

Preliminary Analysis of Nuclei

Classification (Break Apart and Fusion)

Classification	Count	Percentage
ExpectedCountable	103	95.5
ExpectedNotCountable	4	3.6
SingleFusion	10	9.3
DoubleFusion	5	4.6
TotalCount	122	113.0

Enumeration of Probes

Nuclei	Class	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12	#13
C	2	2	0361	0001	0004	19	52	224						
C	2	2	0363	0003	0011	11	64	90						
C	2	2	0362	0003	0013	11	64	90						
C	2	2	0427	0005	0018	15	64	192						
C	2	2	0429	0006	0023	13	83	147						
C	2	2	0428	0006	0025	13	83	147						
C	2	2	0407	0007	0031	17	83	84						
C	2	2	0361	0008	0033	16	65	121						
C	2	2	0364	0009	0037	14	71	171						
C	2	2	0408	0010	0043	17	62	144						
C	2	2	0363	0011	0047	17	52	236						
C	2	2	0406	0012	0050	25	43	177						
C	2	2	0407	0013	0053	15	61	104						
C	2	2	0407	0013	0055	15	61	104						
C	2	2	0395	0014	0059	14	57	145						
C	2	2	0395	0014	0063	14	57	145						
C	2	2	0395	0014	0061	14	57	145						
C	2	2	0361	0015	0066	13	50	72						
C	2	2	0406	0017	0074	13	55	157						
C	2	2	0406	0017	0078	13	55	157						
C	2	2	0428	0018	0079	12	59	163						
C	2	2	0428	0018	0083	12	59	163						
C	2	2	0393	0019	0087	15	52	127						
C	2	2	0364	0023	0089	15	69	233						
C	2	2	0364	0023	0100	15	69	233						
C	2	2	0428	0024	0104	13	65	129						
C	2	2	0429	0024	0106	13	66	129						
C	2	2	0363	0025	0115	14	61	153						
C	2	2	0428	0027	0116	14	62	88						
C	2	2	0429	0027	0117	14	62	88						
C	2	2	0405	0029	0124	16	65	142						
C	2	2	0405	0029	0126	16	65	142						
C	2	2	0405	0029	0127	16	65	142						
C	2	2	0407	0030	0129	18	52	141						
C	2	2	0427	0031	0131	15	62	133						

Example of viewable results for Abbott LSI® PML/RARA dual color, dual fusion translocation probe assay in normal human blood. The PML gene is labeled in SpectrumOrange®. The LSI RARA gene is labeled in SpectrumGreen®.

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Ikonisoft® explorer

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Get unprecedented scanning versatility with Ikonisoft explorer

- Fully user-definable software lets you program all FISH scanning and analytical parameters, for multiple areas on a single slide.
- Each probe channel can be programmed for Fusion, Break Apart, or Bleed-Through. Spacial parameters and scanning configurations are also user-definable.
- Allows scanning and analysis of multiple FISH probe sets (up to five probes each), making a complex classification process much more robust.
- With both low and high magnification scanning options, provides exceptional scanning flexibility.
- Save the applications you create for future use.

Spend less time setting up your application and more time exploring the results!



User-friendly Ikonisoft explorer makes setting up new applications fast and easy.

The screenshot shows the Ikonisoft Explorer software interface with several callouts pointing to specific settings:

- Define slide type:** Points to the 'Select Depositions' dropdown menu.
- Identify structure of interest:** Points to the 'Structure' dropdown menu for Channel 1.
- Select filter sets:** Points to the 'Filter Set' dropdown menu for Channel 1.
- Select focusing methodology:** Points to the 'Auto Focus Method' dropdown menu for Channel 1.
- Select auto exposure method:** Points to the 'Auto Exposure Method' dropdown menu for Channel 1.
- Select dot counting method:** Points to the 'Dot Counting Method' dropdown menu for Channel 1.
- Select bleed-through correction:** Points to the 'Bleed Through' checkbox for Channel 1.
- Define spatial characteristics of Fusion or Break Apart probes:** Points to the 'Split Signal Definition' dropdown menu for Channel 1.
- Define number of focal planes that system will acquire in high magnification:** Points to the 'Number of Slices' input field in the Scanning Configuration section.
- Define manner in which Ikonisoft explorer returns to objects of interest in high magnification:** Points to the 'Visit Sequence' dropdown menu in the Scanning Configuration section.



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