



Emerging NGS Applications at the Intersection Germline and Somatic Cancer Genetics

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Disclosure Information

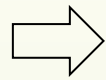
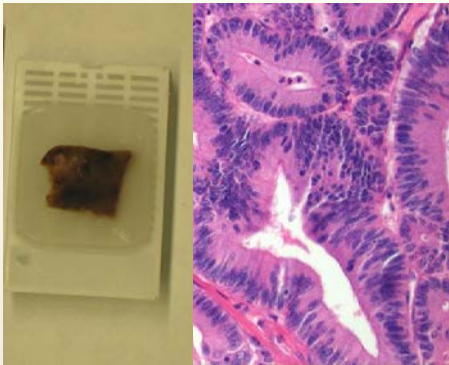
Nothing to disclose

Learning Objectives

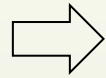
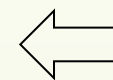
1. Understand when and how testing for inherited mutations in *BRCA1*, *BRCA2*, and other homologous recombination DNA repair genes is used to guide cancer treatment.
2. Describe the clinical scenario and utility of tumor sequencing of mismatch DNA repair genes as part of a Lynch syndrome workup.
3. List at least two types of tumor findings that increase the probability that a germline variant in a cancer predisposition gene is pathogenic.

Interplay

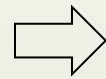
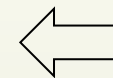
Tumor



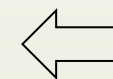
Targeted Therapy



Cancer Syndrome Screening



Variant Interpretation



Germline



Outline

- DNA repair gene mutations and cancer treatment
 - Background
 - Testing Approaches
- Tumor sequencing in a Lynch workup
- How tumors can help with variant classification
- Case vignette

DNA Repair Genes Guide Cancer Treatment

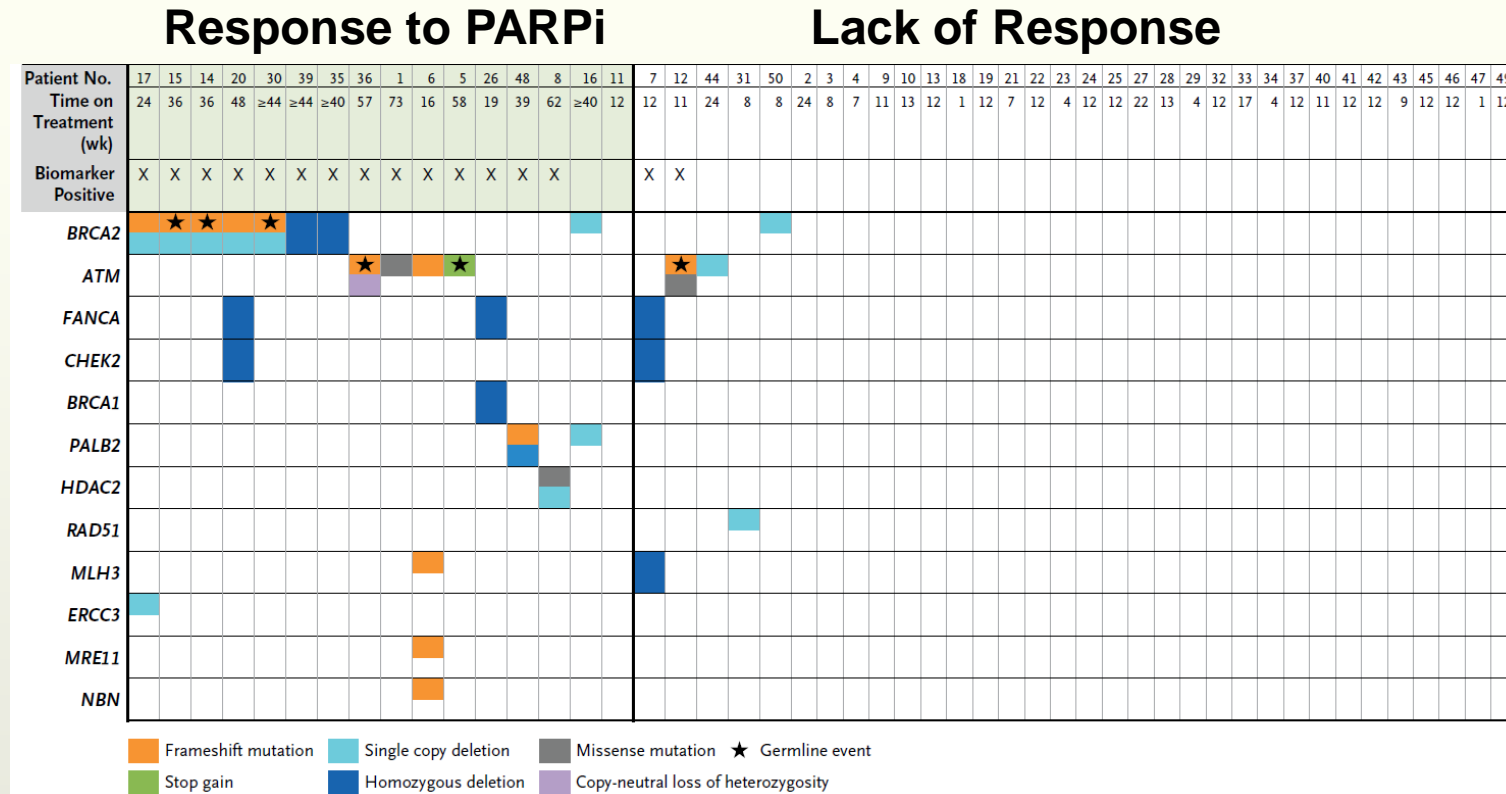
DNA Repair Pathway	Example Genes	Germline Syndrome	Treatment Implications
Homologous Recombination Repair (HR)	<i>BRCA1</i> , <i>BRCA2</i>	Hereditary breast/ovarian/ prostate	PARPi, platinum
Mismatch Repair (MMR)	<i>MSH2</i> , <i>MLH1</i>	Lynch	PD1/PDL-1 inhibitors

PARPi= poly(ADP) ribose polymerase inhibitor
PD1/PDL-1= programmed cell death 1/ligand 1

FDA Approves PARPi for Ovarian and Breast

- Three PARPi approved, 2014 (ovary), 2018 (breast)
- Two drugs based on *BRCA1/2* mutation status
- Germline + somatic *BRCA1/2* testing now standard
- Other cancers close behind: prostate, pancreatic

Extraordinary PARP Inhibitor Responses in DNA Repair-Mutated Prostate Cancer

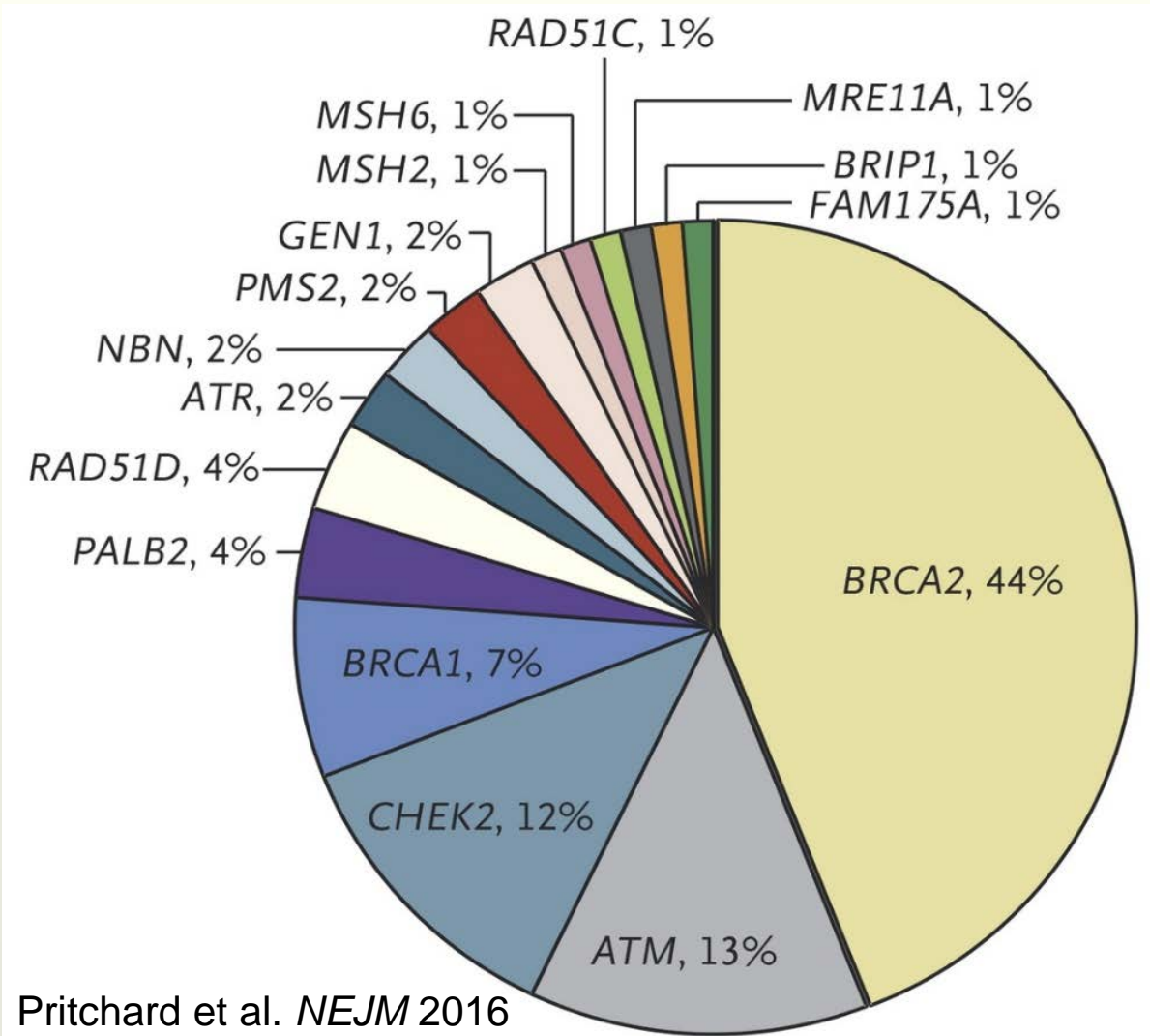


14/16 (88%) with bi-allelic DNA repair defects responded
 2/33 (6%) without bi-allelic DNA repair defects responded

Mateo et al. *NEJM* (2015)



Germline DNA Repair Mutations Are Common in Metastatic Prostate Cancer



12% (82/692)
with deleterious
germline mutations in
16 DNA repair genes

59% (36/61) with avail.
tumors had second
allele loss-of-function
mutation

FDA Approves PD-1 Inhibitor for *Any* MMR-Deficient Cancer



U.S. FOOD & DRUG
ADMINISTRATION


FDA grants accelerated approval to pembrolizumab for first tissue/site agnostic indication

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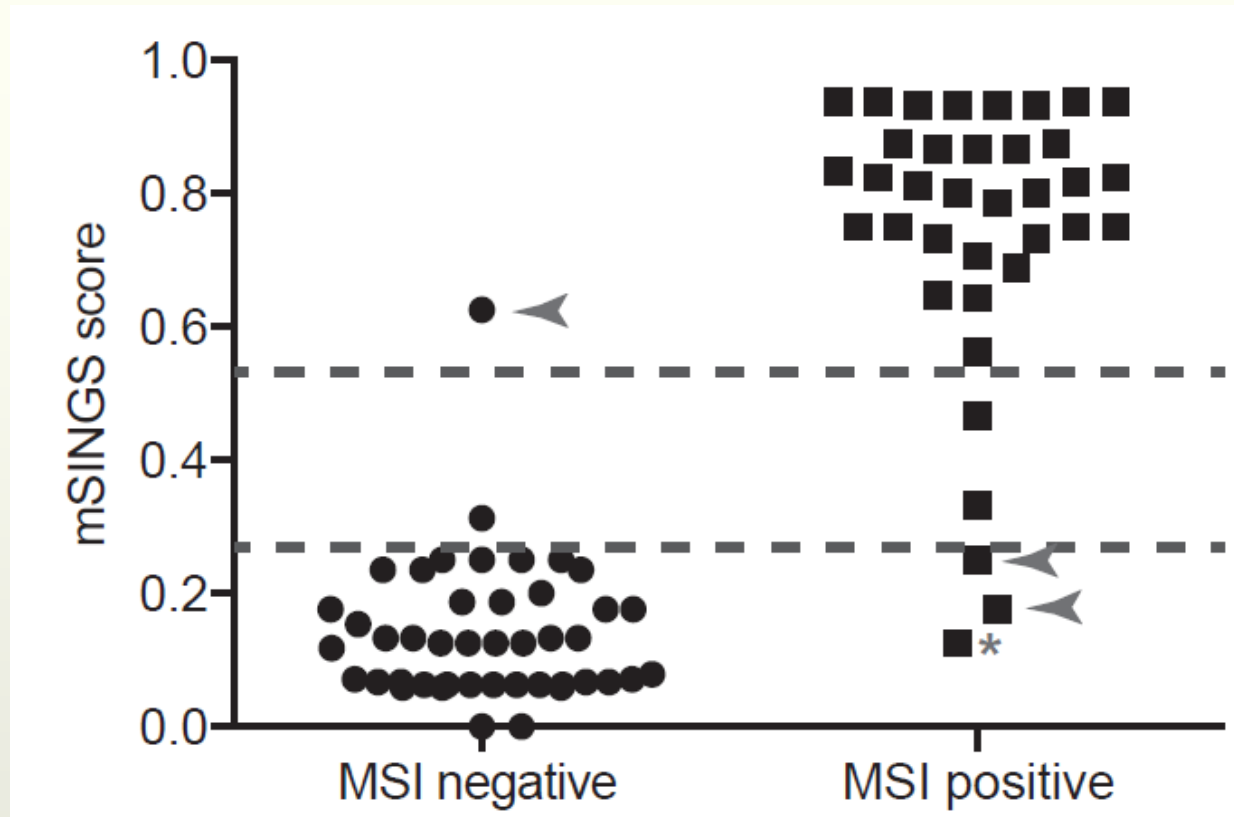
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MSI by NGS (mSINGS)

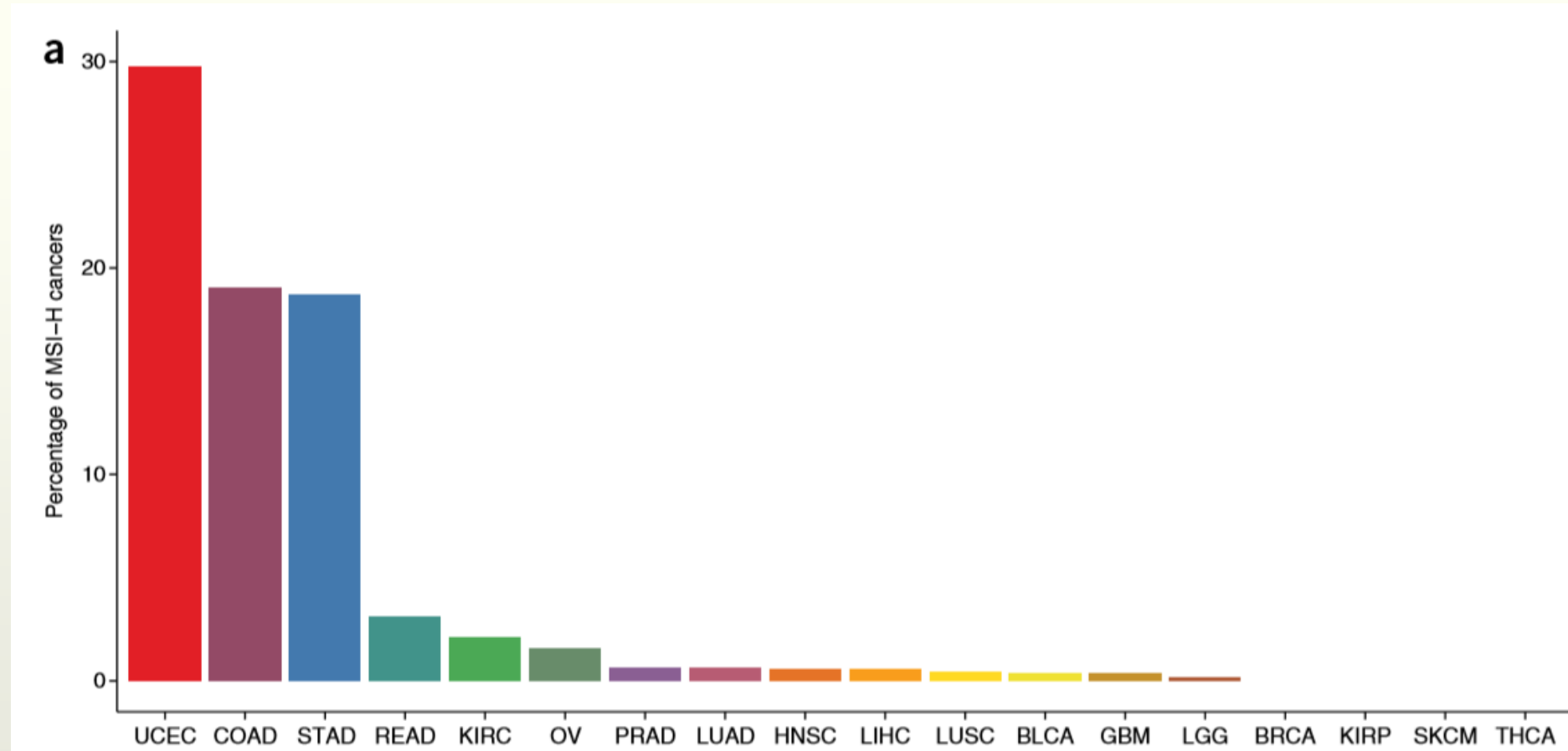
Exome

Large Panel NGS
(e.g. UW-OncoPlex)

Targeted PCR
(MSI-plus)



“Long Tail” of MSI Cancers Now Being Tested for MMR

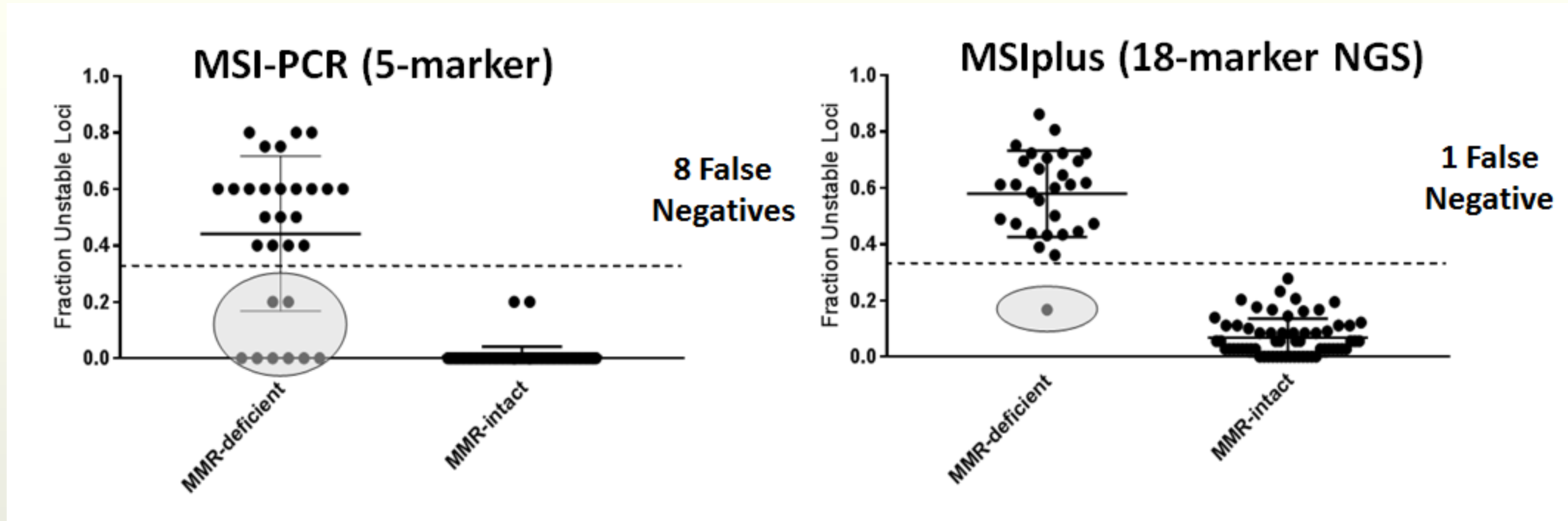


Hause et al. (2016) *Nat. Med.* PMID:27694933

MMR= mismatch DNA repair



MSI by NGS Outperforms Traditional Methods in New Cancer Types



Adapted from Hempelmann et al. (2018) *JITC*. PMID:29665853



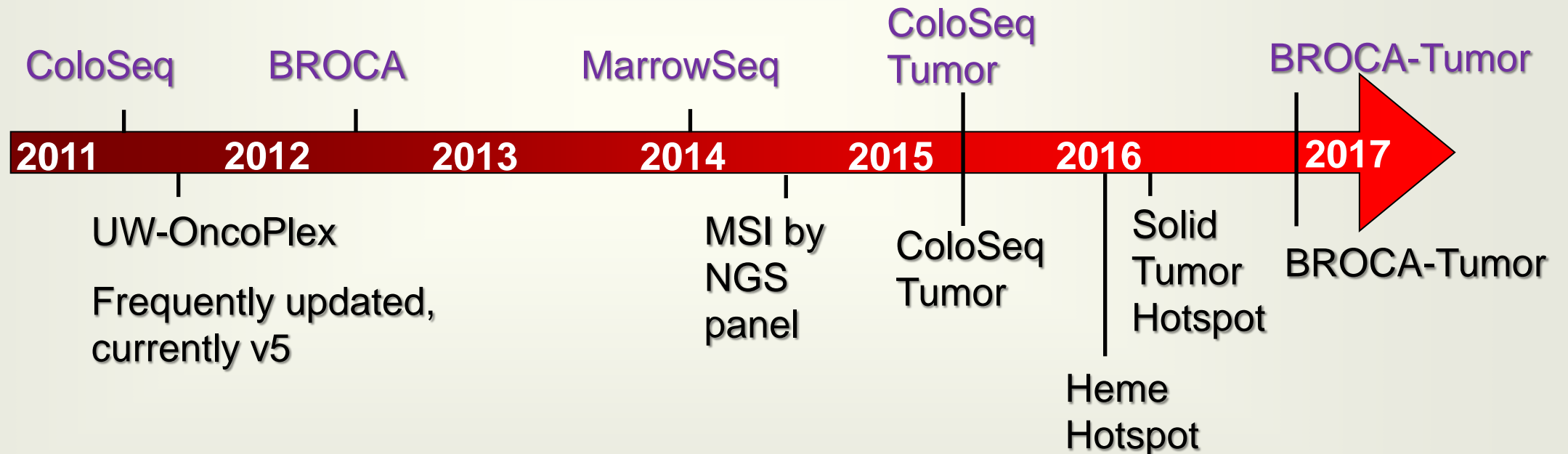
Types of Tests

DNA Repair Pathway	Functional	Mutation-Based
MMR	IHC, MSI	NGS Panel (e.g. ColoSeq), Total Mutation Burden
HR	LOH Burden	NGS panel (e.g. BROCA), HRD Mutation Signature

MMR= mismatch repair, HR= homologous recombination, HRD= homologous recombination deficiency
IHC= immunohistochemistry, MSI= microsatellite instability, LOH= loss of heterozygosity

Implementation of Cancer NGS Testing: *Not One-Size Fits All*

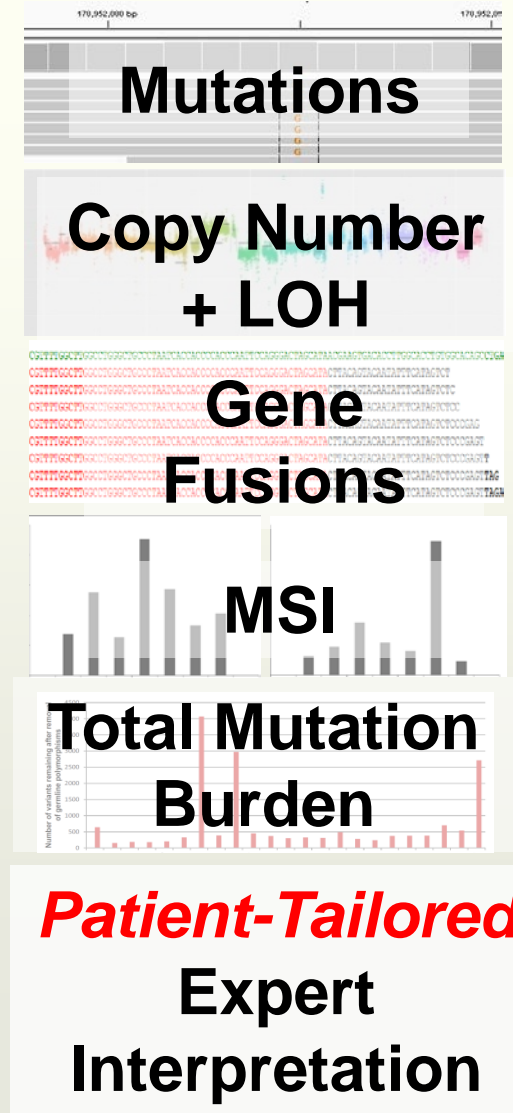
GERMLINE



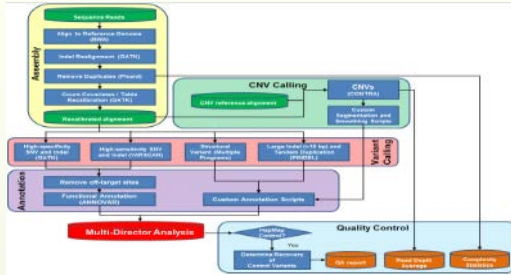
SOMATIC

Approach at UW/BBI/SCCA

- Upfront **germline and tumor** paired sequencing
- DNA repair-focused NGS panels – **exons *AND* introns**
 - e.g. BROCA-tumor



Practice of Genomic Medicine: *Patient-Tailored* Expert Review



**Pipeline
Output**

**Multiple
Director
Review**

**Multi-
Disciplinary
Review**

Report

SCCA Prostate Cancer Genetic Care Clinic (launched 2016, Heather Cheng)



Two-Part Consultation

1. Medical Oncology
 - Discuss genetics (somatic and germline) for treatment planning
 - Discuss trial/research options
2. Genetic Counselor
 - Risk assessment, pre- and post-test counseling, as relevant
 - Education and guidance on discussing with family



Outline

- DNA repair gene mutations and cancer treatment
- **Tumor sequencing in a Lynch workup**
 - **After germline testing**
 - As first-line screening
- How tumors can help with variant classification
- Case vignette

Universal Lynch Syndrome Screening: Colorectal Cancer

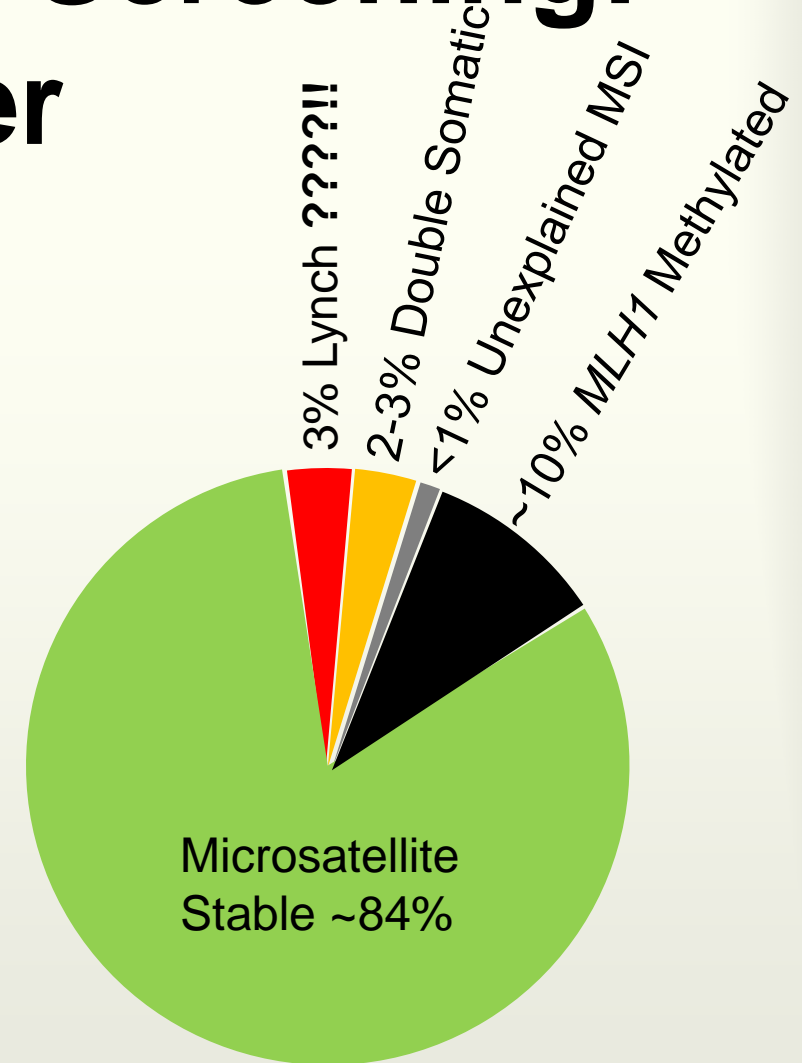
Tumor MSI/IHC **POS**



BRAF V600E/*MLH1* methylation **NEG**



Germline testing **NEG**
Lynch excluded??



MSI Flavors in CRC

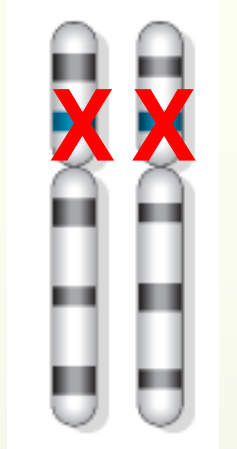
MSI= microsatellite instability, CRC= colorectal cancer

After Germline Testing is Unexpectedly Negative: Sometimes Called “Lynch Like”

- Lynch syndrome in ~3% of colorectal cancer
- “Lynch-like” also in ~2-3% of colorectal cancer
 - Positive tumor screening and no germline mutation
 - **Increasingly clinically important with universal screening**

Double Somatic MMR Mutations Common

- Explain most “Lynch-like” cases (up to 75%)
- About as common as Lynch syndrome
- Positive screening results explained by somatic mutation
- Patients unlikely to have Lynch syndrome (“undiagnosed”)

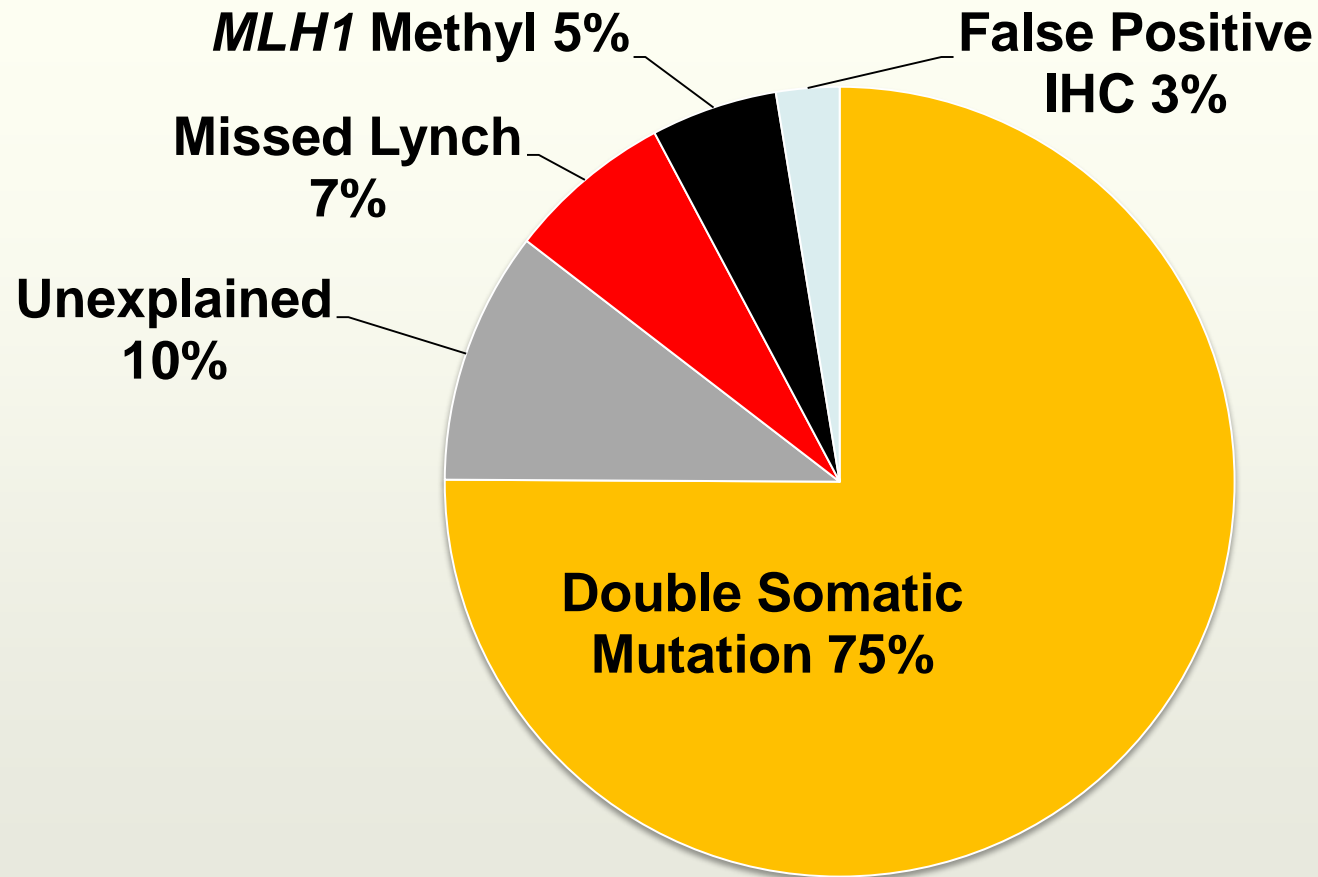


MMR= mismatch repair genes

Recommendation to **consider somatic MMR testing** in some scenarios when germline testing is negative was added to the 2015 NCCN guidelines

MMR= mismatch repair genes

Tumor NGS Can Explain MMR Deficiency After Germline is Unexpectedly Negative



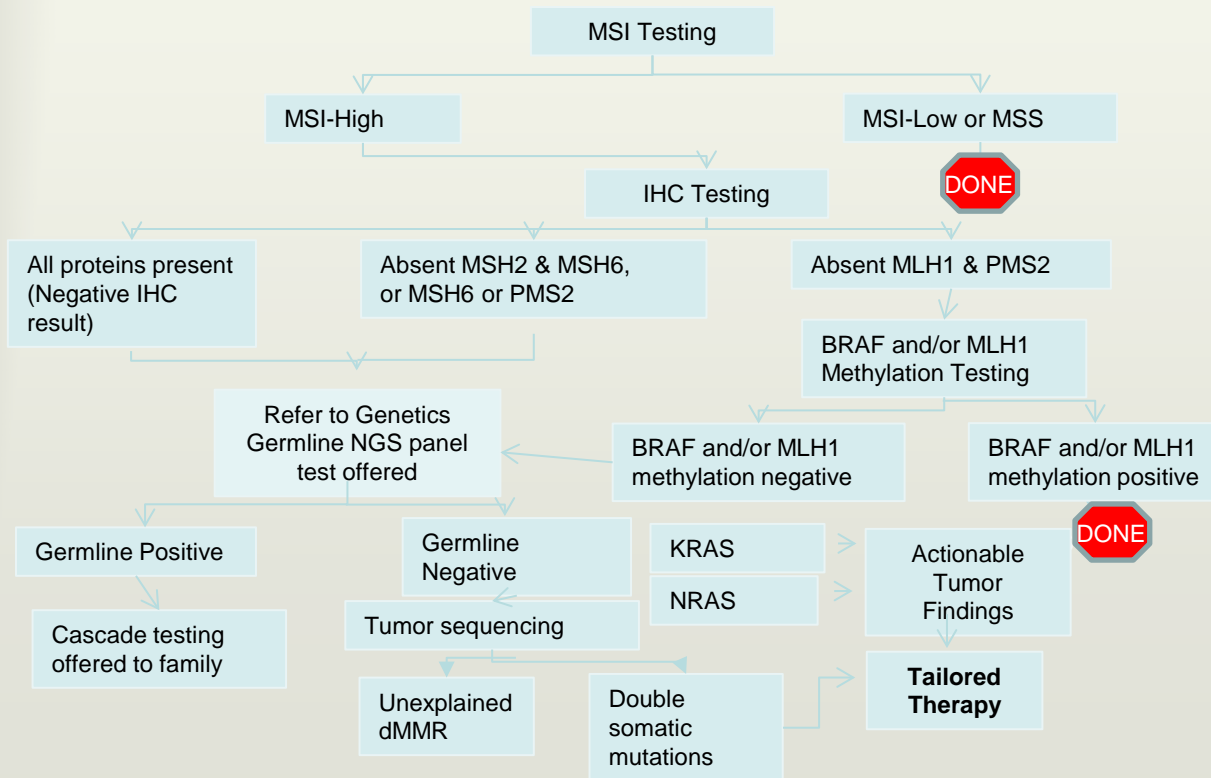
Jacobson et al. (2018), manuscript in preparation

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Tumor Sequencing as First-Line Lynch Screening Can Simplify Testing

TRADITIONAL SCREENING



TUMOR NGS SCREENING

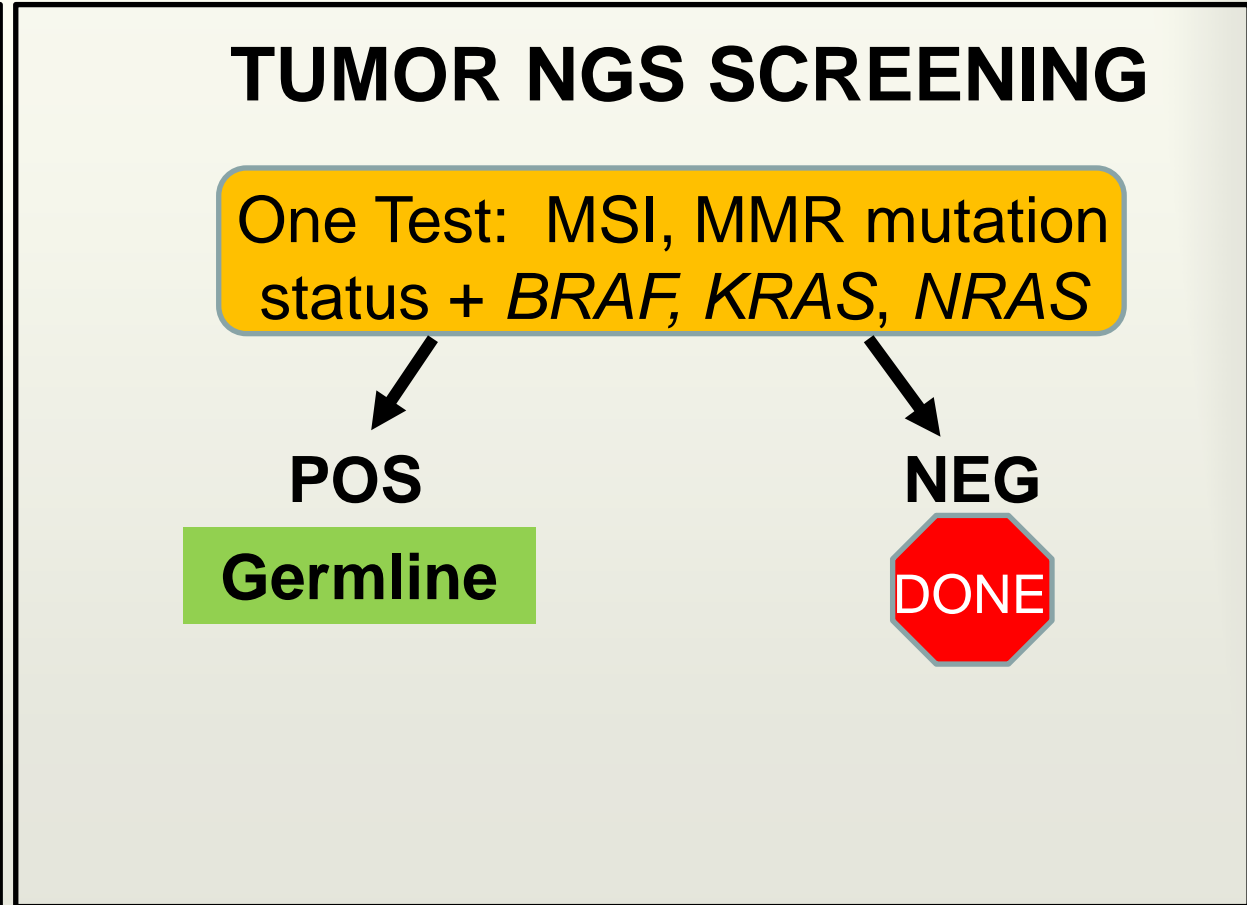
One Test: MSI, MMR mutation status + *BRAF*, *KRAS*, *NRAS*

POS

Germline

NEG

DONE



Study Design

- 419 OSU prospective cases with known MMR IHC, MSI, *BRAF*, *MLH1*-methylation status by conventional assays
- Tumor-only NGS at UW, blinded expert review
- MMR genes, MSI by NGS, *BRAF*, *KRAS*, *NRAS*

Tumor NGS as First-Line Lynch Screening Performs Better Than Traditional Screening

	Tumor NGS	MSI + BRAF	IHC + BRAF
Sensitivity	100% (94-100)	91% (81-97)	90% (79-96)
Specificity	95% (93-97)	95% (92-97)	95% (92-97)
PPV	40% (30-51)	34% (25-45)	33% (24-44)
NPV	>99% (99-100)	>99% (98-100)	>99% (98-100)
Lynch Cases Missed	0 missed	5 missed	6 missed

PPV= positive predictive value;
 NPV= negative predictive value
 (95% confidence intervals)

Hampel et al. *JAMA Oncology* 2018 PMID: 29887214



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- **How tumors can help with variant classification**
 - **In patients with germline VUS**
 - **Incorporating somatic data into classification**
- Case vignette

Tumor Data Is Being Used To Clarify Germline Variants

- Increasing tumor testing to clarify “Lynch-like” cases
- Same tests used in patients with germline MMR VUS

VUS= variant of uncertain significance

MMR= mismatch repair genes

“Lynch-like”= patients with positive Lynch screening tests, but negative germline testing

When Tumor Testing *Might* Help

“High” germline VUS, close to likely pathogenic

OR

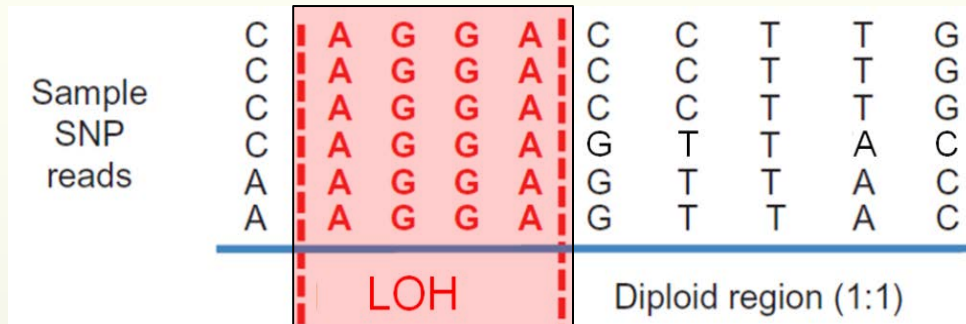
“Low” germline VUS, close to likely benign

VUS= variant of uncertain significance

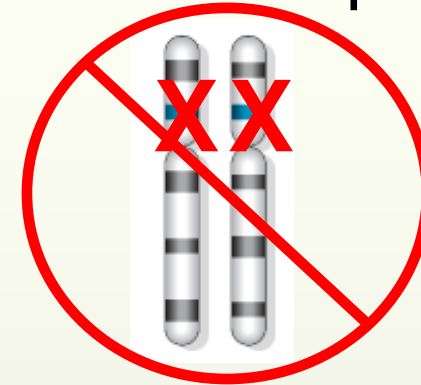


Clues From Tumor: Germline VUS Pathogenic

Loss of Heterozygosity (LOH)

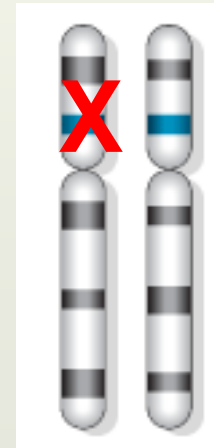


No Somatic Explanation



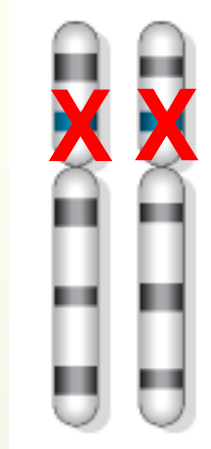
OR

Single Somatic Mutation
Consistent With 2nd Hit



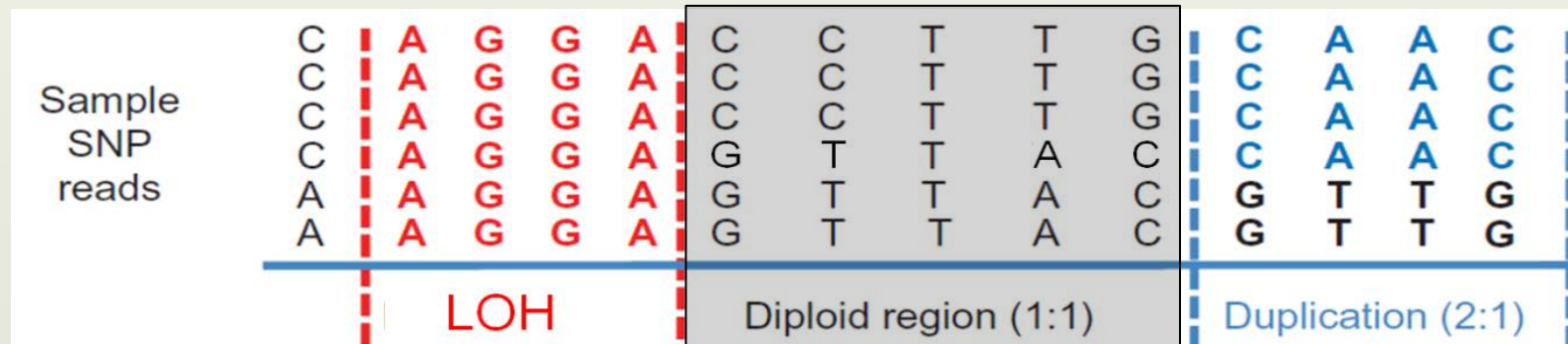
Clues From Tumor: Germline VUS Benign

Double somatic mutation



AND

Absence of LOH



Pitfalls

- Missed germline or somatic mutation
- Double somatic mutations are *in cis*
- Multiple clones

Tumor NGS Enables Variant Re-Classification

- 40 patients with germline MMR VUS
- 5 re-classified based in part on tumor sequencing
 - 4 to likely pathogenic
 - 1 to likely benign



MMR= mismatch repair gene
VUS= variant of uncertain significance

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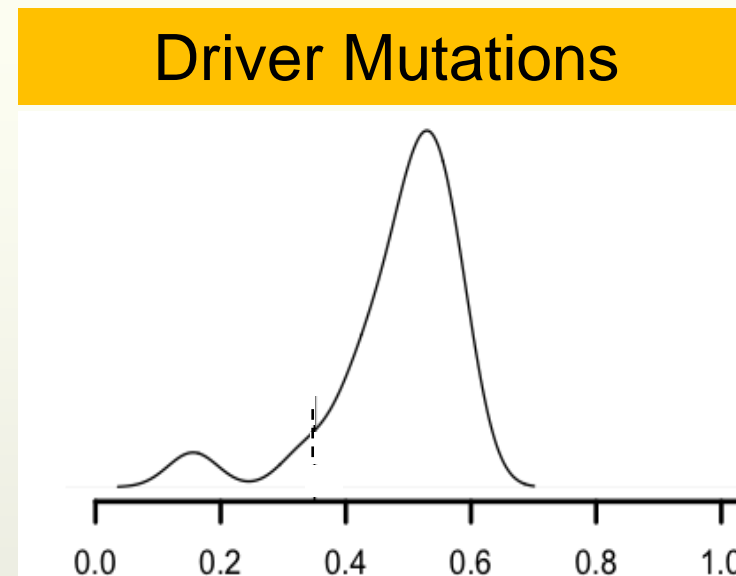
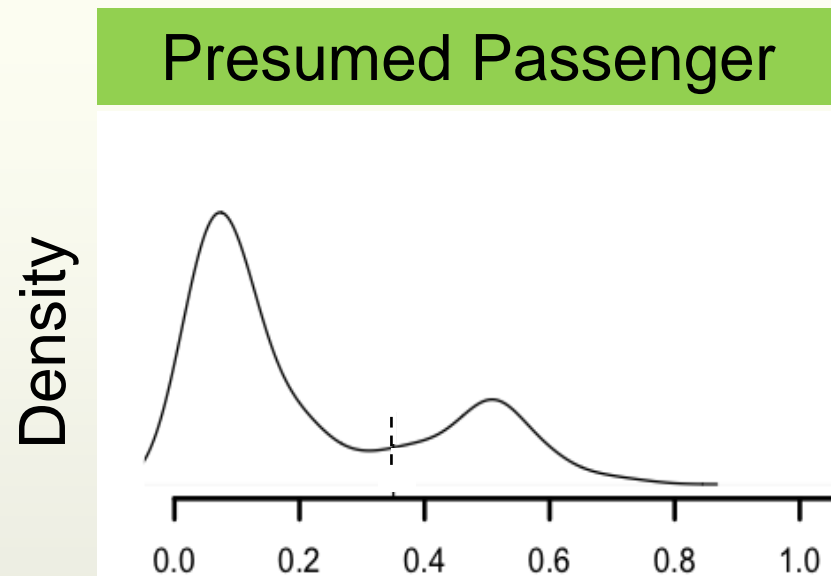
Incorporating Somatic Data into Classification: Lynch is the Perfect Model

- Highly specific tumor phenotype (e.g. MSH2 loss)
- Somatic mutations are *de novo*
- Analogous to *de novo* germline mutation in a patient with a matching phenotype -strong criteria for pathogenicity

Somatic Mutations That Explain IHC

- Somatic missense mutations often explain IHC
- Same mutations may be seen as germline VUS
- Can we use the tumor information to reclassify?
- Yes!

Tumor NGS for Variant Classification: Passenger or Driver?



Brian Shirts

Normalized Variant Allele Fraction

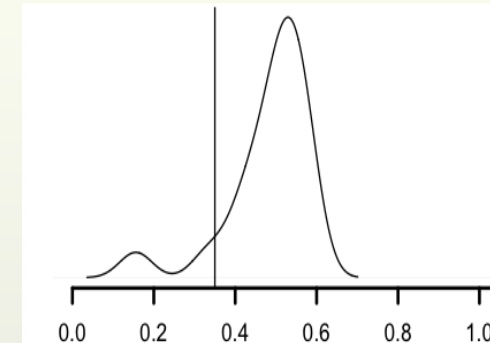
Shirts et al. (2018), *Am. J. Hum Genet.* PMID:29887214

Likelihood Modeling

- Prior probability based on InSiGHT



- Likelihood ratio (LR) from normalized variant allele fraction



- Posterior probability $>95\%$ = Likely Pathogenic

Results

- 61 somatic missense MMR mutations that fit IHC
- 20 reported as germline
 - 10/20 classified as pathogenic/likely pathogenic
 - 10/20 classified as VUS
- **4 of 10 VUS reclassified as pathogenic/likely pathogenic**

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- **Case vignette**

Case

- 45 year old woman with colorectal cancer that loss of MSH2 and MSH6 protein by IHC
- Father had colon cancer at age 55
- Colon cancer predisposition panel testing identifies a rare deep intronic variant in *MSH2*

Case

- Nucleotide position is completely conserved
- Computer prediction strongly suggests the creation of a cryptic splice site
- Variant is reported as VUS with offer of RNA functional studies to follow up

Case: Final Diagnosis

Lynch syndrome caused by an inherited pathogenic deep intronic mutation in *MSH2* that results in the introduction of a cryptic exon and a premature frameshift

Summary

- **Germline and tumor** NGS testing of DNA repair genes is increasingly **needed to guide cancer treatment**
- **Tumor NGS** testing increasingly **used in a Lynch workup**
- **Tumor NGS** testing assists with DNA repair gene **variant classification**

Thank You!

- UW/SCCA/FHCRC/BBI Clinical

- Genetics and Solid Tumors Lab
- NGS Analytics Lab
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