primers for quantitative RT-PCR.

Table S3. Cancer cell fractions in the 8 ESCC samples with mutations of chromatin remodelers.

Sample number	Cancer cell fraction (%)
20	64
85	23
89	87
94	34
126	75
127	45
169	71
176	40