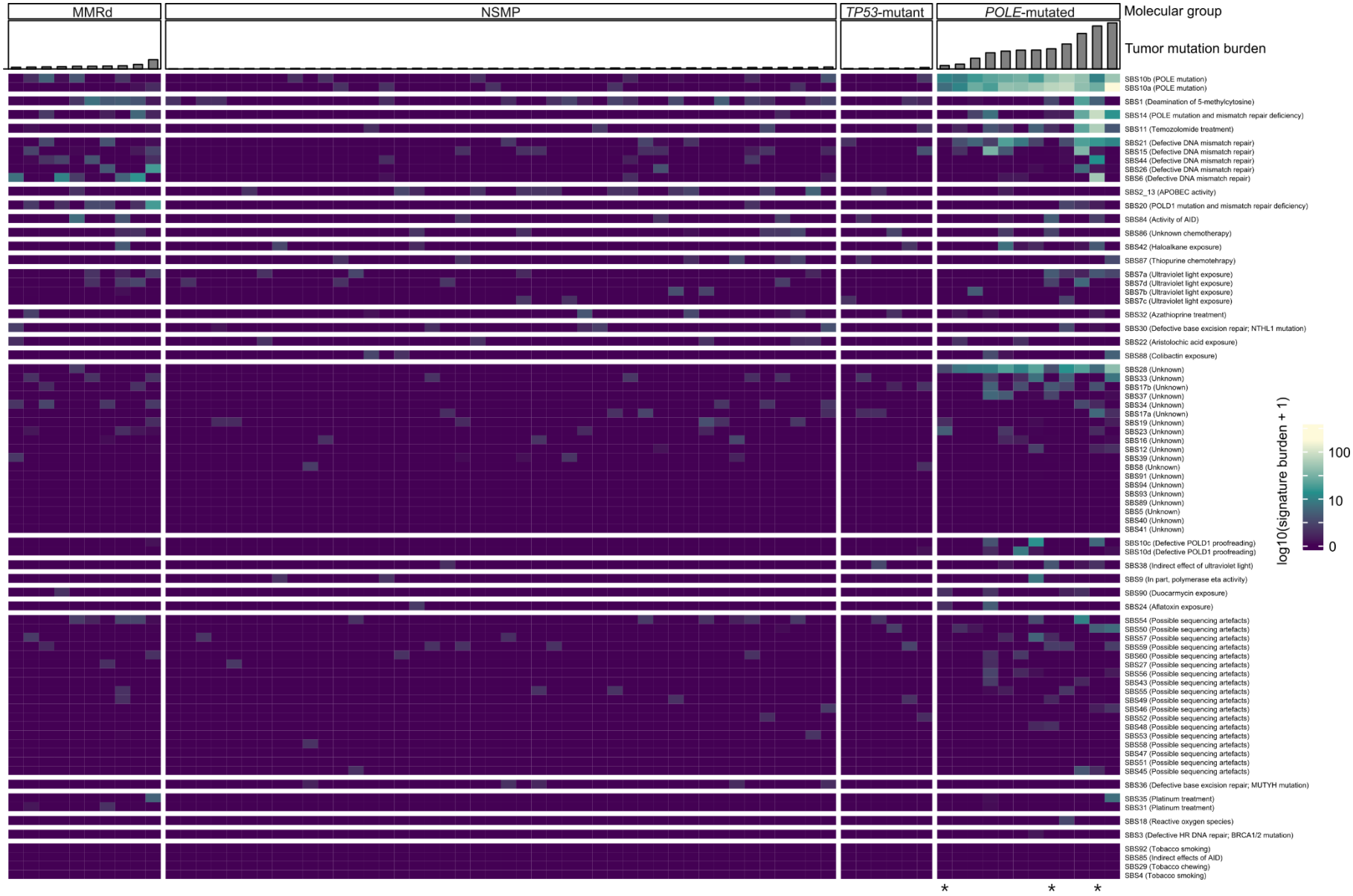

MMRd
NSMP
TP53-mutant
POLE-mutated
Molecular group
Tumor mutation burden
SBS10b (POLE mutation)
SBS10a (POLE mutation)
SBS1 (Deamination of 5-methylcytosine)
SBS14 (POLE mutation and mismatch repair deficiency)
SBS11 (Temozolomide treatment)
SBS21 (Defective DNA mismatch repair)
SBS15 (Defective DNA mismatch repair)
SBS44 (Defective DNA mismatch repair)
SBS26 (Defective DNA mismatch repair)
SBS6 (Defective DNA mismatch repair)
SBS2_13 (APOBEC activity)
SBS20 (POLD1 mutation and mismatch repair deficiency)
SBS84 (Activity of AID)
SBS86 (Unknown chemotherapy)
SBS42 (Haloalkane exposure)
SBS87 (Thiopurine chemotehrapy)
SBS7a (Ultraviolet light exposure)
SBS7d (Ultraviolet light exposure)
SBS7b (Ultraviolet light exposure)
SBS7c (Ultraviolet light exposure)
SBS32 (Azathioprine treatment)
SBS30 (Defective base excision repair; NTHL1 mutation)
SBS22 (Aristolochic acid exposure)
SBS88 (Colibactin exposure)
SBS28 (Unknown)
SBS33 (Unknown)
SBS17b (Unknown)
SBS37 (Unknown)
SBS34 (Unknown)
SBS17a (Unknown)
SBS19 (Unknown)
SBS23 (Unknown)
SBS16 (Unknown)
SBS12 (Unknown)
SBS39 (Unknown)
SBS8 (Unknown)
SBS91 (Unknown)
SBS94 (Unknown)
SBS93 (Unknown)
SBS89 (Unknown)
SBS5 (Unknown)
SBS40 (Unknown)
SBS41 (Unknown)
SBS10c (Defective POLD1 proofreading)
SBS10d (Defective POLD1 proofreading)
SBS38 (Indirect effect of ultraviolet light)
SBS9 (In part, polymerase eta activity)
SBS90 (Duocarmycin exposure)
SBS24 (Aflatoxin exposure)
SBS54 (Possible sequencing artefacts)
SBS50 (Possible sequencing artefacts)
SBS57 (Possible sequencing artefacts)
SBS59 (Possible sequencing artefacts)
SBS60 (Possible sequencing artefacts)
SBS27 (Possible sequencing artefacts)
SBS56 (Possible sequencing artefacts)
SBS43 (Possible sequencing artefacts)
SBS55 (Possible sequencing artefacts)
SBS49 (Possible sequencing artefacts)
SBS46 (Possible sequencing artefacts)
SBS52 (Possible sequencing artefacts)
SBS48 (Possible sequencing artefacts)
SBS53 (Possible sequencing artefacts)
SBS58 (Possible sequencing artefacts)
SBS47 (Possible sequencing artefacts)
SBS51 (Possible sequencing artefacts)
SBS45 (Possible sequencing artefacts)
SBS36 (Defective base excision repair; MUTYH mutation)
SBS35 (Platinum treatment)
SBS31 (Platinum treatment)
SBS18 (Reactive oxygen species)
SBS3 (Defective HR DNA repair; BRCA1/2 mutation)
SBS92 (Tobacco smoking)
SBS85 (Indirect effects of AID)
SBS29 (Tobacco chewing)
SBS4 (Tobacco smoking)
log10(signature burden + 1)
100
10
0
*
*
*

Supplementary Fig. S1. Mutational signature analysis across molecular subtypes of endometrial cancer. The heatmap displays the contributions of SBS mutational signatures across 72 endometrial cancer cases, grouped by molecular subtype: MMRd, NSMP, *TP53*-mutant, and *POLE*-mutated. Each row represents a mutational signature (SBS signatures), and each column represents an individual case. The upper panel shows tumor mutation burden (mut/Mb) for each case. Asterisks (*) denote *POLE*-mutated cases harboring non-hotspot mutations. Color intensity represents log10(signature burden + 1), with signature burden expressed in mut/Mb. Etiologic labels reproduce the COSMIC-associated annotations of computationally attributed signatures and do not indicate documented clinical exposure in an individual patient. SBS, single base substitution; MMRd, mismatch repair deficient; NSMP, no specific molecular profile; COSMIC, Catalogue of Somatic Mutations in Cancer.