

Supplementary Information for

Ionizing Radiation Promotes Epithelial-Mesenchymal Transition Phenotype and Stem Cell Marker in The Lung adenocarcinoma: *In Vitro* and Bioinformatic Studies

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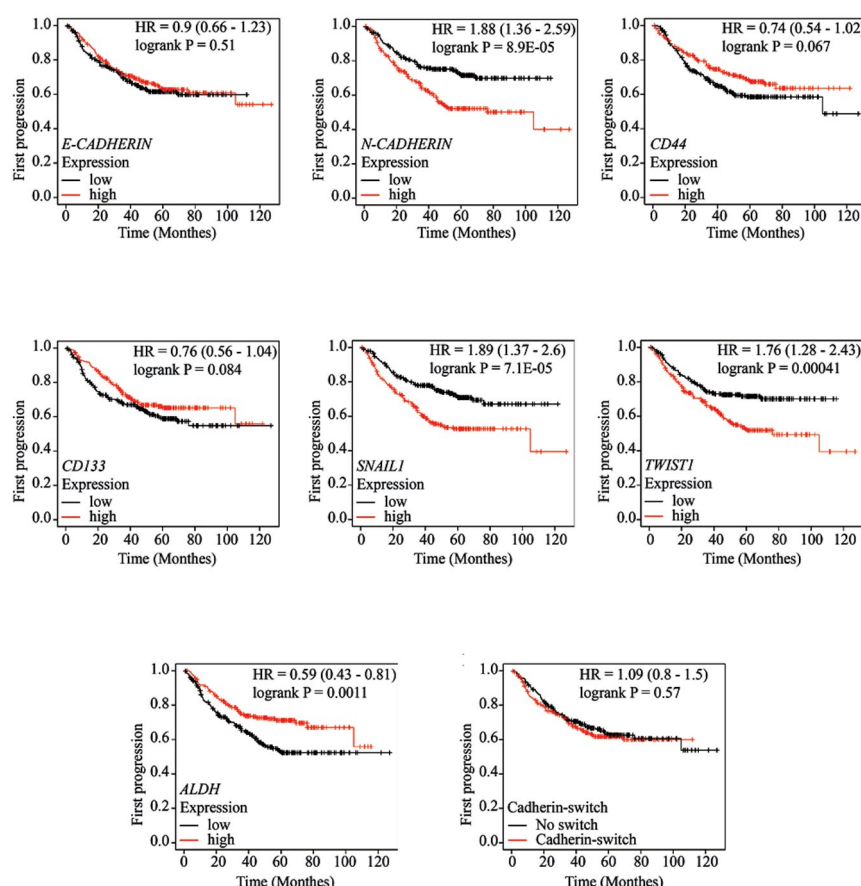


Fig.S1: The association between the first progression (FP) of patients with lung adenocarcinoma (LUAD) and the expression levels of EMT related genes. The FP of patients with lung adenocarcinoma (LUAD) was evaluated in the Cancer Biomedical Informatics Grid (caBIG), The Cancer Genome Atlas (TCGA) and GEO databases using the Kaplan-Meier plotter. Among the EMT related genes, only expression of *CDH2*, *SNAIL1* and *TWIST1* was statistically associated with shorter FP in LUAD patients and the expression of *ALDH1A1* was statistically associated with longer FP in LUAD patients. (number of patients with high (231) and low (230) expression of *CDH1*; probe sets: 201130_s_at and 201131_s_at), (number of patients with high (231) and low (230) expression of *CDH2*; probe sets: 203440_at and 203441_s_at), (number of patients with high (221) and low (222) expression of *CD44*; probe sets: 1557905_s_at, 204489_s_at, 204490_s_at, 209835_x_at, 210916_s_at, 212014_x_at, 212063_at, 216056_at and 217523_at), (number of patients with high (231) and low (230) expression of *PROM1*; probe set: 204304_s_at), (number of patients with high (229) and low (232) expression of *SNAIL1*; probe set: 219480_at), (number of patients with high (231) and low (230) expression of *TWIST1*; probe set: 213943_at), (number of patients with high (231) and low (230) expression of *ALDH1A1*; probe set: 212224_at), (number of patients with cadherin switch (231) and no cadherin switch (230); probe sets: 201130_s_at, 201131_s_at, 203440_at and 203441_s_at).

Table S1: The primer sequences, with their melting temperatures (T_m), the accession number of the targeted refseq mRNA and length of the amplicon

<i>ALDH1A1</i> gene (size of the amplified amplicon: 145)	
F: 5'-GATGCCGACTTGGACAATGC-3' (T _m : 59.90)	R: 5'-TCTTAGCCCGCTCAAACTC-3' (T _m : 59.75)
The accession number of a refseq mRNA begins detected: NM_000689.5	
<i>CD44</i> gene (size of the amplified amplicon: 93)	
F: 5'-CATGGACAAGTTTTGGTGGCAC-3' (T _m : 60.80)	R: 5'-GCAAAGCGGCAGGTTATATTC-3' (T _m : 58.00)
the accession number of a refseq mRNA begins detected: NM_001202555.2, NM_001202556.2, NM_001001389.2, NM_000610.4, NM_001001391.2, NM_001001390.2, NM_001202557.2, NM_001001392.2, NM_001202557.2, XM_006718390.4, XM_011520489.3, XM_017018585.2, XM_011520488.2, XM_011520487.3, XM_017018584.2, XM_005253240.3, XM_011520486.2, XM_005253239.3, XM_005253238.3, XM_011520485.2, XM_011520484.2, XM_011520483.2, XM_011520482.2, XM_017018583.2, XM_005253235.3, XM_006718388.2, XM_005253232.3, XM_005253231.3	
<i>CDH1</i> gene (size of the amplified amplicon: 119)	
F: 5'-CGAGAGCTACACGTTACGG-3' (T _m : 60.79)	R: 5'-GGGTGTCGAGGGAAAAATAGG-3' (T _m : 58.36)
The accession number of a refseq mRNA begins detected: NM_001317185.2, NM_001317186.2, NM_001317184.2, NM_004360.5	
<i>CDH2</i> gene (size of the amplified amplicon: 120)	
F: 5'-AGGCTTCTGGTGAAATCGCA-3' (T _m : 59.96)	R: 5'-TGCAGTTGCTAAACTTCACATTG-3' (T _m : 58.39)
The accession number of a refseq mRNA begins detected: NM_001792.5, XM_017025514.2, XM_011525788.1	
<i>HPRT1</i> gene (size of the amplified amplicon: 160)	
F: 5'-TAGCCCTCTGTGTGCTCAAG-3' (T _m : 59.39)	R: 5'-ACTTTTATGTCCCCTGTTGACTG-3' (T _m : 58.60)
The accession number of a refseq mRNA begins detected: https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&id=1519243938 NM_000194.3	
<i>PROM1</i> gene (size of the amplified amplicon: 167)	
F: 5'-ACCAGCGACAGAAGGAAAATG-3' (T _m : 58.85)	R: 5'-CTTGAAATTGCTATCTGCCAGTT-3' (T _m : 57.68)
The accession number of a refseq mRNA begins detected: NM_001371406.1, NM_001371407.1, NM_001145850.2, NM_001145851.2, NM_001145852.2, NM_001145849.2, NM_001371408.1, NM_006017.3, NM_001145847.2, NM_001145848.2, XM_024454276.1, XM_005248196.5, XM_005248195.5, XM_011513897.3, XM_011513894.3, XM_006713974.3, XM_011513903.2, XM_011513902.2, XM_017008800.1, XM_011513900.2, XM_011513896.2, XM_011513895.2, XM_011513893.2, XM_011513892.2	
<i>SNAIL</i> gene (size of the amplified amplicon: 116)	
F: 5'-CCAGTGCCTCGACCACTATG-3' (T _m : 60.18)	R: 5'-CTGCTGGAAGGTAAACTCTGGA-3' (T _m : 59.70)
The accession number of a refseq mRNA begins detected: NM_005985.4	
<i>Twist1</i> gene (size of the amplified amplicon: 115)	
F: 5'-CTACGCCCTTCTCGGTCTG-3' (T _m : 56.89)	R: 5'-TGGAAACAATGACATCTAGGTCTC-3' (T _m : 58.27)
The accession number of a refseq mRNA begins detected: https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&id=1519243938 NM_000474.4	