

BMB Reports – Manuscript Submission

Manuscript Draft

Manuscript Number: BMB-21-045

Title: Paired analysis of tumor mutation burden calculated by targeted deep sequencing panel and whole exome sequencing in Non-Small Cell Lung Cancer

Article Type: Article

Keywords: targeted exome sequencing; tumor mutational burden; immunotherapy; non-small cell lung cancer; next generation sequencing

Corresponding Author: Myung-Ju Ahn

Authors: Sehhoon Park^{1,#}, Chung Lee^{2,#}, Bo Mi Ku³, Minjae Kim², Woong-Yang Park^{2,4}, Nayoung K.D. Kim², Myung-Ju Ahn^{1,*}

Institution: ¹Division of Hematology-Oncology, Department of Medicine, Samsung Medical Center, Sungkyunkwan University of School of Medicine, Seoul 06351, Republic of Korea,

²Geninus Inc., Seoul 05836, Republic of Korea,

³Research Institute for Future Medicine, Samsung Medical Center, Sungkyunkwan University of School of Medicine, Seoul 06351, Republic of Korea,

⁴Samsung Genome Institute, Samsung Medical Center, Seoul 06351, Republic of Korea,

ORIGINAL ARTICLE**Paired analysis of tumor mutation burden calculated by targeted deep sequencing panel and whole exome sequencing in Non-Small Cell Lung Cancer**

Sehhoon Park^{1,#}, Chung Lee^{2,#}, Bo Mi Ku¹, Minjae Kim², Woong-Yang Park^{2,3}, Nayoung K. D. Kim^{2*}, Myung-Ju Ahn^{1*}

Affiliation: ¹Division of Hematology-Oncology, Department of Medicine, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Republic of Korea, ²Geninus Inc. Seoul, Republic of Korea, Samsung Genome Institute, Samsung Medical Center, Seoul, Republic of Korea

These authors contributed equally

Co-CORRESPONDENCE TO:

Nayoung K.D. Kim, PhD

Jeongeui-Ro 70, Songpa-Gu, Seoul, Republic of Korea

Tel: +82-10-4716-4082

FAX: +82-2-6949-6580

Email: Nayoung.kim@kr-geninus.com

and

Myung-Ju Ahn, MD, PhD

Division of Hematology-Oncology, Department of Medicine, Samsung Medical Center, Sungkyunkwan University School of Medicine

81 Irwon-ro, Gangnam-gu, Seoul 06351, Republic of Korea

Tel: 82-2-3410-3438, fax: 82-2-3410-1754

Email: silkahn@skku.edu or silk.ahn@samsung.com

Funding

This work was supported Bristol Myers Squibb.

Conflicts of Interest

C. Lee is a senior researcher at Geninus. NKD. Kim is a director at Geninus. WY. Park is a chief executive officer at Geninus Inc. No potential conflicts of interest were disclosed by the other authors.

ABSTRACT

Background: Owing to rapid advancements in NGS (next generation sequencing), genomic alteration is now considered an essential predictive biomarkers that impact the treatment decision in many cases of cancer. Among the various predictive biomarkers, tumor mutation burden (TMB) was identified by NGS and was considered to be useful in predicting a clinical response in cancer cases treated by immunotherapy. In this study, we directly compared the lab-developed-test (LDT) results by target sequencing panel, K-MASTER panel v3.0 and whole-exome sequencing (WES) to evaluate the concordance of TMB.

Methods: As an initial step, the reference materials ($n = 3$) with known TMB status were used as an exploratory test. To validate and evaluate TMB, we used one hundred samples that were acquired from surgically resected tissues of non-small cell lung cancer (NSCLC) patients. The TMB of each sample was tested by using both LDT and WES methods, which extracted the DNA from samples at the same time. In addition, we evaluated the impact of capture region, which might lead to different values of TMB; the evaluation of capture region was based on the size of NGS and target sequencing panels.

Results: In this pilot study, TMB was evaluated by LDT and WES by using duplicated reference samples; the results of TMB showed high concordance rate ($R^2 = 0.887$). This was also reflected in clinical samples ($n = 100$), which showed R^2 of 0.71. The difference between the coding sequence ratio (3.49%) and the ratio of mutations (4.8%) indicated that the LDT panel identified a relatively higher number of mutations.

Conclusions: It was feasible to calculate TMB with LDT panel, which can be useful in clinical practice. Furthermore, a customized approach must be developed for calculating TMB, which differs according to cancer types and specific clinical settings.

KEYWORDS: targeted exome sequencing, tumor mutation burden, immunotherapy, next generation sequencing

INTRODUCTION

Next-generation sequencing (NGS) technique has undergone several advancements in recent times. In clinical practice, comprehensive genome profiling is now done extensively with NGS technique because it has a short turnaround time and an acceptable cost of operation.(1, 2) In particular, cancer patients are being extensively screened with NGS technique. The results are used to devise actionable genomic alteration, which is now an essential step in deciding the preferred mode of treatment.(3) As the number of target genes increases, an optimized panel of contents and size have been constructed by targeting genes related to specific cancer types. This has been widely the conventional mode of NGS technique for the past several years.(4, 5)

The initial treatment decision is usually made after performing NGS technique, which accurately detects following mutations: single nucleotide variation (SNV), insertion and deletions (INDEL), copy number variation (CNV), and fusion. Recently, an immune checkpoint inhibitor (ICI) that targets PD-1 and PD-L1 axis has become the standard mode of treatment for patients with different types of cancer(6, 7) including non-small cell lung cancer (NSCLC). Therefore, several efforts are being made to develop a predictive biomarker that measures genomic alteration, which is a daunting task in genomics. Presently, tumor mutation burden (TMB) is considered as a candidate biomarker because several studies have reported that tumors with a high mutation burden are more likely to respond to ICI treatment.(8-10) Interestingly, this finding has also been observed in patients with same types of cancer. In many retrospective studies of NSCLC patients, it has been reported that clinical outcomes of ICI treatment were better in patients with high mutation burden, which was determined by whole exome sequencing.(11) Moreover, this finding was confirmed by evaluating TMB with target sequencing panel.(12) Therefore, target sequencing panel can be effectively used in cancer treatment: it is not only a companion diagnostic test that detects oncogenic drivers for targeted therapy, but it is also used to determine microsatellite instability (MSI) and TMB for cancer immunotherapy. (13, 14)

The TMB value indicates the total number of mutations in the analyzed genomic region, and it is reported that there are variations for each type of tumor.(15) While assessing the value of TMB, oncologists usually count somatic mutations in the entire exonic region: all the mutations are counted by the whole exome sequencing (WES) method, regardless of whether they are synonymous or non-synonymous in nature.(11, 16) In contrast, oncologists encounter several challenges while calculating TMB by target sequencing panel. Firstly, there are limited number of genes in the target sequencing panel, so representative value becomes an issue for a small sized panel.

Therefore, scientists have suggested using a panel whose size is larger than at least 1 megabase pair (Mbp).(17, 18) Secondly, while calculating TMB, scientists use specific methods for evaluating mutation scoring and for defining cutoff levels. These parameters indicate deleterious and clinically significant variants, which are not standardized till date.(19, 20) These uncertain parameters have generated a controversy in defining high versus low TMBs. Moreover, certain studies show that the difference between carcinomas is obvious, and no cutoff value can be used universally.(21) Last but not the least, very few studies have illustrated the prospective clinical benefits of using TMB, which is calculated by target sequencing panel.

Since target sequencing test is a laboratory developed test (LDT) and used in clinical practice, it is necessary to validate its results with gold standard methods in advance. Based on the results, scientists can decide its clinical implementation. CancerSCAN® (Twist Biosciences, CA, USA), which is a next generation cancer gene panel, is considered as a pipeline that targets cancer related genes; its clinical efficacy is found to be high in target therapy, which is based on genomic alteration and is used to treat many types of cancer.(22) More than 15,000 patients have undergone genome profiling through CancerSCAN® panel till date, and it has been used for analyzing various clinical specimens.(23-25) Recently, we have developed TMB calculation algorithms by using CancerSCAN®. In this study, we analyzed the efficacy with which CancerSCAN (pTMB) could detect TMB in NSCLC samples, and we compared it with TMB calculated by WES method (wTMB).

RESULTS

Exploratory analysis using reference materials

As an initial step, we compared the outcomes of pTMB and wTMB by using reference samples, whose TMB value ($n = 3$) was already known. The average sequencing depth was above 750 x, and the duplication rate was also stable at an average value of 16.3% (Supplement table 2). When the first set was sequenced and analyzed in CancerSCAN, the absolute number of variants identified from each sample were as follows: 8, 18, and 23. When this set was divided by the total target coding region 1.1 Mb, the TMB scores were found to be 6.9, 15.5, and 19.8 (Table 2). Using three identical samples, WES method identified the absolute number of variants as 280, 560, and 721, respectively in the three samples, and it processed wTMB as 8.43, 16.86, and 21.7, respectively, after being divided by the total target region of 33 Mb. The processed pTMB from the duplicated second set was 8.6, 19.8, and 22.4. Similarly, the processed wTMB from the duplicated second set was 8.1, 16.0, and 21.7, respectively. By comparing the data from both the initial and the duplicated dataset, we found that the concordance rate between pTMB and wTMB was $R^2 = 0.887$ (Figure 1).

The concordance of TMR in clinical samples

The clinical samples were obtained by surgically resecting NSCLC ($n=100$) tissues; these samples were sequenced with CancerSCAN at a mean depth of 1228.6 x (Supplementary table 3). In all the specimens, the tumor purity value was found to be more than 30% in pathological laboratory. Moreover, when the tumor purity value was calculated using the actually produced sequencing data, it was found to be very high at an average value of more than 80%. On an average, the on-target sequencing coverage was found to be 68.9%. The WES method was conducted on the same specimens and matched with normal samples; the average coverage was 209.4 x from tumor sample and 68.0 x from normal sample. The pre-defined cutoff value for high TMB were as follows: 10 mut/Mb for wTMB and 16 mut/Mb for pTMB. Based on these values, clinical samples were categorized as either high TMB (TMB-h) or low TMB (TMB-l). The raw data was presented on the scatter plot, and it showed a positive correlation between samples ($R^2 = 0.71$, Figure 2). In terms of categorization, most of the samples (92.0%) showed no discrepancy between pTMB and wTMB. However, 8 samples

(8.0%) were found to be as TMB-h by wTMB method and as TMB-l by pTMB method. Among the concordant samples ($n = 92$), TMB-h ratio was found to be 8.7% (8 out of 92 samples). We reviewed the 8 cases, which were underestimated by pTMB. In most cases, a relatively higher number of mutations were detected in the genes that were not included in CancerSCAN method (pTMB). As shown in Figure 3B, representative genes were the ones marked in orange (described in detail later).

An additional analysis was conducted to determine the tumor purity pathologically, the histology subtypes, and the differentiation of tumor tissues. The concordance between pTMB and wTMB was accurately found to be more than 95.0%. The high concordance was observed regardless of the surgical stage (supplementary table 4).

A comparison of common target regions covered by both WES and CancerSCAN

By directly comparing the values of pTMB and wTMB, we found that the number of wTMB were slightly lower than that of pTMB (Figure 2, $R^2 = 0.71$). To evaluate the difference between pTMB and wTMB, we compared the ratio of the coding region by panel sequencing and whole exome sequencing (3.5%). In addition, we also calculated the ratio of variants identified by target sequencing and WES in the entire population (4.8%) (Figure 3A). Based on this result, we inferred that the mutation detected with target sequencing was found to be relatively more than that detected with WES.

As a further step, we compared the number of mutations of each gene by using WES and target sequencing panel (Figure 3B). We ranked the top 50 genes based on the number of mutations identified by WES. Although most of the genes included here were not related to cancer, the list included five genes that were also identified by target sequencing panel. Last but not the least, we determined the variant allele frequency (VAF) and the number of mutations found by both target sequencing panel and WES, which was based on the variant type (Figure 3C). The patterns of mutation were generally found to be similar in both the platforms, which showed the highest frequency of missense mutation.

Finally, we investigated the expected CancerSCAN TMB value, which was determined by comparing WES results with CancerSCAN panel content (Supplementary table 5). The tumor samples sequenced by WES were classified as TMB-high or TMB-low, and 10 mut/Mb was used as the cutoff value. By using the same method for comparing WES results with that of CancerSCAN panel content, the expected values of TMB-high and TMB-low classifications were found to be similar to the experimentally determined values.

DISCUSSION

Several evidences indicate that TMB is a predictive biomarker related to ICI in several types of cancer.(3) Moreover, TMB is now considered to be a component of the treatment guidelines related to ICI in some types of solid cancer. However, there is no consensus on how to measure TMB.

Compared to WES, which is considered as the gold standard method for TMB calculation, target sequencing offers more benefits in terms of shorter turnaround time and cost-effectiveness. However, there are various technical differences among the two target sequencing platforms, including the number of genes, the coverage of sequence, the variant calling algorithms, etc; therefore, it is difficult to compare the efficacy of the two methods. In particular, each component directly impacts the number of variants identified from the sample, which consequently causes differences in the TMB values of the two methods. Last but not the least, different algorithms may be used to filter out the irrelevant variants associated with TMB calculation; these algorithms differ according to the characteristics of each target sequencing panel. Therefore, an extensive validation of LDT target sequencing panel must be conducted with the standard method. Hence, WES should be performed before clinically selecting patients, who are most likely to benefit from ICI.

In this study, we evaluated the efficacy of LDT target sequencing panel and CancerSCAN by detecting a sample with high mutation burden and comparing it with the WES results of surgically resected NSCLC (n = 100) samples. The CancerSCAN technique was applied at a clinical level to determine the genomic alterations of target therapy.(26-33) In addition, CancerSCAN results showed that a definite number of mutations could be identified and processed as TMB for references. The CancerSCAN's panel target was 1.1 Mb, and it identified the variant according to an annotation database, which presented ethnicity specific mutation without matching normal samples. Since this panel was initially designed for cancer patients, most of the genes included in the panel were cancer-related genes, such as the oncogene and tumor suppressor genes. In addition, the panel was also developed to identify the variants with low VAF. This implies that more mutation, which was missed with a coverage of 100 x to 200 x, was captured in this experiment. All these factors are considered as key elements, which consequently caused a discrepancy between pTMB and wTMB values, thereby compelling us to make a direct comparison with the standard method.

In this study, we observed a high correlation between pTMB and wTMB values ($R^2 = 0.71$). For the high TMB values detected by panel sequencing and WES, the

concordance was found to be 93.0% for the samples. For the analysis, we made several stepwise approaches and the assumption was made in advance. Firstly, several exploratory analyses were made to evaluate the potential bias. We tested the technical issue by using known TMB values of reference samples in advance. Secondly, we used higher cut-off values for the pTMB. The various cut-off values were proposed from a number of studies, which tested different cancer types with different methods.(15, 20, 34, 35) These findings indicate that it is challenging to define a standardized cut-off value for high TMB because of the unique components among variable individual panels. The same issue was faced during the fine-tuning of CancerSCAN, that is, the TMB based on HLA was adjusted after considering the characteristics of the patient.(20) Hence, we set a relatively high cutoff value of 16 or more mutations per megabase, for the identification of TMB-h patients. Lastly, the variant filtering process was performed in seven steps, which were used for the calculation of TMB.

This study has some limitations. Our samples were acquired from surgically resected tissues, whose clinical response data related to ICI was limited. In addition, the samples used for this study were pre-selected as histologic, and their tumor purity was pathologically found to be more than 30%. Therefore, interpretation was difficult in samples of low purity. Although we considered factors that affected TMB calculation, such as sample type, cancer type, and sequencing technique, our study established that TMB of well curated LDT was based on pre-defined criteria, which can be used as an alternative to WES method.

ACKNOWLEDGEMENTS

This study was supported by Bristol Myers Squibb. The biospecimens of this study were provided by Samsung Medical Center BioBank (2019-0029).

FIGURES

Figure 1. A comparison of the tumor mutation burden (TMB), which was calculated by CancerSCAN and whole exome sequencing by using reference sample known to harbor TMB of 7, 20, 24 per megabase in number. The X-axis indicates the number of TMB determined by exome (mut/Mb). The Y-axis indicates the number of TMB determined by CancerSCAN (mut/Mb). A high correlation was found between replicates produced in the two batches ($R^2=0.887$). Blue color indicates a sample with TMB of 7 mut/Mb,

red color indicates a sample with TMB of 20 mut/Mb, and green color indicates a sample with TMB of 24 mut/Mb. Circles and triangles represent each replicate.

Figure 2. Scatter and distribution plot of processed TMB(mutation per Mega), which were calculated from CancerSCAN and WES.

Figure 3. (A) The ratio of coding region (CDS length), which were analyzed by CancerSCAN and compared with that analyzed by whole exome sequencing (WES), and the ratio of detected variants. When the ratio of variants was higher than the ratio of CDS length, it indicated a relatively higher detection rates of CancerSCAN. **(B)** The top ranked 50 genes were identified by WES. Orange color indicated a gene that was identified by both CancerSCAN and WES. **(C)** A comparison of the number of mutations corresponding to the interval of each variant allele frequency (VAF), which was determined by WES and CancerSCAN.

Supplementary figure 1. The number of SNVs and INDELs before and after implementing the filtering algorithm for each VAF interval (0-100%). The number of variations before and after implementing the filtering algorithm for each VAF interval. To include only the somatic variant in TMB calculation and to include the characteristics of deep sequencing panel and the tumor-only panel, we performed strict mutation filtering by using the allele frequency and in-house DB.

TABLES

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Supplementary table 5. Classification of clinical samples as TMB-high or TMB-low

Supplementary table 6. Comparison of the number of genes, target genomic region size, and tumor mutation burden (TMB) calculation method from commercially available panels and whole exome sequencing

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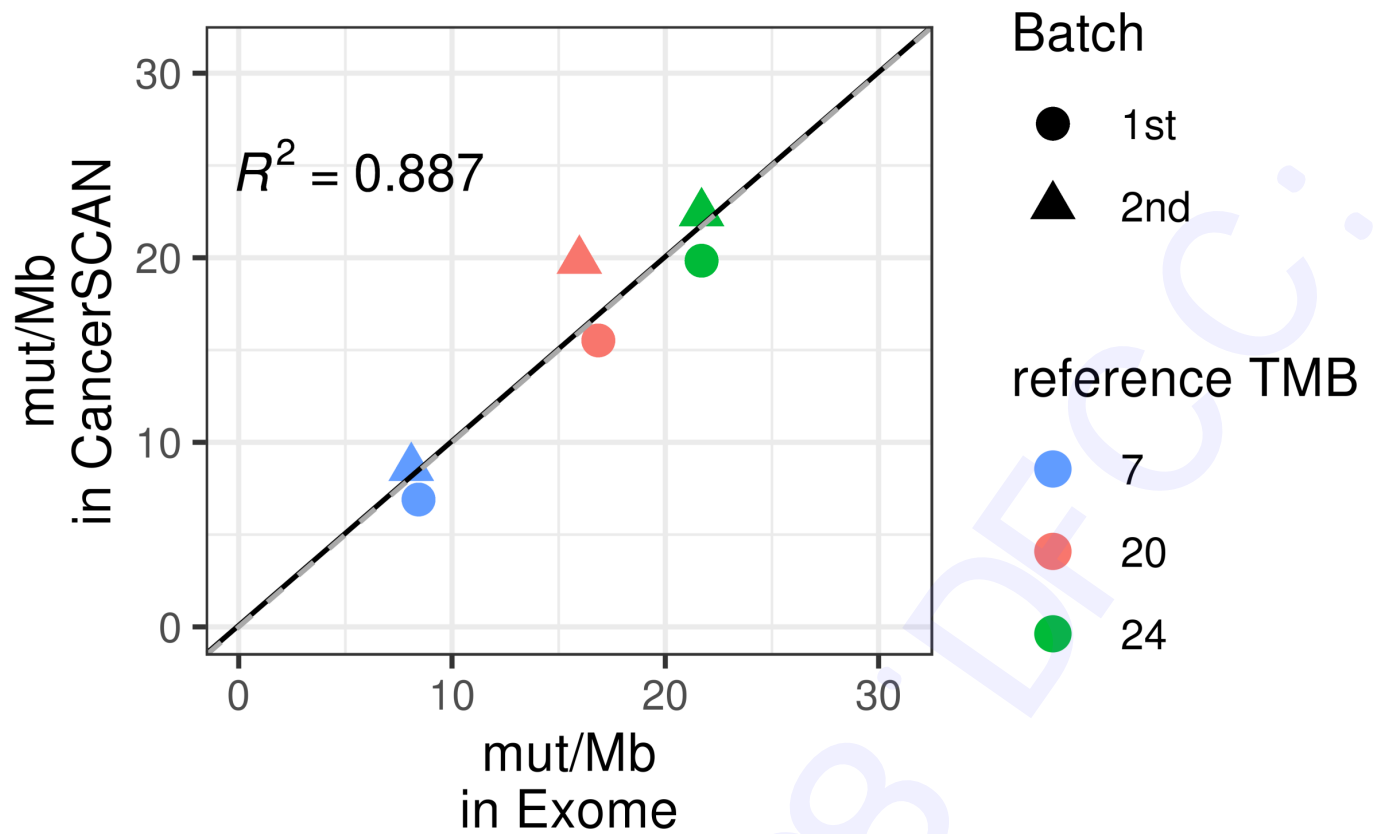


Fig. 1. . The comparison of TMB calculated by CancerSCAN and WES using reference sample known to harbor TMB of 7, 20, 24 per megabase in number. X-axis indicate number of TMB identified by exome (mut/Mb), Y-axis indicate number of TMB identified by CancerSCAN (mut/Mb). The correlation between replicates produced in the two batches was high ($R^2=0.887$). Blue indicate sample with TMB of 7mut/Mb, red indicate 20mut/Mb and green indicates 24 mut/Mb. Circles and triangles represent each replicate.

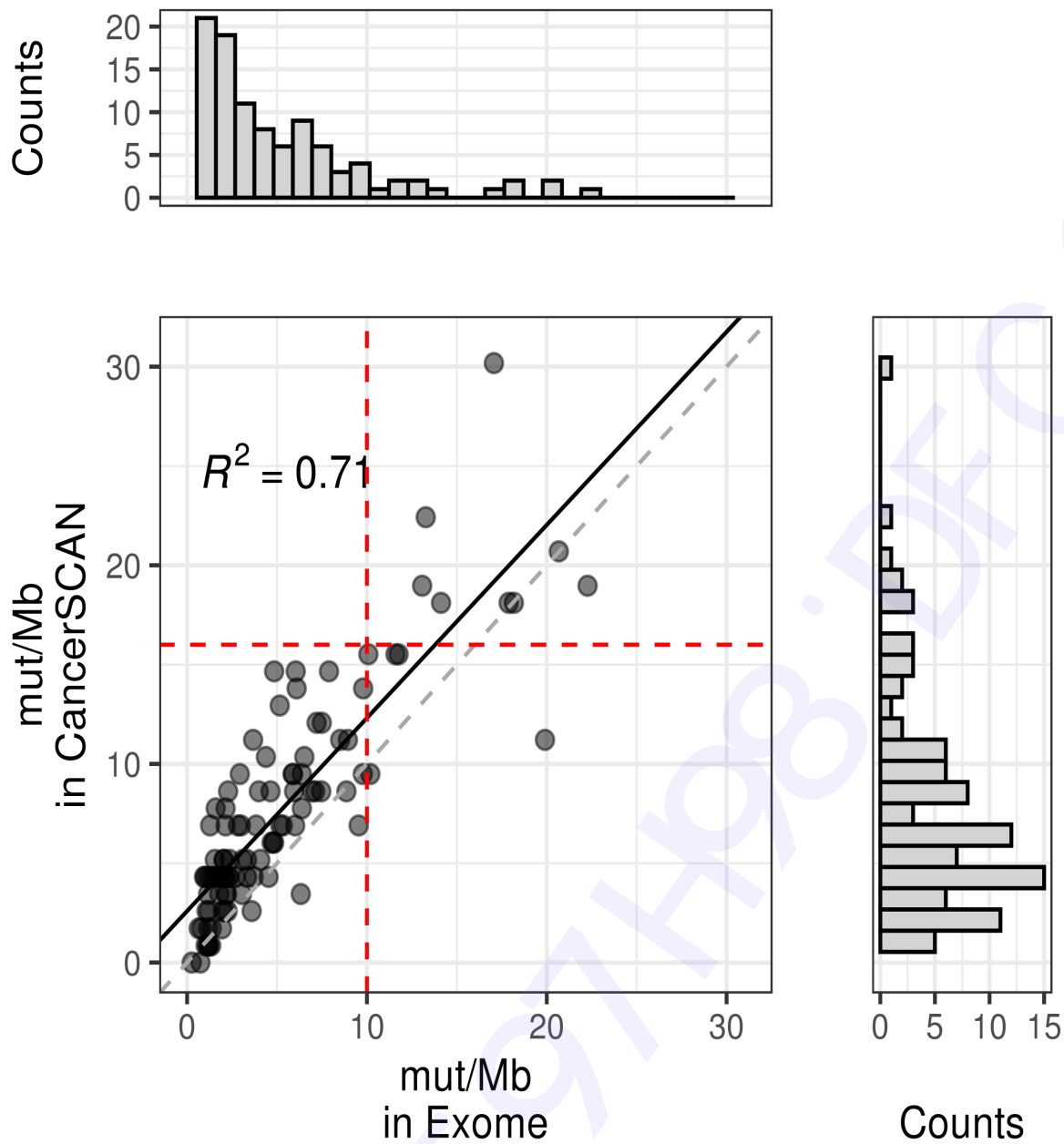


Fig. 2. Scatter and distribution plot of processed TMB (mutation per Megabases) from CancerSCAN and WES.

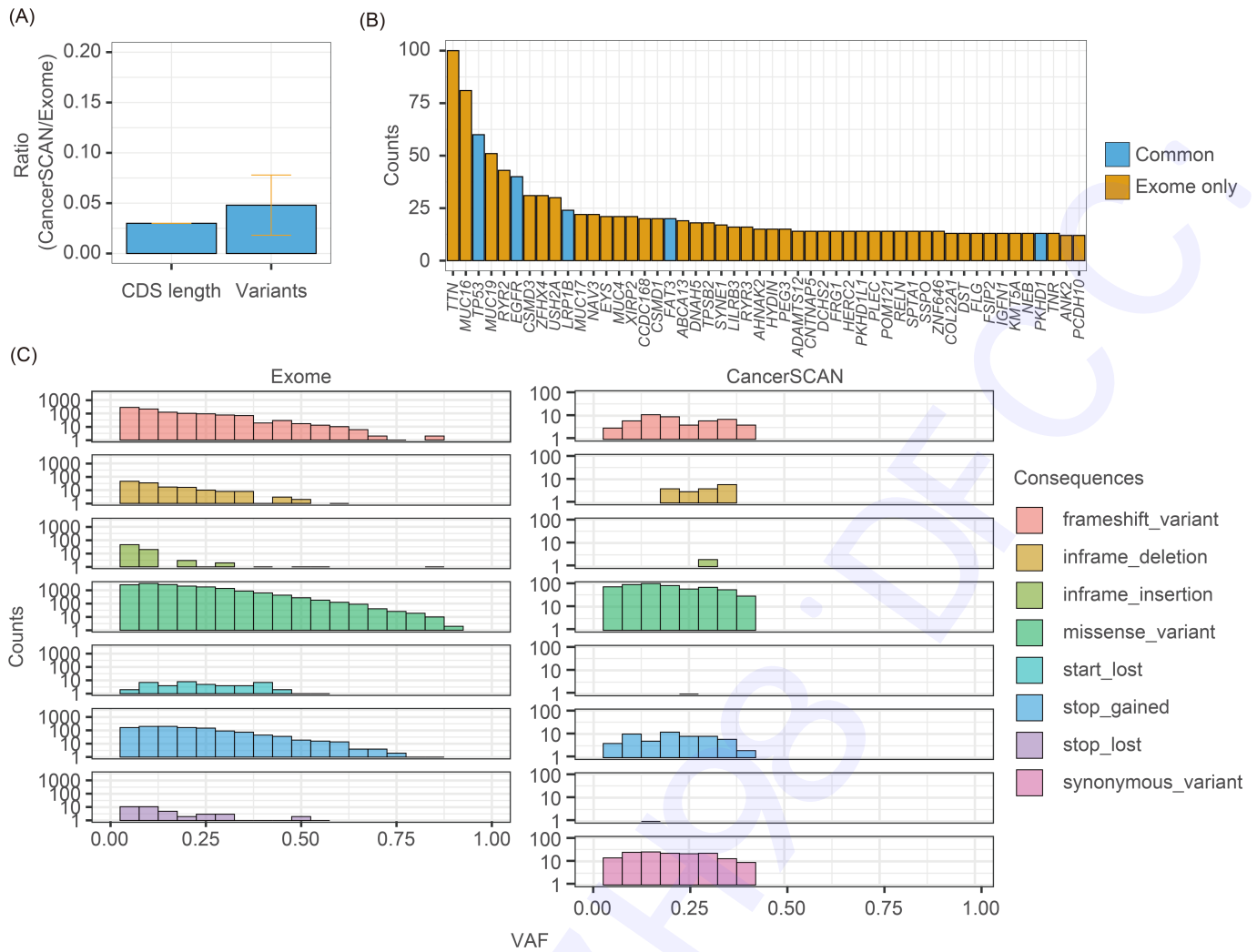


Fig. 3. The Comparison of various properties used in TMB calculations between CancerSCAN and TMB. (A) The ratio of coding region covered by CancerSCAN compared to the WES. (B) The top ranked 50 genes identified by WES. Sky blue indicate gene both covered by CancerSCAN and WES. (C) Comparison of the number of mutations corresponding to the interval of each VAF in WES and CancerSCAN.

Table 1. Variant filtering steps for the TMB calculation using CancerSCAN v3.0.

Steps	Category	Filter out criteria
1	Consequence of variants	None coding region with splice site
2	Chromosomal location	Mitochondrial DNA
3	Variants allele frequency (VAF)	LowVAF < 0.05 or HighVAF > 0.4
4	Supporting reads	Reads ≤ 4
5	Clinical significance	Benign
6	Minor allele frequency	gnomAD ≥ 0.0001 or 1000G EAS, KRGDB, KOVA ≥ 0.001
7	Strand bias between forward and reverse reads	P value ≥ 0.05 by fisher's exact test

Supplementary table 1. Sample information

	Reference materials	Clinical samples
Samples	Samples known for TMB (7, 20, 26) (n=3)	Randomly selected surgically resected non-small cell lung cancer fresh tissue acquired from the tissue-bank (n=100)
Comparison method	CancerSCAN v3.0 and Whole exome sequencing	CancerSCAN v3.0 and Whole exome sequencing

Supplementary table 2. Sequencing metrics for the duplicated reference materials

SAMPLE_ID	CS_1_re p1	CS_2_re p1	CS_3_re p1	CS_1_re p2	CS_2_re p2	CS_3_re p2
ON_BAIT_BASES	13666153 29	11240111 27	11884709 06	15154340 96	14629840 17	12162238 38
NEAR_BAIT_BASE S	18792253 77	16006337 13	17326179 72	21653780 64	20957432 88	17863906 43
OFF_BAIT_BASES	33697006 95	28453971 84	31346552 34	24511801 41	23313437 25	19771505 07
MEAN_BAIT_COV ERAGE	791.1592 9	650.7111 59	688.0281 37	877.3132 7	846.9489 34	704.0948 3
SAMPLE ID	WES_1_r ep1	WES_2_r ep1	WES_3_r ep1	WES_1_r ep2	WES_2_r ep2	WES_3_r ep2
ON_BAIT_BASES	46069588 9	37819896 9	34258553 0	48996297 9	39177129 0	47717617 2
NEAR_BAIT_BASE S	26732086 5	21475654 8	18541214 0	25686642 8	20111011 4	22978866 2
OFF_BAIT_BASES	18664497 652	15253917 820	13395796 956	19232030 163	15281239 695	17969213 718
MEAN_BAIT_COV ERAGE	266.7055 06	218.9464 89	198.3292	283.6487 74	226.8037 6	276.2462 51

CS: CancerSCAN; rep1 and rep 2 indicates same samples which are duplicated

Supplementary Table 3. Expected and identified tumor mutation burden from exploratory reference samples using CancerSCAN v3.0 and whole exome sequencing

Per megabase	Expected TMB	Observed TMB by CancerSCAN v 3.0	Observed TMB by WES
Reference sample #1	7.2±0.4	6.9	8.4
Reference sample #2	18.6±0.5	15.5	16.9
Reference sample #3	22.8±3.6	19.8	21.7
Reference sample #1 replicated	7.2±0.4	8.6	8.1
Reference sample #2 replicated	18.6±0.5	19.8	16.0
Reference sample #3 replicated	22.8±3.6	22.4	21.7

Supplementary table 4. Sequencing metrics for the non-small cell lung cancer clinical samples (n=100)

Attached separately in Excel

Supplementary table 5. The tumor mutation burden based on the pathology based tumor purity, histology subtype and tumor differentiation.

A. Analyses by pathology based tumor purity

	Tumor purity (%)	Sample (N)	TMB high (observed CancerSCAN)	TMB low (observed CancerSCAN)	Accuracy (%)
TMB high (WES)	30~50	6	1	0	100%
TMB low (WES)			0	5	
TMB high (WES)	55~80	36	2	3	91.6%
TMB low (WES)			0	31	
TMB high (WES)	85~100	58	5	2	96.6%
TMB low (WES)			0	51	

B. Analyses by histology subtype

	Histology	Sample (N)	TMB high (observed CancerSCAN)	TMB low (observed CancerSCAN)	Accuracy (%)
TMB high (WES)	Squamous cell carcinoma	30	3	1	96.7%
TMB low (WES)			0	26	
TMB high (WES)	Adenocarcinoma	70	5	4	94.3%
TMB low (WES)			0	61	

C. Analyses by tumor differentiation

	Differentiated	Sample (N)	TMB high (observed CancerSCAN)	TMB low (observed CancerSCAN)	Accuracy (%)
TMB high (WES)	Poorly differentiated	35	3	2	94.3%
TMB low (WES)			0	30	
TMB high (WES)	Moderately differentiated	65	5	3	95.4%
TMB low (WES)			0	57	

D. Analyses by surgical stage

	Stage	Sample (N)	TMB high (observed CancerSCAN)	TMB low (observed CancerSCAN)	Accuracy (%)
TMB high (WES)	I	29	3	3	89.7%
TMB low (WES)			0	23	
TMB high (WES)	II	37	4	0	100%
TMB low (WES)			0	33	
TMB high (WES)	III	33	1	2	93.9%
TMB low (WES)			0	30	
TMB high (WES)	IV	1	0	0	100%
TMB low (WES)			0	1	

Supplementary table 6. Classification of clinical samples as TMB-high or TMB-low

	TMB high (expected CancerSCAN)	TMB low (expected CancerSCAN)	Accuracy (%)
TMB high (WES)	2	11	87%
TMB low (WES)	2	85	
	TMB high (observed CancerSCAN)	TMB low (observed CancerSCAN)	Accuracy (%)
TMB high (WES)	8	5	95%
TMB low (WES)	0	87	

Supplementary table 7. Comparison of the number of genes, target genomic region size, and tumor mutation burden (TMB) calculation method from commercially available panels and whole exome sequencing

	Whole exome sequencing	MSK-IMPACT	FoundationOne CDx	CancerSCAN
Genes	~22000	468	324	407
Size	~30 Mbp	1.22Mbp	0.8Mbp	1.1 Mbp
Germline	Blood	Blood	Internal/external database	Internal/external database
TMB calculation	Somatic, coding mutation (non-syn)/Exome	Somatic, coding mutation (non-syn)/Mbp	Somatic, coding mutation (non-syn+indel+syn) /Mbp	Somatic, coding mutation (non-syn+indel+syn) /Mbp
Reference	Rizvi NA, 2015 Peters S, 2017 Hellmann MD, 2018, etc	Samstein RM, 2019	Hellmann MD, 2018 Ramalingam SS, 2018	Shin HT, 2017

MBp: megabase pair, syn: synonymous, indel: insertion and deletion

Supplementary table 4. Sequencing metrics for the non-small cell lung cancer clinical samples (n=100)

STUDY_ID	Type	NGS Panel	GENIUS_ID	TARGET_TERRITORY	TOTAL_READS	PF_READS	PF_UNIQUE_READS	PF_LIQ_READS_ALIGNED	PF_LIQ_BASES_ALIGNED	ON_BAIT_BASES	NEAR_BAIT_BASES	OFF_BAIT_BASES	ON_TARGET_BASES	PCT_SELECTED_BASES	PCT_OFF_BAIT	ON_BAIT_VS_SELECTED	MEAN_BAIT_COVERAGE	MEAN_TARGET_COVERAGE	PCT_USABLE_BASES_ON_BAIT	PCT_USABLE_BASES_ON_TARGET	ZERO_CVG_TARGETS_PCT	PCT_TARGET_BASES_2X	PCT_TARGET_BASES_10X	PCT_TARGET_BASES_20X	PCT_TARGET_BASES_30X	PCT_TARGET_BASES_40X	PCT_TARGET_BASES_50X	PCT_TARGET_BASES_100X
WES_K_001	paired normal	Exome	CD_19_09251_XN_WES	74569526	37873706	37873706	34811730	34749903	3449771831	2554901851	690550104	508019331	1793032927	0.8647	0.1353	0.7872	34.26	24.05	0.6679	0.4687	0.1557	0.6736	0.6144	0.5229	0.4106	0.2836	0.1617	0.0008
	FFPE tumor	Exome	CD_19_09351_DP_WES	74569526	111216428	111216428	101830368	101632441	10085282535	7363064655	2209107806	1443975835	5158771368	0.8689	0.1311	0.7692	98.74	69.18	0.6555	0.4593	0.1185	0.7025	0.6576	0.6336	0.6090	0.5792	0.5455	0.3519
	FFPE tumor	CancerSCAN	CD_19_09144_DP_CS	74569526	59427396	59427396	59427396	59427396	5834156726	1630953869	1770288987	2432913870	1631266750	0.5830	0.4170	0.4795	944.19	943.35	0.2717	0.2718	0.0046	0.9971	0.9956	0.9953	0.9950	0.9949	0.9947	0.9938
WES_K_002	paired normal	Exome	CD_19_09252_XN_WES	74569526	39369716	39369716	36129534	36058870	3584317559	2632006304	749081070	525039375	1878650588	0.8656	0.1344	0.7785	35.30	25.19	0.6619	0.4725	0.1530	0.6780	0.6216	0.5345	0.4267	0.3045	0.1854	0.0010
	FFPE tumor	Exome	CD_19_09352_DP_WES	74569526	130343986	130343986	116236768	115999838	11520275448	8548882176	2568257187	1803763770	5849164536	0.8604	0.1396	0.7690	114.64	78.44	0.6494	0.4443	0.1036	0.7081	0.6620	0.6398	0.6195	0.5955	0.5676	0.4027
	FFPE tumor	CancerSCAN	CD_19_09145_DP_CS	74569526	46760182	46760182	46760182	4602656129	1283803709	1429383749	1889468671	1284091112	0.5895	0.4105	0.4732	743.22	742.52	0.2718	0.2719	0.0042	0.9970	0.9955	0.9952	0.9950	0.9948	0.9947	0.9935	
WES_K_003	paired normal	Exome	CD_19_09253_XN_WES	74569526	36550006	36550006	33493446	33425349	3320802046	2458591466	6827206469	478399553	1738714734	0.8680	0.1320	0.7815	32.97	23.32	0.6660	0.4710	0.1571	0.6752	0.6146	0.5183	0.3990	0.2658	0.1431	0.0007
	FFPE tumor	Exome	CD_19_09353_DP_WES	74569526	114221896	114221896	104406755	103864915	10317901255	7590460466	2272230588	1463457642	5308892998	0.8708	0.1292	0.7696	101.79	71.19	0.6580	0.4602	0.1203	0.7035	0.6587	0.6345	0.6098	0.5800	0.5467	0.3483
	FFPE tumor	CancerSCAN	CD_19_09146_DP_CS	74569526	48960396	48960396	48960396	48960396	4813284713	1309728495	1503888947	199667271	1310021837	0.5846	0.4154	0.4655	758.23	757.41	0.2649	0.2649	0.0049	0.9969	0.9955	0.9953	0.9951	0.9949	0.9948	0.9938
WES_K_004	paired normal	Exome	CD_19_09254_XN_WES	74569526	39587742	39587742	36101063	36028325	3579450696	2654967229	746358989	524215637	1871853494	0.8665	0.1335	0.7806	35.60	25.10	0.6640	0.4682	0.1545	0.6774	0.6204	0.5327	0.4247	0.3031	0.1844	0.0011
	FFPE tumor	Exome	CD_19_09354_DP_WES	74569526	119885644	119885644	108026550	107811023	10704480017	7899647337	2374859965	1607005005	5458487866	0.8647	0.1353	0.7689	105.94	73.20	0.6524	0.4508	0.1127	0.7062	0.6607	0.6369	0.6135	0.5855	0.5539	0.3668
	FFPE tumor	CancerSCAN	CD_19_09147_DP_CS	74569526	41982391	41982391	41982391	41982391	4135282418	1140264375	1318974450	1676043575	1140502363	0.5947	0.4053	0.4637	660.12	659.79	0.2689	0.2690	0.0050	0.9966	0.9954	0.9952	0.9950	0.9948	0.9946	0.9932
WES_K_005	paired normal	Exome	CD_19_09255_XN_WES	74569526	37552972	37552972	34387798	34322501	3397523803	2558545897	654994997	496925622	1748614767	0.8661	0.1339	0.7962	34.31	23.45	0.6746	0.4610	0.1608	0.6703	0.6080	0.5126	0.3981	0.2717	0.1530	0.0008
	FFPE tumor	Exome	CD_19_09355_DP_WES	74569526	109265400	109265400	98948955	98746835	9816066162	7218276900	2207387575	1415659853	5036898731	0.8694	0.1306	0.7658	96.80	67.55	0.6541	0.4564	0.1200	0.7027	0.6580	0.6332	0.6075	0.5763	0.5412	0.3377
	FFPE tumor	CancerSCAN	CD_19_09148_DP_CS	74569526	47960710	47960710	47960710	47960710	4716358990	1308084698	1433937785	1974336507	1308373998	0.5814	0.4186	0.4771	757.27	756.67	0.2700	0.2701	0.0041	0.9969	0.9956	0.9953	0.9950	0.9948	0.9946	0.9934
WES_K_006	paired normal	Exome	CD_19_09256_XN_WES	74569526	37591994	37591994	34594409	34524301	3430675275	2515980725	704822372	507520114	1787687703	0.8639	0.1361	0.7812	33.74	23.97	0.6627	0.4708	0.1562	0.6764	0.6165	0.5228	0.4080	0.2798	0.1595	0.0008
	FFPE tumor	Exome	CD_19_09356_DP_WES	74569526	14039130	14039130	126852149	126602265	12573373241	9244071205	2803289574	1865457530	6404687746	0.8659	0.1341	0.7673	123.97	85.89	0.6521	0.4518	0.1067	0.7098	0.6640	0.6426	0.6239	0.6025	0.5777	0.4292
	FFPE tumor	CancerSCAN	CD_19_09149_DP_CS	74569526	61299050	61299050	61299050	61299050	6029348369	1701925374	1827563349	2498989646	1702360205	0.5854	0.4146	0.4822	985.28	984.23	0.2749	0.2750	0.0040	0.9972	0.9956	0.9952	0.9950	0.9948	0.9946	0.9938
WES_K_007	paired normal	Exome	CD_19_09257_XN_WES	74569526	31871414	31871414	29572080	29516571	2933005209	2139545476	608419426	413406224	1540731360	0.8692	0.1308	0.7786	28.69	20.66	0.6647	0.4786	0.1589	0.6738	0.6048	0.4902	0.3474	0.1989	0.0848	0.0004
	FFPE tumor	Exome	CD_19_09357_DP_WES	74569526	106230206	106230206	96528175	96351590	9579367587	7021916196	2115511995	1406173259	4913328205	0.8666	0.1334	0.7685	94.17	65.89	0.6545	0.4579	0.1183	0.7026	0.6573	0.6321	0.6056	0.5735	0.5376	0.3232
	FFPE tumor	CancerSCAN	CD_19_09150_DP_CS	74569526	47825715	47825715	47825715	47825715	4705116435	1280297152	1470421780	1954397503	1280575010	0.5846	0.4154	0.4654	741.19	740.82	0.2651	0.2651	0.0061	0.9967	0.9952	0.9949	0.9947	0.9946	0.9943	0.9931
WES_K_008	paired normal	Exome	CD_19_09258_XN_WES	74569526	39893784	39893784	36702748	36625786	3639005404	2675971805	753819715	525937090	1903348146	0.8670	0.1330	0.7802	35.89	25.52	0.6641	0.4724	0.1551	0.6777	0.6217	0.5361	0.4308	0.3115	0.1932	0.0012
	FFPE tumor	Exome	CD_19_09358_DP_WES	74569526	125641250	125641250	113172949	112947649	1121662008	8226718259	2498443819	1729251712	5699239000	0.8612	0.1388	0.7670	110.32	76.43	0.6483	0.4491	0.1040	0.7083	0.6606	0.6359	0.6111	0.5823	0.5500	0.3612
	FFPE																											

WES_K_042	paired normal	Exome	CD_19_09292_XN_WES	74569526	35257010	35257010	32020275	31959758	3171002784	2304796634	686386581	500746193	1663190744	0.8566	0.1434	0.7705	30.91	22.30	0.6472	0.4671	0.1585	0.6720	0.6083	0.5037	0.3736	0.2372	0.1239	0.0010
	FFPE tumor	Exome	CD_19_09292_DP_WES	74569526	127091944	127091944	115759590	115521495	11520607188	8268481364	2641184705	1739941711	5982126875	0.8625	0.1375	0.5759	110.88	80.22	0.6441	0.4660	0.1110	0.7105	0.6689	0.6049	0.6321	0.6112	0.5860	0.4210
WES_K_043	paired normal	Exome	CD_19_09293_XN_WES	74569526	39136440	39136440	35321328	35249778	3501129428	2556798687	772451534	550513580	1842637030	0.8581	0.1419	0.7680	34.29	24.71	0.6468	0.4662	0.1562	0.6745	0.6180	0.5286	0.4143	0.2882	0.1721	0.0020
	FFPE tumor	Exome	CD_19_09293_DP_WES	74569526	107706882	107706882	98575699	98380534	9809975672	6961623935	2249271214	1509078641	5066991660	0.8592	0.1408	0.7558	93.36	67.95	0.6400	0.4658	0.1135	0.7092	0.6656	0.6439	0.6212	0.5925	0.5586	0.3417
WES_K_044	paired normal	Exome	CD_19_09294_XN_WES	74569526	47056710	47056710	42068456	41965573	4162167455	698360773	4162167455	1527955827	1752720486	0.8435	0.1466	0.7456	884.56	883.52	0.2415	0.2416	0.0043	0.9972	0.9957	0.9953	0.9950	0.9948	0.9946	0.9936
	FFPE tumor	Exome	CD_19_09294_DP_WES	74569526	143519646	143519646	129162043	128899994	12864353915	9307657889	3009146054	1979973059	6675846237	0.8615	0.1385	0.7557	124.82	89.53	0.6421	0.4605	0.1051	0.7153	0.6724	0.6530	0.6366	0.6176	0.5949	0.4457
WES_K_045	paired normal	Exome	CD_19_09295_XN_WES	74569526	64984270	64984270	58149116	58034693	5755839282	4253504812	1237946254	941744156	3004393165	0.8536	0.1464	0.7746	57.04	40.29	0.6481	0.4577	0.1422	0.6825	0.6417	0.5985	0.5427	0.4776	0.4053	0.0753
	FFPE tumor	Exome	CD_19_09295_DP_WES	74569526	109592756	109592756	99643010	99451417	9922137159	7142857833	2308828502	1462262615	5171334670	0.8660	0.1340	0.7557	95.79	69.35	0.6453	0.4672	0.1182	0.7086	0.6661	0.6445	0.6223	0.5943	0.5613	0.3507
WES_K_046	paired normal	Exome	CD_19_09296_XN_WES	74569526	41445944	41445944	37342618	37267651	3698358352	2720154139	791742434	593352579	1933382226	0.8585	0.1445	0.7746	36.48	25.93	0.6498	0.4619	0.1546	0.6738	0.6190	0.5354	0.4302	0.3130	0.1995	0.0029
	FFPE tumor	Exome	CD_19_09296_DP_WES	74569526	139144234	139144234	124955323	124338168	12405706775	91477114629	2916748204	1792778538	6502464490	0.8706	0.1294	0.7582	122.67	87.20	0.6509	0.4627	0.1146	0.7130	0.6718	0.6532	0.6377	0.6197	0.5980	0.4539
WES_K_047	paired normal	Exome	CD_19_09297_XN_WES	74569526	42309572	42309572	37797308	37726151	3737011391	2774887755	793619592	615385268	1942126167	0.8529	0.1471	0.7776	37.21	26.04	0.6493	0.4545	0.1559	0.6727	0.6176	0.5346	0.4306	0.3147	0.2027	0.0030
	FFPE tumor	Exome	CD_19_09297_DP_WES	74569526	113445154	113445154	102911518	102710890	10252980354	7354216448	2411097265	1538614440	5339451907	0.8639	0.1361	0.7531	98.62	71.60	0.6418	0.4660	0.1161	0.7115	0.6679	0.6455	0.6227	0.5947	0.5615	0.3477
WES_K_048	paired normal	Exome	CD_19_09298_XN_WES	74569526	49624162	49624162	44428531	44306165	4416270330	3100837966	1018404647	814376416	2290078109	0.8349	0.1651	0.7528	41.58	30.71	0.6187	0.4569	0.1303	0.6836	0.6340	0.5690	0.4819	0.3832	0.2814	0.0117
	FFPE tumor	Exome	CD_19_09298_DP_WES	74569526	139682124	139682124	126337109	126706412	12578255567	8951558828	2925103753	2032200643	589427769	0.8539	0.1461	0.7537	120.04	86.50	0.6345	0.4572	0.0966	0.7173	0.6726	0.6530	0.6365	0.6172	0.5941	0.4418
WES_K_049	paired normal	Exome	CD_19_09299_XN_WES	74569526	39679554	39679554	35914127	35844713	3557407071	2614573684	765955494	550532729	1869796384	0.8600	0.1400	0.7734	35.06	25.07	0.6524	0.4666	0.1546	0.6748	0.6192	0.5319	0.4215	0.2979	0.1804	0.0019
	FFPE tumor	Exome	CD_19_09299_DP_WES	74569526	127277410	127277410	114511485	114261600	11425035297	8199323594	2704425702	1796844809	5992766840	0.8585	0.1415	0.7520	109.96	80.36	0.6378	0.4662	0.1101	0.7073	0.6641	0.6432	0.6231	0.5989	0.5705	0.3868
WES_K_050	paired normal	Exome	CD_19_09300_XN_WES	74569526	36861786	36861786	33126076	33063915	3272865565	2438876826	679701932	532972547	1699844955	0.8562	0.1438	0.7820	32.71	22.80	0.6551	0.4566	0.1581	0.6708	0.6080	0.5071	0.3829	0.2508	0.1360	0.0010
	FFPE tumor	Exome	CD_19_09300_DP_WES	74569526	155606692	155606692	138477419	138170945	13822614630	1011419500	3349599385	2071297863	7365664365	0.8667	0.1333	0.7512	135.63	98.78	0.6435	0.4687	0.1106	0.7111	0.6706	0.6523	0.6381	0.6231	0.6053	0.4818
WES_K_051	paired normal	Exome	CD_19_09301_XN_WES	74569526	39339998	39339998	35529632	35465190	3519411962	2618518903	749871320	529175133	1855538826	0.8642	0.1358	0.7774	35.12	24.88	0.6590	0.4670	0.1592	0.6728	0.6165	0.5282	0.4174	0.2941	0.1776	0.0020
	FFPE tumor	Exome	CD_19_09301_DP_WES	74569526	125247868	125247868	112156475	111971142	11203008164	8106718059	2747749274	1658482771	5979726812	0.8675	0.1325	0.7469	108.71	80.19	0.6408	0.4727	0.1182	0.7085	0.6661	0.6451	0.6260	0.6033	0.5763	0.3924
WES_K_052	paired normal	Exome	CD_19_09302_XN_WES	74569526	41288022	41288022	37100507	37014720	3666688118	2696358524	778798904	606117344	1908887046	0.8515	0.1485	0.7759	36.16	25.60	0.6466	0.4578	0.1486	0.6740	0.6194	0.5344	0.4269	0.3070	0.1919	0.0025
	FFPE tumor	Exome	CD_19_09302_DP_WES	74569526	181051352	181051352	155672197	155325175	15535691428	11685021498	3941905027	2447962124	8220424478	0.8646	0.1354	0.7477	156.70	110.24	0.6390	0.4495	0.1037	0.7175	0.6740	0.6551	0.6404	0.6252	0.6077	0.4861
WES_K_053	paired normal	Exome	CD_19_09303_XN_WES	74569526	39251662	39251662	35156999	35089558	3455033201	2613305335	678294041	566306295	1765484120	0.8532	0.1468	0.7939	35.05	23.68	0.6592	0.4453	0.1604	0.6671	0.6053	0.5099	0.3953	0.2716	0.1586	0.0016
	FFPE tumor	Exome	CD_19_09303_DP_WES	74569526	142526886	142526886	126130602	125858478	12583867111	9163354836	3102702850	1956848756	6661483565	0.8624	0.1376	0.7471	122.88	89.33	0.6366	0.4628	0.1106	0.7117	0.6693	0.6496	0.6328	0.6138	0.5910	0.4357
WES_K_054	paired normal	Exome	CD_19_09304_XN_WES	74569526	37348095	37348095	33480895	33480895	33480895	7264363592	1642744684	2034525762	6387093146	0.8518	0.1437	0.7467	95.02	95.02	0.6378	0.4622	0.1101	0.7073	0.6641	0.6432	0.6231	0.5989	0.5705	0.3868
	FFPE tumor	Exome	CD_19_09304_DP_WES	74569526	43063494	43063494	38709254	38632007	3824948572	2869620384	793828687	592522171	1995745786	0.8608	0.1392	0.7833	38.48	26.76	0.6598	0.4589	0.1575	0.6729	0.6197	0.5395	0.4400	0.3284	0.2178	0.0035
WES_K_055	paired normal	Exome	CD_19_09305_XN_WES	74569526	133355516	133355516	119108486	118858210	11891246043	8106718059	2939208723	1763534014	6867412080	0.8674	0.1326	0.7455	115.48	84.88	0.6394	0.4699	0.1189	0.7102	0.6684	0.6484	0.6313	0.6113	0.5877	0.4258
	FFPE tumor	Exome	CD_19_09305_DP_WES	74569526	38687338	38687338	34560704	34498268	3441383914	2578007780	709084268	532413762	1780304837	0.8606	0.1394	0.7843	34.57	23.87	0.6598	0.4556	0.1612	0.6699	0.6107	0.5165	0.3999	0.2735	0.1583	0.0016
WES_K_056	paired normal	Exome	CD_19_09306_XN_WES	74569526	146793936	146793936	129351334	129074142	12910862499	9483073474	3192959493	1976614205	6848568279	0.8651	0.1349	0.7482	127.20	91.84	0.6398	0.4619	0.1151	0.7113	0.6692	0.6497	0.6397	0.6157	0.5944	0.4476
	FFPE tumor	Exome	CD_19_09306_DP_WES	74569526	56137513	56137513	56137513	56137513	56137513	56137513	56137513	56137513	56137513	0.8651	0.1349	0.7482	127.20	91.84	0.6398	0.4619	0.1151	0.7113	0.6692	0.6497	0.6397	0.6157	0.5944	0.4476
WES_K_057	paired normal	Exome	CD_19_09307_XN_WES	74569526	37348095	37348095	33480895	33480895	33480895	7264363592	1642744684	2034525762	6387093146	0.8518	0.1437	0.7467	95.02	95.02	0.6378	0.4622	0.1101	0.7073	0.6641	0.6432	0.6231	0.5989	0.5705	0.3868
	FFPE tumor	Exome	CD_19_09307_DP_WES	74569526	43063494	43063494	38709254	38632007	3824948572	2869620384	793828687	592522171	1995745786	0.8608	0.1392	0.7833	38.48	26.76	0.6598	0.4589	0.1575	0.6729	0.6197	0.5395	0.4400	0.3284	0.2178	0.0035
WES_K_058	paired normal	Exome	CD_19_09308_XN_WES	74569526	133355516	133355516	119108486	118858210	11891246043	8106718059	2939208723	1763534014	6867412080	0.8674	0.1326	0.7455	115.48	84.88	0.6394	0.4699	0.1189	0.7102	0.6684	0.6484	0.6313	0.6113	0.5877	0.4258
	FFPE tumor	Exome	CD_19_09308_DP_WES	74569526	38687338	38687338	34560704	34498268	3441383914	2578007780	709084268	532413762	1780304837	0.8606	0.1394	0.7843	34.57	23.87	0.6598	0.4556	0.1612	0.6699	0.6107	0.5165	0.3999	0.2735	0.1583	0.0016
WES_K_059	paired normal	Exome	CD_19_09309_XN_WES	74569526	146793936	146793936	129351334	129074142	12910862499	9483073474	3192959493	1976614205	6848568279	0.8651	0.1349	0.7482	127.20											

WES_K_086	paired normal	Exome	CD_19_09336_XN_WES	74569526	41724110	41724110	37116159	37031355	3689607207	2563530920	961666936	623253749	1905769270	0.8498	0.1502	0.7272	34.38	25.56	0.6083	0.4522	0.1444	0.6895	0.6319	0.5455	0.4276	0.2980	0.1798	0.0029
	FFPE tumor	Exome	CD_19_09436_DP_WES	74569526	111005820	111005820	98047633	97857637	9688455004	7204990576	1982936635	1783119045	4774054797	0.8375	0.1625	0.7842	96.62	64.02	0.6426	0.4258	0.1488	0.6831	0.6459	0.6151	0.5801	0.5406	0.4976	0.2738
	FFPE tumor	CancerSCAN	CD_19_09229_DP_CS	1733178	38263145	38263145	38263145	38263145	3835245189	1691865079	1740649974	402730136	1692120657	0.8950	0.1050	0.4929	979.45	982.87	0.4378	0.4379	0.0221	0.9922	0.9845	0.9831	0.9821	0.9812	0.9807	0.9774
WES_K_087	paired normal	Exome	CD_19_09337_XN_WES	74569526	40902388	40902388	36456362	36372669	3633009744	2491969936	965254126	619673602	1879265188	0.8480	0.1520	0.7208	33.42	25.20	0.6032	0.4549	0.1412	0.6905	0.6326	0.5451	0.4232	0.2896	0.1703	0.0025
	FFPE tumor	Exome	CD_19_09437_DP_WES	74569526	101684918	101684918	90593855	90409316	8983486185	6555636795	1938685463	1590927924	4517635281	0.8423	0.1577	0.7718	87.91	60.58	0.6383	0.4399	0.1477	0.6854	0.6470	0.6154	0.5777	0.5342	0.4864	0.2425
	FFPE tumor	CancerSCAN	CD_19_09230_DP_CS	1733178	43378913	43378913	43378913	43378913	4335692005	1921010010	1996682875	417999120	1921299868	0.9036	0.0964	0.4903	1112.11	1117.73	0.4385	0.4385	0.0319	0.9906	0.9850	0.9840	0.9833	0.9826	0.9818	0.9788
WES_K_088	paired normal	Exome	CD_19_09338_XN_WES	74569526	43119732	43119732	38218465	38138605	3806467542	2683998541	993737108	617713155	1989382506	0.8562	0.1438	0.7298	35.99	26.68	0.6163	0.4568	0.1474	0.6884	0.6336	0.5541	0.4436	0.3193	0.2018	0.0043
	FFPE tumor	Exome	CD_19_09438_DP_WES	74569526	114688518	114688518	101742819	101539941	10086132136	7414321324	2165506175	1791752901	5061251482	0.8424	0.1576	0.7740	99.43	67.87	0.6401	0.4369	0.1457	0.6865	0.6500	0.6232	0.5923	0.5566	0.5169	0.2954
	FFPE tumor	CancerSCAN	CD_19_09231_DP_CS	1733178	37651956	37651956	37651956	37651956	3757816638	1681500025	1675377365	400939248	1681759984	0.8933	0.1067	0.5009	973.45	977.37	0.4422	0.4422	0.0252	0.9916	0.9846	0.9835	0.9826	0.9817	0.9808	0.9772
WES_K_089	paired normal	Exome	CD_19_09339_XN_WES	74569526	43040430	43040430	37790917	37707399	3756880774	2665019361	990372681	624208535	1956265832	0.8541	0.1459	0.7291	35.74	26.23	0.6131	0.4500	0.1469	0.6896	0.6347	0.5525	0.4383	0.3105	0.1918	0.0037
	FFPE tumor	Exome	CD_19_09439_DP_WES	74569526	113193178	113193178	98948246	98727999	9773557960	6962349392	2020266125	2199646206	4625239562	0.8033	0.1967	0.7751	93.37	62.03	0.6090	0.4046	0.1502	0.6828	0.6454	0.6116	0.5718	0.5270	0.4788	0.2444
	FFPE tumor	CancerSCAN	CD_19_09232_DP_CS	1733178	40178634	40178634	40178634	40178634	4013525770	1791250817	1813219498	409055455	1791499645	0.8981	0.1019	0.4970	1036.99	1042.74	0.4414	0.4415	0.0301	0.9905	0.9841	0.9829	0.9821	0.9811	0.9805	0.9775
WES_K_090	paired normal	Exome	CD_19_09340_XN_WES	74569526	39787502	39787502	35417284	35337505	3527657791	2450264264	947474377	565930136	1848221815	0.8572	0.1428	0.7211	32.86	24.79	0.6097	0.4599	0.1468	0.6910	0.6339	0.5440	0.4185	0.2810	0.1600	0.0021
	FFPE tumor	Exome	CD_19_09440_DP_WES	74569526	120913484	120913484	104064367	103840966	10272596271	7482674310	2223495570	2232098991	4912488880	0.8130	0.1870	0.7709	100.34	65.88	0.6127	0.4023	0.1507	0.6857	0.6488	0.6179	0.5821	0.5412	0.4965	0.2680
	FFPE tumor	CancerSCAN	CD_19_09233_DP_CS	1733178	37579087	37579087	37579087	3752643562	1679580246	1707225615	365837701	1679815022	0.9025	0.0975	0.4959	972.34	979.25	0.4425	0.4426	0.0384	0.9889	0.9845	0.9835	0.9828	0.9820	0.9813	0.9778	
WES_K_091	paired normal	Exome	CD_19_09341_XN_WES	74569526	43873410	43873410	38705016	38611411	3856372963	2682140146	1055180171	635010130	2015018399	0.8548	0.1452	0.7177	35.97	27.02	0.6053	0.4547	0.1437	0.6945	0.6406	0.5632	0.4520	0.3258	0.2056	0.0036
	FFPE tumor	Exome	CD_19_09441_DP_WES	74569526	110872904	110872904	97715157	97510644	9649147388	6802144983	1978028421	2169527990	4548753684	0.8019	0.1981	0.7747	91.22	61.00	0.6074	0.4062	0.1500	0.6823	0.6436	0.6071	0.5647	0.5178	0.4680	0.2334
	FFPE tumor	CancerSCAN	CD_19_09234_DP_CS	1733178	48606545	48606545	48606545	48606545	4856535510	2155774555	2219733120	481027835	2156117056	0.9010	0.0990	0.4927	1248.02	1257.15	0.4391	0.4392	0.0374	0.9884	0.9837	0.9826	0.9819	0.9813	0.9808	0.9780
WES_K_092	paired normal	Exome	CD_19_09342_XN_WES	74569526	42104162	42104162	37171798	37086025	3704801976	2574748976	998043468	624490171	1933016811	0.8512	0.1488	0.7207	34.53	25.92	0.6055	0.4546	0.1443	0.6921	0.6368	0.5533	0.4354	0.3042	0.1838	0.0028
	FFPE tumor	Exome	CD_19_09442_DP_WES	74569526	130872468	130872468	110683704	110447843	10909594651	7993212182	2627527813	2642047406	5102736263	0.7952	0.2048	0.7790	107.19	68.43	0.6047	0.3860	0.1464	0.6842	0.6485	0.6193	0.5860	0.5081	0.2937	
	FFPE tumor	CancerSCAN	CD_19_09235_DP_CS	1733178	44713894	44713894	44713894	44713894	4461637313	1996708871	1961445108	503483334	1997002161	0.8872	0.1128	0.5045	1155.93	1157.73	0.4421	0.4422	0.0134	0.9944	0.9856	0.9839	0.9831	0.9825	0.9817	0.9787
WES_K_093	paired normal	Exome	CD_19_09343_XN_WES	74569526	43600056	43600056	38356284	38263635	3823610882	2667914435	1044614815	634824328	1998279152	0.8540	0.1460	0.7186	35.78	26.80	0.6058	0.4538	0.1435	0.6938	0.6396	0.5612	0.4493	0.3220	0.2016	0.0034
	FFPE tumor	Exome	CD_19_09443_DP_WES	74569526	93030646	93030646	82276372	82108733	8099631994	5721025971	1625381485	1812982240	3786434552	0.8021	0.1979	0.7788	76.72	50.78	0.6089	0.4030	0.1525	0.6792	0.6384	0.5965	0.5473	0.4927	0.4350	0.1736
	FFPE tumor	CancerSCAN	CD_19_09236_DP_CS	1733178	53372003	53372003	53372003	53372003	5332184471	2332663252	2460696450	593424769	233051368	0.8887	0.1113	0.4923	1350.42	1357.22	0.4327	0.4328	0.0327	0.9908	0.9858	0.9850	0.9844	0.9837	0.9832	0.9810
WES_K_094	paired normal	Exome	CD_19_09344_XN_WES	74569526	40002900	40002900	35424960	35341848	3529978428	2462837581	963668273	560438052	1855582750	0.8594	0.1406	0.7188	33.03	24.88	0.6096	0.4593	0.1468	0.6916	0.6347	0.5456	0.4199	0.2824	0.1612	0.0020
	FFPE tumor	Exome	CD_19_09444_DP_WES	74569526	120272066	120272066	105791555	105563593	10424101384	7415281448	2125595246	2310942304	4906627396	0.8050	0.1950	0.7772	99.44	65.80	0.6104	0.4039	0.1506	0.6832	0.6467	0.6152	0.5790	0.5385	0.4946	0.2715
	FFPE tumor	CancerSCAN	CD_19_09237_DP_CS	1733178	35350798	35350798	35350798	35350798	3536293627	1527065324	1616974210	392254093	1527303826	0.8891	0.1109	0.4857	884.05	889.29	0.4277	0.4278	0.0338	0.9897	0.9850	0.9837	0.9828	0.9821	0.9816	0.9776
WES_K_095	paired normal	Exome	CD_19_09345_XN_WES	74569526	45825568	45825568	40035003	39943056	3992463098	2810532911	1106658726	653733109	2095117384	0.8570	0.1430	0.7175	37.69	28.10	0.6072	0.4527	0.1441	0.6946	0.6425	0.5705	0.4661	0.3453	0.2268	0.0049
	FFPE tumor	Exome	CD_19_09445_DP_WES	74569526	98185384	98185384	86611328	86432608	8561242361	6064399927	1734938509	1907337328	4026761426	0.8035	0.1965	0.7776	81.33	54.00	0.6115	0.4061	0.1533	0.6800	0.6403	0.6005	0.5541	0.5025	0.4476	0.1970
	FFPE tumor	CancerSCAN	CD_19_09238_DP_CS	1733178	45990882	45990882	45990882	45990882	4593965396	1989962733	2089381920	514620743	1990282006	0.8880	0.1120	0.4878	1152.03	1158.70	0.4284	0.4285	0.0334	0.9901	0.9853	0.9844	0.9837	0.9832	0.9827	0.9800
WES_K_096	paired normal	Exome	CD_19_09346_XN_WES	74569526	40718644	40718644	36264366	36181715	3618358834	2484452949	984708544	594387262	1898507907	0.8537	0.1463	0.7162	33.32	25.46	0.6041	0.4616	0.1454	0.6921	0.6364	0.5509	0.4292	0.2947	0.1738	0.0023
	FFPE tumor	Exome	CD_19_09446_DP_WES	74569526	120979956	120979956	104861281	104627306	10332682902	7451212293	2085637189	2386375598	4803635212	0.7999	0.2001	0.7813	99.92	64.42	0.6098	0.3931	0.1517	0.6810	0.6443	0.6>				