

Figure S1. LD pattern in rs9390123 surrounding 20 kb region for (A) CEU, (B) CHB and (C) YRI populations. Each square denotes one single nucleotide polymorphism(SNP). The color from white to black corresponds to the r^2 value. The arrow indicates the position of rs9390123. LD, linkage disequilibrium; CEU, Utah Residents with Northern and Western European Ancestry; CHB, Han Chinese in Beijing; YRI, Yoruba in Ibadan, Nigeria.

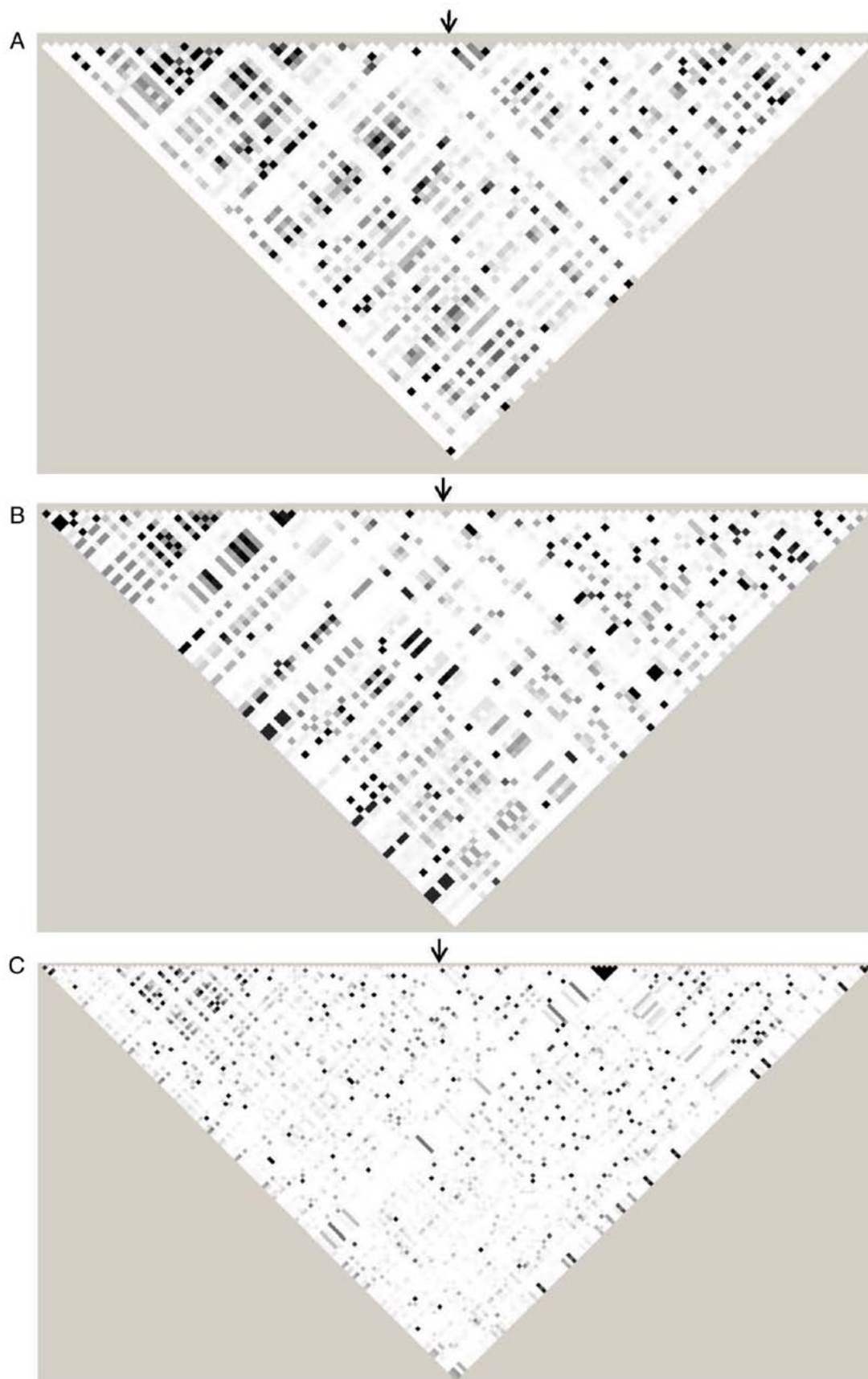


Figure S2. Histone modification in lung cell line A549 for the segment surrounding rs9390123. The yellow line indicates the location of rs9390123.



Figure S3. Ratio between the nuclear and total transcript of *PHACTR2-AS1*. The data are displayed as mean $\pm$ SD. U6 and *GAPDH* are utilized as positive controls. *PHACTR2*, phosphatase and actin regulator 2; AS1, antisense RNA 1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

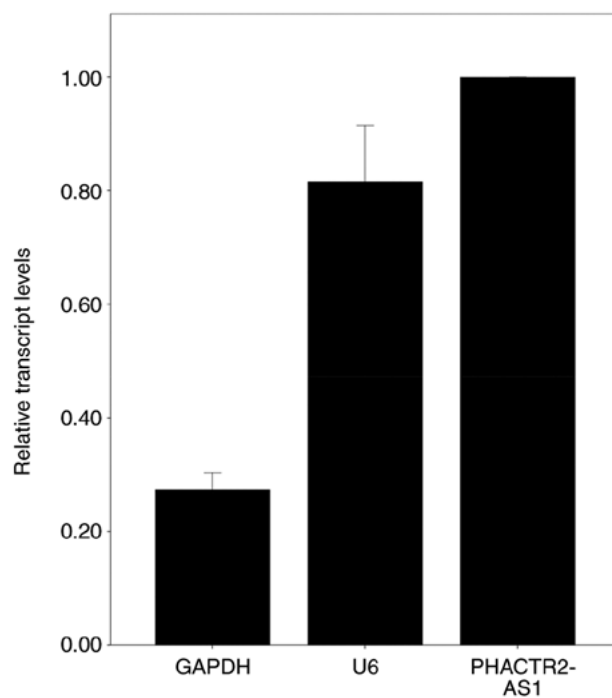


Figure S4. Boxplot of *PEX3* expression in normal and lung adenocarcinoma tissues. The y-axis indicates *PEX3* expression (log-transformed) and is reported in RPKM (reads per kilobase per million mapped reads) units. *PEX3*, peroxisomal biogenesis factor 3.

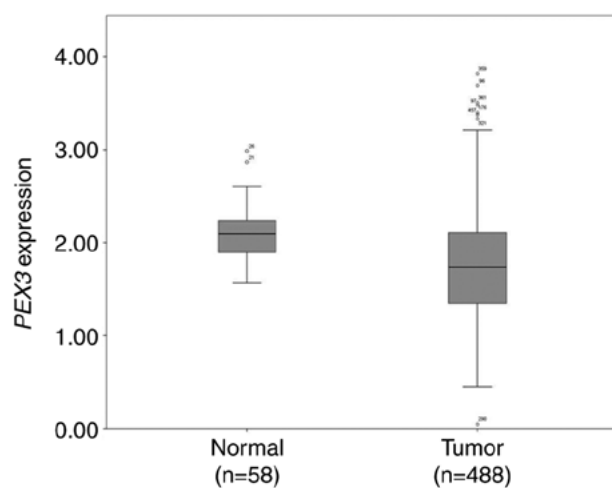


Table SI. Primers in mutagenesis.

SNP	Primer ^a	Annealing temperature (°C)
rs9390123	AGCTAGGTTAcATCTTTTAATGTTTC GTCCACCTCCATTATGTC	58
rs9399451	CTTGATTTTTgTTTGTGTGTGTTTG GTTCACAAGGACTTTTCTG	58

^aThe target site is indicated in lower case. SNP, single nucleotide polymorphism.

Table SII. Primers in 3C-qPCR.

Primer name	Primer sequence	Location in genome ^a	Restrictive segment location	Target element
Target primer 1	GTTTCAGCAGTCTGCCCTTTTCATT	Chr6:143767367-143767391	chr6:143766702-143767459	PEX3 promoter
Target primer 2	CTGAAGGGAGTGAGGGAAGGAAGT	Chr6:143771214-143771237	chr6:143767459-143771280	
Target primer 3	TGTGTTGGACCAAAAGCACATTCT	Chr6:143774212-143774236	chr6:143771280-143774347	
Target primer 4	CAGTTTATGAAGAAGAAACATATAAGCAGATTG	Chr6:143785241-143785274	chr6:143783475-143785307	
Target primer 5	GCAAGATATTCGTTATTTTGCAAGTAGTGATA	Chr6:143801434-143801465	chr6:143799979-143801506	FUCA2 promoter
Target primer 6	GAGCTGATAATATATAGGCACCTTGTAAT	Chr6:143812776-143812806	chr6:143811067-143812901	
Target primer 7	CAGAAAGTTGCCTGACTTCGTAGC	Chr6:143824414-143824437	chr6:143820251-143824460	
Target primer 8	ATACAGTGTTTTAAAAATCAAGTCCTCAAA	Chr6:143846387-143846417	chr6:143831209-143846497	
Target primer 9	CCGAAAAAGGACAGCAAAGACAT	Chr6:143860247-143860269	chr6:143857664-143860292	PHACTR2-AS1 promoter
Target primer 10	AATTGGCTTCTGGGACTTCTCTGA	Chr6:143871770-143871794	chr6:143870775-143871826	
Target primer 11	GTGCTCTCTGTGTGTTGGAATAATCTG	Chr6:143883276-143883303	chr6:143876509-143883408	
Target primer 12	CAGGCCGGTCAAKCATACTC	Chr6:143892759-143892779	chr6:143883929-143892800	
Target primer 13	GACGATCATCTATTTGCCATCGTG	Chr6:143907263-143907286	chr6:143905489-143907391	PHACTR2 promoter
Target primer 14	CTAAGTTAAGTATGTCAAATGACACACTAAAGGC	Chr6:143916367-143916400	chr6:143911831-143916422	
Target primer 15	ACCTAGGRGAATCCTGTGACAAAATAGT	Chr6:143926913-143926940	chr6:143922455-143927042	
Target primer 16	GCACAAAATGCTCTGAAATACCCCTACT	Chr6:143940621-143940648	chr6:143935776-143940671	
Target primer 17	TCACAGTTGTTGTGCTGTCATAGTGC	Chr6:143961201-143961226	chr6:143953777-143961316	Enhancer region
Target primer 18	ATTGAAAGCCACTACTTGCTTTTCATTTC	Chr6:143973318-143973345	chr6:143972912-143973439	
Constant primer	AGCAATGCTCAATCCCTGAAGAATAAC	Chr6:143944851-143944877	chr6:143941597-143944940	

^aRelative to human genome build 37. 3C, chromosome conformation capture.

Table SIII. Primers in ChIP-qPCR.

SNP	Primer sequence	Primer location ^a
rs9390123	CGGTTGATTCCTGGTTCTTGACAT	Chr6:143943266-143943290
	GTTTTGGGCTTGAATTTTATCCTGAG	Chr6:143943372-143943397
rs9399451	AGAAATGTAGCCAAATGCAAACGATG	Chr6:143943775-143943800
	GGAATCCCTACAAAATATATATTTTAAATTCTAAA	Chr6:143943900-143943935

^aRelative to human genome build37. ChIP, chromatin immunoprecipitation; SNP, single nucleotide polymorphism.

Table SIV. Primers in POU2F1 coding region amplification.

Round	Strand	Primer sequence	Annealing temperature (°C)	Primer location ^a
First	Forward	ATCCACTTTCCACCCTACGCAACC	62	59-82
	reverse	TCTCCAATCCATGAAGCAATCCTG		2713-2736
Second	Forward	CAGTC-AAGCTT-TTCCCCACCCCAAAGTCTAC	71	139-159
	reverse	CAGTC-GGTACC-TCACAACACGGCGAGAGGAA		2569-2588

^aRelative to POU2F1 mRNA sequence (Genbank ID NM_001198783.2). POU2F1, POU class 2 homeobox 1.

Table SV. qPCR primers for gene expression.

	Primer sequence
<i>POU2F1</i>	ATGAACAATCCGTCAGAAACCAG GATGGAGATGTCCAAGGAAAGC
<i>PEX3</i>	GCCCAAGCACGACGACAATATCA GGACCCGCAAAAGAACAACCAG
<i>PHACTR2-AS1</i>	ACCAATCACATAGCCCTGCC TCAGAGCTGCAGATGTGGTC
<i>U6</i>	CTCGCTTCGGCAGCACA AACGCTTCACGAATTTGCGT
<i>GAPDH</i>	GAAGGTGAAGGTCGGAGTC GAAGATGGTGATGGGATTTTC

POU2F1, POU class 2 homeobox 1; PEX3, peroxisomal biogenesis factor 3; PHACTR2-AS1, phosphatase and actin regulator 2 antisense RNA 1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

Table SVI. Probes for rs9390123 and rs9399451 in EMSA.

SNP	Allele	Probe sequence ^a
rs9390123	C allele	GACAGCTAGGTTACATCTTTTAATGTT AACATTAAAAGATGTAACCTAGCTGTC
	T allele	GACAGCTAGGTTATATCTTTTAATGTT AACATTAAAAGATATAACCTAGCTGTC
rs9399451	G allele	AACCTTGATTTTTGTTTGTGTGTGTTT AAACACACACAAACAAAAATCAAGGTT
	T allele	AACCTTGATTTTTTTTGTGTGTGTGTTT AAACACACACAAAATAAAAAATCAAGGTT

^aThe target sites are underlined. EMSA, electrophoretic mobility shift assay; SNP, single nucleotide polymorphism.