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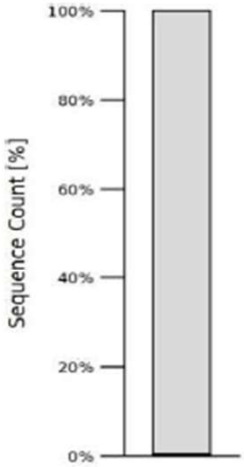
CLIA # 22D2300979

Patient Name	LastName, FirstName	Treatment Date	15-Dec-2019	ProtaGene ID	CLIA20010101BGW_01
MRN	999999999	Collection Date	16-Dec-2019	Visit #	1
DOB	01-J[illegible]9	Received Date	01-Jan-2020	Treatment	Treatment
Gender	M	Analysis Date	01-Feb-2020	Facility Sample ID	19-12-000001
Diagnosis	Dx	Approval Date	15-Feb-2020	Facility Name	Facility Name
Referring Physician	R[illegible]rring, MD	Sample Type	Blood		

[illegible]TEGRATION SITE (IS) ANALYSIS SUMMARY REPORT

Test Summary: IS analysis as [illegible]ine [illegible]afety evaluation to monitor for potential oncogenesis determined IS locations in DNA of the provided sampl[illegible] and [illegible]eir relative abundance as clonality measurement by S-EPTS/LM-PCR, next-generation sequencing, and bioinfo[illegible]atics[illegible]sis.

Result: IS profile is presented as relati[illegible]contrib[illegible]s of the ten most abundant IS.



Ran[illegible]	Gene	Freq. [%]	Location
Top1	ABCD1	0.098	3-49730512
Top2	ABCD2	0.087	5+128137918
Top3	ABCD3	0.076	9+31575888
Top4	[illegible]BCD4	0.065	17-76559300
Top5	[illegible]CD5	0.054	19-3684336
Top6	A[illegible]D6	0.043	X-53679022
Top7	ABCD7	0.032	20-62934580
Top8	ABCD8	0.021	7+135582483
Top9	ABC[illegible]	0.010	2-94552609
Top10	A[illegible]0	0.099	4+109488482
#All Other mapp. IS	[illegible]432	99.415	
Seq Count 10 strongest	[illegible]0		
Seq Count all other mapp. IS	190000		
Total Seq Counts Used	200000		

Caption: Gene name corresponds to RefSeq identification of genes located next to (or at) [illegible]. Loca[illegible] contains the chromosome number, sequence orientation (plus or minus strand), and locus of the IS (based on human reference ge[illegible]ome hg[illegible]

Comments: While increasing IS contribution may be associated with an increased ri[illegible]r a mali[illegible]ancy, it will not *a priori* result in a malignancy. Therefore, regular IS testing and timely trigger of enhanc[illegible] monitorin[illegible]s essential mitigation measure.

Note that sequencing reads mapping to multiple locations in the reference genome have been r[illegible]d from analysis. Frequency of the high contributing IS were not substantially changed. IS test results shoul[illegible]be t[illegible] sole basis for patient management. Results should be interpreted in consultation with a qualified licensed [illegible]alth [illegible]ctioner.

Approval: Result was reviewed and approved by the Laboratory Director, Pertti T.K. Toivola, PhD.

Report Version: V1