

Figure S1 Disease-related to PD-1 target molecules. PD-1, programmed cell death protein 1.

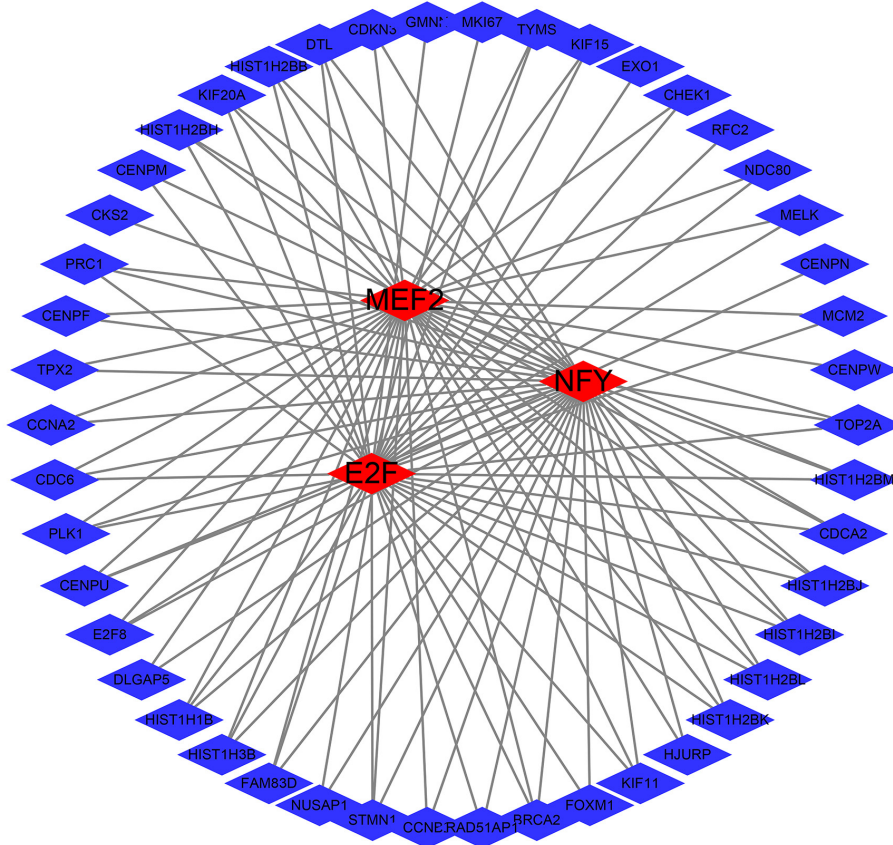


Figure S2 The relationship between transcription factors and PD-1 target molecules. PD-1, programmed cell death protein 1.

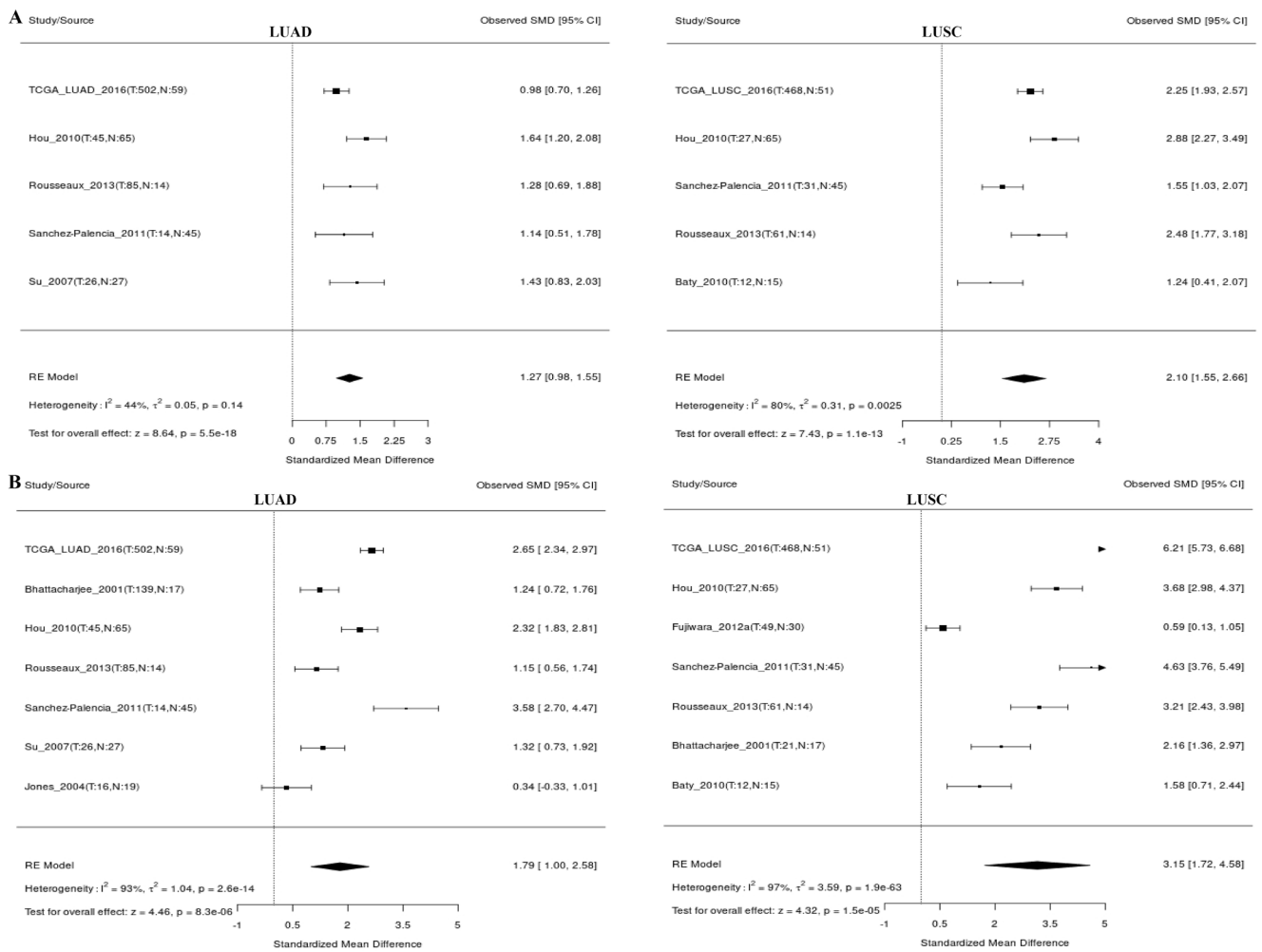


Figure S3 HIST1H2B and PLK1 were unusual expression in LUAD and LUSC via the meta-analysis. (A) HIST1H2B; (B) PLK1. LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma.

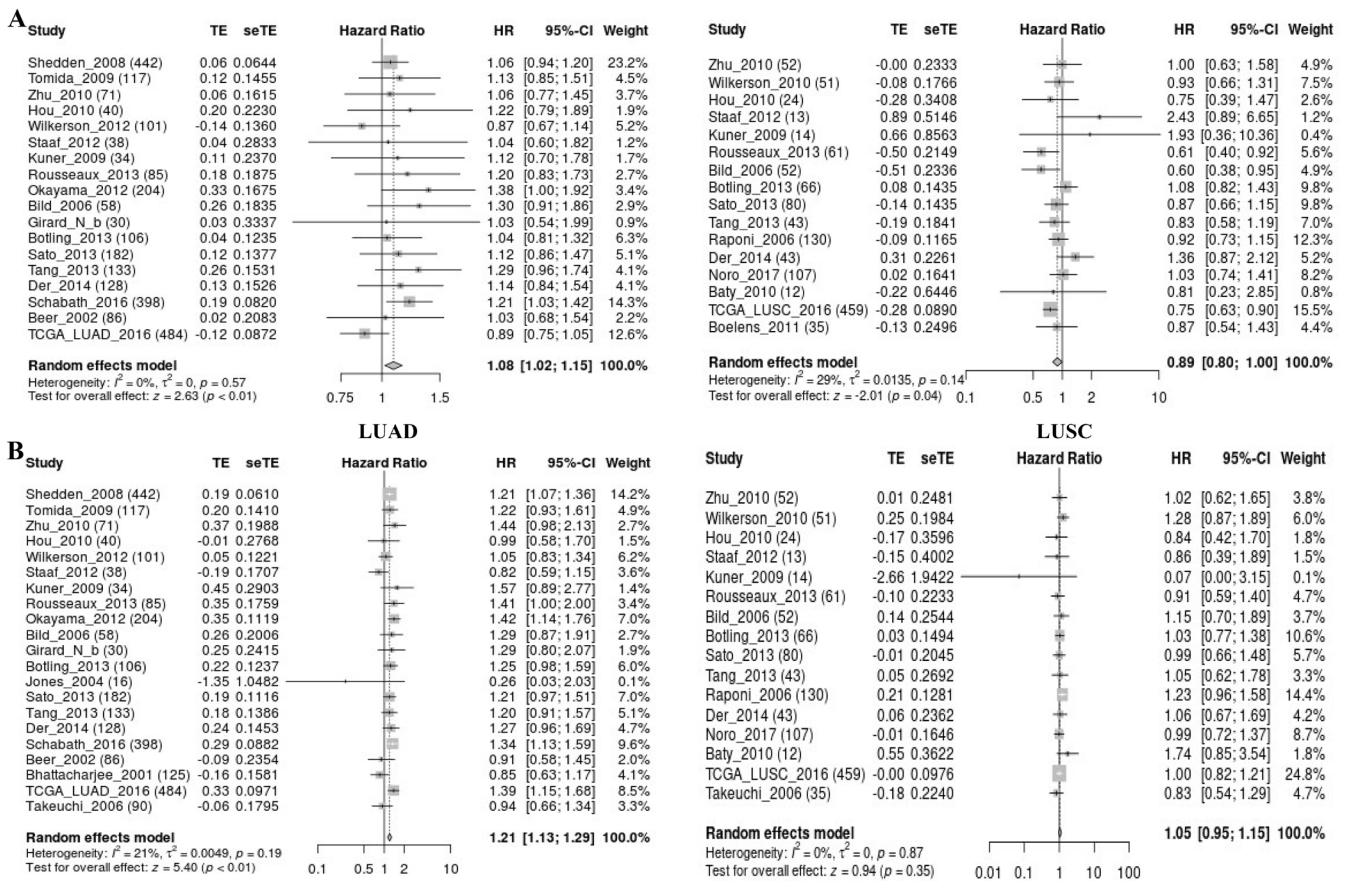


Figure S4 HIST1H2B and PLK1 expression level were related to the OS in LUAD and LUSC tissues via the metaanalysis. (A) HIST1H2B; (B) PLK1. OS, overall survival; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma.

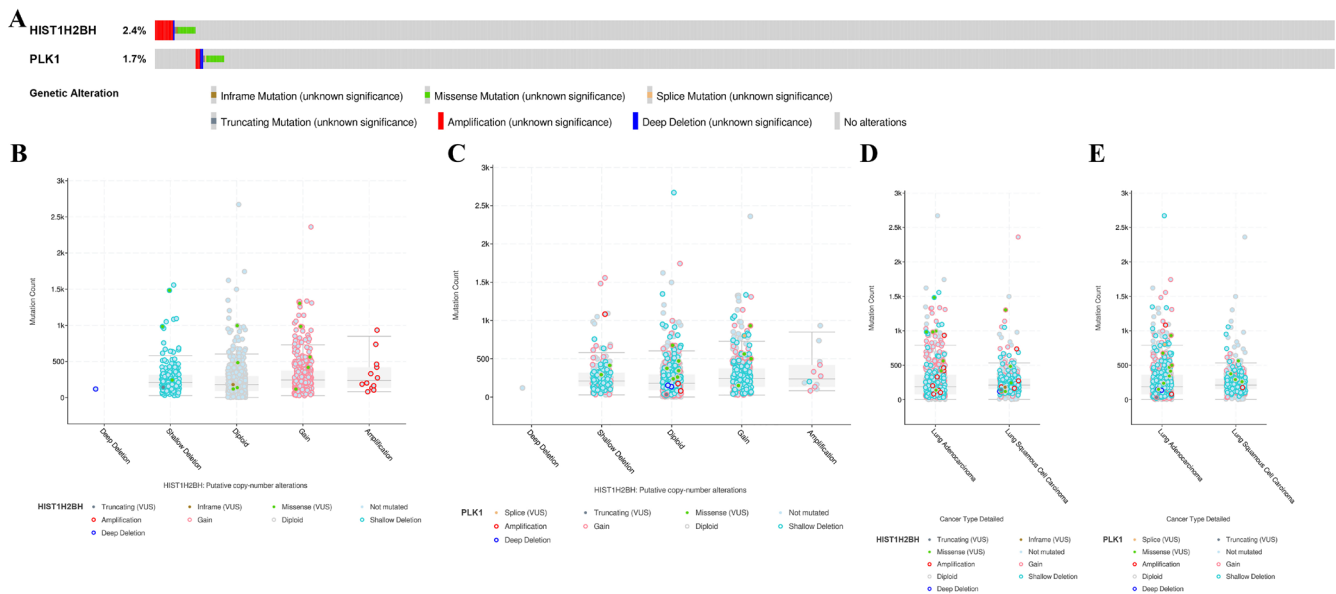


Figure S5 HIST1H2BH and PLK1 had significant mutations in NSCLC. NSCLC, non-small cell lung cancer.

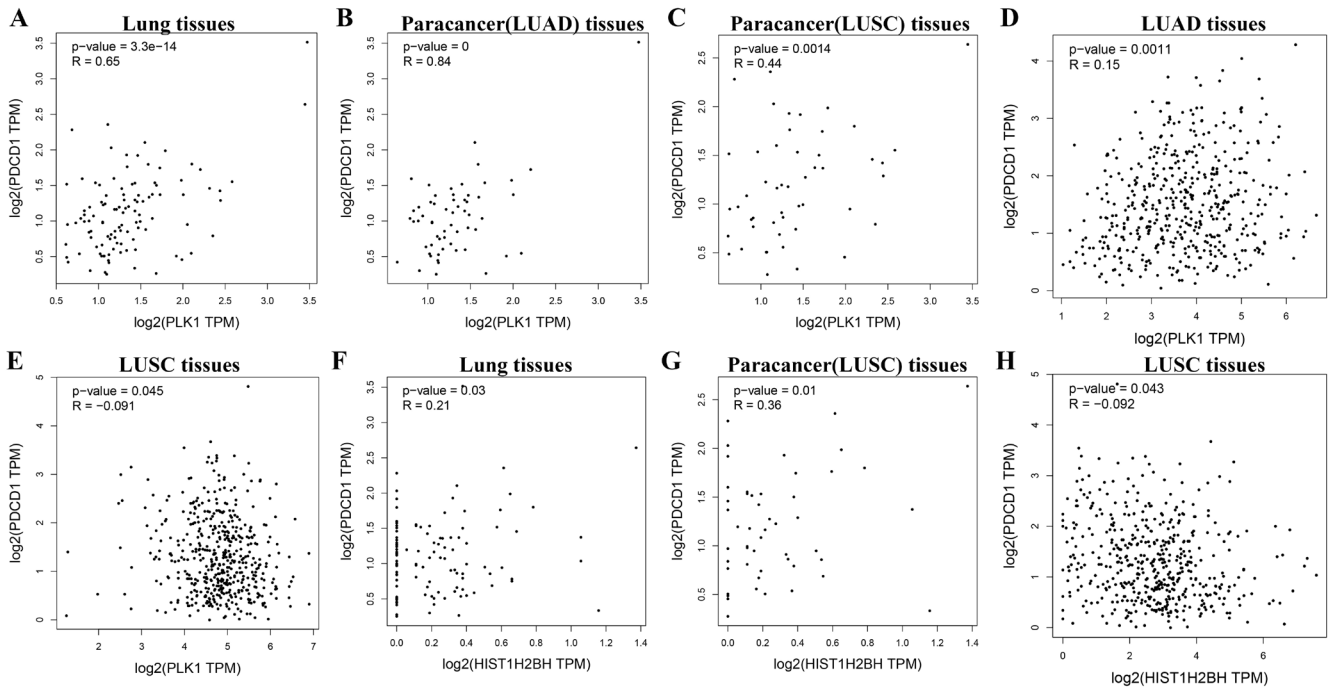


Figure S6 The expression levels of HIST1H2BH and PLK1 were correlated with PD-1 expression level. PD-1, programmed cell death protein 1.

Table S1 The biological functions of PD-1 target molecules via the GO

Category	Term	Count	P
BP	GO:0006334~nucleosome assembly	11	7.15E-13
BP	GO:0007067~mitotic nuclear division	13	2.06E-12
BP	GO:0007059~chromosome segregation	8	6.14E-10
BP	GO:0051301~cell division	11	2.85E-08
BP	GO:0008283~cell proliferation	11	4.34E-08
BP	GO:0034080~CENP-A containing nucleosome assembly	5	5.62E-06
BP	GO:0007062~sister chromatid cohesion	6	8.84E-06
BP	GO:0000086~G2/M transition of mitotic cell cycle	6	3.52E-05
BP	GO:0002227~innate immune response in mucosa	4	4.24E-05
BP	GO:0006260~DNA replication	6	6.35E-05
BP	GO:0000281~mitotic cytokinesis	4	6.69E-05
BP	GO:0019731~antibacterial humoral response	4	2.36E-04
BP	GO:0000910~cytokinesis	4	3.05E-04
BP	GO:0051726~regulation of cell cycle	5	3.64E-04
BP	GO:0051310~metaphase plate congression	3	4.76E-04
BP	GO:0031572~G2 DNA damage checkpoint	3	0.001351749
BP	GO:0050830~defense response to Gram-positive bacterium	4	0.001623959
BP	GO:0000070~mitotic sister chromatid segregation	3	0.002115826
BP	GO:0001578~microtubule bundle formation	3	0.002115826
BP	GO:0000732~strand displacement	3	0.002288156
BP	GO:0000082~G1/S transition of mitotic cell cycle	4	0.002732956
BP	GO:0007049~cell cycle	5	0.002894716
BP	GO:0007052~mitotic spindle organization	3	0.003041358
BP	GO:0000731~DNA synthesis involved in DNA repair	3	0.004123996
BP	GO:1901796~regulation of signal transduction by p53 class mediator	4	0.004733673
BP	GO:0000079~regulation of cyclin-dependent protein serine/threonine kinase activity	3	0.005100354
BP	GO:0046602~regulation of mitotic centrosome separation	2	0.010913626
BP	GO:0007018~microtubule-based movement	3	0.020737582
BP	GO:0030071~regulation of mitotic metaphase/anaphase transition	2	0.024391909
BP	GO:0006281~DNA repair	4	0.026418072
BP	GO:0006268~DNA unwinding involved in DNA replication	2	0.027065923
BP	GO:0001833~inner cell mass cell proliferation	2	0.032392459
BP	GO:0051382~kinetochore assembly	2	0.032392459
BP	GO:0010569~regulation of double-strand break repair via homologous recombination	2	0.042960087

Table S1 (continued)

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Category	Term	Count	P
BP	GO:0006978~DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	2	0.042960087
CC	GO:0005654~nucleoplasm	34	1.21E-17
CC	GO:0000788~nuclear nucleosome	9	1.44E-13
CC	GO:0000786~nucleosome	9	8.22E-11
CC	GO:0005634~nucleus	35	7.53E-10
CC	GO:0005819~spindle	8	2.06E-08
CC	GO:0000775~chromosome, centromeric region	6	3.11E-07
CC	GO:0005737~cytoplasm	30	1.27E-06
CC	GO:0000777~condensed chromosome kinetochore	6	2.59E-06
CC	GO:0000922~spindle pole	6	7.87E-06
CC	GO:0005876~spindle microtubule	4	1.85E-04
CC	GO:0015630~microtubule cytoskeleton	5	3.90E-04
CC	GO:0005813~centrosome	7	6.69E-04
CC	GO:0005874~microtubule	6	0.00108309
CC	GO:0000776~kinetochore	4	0.001118872
CC	GO:0000785~chromatin	4	0.001468433
CC	GO:0030496~midbody	4	0.004212549
CC	GO:0000784~nuclear chromosome, telomeric region	4	0.004304501
CC	GO:0005730~nucleolus	8	0.005348436
CC	GO:0000942~condensed nuclear chromosome outer kinetochore	2	0.010059237
CC	GO:0005829~cytosol	16	0.013417391
CC	GO:0005694~chromosome	3	0.02886921
CC	GO:0051233~spindle midzone	2	0.046907317
MF	GO:0046982~protein heterodimerization activity	11	2.45E-07
MF	GO:0003677~DNA binding	18	4.03E-07
MF	GO:0019901~protein kinase binding	9	4.94E-06
MF	GO:0008017~microtubule binding	7	1.56E-05
MF	GO:0005515~protein binding	36	1.49E-04
MF	GO:0005524~ATP binding	12	0.001252552
MF	GO:0042393~histone binding	4	0.003930198
MF	GO:0008022~protein C-terminus binding	4	0.011807477
MF	GO:0003777~microtubule motor activity	3	0.018448317
MF	GO:0042826~histone deacetylase binding	3	0.029009124

PD-1, programmed cell death protein 1; GO, gene ontology; BP, biological processes; CC, cellular component; MF, molecular function.