SITC/World Immunotherapy Council's Young Investigator Symposium

Genomic Instability, Tumor Mutation Burden and Biomarkers in Lung Cancer and other solid tumors

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www.cahon.org

Disclosure

- Clinical trial and research funding as investigator or institutional support
 - BMS, Merck, Adapimmune, Iovance, Mirati, Genentech, Amgen, GSK
- Advisor/Consultant Perthera, BMS, Geneplus





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Genomic Instability (MMRd), TMB and ICB outcomes

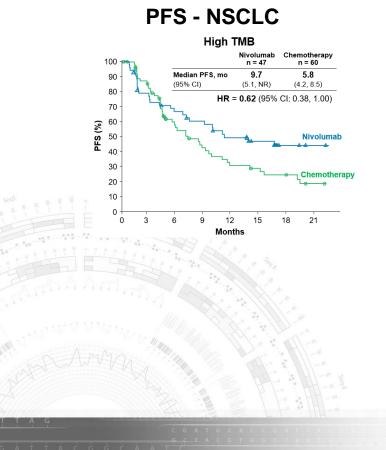
PFS OS 1.0 P=0.03 by log-rank test 1.0-P<0.001 by log-rank test Probability of Overall Survival Probability of Progression-free Survival 0.8 0.8 Mismatch repair-deficient 0.6 0.6-Mismatch repair-deficient 0.4 0.4-Mismatch repair-proficient 0.2-0.2-Mismatch repair-proficient 0.0 0.0ò 3 6 9 Ó 12 15 7 Months Months 5000 5000 P=0.007 P=0.02 4000 Somatic mutations per tumor 4000 Somatic mutations per turnor 3000 3000 2000 2000 1000 1000 **Objective Response** MMR-deficient tumors MMR-proficient tumors

.... Stable Disease Progressive Disease Le et al, N Engl J Med 2015; 372:2509-2520 The James

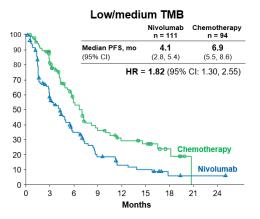


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TMB and ICB outcomes in NSCLC



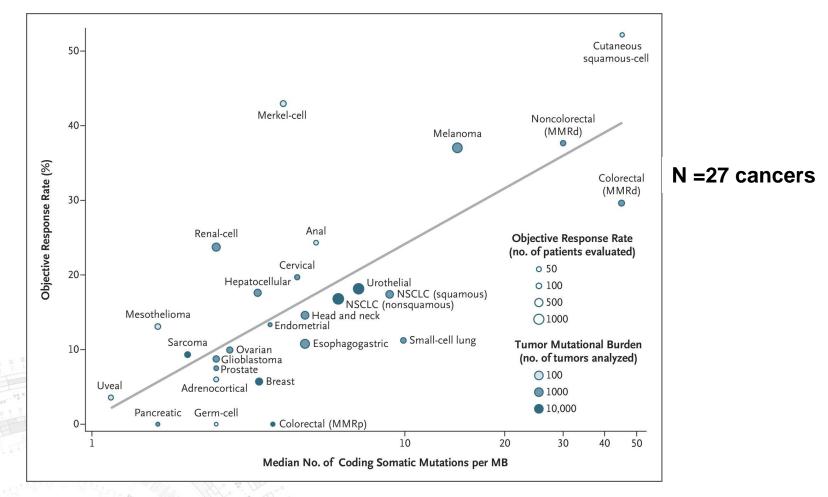
PFS - NSCLC



Carbone et al. N Engl J Med. 2017;376:2415–2426 The James



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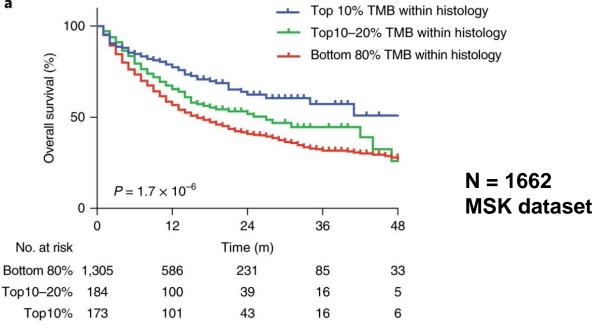


Yarchoan M, Hopkins M, Jaffee EM N Engl J Med, 2017.



Overall survival vs TMB across cancer types

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Nat Genet. 2019 Feb;51(2):202-206

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Effect of nonsynonymous mutational load on overall survival after ICB

	No. of patients		Cutoff	P-value
All samples in cohort	1,662	⊦= -1	-	1.59×10^{-6}
Cancer type				
Bladder	214	├── ■──┥	17.6	0.040
Breast	45	┝─────┤	5.9	0.605
ER+	24	├───₽ ──┤	6.8	0.287
ER-	21	┝────┫	4.4	0.731
Unknown primary	90	├───ड ──┤	14.2	0.155
Colorectal	110	├───■ ───┤	52.2	0.031
Esophagogastric	126	┝──┳──┤	8.8	0.221
Glioma	117	┝┼═╾┥	5.9	0.465
Head and neck	138	┝──■──┤	10.3	7.42 × 10 ^{−3}
Melanoma	321	┝╌┲╌┤	30.7	0.067
Non-small cell lung	350	┠╌═╌┨	13.8	2.30×10^{-4}
Renal cell carcinoma	151	├─── ┤	5.9	0.569
Drug class				
Combo	260	┝──┳──┥	-	0.018
CTLA4	146	⊢	-	1.89 × 10 ⁻³
PD-1/PDL-1	1,256	}=-1	-	6.95×10^{-4}
		0.12 0.25 0.50 1.0 2.0 4.0		

<-- Better overall survival-----HR------Worse overall survival-->

Nat Genet. 2019 Feb;51(2):202-206



The Landscape of Somatic Alteration of DNA Integrity-Related Genes, Smoking and Their Association with TMB in NSCLC

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We examined 182 DNA repair genes in 15 repair pathways in TCGA lung dataset

BER	NER	DR	MMR	HR	NHEJ	FA	Conserved [
21	30	3	13	21	8	17	16
APEX1 (APE1) APEX2 APLF (C2ORF13) LIG3, MB4 MPG MUTYH (MYH) NEIL1, NEIL2 NEIL3 NTHL1 (NTH1) OGG1 PARP1 (ADPRT) PARP2 (ADPRTL2) PNKP SMUG1 TDG UNG XRCC1 PARP3 (ADPRTL3)	CETN2, FBL3 (FBXL2), RAD23A, RAD23B, RPA1 RPA2, RPA3, XPA, XPC, ERCC6 (CSB) ERCC8 (CSA), MMS19, UVSSA (KIAA1530), XAB2 (HCNP), CCNH, CDK7 DDB1, DDB2 (XPE), ERCC1, ERCC2 (XPD) ERCC3 (XPB) ERCC4 (XPF) ERCC5 (XPB) ERCC5 (XPG) GTF2H1, GTF2H2 GTF2H3, GTF2H4 GTF2H5 (TTDA) LIG1, MNAT1		MLH1 MLH3 MSH2 MSH3 MSH4 MSH5 PM51 PM52 PM52L3 (PMS5) DUT NUDT1 (MTH1) RRM2B (p53R2)	BRCA1 DMC1 EME1 (MMS4L) EME2 GEN1 GIYD1 (SLX1A) GIYD2 (SLX1A) MRE11A MUS81 NBN (NBS1,RAD21) RAD50, RAD51 RAD51B, RAD51D RAD52 RAD54B RAD54B RAD54L SHFM1 (DSS1) SMC6L1 XRCC2, XRCC3	DCLRE1C (Artemis) LIG4 NHEJ1 (XLF, Cernunnos) PRKDC (DNA-PK) SIRT1 XRCC4 XRCC5 (Ku80) XRCC6 (Ku70)	BRCA2 (FANCD1) BRIP1 (FANCJ) BTBD12 (SLX4) (FANCP) FAAP20 (C1off86) FAAP24 (C19orf40) FANCA FANCA FANCC FANCC FANCC FANCC FANCC FANCF FANCG (XRCC9) FANCI (KIAA1794) FANCL FANCM PALB2 (FANCN) RAD51C (FANCO)	ATR CHEK1 CHEK2 CLK2 HUS1 MDC1 PER1 RAD17 (RAD24) RAD9A RIF1 RRM1 RRM2 TOPBP1 TP53 TP53BP1 (53BP1)
Defective in Disease	Repair Crosslink	Chromatin structure	Polymerase	Nuclease	Ubiquitination	Other	Total
5	2	3	15	8	11	9	182 genes
ATM BLM RBBP8 (CtIP) RECQL4 WRN	TDP1 TDP2 (TTRAP)	CHAF1A (CAF1) H2AFX (H2AX) SETMAR (METNASE)	MAD2L2 (REV7) PCNA, POLB POLD1, POLE POLG, POLH POLI (RAD30B) POLK (DINB1) POLL, POLM POLN (POL4P)	APTX (aprataxin) ENDOV EXO1 (HEX1) FAN1 (MTMR15) FEN1 (DNase IV) SPO11 TREX1 (DNase III) TREX2	HLTF (SMARCA3) RAD18, RNF168 RNF4, RNF8 SHPRH SPRTN (c1orf124) UBE2A (RAD6A) UBE2B (RAD6B) UBE2B (UBC13)	DCLRE1A (SNM1) DCLRE1B (SNM1B) HELQ (HEL308) OBFC2B (SSB1) PRPF19 (PSO4) RDM1 (RAD52B) RECQL (RECQ1) RECQL5	

POLQ

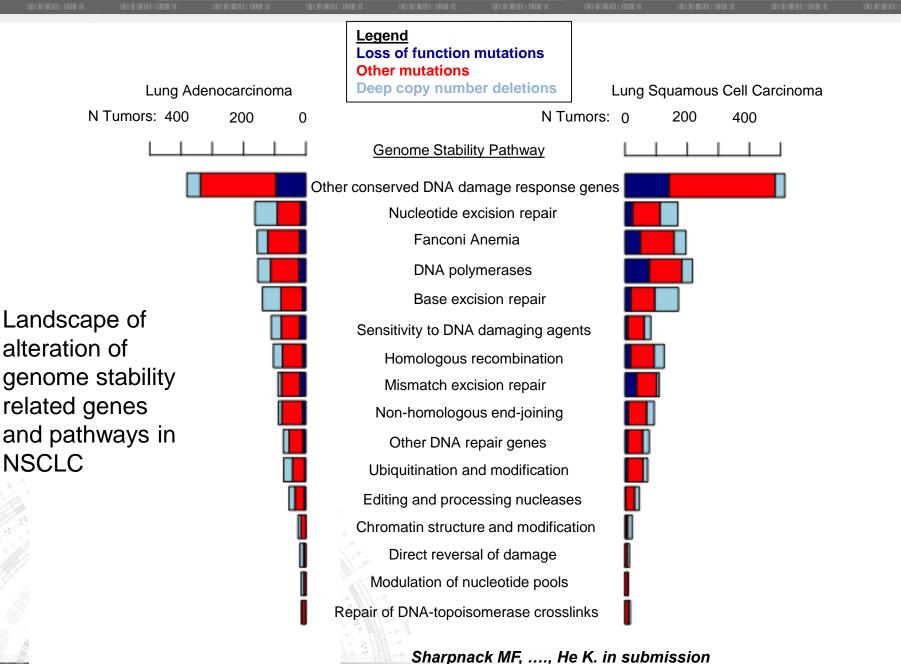
REV1L (REV1) REV3L (POLZ)

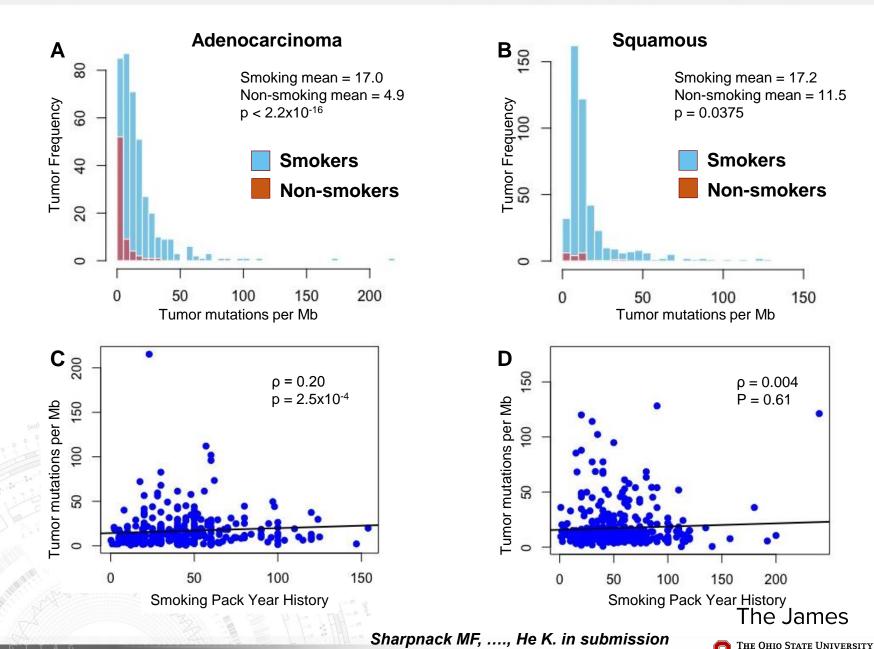
Wood RD et al., *Sicence* 291 (2001) and *Mutation Res.* 577, 275 (2005) DNA Repair and Mutagenesis, 2nd edition (ASM Press, Washington, DC) Lange SS et al, *Nature Reviews Cancer* 11, 96 (2011)

RPA4

UBE2V2 (MMS2)

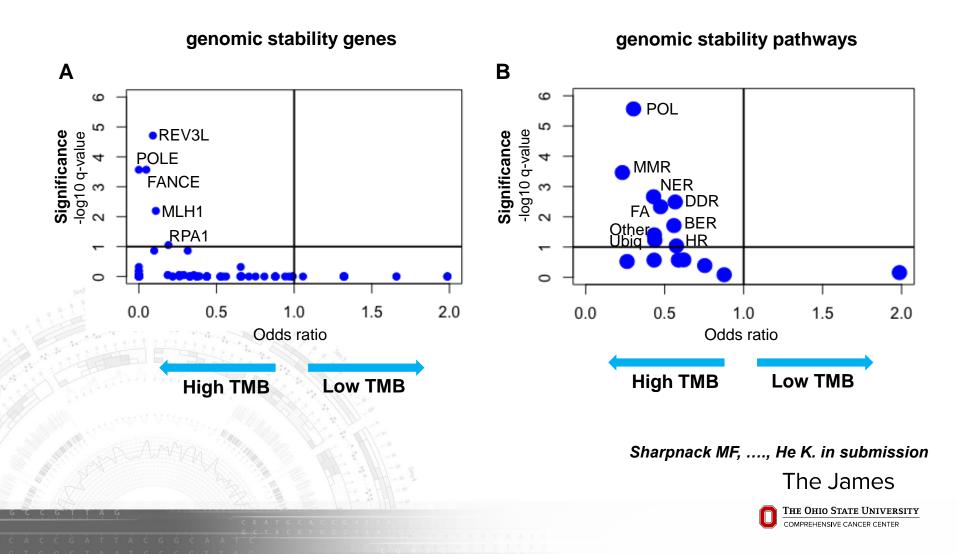






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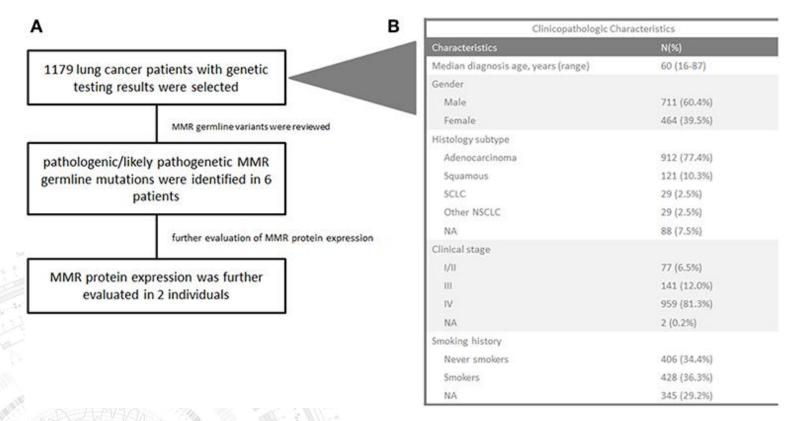
Inactivation of genomic stability related genes and pathways vs TMB in NSCLC



The Germline Alteration of DNA Integrity-Related Genes and Their Association with TMB in NSCLC

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Sun et al, Front. Oncol., 26 June 2019



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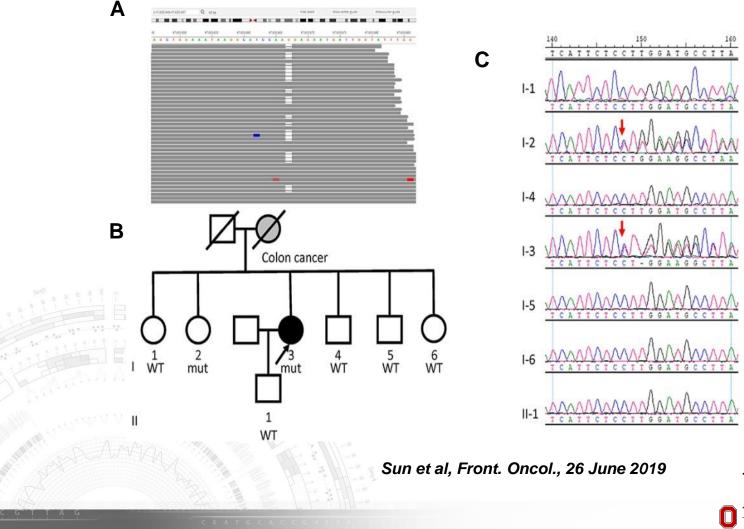
Baseline Characteristics and Genetic Testing Results of Lung Cancer Patients with Germline MMR Mutations

Case	Age range at diagnosis	Smoking status	Family history	Histological subtype	Sample type	Germline mutation	TMB (muts/Mb)	MSI	MMR expression	Genes with somatic mutations
1	60–65	NS	Mother, colon cancer	ADC	PB	<i>MSH2</i> NM_000251.2, c.340delG, p.E114Rfs*60	1	N/A	Intact	MAP2K2, GNAS
2	70–75	NS	No	ADC	PB	<i>PMS2</i> NM_000535.5, c.943C>T, p.R315*	1	MSS (PCR)	Intact	PTCH1
3	70–75	NS	No	ADC	FFPE	<i>PMS2</i> NM_000535.5 c.1053delG, p.L351Ffs*5	5	MSS (NGS)	N/A	GNAS, EGFR, MTOR, CUL3, CREBBP, FGFR4, ABCB1
4	55-60	NS	Mother, colon cancer	ADC	FFPE	<i>MSH</i> 6 NM_000179.2 c.3118T[3>1], p.F1040*	4	MSS (NGS)	N/A	MLL3, EGFR, TP53, RB1, NXF5, CBL
5	65–70	S	No	NSCLC	FFPE	<i>MSH6</i> NM_000179.2 c.4001G>A p.R1334Q	6	MSS (NGS)	N/A	IGF1R, TP53, ARID2, XRCC3, MET, SLC34A2, LRP1B, DICER1
6	75–80	S	Brother, gastric cancer	SCC	FFPE	MSH6 NM_000179.2 c.2552_2553dupGC, p.K852Afs*17	8	MSS (NGS)	N/A	ALK, LRP1B, TP53, DNMT3A, HRAS, DDR2, NTM, TCF7L2, POLE

NS, never-smoker; S, smoker; ADC, adenocarcinoma; NSCLC, non-small-cell lung cancer, SCC, squamous-cell carcinoma; PB, peripheral blood; FFPE, formalin fixation and paraffin embedding tissue; TMB, tumor mutation burden, MSI, microsatellite instability; MSS, microsatellite stable; N/A, not available.

Sun et al, Front. Oncol., 26 June 2019







NUMBER OF STREET

Germline Mutations Identified in Patients and Their Family Members 2.

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Clinical Characteristics of Lung Cancer Patients with Germline Mutation Detected on Routine NGS at OSU

Year	Age	Sex	Histology	Stage	Smoking history	Other cancer	Germline mutation	Other somatic gene alteration	Targeted therapy	Response
2014	37	F	Ad	IA	Former smoker (2 pack year)	No	BRCA2	not evaluated	—	—
2014	72	F	Ad	IV	Former smoker	Breast cancer Lung cancer	EGFR T790M	EGFR G719S	Rociletinib	SD
2015	69	F	Ad	IIIA	Former smoker	Breast cancer Uterine cancer	BRCA2	EGFR L858R	_	—
2015	50	F	SCLC	IA	Never smoker	Breast cancer	<i>TP53</i> Y236* <i>PARK2</i> Q347*	FGFR2 amplification	—	—
2016	34	F	Ad	IV	Former smoker	No	<i>BRCA2</i> L3061*	MET 3028+2T>C (splice site mutation)	Crizotinib	PR
2016	44	80 P	Ad a s	IV	Never smoker	Orbital Rhabdomyosarco ma	TP53	ALK fusion	Crizotinib	PR
2017	62	F	SCLC	IV	Former smoker	Breast cancer	BRCA1	not evaluated	-	_

Abbreviations: F, Female; Ad, Adenocarcinoma; SCLC, Small Cell Lung Cancer; SD, Stable Disease; PR, Partial Response

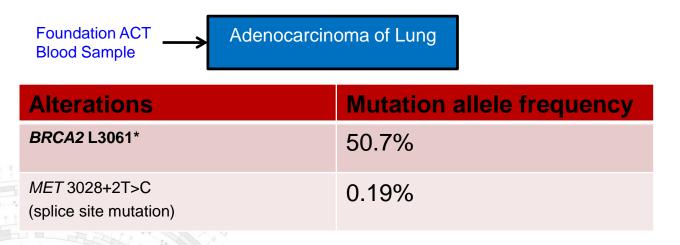
Shukuya et al, J Thorac Oncol. 2018 Feb;13(2)



Case:

A 34 year old female former smoker with lung adenocarcinoma (metastatic pleural effusion) patient with *BRCA2* L3061*.

She has no personal or family history of breast or ovarian cancer. She was treated with pleural catheter placement, four cycles of carboplatin plus pemetrexed followed by two cycles of maintenance pemetrexed, and four doses of nivolumab. She had germline genetic testing which confirmed the *BRCA* mutation.



Shukuya et al, J Thorac Oncol. 2018 Feb;13(2)

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and Other Genes in Pan-Cancers

Identification GPV Using Matched Tumor-Normal Sequencing in Pan-Cancer Patients in China

- Surveyed the germline variants in 7363 Chinese patients across more than 18 diverse cancer types.
- 2. Germline variants in 62 cancer-susceptibility genes were called from a 1021 gene NGS panel analyzing matched normal DNA.
- 3. Investigated the germline mutations in DNA integrity-related genes and their impacts on somatic mutation landscape.

Sharpnack M,...., He K, ASCO 2018, manscript in submittion



Summary

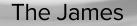


- 1. Inactivation selected DNA instability related genes and pathways are associated with increased TMB in NSCLC
- 2. Smoking is not a sufficient substitute biomarker for TMB in NSCLC.
- 3. PGVs in MMR genes were detected in 6/1,179 NSCLC patients. All of them are heterozygous and MSS. TMB was 4.5 muts/MB. Testing of family members identified new Lynch syndrome cases in two firstdegree relatives.
- 4. Targeted matched tumor-normal NGS reveals PGVs commonly exist in patients with cancers of diverse tissue origin, which is valuable in therapeutic interventions and genetic risk analysis.
- 5. We are creating a multivariate model of tumor mutation burden and studying the potential role as therapeutic biomarkers of immune checkpoint inhibition in NSCLC.



Acknowledgments

- The patients and families who made clinical trials and studies possible.
- OSU James Thoracic Oncology Center: David P. Carbone, MD, PhD, Director, and others.
- Lab members working with me: Drs. Ju Hwan Cho, Sumei Lu, Filiz Oezkan and Lei Fu; Michael Sharpnack, MD/PhD candidate
- Bioinformatics: Kun Huang, PhD (IU);
- Other Collaborators: Renhua Guo, MD, Nangjing, Geneplus, Beijing, China; James Herman, MD (UPMC), and others
- Appreciate CAHON support!





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Thank you!





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