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CROSS CARE

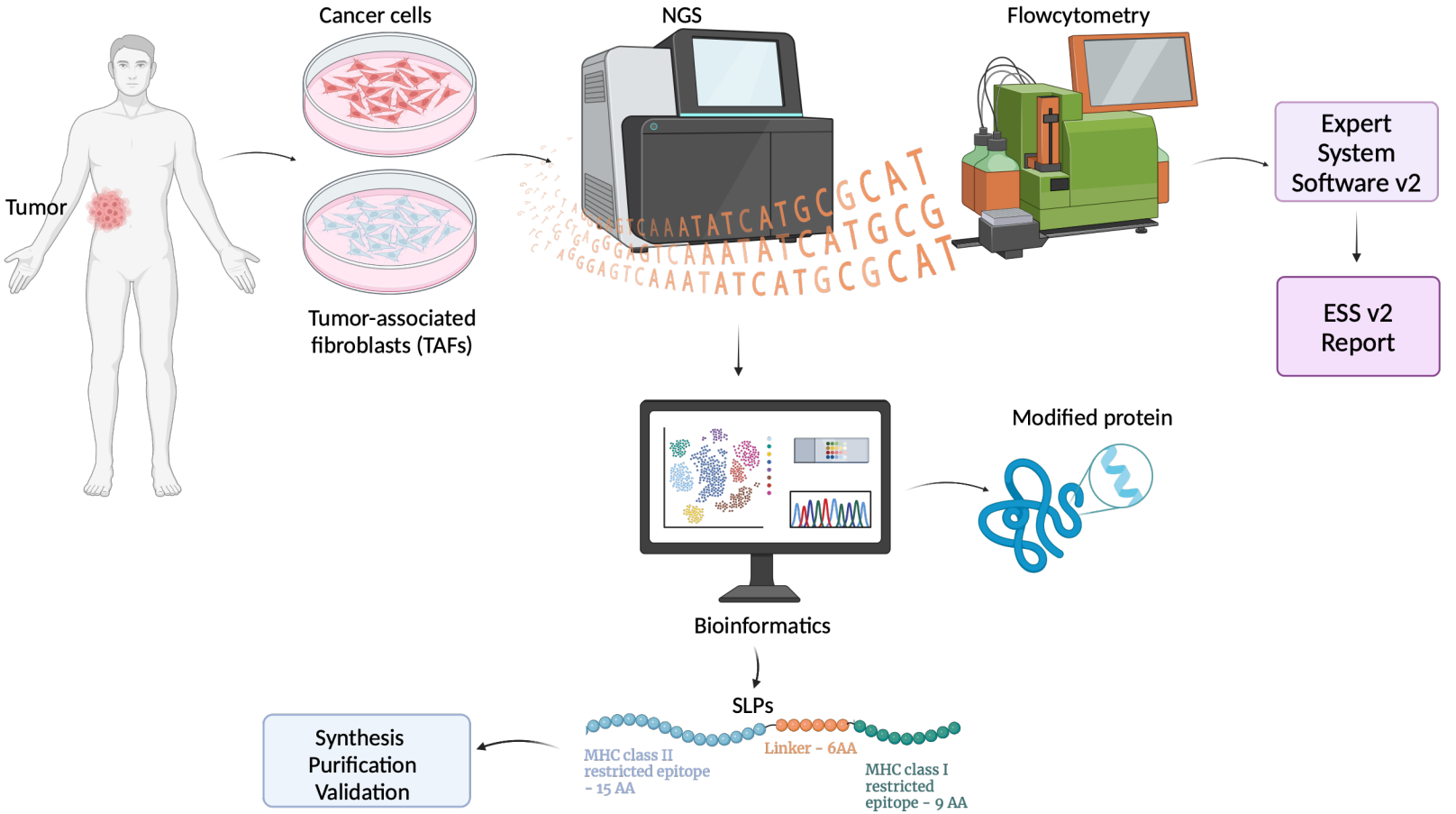
Benefits of implementing the Expert System Software in diagnostic and treatment of oncologic patients

OncoGen-Clinical Emergency County Hospital “Pius Brinzeu” Timisoara

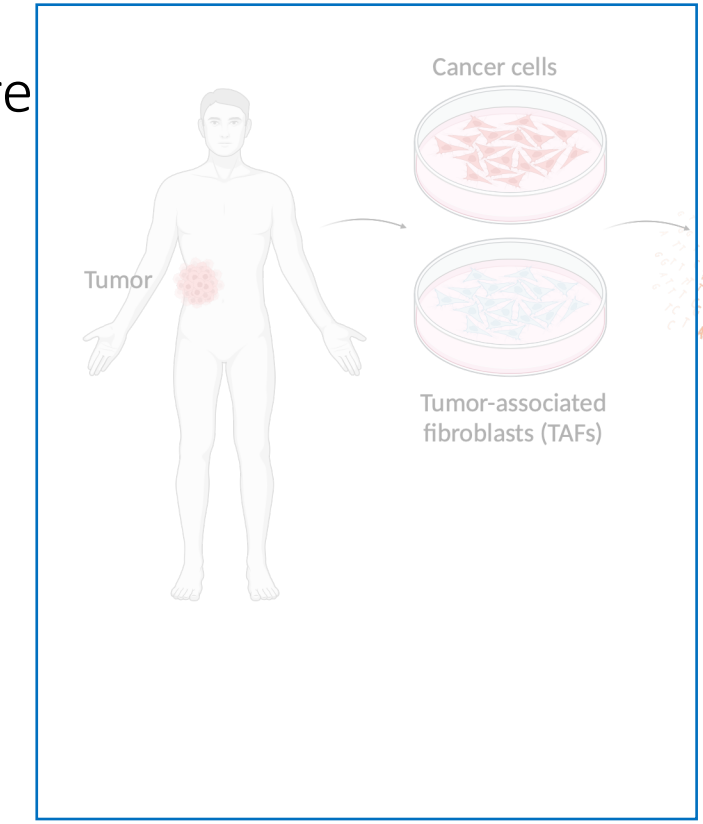
Medical and research team: Bojin Florina, Gavriliuc Oana, Cristea Mirabela, Buzan Roxana, Zbîrcea Lauriana, Grijincu Manuela, Simina Alina, Furdui Marieta, Șerban Daniela, Stanciu Claudia, Popoiu Tudor

Spitalul Clinic Județean de Urgență „Pius Brînzeu” Timișoara
OncoGen® Excellence Research Center
Општа болница "Борђе Јовановић" Opšta bolnica "Đorđe Joanović" 1895

The project

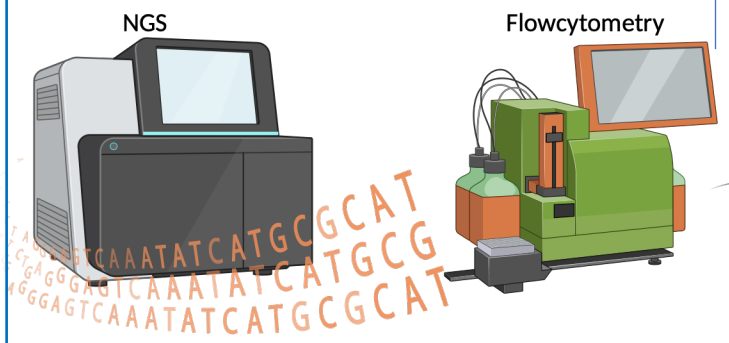

Tumor
Cancer cells
Tumor-associated fibroblasts (TAFs)
NGS
Flowcytometry
Expert System Software v2
ESS v2 Report
Modified protein
Bioinformatics
SLPs
MHC class II restricted epitope - 15 AA
Linker - 6AA
MHC class I restricted epitope - 9 AA
Synthesis
Purification
Validation
Timeline

Where we are

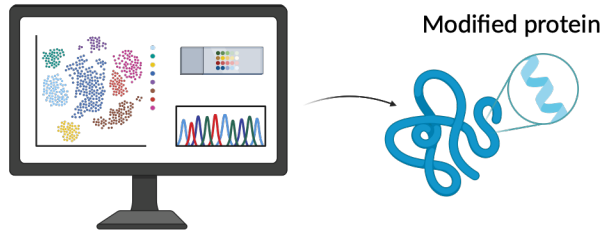


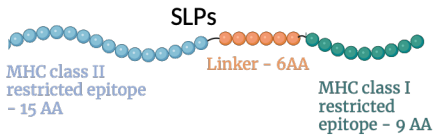
96 samples analyzed by NGS

121 samples analyzed by Cytek Northern Lights spectral flowcytometer



Demo version of the Expert System Software





- 205 blood and tumor tissue samples from SRB
- 103 blood and tumor tissue samples from RO

→ 1 peptide synthesized - FAP

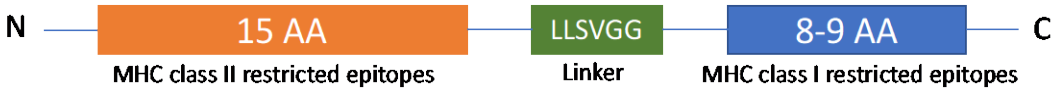
Timeline →

Protein synthesis

Liberty Blue 2.0
Automated Microwave Peptide Synthesizer

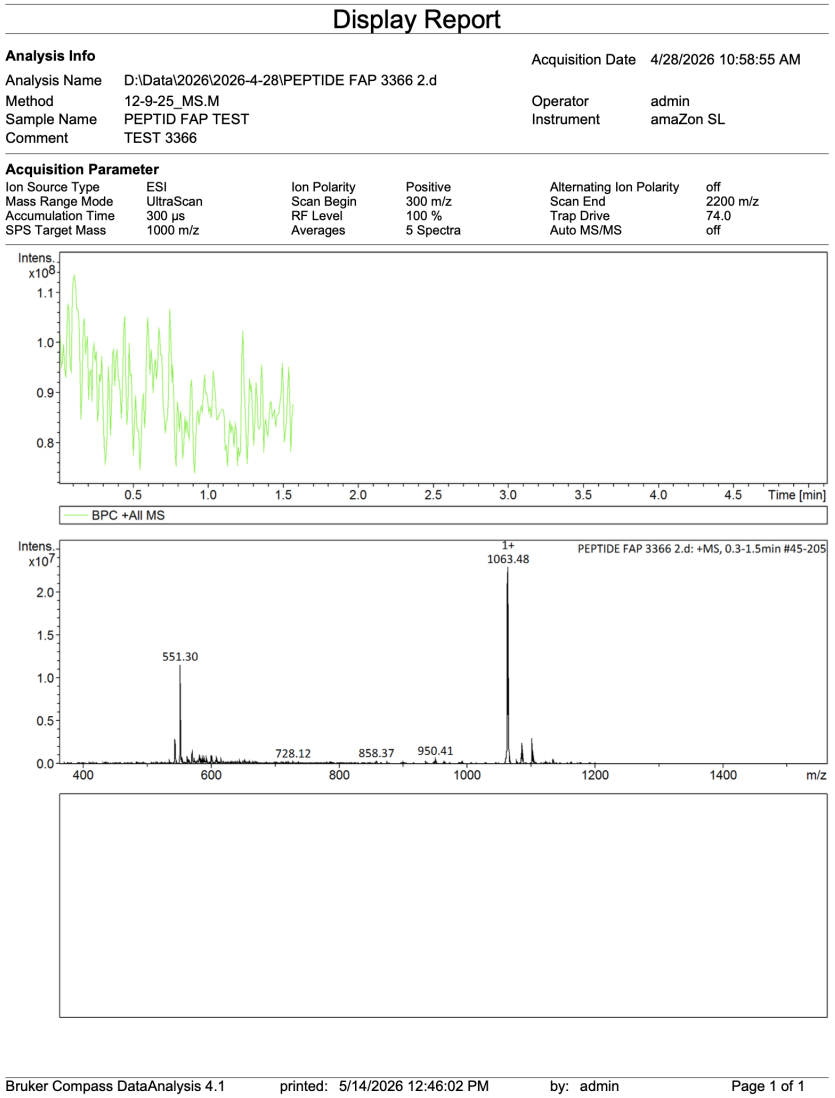
Protein synthesis

FAP_SLP_CrossCare
22.04.2026



FAP: Fibroblast activation protein
MHC class I: HLA A*02:01
MHC class II: strong for DRB1*01:01; very strong for DRB1*10:01; weak but still decent for DRB1*04:03

PDRQFVYLESDYSKL-LLSVGG-GLSGLSTNHL
(15 different AA)


Display Report

Analysis Info
Analysis Name D:\Data\2026\2026-4-28\PEPTIDE FAP 3366 2.d
Method 12-9-25_MS.M
Sample Name PEPTID FAP TEST
Comment TEST 3366
Acquisition Date 4/28/2026 10:58:55 AM
Operator admin
Instrument amaZon SL

Acquisition Parameter
Ion Source Type ESI | Ion Polarity Positive | Alternating Ion Polarity off
Mass Range Mode UltraScan | Scan Begin 300 m/z | Scan End 2200 m/z
Accumulation Time 300 µs | RF Level 100 % | Trap Drive 74.0
SPS Target Mass 1000 m/z | Averages 5 Spectra | Auto MS/MS off

Bruker Compass DataAnalysis 4.1 printed: 5/14/2026 12:46:02 PM by: admin Page 1 of 1

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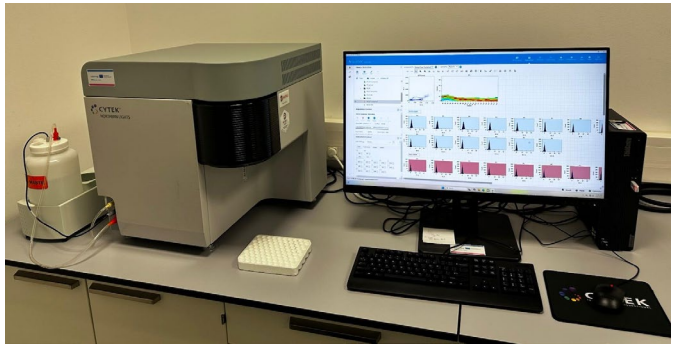
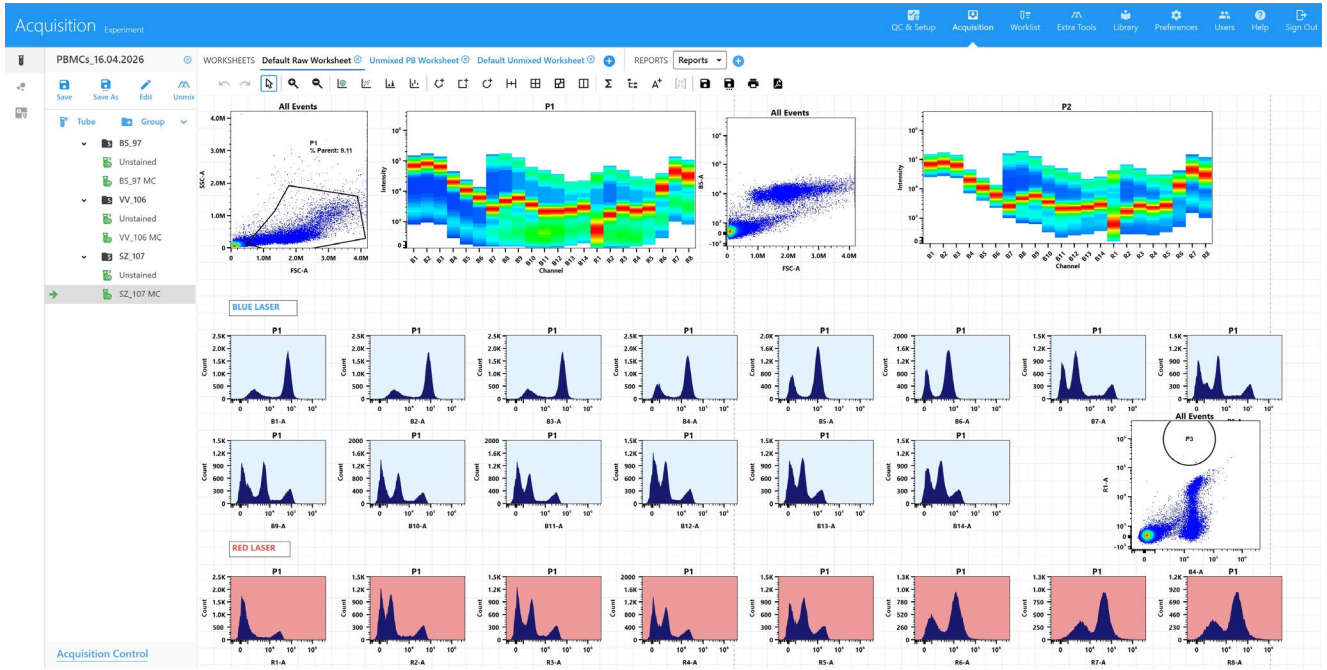
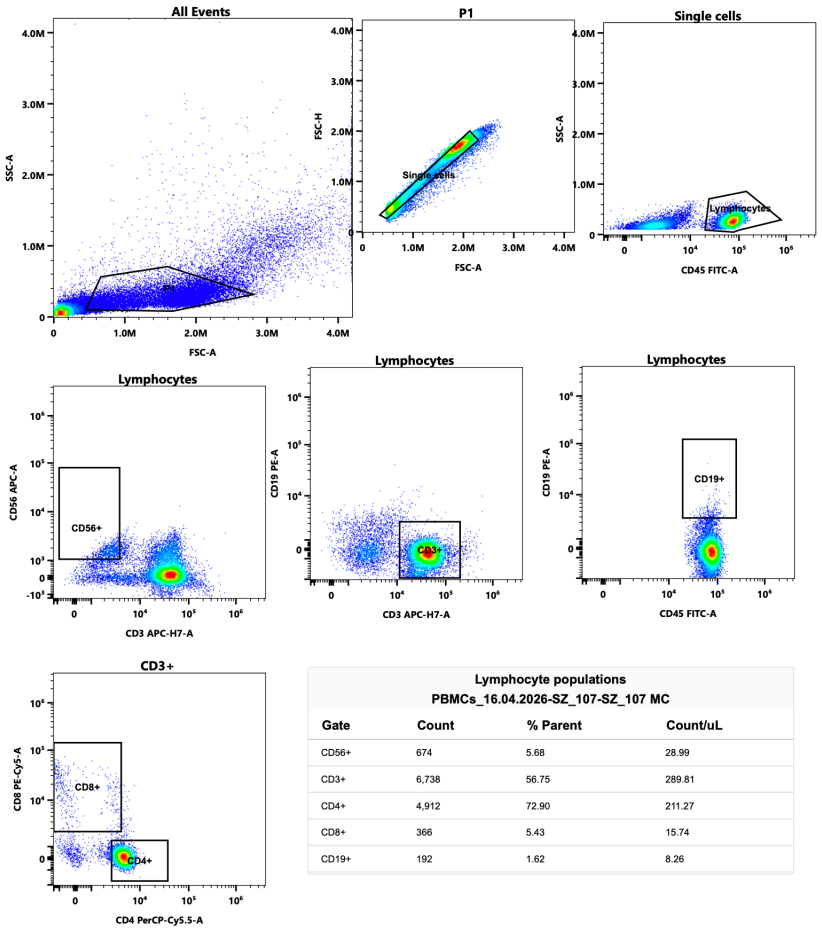
Cell analysis – flowcytometry
PBMCs / Peripheral blood







Lymphocyte populations
PBMCs_16.04.2026-SZ_107-SZ_107 MC

Gate	Count	% Parent	Count/uL
CD56+	674	5.68	28.99
CD3+	6,738	56.75	289.81
CD4+	4,912	72.90	211.27
CD8+	366	5.43	15.74
CD19+	192	1.62	8.26

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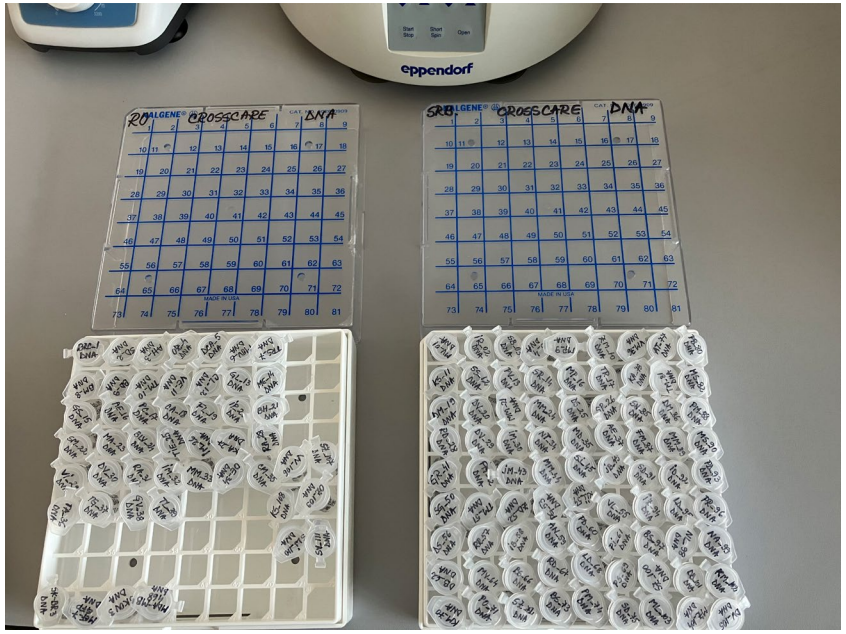
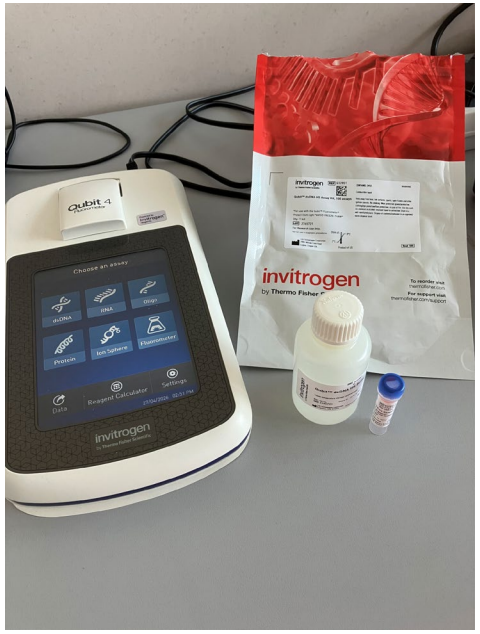
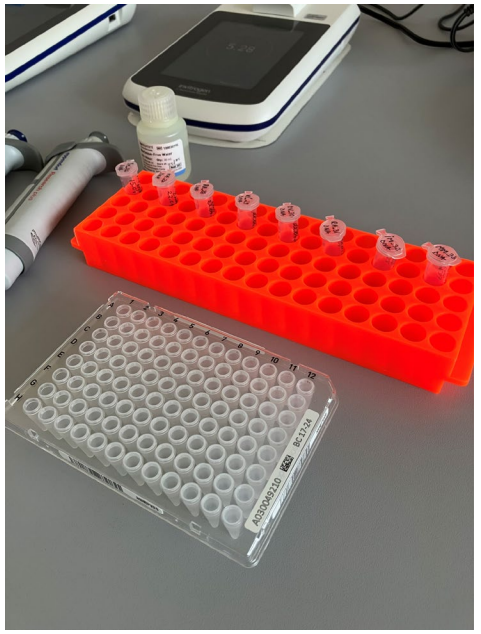
Tumor tissue analysis – Next generation Sequencing (NGS)



DNA purification

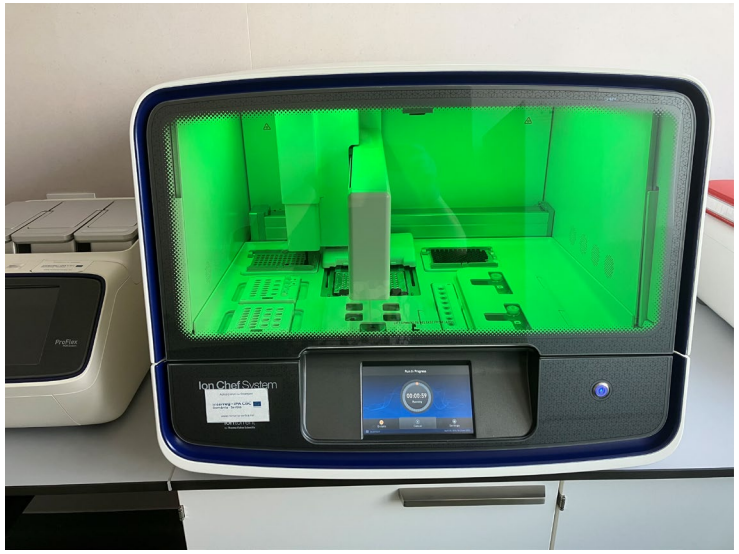


DNA quantification



8 sample libraries preparation

Tumor tissue analysis – Next generation Sequencing (NGS)



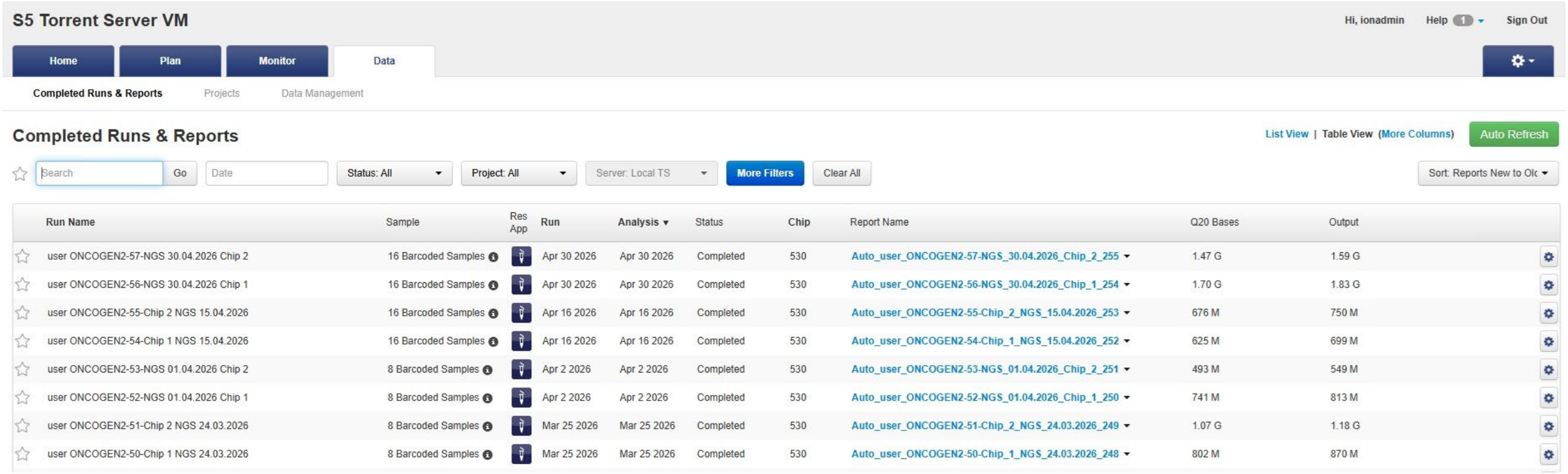
Library preparation / templating
Ion Chef

Sequencing
reagents

530 sequencing
chips

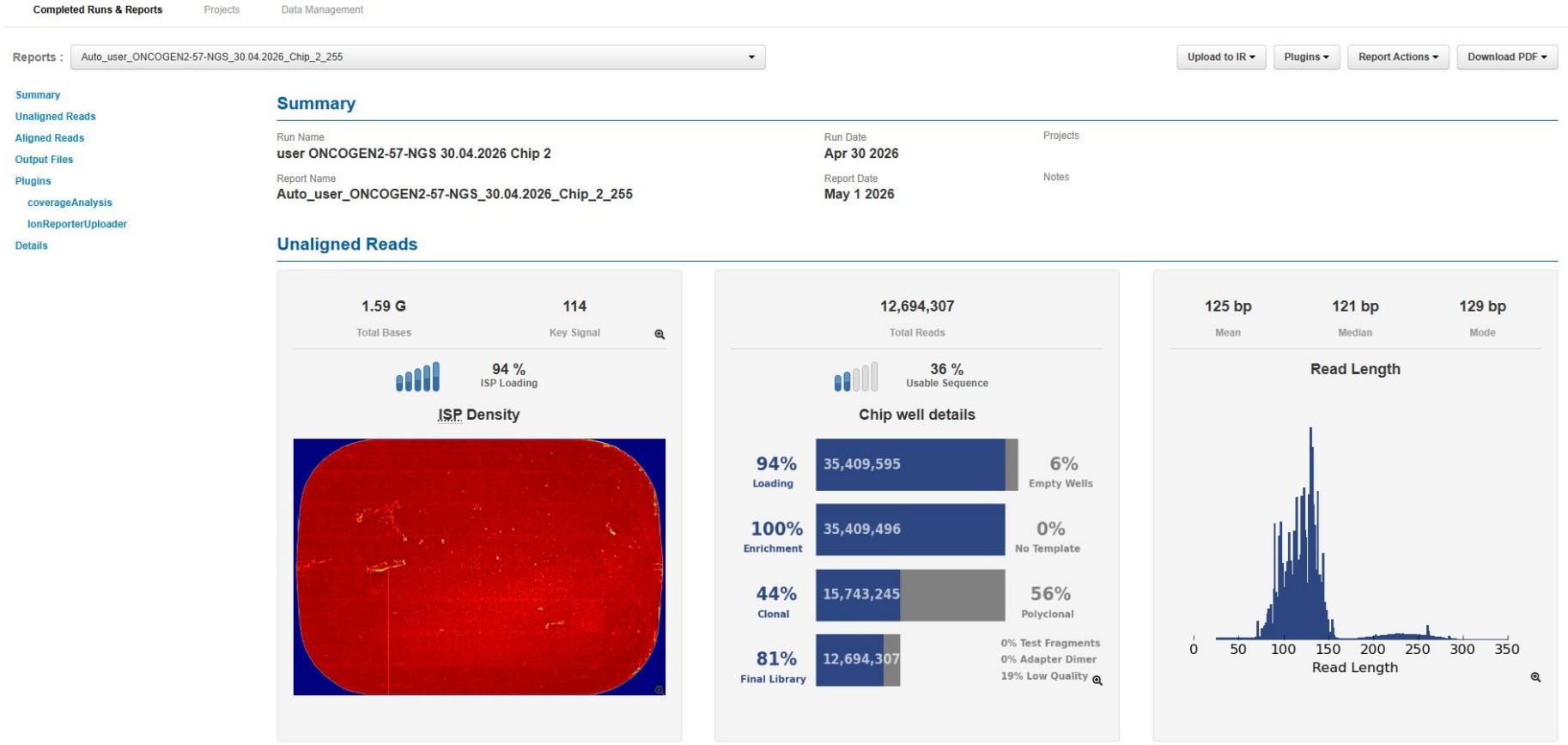
Sequencing
Ion GeneStudio S5

Tumor tissue analysis – Next generation Sequencing (NGS)



Run Name	Sample	Res App	Run	Analysis	Status	Chip	Report Name	Q20 Bases	Output
user ONCOGEN2-57-NGS 30.04.2026 Chip 2	16 Barcoded Samples		Apr 30 2026	Apr 30 2026	Completed	530	Auto_user_ONCOGEN2-57-NGS_30.04.2026_Chip_2_255	1.47 G	1.59 G
user ONCOGEN2-56-NGS 30.04.2026 Chip 1	16 Barcoded Samples		Apr 30 2026	Apr 30 2026	Completed	530	Auto_user_ONCOGEN2-56-NGS_30.04.2026_Chip_1_254	1.70 G	1.83 G
user ONCOGEN2-55-Chip 2 NGS 15.04.2026	16 Barcoded Samples		Apr 16 2026	Apr 16 2026	Completed	530	Auto_user_ONCOGEN2-55-Chip_2_NGS_15.04.2026_253	676 M	750 M
user ONCOGEN2-54-Chip 1 NGS 15.04.2026	16 Barcoded Samples		Apr 16 2026	Apr 16 2026	Completed	530	Auto_user_ONCOGEN2-54-Chip_1_NGS_15.04.2026_252	625 M	699 M
user ONCOGEN2-53-NGS 01.04.2026 Chip 2	8 Barcoded Samples		Apr 2 2026	Apr 2 2026	Completed	530	Auto_user_ONCOGEN2-53-NGS_01.04.2026_Chip_2_251	493 M	549 M
user ONCOGEN2-52-NGS 01.04.2026 Chip 1	8 Barcoded Samples		Apr 2 2026	Apr 2 2026	Completed	530	Auto_user_ONCOGEN2-52-NGS_01.04.2026_Chip_1_250	741 M	813 M
user ONCOGEN2-51-Chip 2 NGS 24.03.2026	8 Barcoded Samples		Mar 25 2026	Mar 25 2026	Completed	530	Auto_user_ONCOGEN2-51-Chip_2_NGS_24.03.2026_249	1.07 G	1.18 G
user ONCOGEN2-50-Chip 1 NGS 24.03.2026	8 Barcoded Samples		Mar 25 2026	Mar 25 2026	Completed	530	Auto_user_ONCOGEN2-50-Chip_1_NGS_24.03.2026_248	802 M	870 M

Tumor tissue analysis – Next generation Sequencing (NGS)



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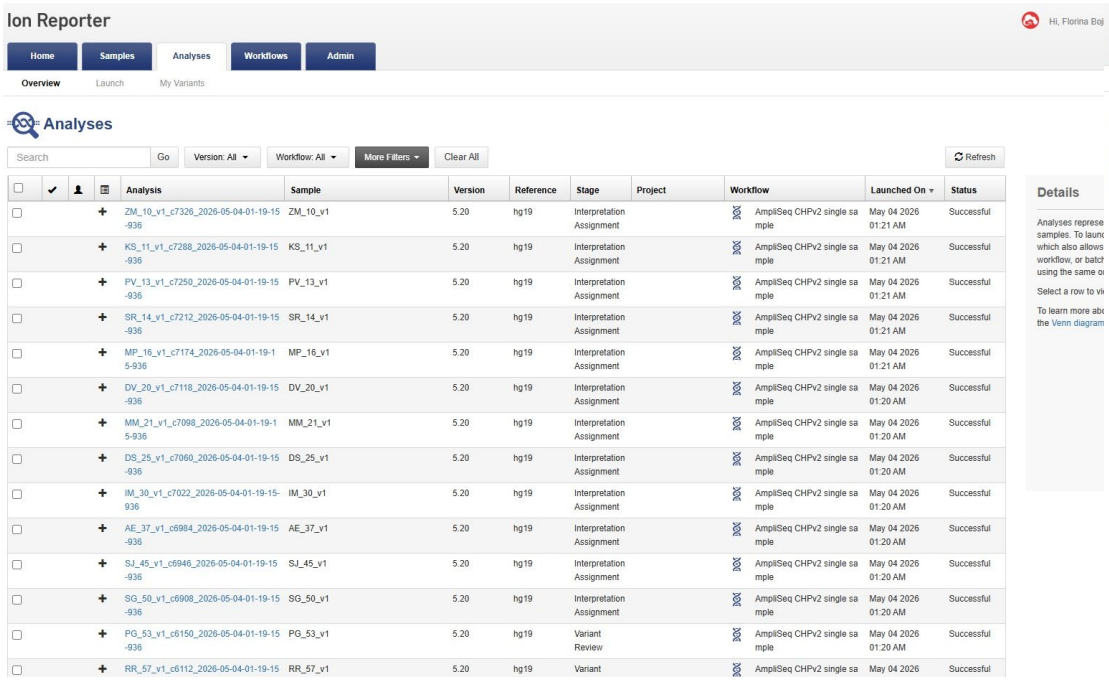
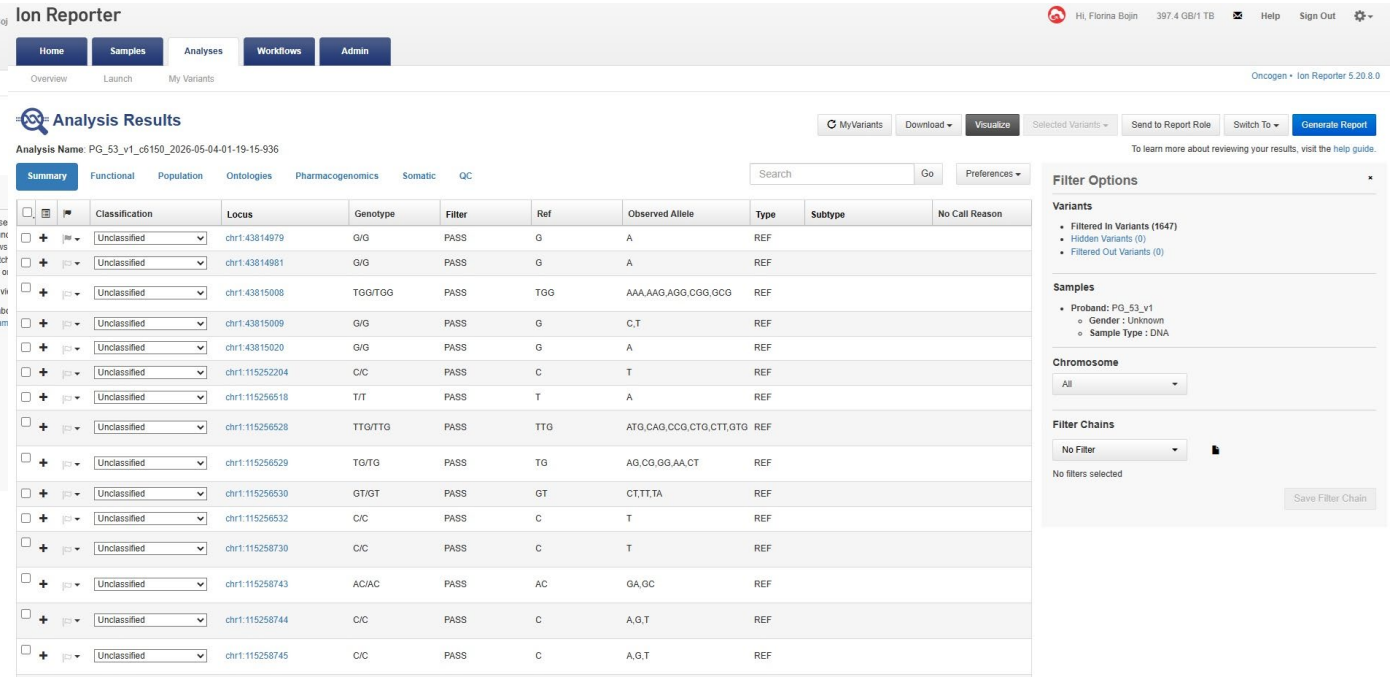
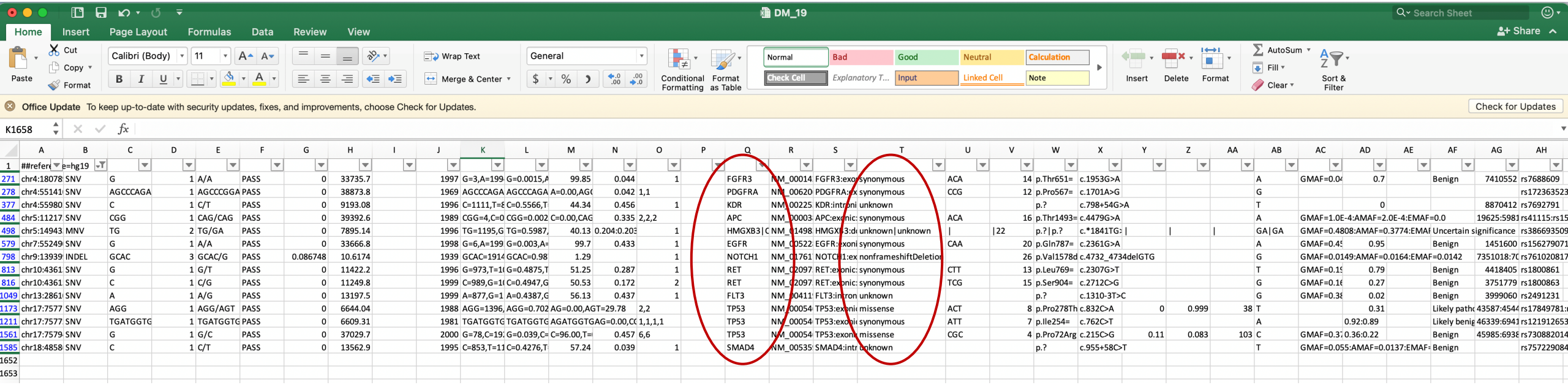
Tumor tissue analysis – IonReporter





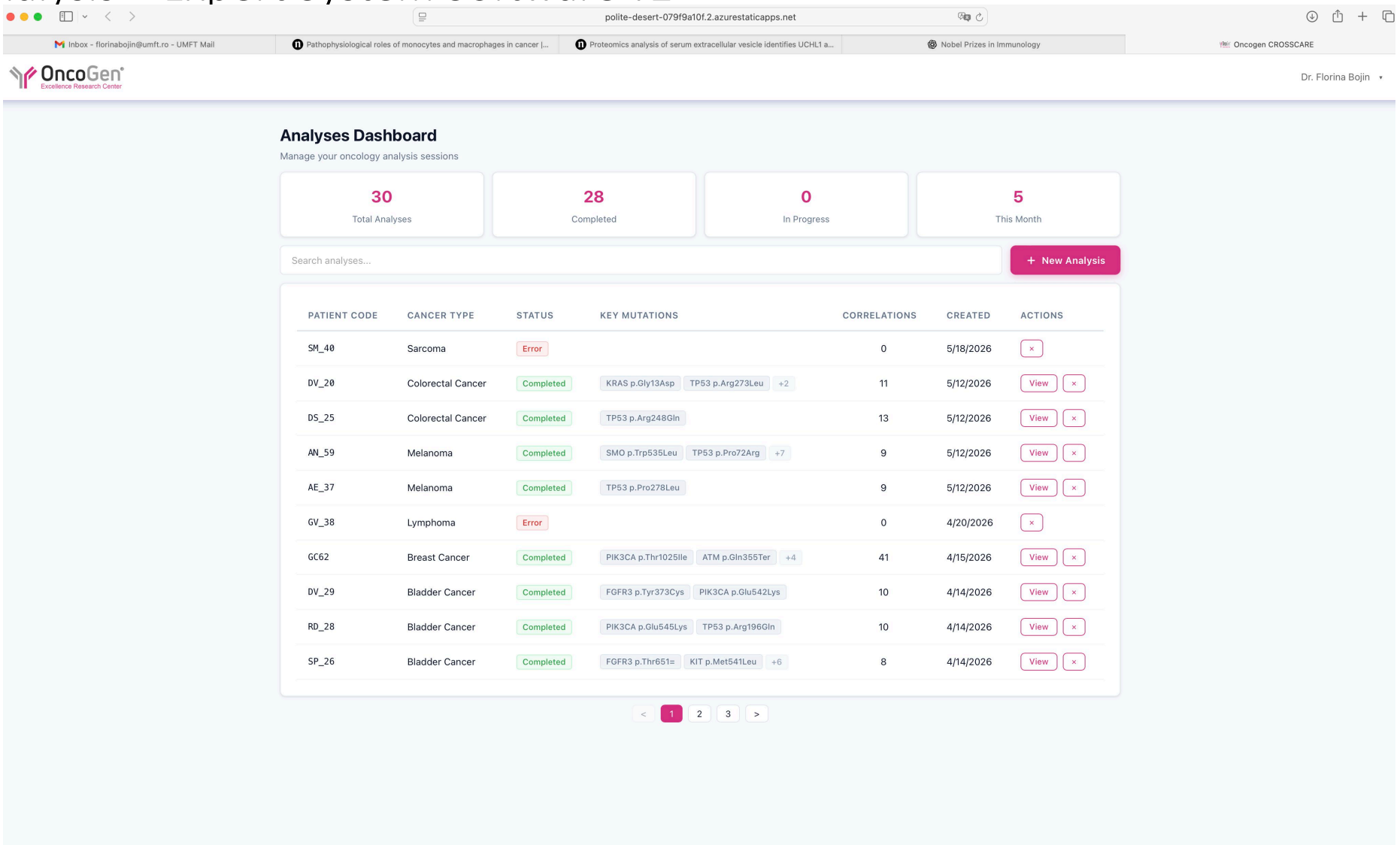
Tumor tissue analysis – IonReporter



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH
1	##refere	e=hg19																																
271	chr4:18078	SNV	G	1	A/A	PASS	0	33735.7		1997	G=3,A=199	G=0.0015,A	99.85	0.044	1		FGFR3	NM_00014	FGFR3:exon	synonymous	ACA	14	p.Thr651=	c.1953G>A				A	GMAF=0.04	0.7		Benign	7410552	rs7688609
278	chr4:55141	SNV	AGCCCAGA	1	AGCCCGGA	PASS	0	38873.8		1969	AGCCCAGA	AGCCCAGA	A=0.00,AG	0.042	1,1		PDGFRA	NM_00620	PDGFRA:ex	synonymous	CCG	12	p.Pro567=	c.1701A>G				G						rs172363523
377	chr4:55980	SNV	C	1	C/T	PASS	0	9193.08		1996	C=1111,T=8	C=0.5566,T	44.34	0.456	1		KDR	NM_00225	KDR:intron	unknown			p.?	c.798+54G>A				T		0			8870412	rs7692791
484	chr5:11217	SNV	CGG	1	CAG/CAG	PASS	0	39392.6		1989	CGG=4,C=0	CGG=0.002	C=0.00,CAG	0.335	2,2,2		APC	NM_00003	APC:exonic:	synonymous	ACA	16	p.Thr1493=	c.4479G>A				A	GMAF=1.0E-4	AMAF=2.0E-4	EMAF=0.0		19625:5981	rs41115:rs15
498	chr5:14943	MNV	TG	2	TG/GA	PASS	0	7895.14		1996	TG=1195,G	TG=0.5987,	40.13	0.204:0.203	1		HMGXB3|C	NM_01498	HMGXB3:de	unknown|unknown	|	|22	p.?|p.?	c.*1841TG>	|	|	|	GA|GA	GMAF=0.4808	AMAF=0.3774	EMAF	Uncertain significance		rs386693509
579	chr7:55249	SNV	G	1	A/A	PASS	0	33666.8		1998	G=6,A=199	G=0.003,A=	99.7	0.433	1		EGFR	NM_00522	EGFR:exon	synonymous	CAA	20	p.Gln787=	c.2361G>A				A	GMAF=0.45	0.95		Benign	1451600	rs156279071
798	chr9:13939	INDEL	GCAC	3	GCAC/G	PASS	0.086748	10.6174		1939	GCAC=1914	GCAC=0.98	1.29		1		NOTCH1	NM_01761	NOTCH1:ex	nonframeshiftDeletion		26	p.Val1578d	c.4732_4734delGTG				G	GMAF=0.0149	AMAF=0.0164	EMAF=0.0142		7351018:7(	rs761020817
813	chr10:4361	SNV	G	1	G/T	PASS	0	11422.2		1996	G=973,T=1(	G=0.4875,T	51.25	0.287	1		RET	NM_02097	RET:exonic:	synonymous	CTT	13	p.Leu769=	c.2307G>T				T	GMAF=0.19	0.79		Benign	4418405	rs1800861
816	chr10:4361	SNV	C	1	C/G	PASS	0	11249.8		1999	C=989,G=1(	C=0.4947,G	50.53	0.172	2		RET	NM_02097	RET:exonic:	synonymous	TCG	15	p.Ser904=	c.2712C>G				G	GMAF=0.16	0.27		Benign	3751779	rs1800863
1049	chr13:2861	SNV	A	1	A/G	PASS	0	13197.5		1999	A=877,G=1	A=0.4387,G	56.13	0.437	1		FLT3	NM_00411	FLT3:intron	unknown			p.?	c.1310-3T>C				G	GMAF=0.38	0.02		Benign	3999060	rs2491231
1173	chr17:7577	SNV	AGG	1	AGG/AGT	PASS	0	6644.04		1988	AGG=1396,	AGG=0.702	AG=0.00,AGT=29.78		2,2		TP53	NM_00054	TP53:exonic	missense	ACT	8	p.Pro278Th	c.832C>A	0	0.999	38	T		0.31		Likely patho	43587:4544	rs17849781:r
1211	chr17:7577	SNV	TGATGGTG	1	TGATGGTG	PASS	0	6609.31		1981	TGATGGTG	TGATGGTG	AGATGGTGAG=0.00,CC		1,1,1,1		TP53	NM_00054	TP53:exonic	synonymous	ATT	7	p.Ile254=	c.762C>T				A		0.92:0.89		Likely benig	46339:6941	rs121912653
1561	chr17:7579	SNV	G	1	G/C	PASS	0	37029.7		2000	G=78,C=19	G=0.039,C=	C=96.00,T=	0.457	6,6		TP53	NM_00054	TP53:exonic	missense	CGC	4	p.Pro72Arg	c.215C>G	0.11	0.083	103	C	GMAF=0.37	0.36:0.22		Benign	45985:6938	rs730882014
1585	chr18:4858	SNV	C	1	C/T	PASS	0	13562.9		1995	C=853,T=11	C=0.4276,T	57.24	0.039	1		SMAD4	NM_00535	SMAD4:intr	unknown			p.?	c.955+58C>T				T	GMAF=0.055	AMAF=0.0137	EMAF=	Benign		rs757229084
1652																																		
1653																																		

Generation of .xlsx file which is uploaded into Expert System Software v2

Integrated analysis – Expert System Software v2



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Analyses Dashboard

Manage your oncology analysis sessions

30	28	0	5
Total Analyses	Completed	In Progress	This Month

Search analyses...

+ New Analysis

PATIENT CODE	CANCER TYPE	STATUS	KEY MUTATIONS	CORRELATIONS	CREATED	ACTIONS
SM_40	Sarcoma	Error		0	5/18/2026	×
DV_20	Colorectal Cancer	Completed	KRAS p.Gly13Asp, TP53 p.Arg273Leu, +2	11	5/12/2026	View ×
DS_25	Colorectal Cancer	Completed	TP53 p.Arg248Gln	13	5/12/2026	View ×
AN_59	Melanoma	Completed	SMO p.Trp535Leu, TP53 p.Pro72Arg, +7	9	5/12/2026	View ×
AE_37	Melanoma	Completed	TP53 p.Pro278Leu	9	5/12/2026	View ×
GV_38	Lymphoma	Error		0	4/20/2026	×
GC62	Breast Cancer	Completed	PIK3CA p.Thr1025Ile, ATM p.Gln355Ter, +4	41	4/15/2026	View ×
DV_29	Bladder Cancer	Completed	FGFR3 p.Tyr373Cys, PIK3CA p.Glu542Lys	10	4/14/2026	View ×
RD_28	Bladder Cancer	Completed	PIK3CA p.Glu545Lys, TP53 p.Arg196Gln	10	4/14/2026	View ×
SP_26	Bladder Cancer	Completed	FGFR3 p.Thr651=, KIT p.Met541Leu, +6	8	4/14/2026	View ×

< 1 2 3 >

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1 Upload — 2 Review — 3 Markers — 4 Correlate

Analysing variants...

Running variant analysis pipeline — enrichment, guideline therapy research, and ranking

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Upload — 2 Review — 3 Markers — 4 Correlate

Review Extracted Data

8 variants analysed, 1 actionable (Tier I/II)

Patient Information

PATIENT CODE	CANCER TYPE	VARIANTS	ACTIONABLE
DS	Colorectal Cancer	8	1

Actionable Variants (1)

TIER	GENE	VARIANT	TYPE	SCORE
Tier I	KRAS	p.Gly12Asp	missense	83.7

Other Variants (7)

TIER	GENE	VARIANT	TYPE	SCORE
Tier IV	TP53	p.Pro72Arg	missense	6.2
Tier IV	KIT	p.Met541Leu	missense	5.2
Tier IV	APC	p.Thr1493=	synonymous	3.3
Tier IV	EGFR	p.Gln787=	synonymous	2.8
Tier IV	HRAS	p.His27=	synonymous	2.4
Tier IV	FGFR3	p.Thr651=	synonymous	2.3
Tier IV	PDGFRA	p.Pro567=	synonymous	2.3

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Upload — Review — Markers — 4 Correlate

AI Correlation

Correlating patient data with scientific literature, clinical trials, and pharmacogenomics databases.

✓ SAVING MARKERS ✓ GUIDELINE RESEARCH ✓ PERSISTING THERAPIES ✓ FINALISED

Finalizing

Processing Log

```
12:48:28 PM  Saving biomarkers and immune markers…
12:48:31 PM  Starting guideline therapy research for 1 actionable genes: KRAS
12:48:35 PM  Starting PubMed Enrichment in parallel…
12:54:59 PM  Found therapies for 0 genes, persisting…
12:55:00 PM  Synthesizing findings…
12:57:34 PM  Research Synthesis complete
             (cache_key=7e3c4b64d76656d19bd3b21ff514dd4b710ac8fc401d47e379166299b06d3d72)
12:57:34 PM  Finalizing report…
```

View Correlation Report →

Input Summary

PATIENT

DS · Colorectal Cancer

MUTATIONS (8)

- **KRAS** p.Gly12Asp
- **TP53** p.Pro72Arg
- **KIT** p.Met541Leu
- **APC** p.Thr1493=
- **EGFR** p.Gln787=

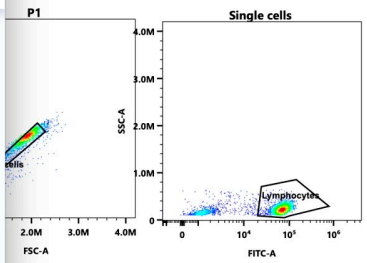
+3 more

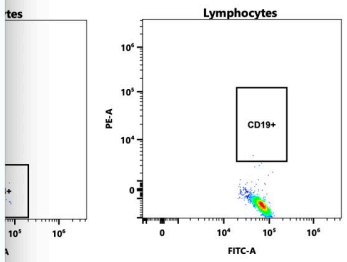
BIOMARKERS (0)

None selected

IMMUNE PROFILE (5)

- B cells (Lymphocytes): low
- CD3 (Lymphocytes): low
- CD4 (CD3): low
- CD8 (CD3): low
- NK cells (Lymphocytes): low





Lymphocyte populations
PBMC_06.03.2026-DS_25-DS_25 MC

	% Parent	Count/uL
	16.82	154.73
	9.17	84.36
	50.73	42.80
	29.27	24.69
	0.04	0.41

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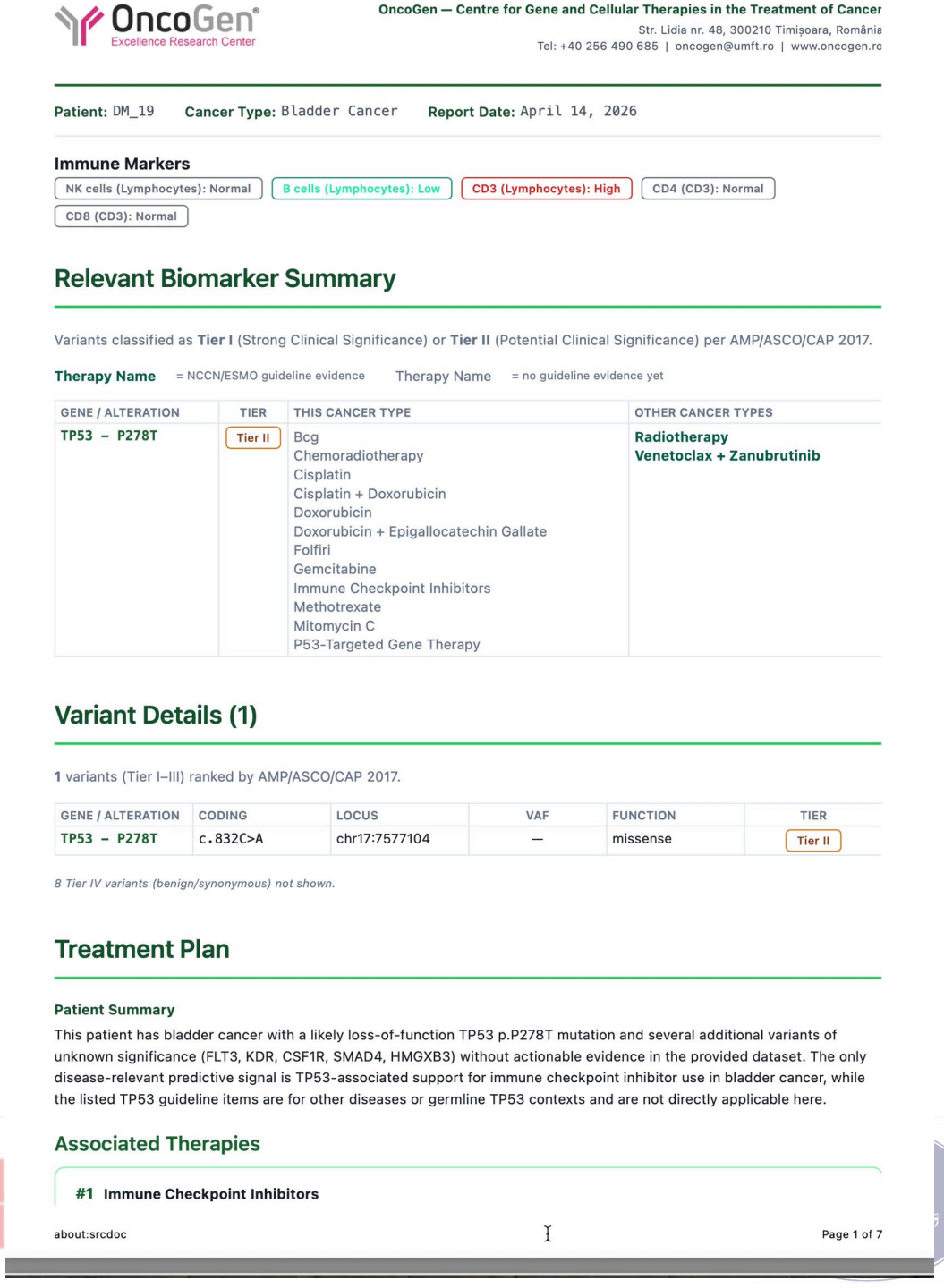
IPA Romania – Serbia
Co-funded by the European Union

CROSS CARE

Integrated analysis – Expert System Software v2



OncoGen
Excellence Research Center

OncoGen — Centre for Gene and Cellular Therapies in the Treatment of Cancer
Str. Lidia nr. 48, 300210 Timișoara, România
Tel: +40 256 490 685 | oncogen@umft.ro | www.oncogen.ro

Patient: DM_19 **Cancer Type:** Bladder Cancer **Report Date:** April 14, 2026

Immune Markers

NK cells (Lymphocytes): Normal | B cells (Lymphocytes): Low | CD3 (Lymphocytes): High | CD4 (CD3): Normal | CD8 (CD3): Normal

Relevant Biomarker Summary

Variants classified as **Tier I** (Strong Clinical Significance) or **Tier II** (Potential Clinical Significance) per AMP/ASCO/CAP 2017.

Therapy Name = NCCN/ESMO guideline evidence Therapy Name = no guideline evidence yet

GENE / ALTERATION	TIER	THIS CANCER TYPE	OTHER CANCER TYPES
TP53 – P278T	Tier II	Bcg Chemoradiotherapy Cisplatin Cisplatin + Doxorubicin Doxorubicin Doxorubicin + Epigallocatechin Gallate Folfiri Gemcitabine Immune Checkpoint Inhibitors Methotrexate Mitomycin C P53-Targeted Gene Therapy	**Radiotherapy** **Venetoclax + Zanubrutinib**

Variant Details (1)

1 variants (Tier I–III) ranked by AMP/ASCO/CAP 2017.

GENE / ALTERATION	CODING	LOCUS	VAF	FUNCTION	TIER
TP53 – P278T	c.832C>A	chr17:7577104	—	missense	Tier II

8 Tier IV variants (benign/synonymous) not shown.

Treatment Plan

Patient Summary

This patient has bladder cancer with a likely loss-of-function TP53 p.P278T mutation and several additional variants of unknown significance (FLT3, KDR, CSF1R, SMAD4, HMGXB3) without actionable evidence in the provided dataset. The only disease-relevant predictive signal is TP53-associated support for immune checkpoint inhibitor use in bladder cancer, while the listed TP53 guideline items are for other diseases or germline TP53 contexts and are not directly applicable here.

Associated Therapies

#1 Immune Checkpoint Inhibitors

about:srcdoc

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Patient: DM_19 **Cancer Type:** Bladder Cancer **Report Date:** April 14, 2026

Patient Summary

Patient Code	DM_19
Diagnosis	Bladder Cancer
Total Variants Analyzed	9
Actionable Findings	1
Key Mutations	TP53 (p.Pro278Thr)
Immune Markers	NK cells (Lymphocytes): normal, B cells (Lymphocytes): low, CD3 (Lymphocytes): high, CD4 (CD3): normal, CD8 (CD3): normal

Genomic Analysis & Associated Therapies

Your tumour sample was analysed for genetic changes. For each relevant gene below, we list the associated therapies — both for your specific cancer type and for other cancers where the same gene is targeted. All treatment decisions should be made by your oncology team.

● Indicated for this cancer type ○ Indicated for other cancer types

TP53 Potential clinical significance

TP53 P278T is a likely loss-of-function missense alteration in a tumor suppressor gene that is frequently

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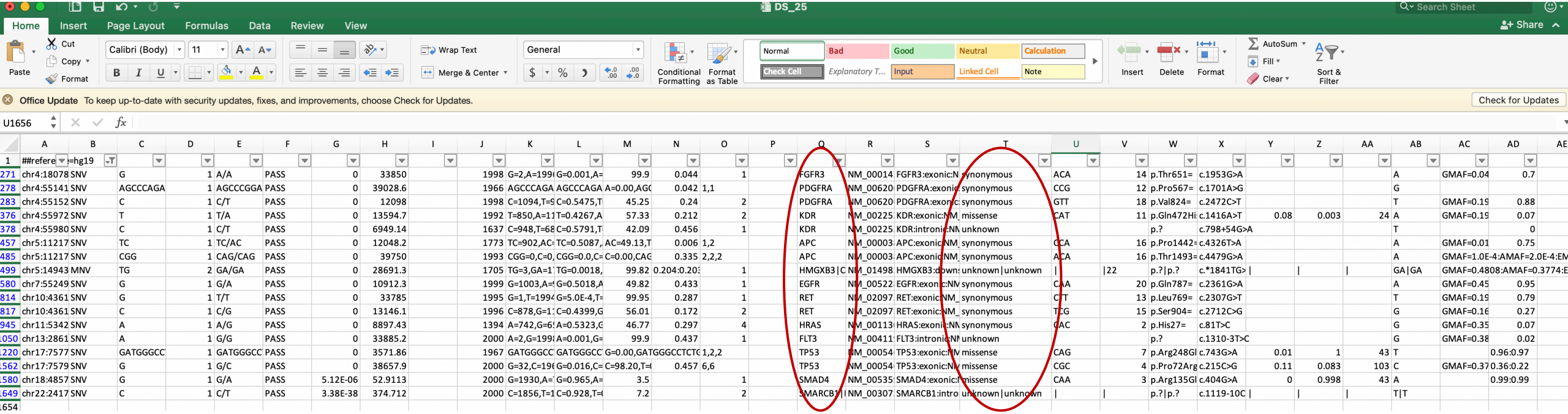
Tumor tissue analysis – IonReporter



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	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE
1	##refere	=hg19																													
271	chr4:18078	SNV	G	1	A/A	PASS	0	33850		1998	G=2,A=199	G=0.001,A=	99.9	0.044	1		FGFR3	NM_00014	FGFR3:exonic:N	synonymous	ACA	14	p.Thr651=	c.1953G>A				A	GMAF=0.04	0.7	
278	chr4:55141	SNV	AGCCCAGA	1	AGCCCGGA	PASS	0	39028.6		1966	AGCCCAGA	AGCCCAGA	A=0.00,AG	0.042	1,1		PDGFRA	NM_00620	PDGFRA:exonic	synonymous	CCG	12	p.Pro567=	c.1701A>G				G			
283	chr4:55152	SNV	C	1	C/T	PASS	0	12098		1998	C=1094,T=9	C=0.5475,T	45.25	0.24	2		PDGFRA	NM_00620	PDGFRA:exonic:	synonymous	GTT	18	p.Val824=	c.2472C>T				T	GMAF=0.19	0.88	
376	chr4:55972	SNV	T	1	T/A	PASS	0	13594.7		1992	T=850,A=11	T=0.4267,A	57.33	0.212	2		KDR	NM_00225	KDR:exonic:NM_	missense	CAT	11	p.Gln472Hi	c.1416A>T	0.08	0.003	24	A	GMAF=0.19	0.07	
378	chr4:55980	SNV	C	1	C/T	PASS	0	6949.14		1637	C=948,T=68	C=0.5791,T	42.09	0.456	1		KDR	NM_00225	KDR:intronic:NM	unknown			p.?	c.798+54G>A				T		0	
457	chr5:11217	SNV	TC	1	TC/AC	PASS	0	12048.2		1773	TC=902,AC=	TC=0.5087,	AC=49.13,T	0.006	1,2		APC	NM_00003	APC:exonic:NM_	synonymous	CCA	16	p.Pro1442=	c.4326T>A				A	GMAF=0.01	0.75	
485	chr5:11217	SNV	CGG	1	CAG/CAG	PASS	0	39750		1993	CGG=0,C=0,	CGG=0.0,C=	C=0.00,CAG	0.335	2,2,2		APC	NM_00003	APC:exonic:NM_	synonymous	ACA	16	p.Thr1493=	c.4479G>A				A	GMAF=1.0E-4:AMAF=2.0E-4:EM		
499	chr5:14943	MNV	TG	2	GA/GA	PASS	0	28691.3		1705	TG=3,GA=1	TG=0.0018,	99.82	0.204:0.203	1		HMGXB3|C	NM_01498	HMGXB3:down	unknown|unknown	|	|22	p.?|p.?	c.*1841TG>	|	|	|	GA|GA	GMAF=0.4808:AMAF=0.3774:E		
580	chr7:55249	SNV	G	1	G/A	PASS	0	10912.3		1999	G=1003,A=	G=0.5018,A	49.82	0.433	1		EGFR	NM_00522	EGFR:exon	synonymous	CAA	20	p.Gln787=	c.2361G>A				A	GMAF=0.45	0.95	
814	chr10:4361	SNV	G	1	T/T	PASS	0	33785		1995	G=1,T=199	G=5.0E-4,T=	99.95	0.287	1		RET	NM_02097	RET:exonic:NM_	synonymous	CTT	13	p.Leu769=	c.2307G>T				T	GMAF=0.19	0.79	
817	chr10:4361	SNV	C	1	C/G	PASS	0	13146.1		1996	C=878,G=1	C=0.4399,G	56.01	0.172	2		RET	NM_02097	RET:exonic:NM_	synonymous	TCG	15	p.Ser904=	c.2712C>G				G	GMAF=0.16	0.27	
945	chr11:5342	SNV	A	1	A/G	PASS	0	8897.43		1394	A=742,G=6	A=0.5323,G	46.77	0.297	4		HRAS	NM_00113	HRAS:exonic:NM	synonymous	CAC	2	p.His27=	c.81T>C				G	GMAF=0.35	0.07	
1050	chr13:2861	SNV	A	1	G/G	PASS	0	33885.2		2000	A=2,G=199	A=0.001,G=	99.9	0.437	1		FLT3	NM_00411	FLT3:intronic:NM	unknown			p.?	c.1310-3T>C				G	GMAF=0.38	0.02	
1220	chr17:7577	SNV	GATGGGCC	1	GATGGGCC	PASS	0	3571.86		1967	GATGGGCC	GATGGGCC	G=0.00,GATGGGCCTCTC		1,2,2		TP53	NM_00054	TP53:exonic:NM	missense	CAG	7	p.Arg248Gl	c.743G>A	0.01	1	43	T		0.96:0.97	
1562	chr17:7579	SNV	G	1	G/C	PASS	0	38657.9		2000	G=32,C=19	G=0.016,C=	C=98.20,T=	0.457	6,6		TP53	NM_00054	TP53:exonic:NM	missense	CGC	4	p.Pro72Arg	c.215C>G	0.11	0.083	103	C	GMAF=0.37	0.36:0.22	
1580	chr18:4857	SNV	G	1	G/A	PASS	5.12E-06	52.9113		2000	G=1930,A=	G=0.965,A=	3.5		1		SMAD4	NM_00535	SMAD4:exonic:	missense	CAA	3	p.Arg135Gl	c.404G>A	0	0.998	43	A		0.99:0.99	
1649	chr22:2417	SNV	C	1	C/T	PASS	3.38E-38	374.712		2000	C=1856,T=1	C=0.928,T=	7.2		2		SMARCB1|	NM_00307	SMARCB1:intro	unknown|unknown	|	|	p.?|p.?	c.1119-10C	|	|	|	T|T			
1654																															

Spitalul Clinic Județean de Urgență „Pius Brînzeu" Timișoara

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Patient: DS_25 **Cancer Type:** Colorectal Cancer **Report Date:** May 12, 2026

Immune Markers

B cells (Lymphocytes): Low | CD3 (Lymphocytes): Low | CD4 (CD3): Normal | CD8 (CD3): Normal | NK cells (Lymphocytes): Normal

Relevant Biomarker Summary

Variants classified as **Tier I** (Strong Clinical Significance) or **Tier II** (Potential Clinical Significance) per AMP/ASCO/CAP 2017.

Therapy Name = NCCN/ESMO guideline evidence Therapy Name = no guideline evidence yet

GENE / ALTERATION	TIER	THIS CANCER TYPE	OTHER CANCER TYPES
TP53 – R248Q	Tier II	5-Fluorouracil 5-Fluorouracil + Genistein Bevacizumab Bevacizumab + Oxaliplatin + Uft Celecoxib Cetuximab Cetuximab + Oxaliplatin + Uft Irinotecan Mdm2-P53 Interaction Inhibitors Nutlin-3 Olaparib Olaparib + Ku55933 Oxaliplatin P53 Inhibition P53 Reactivating Compounds P53 Restoration / P53 Pathway Restoration P53-Targeted Immunotherapy / Neoantigen T-Cell Therapy Radiotherapy Regorafenib Regorafenib + Other Targeted Therapy Combinations Rita	—

Variant Details (2)

2 variants (Tier I–III) ranked by AMP/ASCO/CAP 2017.

GENE / ALTERATION	CODING	LOCUS	VAF	FUNCTION	TIER
TP53 – R248Q	c.743G>A	chr17:7577528	—	missense	Tier II
SMAD4 – R135Q	c.404G>A	chr18:48575210	—	missense	Tier III

11 Tier IV variants (benign/synonymous) not shown.

Treatment Plan

Conclusions and Next steps

Integration of complex oncologic data improves precision medicine approaches

Expert System Software v2 demonstrates that the integration of **NGS data**, **immune profile**, and **circulating tumor biomarkers** into a single AI-based platform can support a more comprehensive characterization of oncologic patients and facilitate personalized therapeutic decisions.

Artificial intelligence can accelerate translational oncology

By automatically correlating molecular findings with **scientific literature**, **clinical databases**, and **international treatment guidelines**, the platform significantly reduces the time required for data interpretation and supports faster translation of research discoveries into clinical practice.

Multidisciplinary decision-making benefits from digital clinical support systems

The software provides clinicians and tumor boards with structured, evidence-based information derived from **NCCN**, **ESMO**, **FDA**, **EMA**, **ClinVar**, and **ongoing clinical trials**, thus improving access to updated oncologic knowledge and supporting standardized clinical decision-making.

Conclusions and Next steps

AI-assisted platforms may contribute to more personalized and adaptive cancer treatment

The integration of molecular and immunological patient profiles allows the identification of actionable mutations, predictive biomarkers, and potential targeted or immunotherapeutic strategies, supporting the transition from conventional oncology toward precision and personalized medicine.

Cross-border collaborative digital infrastructures represent an important direction for future oncology care

The development of **Expert System Software v2** within the **CrossCare project** highlights the importance of international collaboration in digital health, AI-assisted diagnostics, and interoperable oncologic platforms, with the potential to improve patient access to advanced diagnostic and therapeutic strategies across regions.

Next steps include the sequencing and integrative analysis of additional tumor samples, alongside the continuous optimization of **Expert System Software v2** for faster data processing and dynamic updating of oncologic knowledge databases.

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BETTER diagnosis, care, lives!

Thank you!

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