Molecular Subtypes of Endometrial Cancers: Approaches and Considerations for Testing

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Objectives

• Understand the reasoning and rational for developing a molecular based classification of endometrial cancers

Select correct testing and order of testing for clinical situations

2

3

4

• Describe the testing considerations for each molecular classification

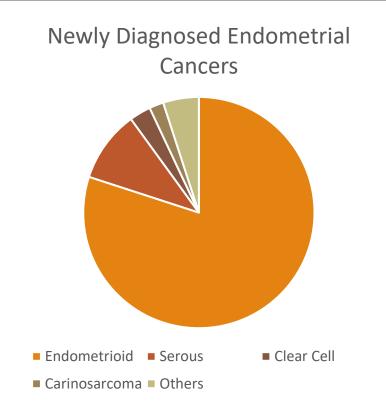
• Understand the recurrent genetic alterations for the molecular classifications

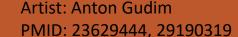
Endometrial cancer

Endometrial cancer is increasing in incidence and mortality

Survival has not increased for the last 4 decades

"In 2013, National Institutes of Health (NIH)-directed funding for EC was \$14 million compared with \$631 million for breast cancer research. Our understanding of this disease lags far behind other cancers; and, for decades, there has been very little change in the approach to EC from what our grandmother would have been offered" – McAlpine et al





Prognostic differentiation

YES,

Bokhman (1983): type I and type II endometrial cancer

- Type I: estrogen driven, low-grade
- Type II: estrogen independent, high-grade, biologically aggressive

Histotype

Disease grade

FIGO stage

Presence of lympho-vascular space invasion

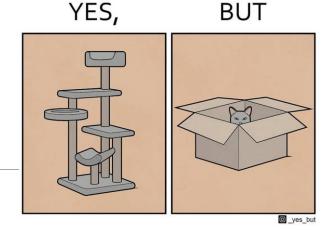
Deep myometrial invasion

~20% of women with type I endometrial cancer experience a relapse while ~50% of those with type II do not

Histological subtype and grade have poor reproducibility even amongst expert pathologists

FIGO stage and LVSI are only available posthysterectomy





Guin

Objectives of molecular classification

A validated risk-stratification model that accurately defines risk of disease recurrence and death will guide clinical care by allowing for treatment de-escalation for those at lowest risk and intensification for those at high risk

- Optimal follow up to monitor for recurrence
- Primary treatments for selected types



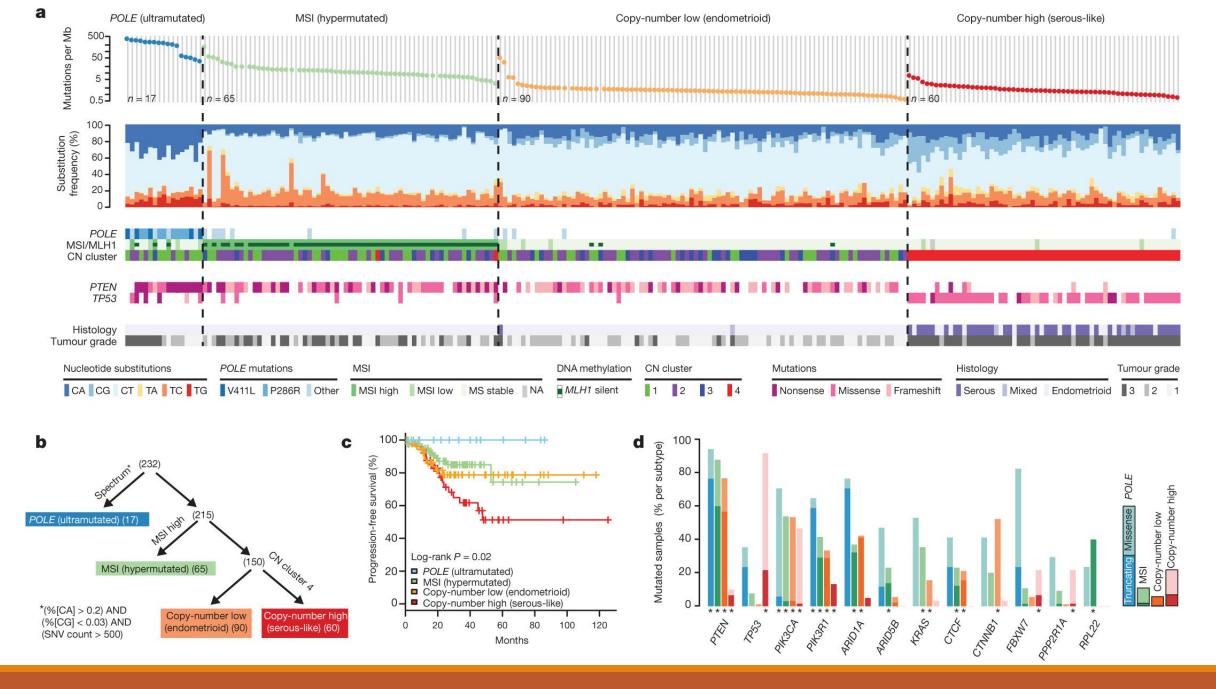
TCGA

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Integrated genomic, transcriptomic and proteomic characterization of 373 endometrial carcinomas



Private Information



PORTEC trails

Retrospective analysis of PORTEC 1 and 2 trails

 Integration of prognostic molecular alterations with established clinicopathologic factors resulted in a stronger model

Retrospective analysis of PORTEC 3

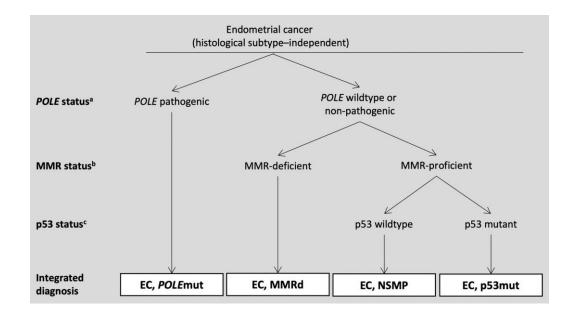
 Molecular classification has strong prognostic value in high-risk EC, with significantly improved RFS with adjuvant CTRT for p53abn tumors, regardless of histologic type. Patients with POLE mut EC had an excellent RFS in both trial arms.

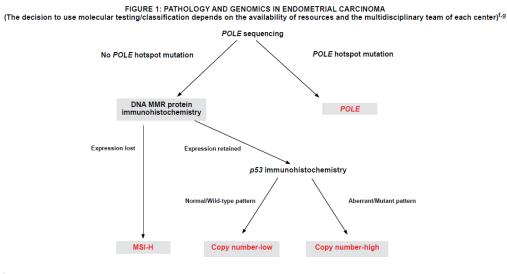
WHO and NCCN guidelines

WHO FEMALE GENITAL TUMORS, 5^{TH} EDITION

NCCN GUIDANCE – V1.2024

PRINCIPLES OF MOLECULAR ANALYSIS





^f Adapted with permission from Murali R, Delair DF, Bean SM, et al. Evolving roles of histologic evaluation and molecular/genomic profiling in the management of endometrial cancer. J Nat Compr Canc Netw 2018;16:201-209.

So, pathology, why aren't you testing for all these things??

The rest of the TPC

Post Operative Radiation Therapy in Endometrial Carcinoma (PORTEC)

PORTEC 1: post-operative pelvic external beam radiotherapy compared to no additional treatment.

PORTEC-2, Postoperative Radiation Therapy for Endometrial Carcinoma - A Multicenter Randomized Phase III Trial Comparing External Beam Radiation and Vaginal Brachytherapy

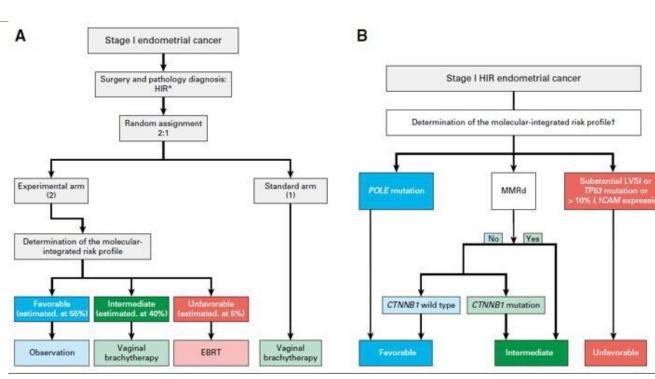
PORTEC 3: randomized phase III trial is studying chemotherapy and radiation therapy to see how well they work compared with radiation therapy alone in treating patients with high-risk, stage I, stage II, or stage III endometrial cancer.

PORTEC 4a

PORTEC 4a: Randomized Phase III Trial of Molecular Profile-based Versus Standard Recommendations for Adjuvant Radiotherapy for Women With Early Stage Endometrial Cancer

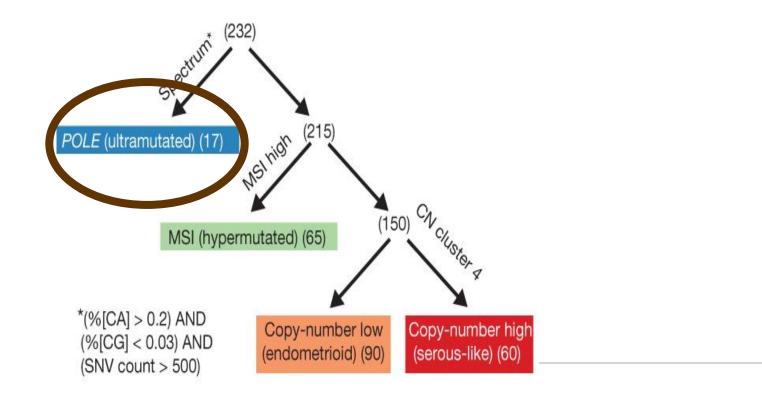
First trial to introduce molecular factors in the adjuvant treatment of endometrial cancer

 Omitting treatment in cases of favorable molecular profiles is safe and effective



Data coming soon!

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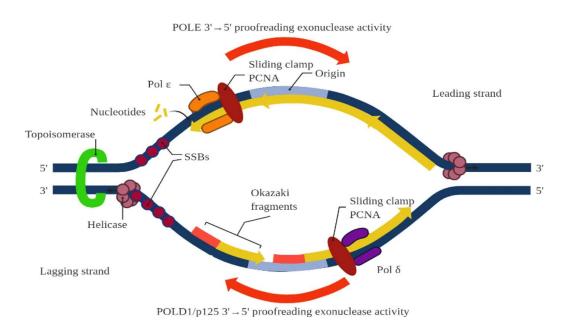


POLE

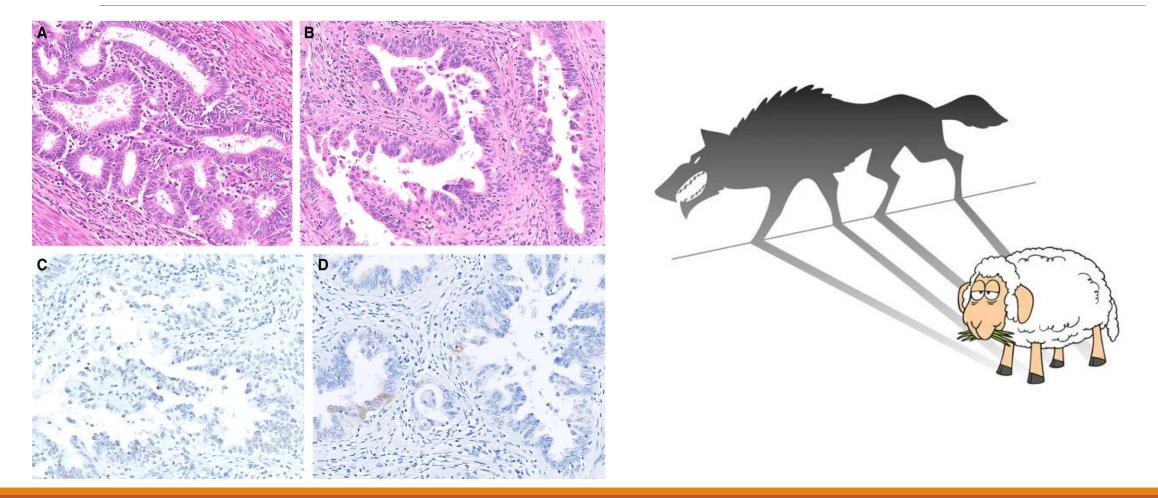
Mechanism

DNA proof-reading function

- POLE encodes the major catalytic proofreading subunits of the PolE DNA polymerase enzyme complex and PolE enzyme complex synthesizes the leading strand
- Exonuclease function locates and replaces erroneous bases in the daughter strand through failed complementary pairing with the parental strand
- Exonuclease domain mutations increase spontaneous mutation rates (mouse models)



POLE mutation and histology



PMID: 28795426 https://www.everypixel.com/q/wolves-sheep

Should we test based on morphology?

MORPHOLOGY/IHC

Prominent immune infiltrate:

Peritumoral or infiltrating lymphocytes

Giant cells

Focal Serous-like features

p16 unhelpful

Grade not significantly different

BOOLEAN MODELING

Sensitivity of 80% and specificity of 88%, assuming prevalence of 7%, PPV is 33%

- MLH1 wild-type expression OR p53 wild type expression
- Endometrioid-type EC
- Peritumoral lymphocytes OR tumor grade 3

Sequencing

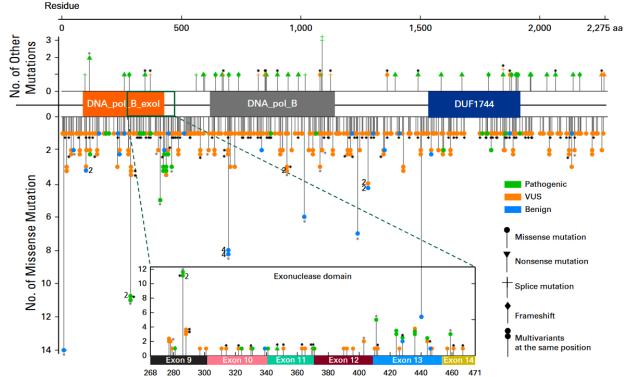
Majority of studies showing prognosis are based on

Expensive/insurance may only reimburse once

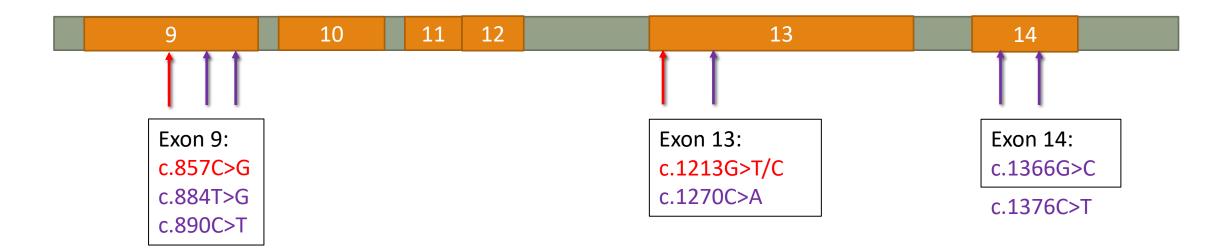
Slow TAT

Not all alterations in POLE are related to prognosis or even clearly pathogenic (n=458, all cancers)

- 15% Pathogenic showed prognostic significance, response to immune checkpoint inhibitor
- 16% Benign
- 69% Variant of unknown significance



Exonuclease domain



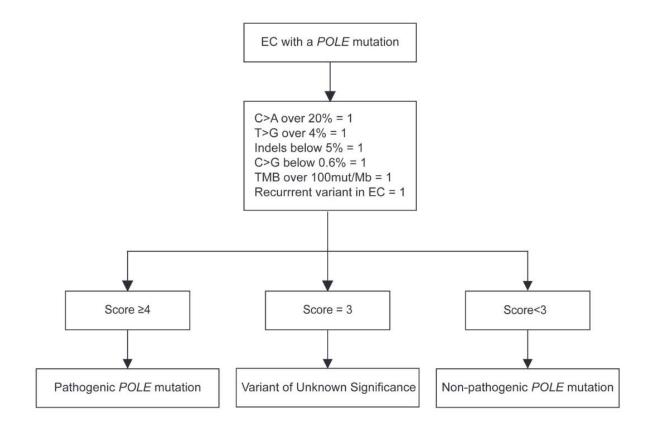
Exons

Red: 2 most common alterations Purple: <10% of alterations

PMID: 23636398, 34910396

Private Information

Scoring System for novel Mutations in POLE



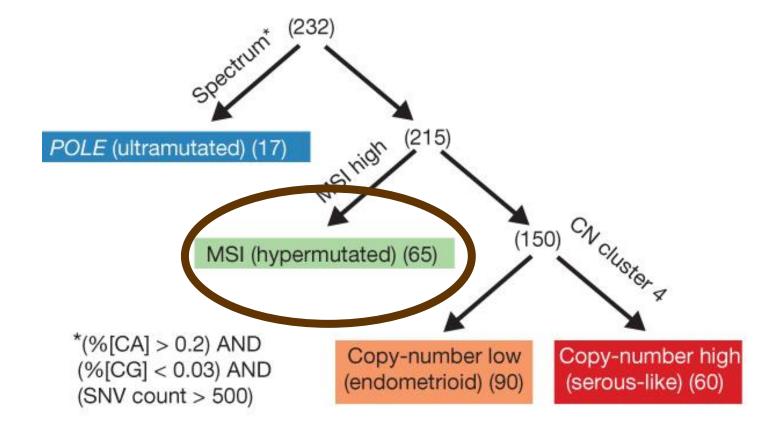
*database searches

PMID: 31829442

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ISGyP 2020 Annual Meeting

"Although treatment implications are suggested by several clinical trials, these cannot be incorporated into routine clinical practice in the absence of prospective data from randomized controlled clinical trials. At the present time, the purpose of classifying EC on a molecular basis, and specifically of POLE testing, is restricted to providing prognostic insight, and for treatment modulation in clinically challenging cases. This is also of diagnostic utility in young patients with p53 abnormal serous-like carcinomas."



Mismatch repair instability

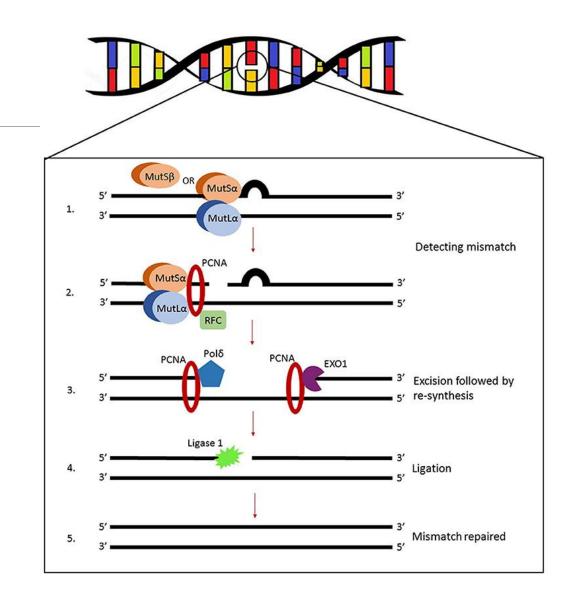
Mismatch repair

Recognition of a mismatch by the MSHs

Recruitment of the MLHs by ATP-bound MSHs that then connect the mismatch recognition signal to the distant DNA strand scission where excision begins

Excision of the DNA strand containing the wrong nucleotide

Resynthesis of the excision gap by the replicative DNA polymerase using the remaining DNA strand as a template (virtually identical to normal replicative DNA synthesis)



Microsatellite Instability Testing

PCR

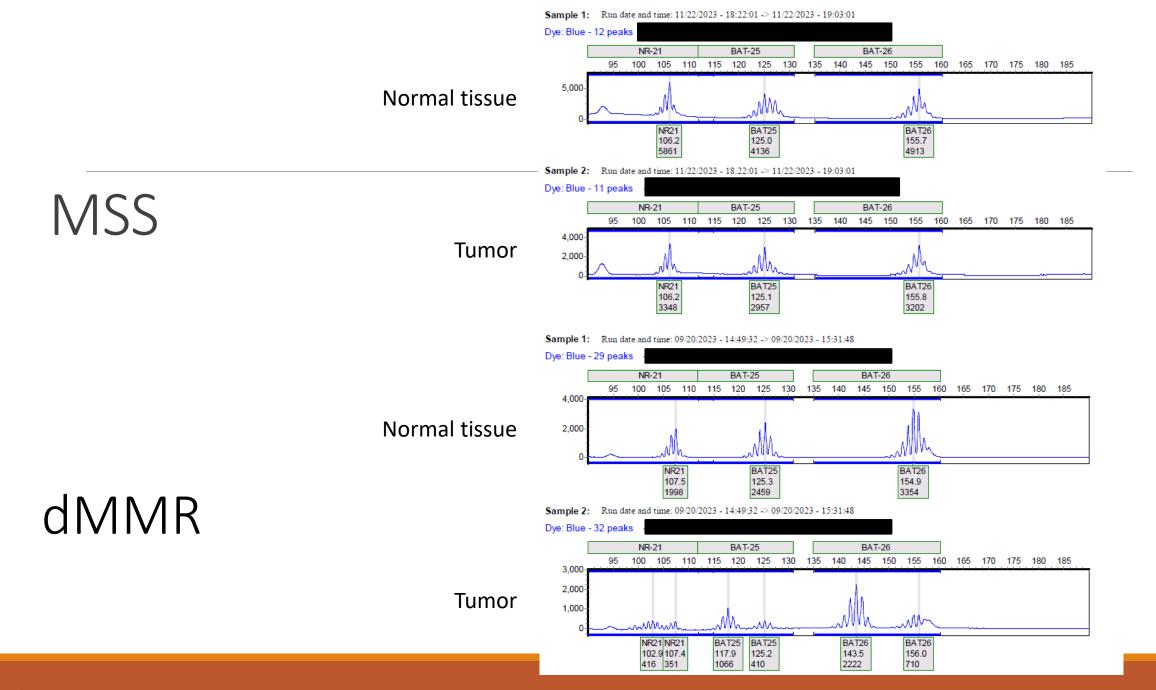
- Microsatellites are variable blocks of short repeating nucleotide sequences: 1-6 base pairs repeated 2-10 times mostly in non-coding regions
 of the genome
- Prone to errors during DNA replication; DNA mismatch repair proteins normally recognize and repair these errors.
- Loss of function \rightarrow high mutagenesis \rightarrow high frequency of changes to length of microsatellites
- The National Cancer Institute microsatellite panel was optimized and correlated with IHC analysis in MMR-deficiency in colorectal cancer
 - 5 microsatellites tested: BAT25, BAT26, D5S346, D2S123, D17S250 (Mononucleotide Dinucleotide)
 - 1 unstable (<40%) = MSI-low or MSI-indeterminate
 - 2 or more unstable (≥40%) = MSI-high
- MSI is defined as a change of any length due to either insertion or deletion of repeating units, in a microsatellite within a tumor when compared to normal tissue (this is limited by the analytical sensitivity of the assay)
- Dinucleotide repeats are less sensitive and specific than mononucleotide repeats for the identification of cancers with MMR deficiencies. A commercially available fluorescent multiplex assay that analyzes five nearly monomorphic mononucleotide microsatellite loci (*BAT-25, BAT-26, NR-21, NR-24,* and *MONO-27*) is available.

IHC

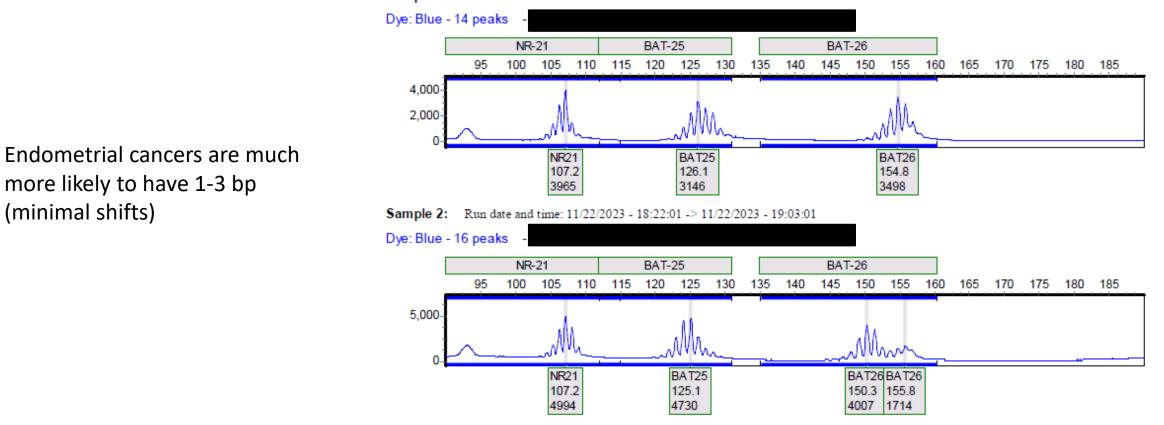
- Staining of MLH1, PMS2, MSH2, and MSH6 proteins
- Cheap, fairly easy to interpret
- Fixation issues

Sequencing

• Can integrate a number of microsatellites to determine MSI



Private Information



Sample 1: Run date and time: 11/22/2023 - 18:22:01 -> 11/22/2023 - 19:03:01

Sample 1: Run date and time: 11/22/2023 - 18:22:01 -> 11/22/2023 - 19:03:01

(minimal shifts)

Immunohistochemistry

MLH1 PMS2 MSH2 MSH6

MSH6 protein loss

Subclonal loss of MLH1/PMS2

Complete loss of MLH1/PMS2

PMID: 27742654

MSI or MMR?

MSI status	MMR protein expression					Coun
	MLH1	PMS2	MSH6	MSH2	Protein expression	
MSS	1	1	1	1	Retained	496
MSS	2	2	1	1	Subclonal loss	6
MSS	1	1	2	2	Subclonal loss	2
MSS	0	0	1	1	Loss	8
MSS	1	1	0	1	Loss	3
MSS	1	1	0	0	Loss	1
MSI-L	1	1	1	1	Retained	1
MSI-L	2	2	1	1	Subclonal loss	2
MSI-L	0	0	1	1	Loss	4
MSI-L	1	0	1	1	Loss	2
MSI-L	1	1	0	1	Loss	2
MSI-H	1	1	1	1	Retained	2
MSI-H	2	2	1	1	Subclonal loss	8
MSI-H	0	0	2	1	Loss/subclonal loss	6
MSI-H	0	0	1	1	Loss	130
MSI-H	1	1	0	0	Loss	10
MSI-H	1	0	1	1	Loss	8
MSI-H	1	1	0	1	Loss	5

Mismatch repair protein expression was scored as following: 0— Complete loss; 1—Retained; 2—Subclonal loss. MMR—mismatch repair, MSS—microsatellite stable, MSI-L/H—microsatellite unstable with low or high frequency.

	Retained	Loss
MSS	496	20
MSI-L	1	10
MSI-H	2	167

Concordant in 655/696, kappa =0.854

Ambiguous cases (n = 41):

- subclonal loss (n=18)
- MSS with loss of MMR protein expression (n=20) [promoter methylation of MLH1 was identified in the majority of cases]
- MSI-L or MSI-H with retained MMR protein expression (n=3)

dMMR – what's next?

MLH1 methylation BRAF V600E

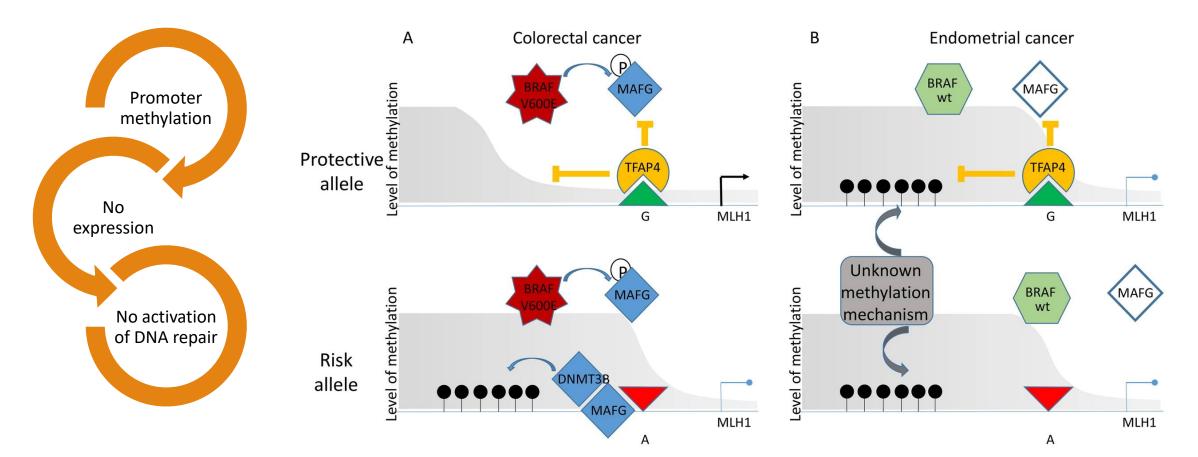
■ methylation ■ mutation



EPCAM deletion

PMID: 10072435

Loss of MLH1 is predominantly due to somatic silencing by promoter hypermethylation



PMID: 32641106

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Subclonal dMMR

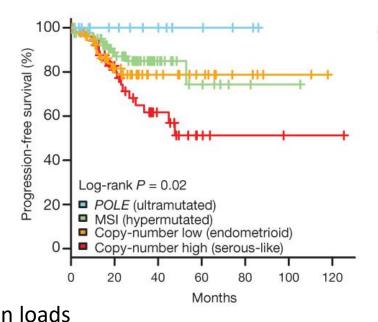
Subclonal loss of MMR protein expression generally corresponded to MLH1 promoter hypermethylation and subclonal MSI within microdissected area of the tumor.

MLH1+PMS2 subclonal loss \rightarrow MLH1 promoter hypermethylation \rightarrow sporadic intratumor heterogeneity

MSH6 +/- MSH2 subclonal loss \rightarrow unclear mechanism

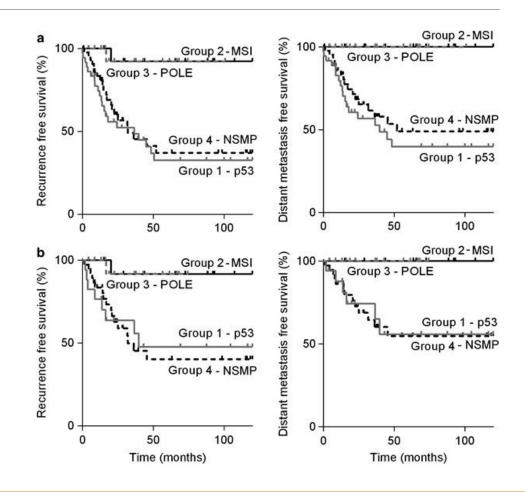
MSH6 subclonal + MLH1/PMS2 complete loss \rightarrow secondary MSI events in MSH6

Improved survival of MMRd and POLE mutants



High neoantigen loads

Increased tumor-infiltrating lymphocytes Overexpression of PD-1 and PD-L1 in TILs and intraepithelial immune cells, but not tumor cells



PMID: 23636398, 25720322, 26181000, 27159395

Check point inhibitors

Pembrolizumab: FDA-approved (in specific settings)

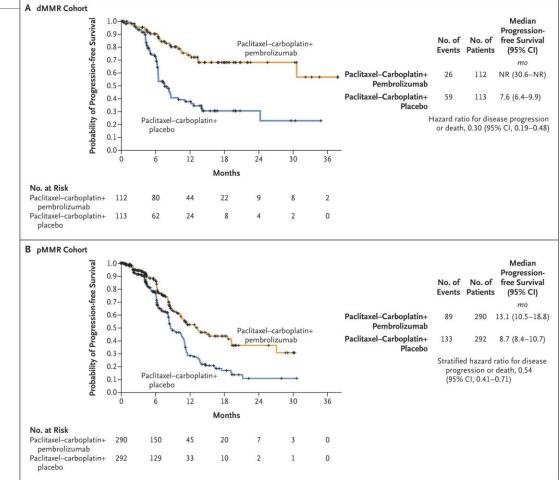
- dMMR as single agent (KEYNOTE-158)
- In combination with Lenvatinib for pMMR (KEYNOTE-775)

Dostarlimab: FDA-approved

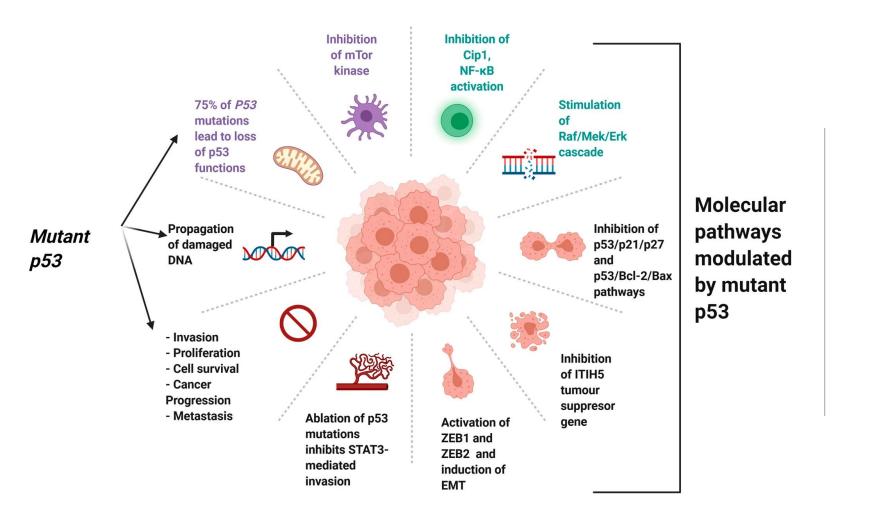
dMMR advanced solid tumors

Recent advances in primary advanced or recurrent endometrial cancer including pMMR

- GY018: additional of Pembrolizumab
- RUBY: addition of Dostarlimab



PMID: 35680043, 36972022, 36972026



Copynumber High

Copy number high, low mutational burden

p53 IHC is a surrogate marker for this tumor group

Non-myoinvasive can present with extrauterine and metastatic disease

Primarily serous, but histologic type did not alter overall survival; stage being a better predictor

• Even grade 1 and 2 endometrioids can harbor TP53 mutations

Associated with HER2-positivity and homologous deficiency (HRD)

- ERBB2 amplification is most common (unfavorable clinical outcomes)
- May also harbor ERBB2 activating hotspot mutations point mutations which have shown association with sensitivity to anti-HER2 therapy in other cancer types

P53 IHC categories

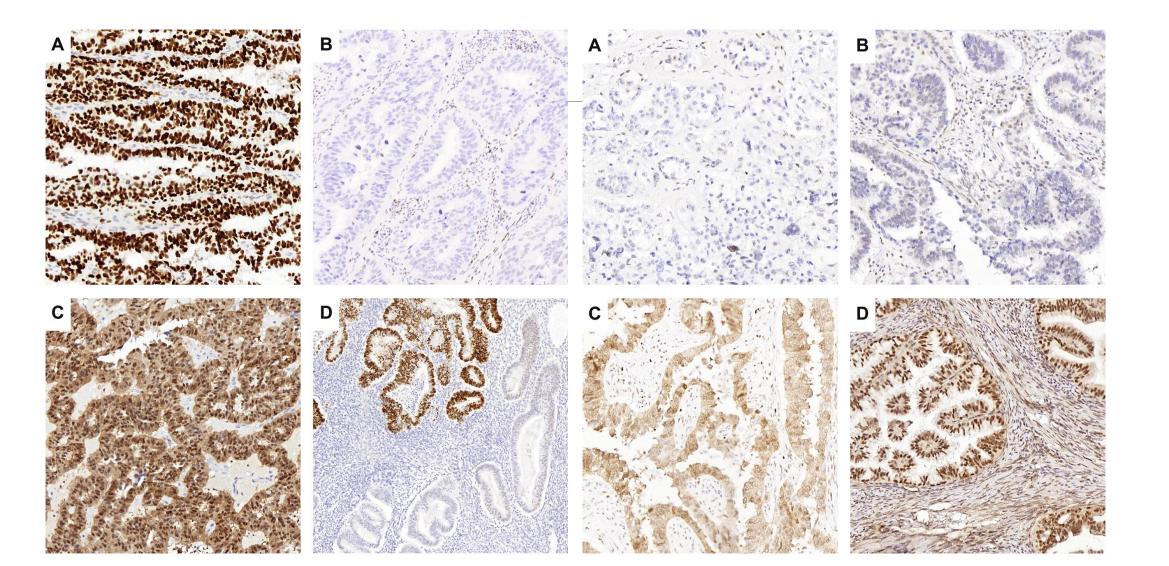
Wild-type/normal: admixture of negative cells, weakly and strongly positive cells

Mutant overexpression: 80-100% of tumor cells show strong nuclear expression of p53. Commonly missense mutations in the DNA binding domain of TP53 resulting in nuclear accumulation of p53

Null mutant pattern: loss of expression of p53 in all tumor cells, positive internal control must be present. Commonly frameshift or nonsense mutations

Cytoplasmic overexpression: unequivocal cytoplasmic staining accompanied by a variable nuclear staining. Commonly mutations in the tetramerization or C-terminal domain of TP53 (suggested >80% of the tumor)

Subclonal abnormal p53 expression: well-defined area within a tumor shows an abnormal p53 IHC pattern. *cutoffs for percent of tumor is unclear, studies have used 10% of tumor, <80% of tumor volume

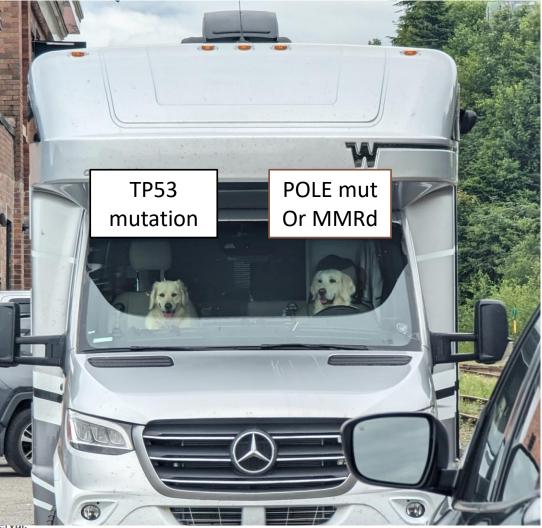


P53 IHC vs Sequencing

	(Likely) pathogenic mutation	n on <i>TP53</i> NGS analysis			
	All EC		POLE wildtype and MMR proficient EC		
p53 IHC	Absent	Present	Absent	Prese	
Wildtype	215	19	96	4	
Abnormal	13	97	6	76	
Total	228	116	102	80	
Accuracy	90.7% (95% CI 87.6–93.8%)	% (95% CI 87.6–93.8%) 94.5% (95% CI 89.4–99.6%)			
Sensitivity	83.6% (95% CI 79.7–87.5%)		95.0% (95% CI 90.2–99.8%)		
Specificity	94.3% (95% CI 91.8–96.7%)		94.1% (95% CI 88.9–99.3%)		

In bold, EC with concordant p53 IHC and sequencing for TP53 mutations.

IHC immunohistochemistry, NGS next generation sequencing, EC endometrial cancer, MMR mismatch repair, CI confidence interval.



Private Information

HER2 Clinical trials

2010 – single agent trastuzumab failed to demonstrate therapeutic benefit

The addition of trastuzumab to carboplatin/paclitaxel increased PFS and OS in HER2+ uterine serosal cancer with the most benefit in stage III/IV disease. (NCT01367002)

NCCN: HER2 IHC testing with reflex to FISH is recommended for all serous and carcinosarcoma tumors. Consider HER2 testing for p53 abnormal carcinomas regardless of histology

Clear HER2 overexpression by IHC or FISH is associated with worse recurrence and survival outcomes in uterine serous carcinoma

HER2 scoring?

No current standard

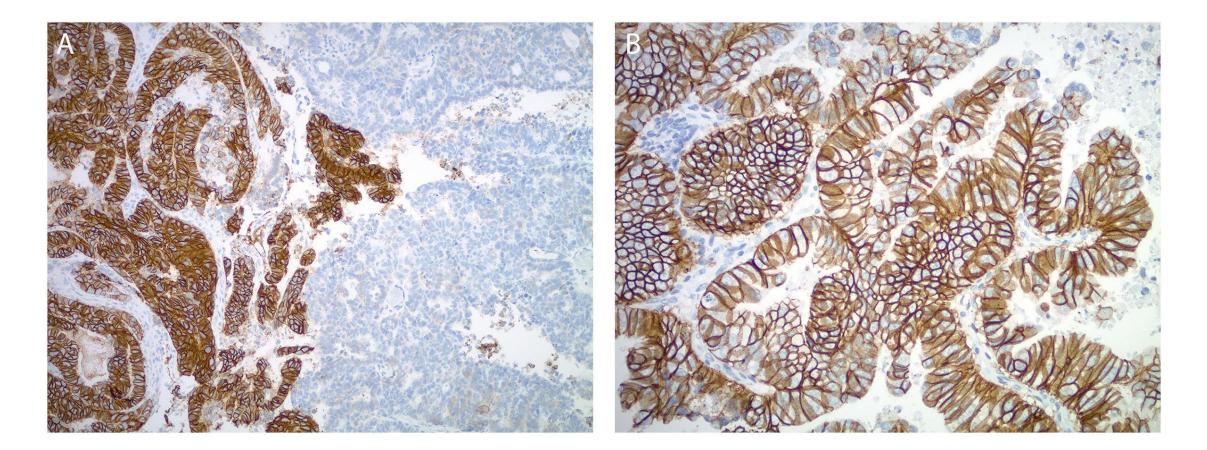
The 2007 ASCO/CAP breast scoring system (>30% circumferential) yielded the highest concordance between IHC and FISH for HER2 expression in uterine serous carcinoma in one study Table 1. Current criteria (approved or proposed) for HER2 positivity by IHC and FISH in different tumour types

	HER2 IHC 3+	HER2 FISH amplification
Breast (ASCO/CAP 2018)	>10% circumferential, strong, complete	HER2/CEP17 ratio ≥2.0 and HER2 signal ≥4.0/nucleus OR ratio <2.0 and HER2 signal ≥6.0/nucleus (if IHC score 2+ or 3+)
Gastric/gastro-oesophageal junction (ASCO/CAP 2016)	≥10%, strong complete, or basolateral/lateral	<i>HER2</i> /CEP17 ratio ≥2.0 OR ratio <2.0 and HER2 signal >6.0/nucleus
Colorectal (HERACLES trial)	≥50% strong complete, or basolateral/lateral	<i>HER2</i> /CEP17 ratio \geq 2.0 in \geq 50% of cells

ASCO, American Society of Clinical Oncology; CAP, College of American Pathologists; FISH, fluorescent *in situ* hybridisation; IHC, immunohistochemistry.

PMID: 36503635, 23765245

Lateral/basolateral membranous staining – still 3+

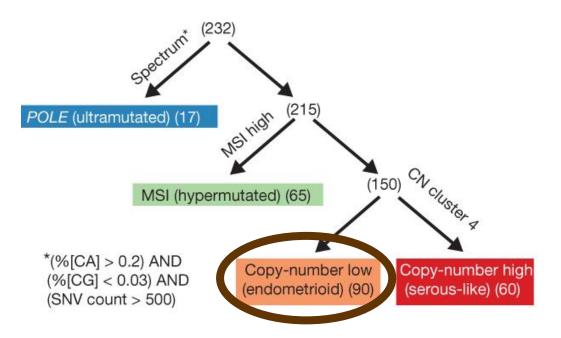


No specific molecular profile (NSMP) / Low copy number

Prognosis between POLE-mutated and copy number-high

Heterogeneous group

In addition to hormonal therapy, maintenance therapy with selinexor (exportin-1 inhibitor) showed potential benefit in *p53*-wildtype cases in a subset analysis and is being investigated prospectively.



Mesonephric like endometrial cancer

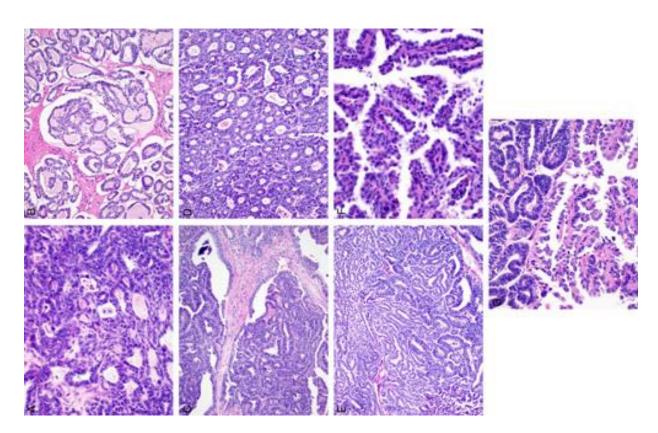
Rare and aggressive histotype

Current data suggest they are NSMP

Appear to harbor KRAS mutations (p.G12 common), absent TP53, PTEN abnormalities

IHC:

- express TTF-1 and/or GATA3, PAX8 positive
- predominantly negative for hormone receptors including estrogen receptor (ER)
- pMMR

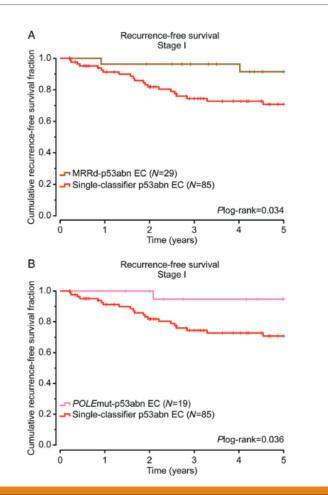


More than one aberrancy?

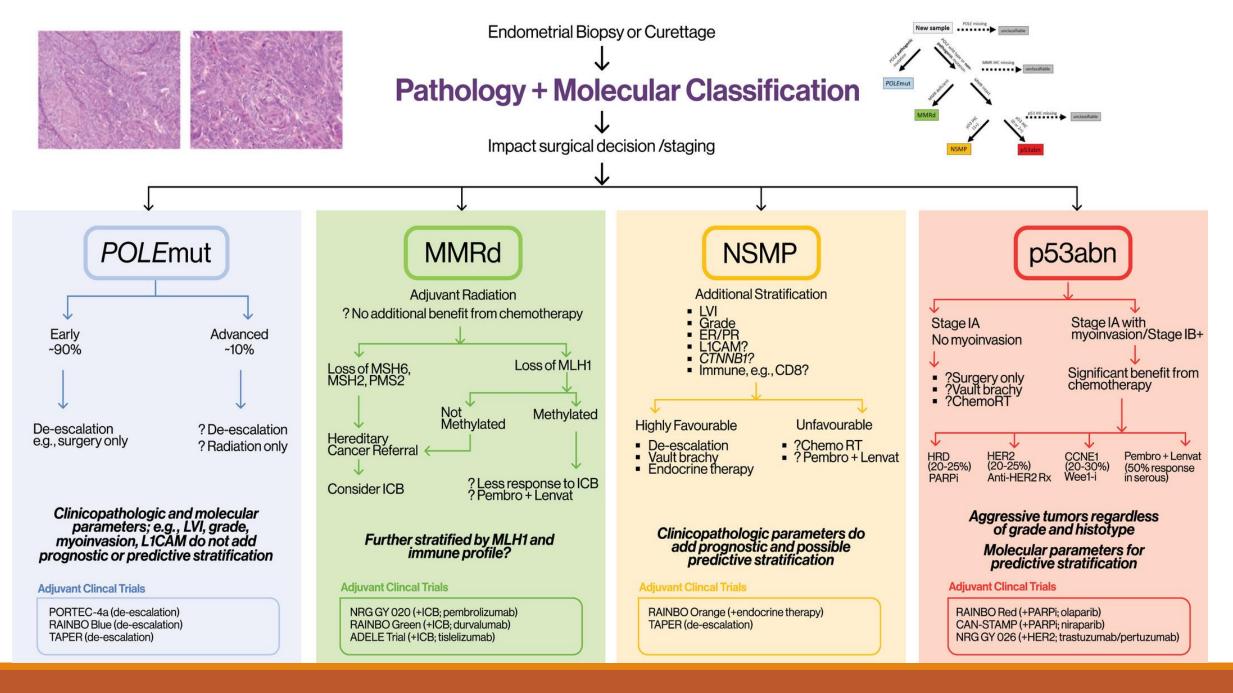
3% (107/3353) of p53 abnormal had an additional aberrancy

- 64 MMRd-p53abn
- 31 POLEmut-p53abn
- 12 MMRd-POLEmut-p53abn

30 MSI-H + POLE EDM: 5yr recurrence-free survival comparable to previously reported POLE-ultramutated



	Use & utility				
	FDA approved EC biomarker	Predictive of response to agent	Prognostic	Exploratory	
dMMR	1	\checkmark	\checkmark		
MSI	\checkmark	\checkmark	\checkmark		
ТМВ-Н	\checkmark	\checkmark			
P53		\checkmark	\checkmark	\checkmark	
HER2		\checkmark	\checkmark		
ER/PR		\checkmark	+/-	\checkmark	
L1CAM			\checkmark	\checkmark	
CTNNB1			\checkmark	\checkmark	
POLE			\checkmark	\checkmark	
PD-L1			+/-	\checkmark	
ARID1A				\checkmark	
PI3K/AKT/mT	OR			\checkmark	



Private Information

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