

SAMPLE INFORMATION

Name:	-	Date Sp. Extracted:	-
Medical ID:	-	Req. Physician:	-
Date Of Birth:	-	Report No:	24MOCKICCGR
Material #1:	PARAFFIN EMBEDDED TISSUE-BLOCK	Date Received:	-
Material #2:	-	Date Of Report:	-
Sample #1 ID:	-	Tumor type:	UNKNOWN PRIMARY

primeDX - 1021 Unique Genes (38 Fusions) analyzed
1. Report Summary

3	Biomarker related approved therapies for indication	1	Biomarker related therapies with potential benefit
0	Biomarker related therapies with potential resistance	0	Biomarker related Clinical Trials

2. Clinically Significant Biomarkers*

Biomarker	Result	Approved therapies for indication	Therapies with potential clinical significance or approved in another type of cancer	Therapies with potential resistance/toxicity	Clinical Trials
	No clinically significant mutation or fusion identified				
Microsatellite Instability (MSI)	Stable (MSS)	-	-	-	-
Tumor Mutational Burden (TMB)	18.24 Muts/MB	Pembrolizumab (1A.1)	Nivolumab (2C.1)	-	-
Immunohistochemistry Biomarkers					
PD-L1 expression (Table S2)	CPS<1	-	-	-	-
Claudin 18.2 expression (IHC)	Claudin-positive (90%)	Zolbetuximab (1A.1)	-	-	-
FOLR1 (FRα) expression (IHC)	FOLR1-positive (90%)	Mirvetuximab soravtansine (1A.1)	-	-	-
ERBB2 (HER2) expression (IHC)	Positive (Score 3+)	anti-ERRB2 therapy (Table S3)	-	-	-

*Note: Variants' Level of Evidence (LoE) (e.g. 1A.1, 2C.1, 1B etc) are based on the Joint consensus recommendation of AMP, ACMG, ASCO and CAP for reporting genetic variants in cancer. For a detailed description of the recommendation please refer to Fig. 1



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3. Important biomarkers findings

Gene	Detected Range	Finding (VAF/Copy Number/Germline Mutation)
EGFR	Exon 18	Not detected
	Exon 19	Not detected
	Exon 20(including T790M)	Not detected
	Exon 21	Not detected
ERBB2(HER2)	Copy number gain	Not detected
	Mutation	Not detected
ESR1	Mutation	Not detected
ALK	Rearrangement	Not detected
ROS1	Rearrangement	Not detected
MET	Copy number gain	Not detected
	Exon 14 skipping	Not detected
RET	Rearrangement	Not detected
BRAF	Codon 600 mutation	Not detected
KIT	Exon 9	Not detected
	Exon 11	Not detected
	Exon 13	Not detected
	Exon 17	Not detected
PDGFRA	Exon 12	Not detected
	Exon 18	Not detected
BRCA1	Mutation	Not detected
BRCA2	Mutation	Not detected
KRAS	Codon 12/13/59/61/117/146 mutation	Not detected
	Other mutations except codon 12/13/59/61/117/146	Not detected
NRAS	Codon 12/13/59/61/117/146 mutation	Not detected
	Other mutations except codon 12/13/59/61/117/146	Not detected
PIK3CA	Mutation	Not detected
FGFR2	Rearrangement	Not detected
	Mutation	Not detected
FGFR3	Rearrangement	Not detected
	Mutation	Not detected
NTRK1	Rearrangement	Not detected
NTRK2	Rearrangement	Not detected
NTRK3	Rearrangement	Not detected
IDH1	Mutation	Not detected

Note:

- 'Not detected/-' indicates the corresponding variations were not detected in this tested individual.
- The genetic variations listed above are covered, but not limited to this list.
- For a detailed information about listed variants, please refer to the Report Summary and the respective Interpretations sections.



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4. Immune Checkpoint inhibitors biomarkers

Biomarker/Variant		Result	Clinical Interpretation
Biomarkers for predicting efficacy			
Tumor mutation burden (TMB)		TMB-H 18.24	PD-1/PD-L1 inhibitors can be considered
Microsatellite instability (MSI)		Stable (MSS)	-
Affect the treatment effect - positive correlation			
PD-L1 amplification		Not detected	-
PBRM1 inactivating mutation Renal clear cell carcinoma)		Not detected	-
MLH1 suspected germline deleterious mutation		Not detected	-
MSH2 suspected germline deleterious mutation		Not detected	-
MSH6 suspected germline deleterious mutation		Not detected	-
PMS2 suspected germline deleterious mutation		Not detected	-
POLE mutation (driver)		Not detected	-
POLD1 mutation (driver)		Not detected	-
Other DNA damage repair (DDR) pathway genes	ATM mutation	Not detected	-
	ATR mutation	Not detected	-
	BAP1 mutation	Not detected	-
	BLM mutation	Not detected	-
	BRCA1 mutation	Not detected	-
	BRCA2 mutation	Not detected	-
	BRIP1 mutation	Not detected	-
	CHEK1 mutation	Not detected	-
	CHEK2 mutation	Not detected	-
	ERCC3 mutation	Not detected	-
	ERCC4 mutation	Not detected	-
	ERCC5 mutation	Not detected	-
	FANCA mutation	Not detected	-
	FANCC mutation	Not detected	-
	MRE11A mutation	Not detected	-
	NBN mutation	Not detected	-
	RAD50 mutation	Not detected	-
	RAD51 mutation	Not detected	-
	RAD51B mutation	Not detected	-
	RAD51D mutation	Not detected	-
	RAD54L mutation	Not detected	-
TP53 mutation		Not detected	-
KRAS mutation		Not detected	-
Biomarker/Variant		Result	Clinical Interpretation



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Affect the treatment effect - negative correlation		
<i>PTEN</i> inactivating mutation	Not detected	-
<i>JAK1</i> inactivating mutation	Not detected	-
<i>JAK2</i> inactivating mutation	Not detected	-
<i>B2M</i> inactivating mutation	Not detected	-
<i>EGFR</i> mutation (L858R/EX19del)	Not detected	-
<i>ALK</i> rearrangement	Not detected	-
<i>STK11</i> inactivating mutation	Not detected	-
<i>KEAP1</i> inactivating mutation	Not detected	-
<i>11q13</i> amplification	Not detected	-
<i>MDM2</i> amplification	Not detected	-
<i>MDM4</i> amplification	Not detected	-
<i>DNMT3A</i> inactivating mutation	Not detected	-
Indicator affecting prognosis of immune checkpoint inhibitor therapy		
HLA-I Zygosity (At least one of type A, B, C is homozygous)	Not detected	-

Note:

- Not detected/- indicates the corresponding variation were not detected in this tested individual.
- The interpretation of the detection results of *PBRM1* inactivating mutations is only applicable to renal clear cell carcinoma.
- The indicators/gene clinical interpretations listed above are for reference only, and the specific decisions need to refer to professional physician instructions.
- For a detailed interpretation, showed in Interpretation for biomarker of checkpoint inhibitor.
- POLE* and *POLD1* mutations are restricted to currently reported mutations that may lead to hypermutation in tumor, resulting in tumor mutation burden increase.
- HLA-I results analyzed by the phenotypes of HLA-A, HLA-B and HLA-C loci detected from tumor samples. Due to the lack of control samples, HLA-I typing cannot be accurately analyzed and it is possible that show homozygosity because of the occurrence of HLA-LOH in the tumor tissue.



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5. Interpretations for targeted therapies

Genetic Variation: *None detected*

VAF: -

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6. Interpretation for polymorphism variants related with chemotherapy drugs

Biomarkers associated with treatment response

Drug Classes	Drug name	Gene	dbSNP	Patient's Genotype	Patient's Variant-Drug Phenotype Annotation	Evidence Level
5-Fluorouracil (5-Fu), Fluoropyrimidines	5-Fu + Oxaliplatin	<i>GSTP1</i>	rs1695	AG	Associated with moderate response to treatment	2A
Anthracyclines	Epirubicin	<i>GSTP1</i>	rs1695	AG	Associated with better response to treatment	2A
Aromatase inhibitors	Letrozole, Anastrozole	<i>CYP19A1</i>	rs4646	CC	Associated with poorer response to treatment	3
	Anastrozole	<i>ABCB1</i>	rs2032582	CC	Associated with poorer response to treatment	3
Cyclophosphamide	Cyclophosphamide	<i>XRCC1</i>	rs25487	CT	Associated with poorer response to treatment	3
	Cyclophosphamide	<i>SOD2</i>	rs4880	AG	Associated with moderate response to treatment	2B
	Cyclophosphamide + Epirubicin	<i>GSTP1</i>	rs1695	AG	Associated with better response to treatment	2A
Methotrexate	Methotrexate	<i>ATIC</i>	rs4673993	TT	Associated with poorer response to treatment	2B
Pemetrexed	Pemetrexed	<i>MTHFR</i>	rs1801133	AA	Associated with poorer response to treatment	3
Platinum-Based Chemotherapy	Carboplatin	<i>MTHFR</i>	rs1801133	AA	Associated with better response to treatment	2A
	Platinum compounds	<i>XRCC1</i>	rs1799782	GG	Associated with poorer response to treatment	NA
	Carboplatin, Cisplatin, Oxaliplatin, Platinum, Platinum compounds	<i>ERCC1</i>	rs11615	AA	Associated with poorer response to treatment	2B
	Carboplatin, Cisplatin, Oxaliplatin, Platinum, Platinum compounds	<i>XRCC1</i>	rs25487	CT	Associated with poorer response to treatment	2B
Taxanes	Paclitaxel + Cisplatin	<i>TP53</i>	rs1042522	CC	Associated with better response to treatment	2B
	Paclitaxel	<i>ABCB1</i>	rs2032582	CC	Associated with poorer response to treatment	3
Vinca alkaloids	Vincristine	<i>ABCB1</i>	rs1045642	AG	Associated with poorer response to treatment	3

Biomarkers associated with drug toxicity

Drug Classes	Drug name	Gene	dbSNP	Patient's Genotype	Patient's Variant-Drug Phenotype Annotation	Evidence Level
5-Fluorouracil (5-Fu), Fluoropyrimidines	5-Fu or Capecitabine	<i>DPYD</i>	rs2297595	TT	Associated with decreased risk of drug toxicity	2A
	5-Fu or Capecitabine	<i>MTHFR</i>	rs1801133	AA	Associated with increased risk of drug toxicity	2A
	5-Fu + Leucovorin or Tegafur + Leucovorin	<i>UMPS</i>	rs1801019	GG	Associated with decreased risk of drug toxicity	2B
	Fluoropyrimidine-based therapy	<i>DPYD</i>	rs67376798	TT	Associated with decreased risk of drug toxicity	1A
	Fluoropyrimidine-based therapy	<i>DPYD</i>	rs55886062	AA	Associated with decreased risk of drug toxicity	1A
	Fluoropyrimidine-based therapy	<i>DPYD</i>	rs3918290	CC	Associated with decreased risk of drug toxicity	1A



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Anthracyclines	Anthracyclines	<i>CBR3</i>	rs1056892	AG	Associated with increased risk of drug toxicity	2B
	Epirubicin	<i>GSTP1</i>	rs1695	AG	Associated with decreased risk of drug toxicity	2A
Capecitabine	Capecitabine-Based Chemotherapy	<i>MTHFR</i>	rs1801131	TT	Associated with decreased risk of drug toxicity	2A
	Capecitabine-Based Chemotherapy	<i>DPYD</i>	rs2297595	TT	Associated with decreased risk of drug toxicity	2A
	5-Fu or Capecitabine	<i>MTHFR</i>	rs1801133	AA	Associated with increased risk of drug toxicity	2A
	Capecitabine	<i>DPYD</i>	rs67376798	TT	Associated with decreased risk of drug toxicity	1A
	Capecitabine	<i>DPYD</i>	rs55886062	AA	Associated with decreased risk of drug toxicity	1A
	Capecitabine	<i>DPYD</i>	rs3918290	CC	Associated with decreased risk of drug toxicity	1A
Cyclophosphamide	Cyclophosphamide	<i>MTHFR</i>	rs1801133	AA	Associated with increased risk of drug toxicity	2A
	Cyclophosphamide + Epirubicin	<i>GSTP1</i>	rs1695	AG	Associated with decreased risk of drug toxicity	2A
Gemcitabine	Gemcitabine	<i>CDA</i>	rs2072671	CC	Associated with increased risk of gastrointestinal toxicity and neutropenia, decreased risk of hematologic toxicity	2B
Irinotecan	Irinotecan	<i>UGT1A1</i>	rs8175347	6TA/7TA	Associated with moderate risk of drug toxicity	2A
	Irinotecan	<i>UGT1A1</i>	rs4148323	GG	Associated with decreased risk of drug toxicity	2A
	Irinotecan	<i>C8orf34</i>	rs1517114	CG	Associated with increased risk of drug toxicity	2B
Methotrexate	Methotrexate	<i>MTRR</i>	rs1801394	AA	Associated with decreased risk of drug toxicity	2B
	Methotrexate	<i>ABCB1</i>	rs1045642	AG	Associated with increased risk of drug toxicity	2A
Platinum-Based Chemotherapy	Cisplatin	<i>XPC</i>	rs2228001	GG	Associated with increased risk of drug toxicity	1B
	Platinum compounds	<i>GSTP1</i>	rs1695	AG	Associated with increased risk of drug toxicity	2A
	Cisplatin, Platinum, Platinum compounds	<i>ERCC1</i>	rs3212986	CC	Associated with increased risk of drug toxicity	2B
	Carboplatin, Cisplatin, Oxaliplatin, Platinum, Platinum compounds	<i>ERCC1</i>	rs11615	AA	Associated with increased risk of drug toxicity	2B
	Carboplatin, Cisplatin, Oxaliplatin, Platinum, Platinum compounds	<i>XRCC1</i>	rs25487	CT	Associated with decreased risk of drug toxicity	2B

Note:

1. The level of variant-drug associations evidence is based on PharmGKB website, for more detailed information please see <http://www.pharmgkb.org/page/clinAnnLevels>.

Level 1A: Annotation for a variant-drug combination in a CPIC- or medical society-endorsed pharmacogenomics guideline, or implemented at a PGRN site, or in another major health system;

Level 1B: Annotation for a variant-drug combination in which the preponderance of evidence shows an association. The association must be replicated in more than one cohort with significant P-values, and, preferably with a strong effect size;

Level 2A: Annotation for a variant-drug combination that qualifies for level 2B where the variant is within a VIP (Very Important Pharmacogene) as defined by PharmGKB. The variants in level 2A are in known pharmacogenes, so functional significance is more likely;



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- Level 2B: Annotation for a variant-drug combination with moderate evidence of an association. The association must be replicated, but there may be some studies that do not show statistical significance, and/or the effect size may be small;
- Level 3: Annotation for a variant-drug combination based on a single significant (not yet replicated) study or annotation for a variant-drug combination evaluated in multiple studies but lacking clear evidence of an association;
- Level 4: Annotation based on a case report, non-significant study, or in vitro, molecular, or functional assay evidence only.
2. The variant-drug correlation relationship derived from multiple independent studies, therefore, the interpretations of the same class of drug for the tested individual may be inconsistent. The final drug instruction needs to combine with the specific clinical situation.
 3. The detection results are only based on the analysis of tumor samples and lack of control, the results of some loci may be specific to tumor tissues due to factors such as loss of heterozygosity.



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***Note:** In this section, damaging variants in genes without clinical actionability or without convincing evidence of cancer association are reported.

Genetic Variation: -

Therapies: -

8. Variants of Uncertain Significance (VUS)

The clinical significance of the variants listed in the below table is uncertain at this time. Until the uncertainty is resolved, these variants should not be used in clinical management decisions.

Gene	Variant	Interpretation
-	-	-



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9. Suspected Germline variants

Gene	Transcript	Exon	c.HGVS	p.HGVS	Zygosity	Classification
-	-	-	-	-	-	-

Note:

- indicates no relevant variations were detected in this test.
- When detected, pathogenic or likely pathogenic variants are reported. Variants of uncertain significance or variants that are benign or likely benign are not reported.
- The somatic or germline origin of the alteration identified cannot be verified due to the absence of control sample analysis (blood or saliva).
- Variant classification interpretation is based on ACMG (American College of Medical Genetics and Genomics) guidelines for the interpretation of germline sequence variants ([PMID:25741868](https://pubmed.ncbi.nlm.nih.gov/25741868/)).

10. HLA-I Polymorphism variation

Somatic HLA-I Zygosity

The anti-tumor activity of immune checkpoint inhibitor therapy is related to CD8+ T cells. The recognition of cancer cells by CD8+ T cells is achieved by HLA-I (human leukocyte antigen class I) molecules presenting tumor antigens.

HLA alleles have the characteristics of polymorphism and codominance. HLA-I loci subdivided into HLA-A, HLA-B and HLA-C. When a patient's HLA-I is homozygous at least one locus, this patient is expected to present less and less diverse tumor neoantigens to T cells compared to patients who are heterozygous at all three loci. In two cohorts, patients with heterozygous HLA-I showed longer OS than those with homozygous alleles, cohort1: HR=1.4 (1.02-1.9), P-value=0.036; cohort2: HR=1.31 (1.03- 1.7), P-value=0.028; among 32 patients with heterozygous HLA-I but at least one locus with LOH (loss of heterozygosity), patients with HLA-I LOH have a higher survival risk (P = 0.05, HR = 1.60, 95% CI 1.03-2.43), and these patients mainly with low mutation burden (P = 0.0006, HR = 3.68, 95% CI 1.64-8.23) ([PMID:29217585](https://pubmed.ncbi.nlm.nih.gov/29217585/)).

Gene	Test Content	Result
HLA-A	Zygosity	Heterozygosity
HLA-B	Zygosity	Heterozygosity
HLA-C	Zygosity	Heterozygosity



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12. Appendix

12.a. Immune checkpoint inhibitors predictive biomarkers

Tumor Mutation Burden (TMB)

Tumor mutation burden (TMB) refers to the number of somatic mutations in the coding region, usually indicated as the total number of somatic mutations within each MB tumor genome region. The clinical utility of TMB as a predictive biomarker for anti-PD1 immunotherapy has been established in the KEYNOTE-158 trial which led to the site-agnostic FDA-approval of pembrolizumab for metastatic/untreatable solid tumors with tissue TMB value ≥ 10 muts/MB (PMID: 32919526). The results of TMB are divided into three types: TMB-H, which means high tumor mutation burden; TMB-L, which means low tumor mutation burden; TMB-U, means that the sample does not meet the TMB assessment conditions (the tissue or pleural and ascites sample may fail to pass the TMB indicator calculation quality index due to low DNA quality and/or low tumor cell content).

Table S1. TMB interpretation and cut-offs.

Tumour Type	Immunotherapy agent	Study/Trial	TMB high cut-off	Type of benefit
TMB assessed through a multi-gene assay				
NSCLC (1L or 2L)	Anti PD-L1	FIR/BIRCH [1]	13.5 Muts/Mb (1L) 17.1 Muts/Mb (2L)	ORR, OS, PFS
NSCLC (2L)	Anti PD-L1	POPLAR [1]	15.8 Muts/Mb	ORR, OS, PFS
NSCLC (2L)	Anti PD-L1	POPLAR/OAK [2-3]	16 Muts/Mb (blood)	OS, PFS
NSCLC (1L)	Anti PD-L1	BFAST and B-F1RST [4-6]	16 Muts/Mb (blood)	DOR, ORR, PFS, OS
NSCLC	Anti PD-L1	Rizvi <i>et al</i> , 2018 [7]	7.4 Muts/Mb	DCB, ORR, PFS
NSCLC	Anti PD-1	Singal <i>et al</i> , 2017 [8]	20 Muts/Mb	OS
NSCLC (1L)	Anti PD-1/Anti-CTL4	CheckMate 227 [9]	10 Muts/Mb	ORR, PFS
NSCLC (1L)	Anti PD-1/Anti-CTL4	CheckMate 568 [10]	10 Muts/Mb	ORR, PFS
NSCLC	various immunotherapies	Rozenblum <i>et al</i> , 2017 [11]	9.6 Muts/Mb	ORR
Melanoma	various immunotherapies	Johnson <i>et al</i> , 2016 [12]	23.1 Muts/Mb	ORR, OS, PFS
Bladder (1L or 2L)	Anti PD-L1	IMvigor 210 [13-14]	16 Muts/Mb	ORR, OS
Bladder (2L)	Anti PD-L1	IMvigor 211 [15]	9.65 Muts/Mb	OS
Multiple solid tumours	various immunotherapies	Goodman <i>et al</i> , 2017 [16]	20 Muts/Mb	ORR, OS, PFS
Multiple solid tumours (2L)	various immunotherapies	Bonta <i>et al</i> , 2017 [17]	8 Muts/Mb	ORR
Multiple solid tumours	anti-CTLA-4 or anti-PD-1	Samstein <i>et al</i> , 2019 [18]	varies across cancer types	OS
mTNBC	Anti PD-1	KEYNOTE-119 [19]	10 Muts/Mb	ORR, OS
All solid tumours	Anti PD-1	KEYNOTE-158 [20]	10 Muts/Mb	ORR

1. Kowanetz M, Zou W, Shames D, et al. J Thorac Oncol 2017;12:S321-S322 | 2. Fabrizio D, Lieber D, Malboeuf C, et al Presented at the AACR Annual Meeting, Chicago, IL, 2018. | 3. Gandara DR, Paul SM, Kowanetz M, et al. Nat Med 2018;24:1441-8 | 4. Fabrizio D, Malboeuf C, Lieber D, et al. Ann Oncol 2017;28:v22-v24. | 5. Velcheti V, Kim ES, Mekhail T, et al. J Clin Oncol ;36:12001. | 6. Mok TSK, Gadgeel S, Kim ES, et al. Ann Oncol 2017;28:v460-v496 | 7. Rizvi H, Sanchez-Vega F, La K, et al. J Clin Oncol 2018;36:633-41. | 8. Singal G, Miller PG, Agarwala V, et al. Ann Oncol 2017;28:v403-427. | 9. Hellmann MD, Ciuleanu TE, Pluzanski A, et al. Med 2018;378:2093-104. | 10. Ready N, Hellmann MD, et al. J Clin Oncol. 2019 Feb 20;JCO1801042 | 11. Rozenblum AB,



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Pembrolizumab



Pembrolizumab is a highly selective IgG4-kappa humanized monoclonal antibody against PD-1 receptor. It was generated by grafting the variable sequences of a very high-affinity mouse antihuman PD-1 antibody onto a human IgG4-kappa isotype with the containing a stabilizing S228P Fc mutation. It contains 32 cysteine residues and the complete folded molecule includes 4 disulfide linkages as interchain bonds and 23 interchain bonds. It was developed by Merck & Co and first approved for the treatment of metastatic malignant melanoma by the FDA on September 4, 2014, becoming the first approved therapy against PD-1. In the time since its initial approval, pembrolizumab has been granted approval in the treatment of a wide variety of cancers. On June 16, 2020, the Food and Drug Administration granted accelerated approval to pembrolizumab (KEYTRUDA, Merck & Co., Inc.) for the treatment of adult and pediatric patients with unresectable or metastatic tumor mutational burden-high (TMB-H) [≥ 10 mutations/megabase (mut/Mb)] solid tumors, as determined by an FDA-approved test, that have progressed following prior treatment and who have no satisfactory alternative treatment options. Efficacy was investigated in a prospectively-planned retrospective analysis of 10 cohorts of patients with various previously treated unresectable or metastatic TMB-H solid tumors enrolled in a multicenter, non-randomized, open-label trial, KEYNOTE-158 (NCT02628067). A total of 102 patients (13%) had tumors identified as TMB-H, defined as TMB ≥ 10 mut/Mb. The ORR for these patients was 29% (95% CI: 21,39), with a 4% complete response rate and 25% partial response rate. This new approval represents the fourth "tissue agnostic" approval by the FDA, following behind pembrolizumab for mismatch repair (MMR)-deficient solid tumors and larotrectinib and entrectinib for NTRK gene fusion-positive solid tumors.

Nivolumab



Nivolumab is a fully human IgG4 antibody targeting the immune checkpoint programmed death receptor-1 (PD-1). This molecule was produced entirely on mice and grafted onto human kappa and IgG4 Fc region with the mutation S228P for additional stability and reduced variability. It was originally FDA approved on December 22, 2014. Since this approval, nivolumab has been approved for a variety of other uses related to cancer therapy. On 2017, was notably approved for the treatment of hepatocellular carcinoma and on July 11, 2018, the FDA approved this agent in combination with low doses of for the treatment of MSI-H/dMMR metastatic colorectal cancer. The CheCUP trial, a multicenter phase II study of combined nivolumab (PD-1 checkpoint inhibitor) and ipilimumab (CTLA-4 checkpoint inhibitor) in patients with unfavorable cancer of unknown primary (CUP) relapsed after or refractory to platinum-based chemotherapy (NCT04131621) showed that 60% of CUP patients with high TMB respond to combined ICI therapy with nivolumab.

Microsatellite Instability (MSI)

MSI (microsatellite instability, MSI) refers to the phenomenon that the sequence of microsatellites increases or decreases. Microsatellite (MS), also called Short Tandem Repeats (STRs) or Simple Sequence Repeat (SSRs), consists of repeated sequences of 1-6 nucleotides. This report uses NGS panel detection and is based on the 1021 Panel platform. The results of MSI are divided into three types: MSI-H, which means microsatellites are highly unstable; MSS, which means microsatellites are stable; MSI-U, which means that the sample does not meet the MSI evaluation conditions (tissues or pleural fluid samples may not have passed the MSI indicator calculation quality control due to the low DNA and/or content of tumor cells).





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FDA approved pembrolizumab for solid tumors with MSI-H or dMMR (highly unstable microsatellites or MMR defects) and approved for MSI-H or dMMR colorectal cancer as the first-line treatment ([PMID: 35680043, 33264544](#)). FDA approved nivolumab for the treatment of children or adults who have progressed after 5-FU/oxaliplatin/irinotecan treatment with MSI-H or dMMR metastatic colorectal cancer. The NCCN clinical practice guidelines for colorectal cancer indicate that pembrolizumab/nivolumab can be used for the treatment of patients with dMMR/MSI-H colorectal cancer ([PMID: 28734759](#)).



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Report No: **24MOCKICCGR****PD-L1 expression****Table S2.** PD-L1 interpretation and cut-offs.

Cancer type	Therapy	PD-L1	Cut-off	We report
Non-Small Cell Lung Cancer (NSCLC)	Anti-PD-1 ^[1-4]	VENTANA (SP263)	1L TPS ≥ 50% 2L TPS ≥ 1%	%TPS
	Anti-PD-L1 ^[5-7]	VENTANA (SP263)	2L TPS ≥ 1%	%TPS
		VENTANA (SP263)	1L TPS ≥ 50%	%TPS
		VENTANA (SP142)	1L TC ≥ 50% or IC ≥ 10%	%TC/%IC
Urothelial Cancer (UC)	Anti-PD-1 + Anti-CTLA-4 ^[8]	VENTANA (SP263)	1L TPS ≥ 1%	%TPS
	Anti-PD-1 ^[9]	Dako 22C3	1L CPS ≥ 10	CPS
	Anti-PD-1 ^[19]	VENTANA (SP263)	1L TC ≥ 1%	%TC
	Anti-PD-L1 ^[10]	VENTANA (SP142)	2L IC ≥ 5%	%IC
Triple Negative Breast Cancer (TNBC)	Anti-PD-L1 ^[11]	VENTANA (SP142)	1L IC ≥ 1%	%IC
	Anti-PD-1 ^[12] + chemotherapy	Dako 22C3	1L CPS ≥ 10	CPS
Cervical cancer	Anti-PD-1 ^[16]	Dako 22C3	2L CPS ≥ 1	CPS
Head and Neck Squamous Cell Carcinoma (HNSCC)	Anti-PD-1 ^[14,15]	Dako 22C3	1L CPS ≥ 1 2L TPS ≥ 50%	CPS and %TPS
Gastric cancer (adenocarcinoma) (HER-2 Positive)	Anti-PD-1 ^[13,20]	Dako 22C3	1L CPS ≥ 1	CPS
Gastric cancer (adenocarcinoma) (HER-2 Negative)	Anti-PD-1 ^[18, 20]	Dako 22C3	1L CPS ≥ 5	CPS
Oesophageal (Adenocarcinoma and squamous carcinoma)	Anti-PD-1 ^[17]	Dako 22C3	1L CPS ≥ 10	CPS
Oesophageal (squamous carcinoma)	Anti-PD-1 ^[17]	Dako 22C3	1L TC ≥ 1%	%TC
Oesophageal (Adenocarcinoma) (HER-2 Negative)	Anti-PD-1 ^[17]	Dako 22C3	1L CPS ≥ 5	CPS
Gastro-oesophageal junction Adenocarcinoma (HER-2 Negative)	Anti-PD-1 ^[17,20] *Depending on PD-L1 inhibitor	Dako 22C3	1L CPS ≥ 5 or* 1L CPS ≥ 10	CPS
		Dako 22C3	1L CPS ≥ 1	
Gastro-oesophageal junction Adenocarcinoma (HER-2 Positive)				

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TPS: Tumor Proportion Score = $\frac{\text{\#PD-L1 positive tumor cells}}{\text{Total \#PD-L1 positive+PD-L1 negative tumor cells}} \times 100$

TC: tumor cell

CPS: Combined Positive Score = $\frac{\text{\#PD-L1 staining cells (tumor cells, lymphocytes, macrophages)}}{\text{Total \# of viable tumor cells}} \times 100$

IC: immune cell

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12.b. Other Immunohistochemistry Biomarkers

Claudin 18.2

Claudin 18.2, a member of the claudin family, is a promising target for the treatment of patients with digestive malignancies, such as gastric cancer (GC), gastroesophageal junction (GEJ) cancer, esophageal cancer, and pancreatic cancer, because of its limited expression in healthy tissues and abnormal overexpression in a range of malignancies. Based on the results from SPOTLIGHT (NCT03504397) and GLOW (NCT03653507) clinical trials, FDA approved zolbetuximab-clzb for the first-line treatment of adults with locally advanced unresectable or metastatic human epidermal growth factor receptor 2 (HER2)-negative gastric or gastroesophageal junction (GEJ) adenocarcinoma whose tumors are CLDN18.2 positive ($\geq 75\%$).).

Zolbetuximab



Zolbetuximab is a claudin 18.2-directed cytolytic antibody. On October 18, 2024, the Food and Drug Administration approved zolbetuximab-clzb, with fluoropyrimidine- and platinum-containing chemotherapy, for the first-line treatment of adults with locally advanced unresectable or metastatic human epidermal growth factor receptor 2 (HER2)-negative gastric or gastroesophageal junction (GEJ) adenocarcinoma whose tumors are CLDN18.2 positive, as determined by an FDA-approved test. Efficacy was evaluated in trials SPOTLIGHT (NCT03504397) and GLOW (NCT03653507).

FOLR1 (FR α)

The *FOLR1* gene encodes the Folate Receptor 1, a protein that binds folate and mediates its transport into cells. Folate is essential for DNA synthesis, repair, and methylation, making FOLR1 important for cell division and growth. Overexpression of FOLR1 has been found in various cancers, such as ovarian, lung, and breast cancers. Based on the results of Study 0416 (MIRASOL, NCT04209855), FDA granted full approval for mirvetuximab soravtansine-gynx, for adult patients with FR α -positive, platinum-resistant epithelial ovarian, Fallopian tube, or primary peritoneal cancer, who have received 1-3 prior systemic treatment regimens.

Mirvetuximabsoravtansine



Mirvetuximab soravtansine is a folate receptor alpha-directed antibody and microtubule inhibitor conjugate. On November 2022, the FDA granted accelerated approval to mirvetuximab soravtansine-gynx for the treatment of adult patients with FR α -positive, platinum-resistant epithelial ovarian, fallopian tube, or primary peritoneal cancer who have received 1-3 prior systemic treatment regimens. This decision was supported by findings from the phase 3 SORAYA trial (NCT04296890). It was subsequently granted full approval in March 2024. Efficacy was evaluated in Study 0416 (MIRASOL, NCT04209855), a multicentre, open-label, active-controlled, randomised, two-arm study.

ERBB2 (HER2) expression

ERBB2, a receptor tyrosine kinase, is altered by mutation, amplification and/or overexpression in various cancer types, most frequently in breast, esophagogastric and endometrial cancers. FDA has granted approval to several anti-ERBB2 regimens, either as single or combination therapy for various cancer types. In addition, recently FDA granted accelerated approval to fam-trastuzumab deruxtecan-nxki, for adult patients with unresectable or metastatic HER2-positive (IHC 3+) solid tumors who have received prior systemic treatment and have no satisfactory alternative treatment options.





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Table S3. Biomarkers associated with treatment response (LoE)				
Cancer Type	3+ IHC	2+ IHC & ≥2 FISH	ERBB2 amplification by NGS	IHC 1+ or IHC 2+/ISH -ve

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Breast Cancer	<u>Trastuzumab Deruxtecan</u> (1A.1) <u>Trastuzumab</u> (1A.1) <u>Ado-Trastuzumab Emtansine</u> (1A.1) <u>Lapatinib + Capecitabine</u> (1A.1) <u>Lapatinib + Letrozole</u> (1A.1) <u>Margetuximab</u> + Chemotherapy (1A.1) <u>Neratinib</u> (1A.1) <u>Neratinib + Capecitabine</u> (1A.1) <u>Trastuzumab + Tucatinib + Capecitabine</u> (1A.1) <u>Trastuzumab</u> + Chemotherapy (1A.1) <u>Trastuzumab + Pertuzumab</u> + Chemotherapy (1A.1)	<u>Trastuzumab Deruxtecan</u> (1A.1) <u>Ado-Trastuzumab Emtansine</u> (1A.1) <u>Lapatinib + Capecitabine</u> (1A.1) <u>Lapatinib + Letrozole</u> (1A.1) <u>Margetuximab</u> + Chemotherapy (1A.1) <u>Neratinib</u> (1A.1) <u>Neratinib + Capecitabine</u> (1A.1) <u>Trastuzumab + Tucatinib + Capecitabine</u> (1A.1) <u>Trastuzumab</u> + Chemotherapy (1A.1) <u>Trastuzumab + Pertuzumab</u> + Chemotherapy (1A.1) <u>Trastuzumab</u> (2C.1)	<u>Trastuzumab Deruxtecan</u> (2C.1) <u>Trastuzumab</u> (2C.1) <u>Ado-Trastuzumab Emtansine</u> (2C.1) <u>Lapatinib + Capecitabine</u> (2C.1) <u>Lapatinib + Letrozole</u> (2C.1) <u>Margetuximab</u> + Chemotherapy (2C.1) <u>Neratinib</u> (2C.1) <u>Neratinib + Capecitabine</u> (2C.1) <u>Trastuzumab + Tucatinib + Capecitabine</u> (2C.1) <u>Trastuzumab</u> + Chemotherapy (2C.1) <u>Trastuzumab + Pertuzumab</u> + Chemotherapy (2C.1)	<u>Trastuzumab Deruxtecan</u> (1A.1)
Colorectal Cancer	<u>Trastuzumab Deruxtecan</u> (1A.1) <u>Tucatinib + Trastuzumab</u> (1A.1) <u>Lapatinib + Trastuzumab</u> (1A.2) <u>Trastuzumab + Pertuzumab</u> (1A.2)	<u>Tucatinib + Trastuzumab</u> (1A.1) <u>Lapatinib + Trastuzumab</u> (1A.2) <u>Trastuzumab + Pertuzumab</u> (1A.2) <u>Trastuzumab Deruxtecan</u> (2C.1)	<u>Tucatinib + Trastuzumab</u> (1A.1) (RAS/BRAF wild type) <u>Trastuzumab Deruxtecan</u> (2C.1) <u>Lapatinib + Trastuzumab</u> (2C.1) (RAS/BRAF wild type) <u>Trastuzumab + Pertuzumab</u> (2C.1) (RAS/BRAF wild type)	N/A
Gastric/GEJ	<u>Trastuzumab Deruxtecan</u> (1A.1) <u>Trastuzumab</u> + Chemotherapy (1A.1) <u>Pembrolizumab + Trastuzumab</u> + Chemotherapy (1A.1) (PD-L1 with CPS>1% required)	<u>Pembrolizumab + Trastuzumab</u> + Chemotherapy (1A.1) (PD-L1 with CPS>1% required) <u>Trastuzumab</u> + Chemotherapy (1A.1) <u>Trastuzumab Deruxtecan</u> (1A.1)	<u>Pembrolizumab + Trastuzumab</u> + Chemotherapy (2C.1) (PD-L1 with CPS>1% required) <u>Trastuzumab</u> + Chemotherapy (2C.1) <u>Trastuzumab Deruxtecan</u> (2C.1)	N/A
Biliary Tract	<u>Trastuzumab Deruxtecan</u> (1A.1) <u>Zanidatamab-hrii</u> (1A.1) <u>Trastuzumab + Pertuzumab</u> (1A.2) <u>Tucatinib + Trastuzumab</u> (1A.2)	<u>Trastuzumab Deruxtecan</u> (2C.1) <u>Zanidatamab-hrii</u> (2C.1) <u>Trastuzumab + Pertuzumab</u> (1A.2) <u>Tucatinib + Trastuzumab</u> (1A.2)	<u>Trastuzumab Deruxtecan</u> (2C.1) <u>Zanidatamab-hrii</u> (2C.1) <u>Trastuzumab + Pertuzumab</u> (2C.1) <u>Tucatinib + Trastuzumab</u> (2C.1)	N/A
Uterine Serous Carcinoma/ Papillary Serous	<u>Trastuzumab Deruxtecan</u> (1A.1) <u>Trastuzumab + Carboplatin-Taxol Regimen</u> (1A.2)	<u>Trastuzumab Deruxtecan</u> (2C.1) <u>Trastuzumab + Carboplatin-Taxol Regimen</u> (2C.1)	<u>Trastuzumab Deruxtecan</u> (2C.1) <u>Trastuzumab + Carboplatin-Taxol Regimen</u> (2C.1)	N/A
Lung Cancer	<u>Trastuzumab Deruxtecan</u> (1A.1)	<u>Trastuzumab Deruxtecan</u> (2C.1)	<u>Trastuzumab Deruxtecan</u> (2C.1)	N/A
All tumors	<u>Trastuzumab Deruxtecan</u> (1A.1)	<u>Trastuzumab Deruxtecan</u> (2C.1)	<u>Trastuzumab Deruxtecan</u> (2C.1)	N/A



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12.c. Methodology

DNA was extracted from the sample under investigation using the MagMax Total Nucleic Acid Isolation Kit (ThermoFisher). A capture based targeted next generation sequencing (NGS) analysis was performed, using the Oncology Multi-Gene Variant Assay (GenePlus) which is a qualitative in vitro diagnostic test that detects variants in 1021 tumor-related genes and gene rearrangements / fusions in 38 genes. Sequencing was carried out on an MGI sequencing platform (DNBSEQ-G400). The analysis includes the entire exon regions of 312 genes, introns/promoters/fusion breakpoint regions of 38 genes and partial coding exons of 709 genes. The test also reports 30+ immune response biomarkers, including Tumor Mutational Burden (TMB) score and Microsatellite Instability (MSI) status.

Sequencing data are analyzed through bioinformatics pipeline for variant calling and interpretation using the Gene+Box data analysis and management system.

Sensitivity: Positive reference standards are tested with the assay, all corresponding mutation sites can be accurately detected, and the positive percent agreement (PPA) for all variants (SNVs, Indels, fusions and CNVs) assessed was 100%. **Specificity:** Negative reference standards are tested with the assay, and the negative percent agreement (NPA) of SNVs, Indels, fusions and CNVs was 100%.

Limit of Detection (LoD): The limit of detection (LoD) of this assay is listed in the table below. The LoD is based on as low as 50 ng of gDNA input for library preparation. The assay can also be used to test the microsatellite instability (MSI) with a tumor cell content as low as 10%.

Variant Type	Limit of Detection
Single nucleotide variations (SNV)	Hotspot: VAF $\geq 2\%$; Non-hotspot: VAF $\geq 5\%$
Insertions/deletions (Indel)	Hotspot: VAF $\geq 2\%$; Non-hotspot: VAF $\geq 5\%$
Fusion (or rearrangement)	VAF $\geq 2\%$

PD-L1 expression by IHC

PD-L1 protein expression is determined by using Combined Positive Score (CPS), which is the number of positive cells (tumor, lymphocytes, and macrophages) showing partial or complete membrane staining (or cytoplasmic for immune cells) at any intensity, divided by the total number of viable tumor cells, multiplied by 100.

DAKO 22C3 (CE IVD) by IHC is a qualitative immunohistochemical assay using Monoclonal Mouse Anti-PD-L1, 22C3 intended for use in the detection of PD-L1 protein in formalin-fixed, paraffin-embedded (FFPE) tissue. The specimen submitted for testing should contain at least 100 viable tumor cells to be considered adequate for evaluation. For cut-off values please refer to Table S2.

Claudin 18.2 expression by IHC

Claudin 18.2 staining is performed in a VENTANA BenchMark Series automated staining instrument using the Claudin 18.2 ZR451 clone (Zeta corporation), on formalin-fixed, paraffin-embedded (FFPE) tissue. In gastric/GEJ adenocarcinomas, immunohistochemical positivity for Claudin 18.2 at a percentage $\geq 75\%$, according to recent studies, has been proposed to be considered as positive expression.



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FOLR1 (FRa) expression by IHC

FOLR1 (FRa) staining is performed in a VENTANA BenchMark Series automated staining instrument using the FRa BN3.2 clone (Leica/Novocastra), on formalin-fixed, paraffin-embedded (FFPE) tissue. FOLR1 expression clinical cut-off is $\geq 75\%$ viable tumor cells (TC) with membrane staining at moderate (2+) and/or strong (3+) intensity levels.

ERBB2 (HER2) expression by IHC

ERBB2 staining is performed in a VENTANA BenchMark Series automated staining instrument using the ERBB2 clone 4B5, on formalin-fixed, paraffin-embedded (FFPE) tissue. The IHC test gives a score of 0 to 3+ that measures the amount of HER2 receptor protein on the surface of cancer cells. Scoring interpretation is as follows:

HER2 IHC positive (score 3+)

HER2 IHC equivocal (score 2+)

HER2 IHC negative (score 0 or 1+)

Scoring is based on the ASCO-CAP HER2 testing guidelines (PMID: 27841667, 37303228).

For mCRC the HERACLES criteria are also used (PMID: 26449765).

Disclaimer

1. This test is mainly used to assist clinical decision-making and the result does not represent clinical decision.
2. The test should be interpreted by combining the actual patient context. The medication information provided only on the basis of genetic test results, and the actual medication should follow the physician's instructions.
3. The clinical trials only present partial relevant clinical recruitment trials. For more comprehensive and updated information, please refer to the website: <https://clinicaltrials.gov/>.
4. As evidence on variants and drugs evolves, previous classifications may later be modified. The interpretation of a variant is based on current available evidence.
5. Sequence variants were reported using Human Genome Variation Society (HGVS) nomenclature. Classification and interpretation of variants follows guidelines of American College of Medical Genetics and Genomics (ACMG), Association of Molecular Pathology (AMP), American Society of Clinical Oncology (ASCO) and College of American Pathologists (CAP).
6. Translocations detected at the DNA level are confirmed by an RNA-based NGS method.
7. Database and references used: Reference genome (GRCh37), annotation using A Locus Reference Genomic (LRG), database referencing 1000G (phaseIII-ucsc), EXAC (0.3.1), dbSNP (147), PolyPhen2/SIFT (ensdb v73), PhyloP (2013-12-06), Clinvar (2018-8) and Cosmic(V80).

Limitations

1. Limited tissue detection may not represent the whole DNA variations of lesions because of tumor heterogeneity.
2. Scientific data show that not all patients carry genomic variations that are associated with targeted drug, therefore not all subjects can be matched with targeted therapies or clear resistance mechanism.
3. Genetic variation beyond the detection range of this test or some non-gene mutation related factors such as drug interactions may affect the clinical effects of drugs.





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4. The detection could not distinguish between somatic mutations and germline mutations effectively without control sample analysis.
5. Fraction of base quality \geq Q30: The proportion of base quality in sequencing data that reaches or exceeds Q30, indicating that the probability of base recognition accuracy rate exceeds 99.9%.
6. Every molecular test has an internal 0.5-1% chance of failure. This is due to rare molecular events and factors related to the preparation and analysis of the samples.



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Quality Control Index		Result	Criterion
Sequencing Quality Assessment	Average effective sequencing depth ¹	1012	≥ 500
	Fraction of target covered with ≥ 50x ²	100%	≥99%
	Fraction of base quality ≥ Q30 ³	94%	≥80%
Tumor cell content ⁴		60%	>20%
Overall Assessment ⁵		PASS	

Note :

1. Average effective sequencing depth: Average sequencing depth on target without duplicated reads.
2. Fraction of target covered with ≥ 50x: The proportion of bases that sequencing depth reach or above 50x on target, this index reflecting the coverage uniformity of sequencing.
3. Fraction of base quality ≥ Q30: The proportion of base quality in sequencing data that reach or above Q30, that is the probability of base recognition accuracy rate exceeds 99.9%.
4. Overall A tumor cell content percentage of ≥ 20% is recommended for the efficient detection of somatic alterations in the sample analyzed.
5. Overall Assessment: The quality control overall assessment results are divided into two levels: "PASS" and "RISK". When the overall quality assessment result is "RISK", 94-96% of coverage was achieved in the genes analysed, hence there is a small range where clinical actionable variations could be undetected.



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312 genes including all exon regions and available for detecting SNV / Indel / CNV

ABL1	ACVR1B	AKT1	AKT2	AKT3	ALK	APC	AR	ARAF	ARID1A
ARID1B	ARID2	ASXL1	ATM	ATR	ATRX	AURKA	AURKB	AXIN1	AXIN2
AXL	B2M	BAP1	BARD1	BCL2	BCL2L1	BCOR	BLM	BMPR1A	BRAF
BRCA1	BRCA2	BRD4	BRIP1	BTK	CARD11	CASP8	CBFB	CBL	CCND1
CCND2	CCND3	CCNE1	CD274	CDC73	CDH1	CDK12	CDK4	CDK6	CDK8
CDKN1A	CDKN1B	CDKN2A	CDKN2B	CDKN2C	CEBPA	CHEK1	CHEK2	CIC	CREBBP
CRKL	CSF1R	CTCF	CTNNA1	CTNNB1	CUL3	CYLD	DAXX	DDR1	DDR2
DICER1	DNMT3A	DOT1L	EGFR	EIF1AX	EMSY	EP300	EPAS1	EPCAM	EPHA2
EPHA3	EPHA5	EPHB1	EPHB6	ERBB2	ERBB3	ERBB4	ERCC1	ERCC3	ERCC4
ERCC5	ERG	ERRF1	ESR1	EXT1	EXT2	EZH2	FAM123B	FAM175A	FANCA
FANCC	FANCD2	FANCE	FANCF	FANCG	FANCL	FANCM	FAS	FAT1	FAT2
FBXW7	FGF19	FGF3	FGF4	FGFR1	FGFR2	FGFR3	FGFR4	FH	FLCN
FLT1	FLT3	FLT4	FOXA1	FOXL2	FOXP1	FUBP1	GALNT12	GATA3	GNA11
GNAQ	GNAS	GRIN2A	GRM3	HDAC1	HGF	HNF1A	HOXB13	HRAS	IDH1
IDH2	IFNG	IFNGR1	IGF1R	IKBKE	IKZF1	IL7R	INPP4B	IRF2	IRS2
JAK1	JAK2	JAK3	JUN	KDM5A	KDM5C	KDM6A	KDR	KEAP1	KIT
KRAS	LRP1B	MAF	MAP2K1	MAP2K2	MAP2K4	MAP3K1	MAPK1	MAX	MCL1
MDM2	MDM4	MED12	MEF2B	MEN1	MET	MITF	MLH1	MLH3	MLL
MLL2	MLL3	MPL	MRE11A	MS4A1	MSH2	MSH3	MSH6	MST1R	MTOR
MUTYH	MYC	MYCL1	MYCN	MYD88	NBN	NCOR1	NF1	NF2	NFE2L2
NFKB1A	NKX2-1	NOTCH1	NOTCH2	NOTCH3	NPM1	NRAS	NSD1	NTHL1	NTRK1
NTRK2	NTRK3	PALB2	PARK2	PARP1	PAX5	PBRM1	PCK1	PDCD1	PDCD1LG2
PDGFRA	PDGFRB	PKD1	PIK3CA	PIK3CB	PIK3CG	PIK3R1	PIK3R2	PMS1	PMS2
POLD1	POLE	POT1	PPP2R1A	PRDM1	PRKAR1A	PTCH1	PTCH2	PTEN	PTPN11
PTPRD	RAC1	RAD50	RAD51	RAD51B	RAD51C	RAD51D	RAD52	RAD54L	RAF1
RARA	RB1	RBM10	RECQL	RECQL4	RET	RHOA	RICTOR	RINT1	RNF43
ROS1	RPTOR	RUNX1	SDHA	SDHAF2	SDHB	SDHC	SDHD	SERPINB3	SERPINB4
SETD2	SF3B1	SLX4	SMAD2	SMAD3	SMAD4	SMARCA4	SMARCB1	SMO	SOCS1
SOX2	SOX9	SPOP	SRC	STAG2	STAT3	STK11	SUFU	SYK	TBX3
TCF7L2	TERC	TET2	TGFBR2	TMEM127	TMPPRSS2	TNFAIP3	TNFRSF14	TOP1	TOP2A
TP53	TSC1	TSC2	TSHR	U2AF1	VEGFA	VHL	WRN	WT1	XPO1
XRCC2	ZMAT3								



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ALK	BCL2L11	BRAF	BRCA1	BRD4	CD74	EGFR	EML4	ERG	ETV6
EZR	FGFR1	FGFR2	FGFR3	KIF5B	KIT	MAML2	MET	MSH2	MYC
MYCL1	NCOA4	NOTCH2	NTRK1	NTRK2	NTRK3	PDGFRA	RAF1	RET	ROS1
RSPO2	SDC4	SLC34A2	TERT	TFE3	TMPPRSS2	TPM3	PMS2		

709 genes including partial exon regions and available for detecting SNV / Indel

ABCA13	ABCB1	ABCC1	ABCC11	ABCC2	ABCG2	ABL2	ACACA	ACIN1	ACTB
ACTG1	ACTG2	ACVR2A	ACVRL1	ADAM29	ADAMTS5	ADCY1	AFF1	AFF2	AFF3
AHNAK	AKAP9	ALB	AMOT	ANGPT1	ANK3	ANKRD11	ANKRD30A	ANKRD30B	APEX1
APOBEC3B	ARAP3	ARFGEF1	ARFGEF2	ARHGAP29	ARHGAP35	ARID4B	ARID5B	ARNT	ASCL4
ASH1L	ASMTL	ASPM	ASTN1	ASXL2	ATIC	ATP11B	ATP12A	ATP1A1	ATP2B3
BAZ2B	BBC3	BBS9	BCAS1	BCL10	BCL11A	BCL11B	BCL2A1	BCL2L11	BCL3
BCL6	BCL9	BCORL1	BCR	BIRC3	BMPR2	BNC2	BPTF	BRD2	BRD3
BRSK1	BRWD1	BTLA	BUB1	C15orf23	C15orf55	C1QA	C1S	C3orf70	C7orf53
C8orf34	CACNA1E	CADM2	CALR	CAMTA1	CASP1	CASQ2	CBLB	CBR1	CBR3
CCDC168	CCNA1	CCNB3	CCT3	CCT5	CCT6B	CD22	CD33	CD5L	CD74
CDA	CDH11	CDH18	CDH23	CDK13	CHD1	CHD1L	CHD4	CHD6	CHD8
CHD9	CHFR	CHI3L1	CHN1	CIITA	CLDN18	CLP1	CLSPN	CLTC	CNOT3
CNOT4	CNTN1	CNTN5	CNTNAP1	CNTNAP5	COL1A1	COL2A1	COL5A1	COL5A2	COL5A3
COPS2	CPS1	CRIPAK	CRLF2	CRNKL1	CRTC1	CSF1	CSF3R	CSMD1	CSMD3
CSNK1A1	CSNK1G3	CTLA4	CTNNA2	CTNND1	CUX1	CXCR4	CYBA	CYP19A1	CYP1A1
CYP1B1	CYP2A13	CYP2C8	CYP2D6	CYP3A4	CYP3A5	DCC	DDX3X	DDX5	DEK
DHX35	DHX9	DIAPH1	DIS3L2	DLC1	DMD	DNAH6	DNAJB1	DNM2	DNMT1
DNMT3B	DOCK2	DOCK7	DPYD	DRGX	DTX1	DUSP22	DYSF	E2F3	EBF1
ECT2L	EED	EEF1A1	EGFL7	EGR3	EIF2AK3	EIF2C3	EIF3A	EIF4A2	EIF4G3
ELAC2	ELF1	ELF3	ELMO1	ELN	EME2	EMID2	EML4	EPC1	EPHA1
EPHA4	EPHA7	EPHB2	EPHB4	EPOR	EPPK1	EPS15	ERBB2IP	ERCC2	ESR2
ETS1	ETV1	ETV5	ETV6	EWSR1	EZR	F8	FAM131B	FAM135B	FAM157B
FAM46C	FAM5C	FAP	FASLG	FAT3	FAT4	FCGR1A	FCGR2A	FCGR2B	FCGR3A
FCRL4	FGF10	FGF12	FGF14	FGF23	FGF6	FLG	FLI1	FLNC	FMN2
FN1	FNDC4	FOXA2	FOXO1	FOXO3	FOXQ1	FRMPD4	FUS	FXR1	FYN
FZD1	G3BP1	G3BP2	GAB2	GABRA6	GATA1	GATA2	GFRAL	GIGYF1	GKN2
GLB1L3	GLI1	GLI2	GLI3	GMPS	GNA13	GNG2	GPC3	GPR124	GPS2
GPX1	GRB7	GSK3B	GSTM5	GSTP1	GUSB	H3F3A	H3F3B	H3F3C	HCLS1
HCN1	HDAC4	HDAC9	HECW1	HEY1	HIST1H1C	HIST1H1D	HIST1H1E	HIST1H2AC	HIST1H2AG
HIST1H2AL	HIST1H2AM	HIST1H2BC	HIST1H2BD	HIST1H2BJ	HIST1H2BK	HIST1H2BO	HIST1H3B	HIST1H3C	HIST1H3D



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HIST1H3F	HIST1H3G	HIST1H3H	HIST1H3I	HIST1H4I	HIST3H3	HLA-A	HLA-B	HLA-C	HLF
HMCN1	HNF1B	HNRPD	HOXA11	HOXA13	HOXA3	HOXA9	HOXC13	HOXD11	HOXD13
HSD3B1	HSP90AA1	HSP90AB1	HSPA8	HSPD1	HSPH1	ICK	ICOSLG	ID3	IFITM3
IGF1	IGF2	IGF2R	IGLL5	IKZF2	IKZF3	IL10	IL1RAPL1	IL21R	IL6
IL6ST	IMPG1	ING1	INHBA	INPP4A	INPPL1	INSR	IRF4	IRF6	IRS1
ITGB3	ITK	ITSN1	JARID2	KALRN	KAT6A	KAT6B	KCNJ5	KCNQ2	KDM2B
KEL	KIF5B	KLF4	KLHL6	KLK1	KRTAP5-5	L3MBTL1	LAMA2	LATS1	LATS2
LCP1	LEF1	LGALS8	LIFR	LPHN2	LPP	LRP2	LRP4	LRP5	LRP6
LRRRC7	LRRK2	LYN	LZTS1	MACF1	MAD1L1	MAGI2	MAML2	MAML3	MAP3K13
MAPK3	MCC	MCM3	MDC1	MECOM	MEF2C	MGA	MIB1	MIOS	MKL1
MLL4	MLLT3	MMP11	MMP2	MN1	MNDA	MNX1	MSH4	MSN	MSR1
MTHFR	MTRR	MUC5B	MYH11	MYH14	MYH9	MYO3A	MYOD1	NAP1L1	NAV3
NCAM2	NCF2	NCF4	NCK1	NCOA3	NCOA4	NCOR2	NCSTN	NDUFA13	NFATC4
NFE2L3	NKX3-1	NLRC3	NOD1	NOS3	NOTCH4	NQO1	NR1I2	NR2F2	NR4A2
NRG1	NRP2	NRXN1	NTM	NUMA1	NUP107	NUP210	NUP93	NUP98	OBSCN
OGDH	OMD	OPCML	OR11G2	OR2T4	OR4A15	OR4C6	OR5L2	OR6F1	P2RY8
P4HB	PABPC1	PABPC3	PAG1	PAK1	PAK3	PASK	PAX3	PAX7	PC
PCDH18	PCSK6	PCSK7	PDCD11	PDE4DIP	PDGFB	PDILT	PER1	PGR	PHF1
PHF6	PIK3C2A	PIK3C2B	PIK3C2G	PIK3C3	PIM1	PKD1L2	PKHD1	PLAG1	PLCB1
PLCG1	PLCG2	PLK1	PLXNA1	PLXNB2	PNRC1	POLQ	POM121	POM121L12	POU2AF1
PPM1D	PPP1R17	PPP6C	PRDM16	PREX2	PRF1	PRKAA1	PRKCB	PRKCI	PRKDC
PRRX1	PRX	PSG2	PSIP1	PSMB1	PSMB5	PTGS1	PTGS2	PTPN13	PTPN2
PTPRB	PTPRK	PTPRO	PTPRS	PTPRT	PTPRU	RAB35	RAC2	RAD21	RAD54B
RANBP2	RASA1	RASGRP1	RBL1	REL	RELN	RFC1	RGS3	RHEB	RHOH
RHOT1	RIT1	RNASEL	ROBO1	ROBO2	ROBO3	ROCK1	RPGR	RPS6KB1	RPS6KB2
RSPO2	RSPO3	RUNX1T1	RUNX2	RXRA	RYR1	RYR2	SBDS	SCUBE2	SDC4
SEC31A	SEMA3A	SEMA3E	SEMA6A	SERPINA7	SETBP1	SETDB1	SF1	SF3A1	SFPQ
SGCZ	SGK1	SH2B3	SH2D1A	SH3PXD2A	SHH	SI	SIN3A	SLC16A1	SLC1A2
SLC22A16	SLC22A18	SLC22A2	SLC22A3	SLC34A2	SLCO1B3	SLIT1	SLIT2	SMARCD1	SMARCE1
SMC1A	SMC1B	SNCAIP	SNTG1	SNX29	SOD2	SOS1	SOX10	SOX17	SPEN
SPRR3	SPSB4	SPTA1	SRD5A2	SRGAP1	SRGAP3	SRSF2	SRSF7	STAG1	STAT1
SUCLG1	SUCLG2	SULT1A1	SUZ12	SVEP1	SYNCRIP	SYNE1	TAF1	TAF15	TAF1L
TAL1	TBL1XR1	TBX15	TBX22	TCEB1	TCF12	TCF3	TCF4	TCL1A	TEC
TENM3	TERT	TET1	TFDP1	TFDP2	TFE3	TGFBR1	THBS2	TJP1	TLE1
TLL2	TLR4	TLX3	TMEM132D	TNFSF11	TNN	TP53BP1	TP63	TP73	TPM3
TPR	TRAF2	TRAF7	TRIM24	TRIM58	TRIO	TRPC5	TRRAP	TSHZ2	TSHZ3
TTF1	TUBA3C	TUBB3	TUSC3	TXNIP	TYMS	TYR	UBE2D2	UBR5	UGT1A1





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UMPS	UPF3B	USH2A	USP6	USP8	VEZF1	VIM	VTCN1	WASF3	WDR90
WDTC1	WHSC1	WHSC1L1	WIPF1	WNK1	WNT5A	WSCD2	WVOX	WWP1	WWP2
XIAP	XPC	XRCC1	XRCC3	YAP1	YY1AP1	ZBTB16	ZC3H11A	ZFH3	ZFP36L1
ZFP36L2	ZFPM2	ZIC3	ZNF217	ZNF384	ZNF521	ZNF638	ZNF750	ZNF804B	
36 HRR genes analyzed									
ATM	ATR	ATRX	BAP1	BARD1	BLM	BRCA1	BRCA2	BRIP1	CDK12
CHEK1	CHEK2	C11orf30	ERCC1	FAM175A	FANCA	FANCC	FANCD2	FANCE	FANCF
FANCG	FANCL	FANCM	MRE11	NBN	PALB2	RAD50	RAD51	RAD51B	RAD51C
RAD51D	RAD52	RAD54L	RECQL	RECQL4	WRN				



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12.f. Levels of Evidence for Genomic Biomarkers

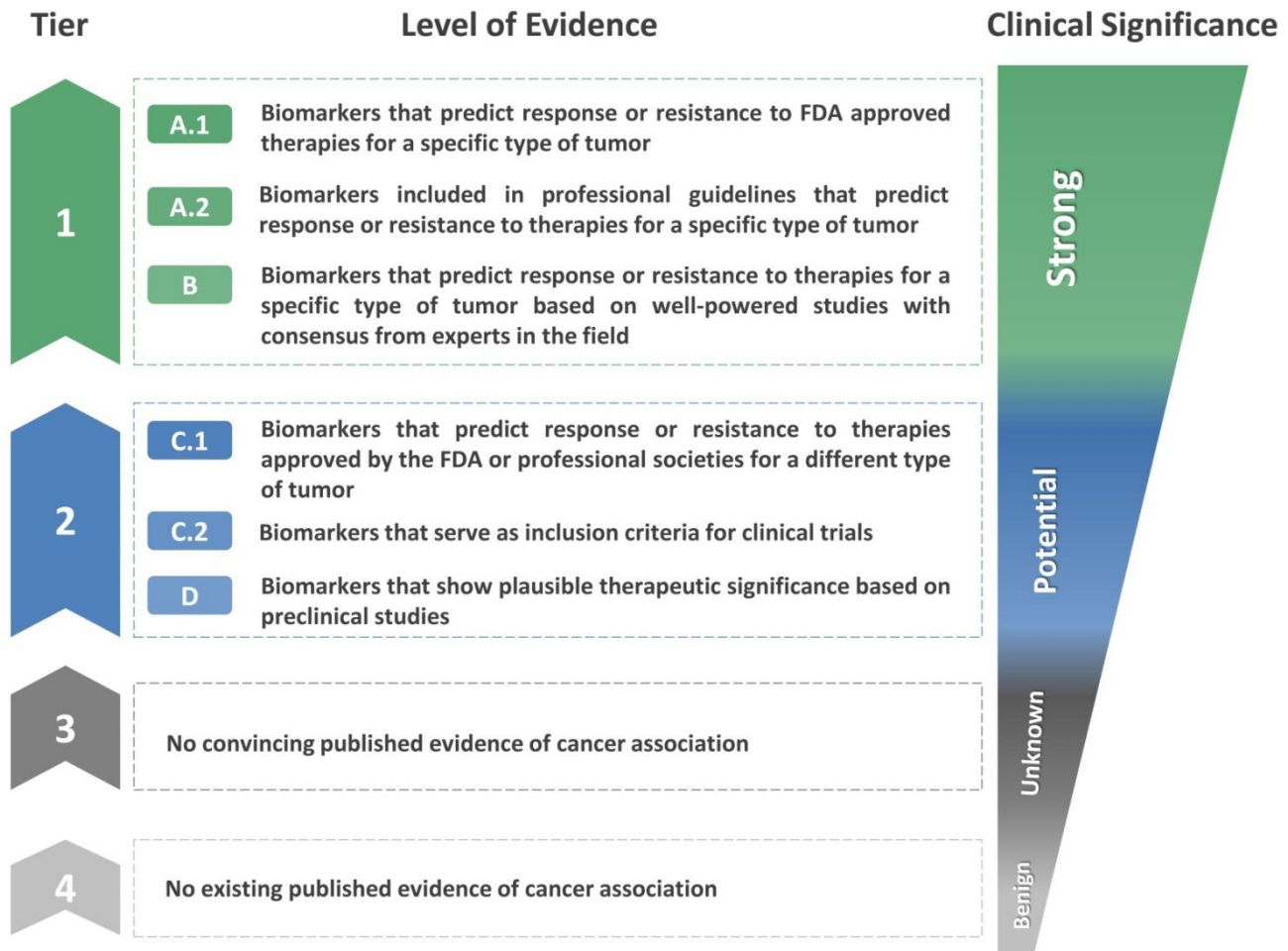


Figure 1. Joint consensus recommendation of AMP, ACMG, ASCO and CAP for reporting genetic variants in cancer. [1-2]

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