**Supplementary Table S1. PCR primer sequences in this study**

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Primer sequence (5' - 3')** | **Method** | **Reference** |
| AR-fl-F | TGGATAGCTACTCCGGACCTTA | RT-PCR |  |
| AR-fl-R | GGAGTTGACATTGGTGAAGGAT | RT-PCR |  |
| AR-45-F | TGACATTGCCTGTCACTTTTTC | RT-PCR |  |
| AR-45-R | CACACACTACACCTGGCTCAAT | RT-PCR |  |
| AR-V7-F | CTACTCCGGACCTTACGGGGACATGCG | RT-PCR |  |
| AR-V7-R | TGCCAACCCGGAATTTTTCTCCC | RT-PCR |  |
| AR-V1-F | AACAGAAGTACCTGTGCGCC | RT-PCR | ([1](#_ENREF_1)) |
| AR-V1-R | TGAGACTCCAAACACCCTCA | RT-PCR | (1) |
| AR-V3-F | TGGATGGATAGCTACTCCGG | RT-PCR | (1) |
| AR-V3-R | GTTCATTCTGAAAAATCCTTCAGC | RT-PCR | (1) |
| ARv567es-F | AATGAACTGGGAGAGAGACAGC | RT-PCR |  |
| ARv567es-R | CAGGTCAAAAGTGAACTGATGC | RT-PCR |  |
| AR-V5-F | AACAGAAGTACCTGTGCGCC | RT-PCR | (1) |
| AR-V5-R | TATGACACTCTGCTGCCTGC | RT-PCR | (1) |
| AR-V4-F | AACAGAAGTACCTGTGCGCC | RT-PCR | (1) |
| AR-V4-R | TTCTGTCAGTCCCATTGGTG | RT-PCR | (1) |
| AR-E1F1 | AGCCTGTTGAACTCTTCTGAGC | Sequencing (Exon1) | ([2](#_ENREF_2)) |
| AR-E1R1 | GGTGGAACTCCCAAAAGTGG | Sequencing (Exon1) | (2) |
| AR-E1F2 | GCTCCCACTTCCTCCAAGGACAATTAC | Sequencing (Exon1) | (2) |
| AR-E1R2 | CGGGTTCTCCAGCTTGATGCG | Sequencing (Exon1) | (2) |
| AR-E1F3 | CCAGAGTCGCGACTACTACAACTTTCC | Sequencing (Exon1) | (2) |
| AR-E1R3 | CCAGAACACAGAGTGACTCTGCC | Sequencing (Exon1) | (2) |
| AR-E2F | TCAGTCACACCCTACAACCATC | Sequencing (Exon2) |  |
| AR-E2R | GCCTTGCCAATGACTCTATTTC | Sequencing (Exon2) |  |
| AR-E3F | TTGTTTGGTGCCATACTCTGTC | Sequencing (Exon3) |  |
| AR-E3R | CTATGAAAGGGTCAGCCTGTGT | Sequencing (Exon3) |  |
| AR-E4F | CTGTGACCAGGGAGAATGGT | Sequencing (Exon4) |  |
| AR-E4R | GCCTGAGTTAATGGGCAGAA | Sequencing (Exon4) |  |
| AR-E5F | CAGACTTAGCTCAACCCGTCA | Sequencing (Exon5) |  |
| AR-E5R | TAGGATTGGTTCTTGGGTGTG | Sequencing (Exon5) |  |
| AR-E6F | CAGCAAGCTCTTCTTGGAAAA | Sequencing (Exon6) |  |
| AR-E6R | AAGAAGGGAAATGTCCAGGAG | Sequencing (Exon6) |  |
| AR-E7F | TCTGTGGTCAGAAAACTTGGTG | Sequencing (Exon7) |  |
| AR-E7R | ACTGTGACCCGTGTTCTTTTCT | Sequencing (Exon7) |  |
| AR-E8F | AAAAGGCTGAAAGACCAAAAATC | Sequencing (Exon8) |  |
| AR-E8R | TAGGGAGGGAAGAAGAAAAAGAA | Sequencing (Exon8) |  |
| AR-fl-QF | TCCCACTTGTGTCAAAAGC | Quantitative RT-PCR |  |
| AR-fl-QR | AAACATGGTCCCTGGCAGTC | Quantitative RT-PCR |  |
| AR-45-QF | AACGAATGCAGAGTGCTCCT | Quantitative RT-PCR |  |
| AR-45-QR | AAACATGGTCCCTGGCAGTC | Quantitative RT-PCR |  |
| AR-V7-QF | CTACTCCGGACCTTACGGGGACATGCG | Quantitative RT-PCR |  |
| AR-V7-QR | TGCCAACCCGGAATTTTTCTCCC | Quantitative RT-PCR |  |
| ACTB-QF | TCACCGAGCGCGGCT | Quantitative RT-PCR |  |
| ACTB-QR | TAATGTCACGCACGATTTCCC | Quantitative RT-PCR |  |

References;

1. Li Y, Alsagabi M, Fan D, Bova GS, Tewfik AH, Dehm SM. Intragenic rearrangement and altered RNA splicing of the androgen receptor in a cell-based model of prostate cancer progression. Cancer Res. 2011;71:2108-17.

2. Gottlieb B, Vasiliou DM, Lumbroso R, Beitel LK, Pinsky L, Trifiro MA. Analysis of exon 1 mutations in the androgen receptor gene. Hum Mutat. 1999;14:527-39.

**Supplementary Table S2. AR IHC and FISH result**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | |  | **Male** | **Female** |
| **AR IHCa** | | |  |  |
|  | Nu | | 15 | 8 |
|  | Nu/Cy | | 1 | 3 |
|  | Negative | | 4 | 4 |
| **AR FISH** | |  |  |  |
| **X chr status in AR(+)** | | |  |  |
|  | Gain | | 7 | 3 |
|  | Loss | | 0 | 1 |
|  | No change | | 9 | 7 |
| **X chr status in AR(-)** | | |  |  |
|  | Gain | | 1 | 2 |
|  | Loss | | 0 | 0 |
|  | No change | | 3 | 2 |

aNu, nuclear positive; Cy, cytoplasmic positive.

**Supplementary Table S3. *AR* mutation detail result in this study.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample** | **AA Mutation** | **CDS Mutation** | **CAG repeat** | **GGN repeat** |
| 49F1 | - | - | 18 | 23 |
| 167H1 | - | - | 24 | 23 |
| 340H1 | - | - | 20 | 19 |
| 401G8 | - | - | 27 | 24 |
| 403H1 | p.E213E | c.639G>A | 18 | 20 |
| 430A8 | p.E213E | c.639G>A | 19 | 24 |
| 438E6 | p.E213E | c.639G>A | 22 | 23 |
| 458A1 | - | - | 18 | 24 |
| 465A4 | - | - | 24 | 23 |
| 495E6 | - | - | 22 | 23 |
| 518F1 | - | - | 27 | 19 |
| 527E5 | - | - | 22 | 23 |
| 530D2 | - | - | 21 | 24 |
| 532H4 | - | - | 25 | 23 |
| 540E3 | - | - | 21 | 22 |
| 544B8 | - | - | 20 | 19 |
| 544C3 | p.E213E | c.639G>A | 22 | 22 |
| 545F2 | - | - | 22 | 23 |
| 548A6 | p.E213E | c.639G>A | 21 | 22 |
| 548B6 | - | - | 19 | 23 |
| 560A1 | - | - | 21 | 23 |
| 563F1 | - | - | 18 | 23 |
| 565E4 | p.E213E | c.639G>A | 22 | 22 |
| 570F3 | - | - | 22 | 23 |
| 599B2 | - | - | 22 | 23 |
| 610B8 | p.E213E | c.639G>A | 18 | 23 |
| 619C7 | p.E213E | c.639G>A | 22 | 23 |
| 623E5 | p.Q24Q | c.72G>A | 20 | 23 |
| 625D3 | - | - | 18 | 23 |
| 629D3 | - | - | 21 | 23 |
| 636A8 | - | - | 21 | 23 |
| 648B4 | p.E213E | c.639G>A | 20 | 24 |
| 650E2 | - | - | 20 | 23 |
| 652G7 | - | - | 25 | 23 |
| 688A5 | - | - | 22 | 23 |
| RET981 cell | - | - | 19 | 20 |

p.E213E (c.639G>A, dbSNP re#; rs6152) has been sequenced in 1000 Genome project as SNP. p.Q24Q (c.72G>A, dbSNP re#; rs199644815)

(-); no mutation.