The comprehensive map of SHOX2: chr3:157,811,666-157,828,577

Replication region of epigenomics[[1-5](#_ENREF_1)]

GTCCCCTGGACAGCCAGGTAATCTCCGTCCCGCCTGCCCGACCGGGGTCGCACGAGCACAGGCGCCCACGCCATGTTGGCTGCCCAAAGGGCTCGCCGCCCAAGCCGGGCCAGAAGGCAGGAGG

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Name | Tm(oC) | GC% | sequence | date | designer | purpose | Sense | Gene&Accession No |
| SHOX2bspf | 58.85 | 75 | GGGATATTGGAGGGGGTATT | 2011/6/9 | 郭士成 | BSP | on | SHOX2 |
| SHOX2bspt | 58.29 | 75 | CTACCCACCTTACCCCAAAC | 2011/6/9 | 郭士成 | BSP | off | SHOX2 |
| SHOX2mf | 56.51 | 77.27 | GTATTTTAGCGGGGTTATACGT | 2011/6/9 | 郭士成 | MSP | on | SHOX2 |
| SHOX2mt | 57.4 | 68.18 | CCGAATAAATTAAAAAACCGAA | 2011/6/9 | 郭士成 | MSP | off | SHOX2 |
| SHOX2uf | 59.59 | 80 | GGGGTATTTTAGTGGGGTTATATGT | 2011/6/9 | 郭士成 | MSP | on | SHOX2 |
| SHOX2ut | 59.26 | 64 | TTCCTCCAAATAAATTAAAAAACCA | 2011/6/9 | 郭士成 | MSP | off | SHOX2 |
| shox2\_3mf | 55.48 | 75 | ATTTTAGCGGGGTTATACGT | 2011/6/9 | 郭士成 | MSP | on | shox2\_3 |
| shox2\_3mt | 54.33 | 61.11 | GAACCAAAATTCCACGAA | 2011/6/9 | 郭士成 | MSP | off | shox2\_3 |
| shox2\_3uf | 56.63 | 79.17 | GGGTATTTTAGTGGGGTTATATGT | 2011/6/9 | 郭士成 | MSP | on | shox2\_3 |
| shox2\_3ut | 57.82 | 65 | ACCAAACCAAAATTCCACAA | 2011/6/9 | 郭士成 | MSP | off | shox2\_3 |
| SHOX2Eurobspf | 54.82 | 36 | TTTGTTGGTTTAATTTAGGAATAAT | 2011/6/9 | 郭士成 | BSP | on | SHOX2Euro |
| SHOX2Eurobspt | 55.45 | 63.64 | CCCTTTAAACAACCAACATAAC | 2011/6/9 | 郭士成 | BSP | off | SHOX2Euro |

>hg19\_cpgIslandExt\_CpG: 71 range=chr3:157822974-157823836 5'pad=0 3'pad=0 strand=+ repeatMasking=none

CGGAGTTCGAGGGGTCTTGGCGGCCCCAAACACCTAGGCGACCGGAGGGT

TAAGCTTTCCACCTCTGCCCCTTCTCCCTCCCGGCAAACTCTGCGCTAGA

GGCTAGCTTTAGTCCCGCCGTCTGGTTCAGCACCCCCTCCTGCAGCCCGG

CCCCGCGAACTTCCACGTCCGCCTGCGGGCCATCCGGGCTGCGGGCCCAT

CCTCCCGCTGGTGAAAAATGCATTTCGGTGGAATGGGAACATCTGGGAAG

GGCGCGCACAAACCCCACACGCTTCCCCCCACGCCACCCCCACAACACAC

TAGGACCCCACCCATGACCGAGCATACCACCGGACCCCCACCCTTCCACT

ATCACTCTAGCTGACAAAGCTGGGGTCCAGGGCCCTCTCCGTGTCCCTCT

CCCCTCCCCGCTGGGCCTCGGAGTCCTCTCCCGCCCGAGAGGAGTCCGGA

AGGCGGGAAGGGGAACCGCTGCCGGGGGTCAGTCAGGTCGTTACCCTCCG

TCAGTCGCGGGCTGCCCGGCTCCCTGCTTCTCTCGGCGGCGCCCATGTCC

AGCTCCCGGACGGGAGAGCGCCCTCCTCCAGCTCCTCCGCCTGCTCCTCC

TCCTCCTACACCTCCTCCGCCTCCTCCGCCGCCGCCTCCGCCTCCTCCGC

CGCCGCCTCCGCCGGCCGCCCGGACTGCCGGGCTGCTGCGGTCGTCGCGG

CCCGCCTCGGTGCAGCCGGTCGGCTCCTTGGCCCCGCGCAGCGGCCCGCT

CTCCAGCACCTCCCGGTACGTGATCGCCTCCTTCTTCTCCTTCACTTTCT

GGTCAAAAGACTTGGAGACGAACGCCGTAAGTTCTTCCATCGCCGCCGCA

CGTCAGCCCGGCG

1. Dietrich D, Hasinger O, Liebenberg V, Field JK, Kristiansen G, Soltermann A: **DNA methylation of the homeobox genes PITX2 and SHOX2 predicts outcome in non-small-cell lung cancer patients**. *Diagnostic molecular pathology : the American journal of surgical pathology, part B* 2012, **21**(2):93-104.

2. Dietrich D, Kneip C, Raji O, Liloglou T, Seegebarth A, Schlegel T, Flemming N, Rausch S, Distler J, Fleischhacker M *et al*: **Performance evaluation of the DNA methylation biomarker SHOX2 for the aid in diagnosis of lung cancer based on the analysis of bronchial aspirates**. *International journal of oncology* 2012, **40**(3):825-832.

3. Kneip C, Schmidt B, Seegebarth A, Weickmann S, Fleischhacker M, Liebenberg V, Field JK, Dietrich D: **SHOX2 DNA methylation is a biomarker for the diagnosis of lung cancer in plasma**. *Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer* 2011, **6**(10):1632-1638.

4. Schneider KU, Dietrich D, Fleischhacker M, Leschber G, Merk J, Schaper F, Stapert HR, Vossenaar ER, Weickmann S, Liebenberg V *et al*: **Correlation of SHOX2 gene amplification and DNA methylation in lung cancer tumors**. *BMC cancer* 2011, **11**:102.

5. Schmidt B, Liebenberg V, Dietrich D, Schlegel T, Kneip C, Seegebarth A, Flemming N, Seemann S, Distler J, Lewin J *et al*: **SHOX2 DNA methylation is a biomarker for the diagnosis of lung cancer based on bronchial aspirates**. *BMC cancer* 2010, **10**:600.