

Personalized CRC Prevention: A case for Hereditary CRC Syndromes

Eduardo Vilar, MD, PhD

Associate Professor & Deputy Chair

Department of Clinical Cancer Prevention

The University of Texas MD Anderson Cancer Center

evilar@mdanderson.org

PragueONCO 2020

January 30th, 2020

Prague, Czech Republic

Disclosure Information

**PragueONCO 2020
Eduardo Vilar, MD, PhD**

Janssen Research & Development (Consulting)

PI on NCI U01 CA231425 ‘Neoantigen Vaccination for Lynch Syndrome Immuneprevention’: a Co-Investigator on this grant is an employee of NousCom, srl

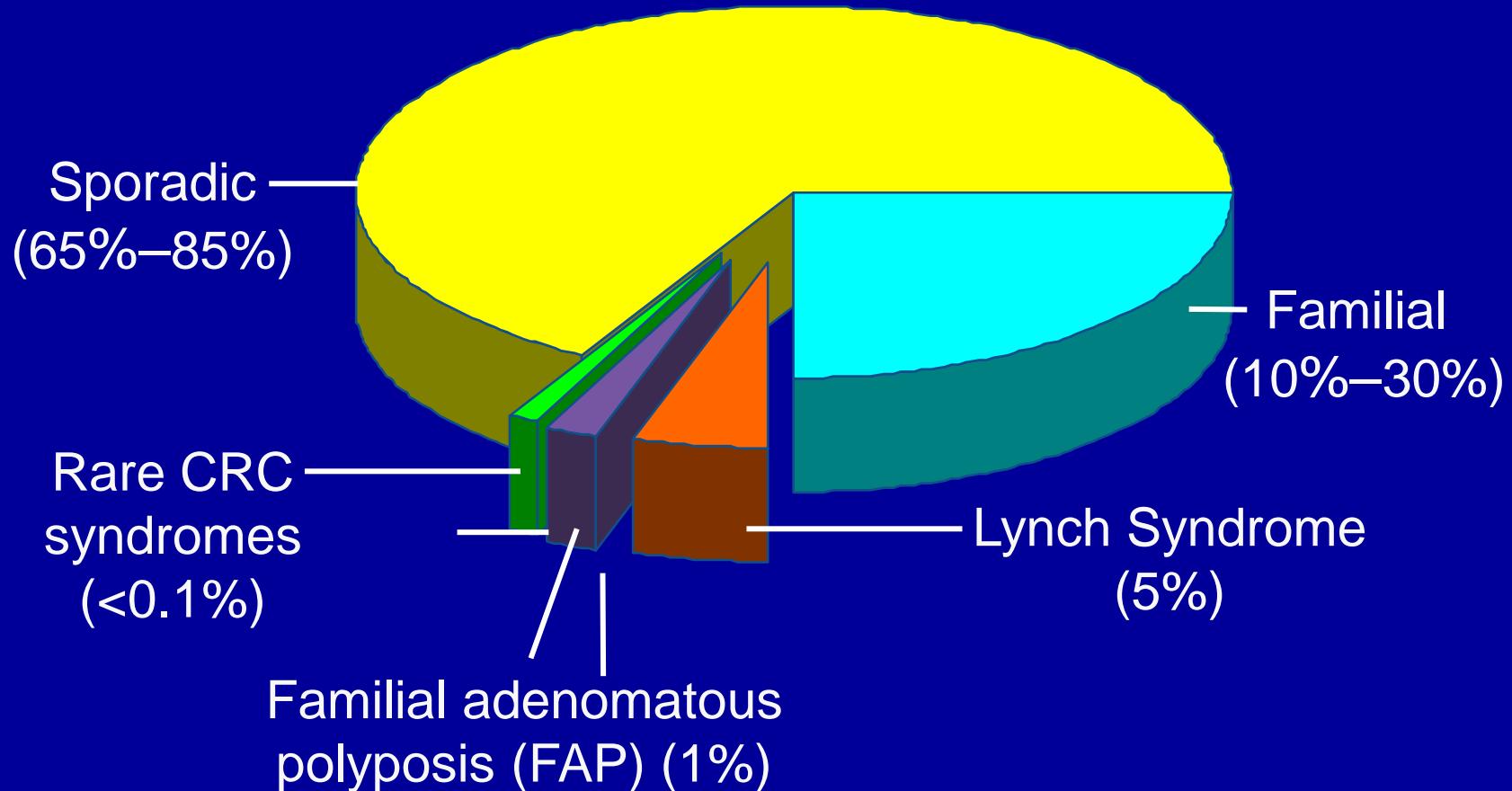
-and-

I will be discussing off label use of agents in this presentation

Outline

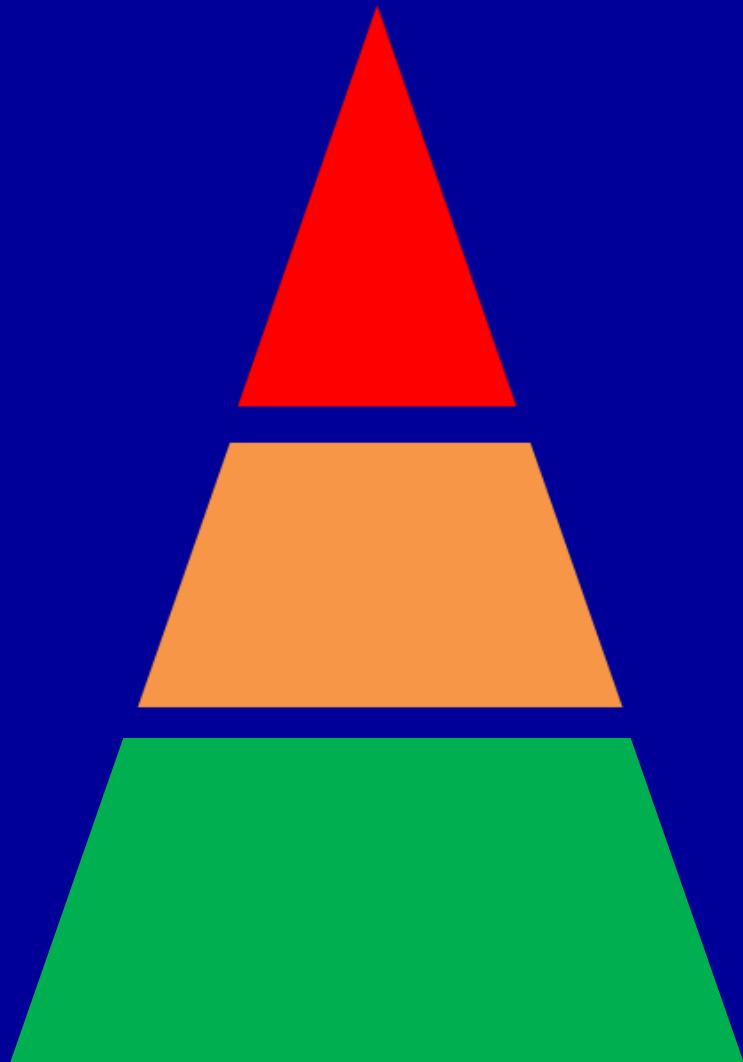
1. The importance of CRC High-risk Populations
2. Immuno-profiling of Lynch Syndrome Pre-Cancers
 - Lynch syndrome clinical trials
 - Lynch Syndrome vaccine development efforts
3. CMS application to Sporadic polyps
 - From Genetics to Sporadics

Causes of Hereditary Susceptibility to CRC



Adapted from Burt RW et al, *Prevention and Early Detection of CRC*, 1996

CRC Risk categories



High Risk

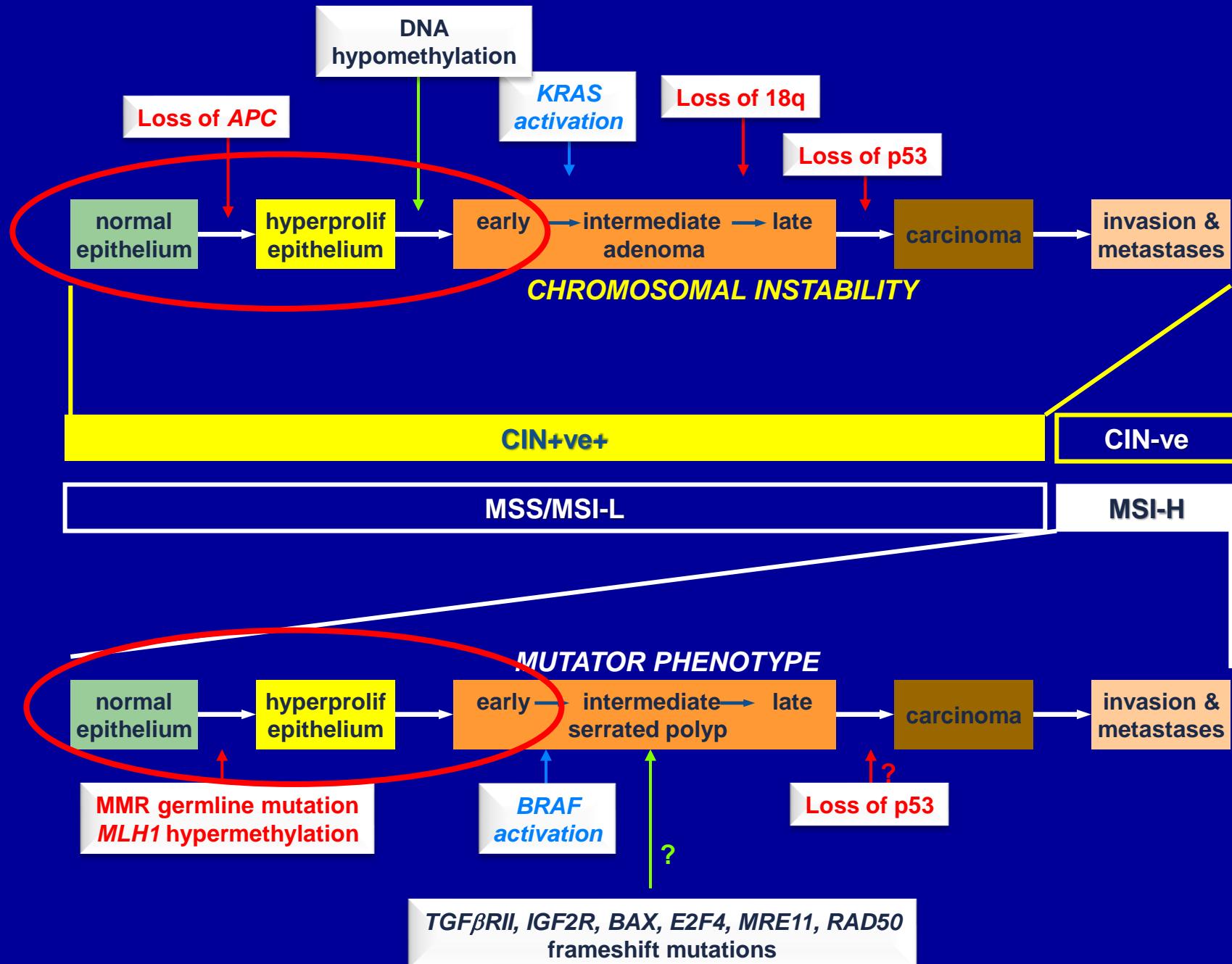
- ✓ Hereditary CRC Syndromes

Increased Risk

- ✓ Personal history of adenoma, SSP, CRC
- ✓ Inflammatory Bowel Disease (UC, CD)
 - ✓ Positive family history

Average Risk

- ✓ Age ≥ 50 y
- ✓ No history of adenoma, SSP or CRC
- ✓ No history of IBD
- ✓ No Family History



Fearon and Vogelstein, *Cell* (1990); Vilar, *Nature Reviews Clinical Oncology* (2010)

Hereditary CRC Syndromes as Models for CRC Carcinogenesis

Polyposis Syndromes

Adenoma

CIN +ve [Non-Hypermut]

Hypermut (MUTYH)

Hamartoma predominant

Peutz-Jeghers Sd (*LKB1, STK11*)
Juvenile polyposis Sd (*BMPR1A, DPC4, PTEN*)
Cowden Sd (*PTEN*)

Hypermut

CIMP-High [Methylators]

Hypermut Sd

Non-polyposis Syndromes

MSI-H [Hypermut]

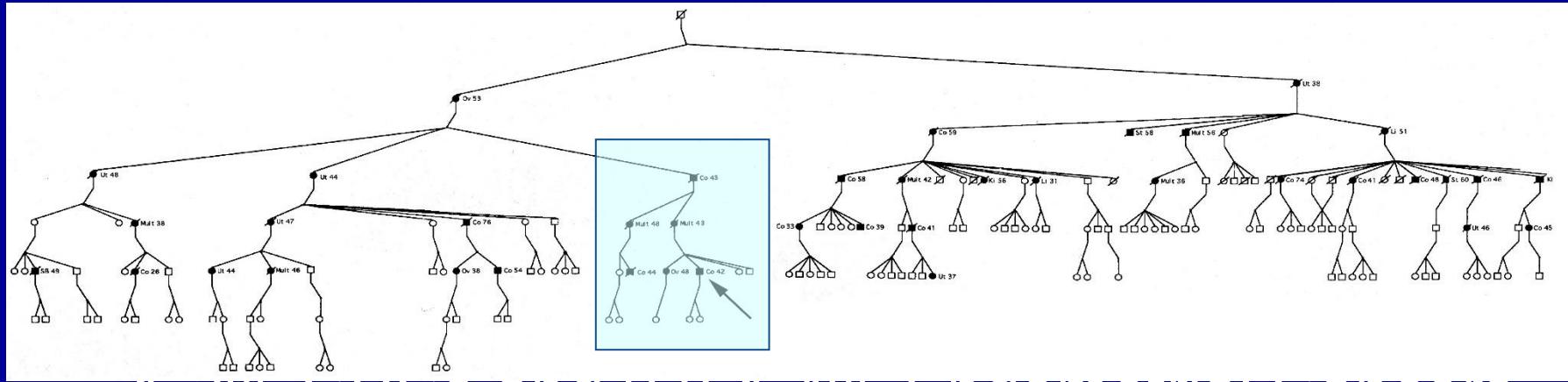
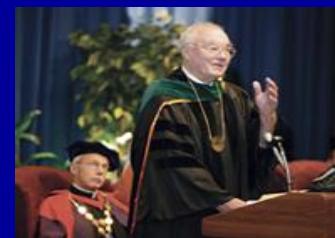
Adenoma, PMS2

Mismatch repair proficient

Familial Colorectal Cancer Type X
Other Syndromes



Lynch Syndrome



- 1-3% CRCs and 18-22% Endometrial Cancers

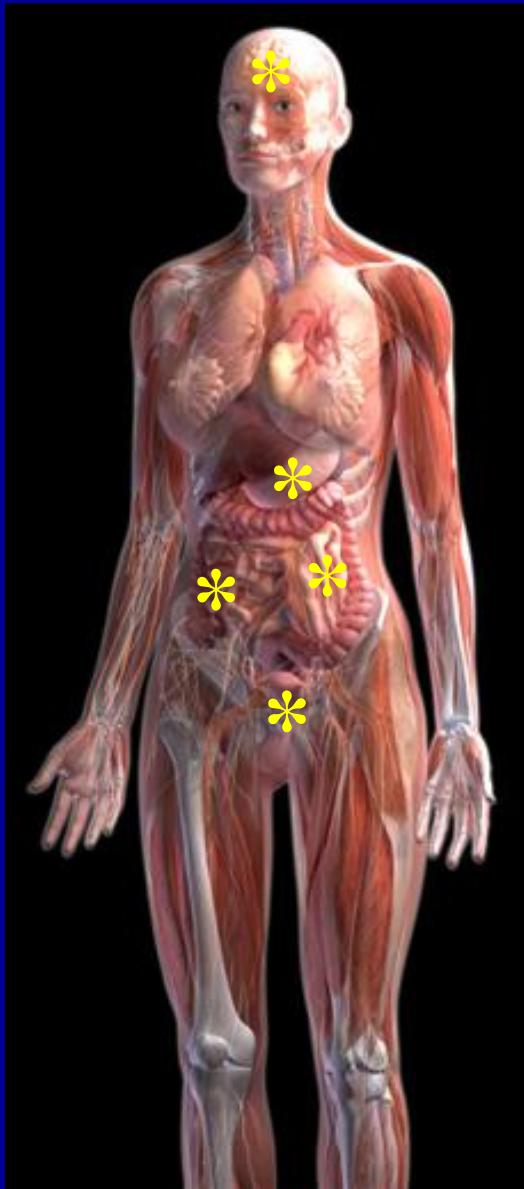
- Caused by mutations in *MLH3*, *MSH2*, *EPCAM*, *MLH1*, *BRCA1*, and *BRCA2*.

- High but variable penetrance
- Variable expression of cancer risk
- Tumors often have microsatellite instability



Hampel and de la Chapelle, CAPR (2011); Gruber, GeneReviews (2012)

Lynch Syndrome

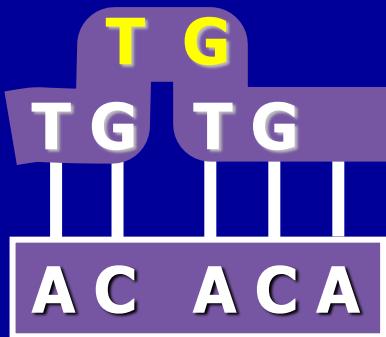


LS-related tumors

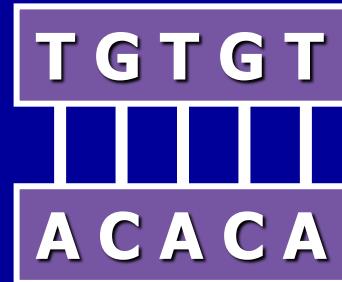
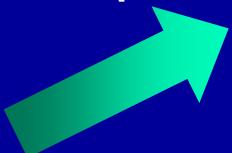
- ✓ Colorectal Cancer (52-82%)
 - ✓ Endometrial Cancer (25-60%)
 - ✓ Ovarian Cancer (4-12%)
 - ✓ Urinary Tract Tumors (1-4%)
 - ✓ Gastric Cancer (6-13%)
 - ✓ Small Bowel (3-6%)
 - ✓ CNS – GBM (1-3%)
 - ✓ Prostate? Breast?
- *Life-time risk

MSI is the molecular marker of Mismatch Repair deficiency

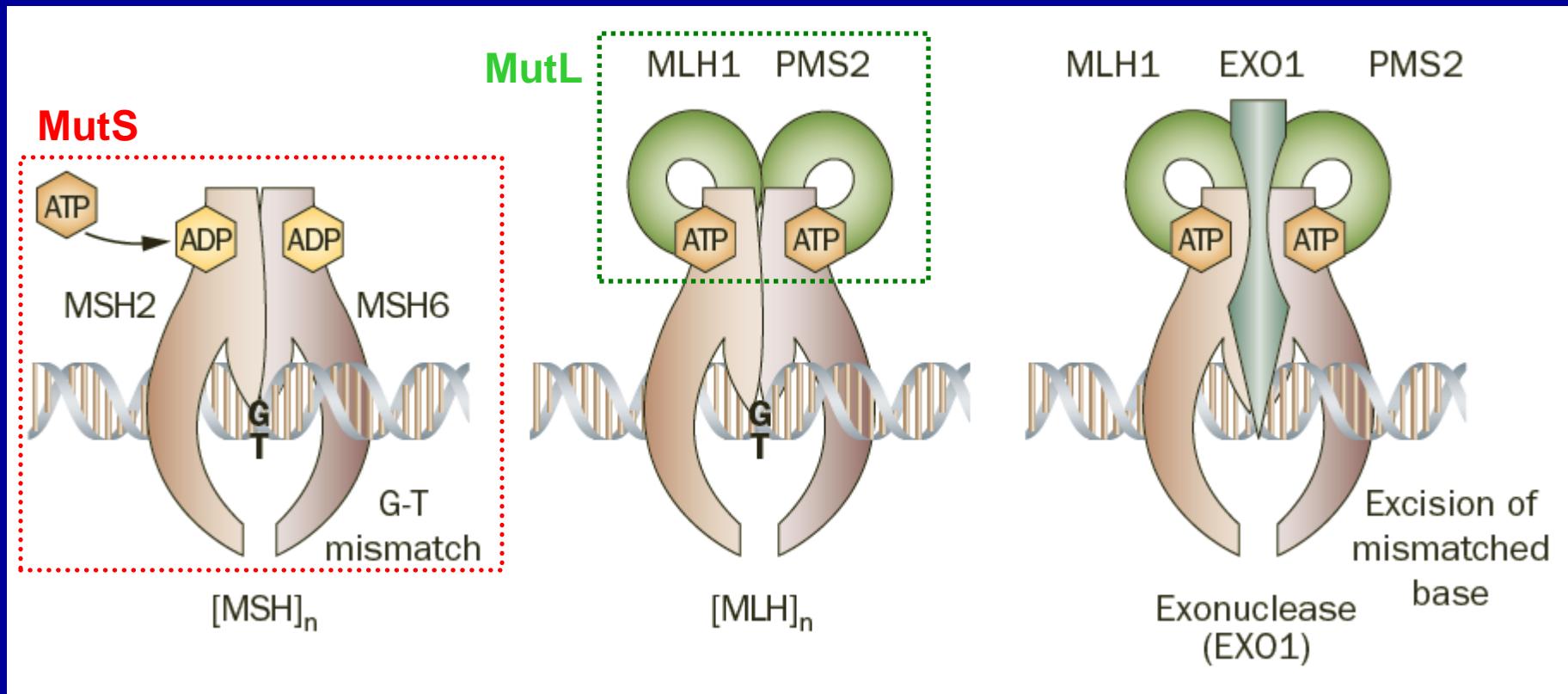
Ins/Del
Loop
Pol slippage



Normal
DNA repair

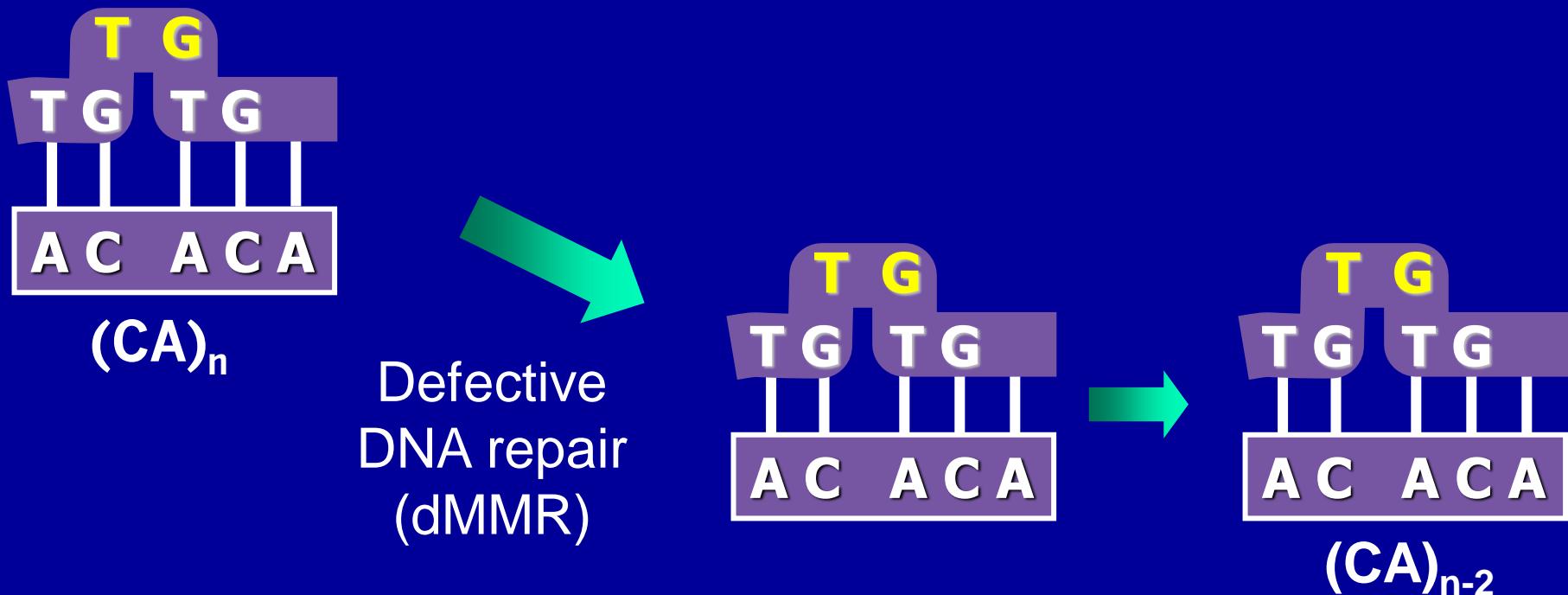


MMR System: MutS sliding clamp binds MutL to form a ternary complex

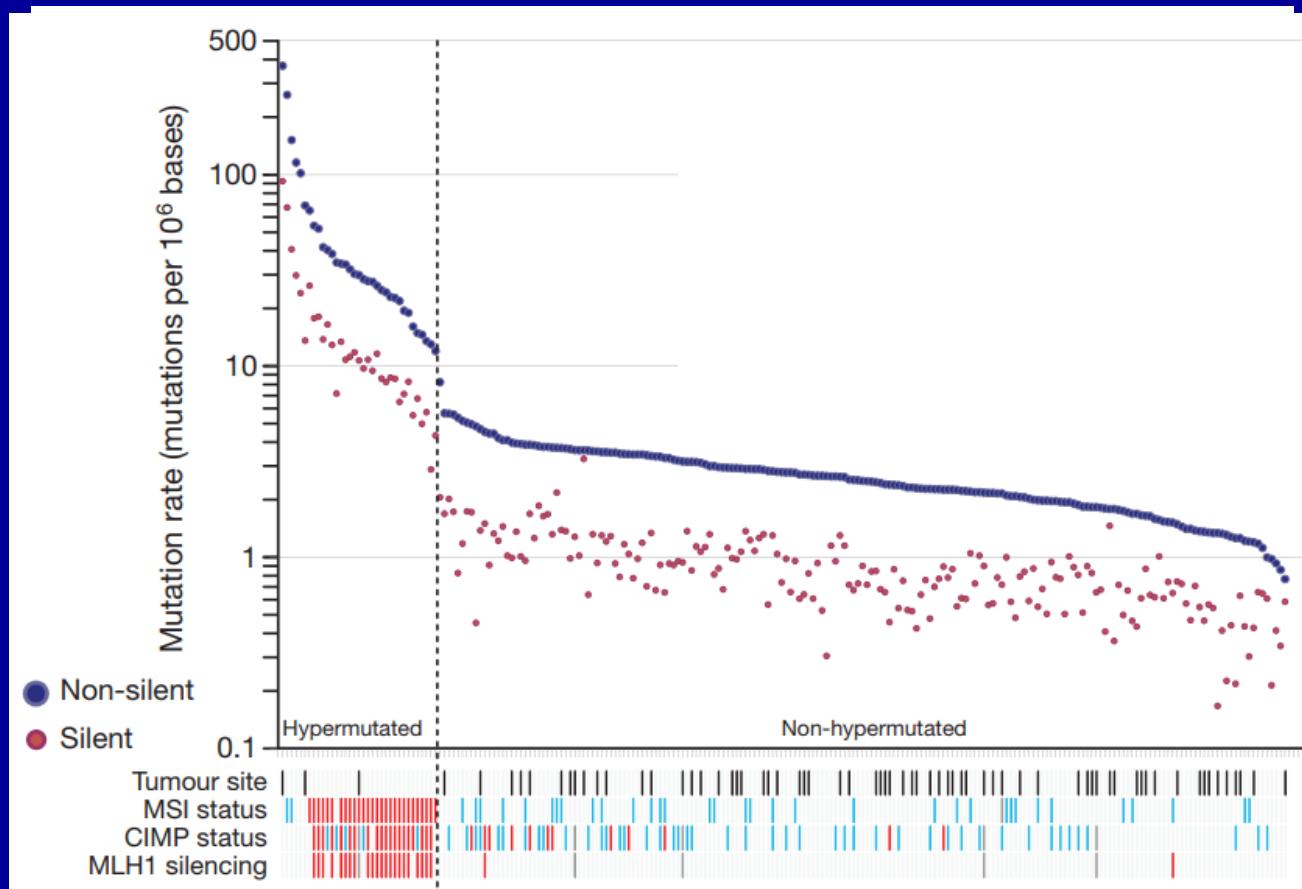


MSI is the molecular marker of Mismatch Repair deficiency

Ins/Del
Loop
Pol slippage

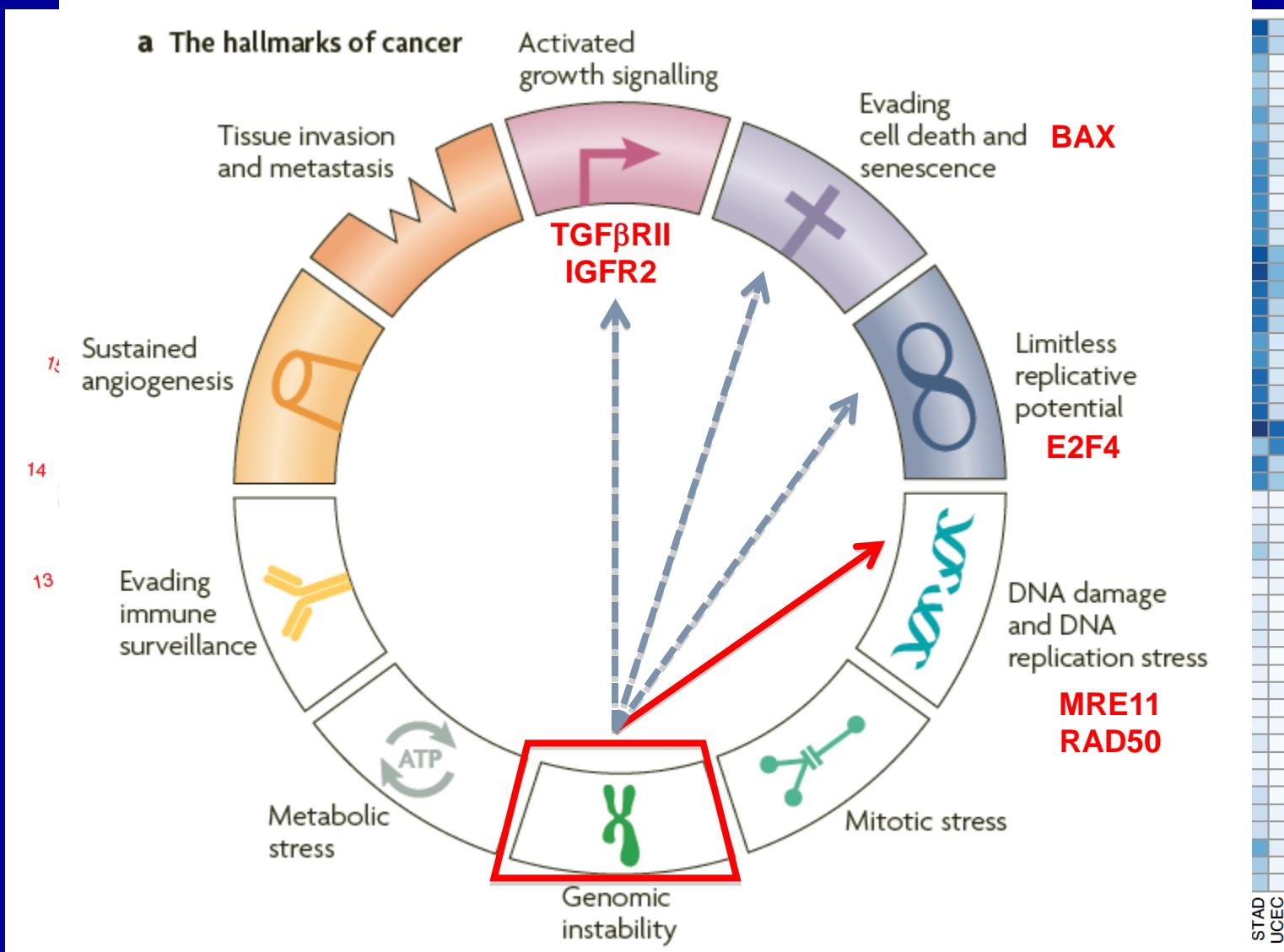


MSI detection: multiple target microsatellites

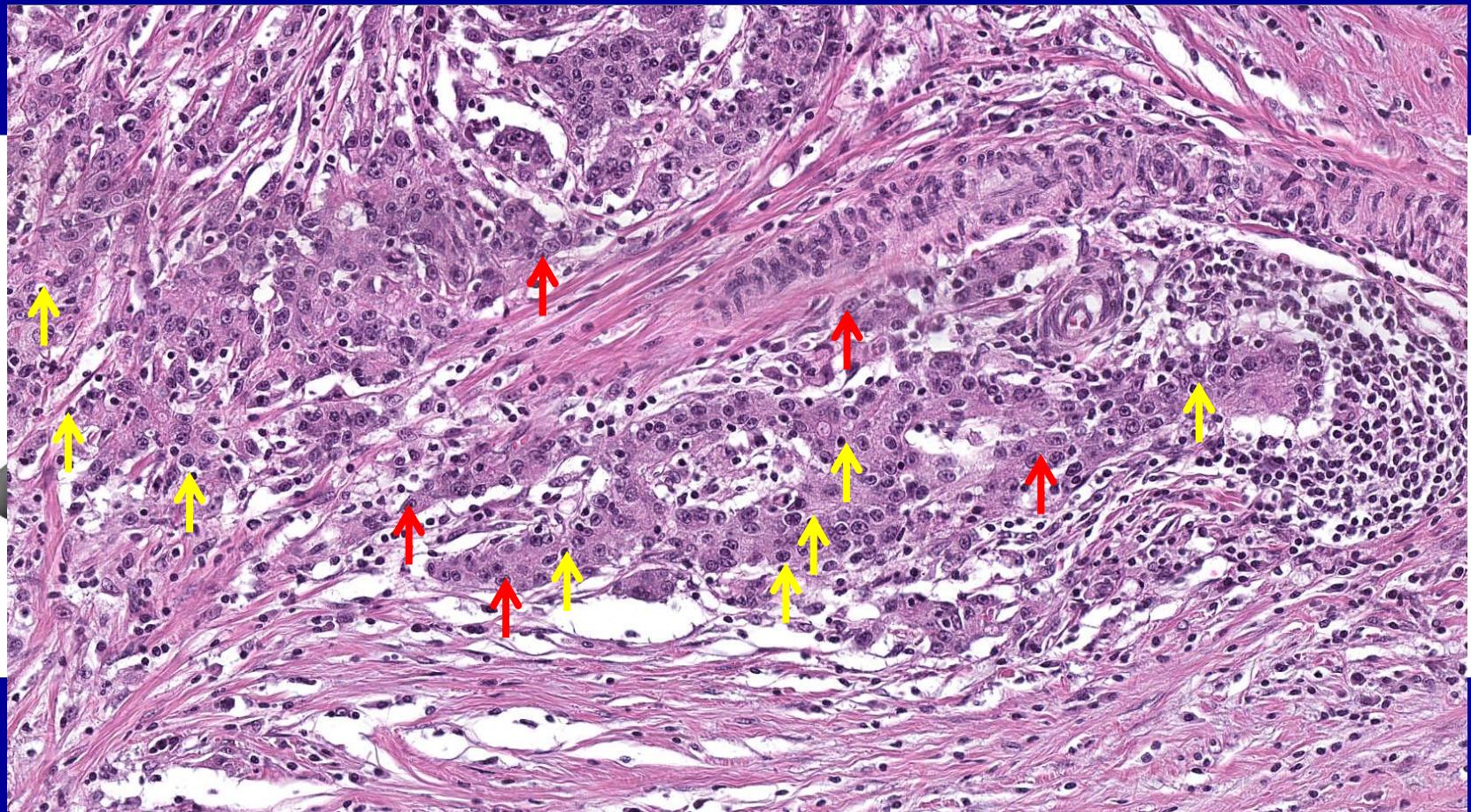


Gryfe, NEJM (2000); Vilar, *Nature Reviews Clinical Oncology* (2010);
TCGA, *Nature* (2012)

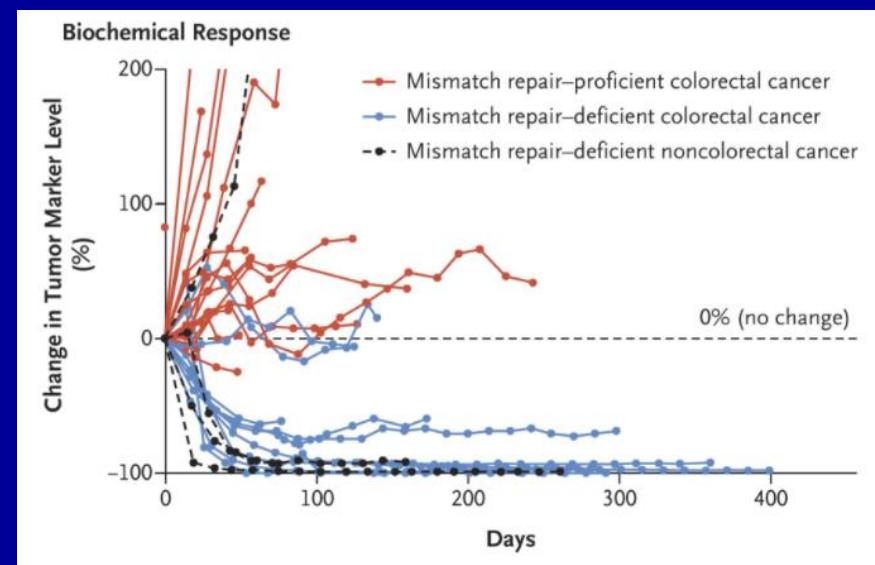
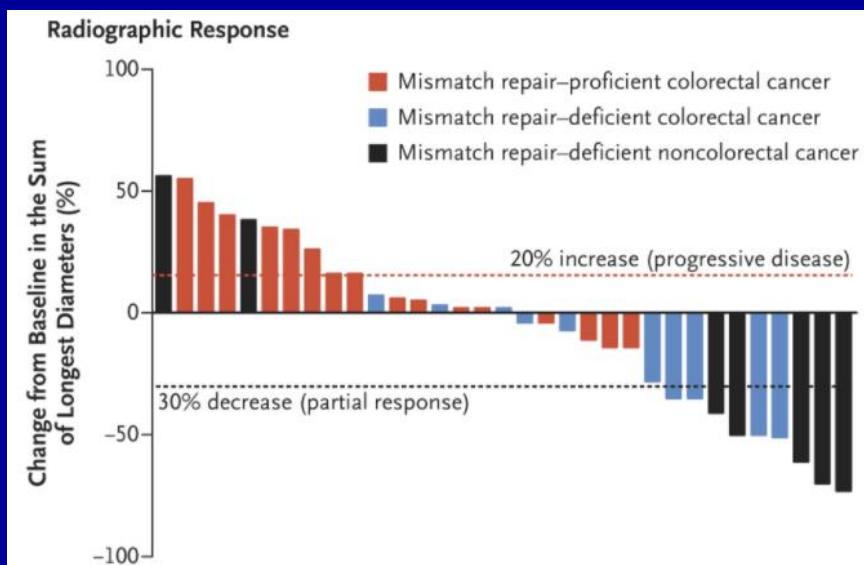
MSI and Secondary mutations



FSP and Tumor Infiltrating Lymphocytes

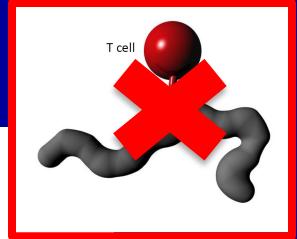
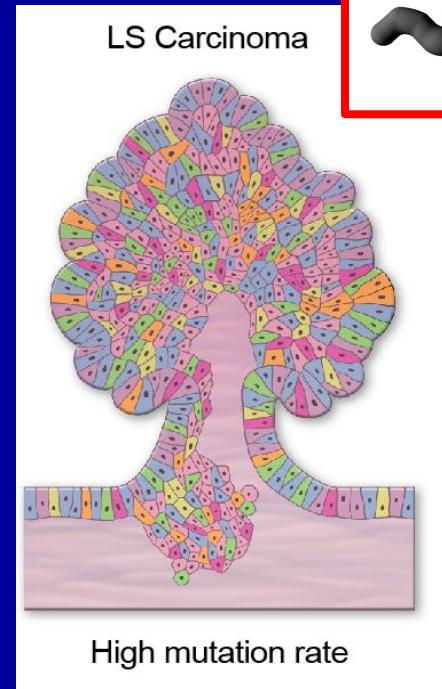
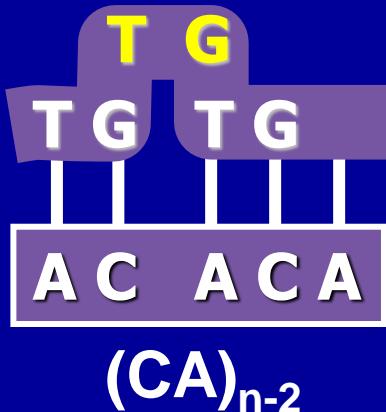
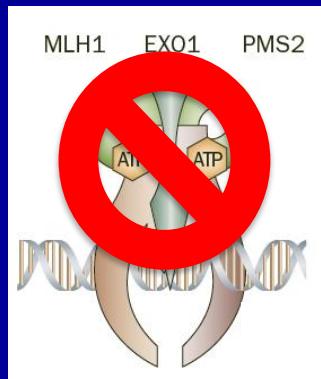


Pembrolizumab in MSI-H CRC

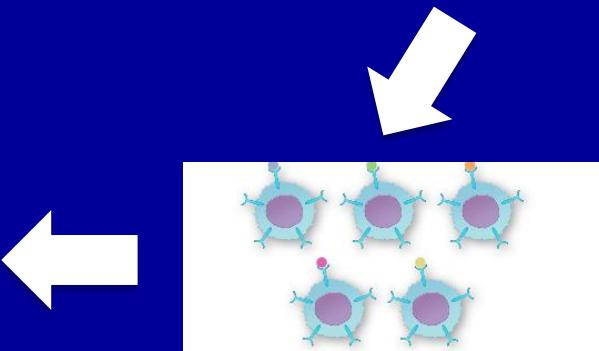


	MMR-deficient CRC N=28	MMR-proficient CRC N=28
Response Rate	57%	0%
Disease Control Rate	89%	16%

Lynch Syndrome



CD4, IFN, PRF1, L~~X~~3,
~~PX~~1, IL12A, TNF
FOXP3, CD~~X~~4
CD8A, GZMB, IL17A,
TGFB1, PTGS2, IL1B,
IL6, IDO1, NOS2, HIF1A



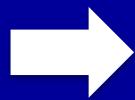
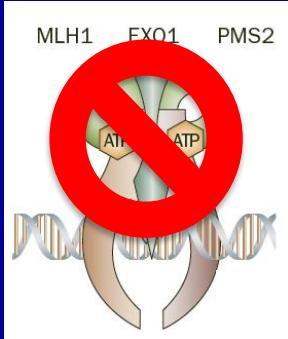
Interception in High-Risk Genetics

***'Treatment without Prevention is
simply unsustainable'***

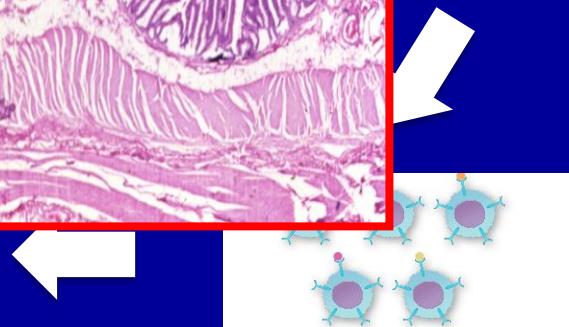
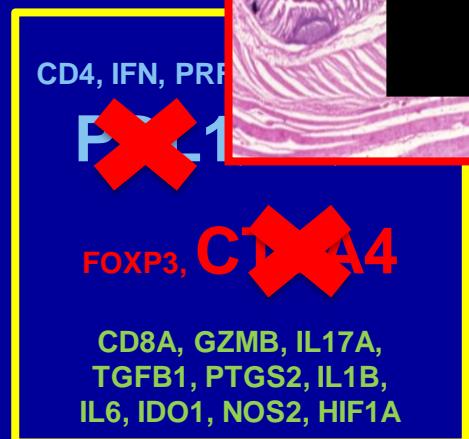
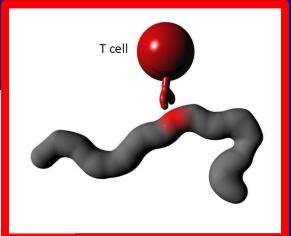
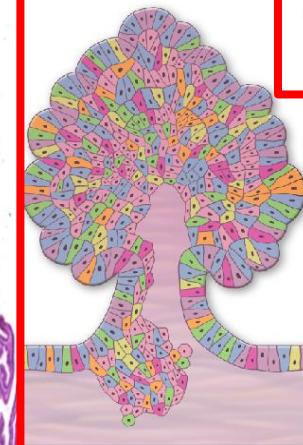
(Bill Gates)

<https://www.gatesfoundation.org/Media-Center/Press-Releases/2006/08/Putting-the-Power-of-HIV-Prevention-in-the-Hands-of-Women>

Lynch Syndrome

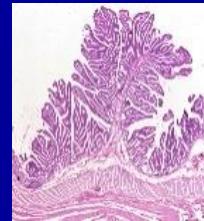
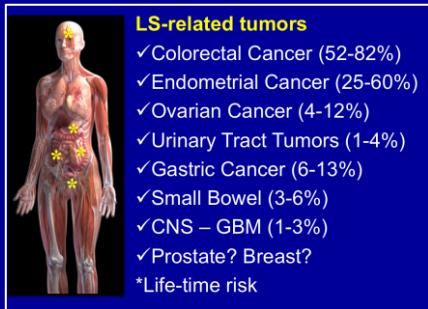


LS Carcinoma



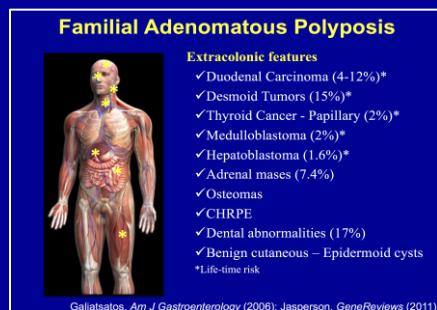
Interception in High-Risk Genetics

14 LS



Pre-Cancers
Tumors
Normal

Colon Polyps
Normal mucosa
Germline
Lynch Syndrome



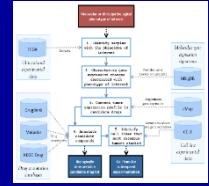
10 FAP



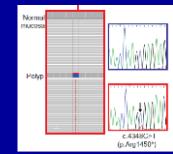
DNA & RNA



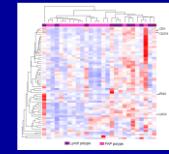
Next-Gen Seq
RNA-seq



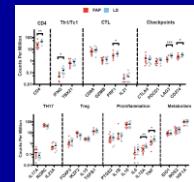
HLA & NeoAg



Mutations

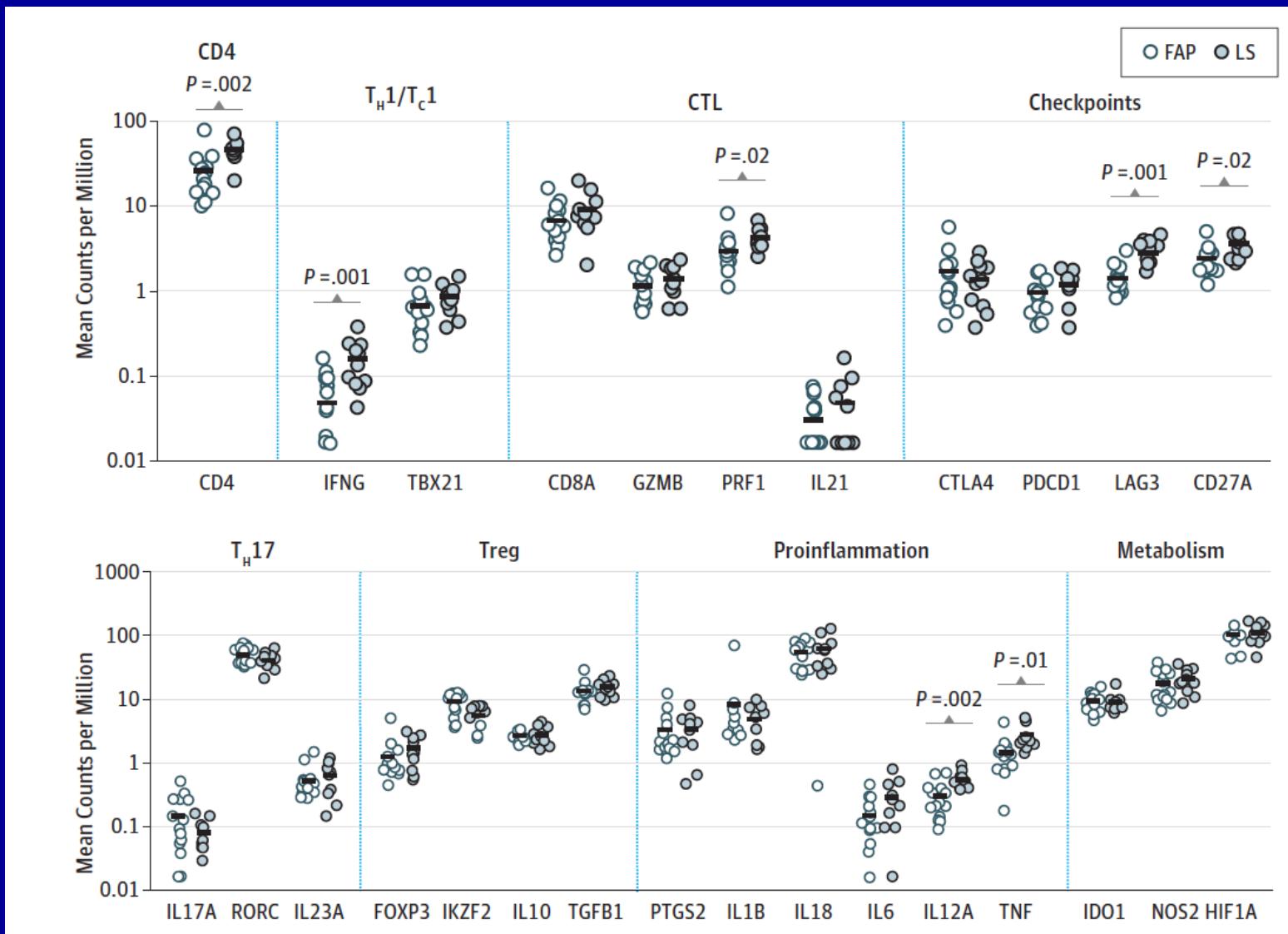


Expression

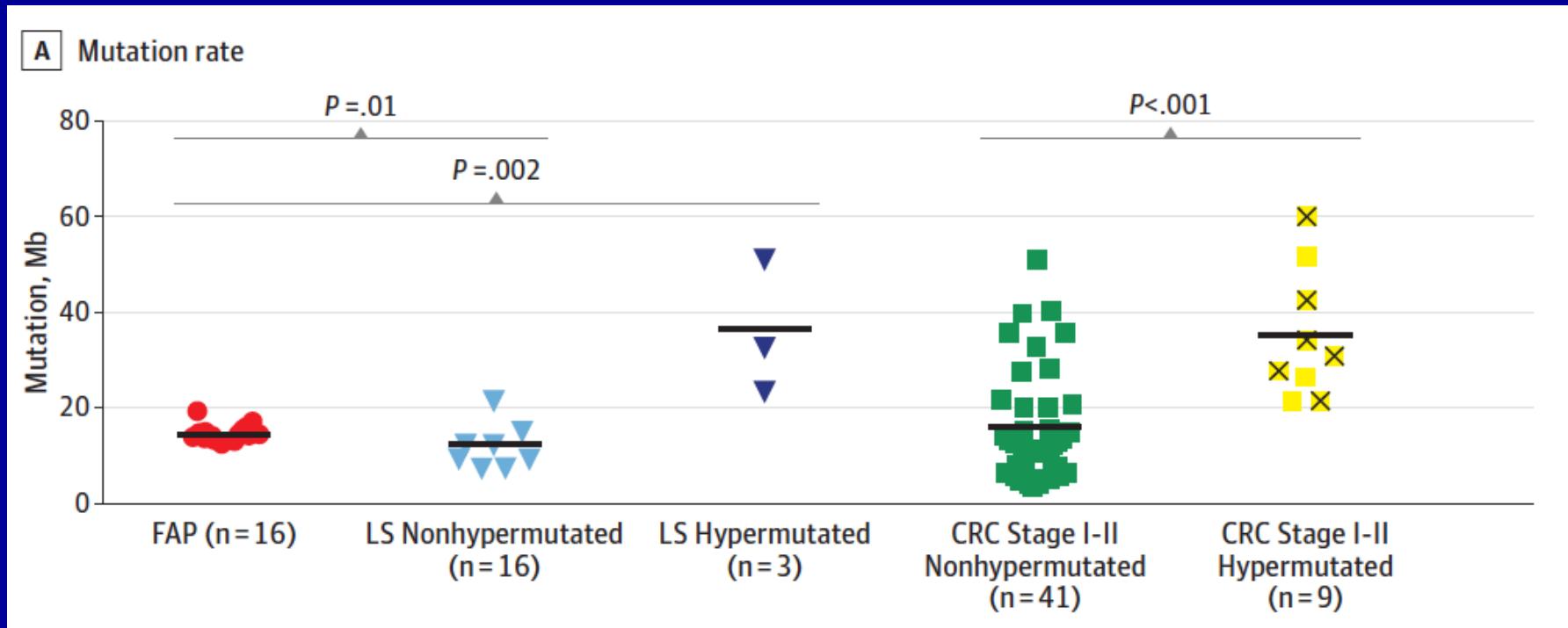


Immune Profile

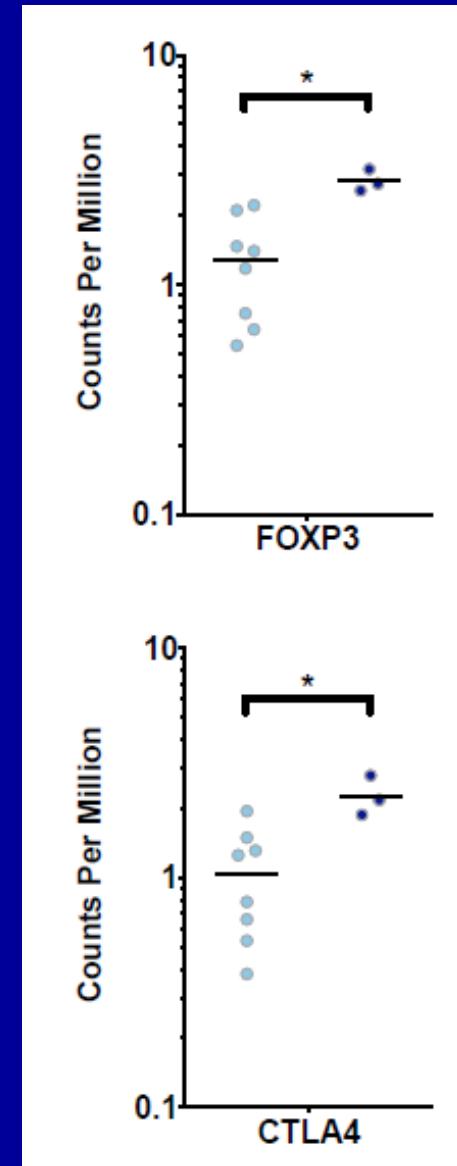
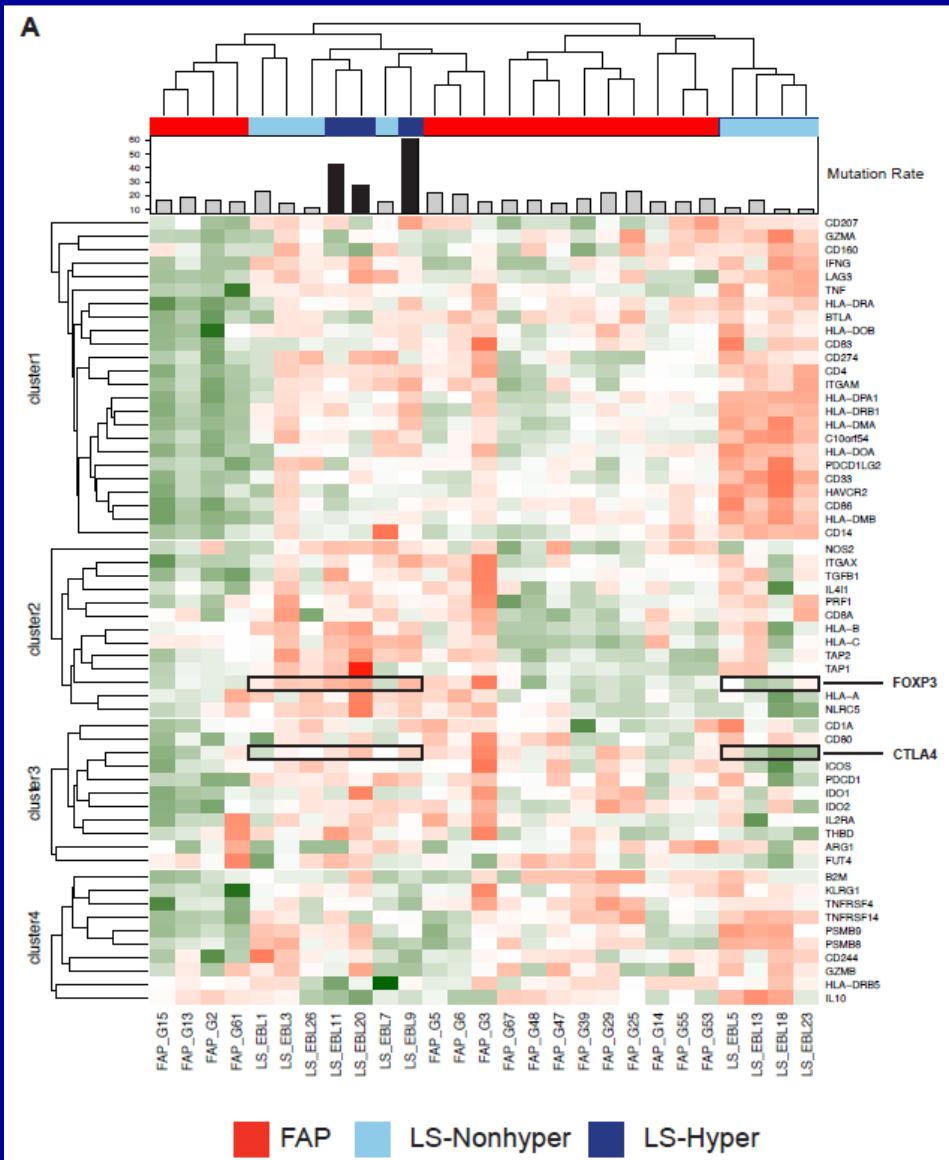
Lynch Syndrome



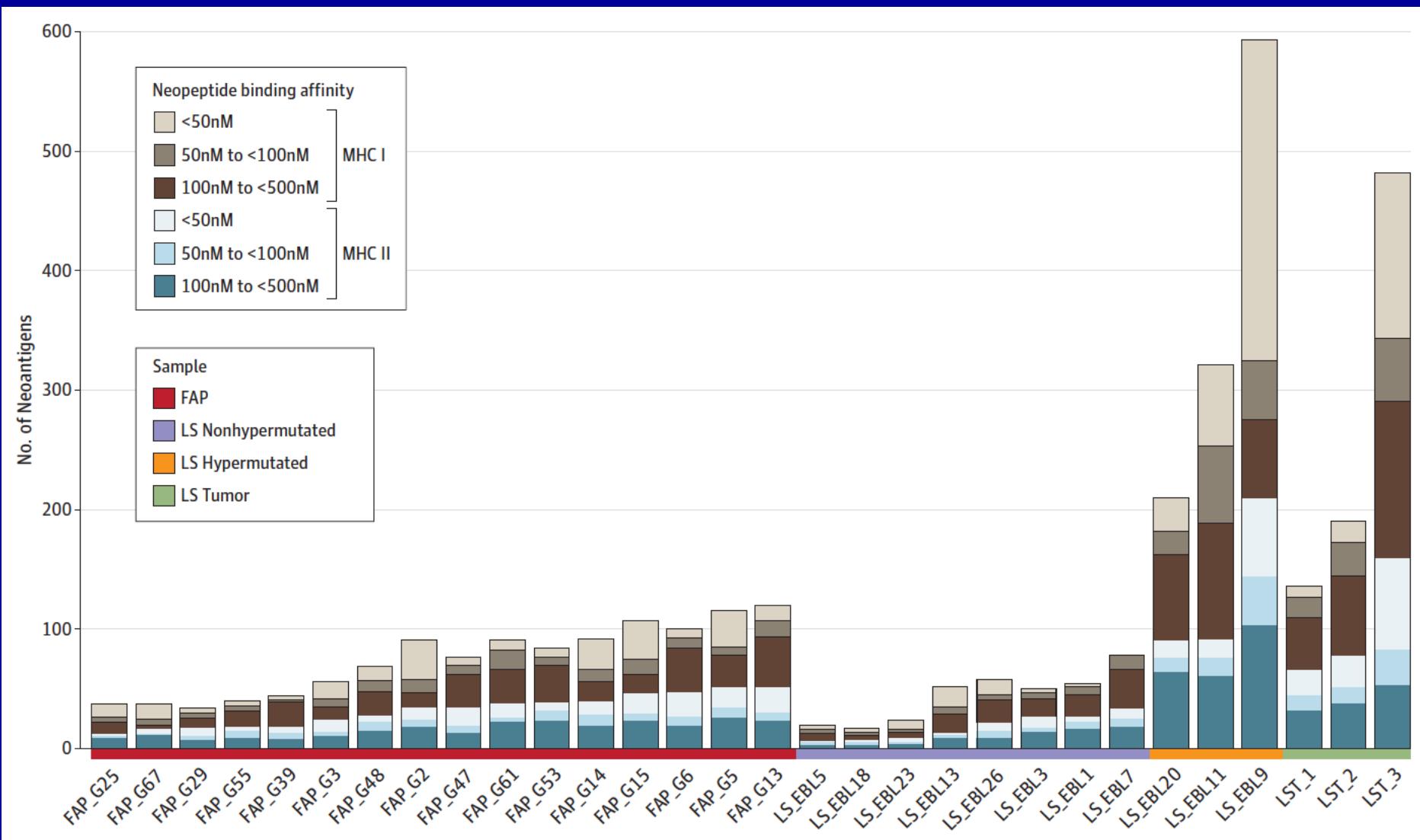
Lynch Syndrome



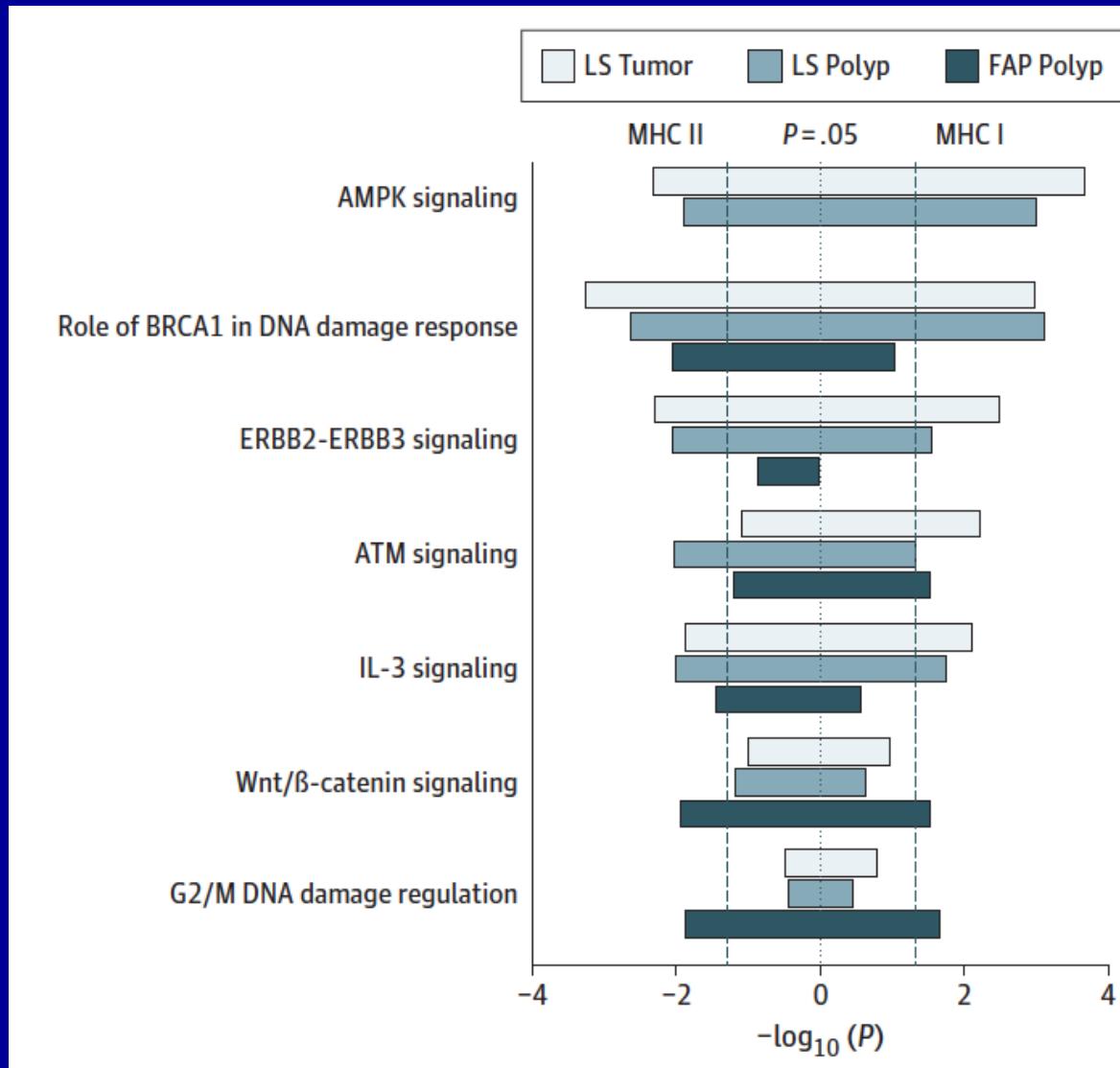
Lynch Syndrome



Lynch Syndrome



Lynch Syndrome

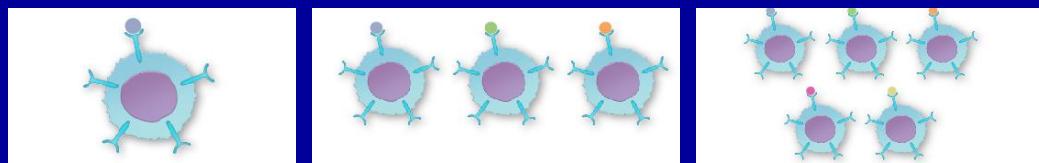


Lynch Syndrome

Epithelium



Neo-Antigens



Immune
Signals
(Activation)

CD4, IFN, PRF1, LAG3,
PDL1, IL12A, TNF

CD4, IFN, PRF1, LAG3,
PDL1, IL12A, TNF

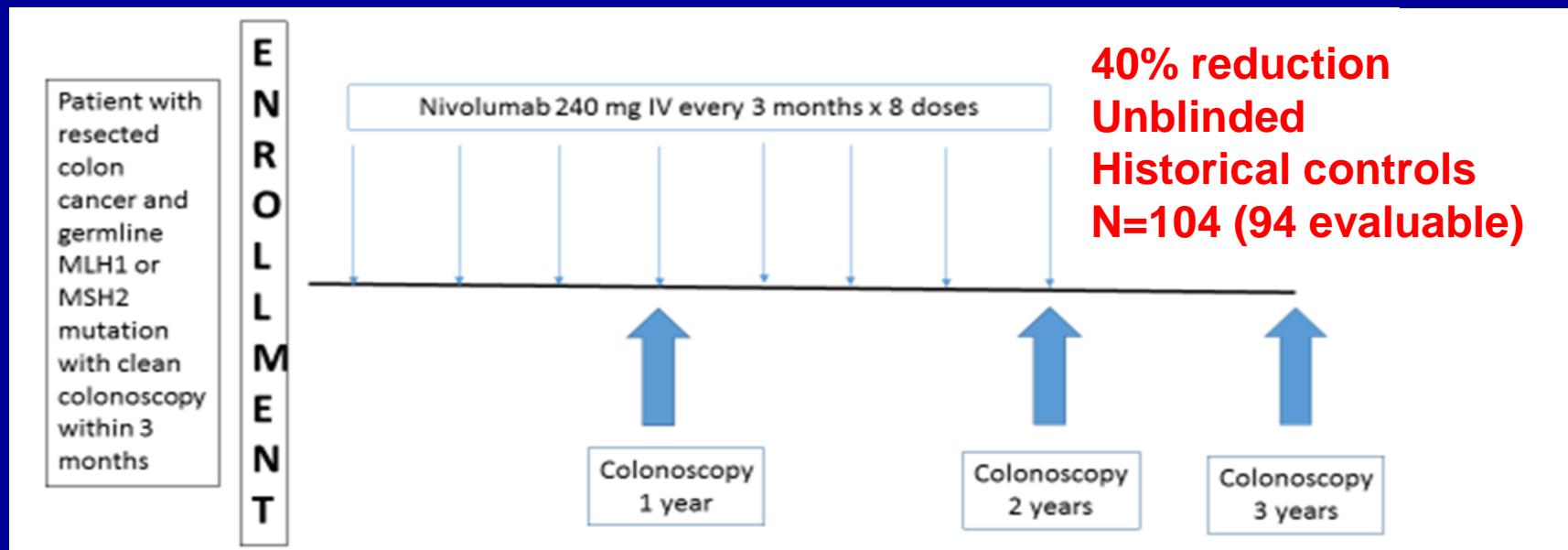
FOXP3, CTLA4

CD4, IFN, PRF1, LAG3,
PDL1, IL12A, TNF

FOXP3, CTLA4

CD8A, GZMB, IL17A,
TGFB1, PTGS2, IL1B,
IL6, IDO1, NOS2, HIF1A

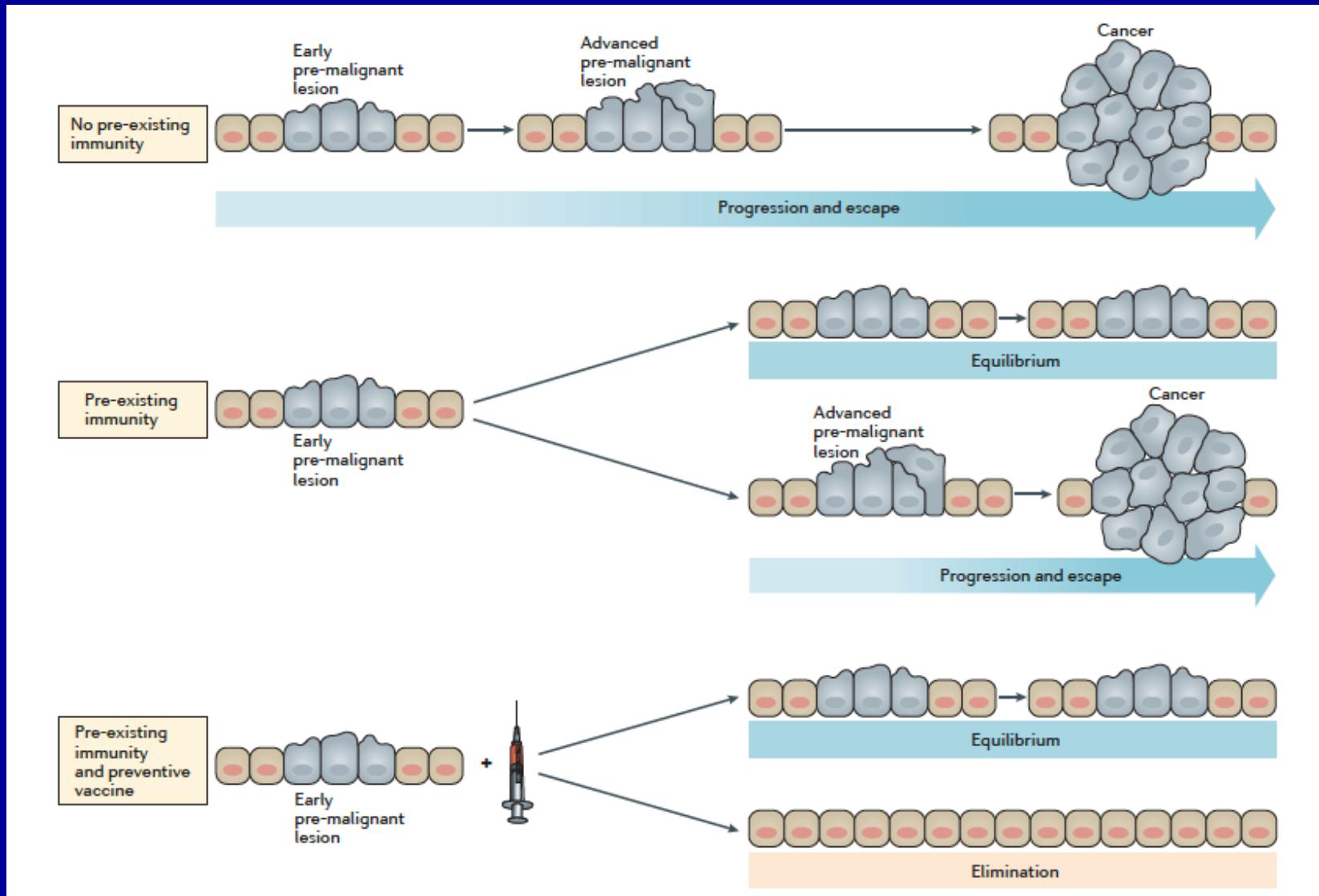
A Phase II Study of PD-1 Inhibition for the Prevention of Colon Adenomas in Patients With Lynch Syndrome and a History of Partial Colectomy



Primary Objective: Reduce incidence of adenomas

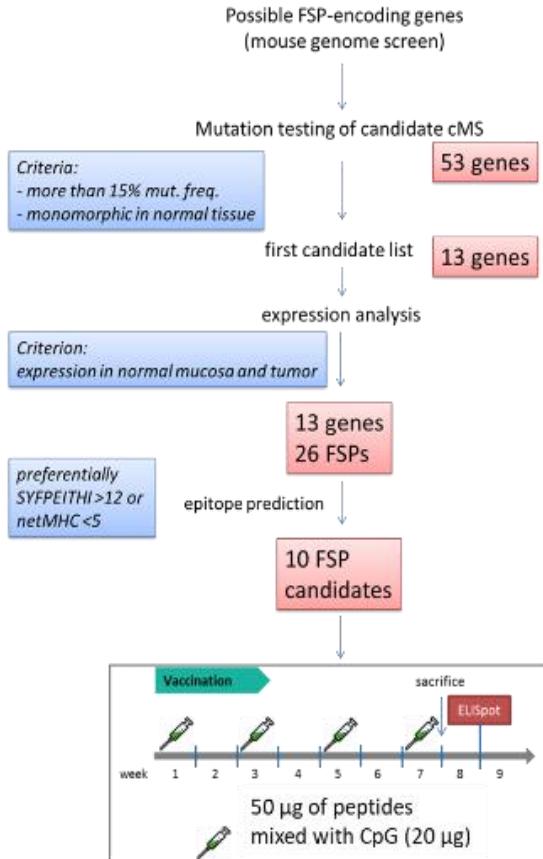
Others: Incidence of advanced adenomas, colon and other LS-related tumors, Safety, and Immunogenicity

Lynch Syndrome Vaccines

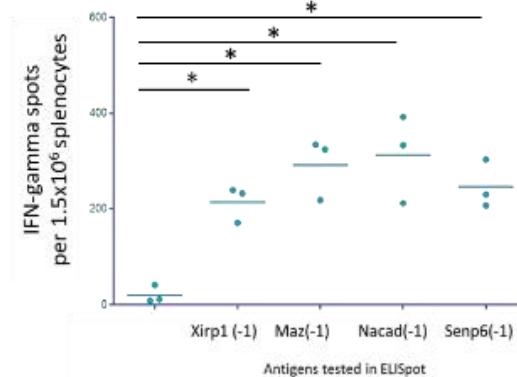


Frameshift Peptide Vaccine for prevention in LS mouse model

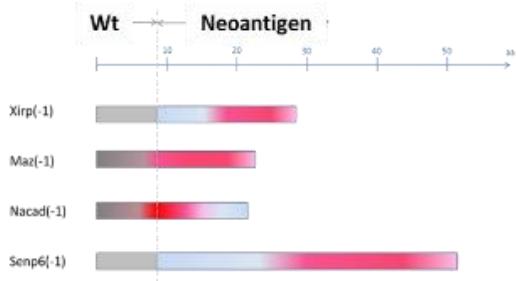
A. Experimental strategy



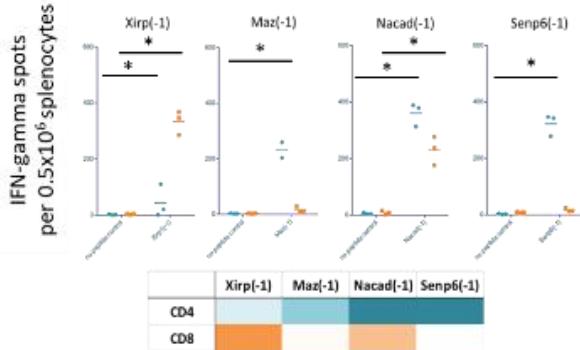
B. IFN- γ ELISPOT



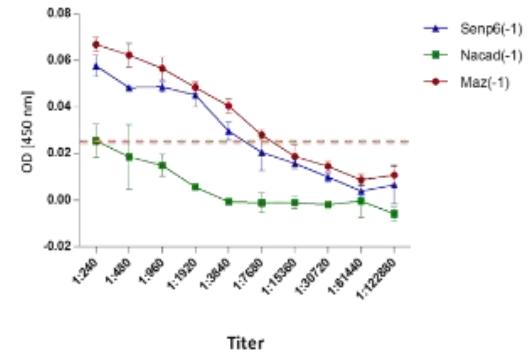
D. Epitopic regions



C. CD4 vs. CD8 responses

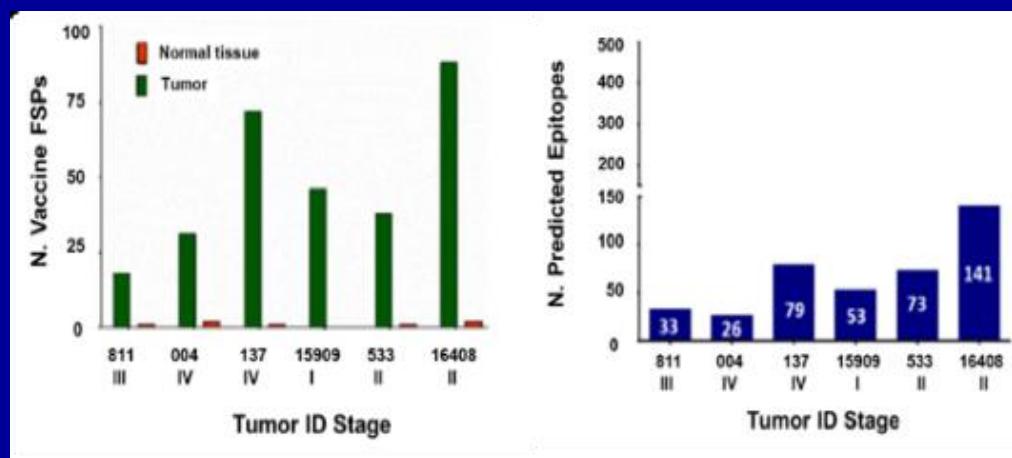
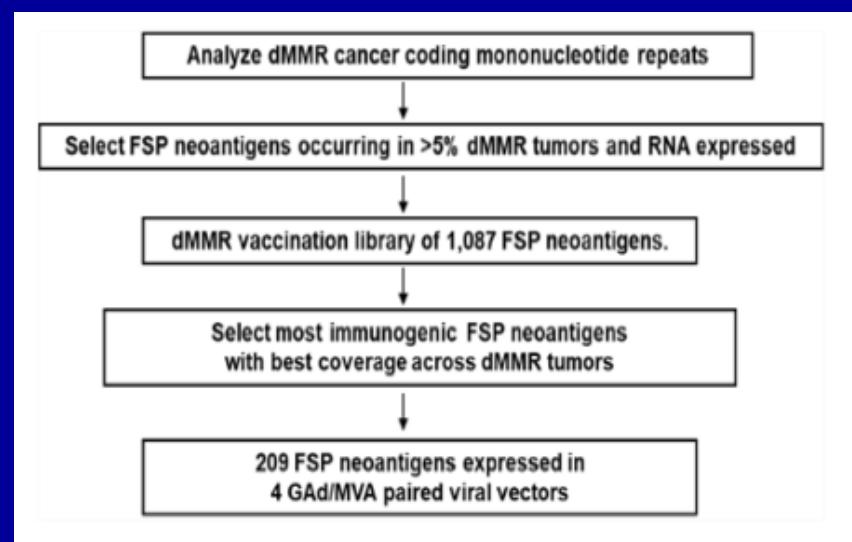


E. Humoral immune responses

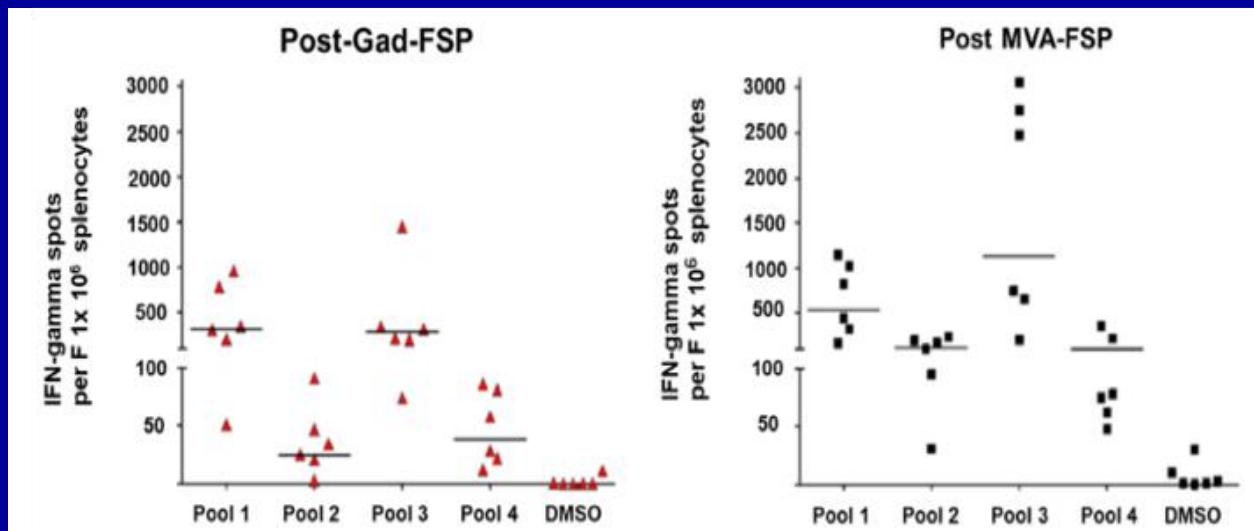
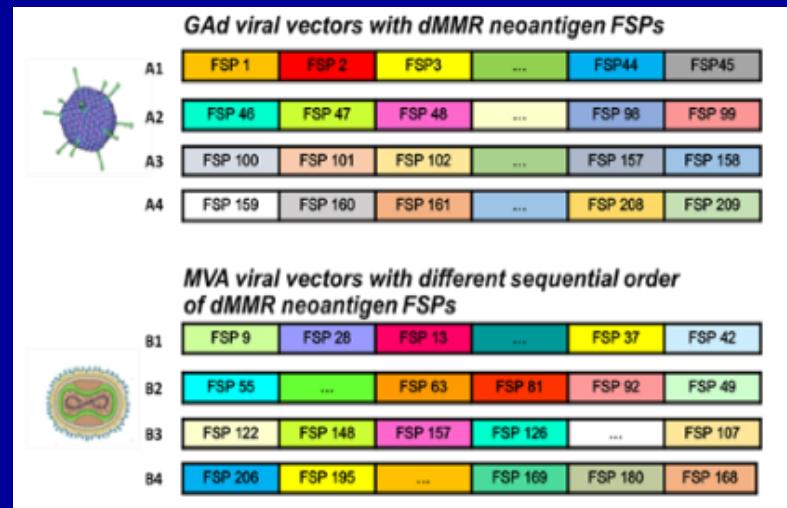
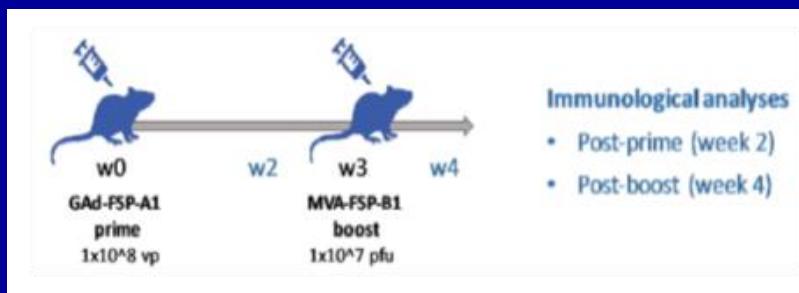
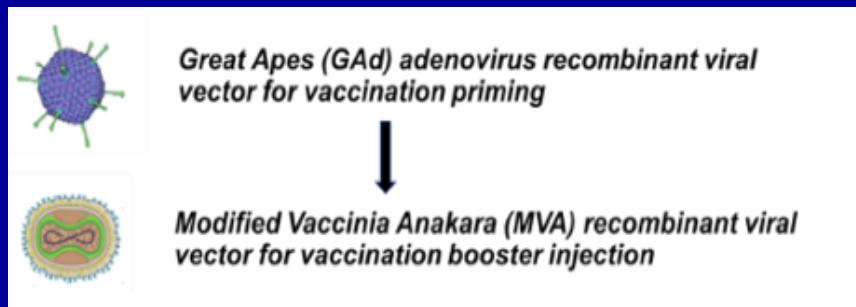


Slide courtesy of Steve Lipkin, MD, PhD;
Confidential – Unpublished Data – PLEASE DO NOT POST

Lynch Syndrome Vaccines



Lynch Syndrome Vaccines



Lynch Syndrome Vaccines

Ph1a Dose Escalation

N=9-12

NOUS-209 (D1 + D2)
+
Pembrolizumab

Ph1b Dose Expansion

N=12

NOUS-209 (RP2D)
+
Pembrolizumab

**Anti-PD-1 checkpoint inhibitor
naïve dMMR or MSI CRC,
gastric, G-E junction**

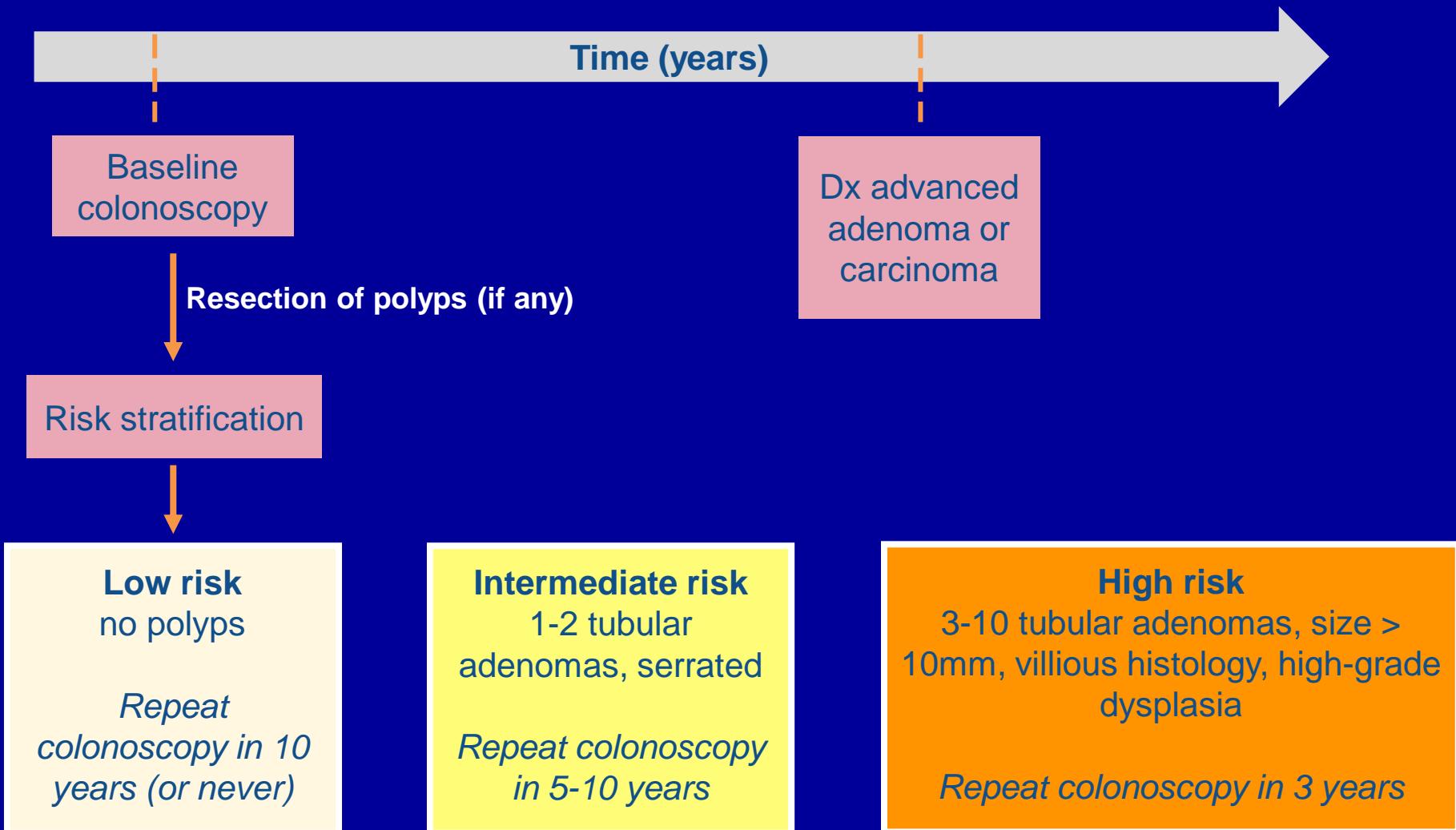
Estimated Start date: September 2019

Courtesy of Paola Antonini & Elisa Scarselli – NousCom – NCT 04041310

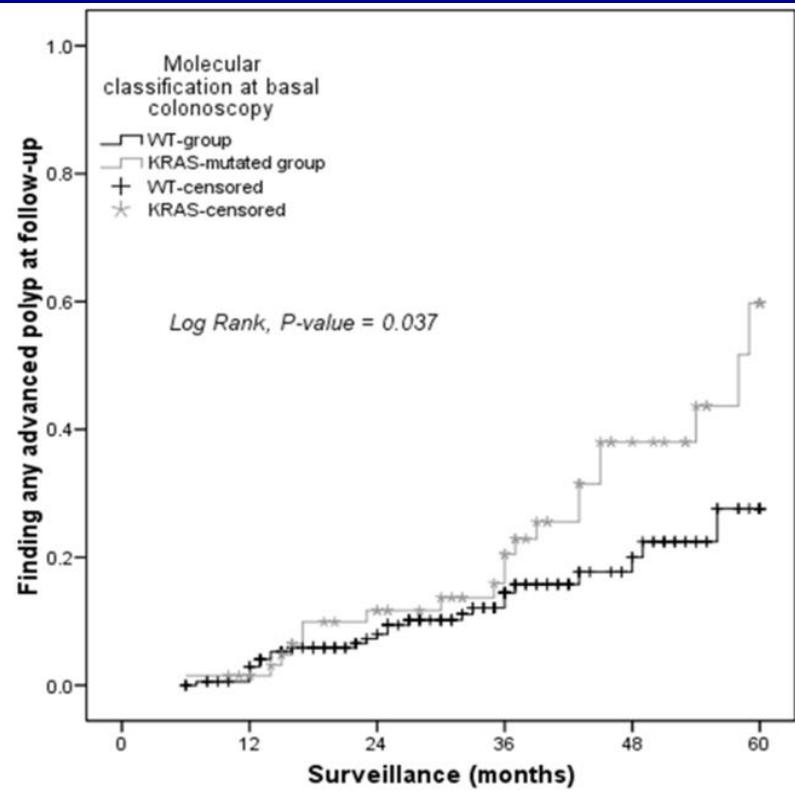
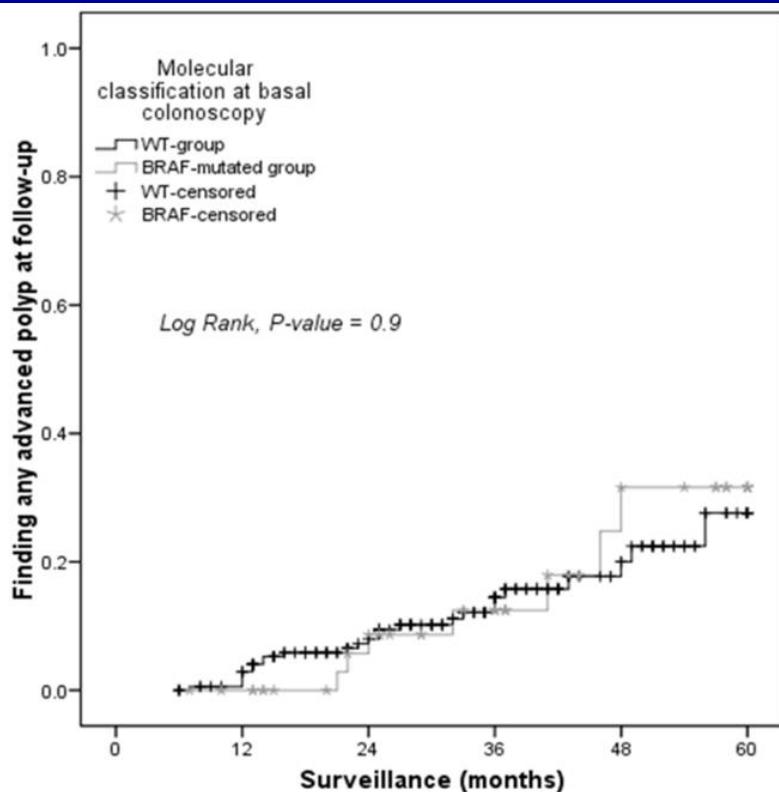
Conclusions

- LS polyps display a unique immunoprofile with overexpression of immune checkpoints
- Activation of the immune system was independent of NeoAg and Mut rates
- Hypemut LS polyps display immune tolerance prior to carcinoma progression
- Neoantigens are involved in DNA repair mechanisms
- Potential use of CPI and vaccines in LS
- Clinical trials in ‘rare’ pops are feasible

Refining CRC surveillance

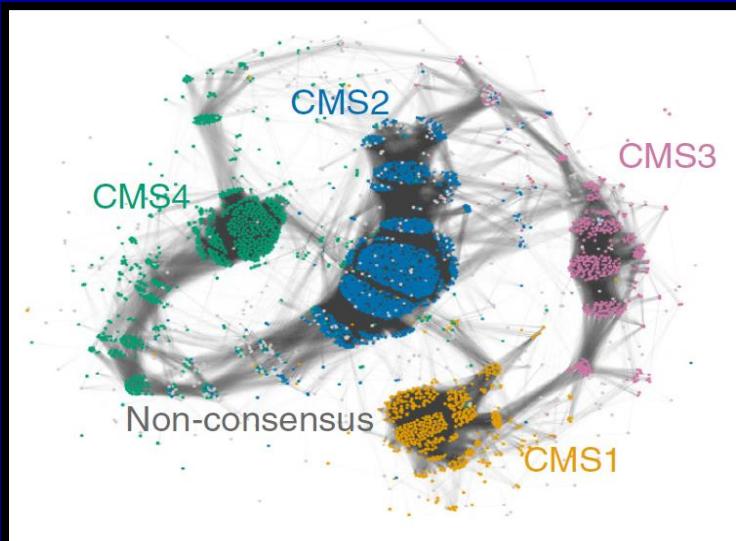


Does the molecular profile of a polyp have prognostic significance?

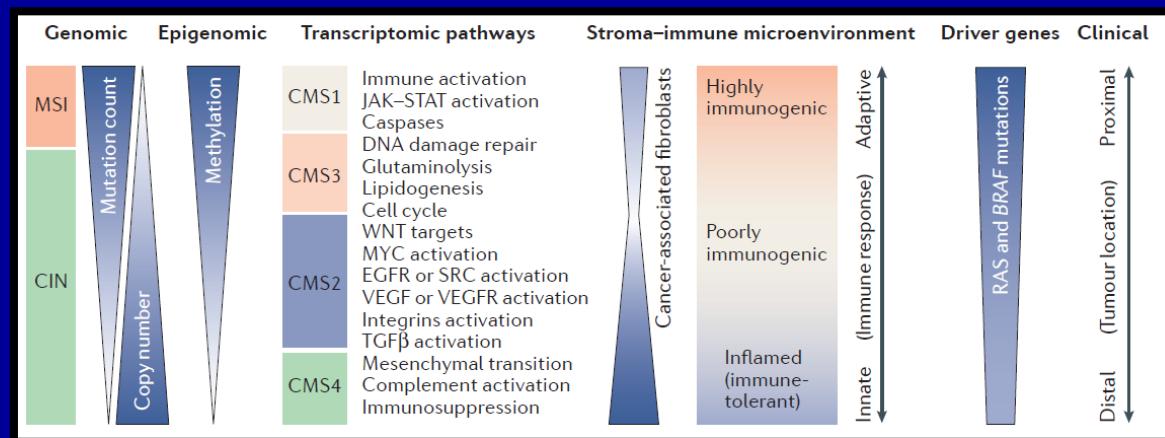


Wild-Type group	180	171	129	74	35	8	Wild-Type group	180	171	129	74	35	8
BRAF-mutated group	43	43	31	21	10	3	KRAS-mutated group	66	62	48	36	15	4

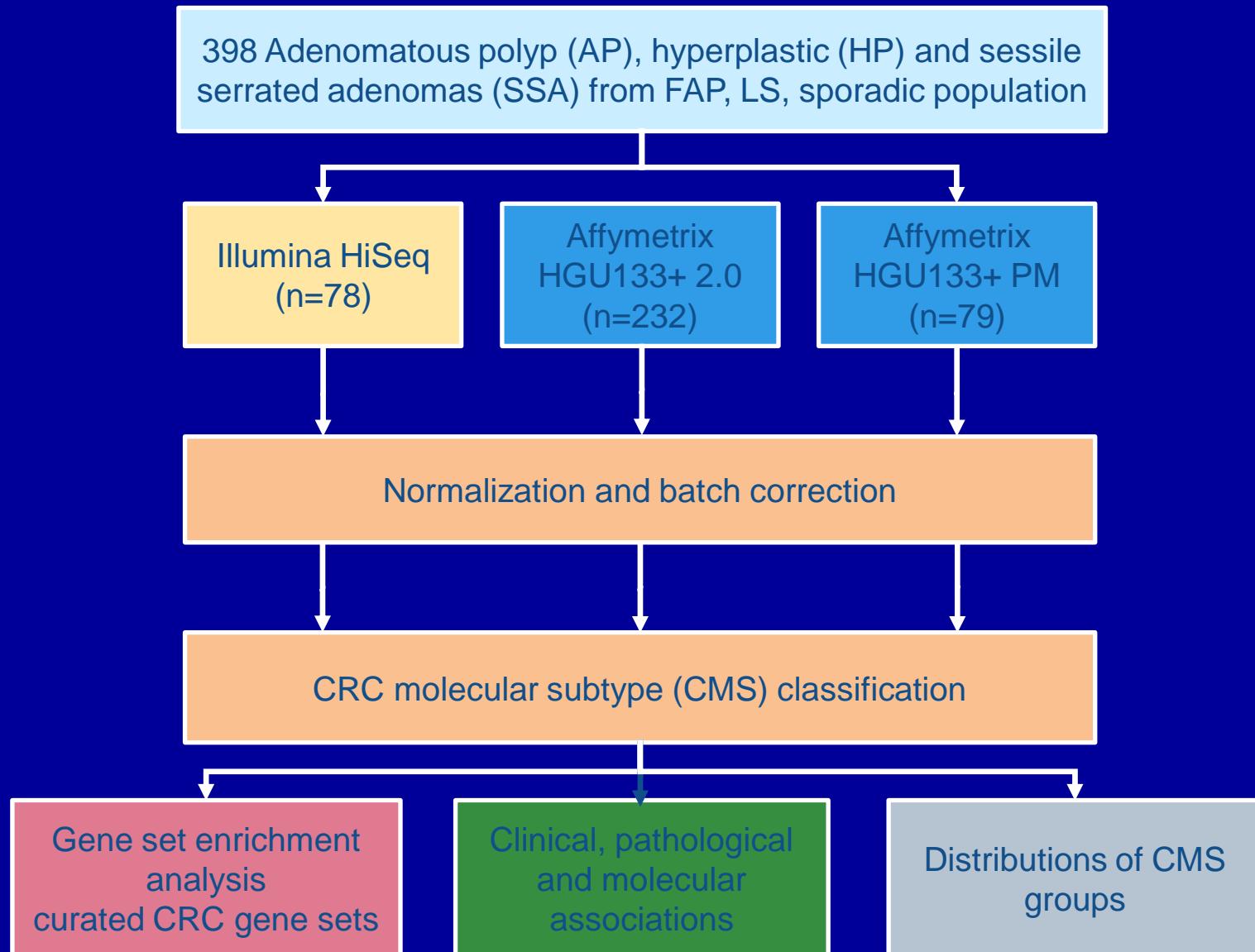
Adenoma CMS subtypes



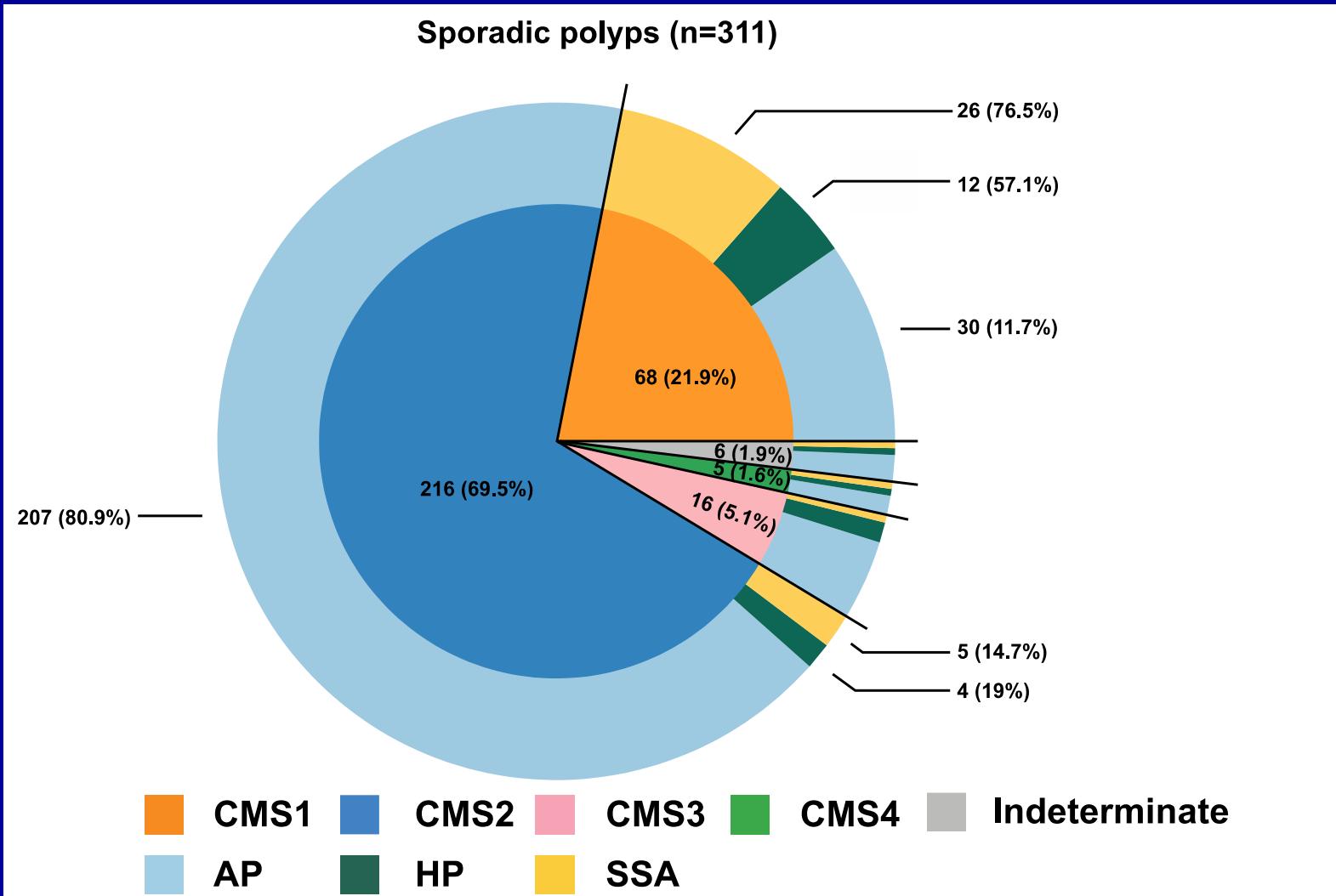
CMS1 MSI immune	CMS2 Canonical	CMS3 Metabolic	CMS4 Mesenchymal
14%	37%	13%	23%
MSI, CIMP high, hypermutation	SCNA high	Mixed MSI status, SCNA low, CIMP low	SCNA high
<i>BRAF</i> mutations		<i>KRAS</i> mutations	
Immune infiltration and activation	WNT and MYC activation	Metabolic deregulation	Stromal infiltration, TGF- β activation, angiogenesis
Worse survival after relapse			Worse relapse-free and overall survival



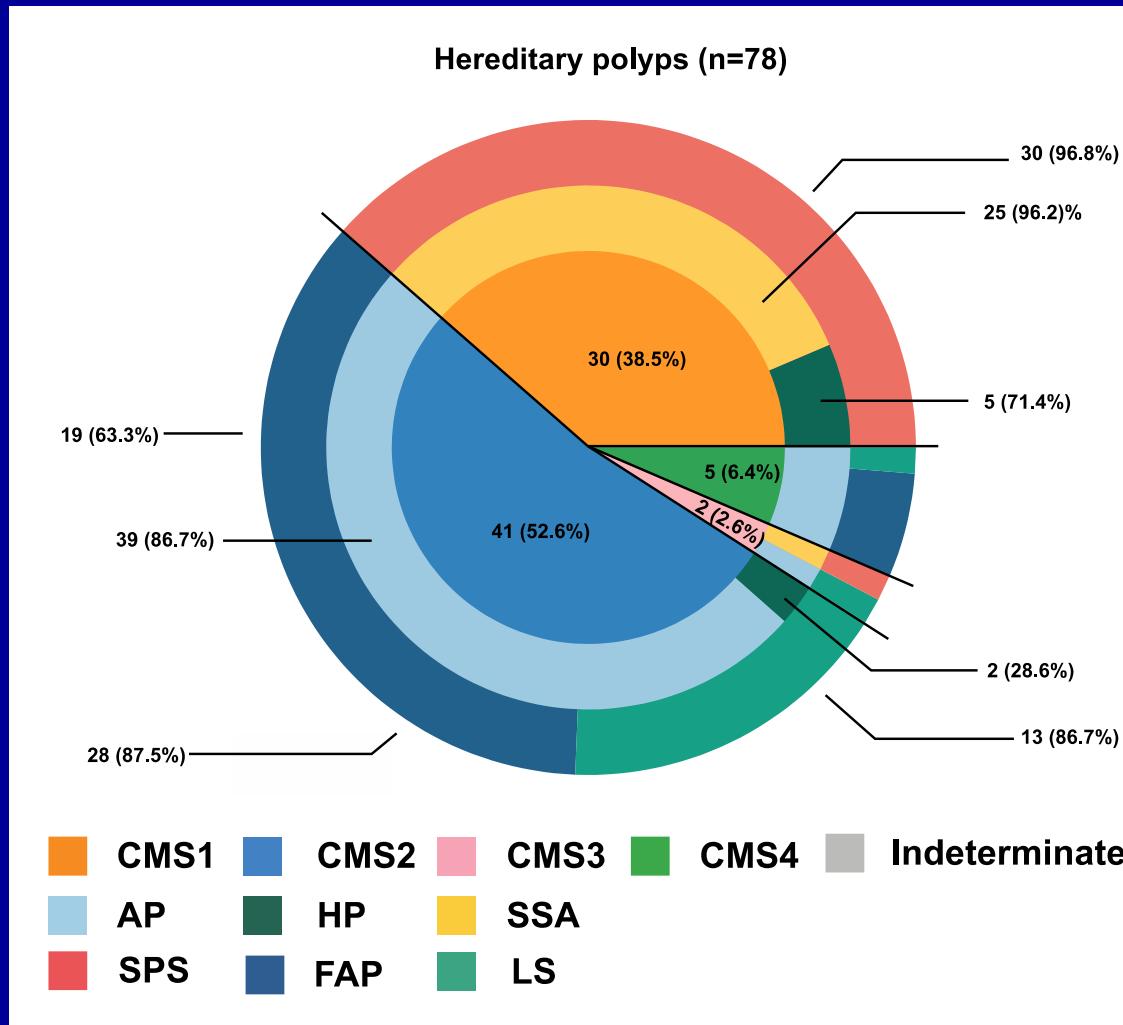
Analysis workflow



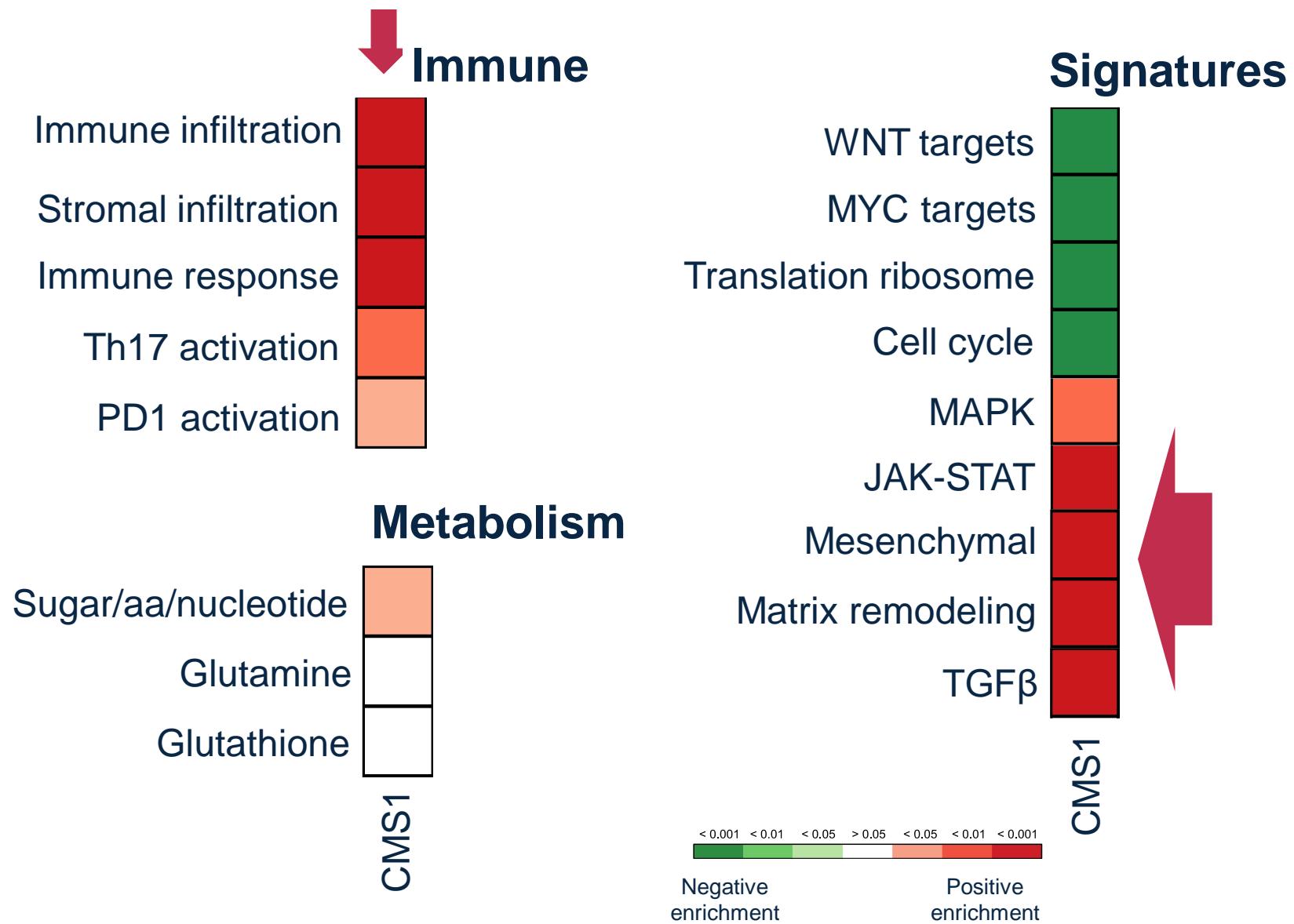
CMS1 and CMS2 are major subtypes in premalignancy



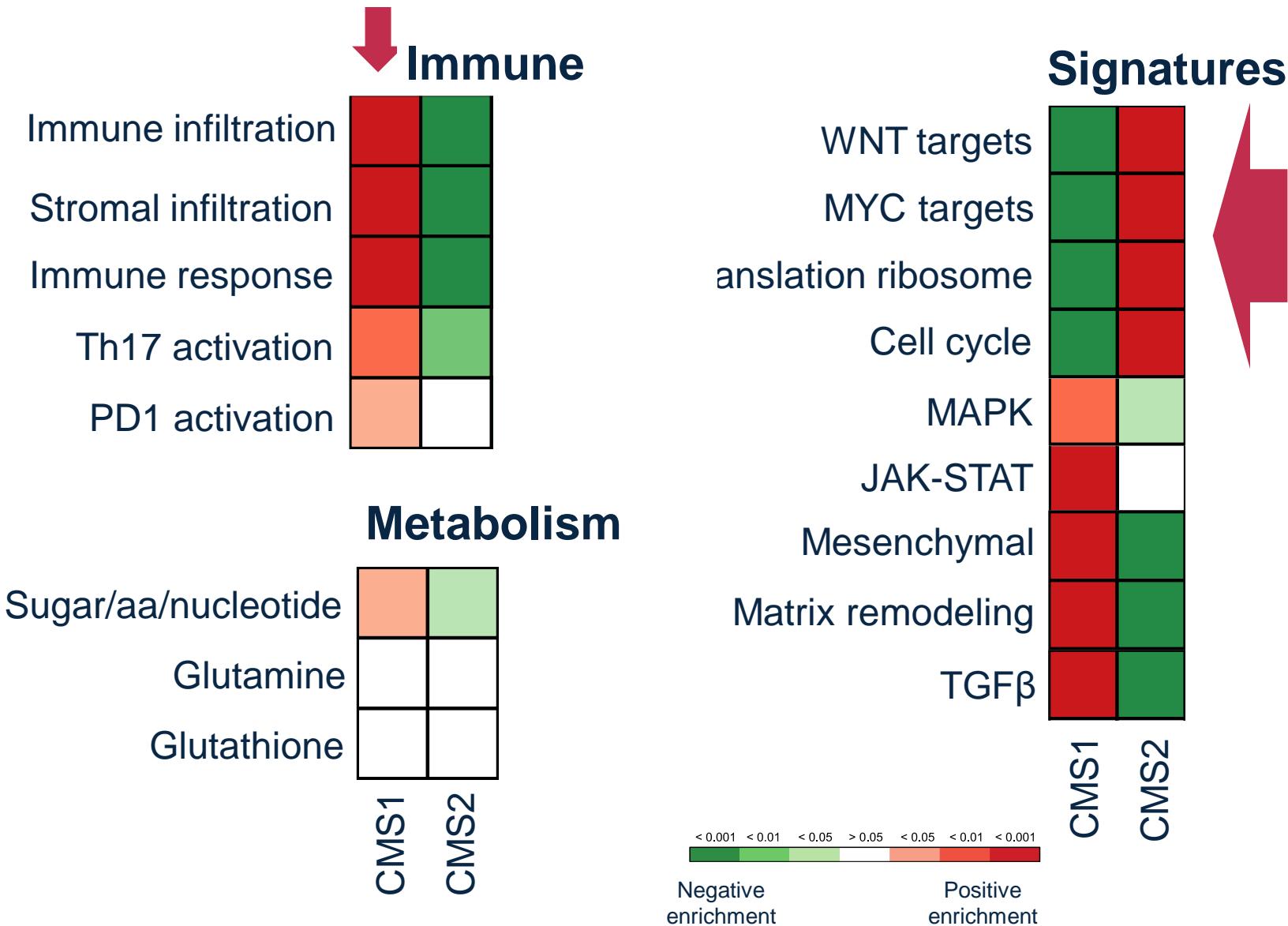
CMS1 and CMS2 are major subtypes in premalignancy



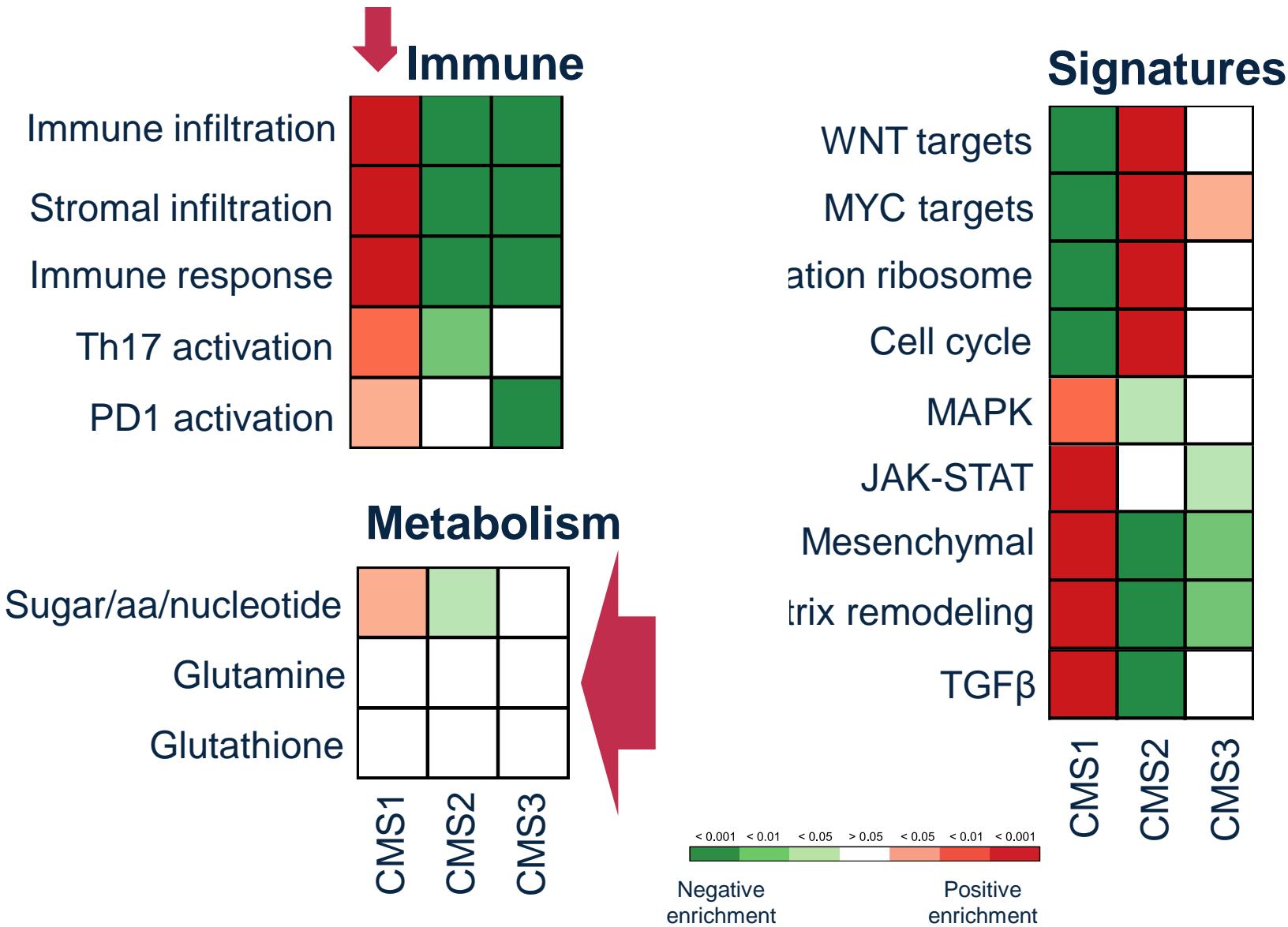
Pathway enrichment analysis



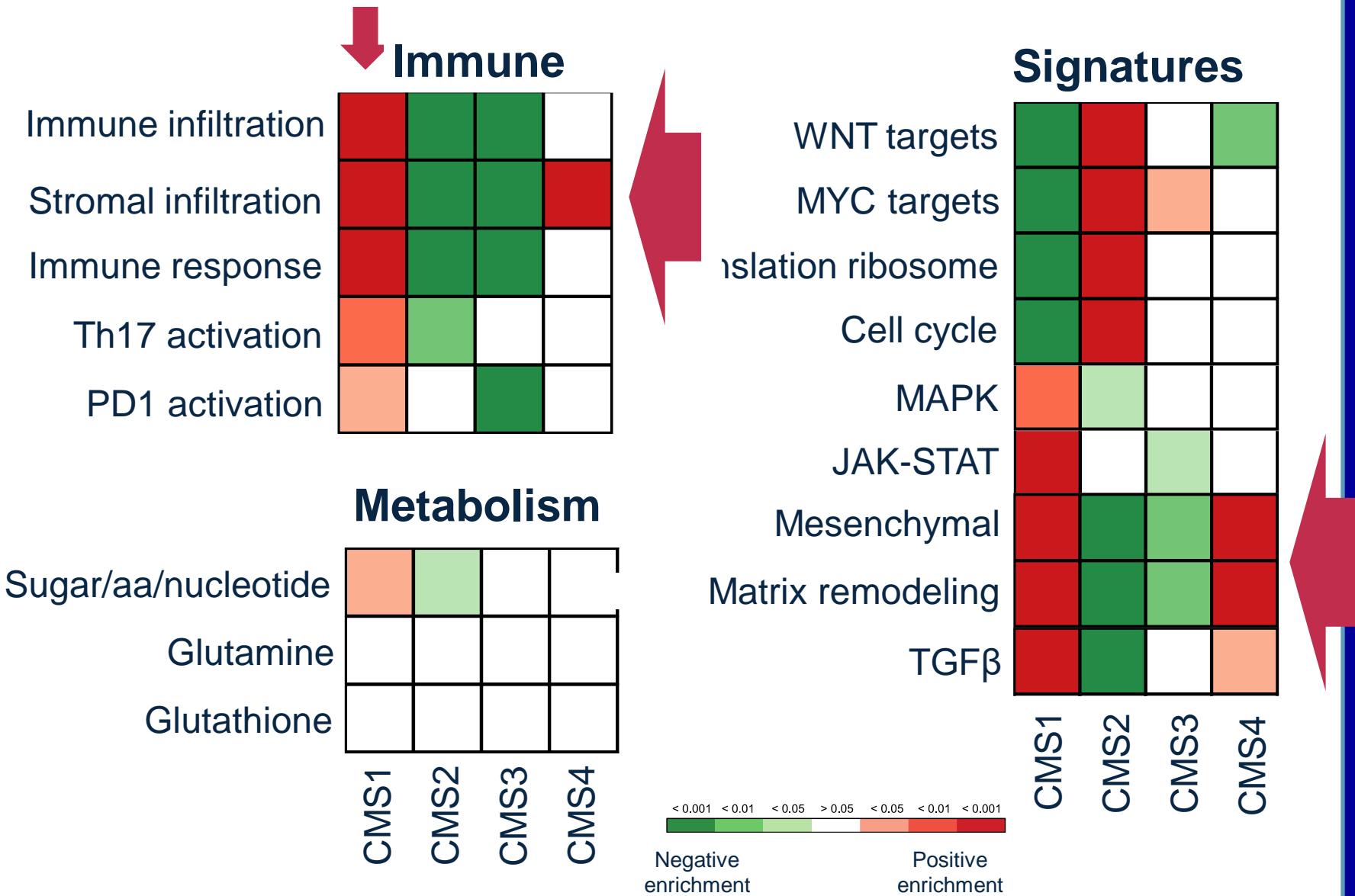
Pathway enrichment analysis



Pathway enrichment analysis



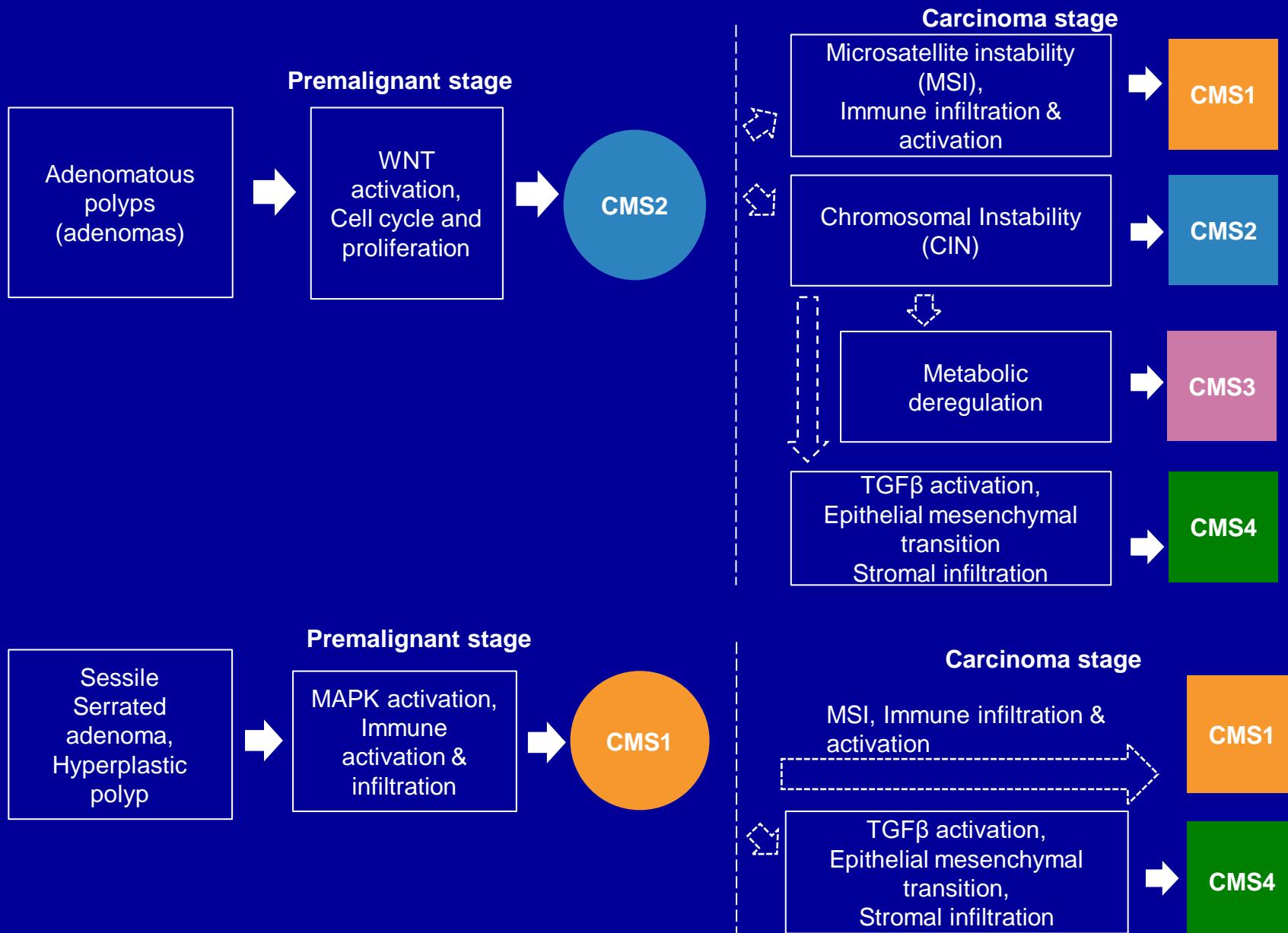
Pathway enrichment analysis



Clinical and pathological associations

Characteristics		CMS1	CMS2	CMS3	CMS4
Gender	n	57	218	12	7
	female	54%	47%	17%	57%
	male	46%	53%	83%	43%
	p-value	2.41E-01	7.91E-01	3.80E-02	7.11E-01
Presence of high-grade dysplasia (HGD)	n	30	246	13	8
	AP	60%	76%	85%	100%
	AP with HGD	40%	24%	15%	0%
	p-value	4.57E-02	5.95E-01	7.42E-01	2.07E-01
Location	n	59	210	11	7
	left	32%	66%	27%	86%
	right	68%	34%	73%	14%
	p-value	1.28E-05	1.27E-05	5.79E-02	2.45E-01
<i>BRAF V600E</i>	n	63	164	8	1
	Mutant	24%	2%	0	0
	Wildtype	76%	98%	100%	100%
	p-value	9.95E-07	7.73E-06	1.00E+00	1.00E+00
<i>KRAS</i> codon 12 and 13	n	51	164	7	1
	Mutant	2%	13%	14%	0
	Wildtype	98%	87%	86%	100%
	p-value	1.94E-02	4.70E-02	5.55E-01	1.00E+00

Pathway activation driving CMS



Acknowledgements

Vilar Lab

Laura Reyes
Prashant Bommi
Lewins Walter
Jason Willis
Hong Wu
Wendy Wu
Kyera Evans
Jennifer Kinnison
Ana Bolivar
Nejla Ozirmak
Chase Bowen

Scheet Lab

Paul Scheet
Kyle Chang

MDA

Florencia McAllister
Ernie Hawk, Powel Brown
Margaret Dunseith
Melissa Taggart – Pathology
Jack Lee, Diane Liu, Shiva Dibaj – Biostats
Diane, Val, Carrie – CCP Research Core
Erika Thompson – SMF Core

Clinical Cancer Genetics - MDA

Patrick Lynch, Nancy You,
Miguel Rodriguez-Bigas
Selvi Thirumurthi
Maureen Mork, Sarah Bannon, Julie Moskowitz

Outside Collaborators

Ramona Lim, Elena Stoffel, Jewel Samadder, Priyanka Kanth
Steve Lipkin, Ozkan Gelincik – VCM
Marjorie Perloff, Ellen Richmond, Asad Umar (NCI)
Ginger Milne, Lawrence Marnett – Vanderbilt University
Winfried Edelmann – AECOM
Elisa Scarselli, Alfredo Nicosia – NousCom
Joanne Jeter – OSU

Grants

R01 CA219463
IOTN U01 CA233056
N01 HHSN261201200034I
MDA Colorectal Cancer Moonshot
MDA GI SPORE – Project #2

**Feinberg Family
Duncan Family Institute**



THE HOPE FOUNDATION

Because answers to cancers come from clinical trials



THE UNIVERSITY OF TEXAS
**MDAnderson
Cancer Center**
Graduate School of Biomedical Sciences