***Supplemental methods***

***qRT–PCR assays and Western blot assays***

Total RNA of A549 and H522 were extracted with TRIzol reagent (Invitrogen) . cDNA were then synthesized from total RNA using reverse transcription reagent kit (Toyobo). Real time PCR was conducted with SYBR Premix Ex Taq II Kit (Takara) on an StepOnePlus Real-Time PCR System. The primers were provided by Sangon, Shanghai, China. Gene expression changes relative to the stated housekeeping gene GAPDH were calculated using the △△CT method.

Western blotting was performed using standard methods. Whole-cell extracts of A549 and H522 were prepared by lysing the cells with NP40 supplemented with Protease inhibitor Cocktail. After separation by SDS-PAGE, proteins were transferred to PVDF membrane, and followed by immunoblotting using indicated antibodies. The primary antibodies for GAPDH, CENP-E and PD-L1(Abcam) were used according to the manufacturer’s instructions. The horseradish peroxidase (HRP)-conjugated secondary antibody was obtained from Santa Crutz. Proteins were visualized using an ECL system (Bio-Rad) . Image acquisition were performed using Chemi Doclt 510 imaging system (UVP).

***Immunohistochemistry and Immunofluorescence***

Lung cancer tissues were collected from Cancer Center, Union Hospital, Tongji Medical College of Huazhong University of Science and Technology, and written informed consent was obtained from patients at the time of enrollment. Before staining, the paraformaldehyde fixed paraffin embedded tumor slides were deparaffinized, rehydrated and followed by heat-mediated antigen retrieval. For immunohistochemistry staining, the specimens were incubated with the anti-human CENP-E (Santa crutz) overnight at 4°C, followed by biotinylated secondary antibody and HRP/DAB detection. For immunofluorescence staining, the samples were stained with anti-human primary antibodies including mouse CENP-E (Santa crutz), rabbit PD-L1 (Abcam) overnight at 4°C. Then the samples were stained with secondary antibodies including FITC-labeled donkey anti-rabbit, Cy3-labeled donkey anti-mouse. 4’, 6-diamidino-2-phenylindole (DAPI) was used for nuclear staining. The images were acquired utilizing a confocal laser-scanning microscope (Carl Zeiss).

***mRNA stability assays***

The cells were seeded in 6 wells plate and cultured overnight. After GSK923295 treatment for 3 days, the cells were treated with ACTD for 0, 1 or 2 hours. Then the total RNA was extracted for the reverse transcription PCR and real time PCR.

***Dual luciferase reporter assays***

 A549 was plated in 96 well plates and the following day co-transfected with renilla luciferase reporter gene plasmid and PD-L1 3'UTR WT or PD-L1 3'UTR MUT luciferase reporter gene plasmid (Addgene) using lipofectamine 2000 (Invitrogen, Carlsbad, CA) according to the manufacturer’s instructions. 24 h after transfection, the cells were treated with GSK923295 for 2 days. After incubation, the cells were collected and subjected to luciferase assays using a Dual-Luciferase Reporter Assay System (Promega), and measured with the Centro LB960 Microplate Luminometer (Berthold Technologies).

***Tansfection, Viral infections***

For transfection with TTP constructs, cells were seeded in a 6 well plate overnight. Then cells were transfected with pcDNA3 Myc2-Hs TTP (Addgene) or with the wild-type pcDNA3 plasmid using lipofectamine 2000 (Invitrogen, Carlsbad, CA) according to the manufacturer’s instructions.

To generate lentivirus expressing shRNA for the knockdown of CENP-E, TTP, UPF1 in A549 and the knockdown of CENP-E in Lewis, we transfected HEK293T cells with shRNA targeting CENP-E, TTP or UPF1 constructs (Sigma) and two packaging plasmids pSPAX2 and pMD2G. shRNA for the knockdown of CENP-E in mice were purchased from GenePharm in Shanghai, China. The shRNA were listed below. Human CENPE-sh1: 5’-CCGGGCAACTACACAGTCGAATTATCTCGAGA TAATTCGACTGTGTAGTT GCTTTTTTG-3’, human CENPE-sh2: 5’-CCGGACC TCATCCAGTTCGCTATTTCTCGAGAAATAGCGAACTGGATGAGGTTTTTTTG-3’, human CENPE-sh3: 5’-CCGGGCCACTAGAGTTGAAAGATAACTCGAGTT ATCTTTCAACTCTAGT GGCTTTTTG-3’. Human TTP-sh1: 5’-CCGGGA CGGAACTCTGTCACAAGTTCTCGAGAACTTGTGACAGAGTTC CGTCTTT TT-3’, human TTP-sh2: 5’-CCGGCCCATCTTCAATCGCATCTCTCTCGAGAGA GATGCGATTGAAGAT GGGTTTTT-3’, human TTP-sh3: 5’-CCGGGATCCGACC CTGATGAATATGCTCGAGCATATTCATCAGGGTCGGA TCTTTTTTG-3’. Human UPF1-sh1: 5’-CCGGGCCTACCAGTACCAGAACATACTCGAGTATGTT CTGGTACTGGTA GGCTTTTT-3’, human UPF1-sh2: 5’-CCGGGCTGAGTTGAA CTTCGAGGAACTCGAGTTCCTCGAAGTTCAACTCAGCTTTTT-3’, human UPF1-sh3: 5’-CCGGGCAAGGTATGGCGTCATCATTCTCGAGAATGATGACGCC ATACCT TGCTTTTT-3’. Mouse CENPE-sh1: 5’-GCTGCTTCCTGTTGTCAAAG A-3’, mouse CENPE-sh2: 5’-GGAGAATACTGTACAGGAAGA-3’, mouse CENPE-sh3: 5’-GCATGAGTCCATCAATAAACG-3’. Twenty-four hours after transfection, the medium was changed, and then the supernatant containing virus was collected and filtered through 0.45μM filters at 24-h intervals. Then the cells were incubated in lentivirus-containing culture medium with polybrene (10μg/mL). Three days after infection, cells were subjected to puromycin selection (1μg/mL) for at least 3 days.

***RNA-immunoprecipitation***

RNA-immunoprecipitation (RNA-IP) assays were conducted using Magna-RIP RNA-IP Kit (Millipore) with IgG control, anti-TTP antibodies according to the manufacturer’s instructions. Total RNA was isolated and the reverse transcription PCR and real time PCR was performed using methods specified in the above section. A % input method was used to calculate RNA enrichment.

***Bioinformatic analysis***

The expression of CENP-E was analyzed within UALCAN. The relationship between survival and CENP-E expression in lung cancer patients was analyzed on Kaplan-Meier plotter. The relationship between the expression of CENP-E and immune molecules in lung cancer was analyzed on Genomics Analysis and Visualization Platform. All the data from TCGA data base.

***Chip assay***

Passage A549 cells, 80% confluent, were synchronized by starving in DMEM 0.1% FBS, for 72 h; then 20% FBS DMEM was readded and ChIP was performed at 0, 6, 12, 16, and 20 h post reinduction. Cells were fixed for 20 min with crosslinking solution (11% formaldehyde, 0.1 M NaCl, 1 mM Na-EDTA pH 8, 0.5 mM Na-EGTA pH 8, 50 mM HEPES pH 8, 1/10 volume (Vol) added to the medium), and blocked in 0.125 M glycine in PBS at room temperature (RT). Cells were collected in 10 ml buffer A (0.25% Triton X-100, 10 mM Na-EDTA pH 8, 0.5 mM Na-EGTA pH 8, 10 mM Tris-HCl pH 8, anti-proteases (10 μg/ml aprotinin, 10 μg/ml leupeptin, 5 mg/ml pepstatin), anti-phosphatases (1 mM sodium orthovanadate, 10 mM tetra-sodium pyrophosphate, 10 mM NaF), and 0.5 mM PMSF), incubated 10 min at 4°C on a wheel, centrifuged for 5 min at 1500 r.p.m., and resuspended in 10 ml of buffer B (0.2 M NaCl, 10 mMNa-EDTA pH 8, 0.5 mM Na-EGTA pH 8, 10 mM Tris-HCl pH 8, 0.5 mMPMSF, anti-proteases, and anti-phosphatases). Incubation and centrifugation steps were repeated, and the pellets were resuspended in 440 μl of sonication buffer (0.2 M NaCl, 10 mM Na-EDTA pH 8, 0.5 mMNa-EGTA pH 8, 10 mM Tris-Cl pH 8, anti-proteases, anti-phosphatases, and 0.5 mM PMSF). Samples were sonicated for 3 × 30 s, yielding genomic DNA fragments with a bulk size of 300–2000 base pairs, and the sonication buffer was adjusted to an RIPA buffer by adding 1% Triton X-100, 0.1% sodium dodecyl sulphate (SDS), and 0.1% sodium deoxycholate (DOC) final concentration. Samples were incubated for 10 min on a wheel at 4°C and then centrifuged for 10 min at 10 000 r.p.m. In all, 50 μl/sample were kept to recover total DNA input, and ChIP was performed, either with 2 μg of anti-Myc N-262 or without antibody. After crosslinking reversal, protein extraction, and ethanol precipitation, DNA was resuspended in TE, 50 μl for total input, and 100 μl for ChIP samples.ChIP DNA (1–2 μl) was used for PCR analysis.

***Supplemental Figures***



**Figure S1** Relationship between CENPE expression and prognosis of 8 cancers. These data were analyzed using Kaplan-Meier plotter from the TCGA database.

LUAD: Lung adenocarcinoma; LUSC: Lung squamous cell carcinoma; BRCA: Breast invasive carcinoma; COAD: Colon adenocarcinoma; SKCM: Skin cutaneous melanoma; STAD: Stomach adenocarcinoma; TGCT: Testicular germ cell tumors; BLCA: Bladder urothelial carcinoma.



**Figure S2**The gating strategy of flow cytometry for T cell subsets.

(A) The gate for CD4 and CD8 T cells; (B) The gate for Treg cells.