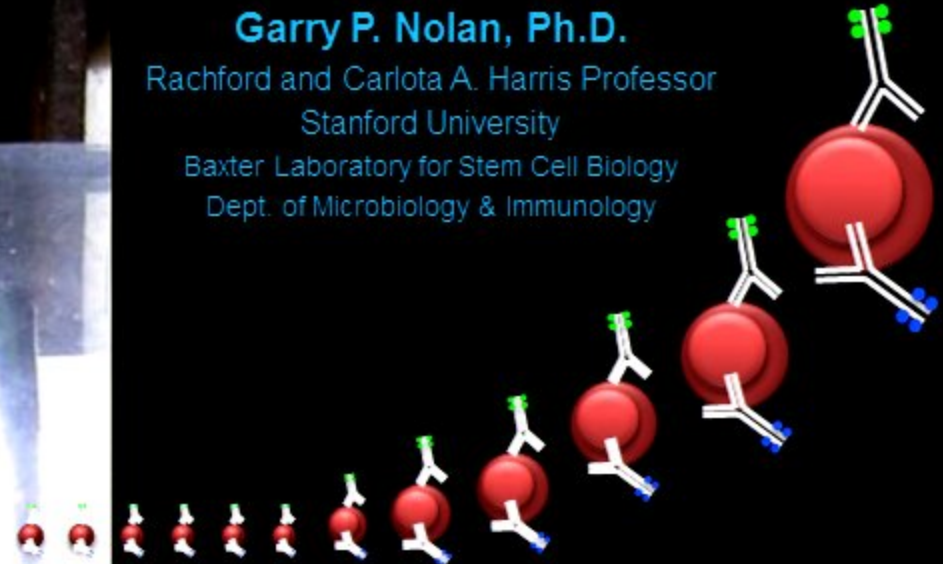
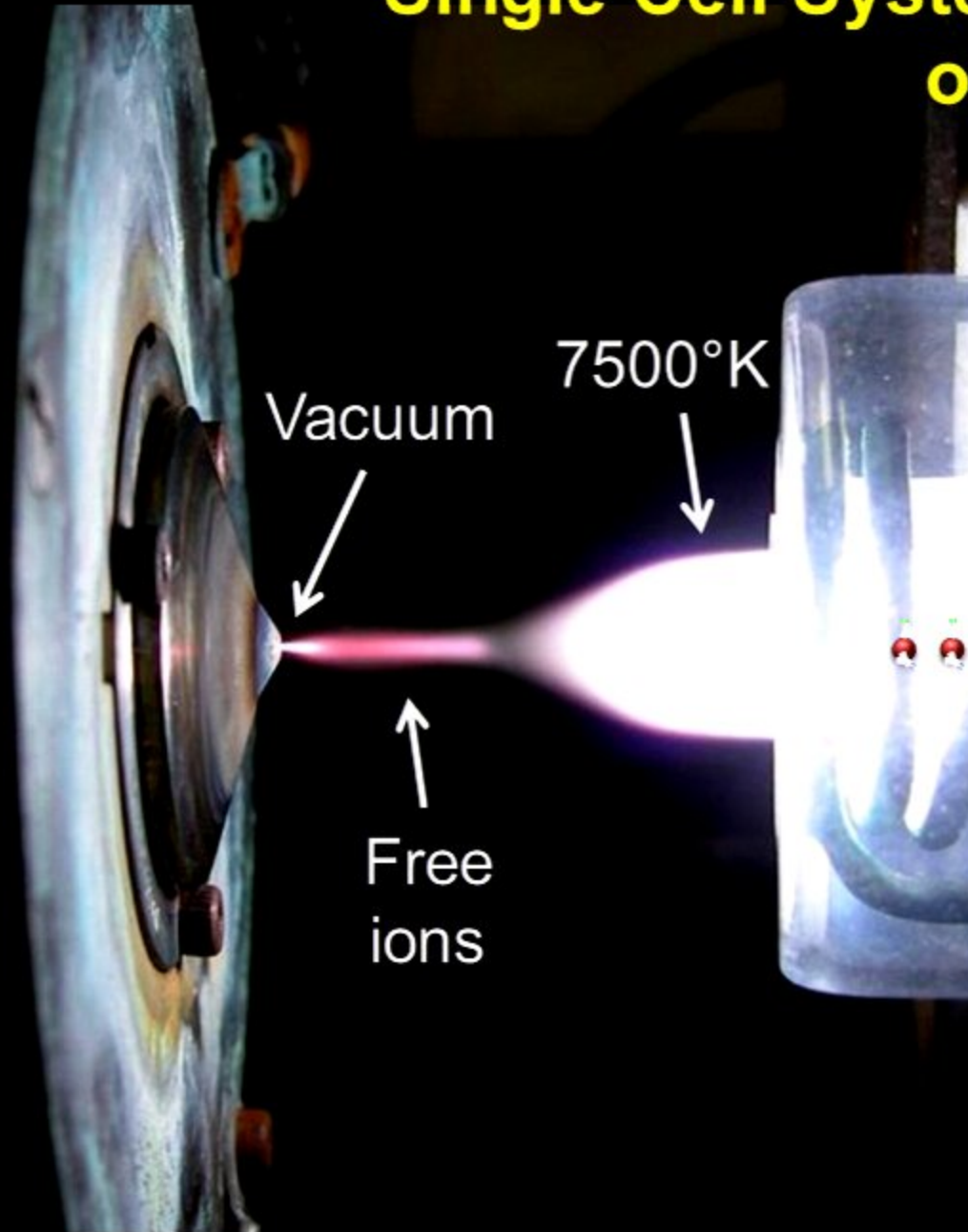


Single Cell Systems-Structured View of Immunity & Cancer

Garry P. Nolan, Ph.D.

Rachford and Carlota A. Harris Professor
Stanford University

Baxter Laboratory for Stem Cell Biology
Dept. of Microbiology & Immunology



Disclosures:

- Nodality: Founder & Chair SAB, Equity
- DVS: Chair SAB, Equity

CyTOF

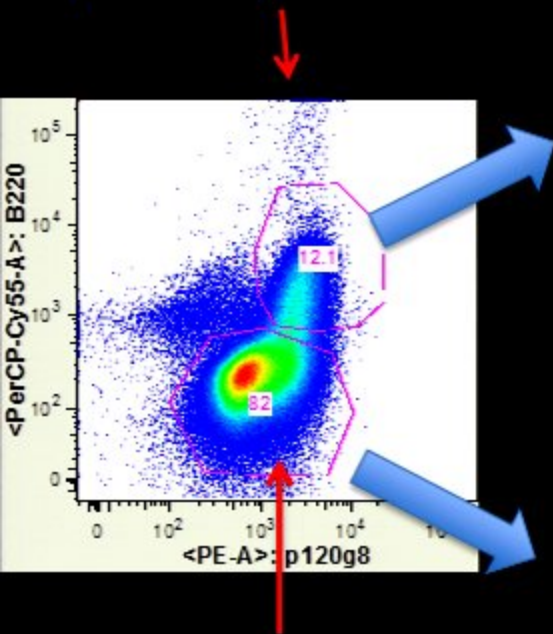
- ~45 parameters right now.
- New encoding system → 100-200 parameters per cell.
- mRNA measured along with Abs
- One main goal is to develop an Immune System Reference Map
- Allows powerful models and hypotheses about immune function—much like is accomplished with genomics datasets.
- 4 CyTOFs on campus
 - 2 in Nolan lab
 - 2 in Human Immune Monitoring Core (HIMC) – Mark Davis & Holden Maecker
 - 5th to be placed in Shared FACS Facility.
- 30 CyTOFs in world now— 4 already in pharma.

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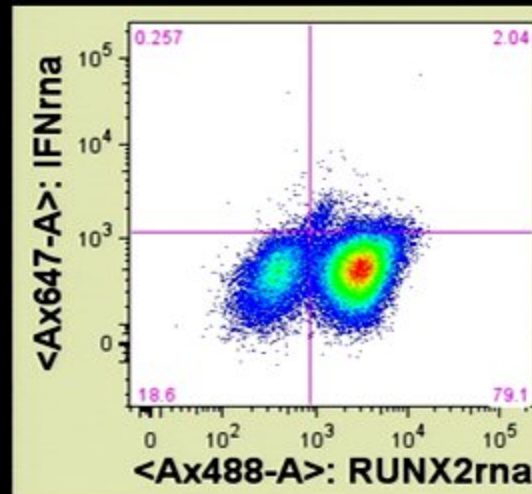
Rflow can be used for cytokine detection

plasmacytoid DC

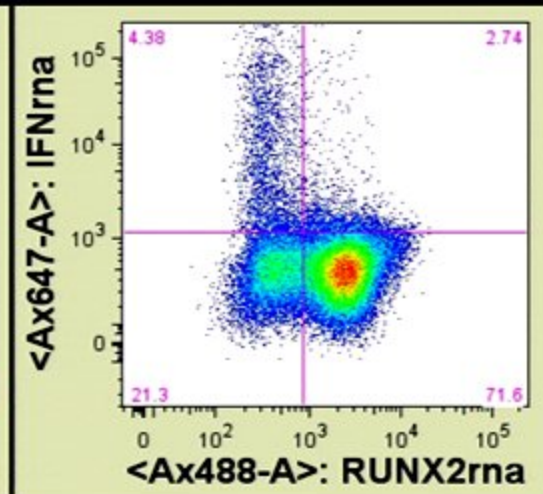


conventional DC

UNstim



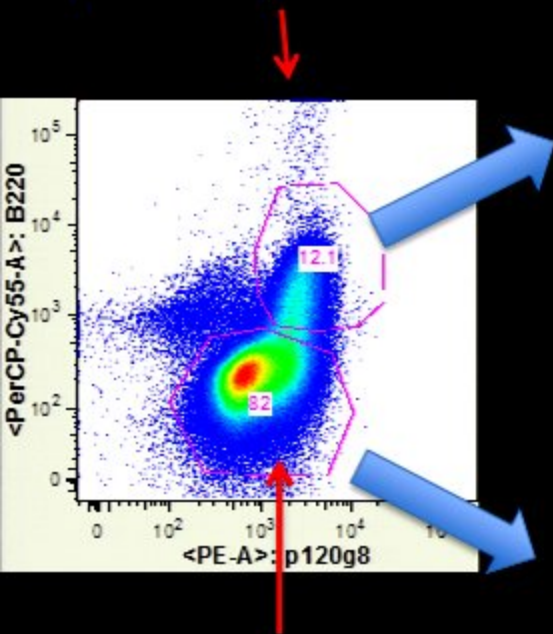
stim



Rflow can be used for cytokine detection



plasmacytoid DC



conventional DC

RNA flow can detect gene expressed as low as 5 copies per cell

Low

high expression

No Probe-0 dot/cell

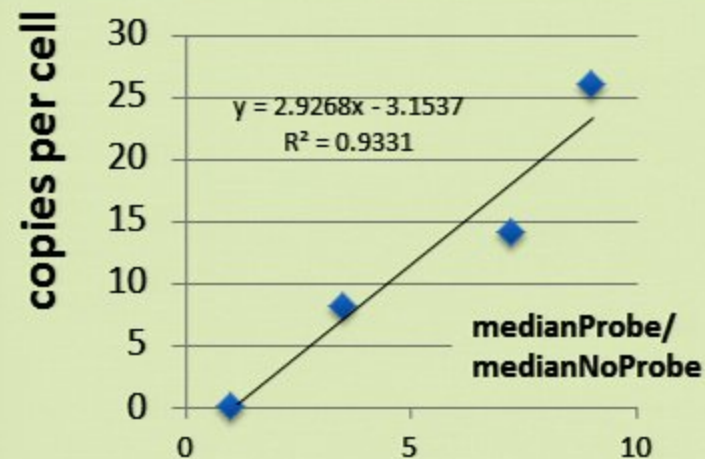
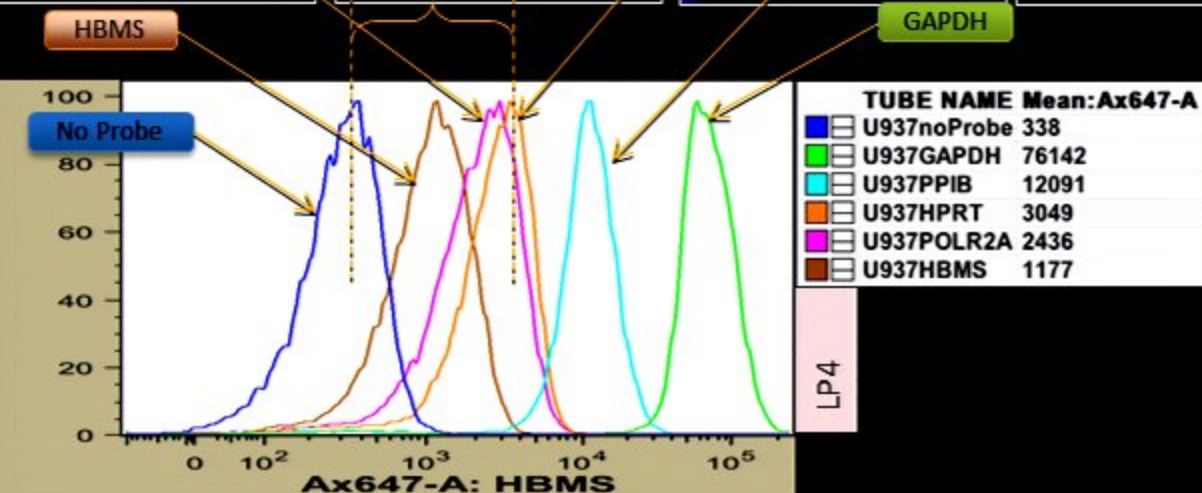
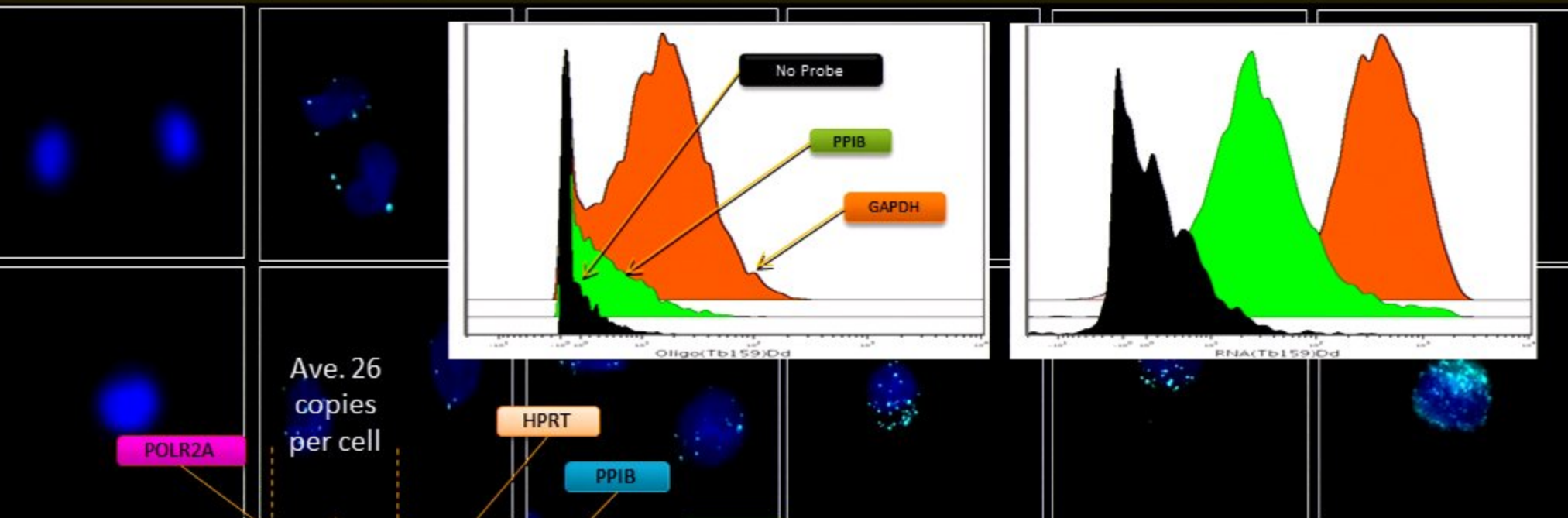
HBMS - 8 dots/cell

POLR2A - 14 dot/cell

HPRT -26dots/cell

PPIB-not count

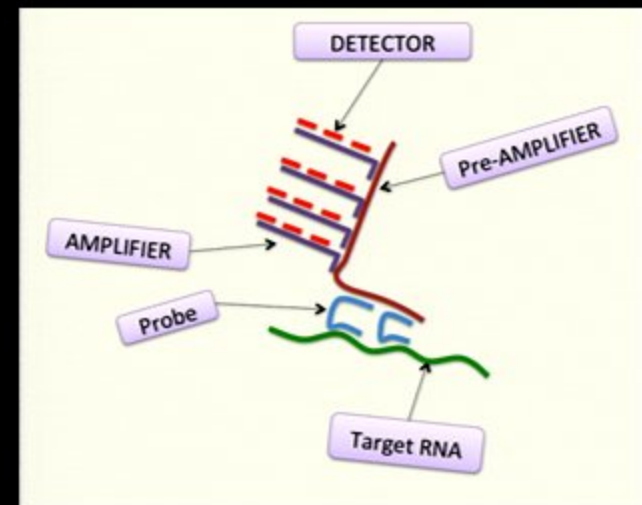
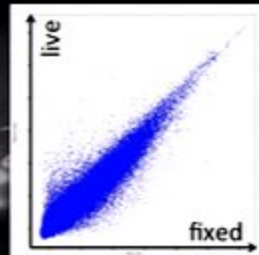
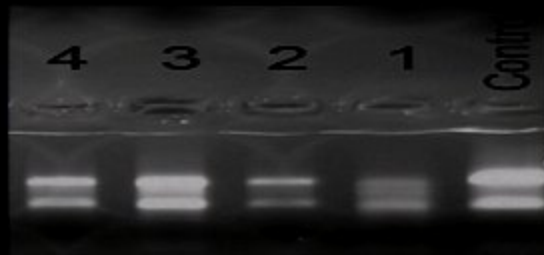
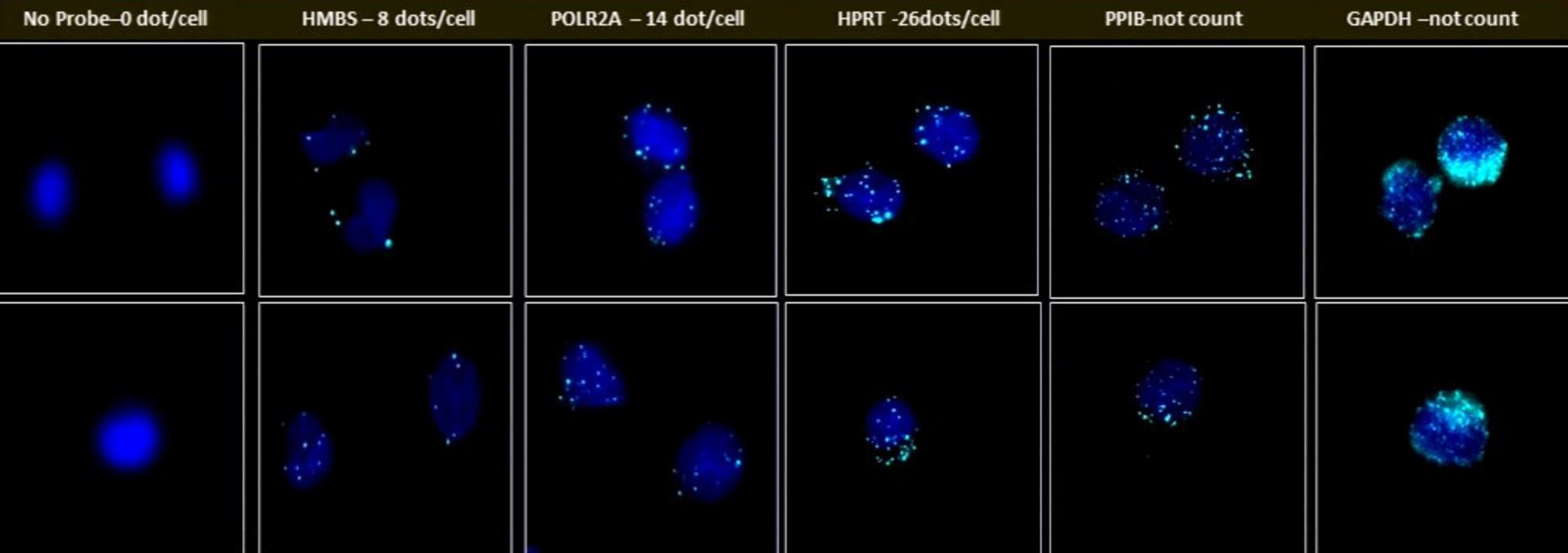
GAPDH -not count



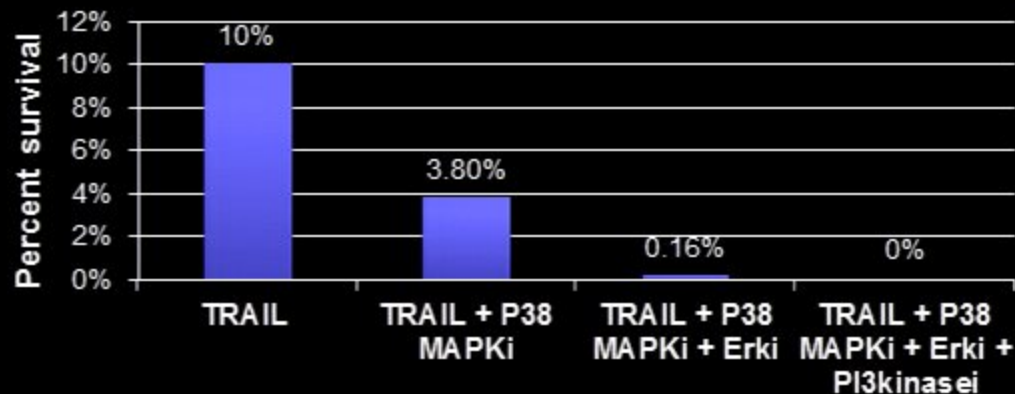
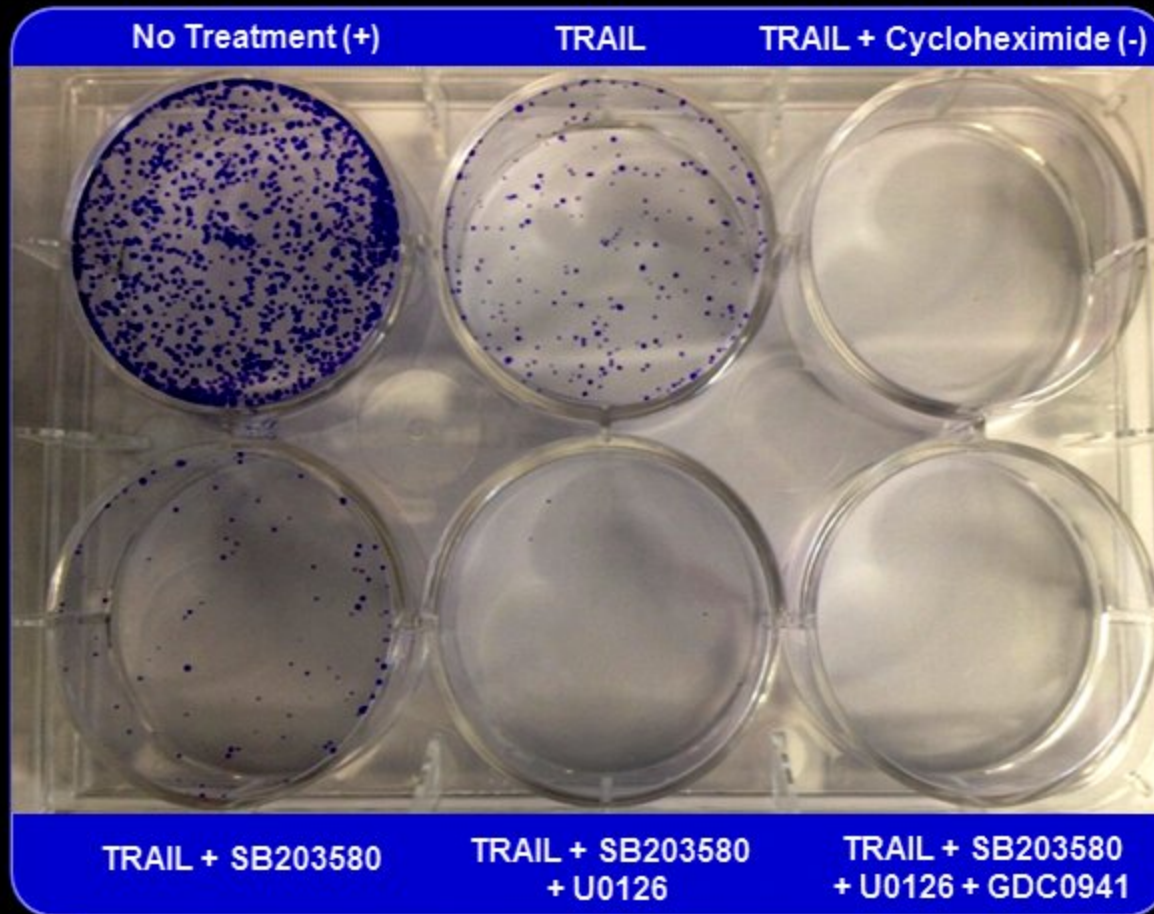
RNA flow can detect gene expressed as low as 5 copies per cell

Low

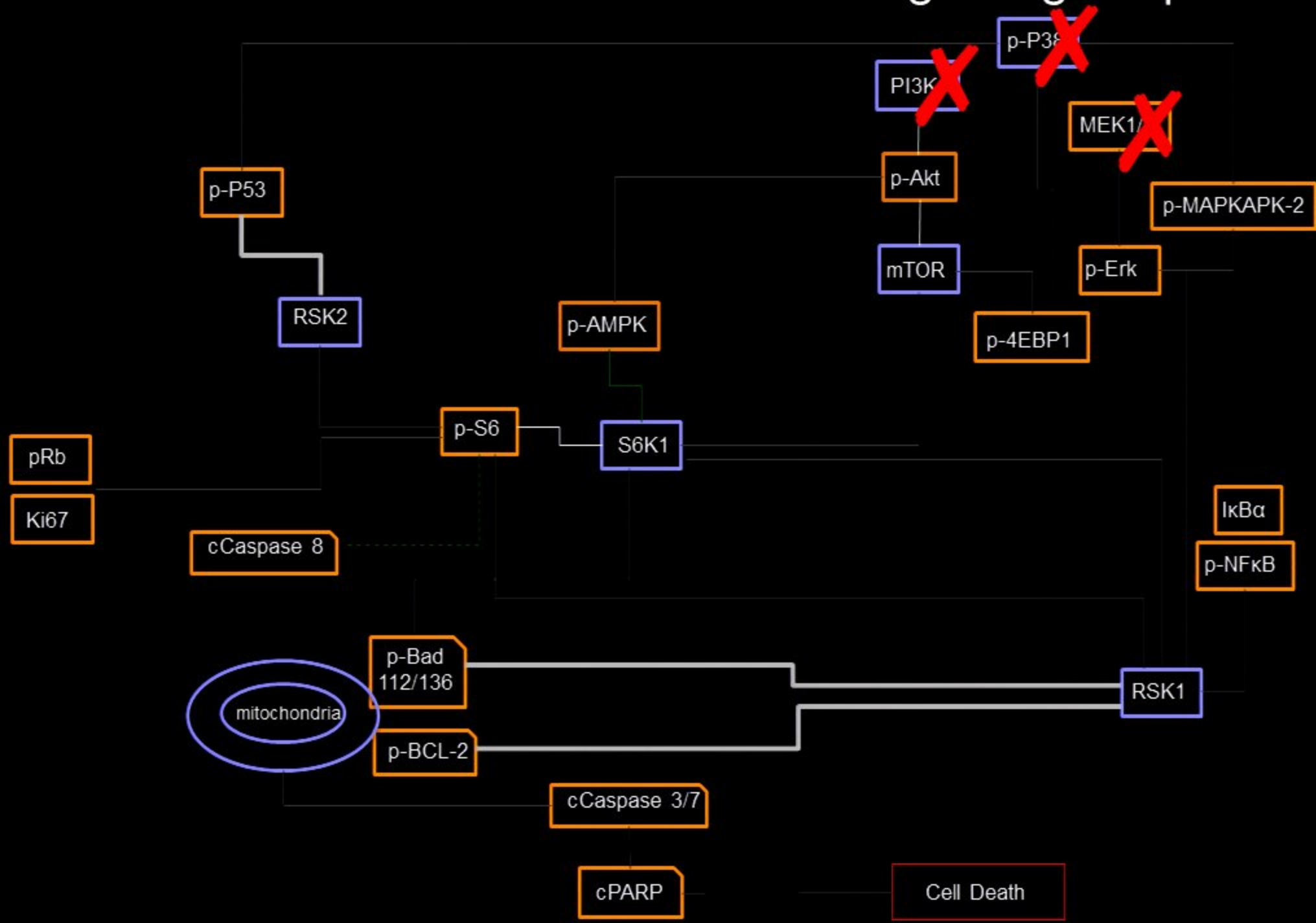
high expression



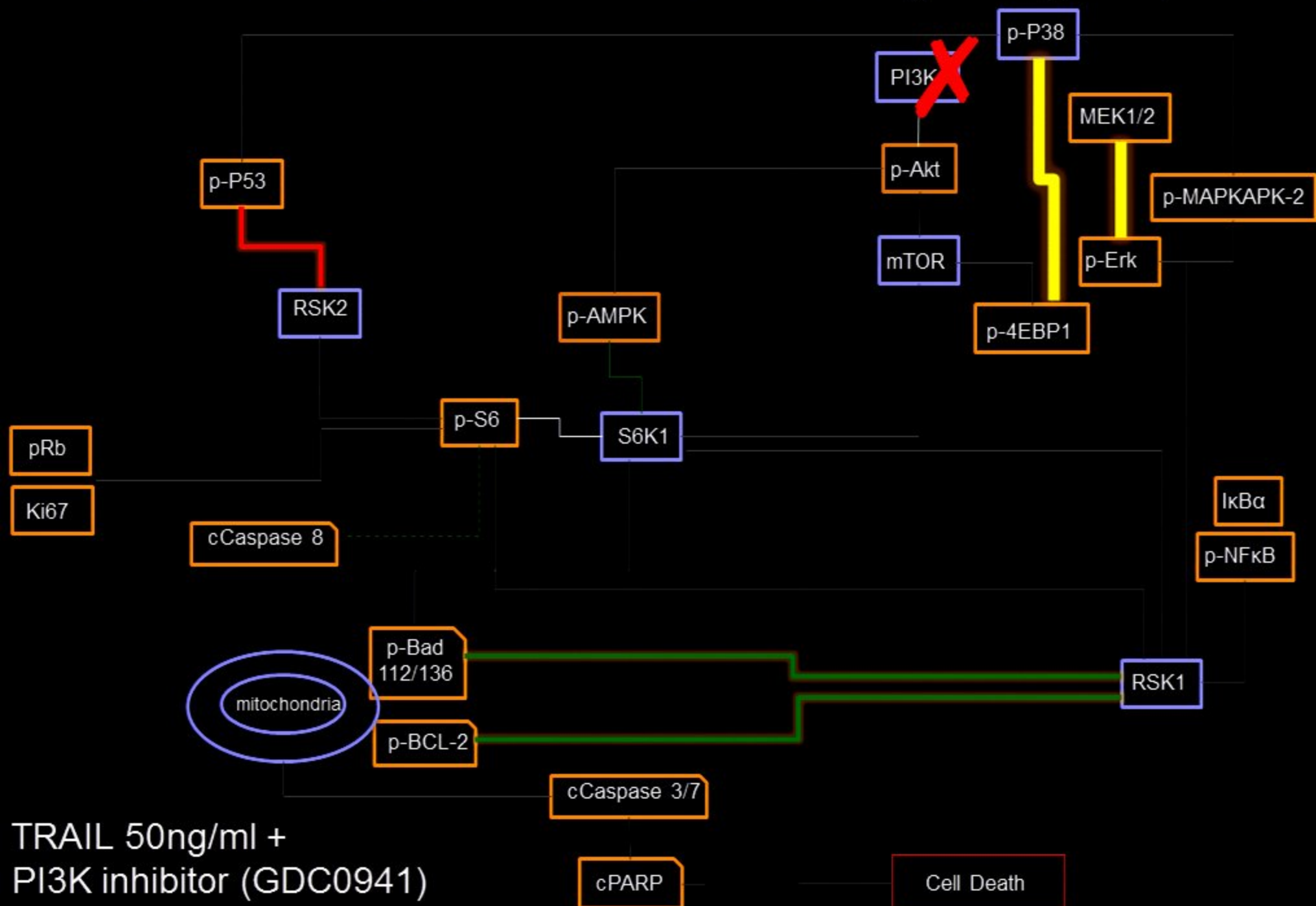
Compensatory signaling off w/ targeted kinase inhibition



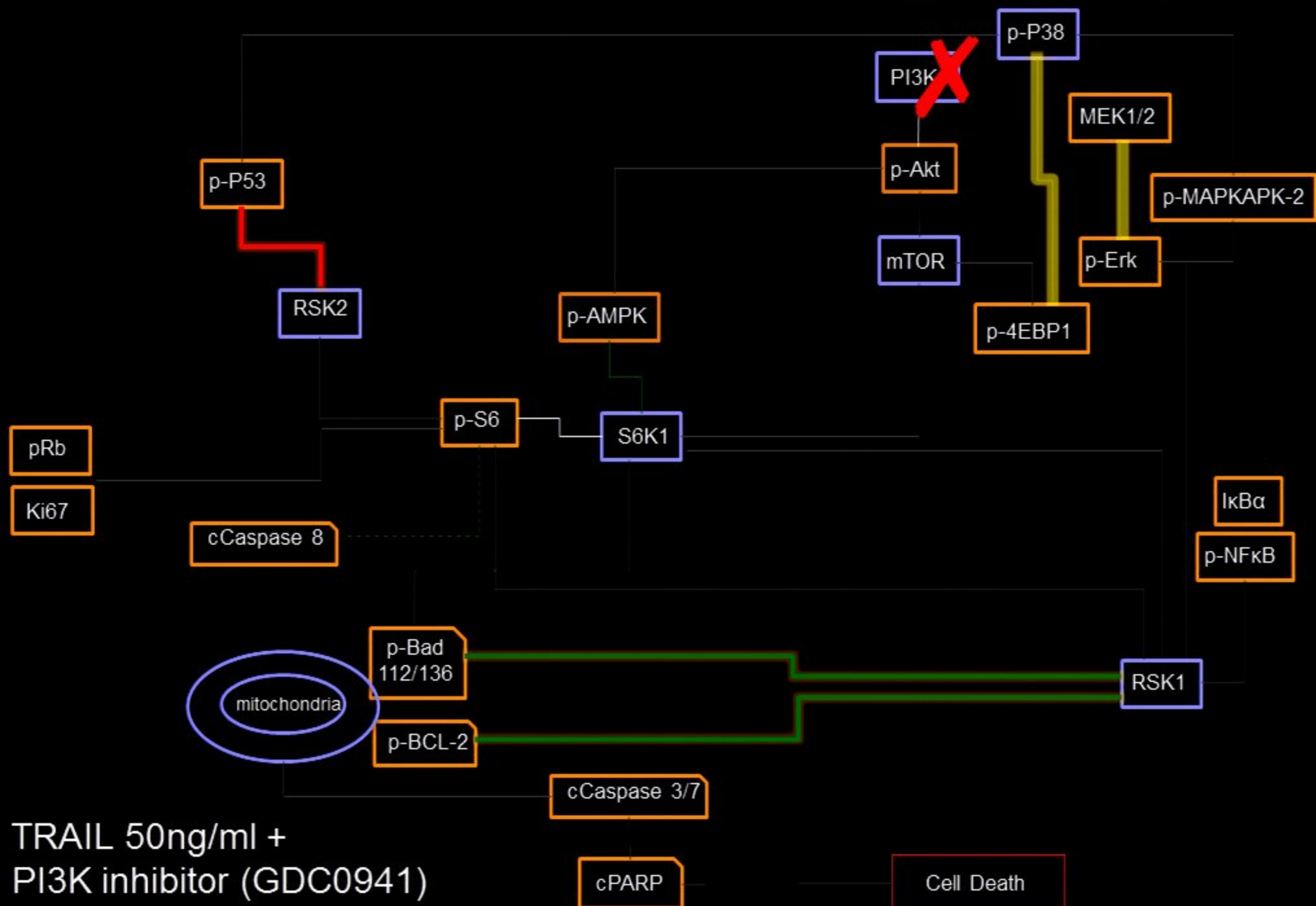
Survival factor/TRAIL interaction signaling map



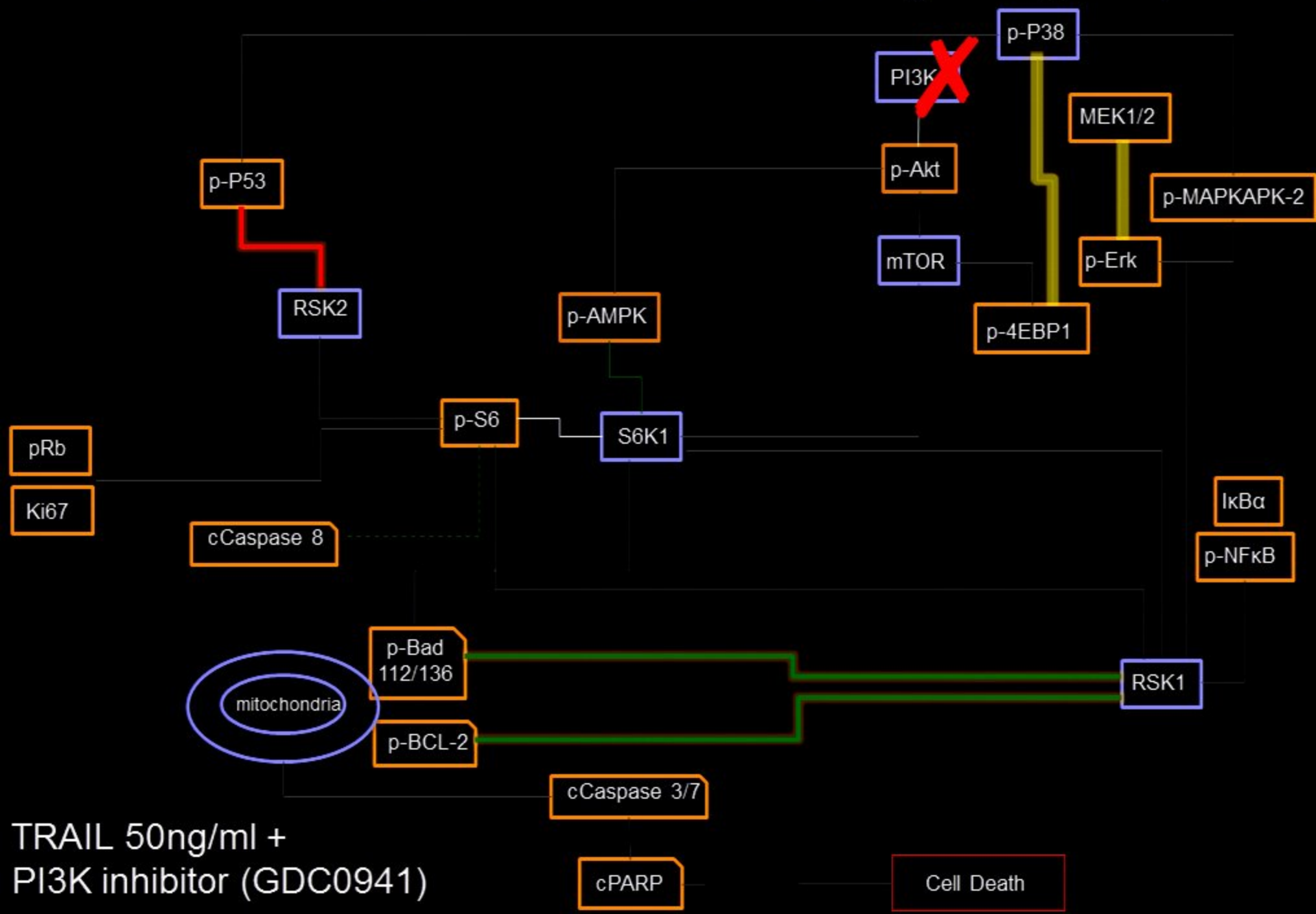
Survival factor/TRAIL interaction signaling map



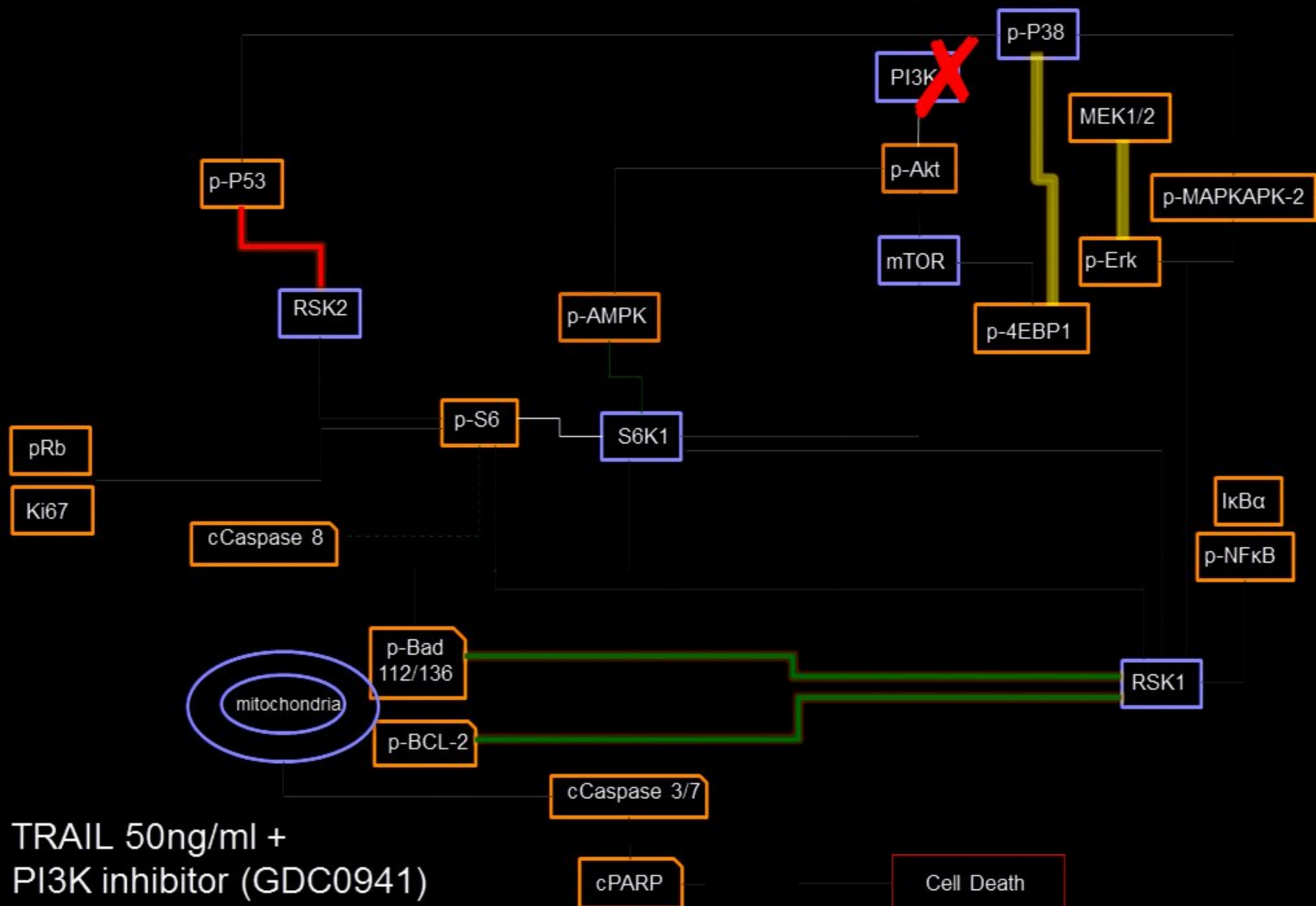
Survival factor/TRAIL interaction signaling map



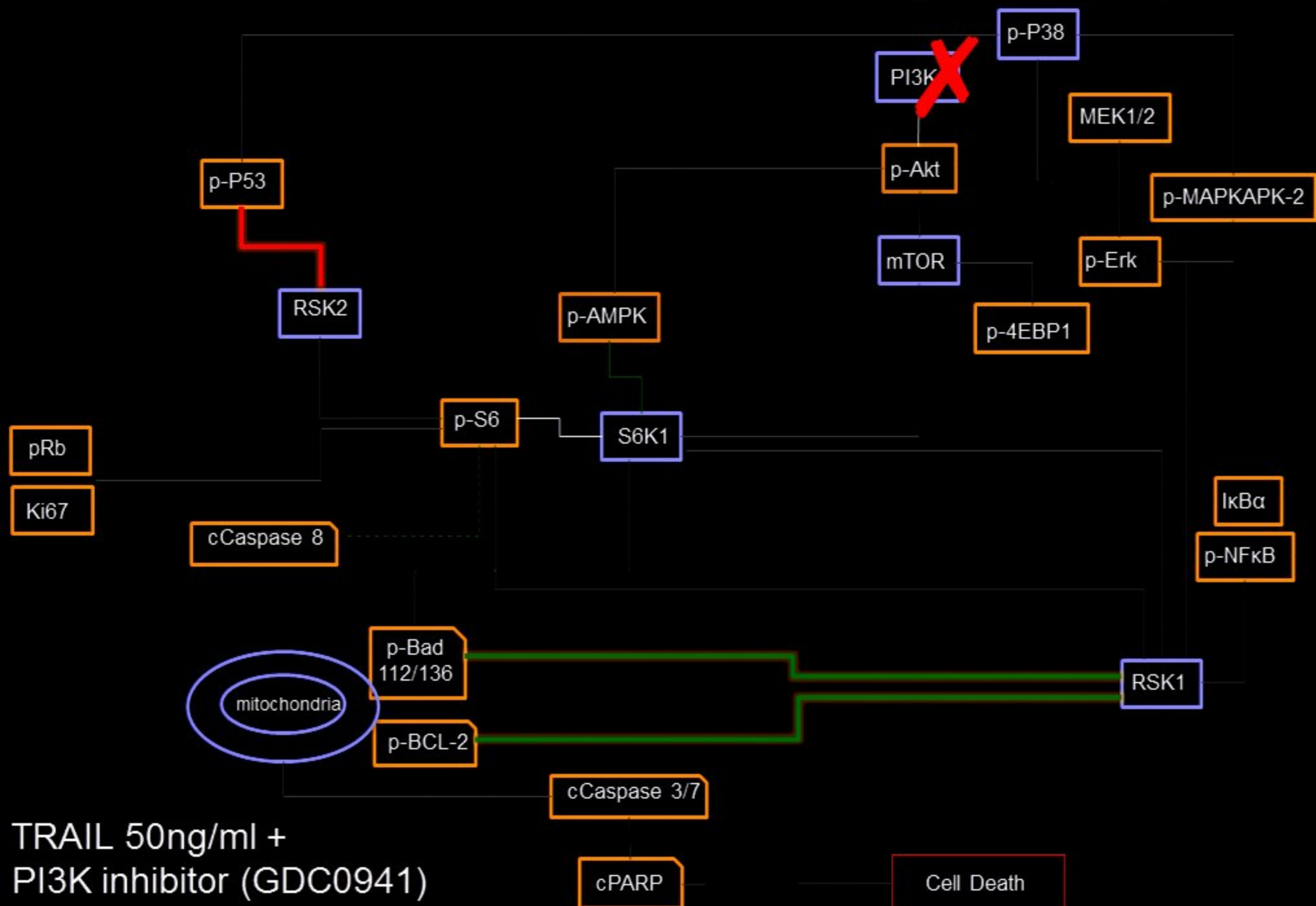
Survival factor/TRAIL interaction signaling map



Survival factor/TRAIL interaction signaling map



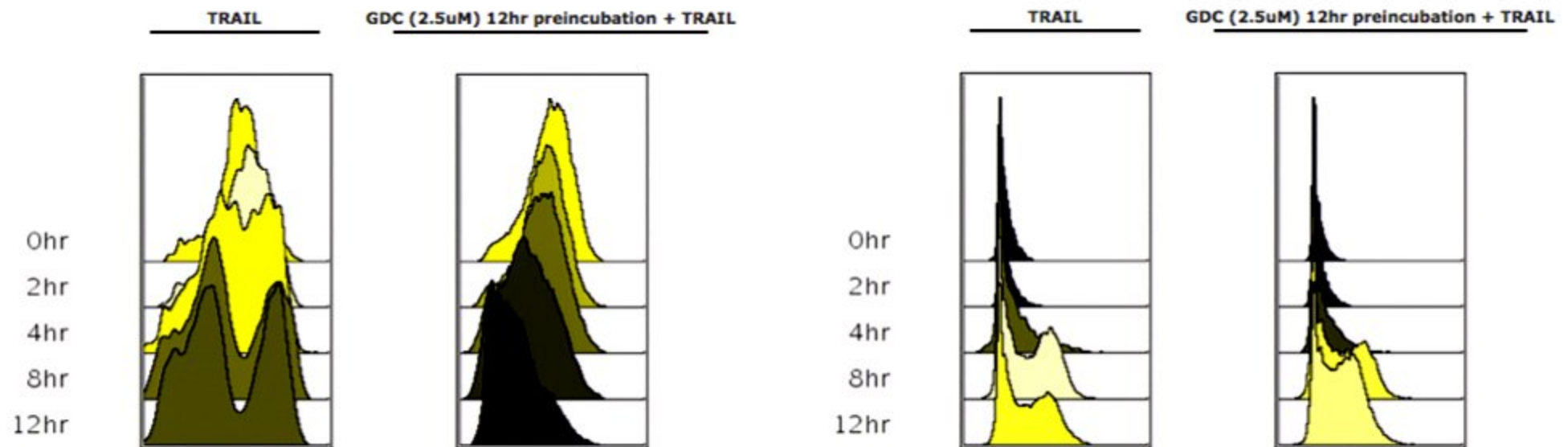
Survival factor/TRAIL interaction signaling map



Inhibiting S6 phosphorylation via a PI3K inhibitor does not have a significant effect on survival

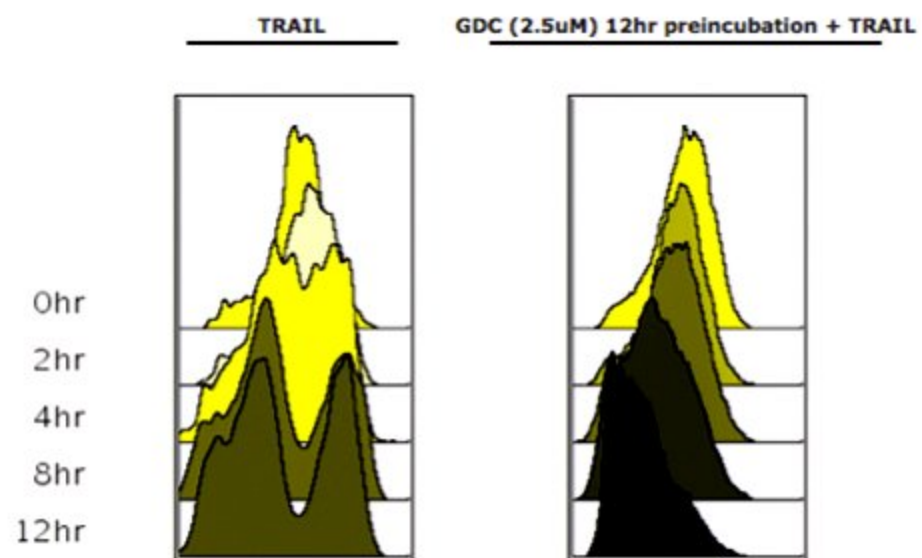
phospho-S6

Viability



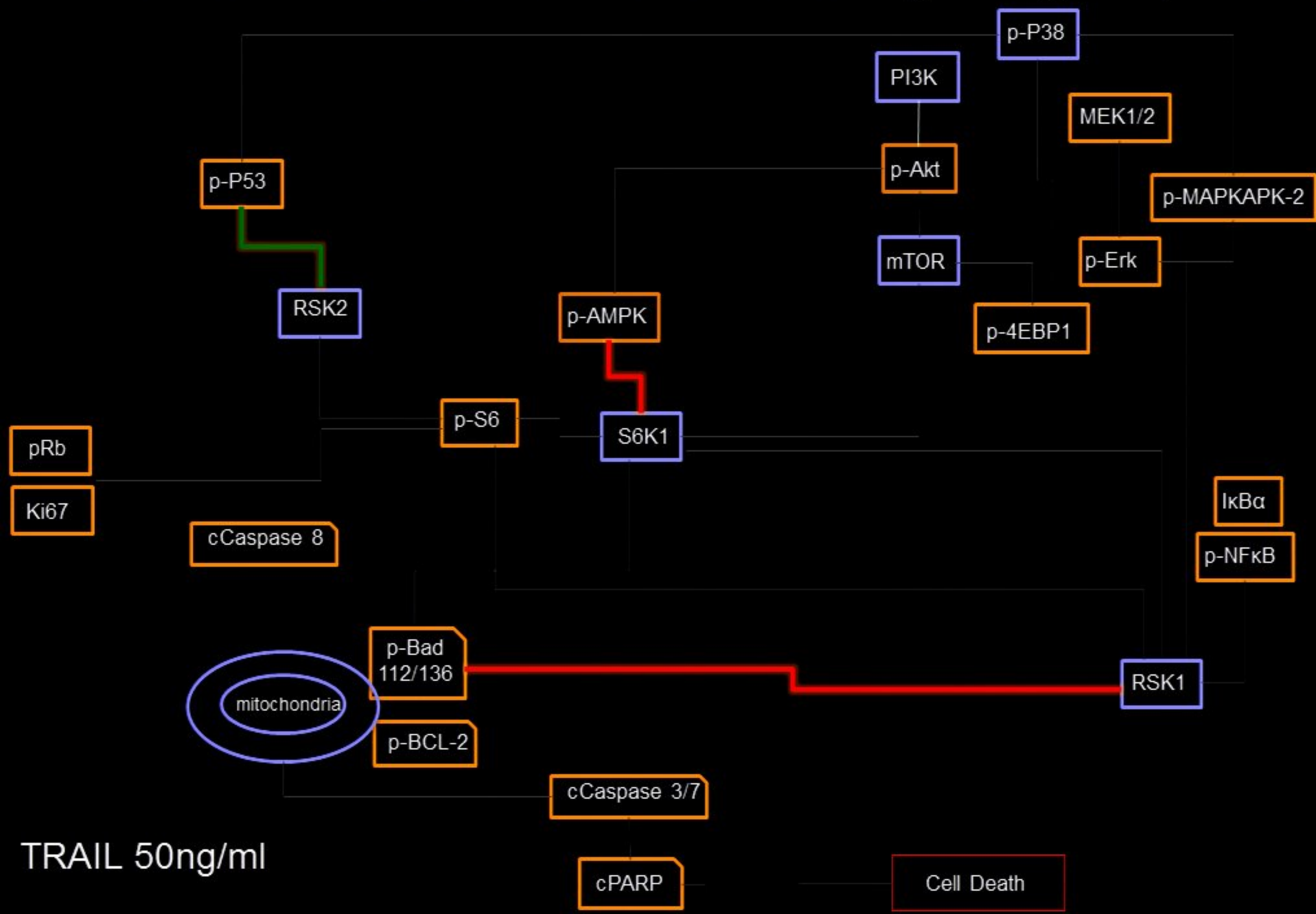
HeLas treated with TRAIL 50ng/ or TRAIL with 12hr pre-incubation with GDC0941

phospho-S6

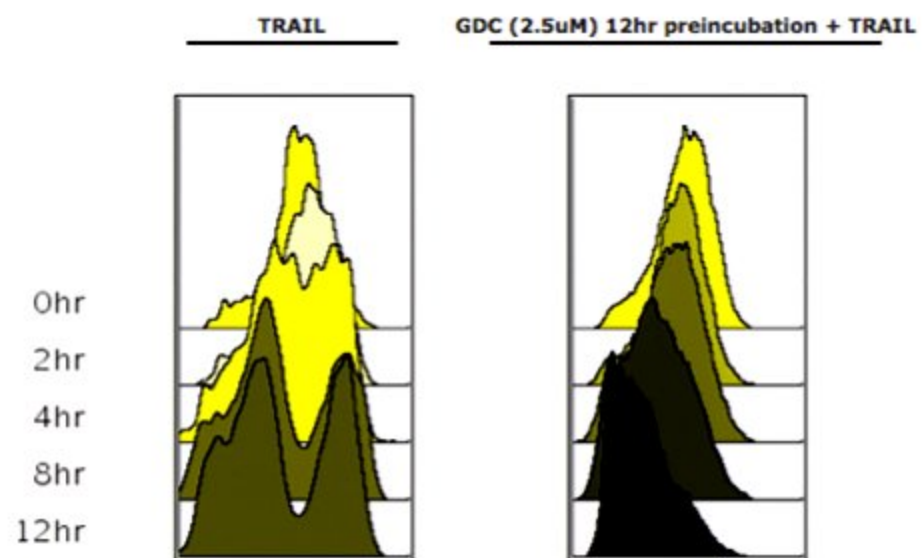


HeLas treated with TRAIL 50ng/ or TRAIL with 12hr pre-incubation with GDC0941

Survival factor/TRAIL interaction signaling map

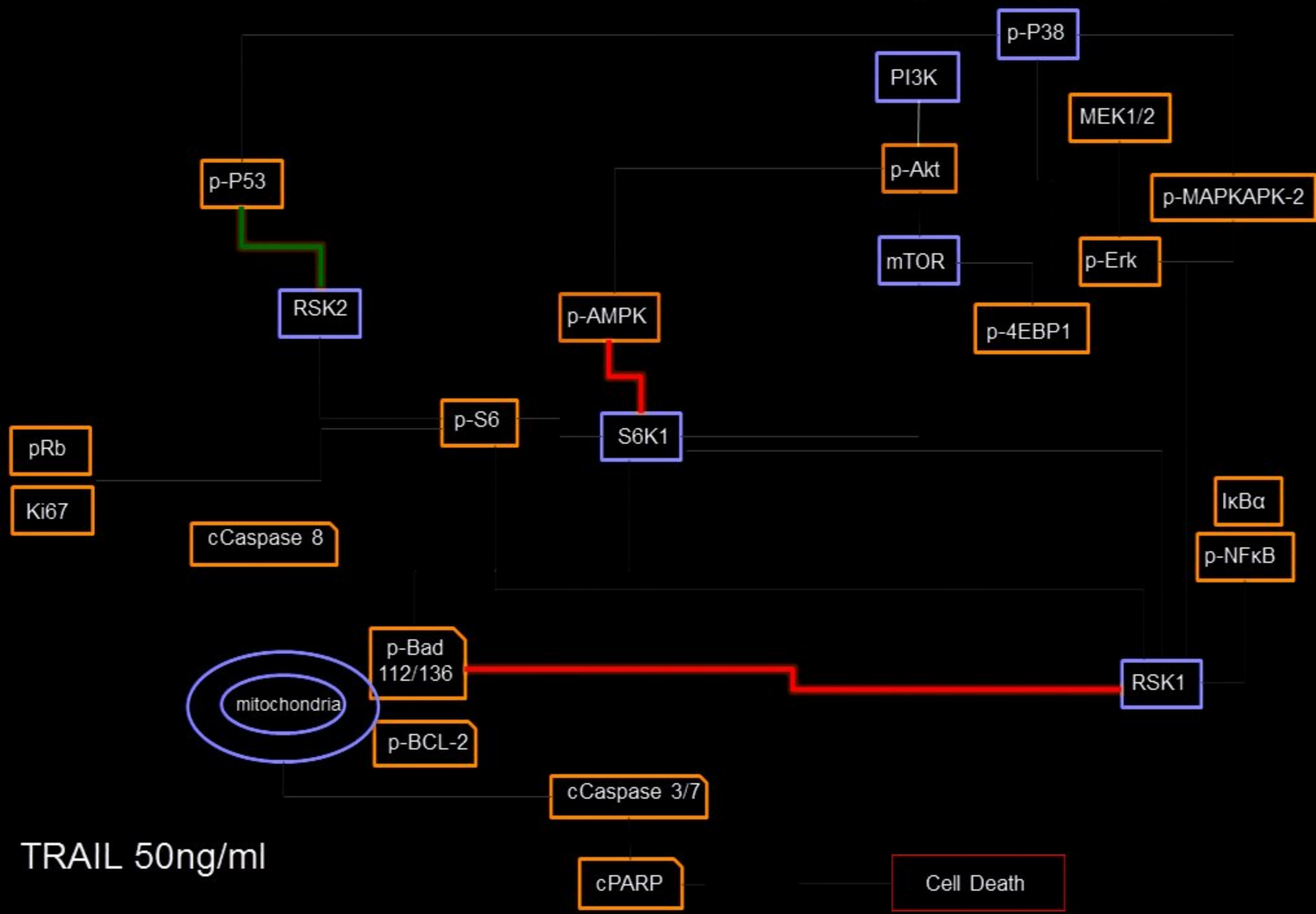


phospho-S6

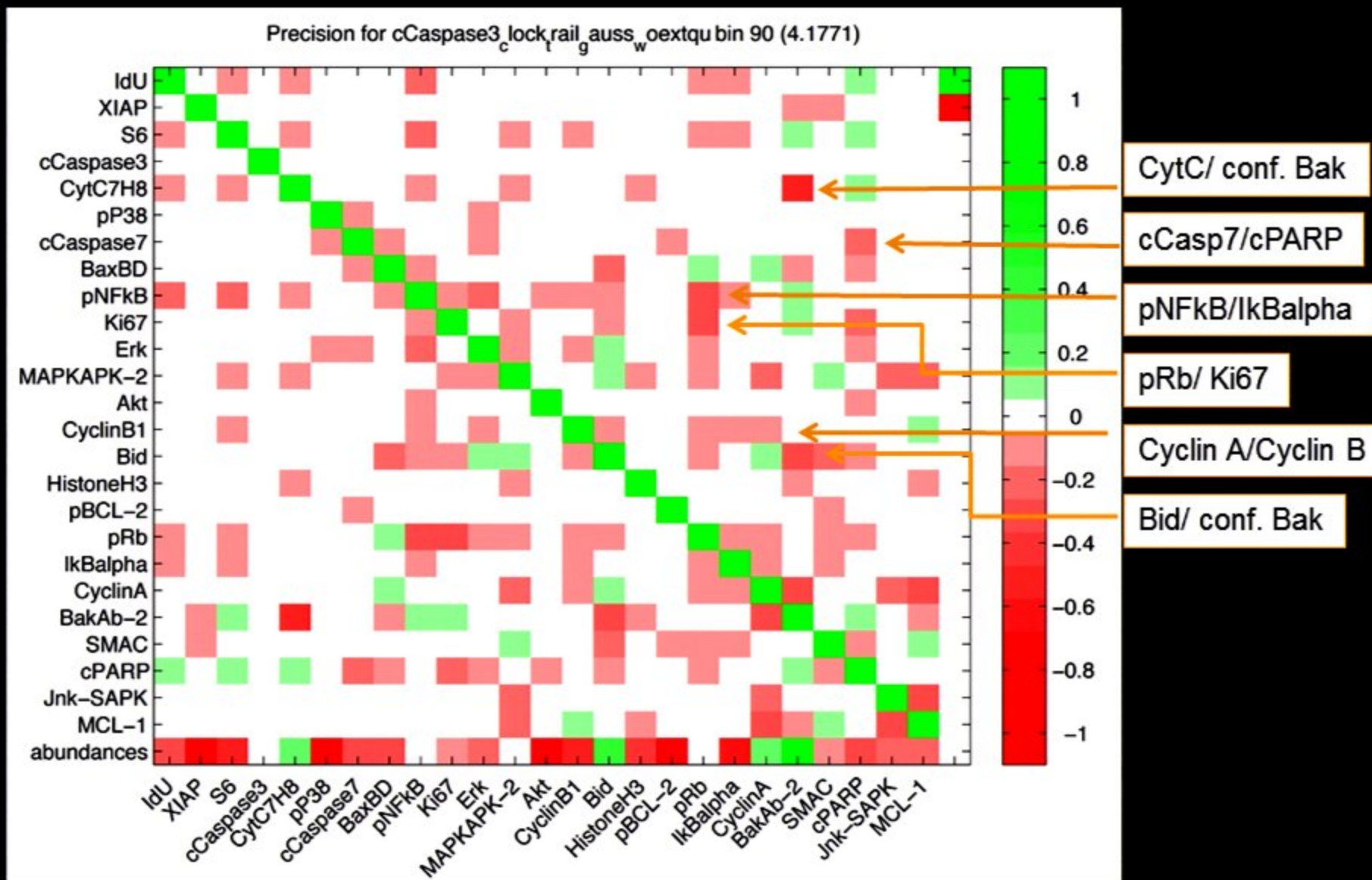


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Survival factor/TRAIL interaction signaling map

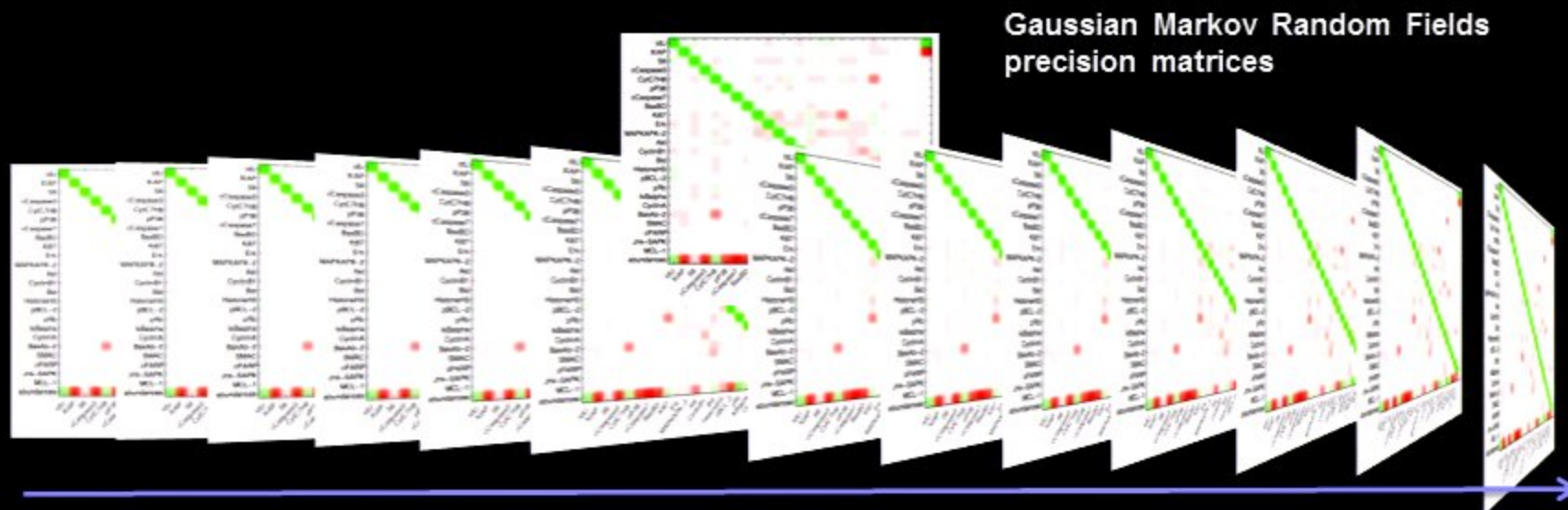


Precision matrices recapitulate expected signaling relationships



Signaling Time with a Molecular Clock

models



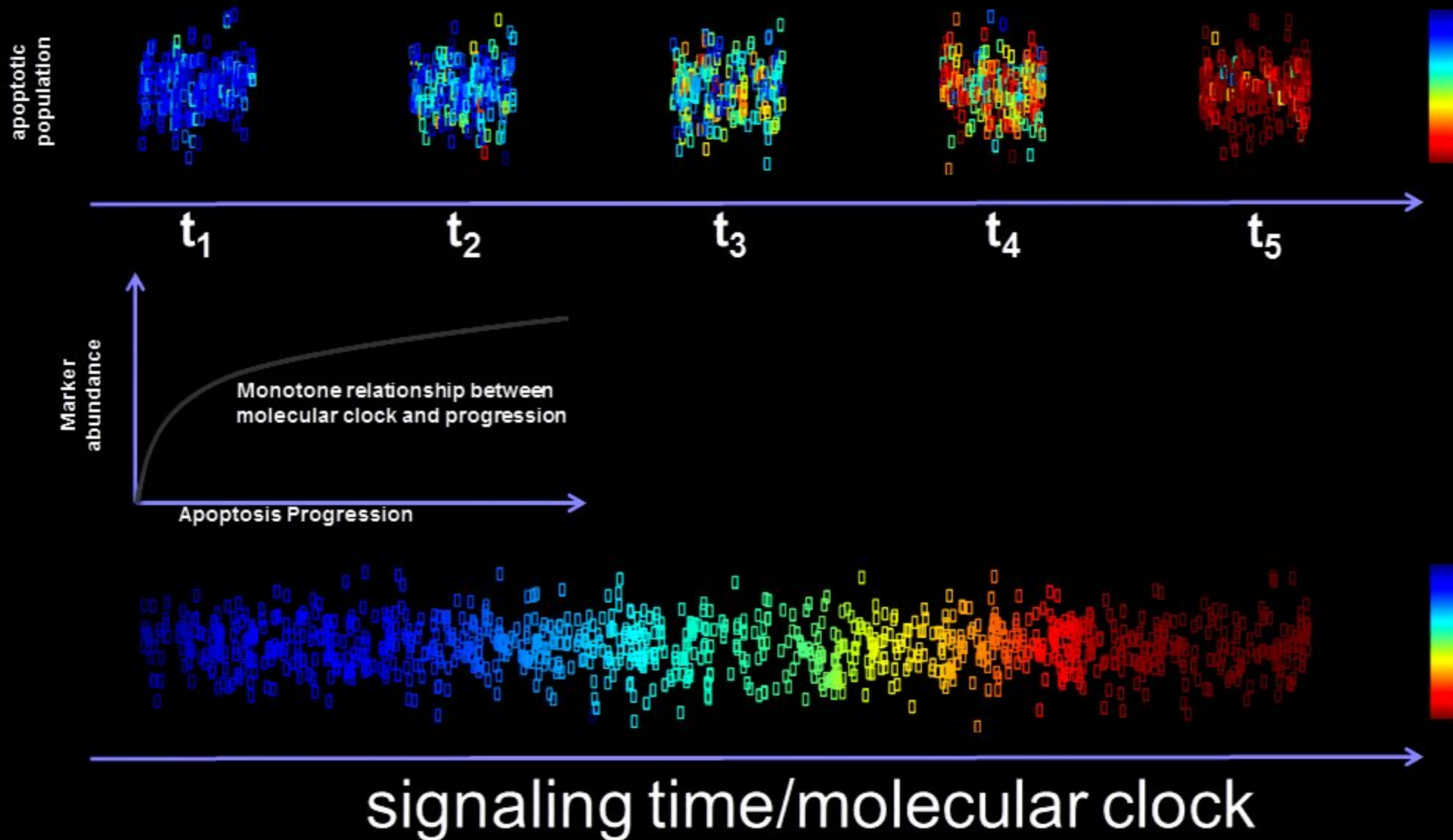
cell population
at consistent
signaling state

Infer signaling state
from cell population

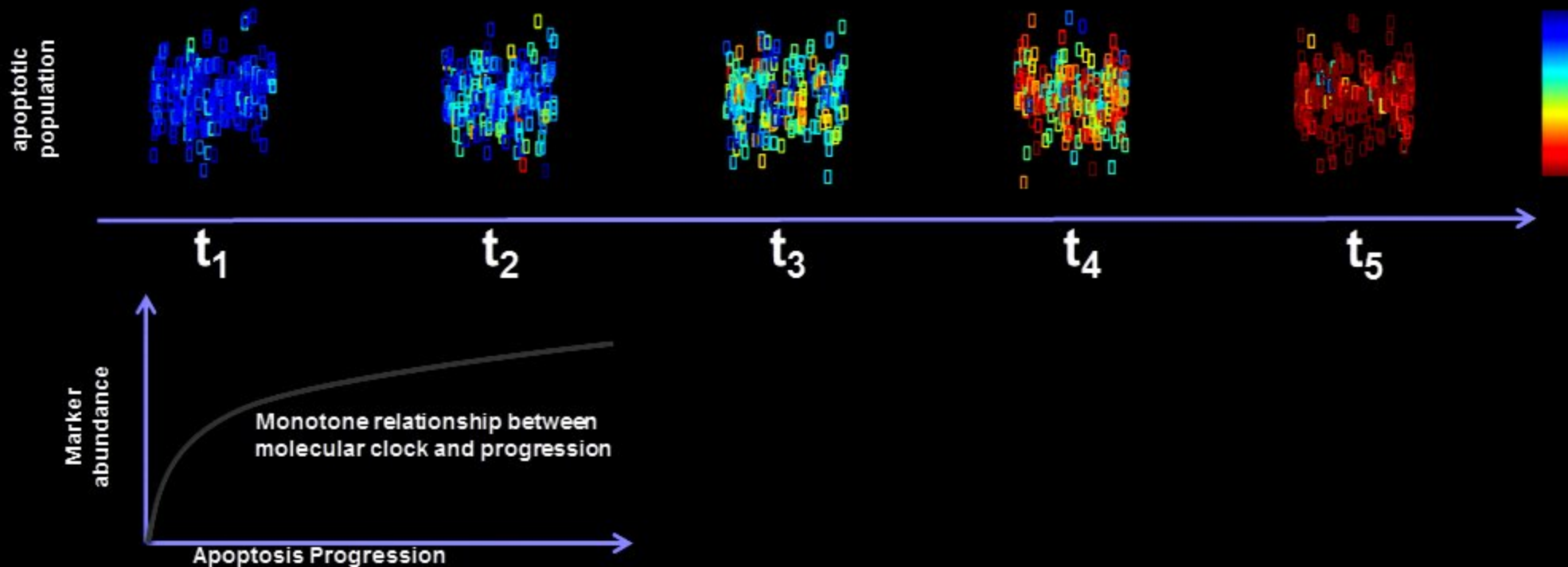


signaling time/molecular clock

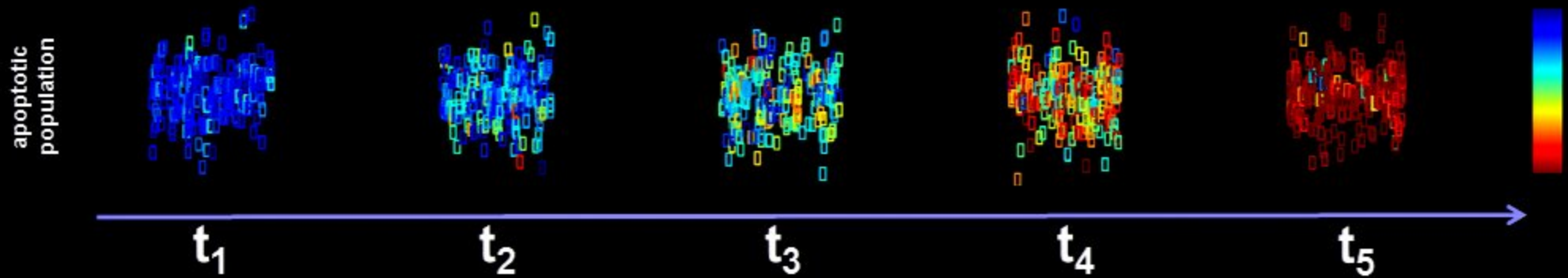
Signaling Time with a Molecular Clock



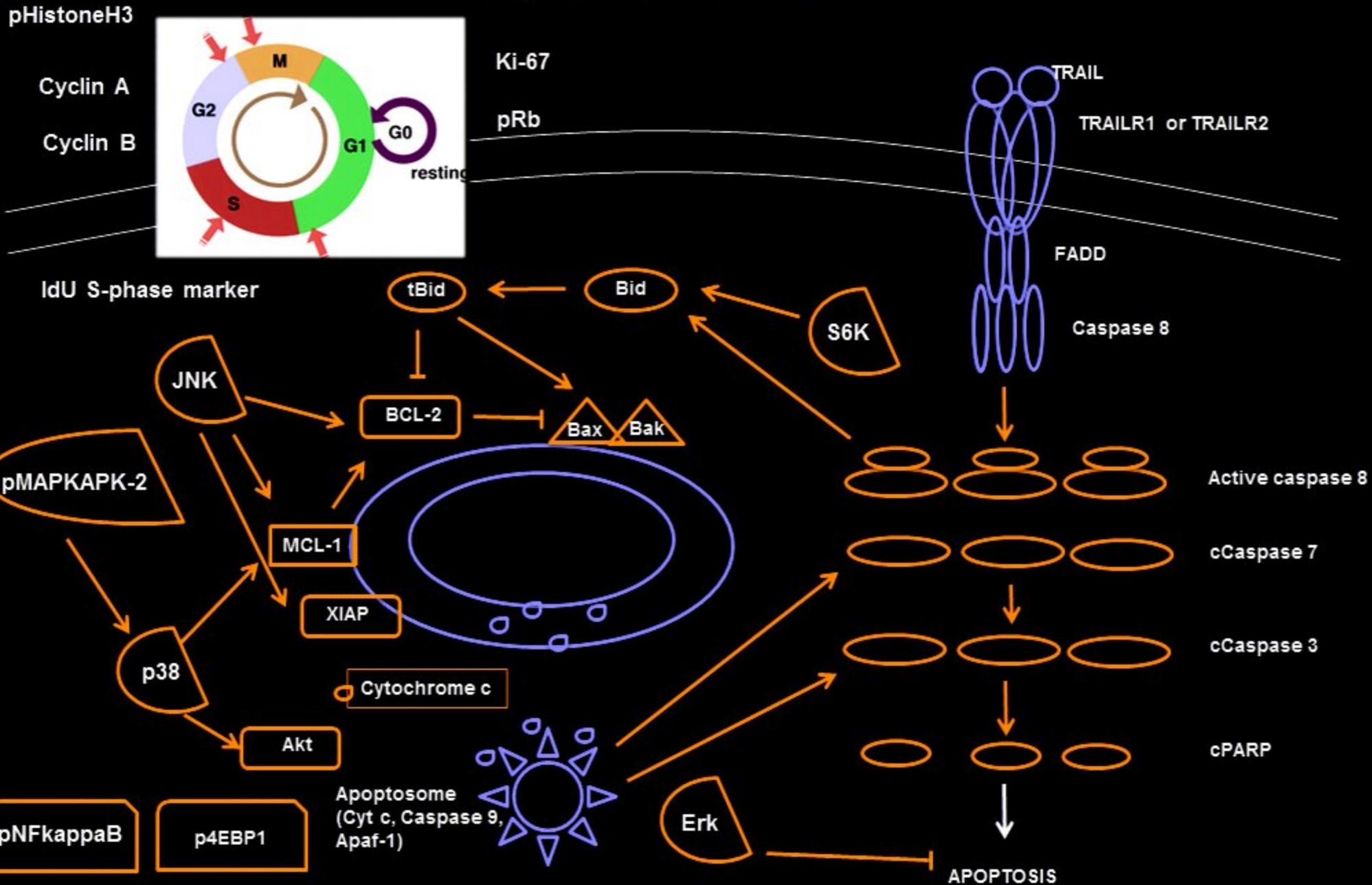
Signaling Time with a Molecular Clock



Signaling Time with a Molecular Clock

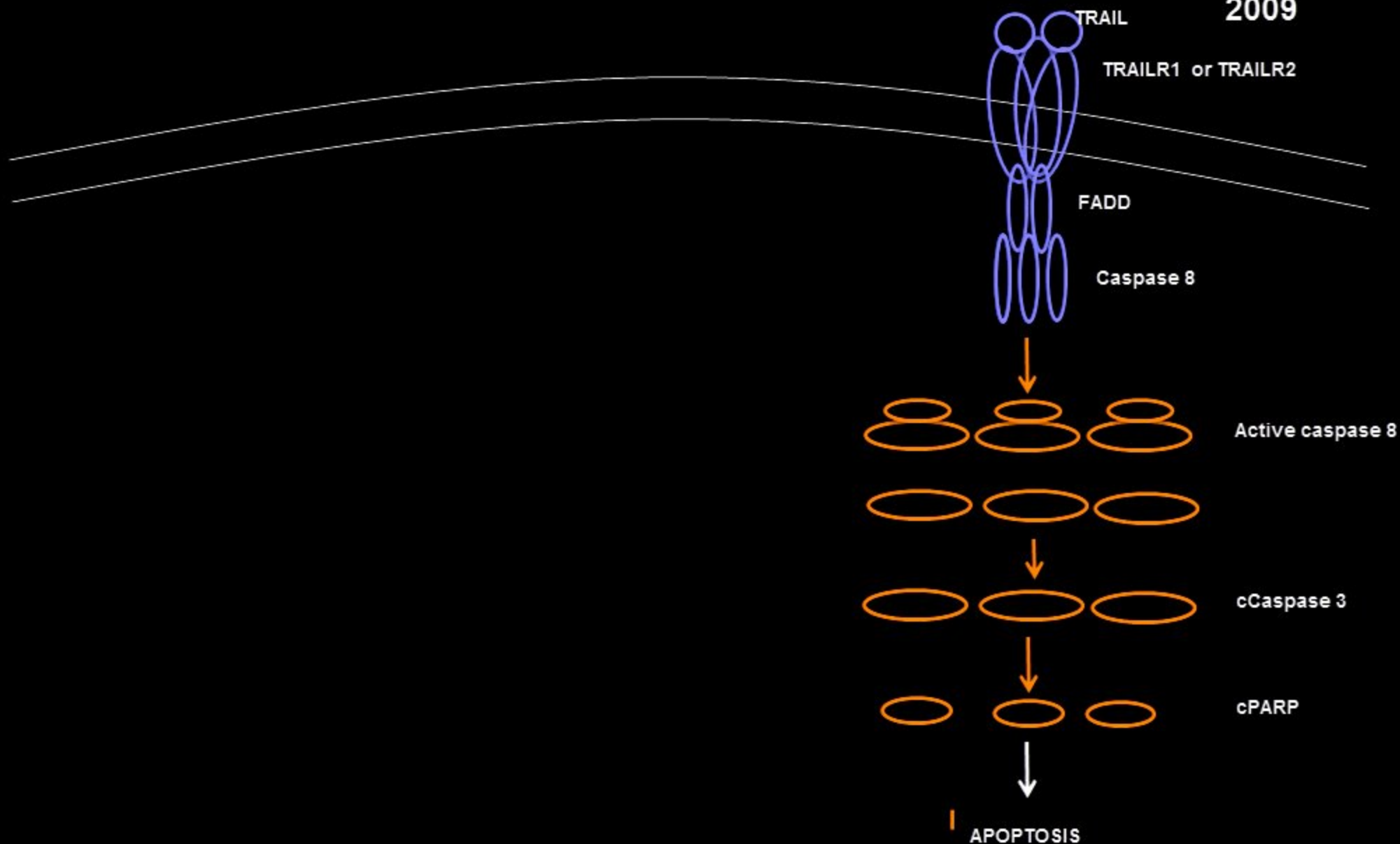


Apoptosis, cell cycle, transcriptional and metabolic system context



Apoptosis, cell cycle, transcriptional and metabolic system context

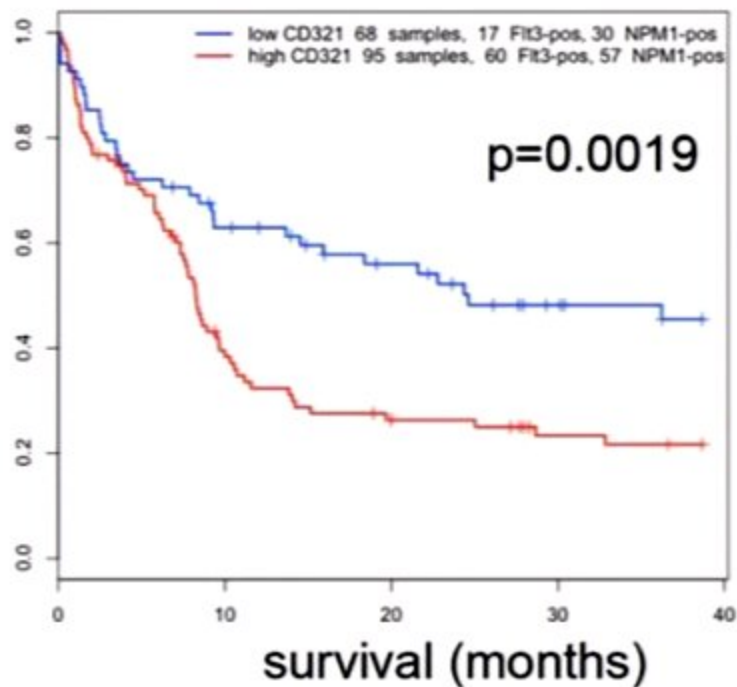
Sorger et al
Nature
2009



CD321 segregates outcome & better with NPM1

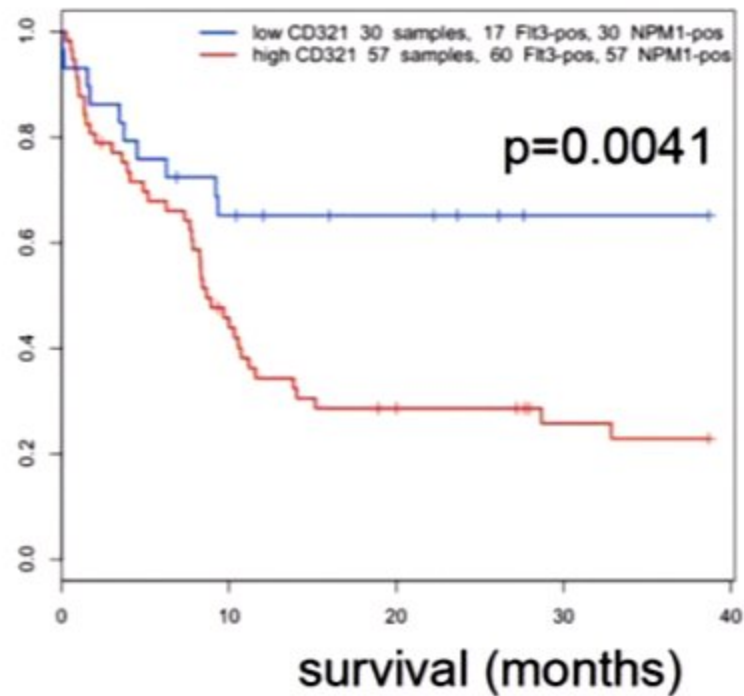
B

all patients - Normal Karyotype



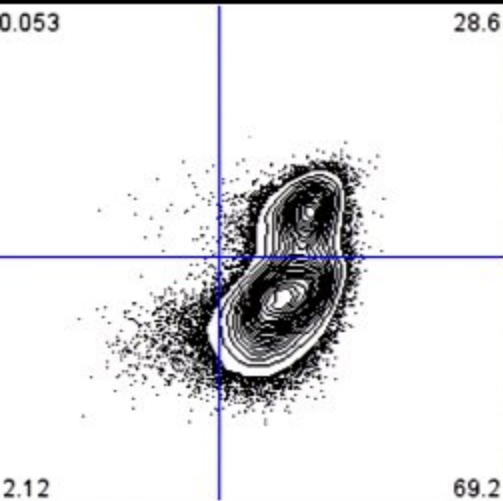
C

NPM1 positive patients

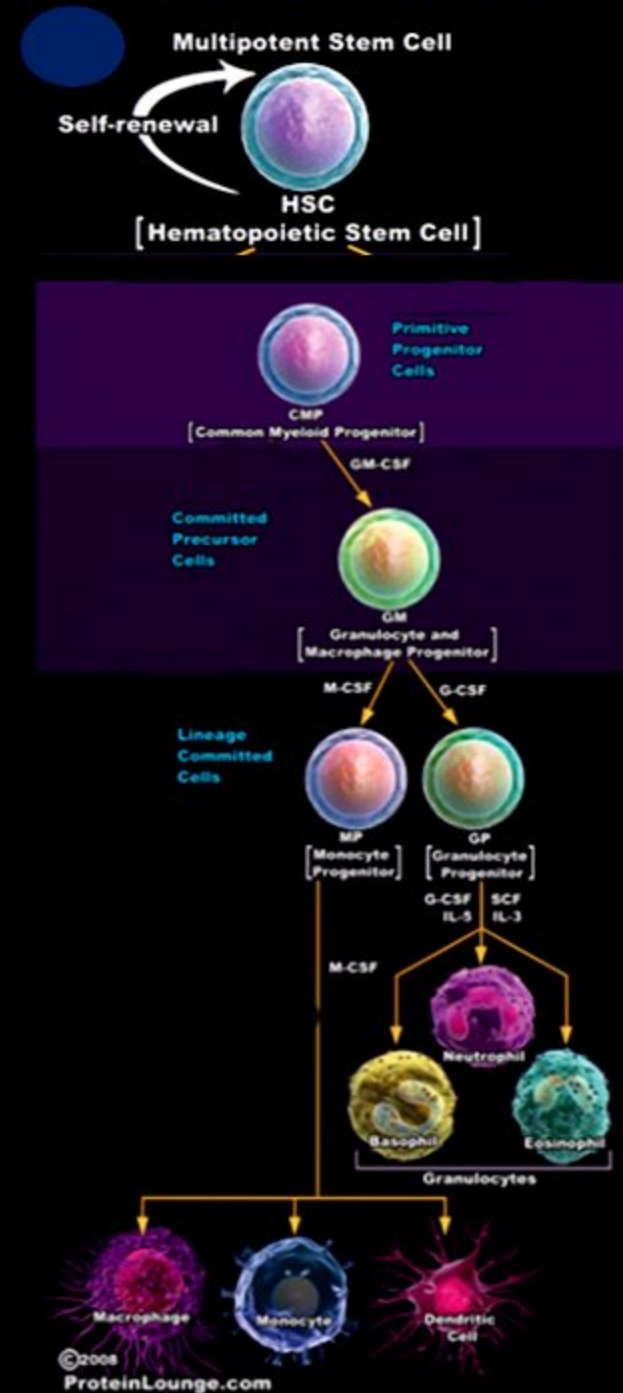


Nucleophosmin (NPM), also known as nucleolar phosphoprotein B23 or numatrin

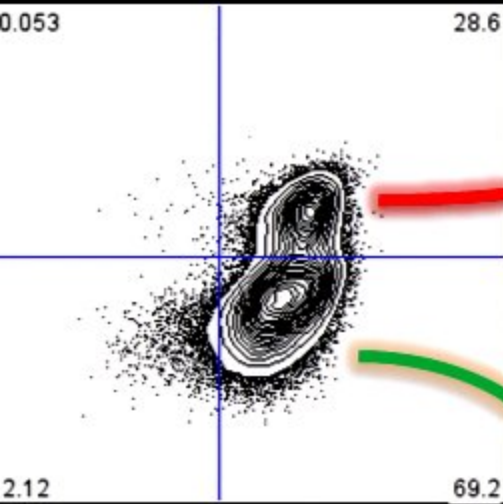
Responding cells are primitive ... Non-responders are mature



Cytokine Feedback

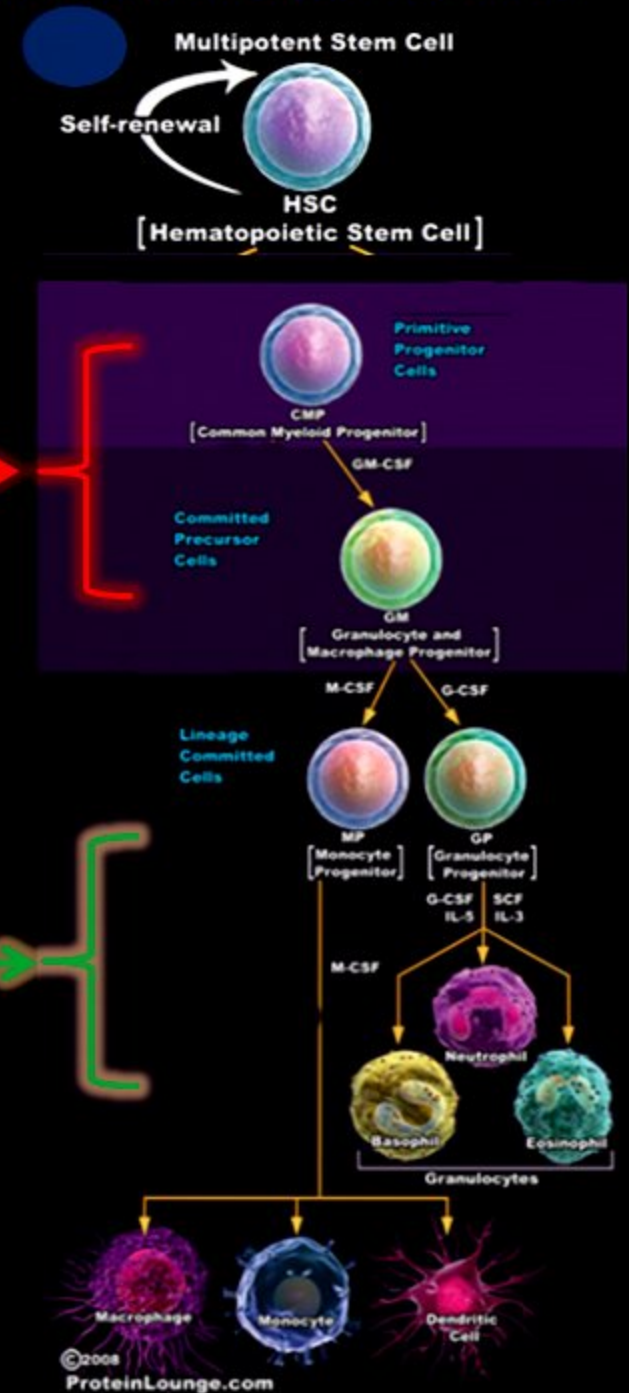
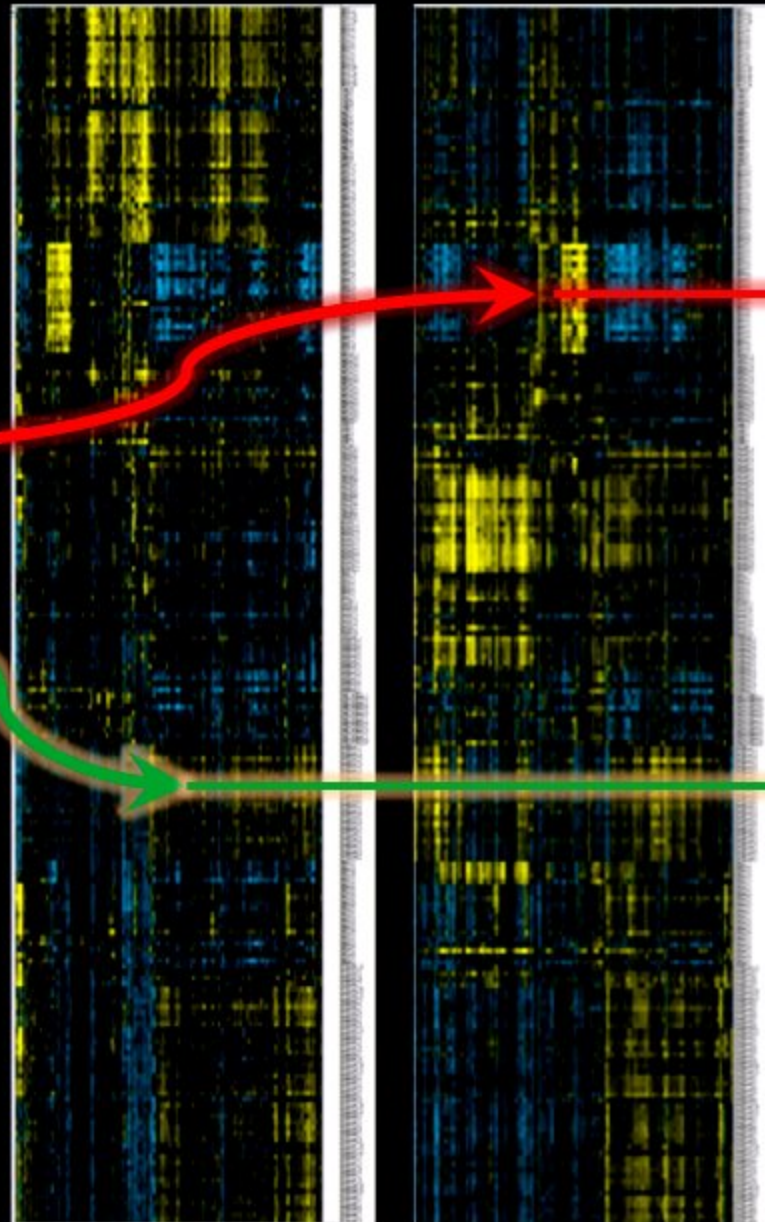


Responding cells are primitive ... Non-responders are mature

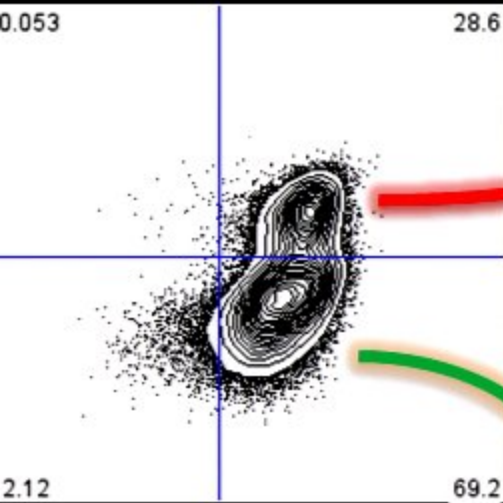


Responders

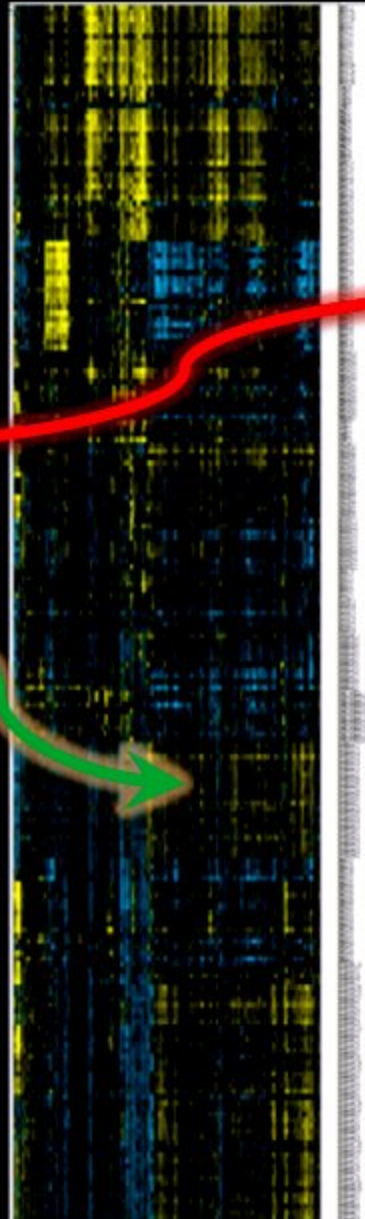
Non-responders



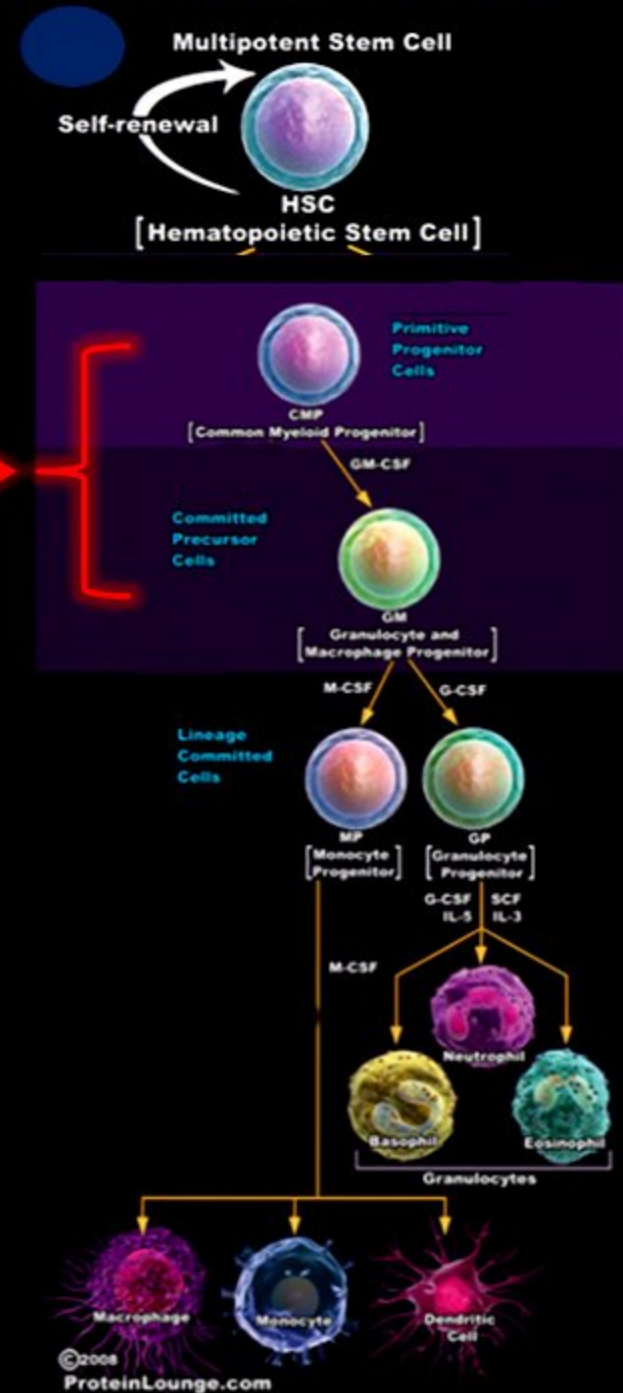
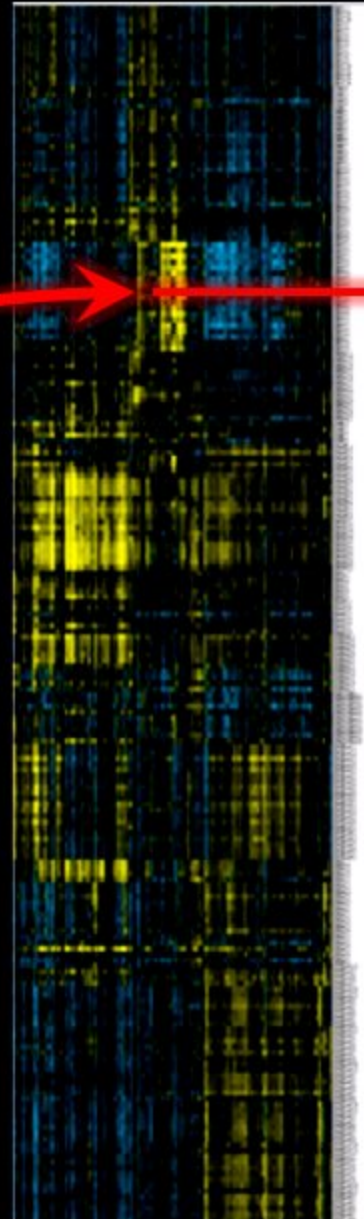
Responding cells are primitive ... Non-responders are mature



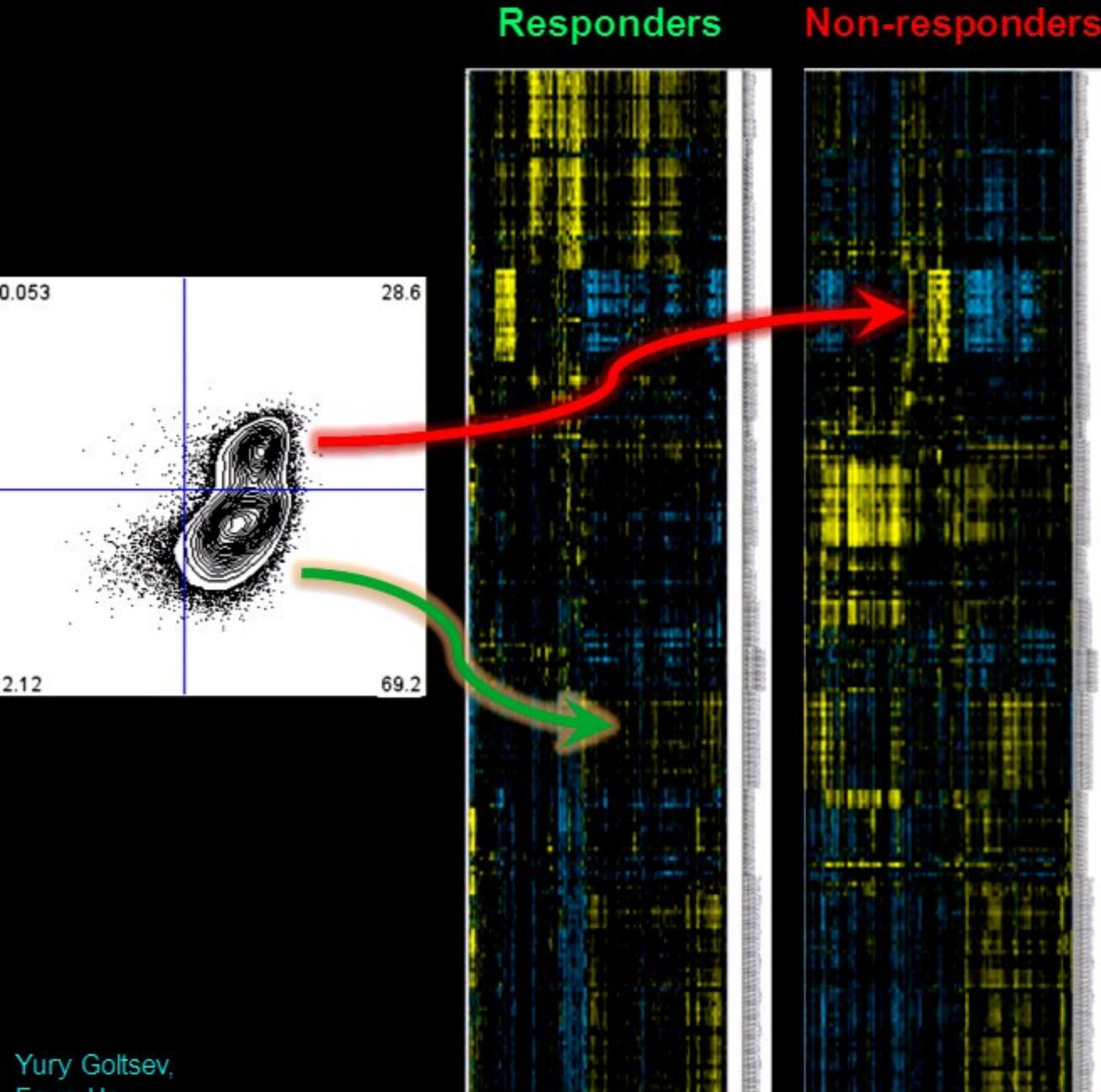
Responders



Non-responders

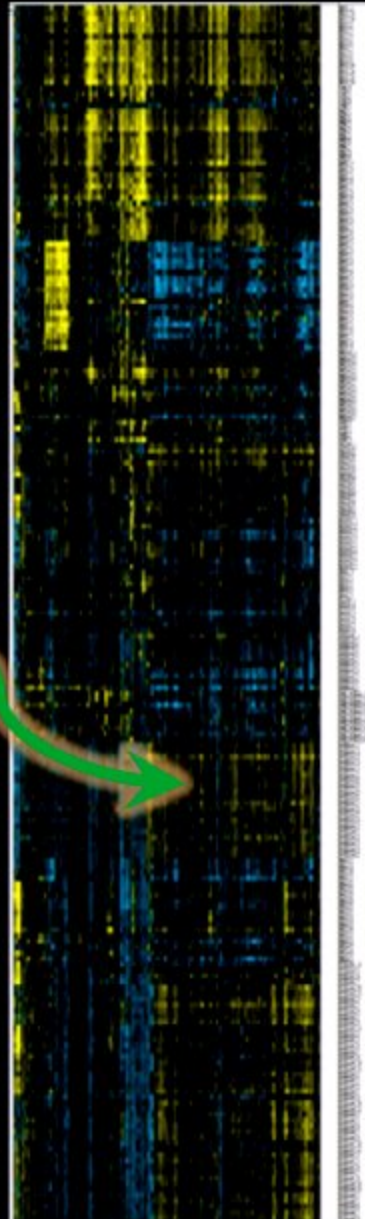
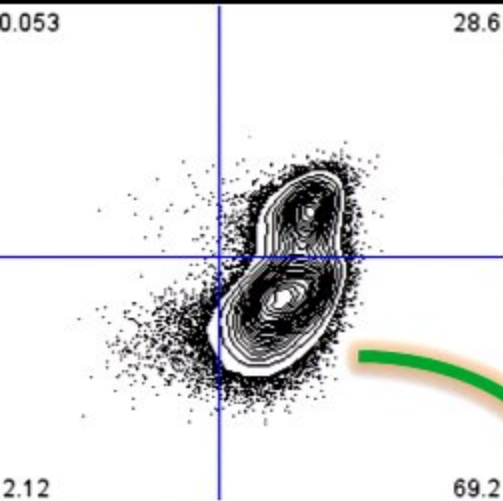


Responding cells are primitive ... Non-responders are mature

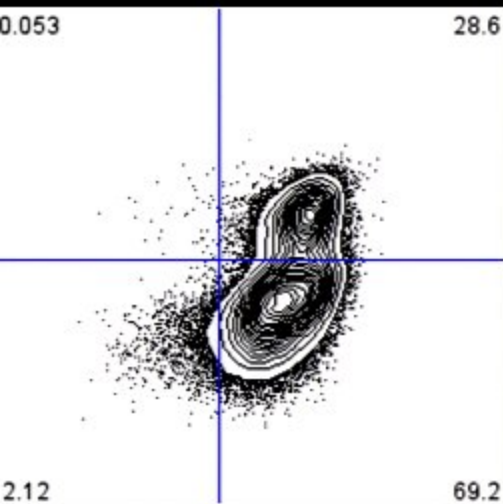


Responding cells are primitive ... Non-responders are mature

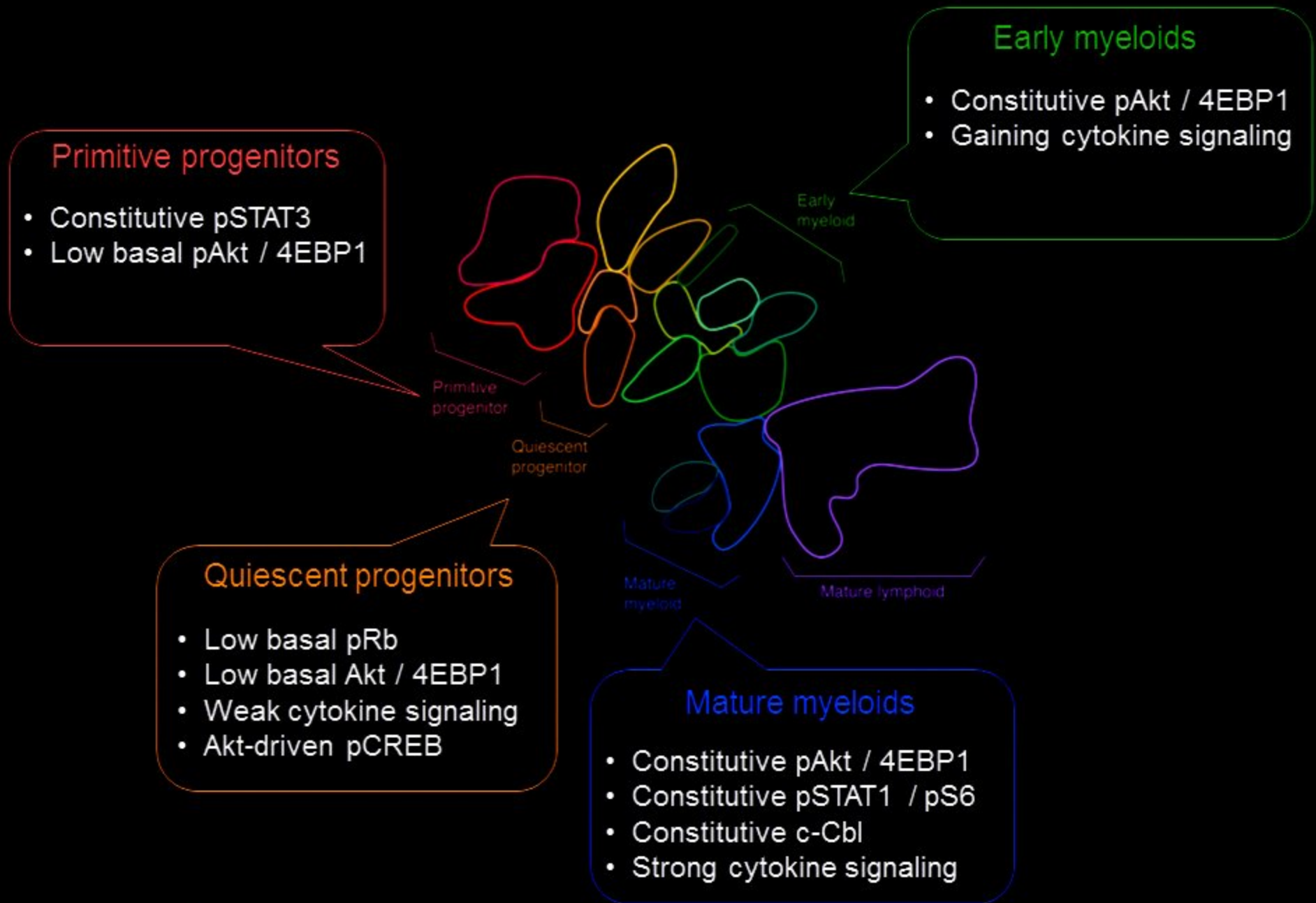
Responders



Responding cells are primitive ... Non-responders are mature



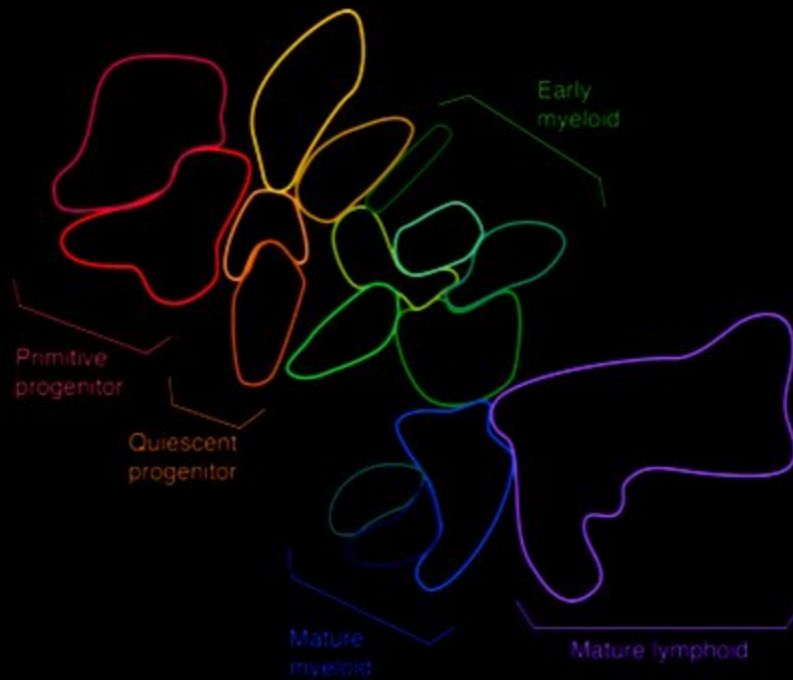
Summary of differential signaling in phenotype groups



Summary of differential signaling in phenotype groups

Primitive progenitors

- Constitutive pSTAT3
- Low basal pAkt / 4EBP1

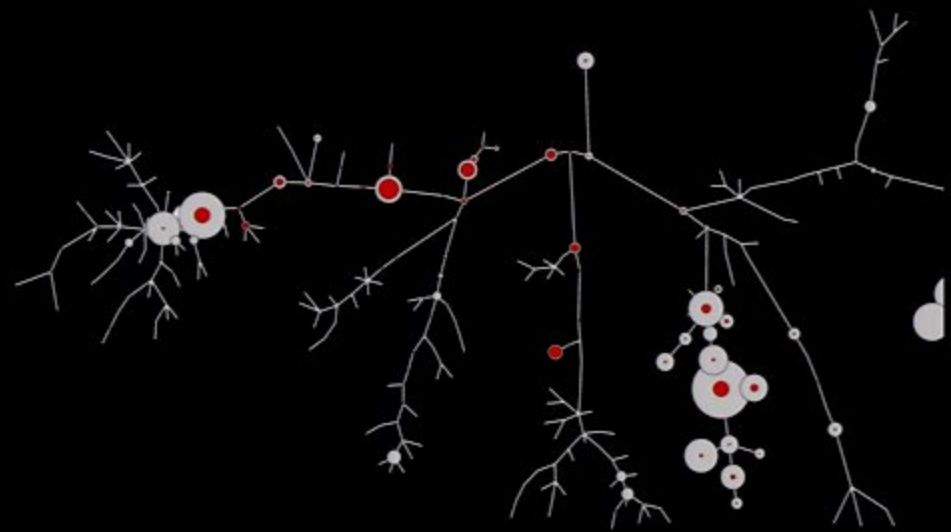
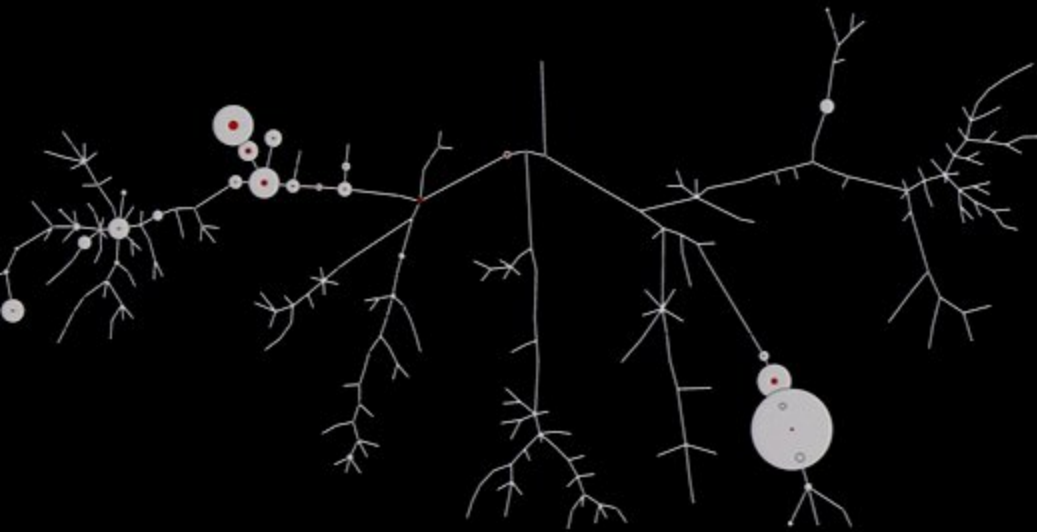


Cell Cycle Distribution Varies Within & Across AML Cell Subsets

AML5

AML9

S

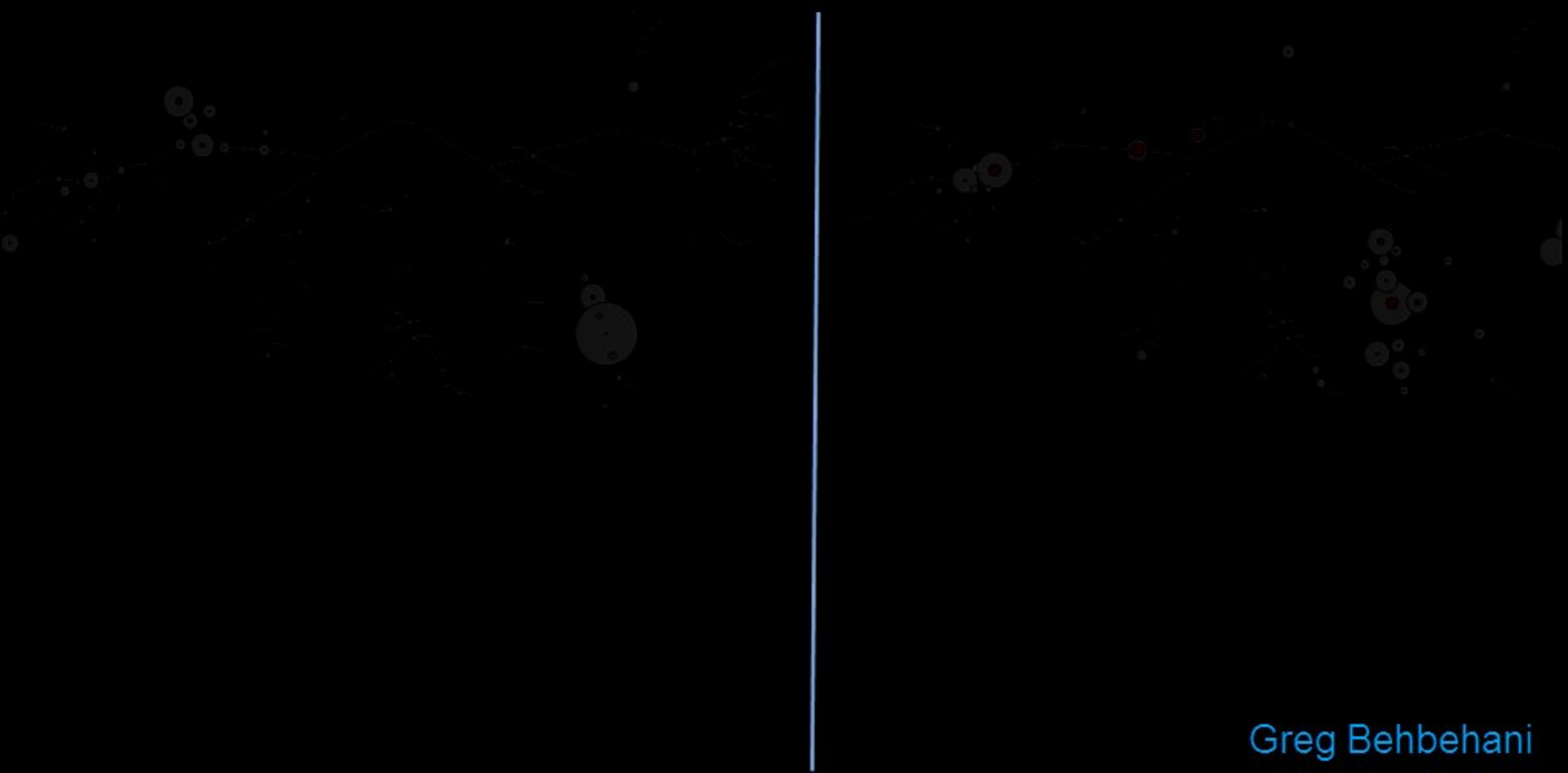


Cell Cycle Distribution Varies Within & Across AML Cell Subsets

AML5

AML9

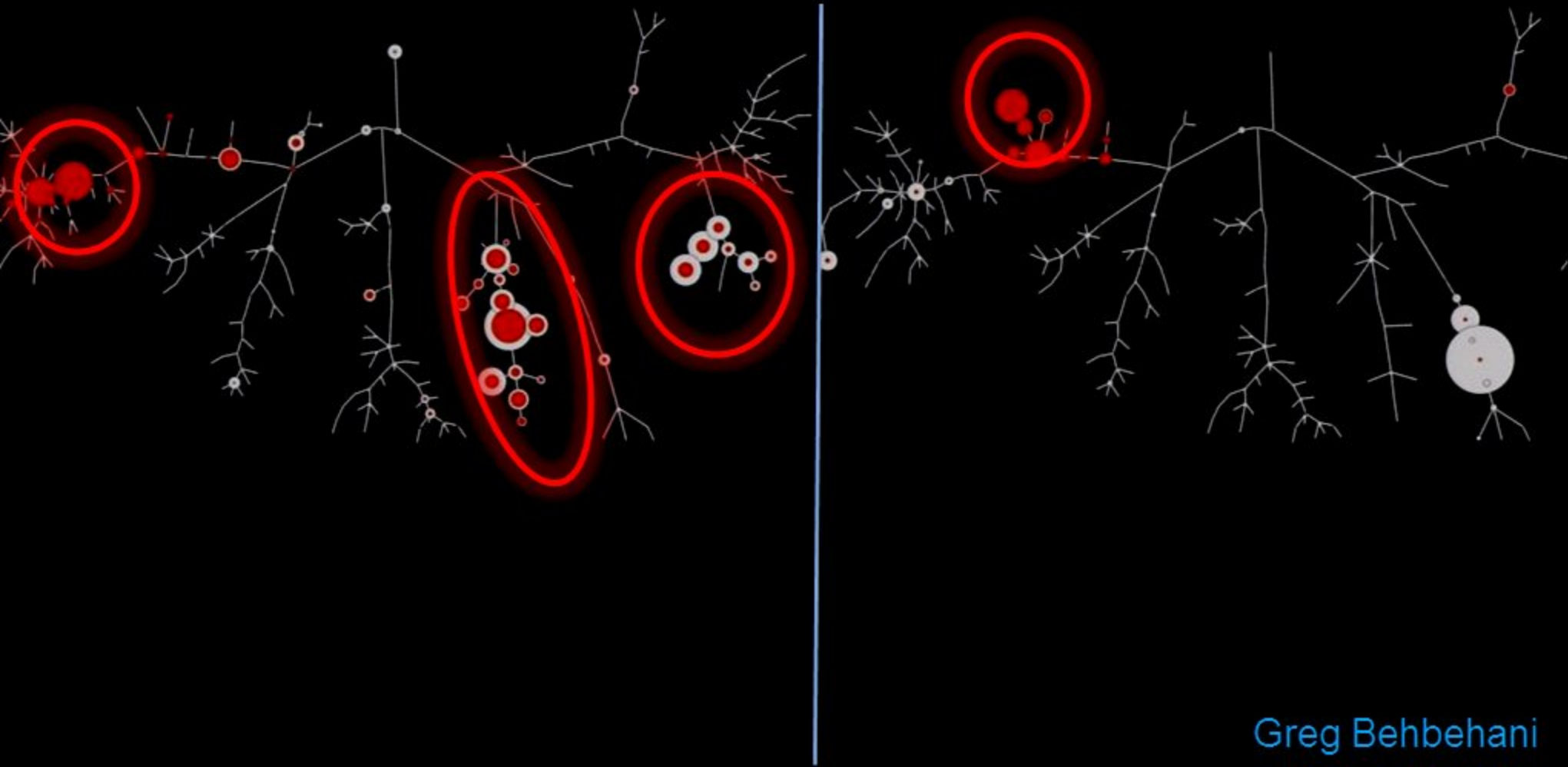
S



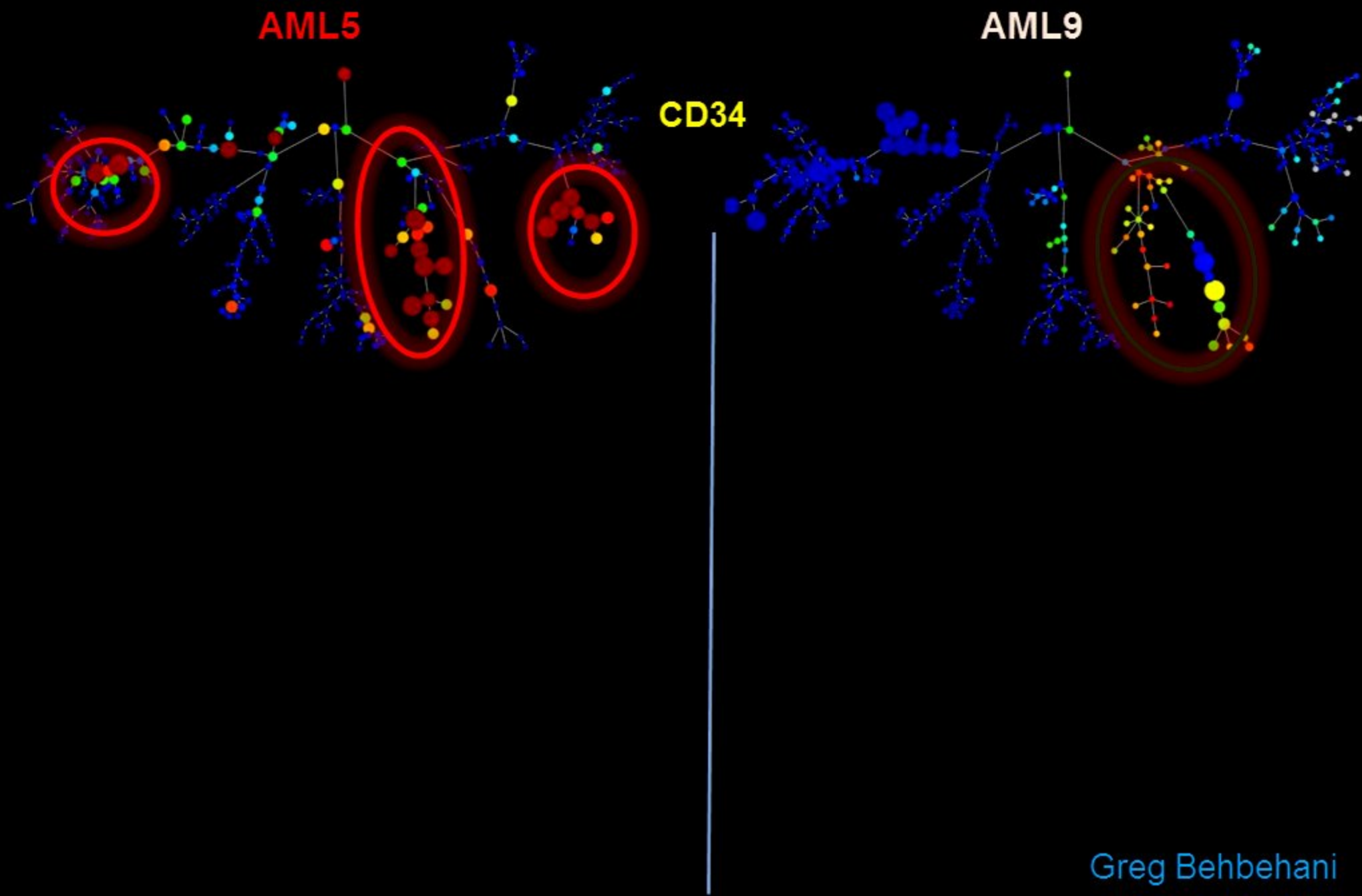
Cell Cycle Distribution Varies Within & Across AML Cell Subsets

AML5

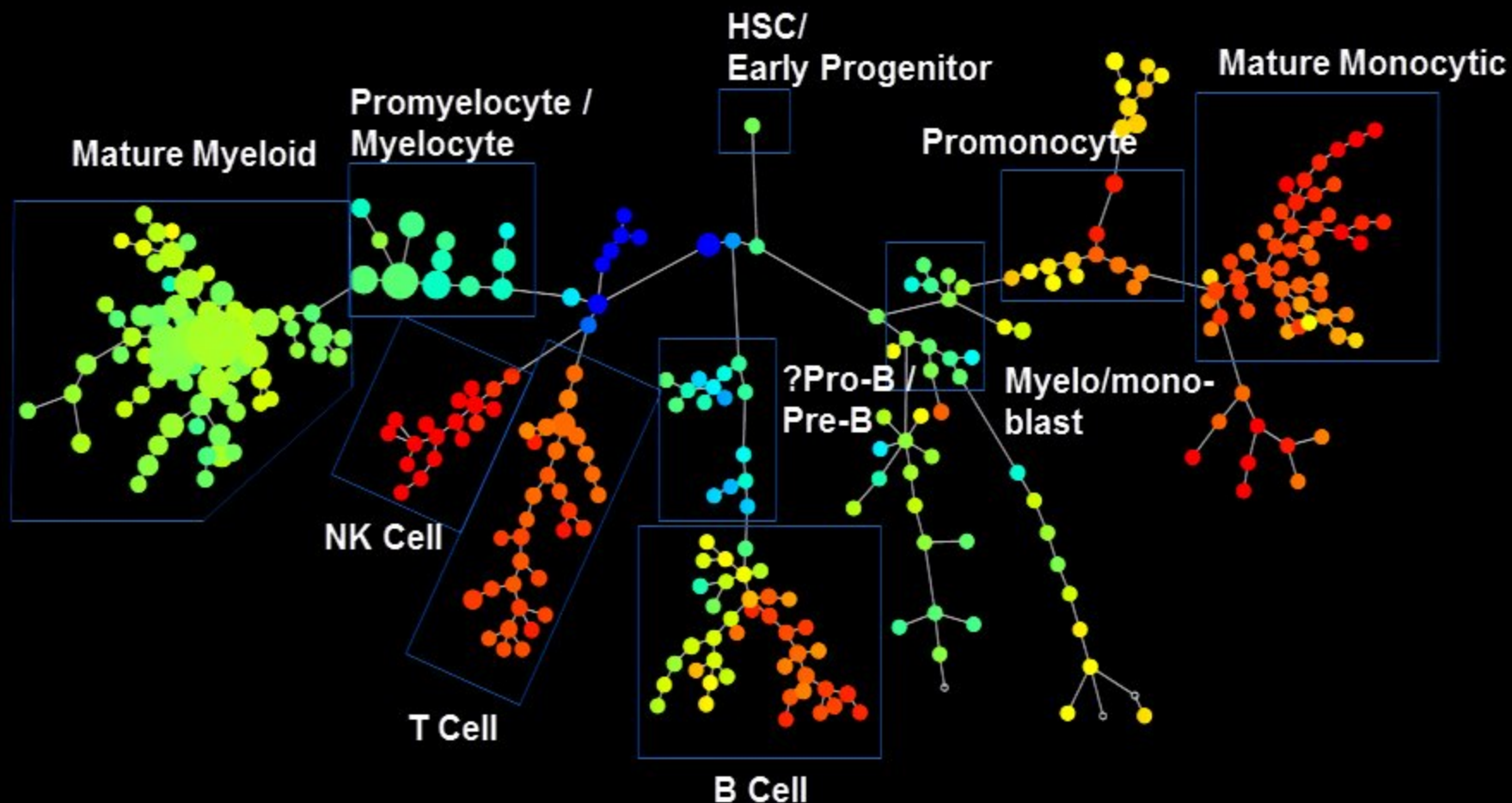
AML9



Cell Cycle Distribution Varies Within & Across AML Cell Subsets



Distinct AML Immuno-phenotypes



Normal human bone marrow
Clustered with AML samples
Colored for CD45

Additional Markers Allow for Complete Cell

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July 2012 | Volume 81A | Issue 7

Cytometry

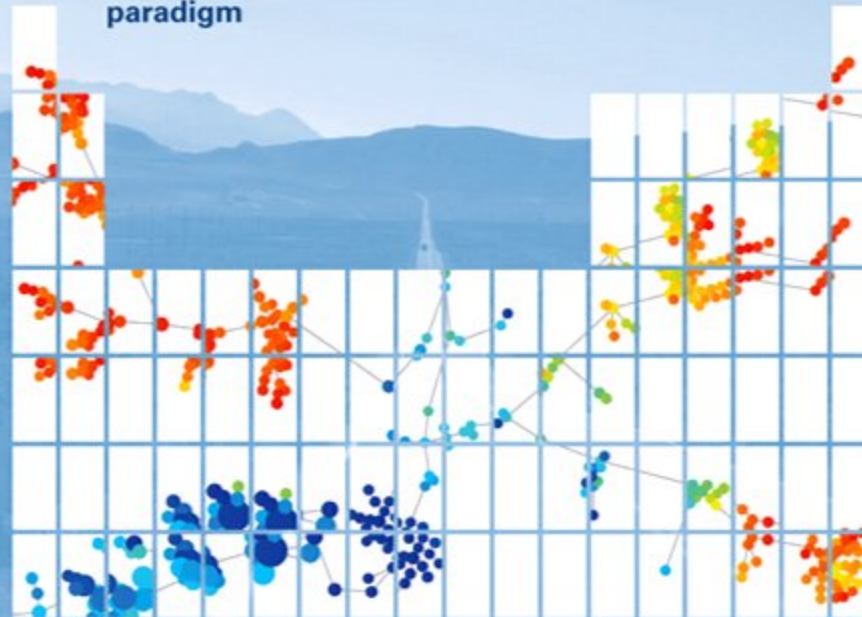
PART A

Journal of the
International Society for
Advancement of Cytometry

Illuminate: a single light source

Ultimate goal: quantification

Mass cytometry: creating a new
paradigm

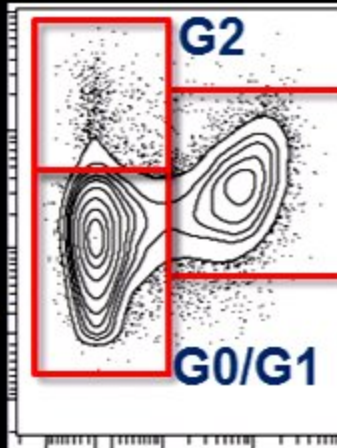


57	58	59	60	61	62	63	64	65	66	67	68	69	70	71
La	Ce	Pr	Nd	Pm	Sm	Eu	Gd	Tb	Dy	Ho	Re	Tm	Yb	Lu
89	90	91	92	93	94	95	96	97	98	99	100	101	102	103
Ac	Th	Ph	U	Np	Pu	Am	Cm	Bk	Cf	Es	Fm	Md	No	Lr



WILEY-BLACKWELL
ISSN 1552-4322

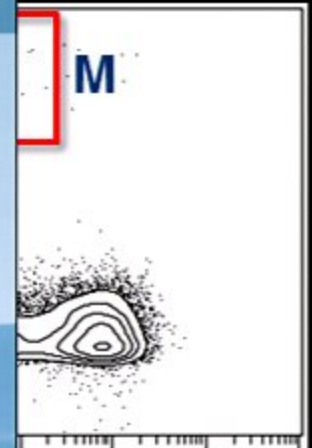
Cyclin B1



IdU

p16
p21
Ki-67
Cyclin A
Cyclin B1
pAMPK

M

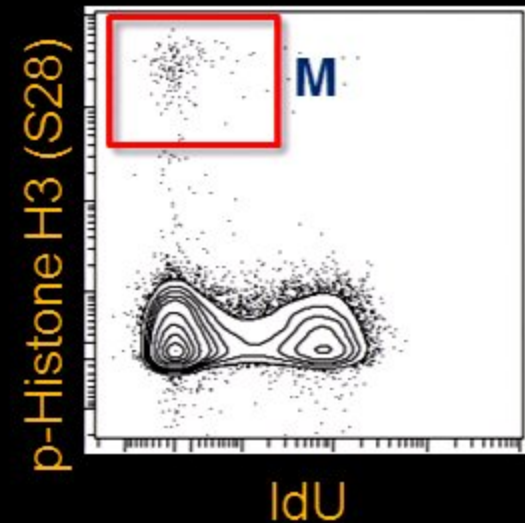
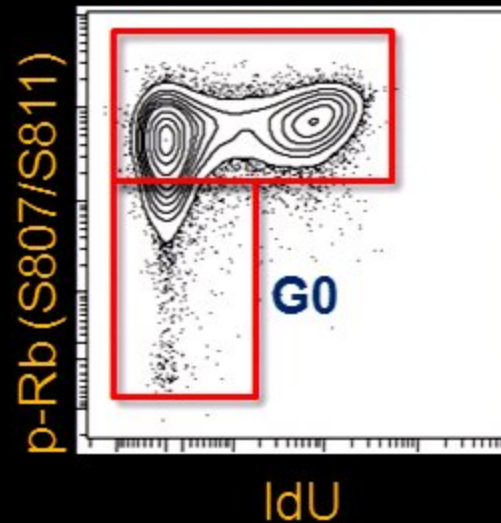
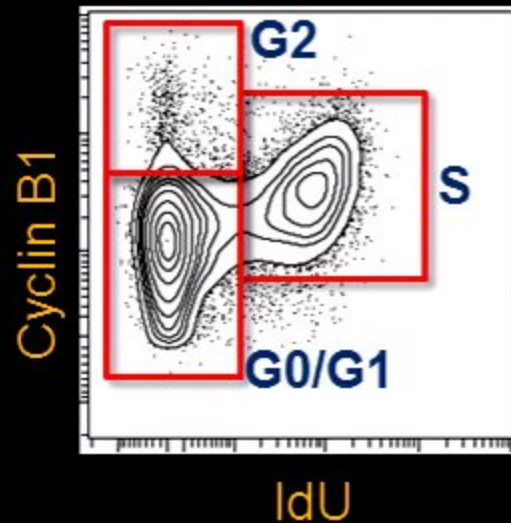


IdU

1
2
C2D
P
P1
oneH3(S28)

Greg Behbehani, et al, Cytometry A

Additional Markers Allow for Complete Cell Cycle State Assignment



p16
p21
Ki-67
Cyclin A
Cyclin B1
pAMPK

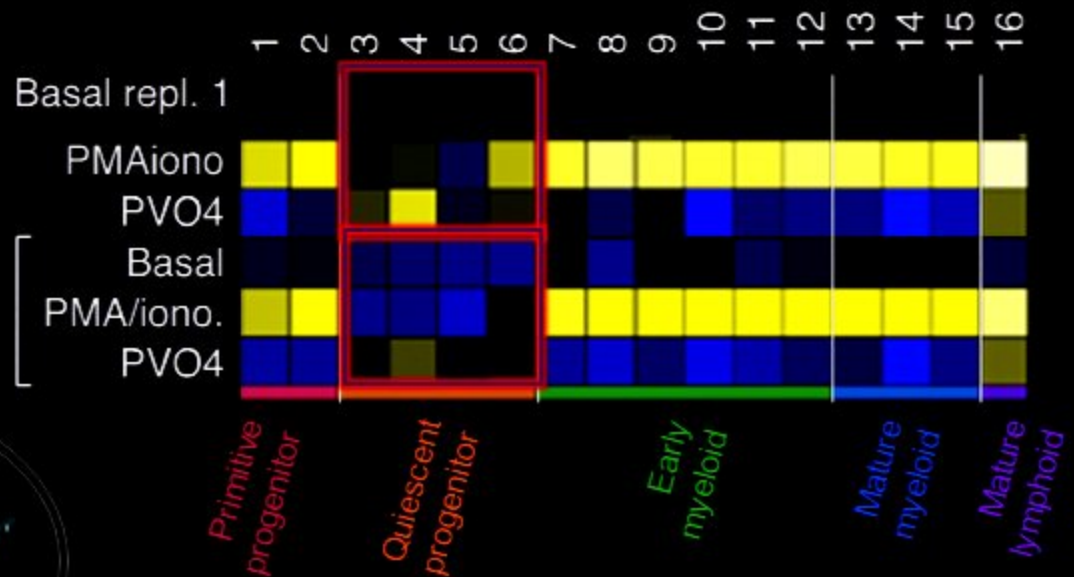
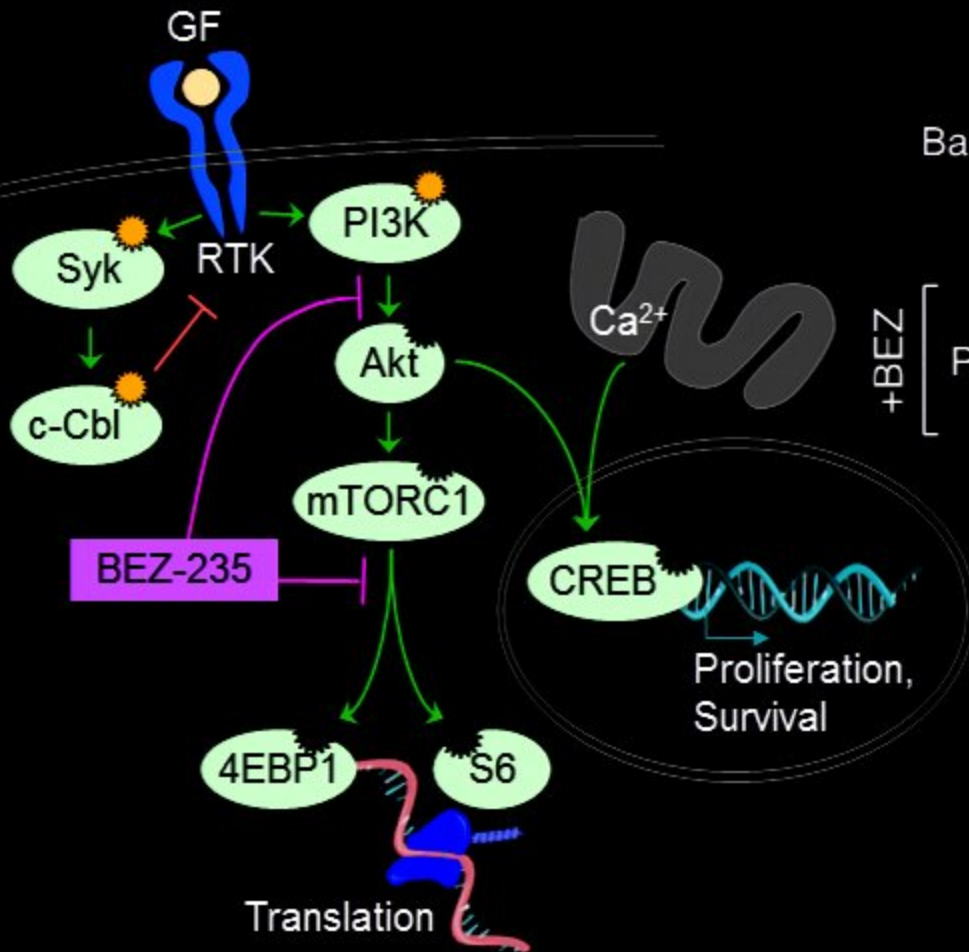
p-pRb (S807/811)
Cyclin D1/2/3
Cyclin E
c-Caspase3
prpS6
pCDK1

p27
p53 (pS15)
p53 (pS20)
pH2AX
pATM
pATR

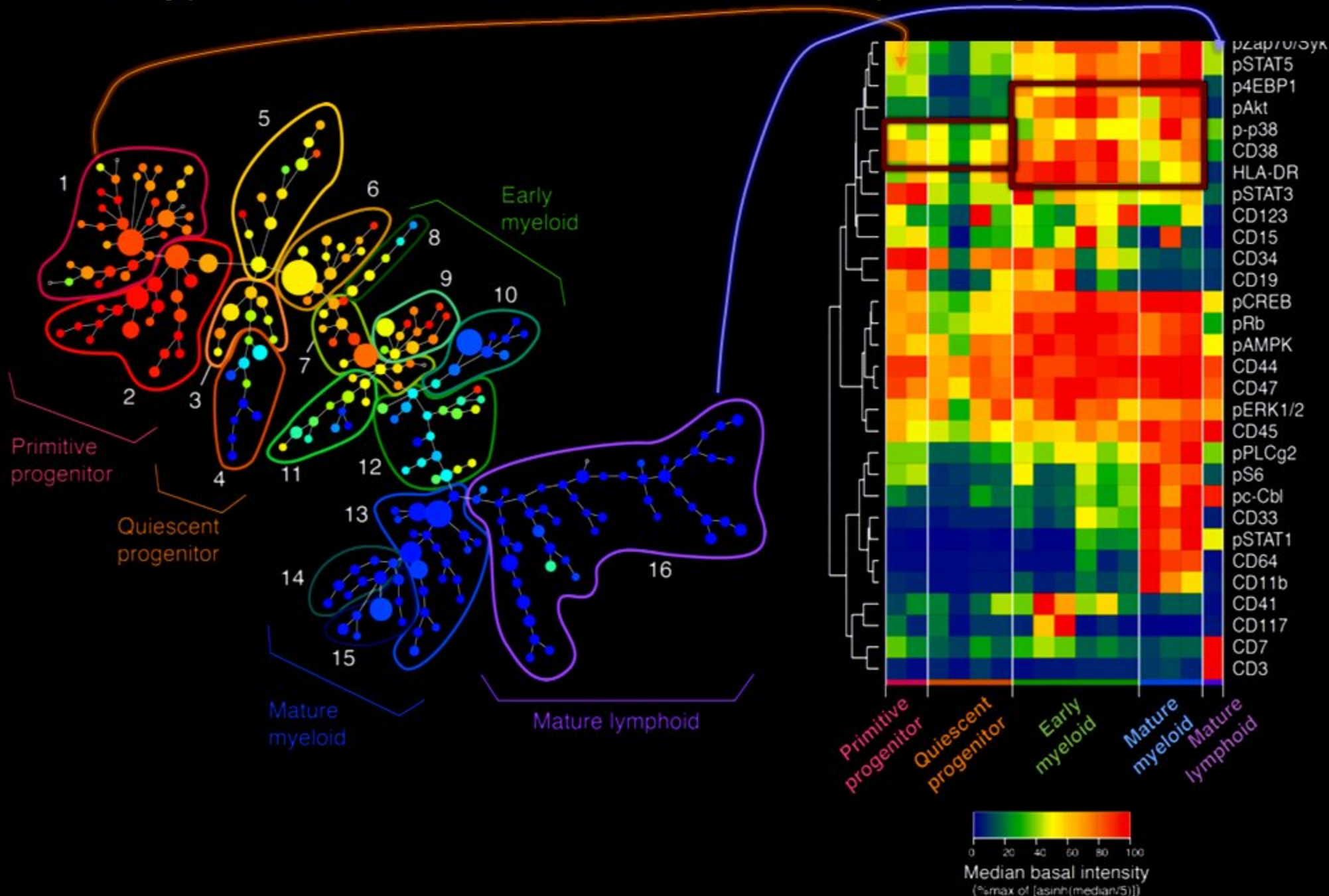
pCHK1
pCHK2
pFANC2D
c-PARP
p53BP1
pHistoneH3(S28)

Quiescent Cells can still be inhibited

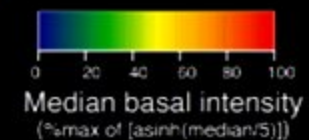
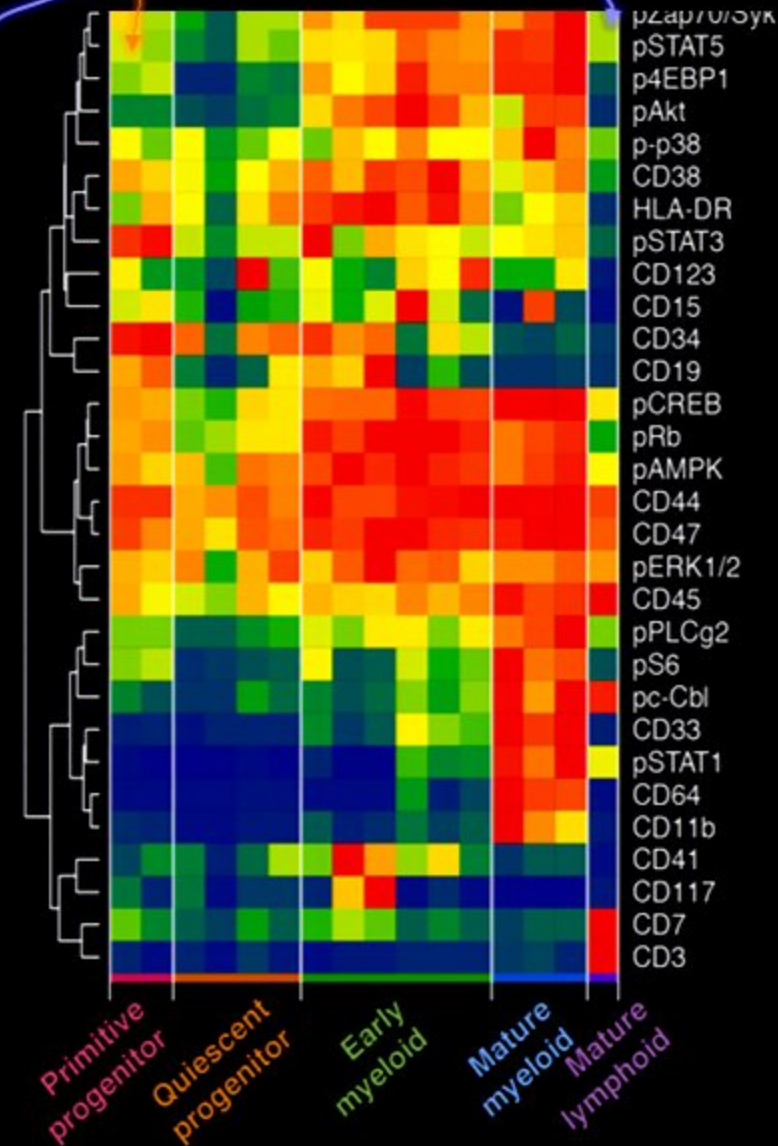
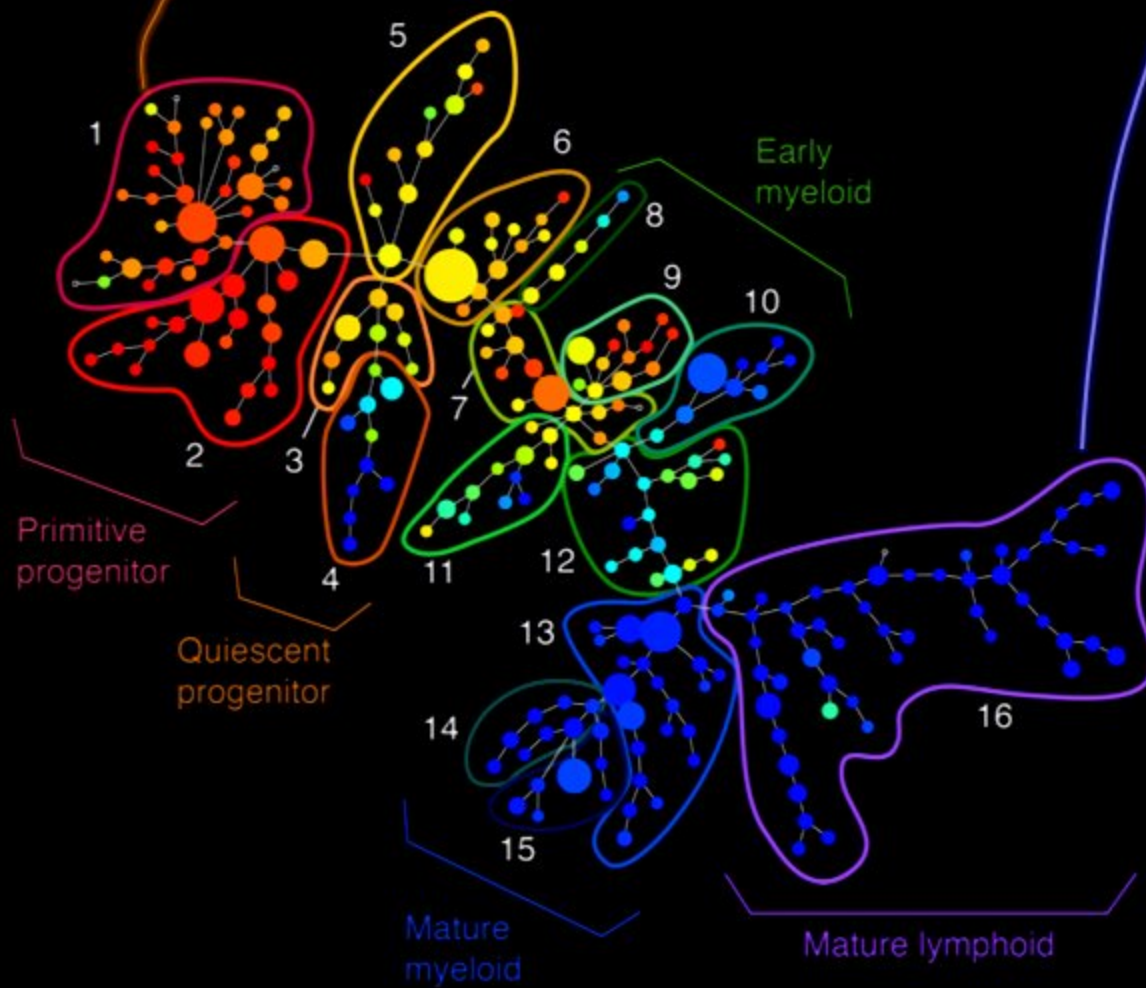
pCREB



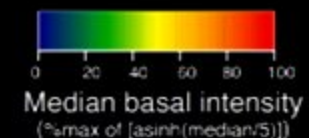
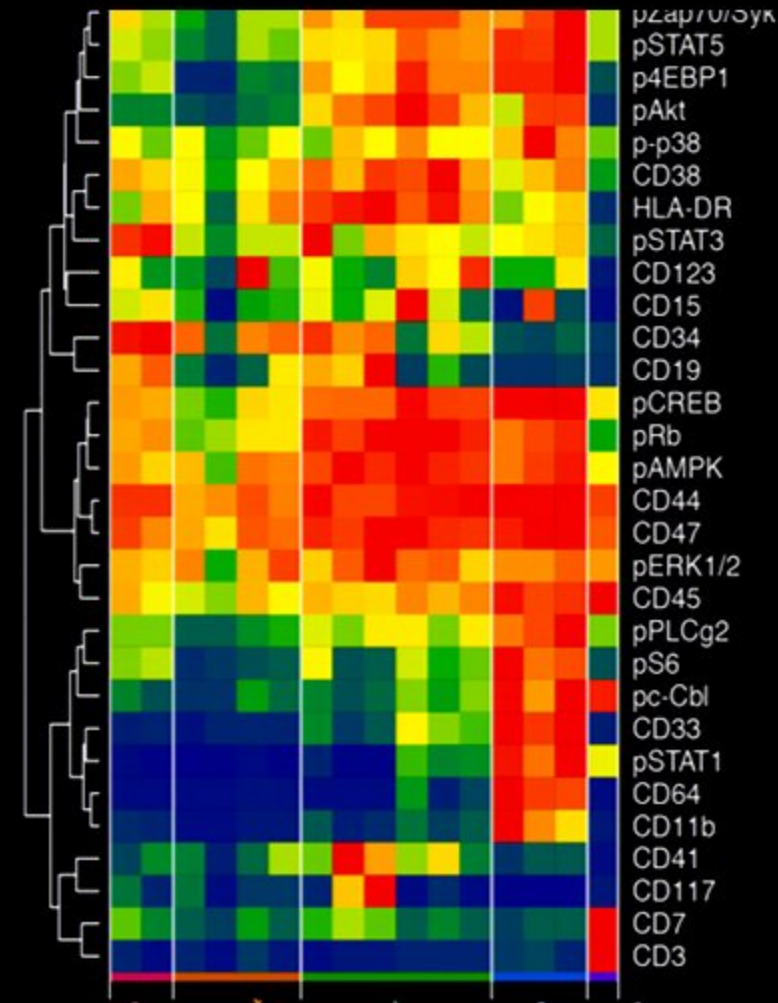
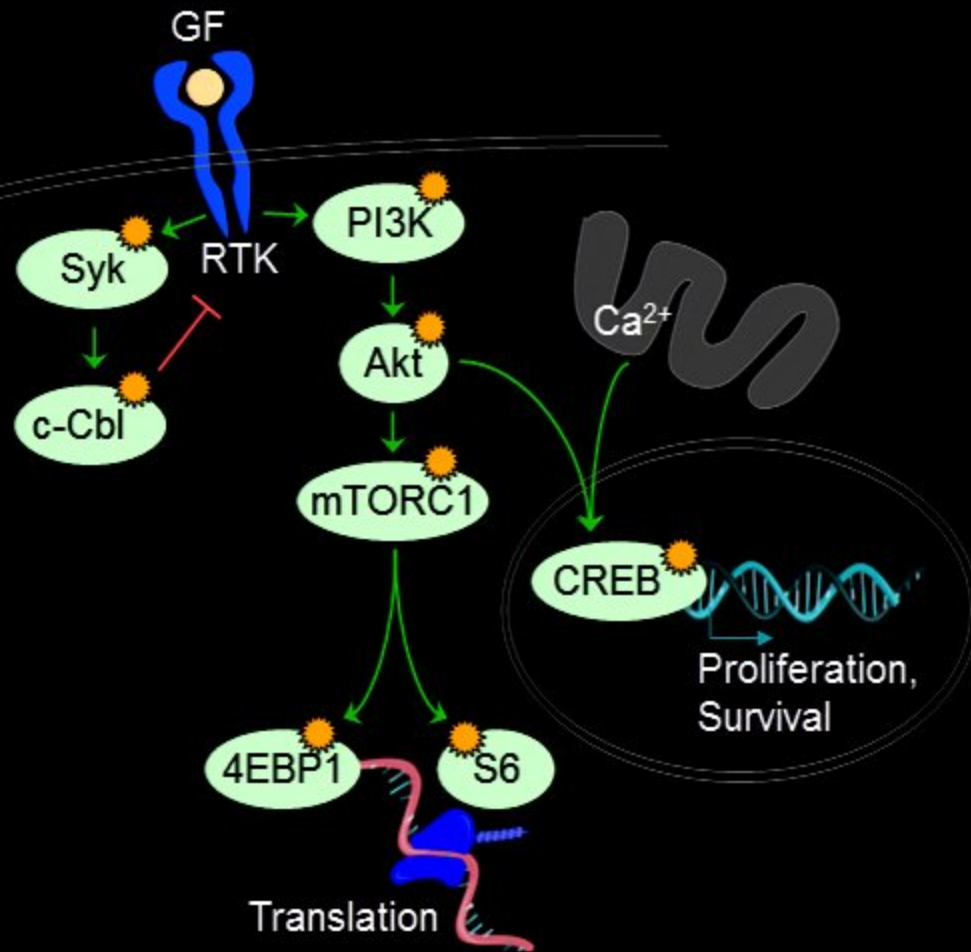
Cell types exhibit differential constitutive pathway activation



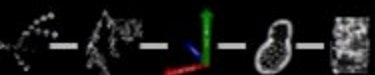
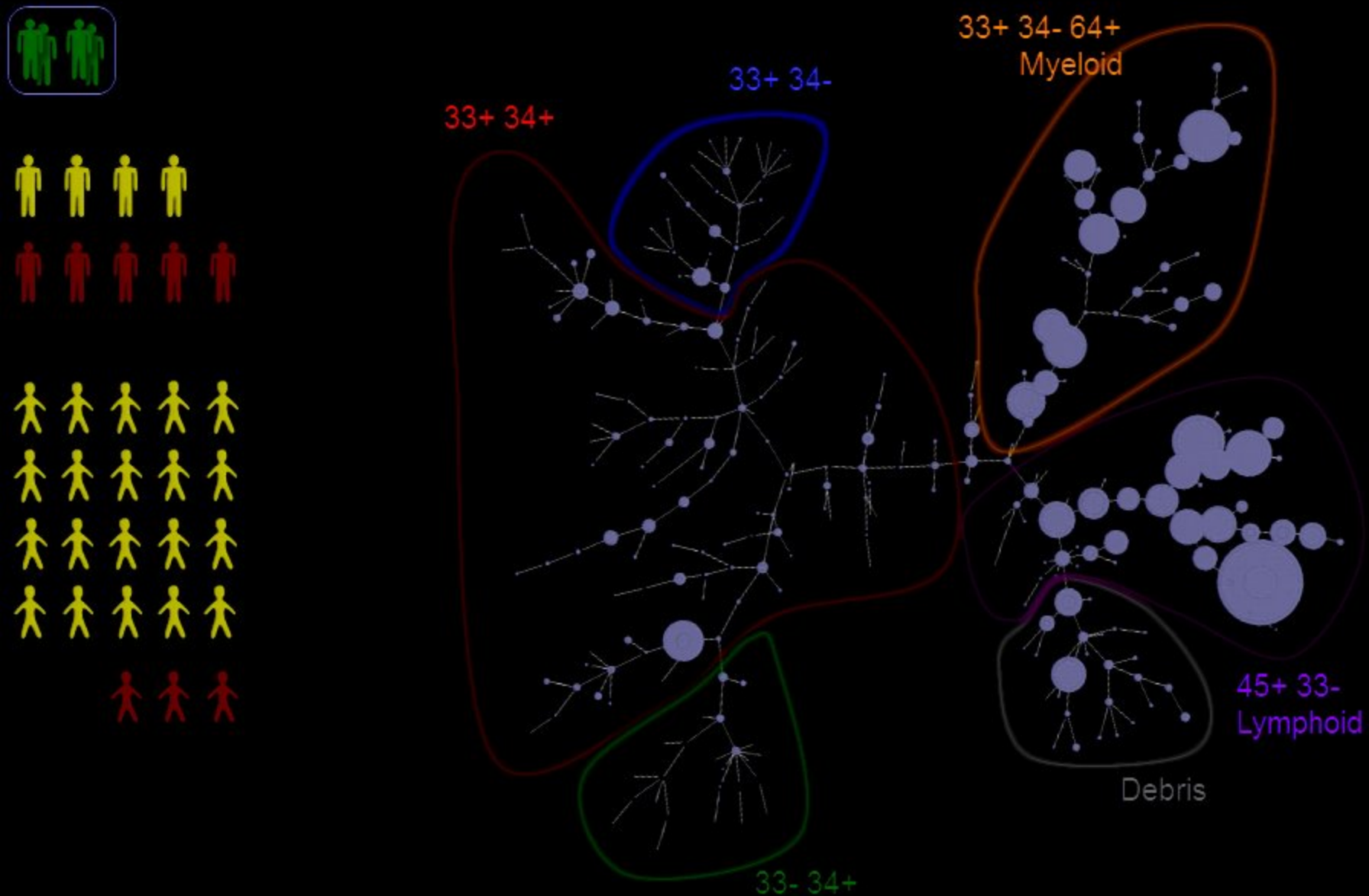
Cell types exhibit differential constitutive pathway activation



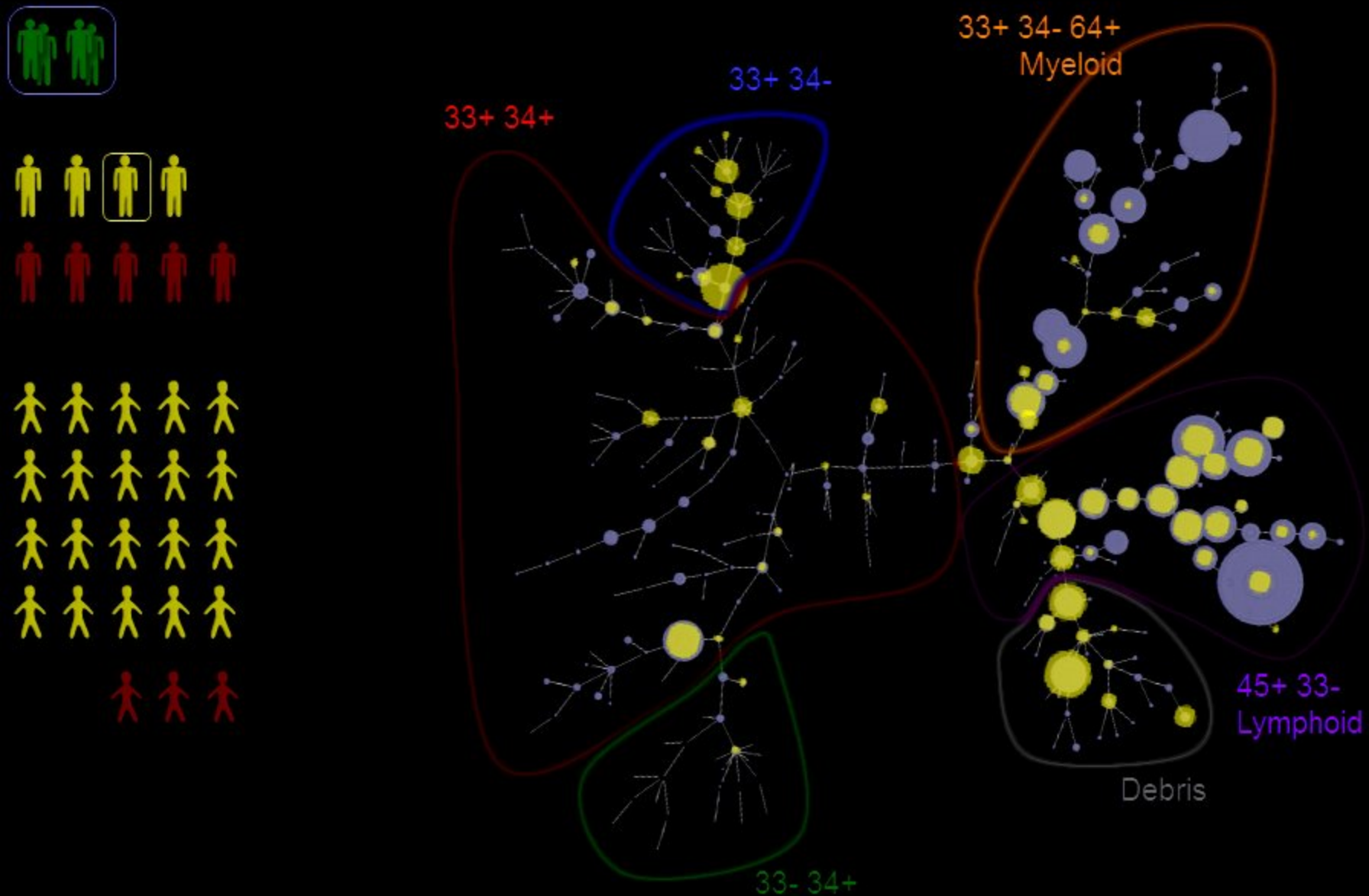
Cell types exhibit differential constitutive pathway activation



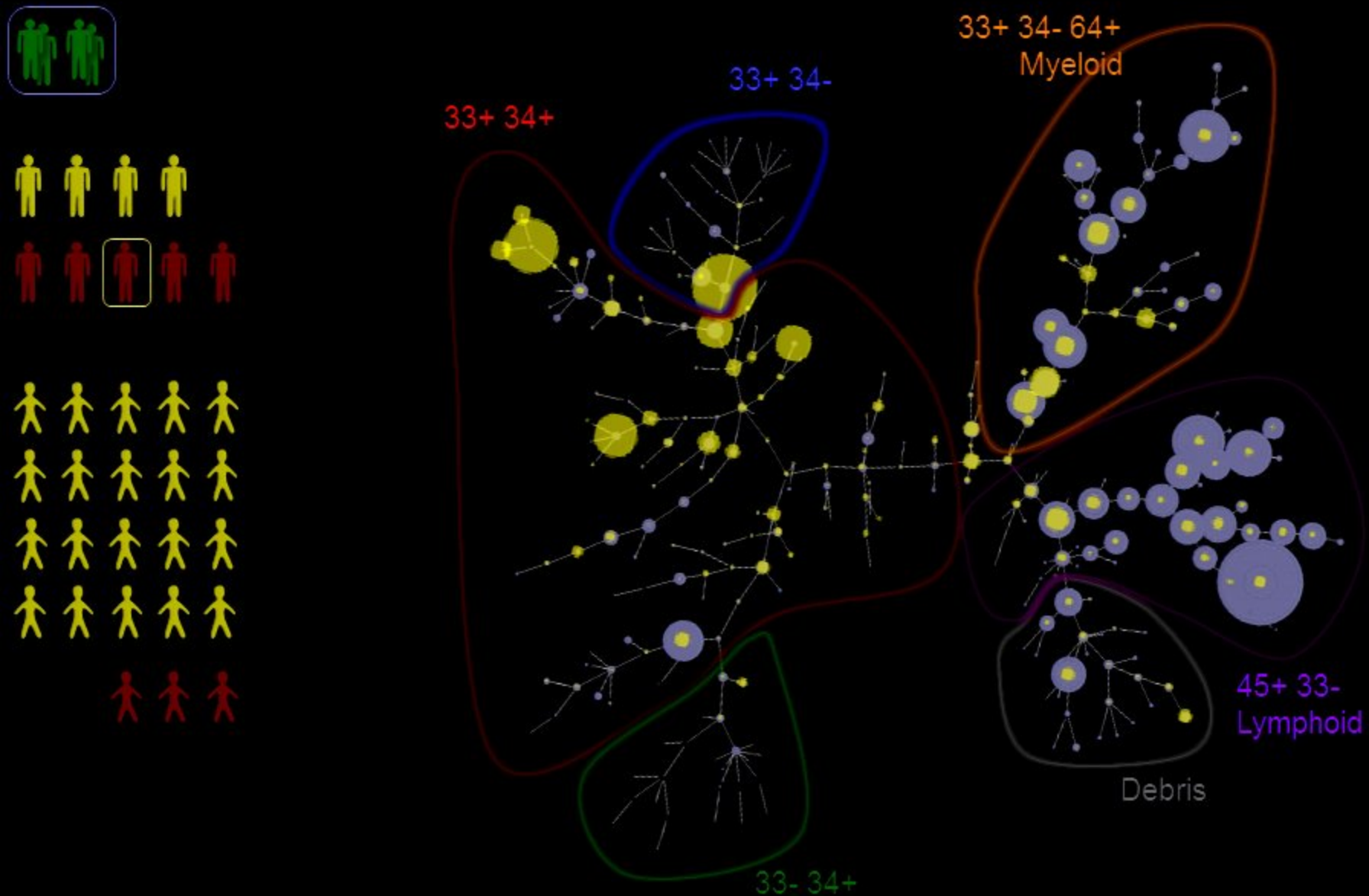
Phenotypic landscape of AML is diverse, but constrained...



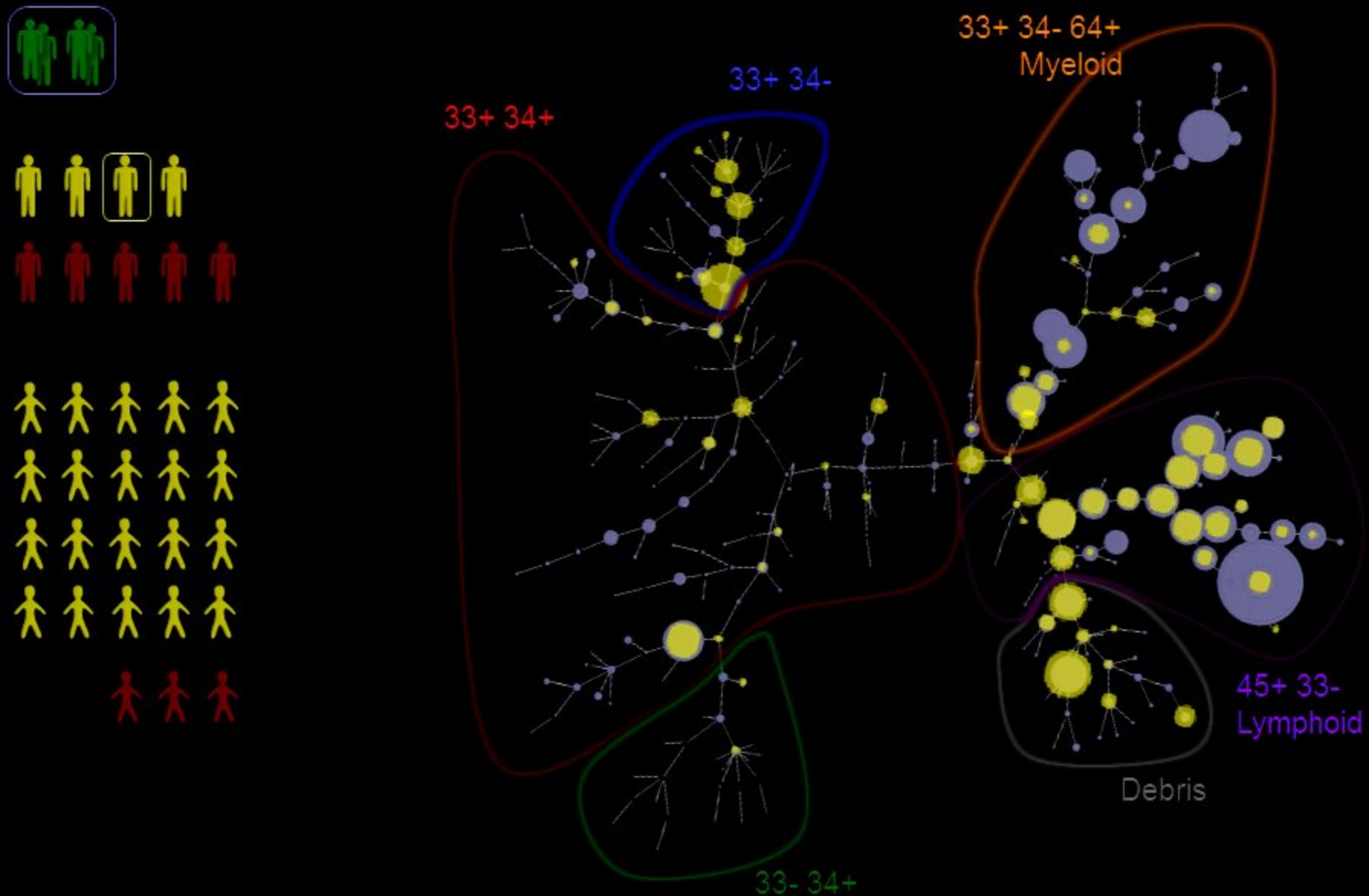
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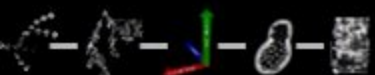
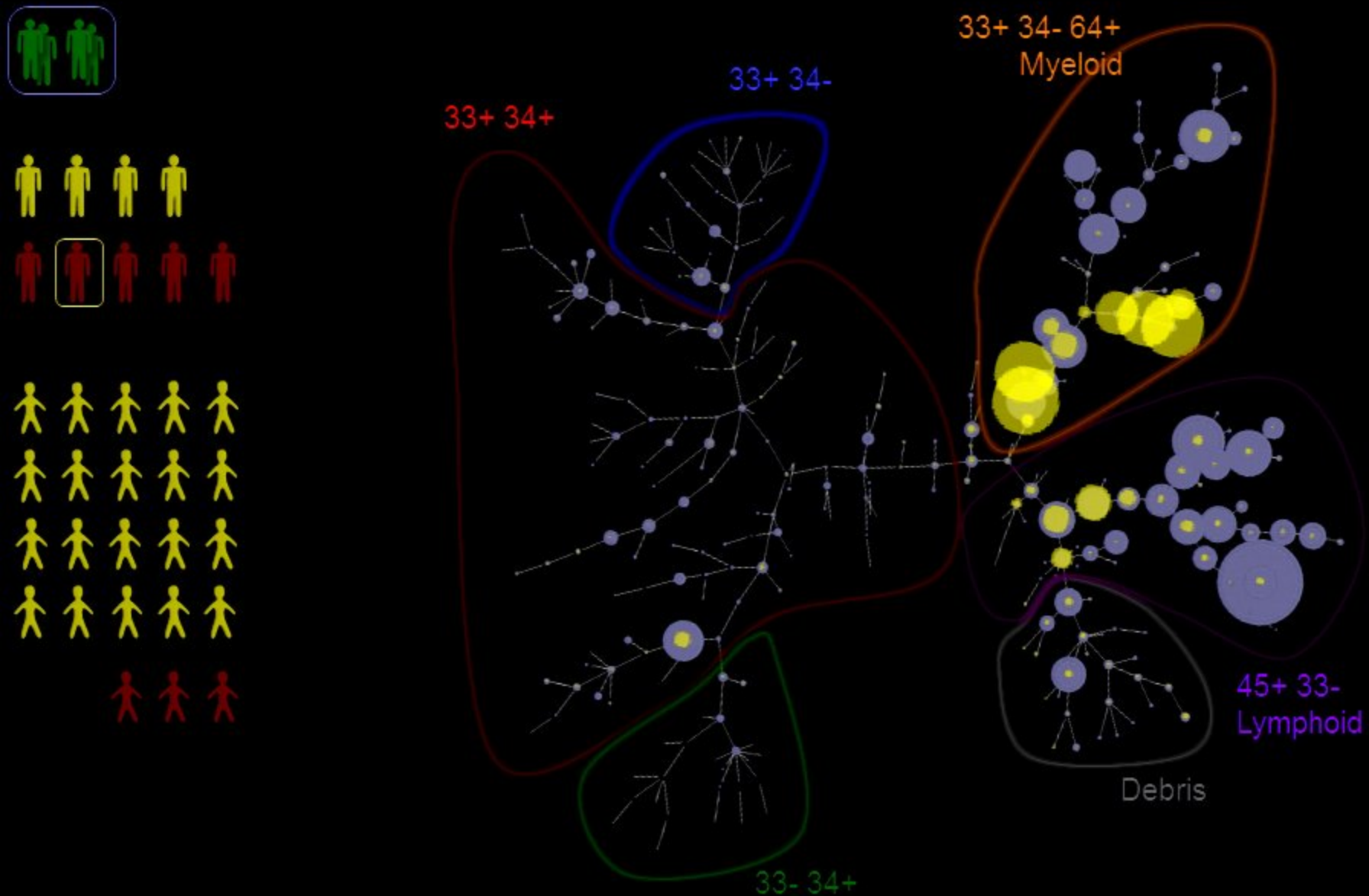
Phenotypic landscape of AML is diverse, but constrained...



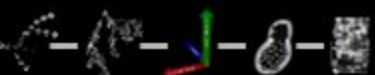
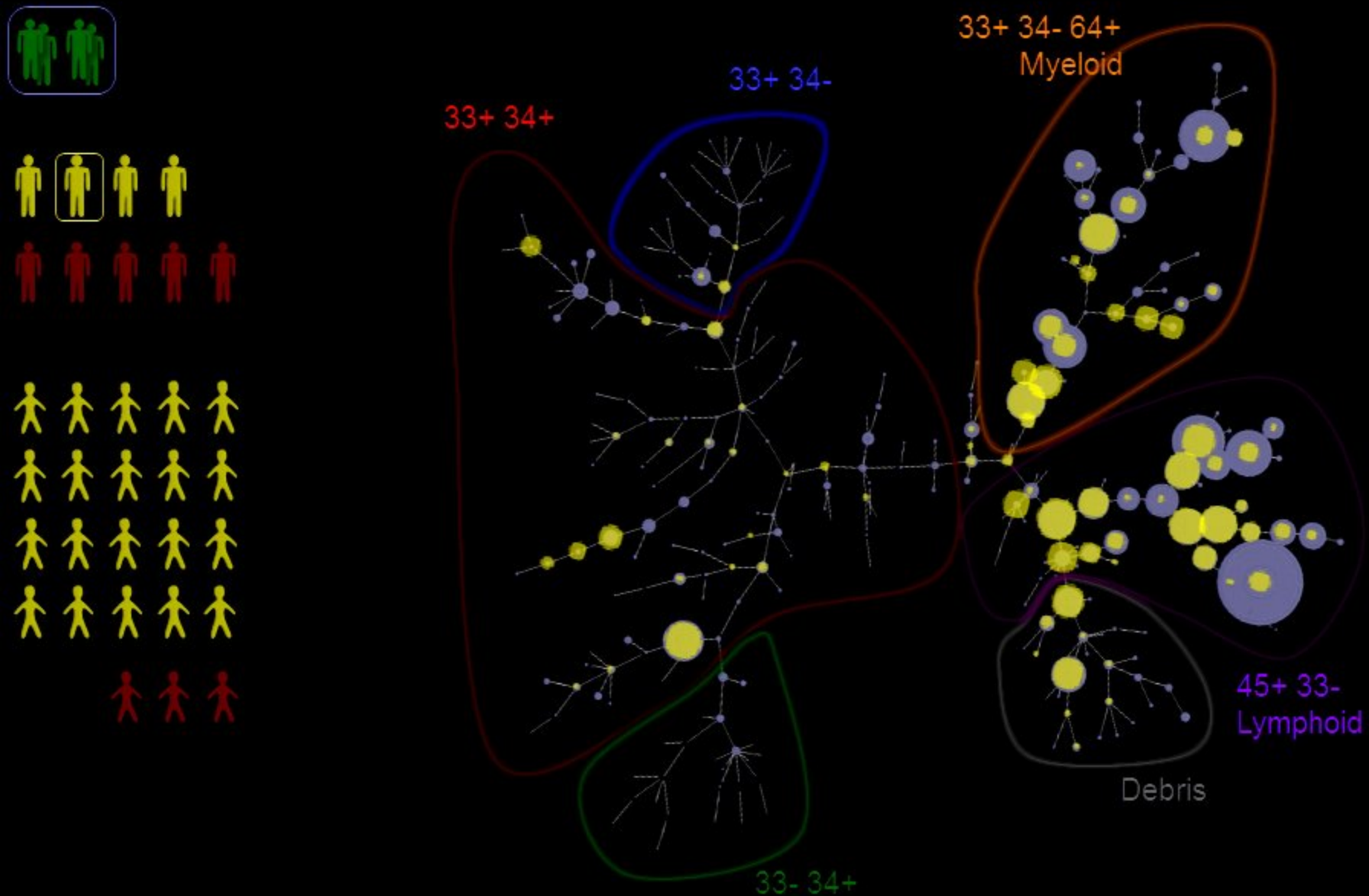
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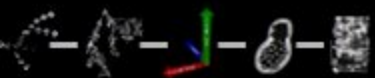
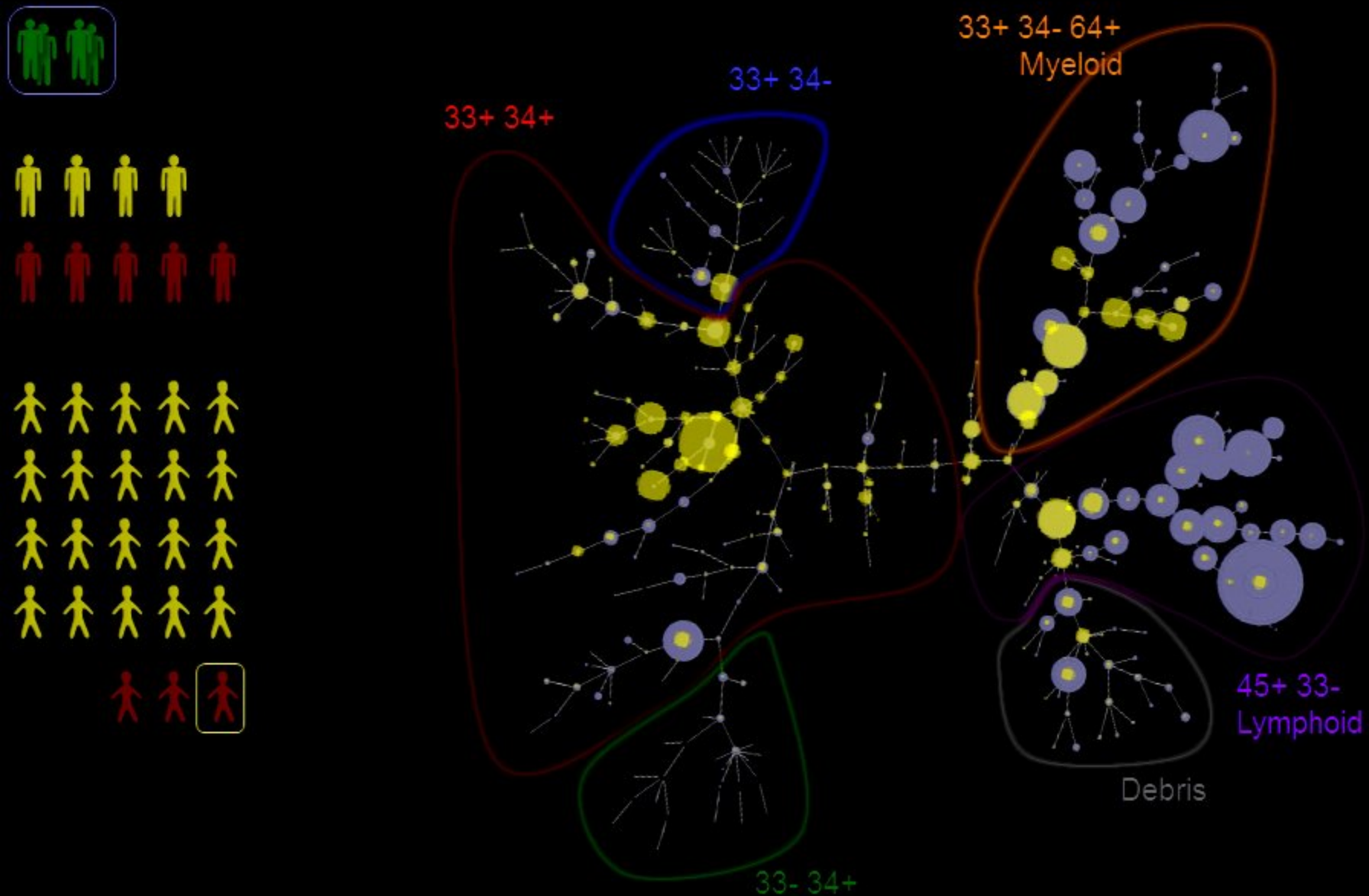
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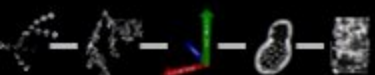
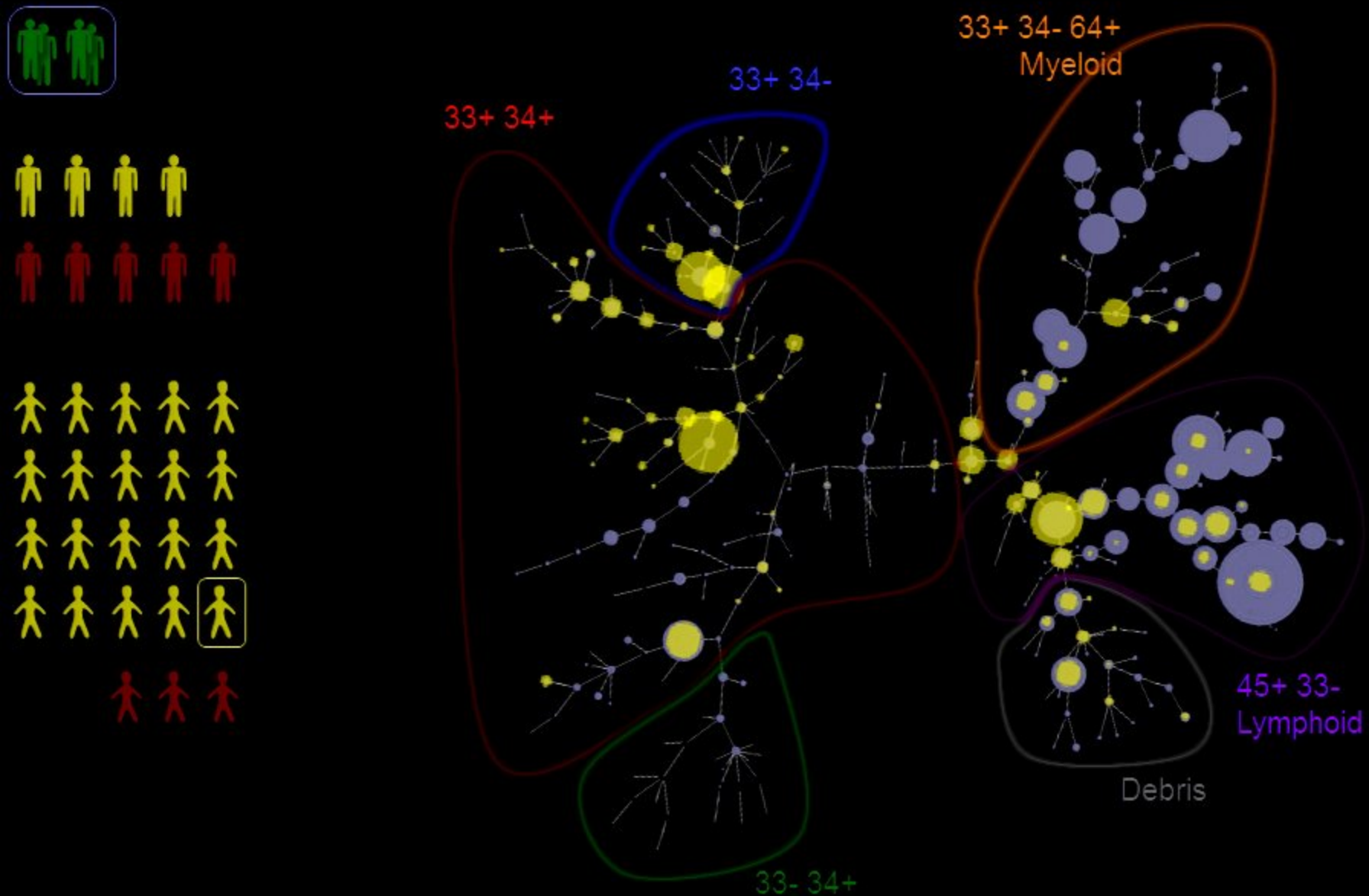
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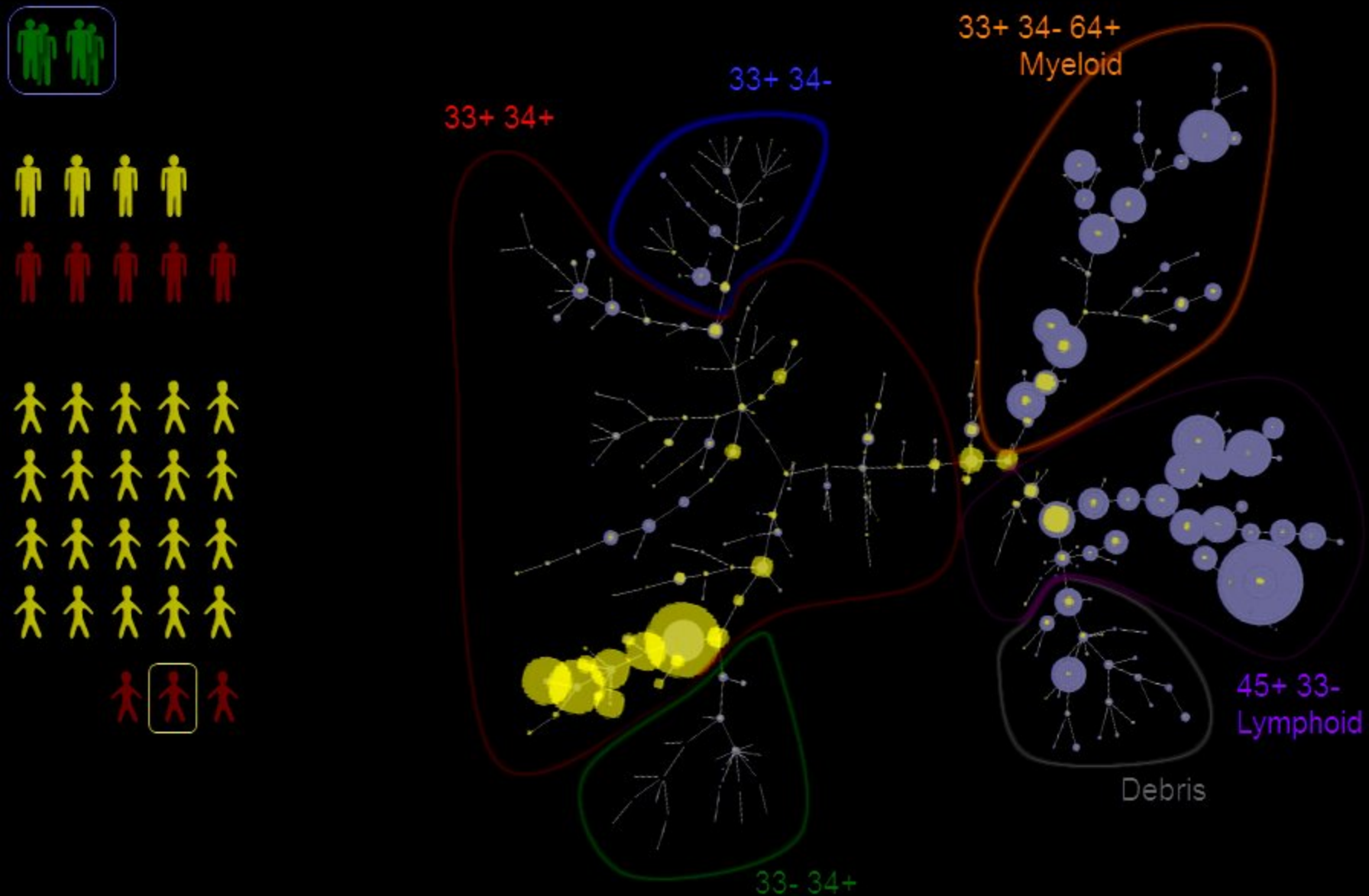
Phenotypic landscape of AML is diverse, but constrained...



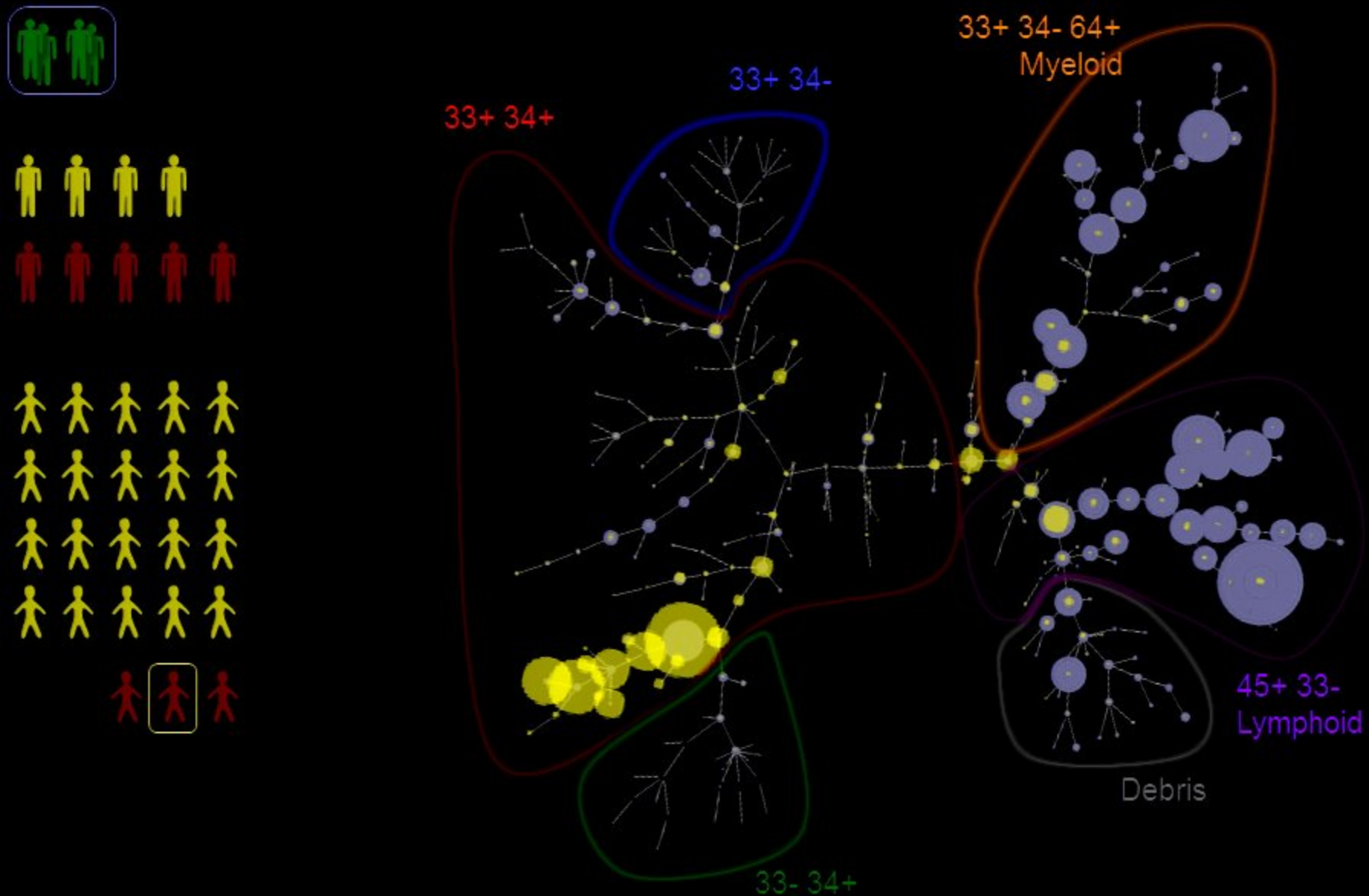
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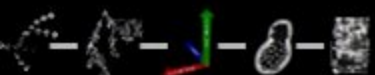
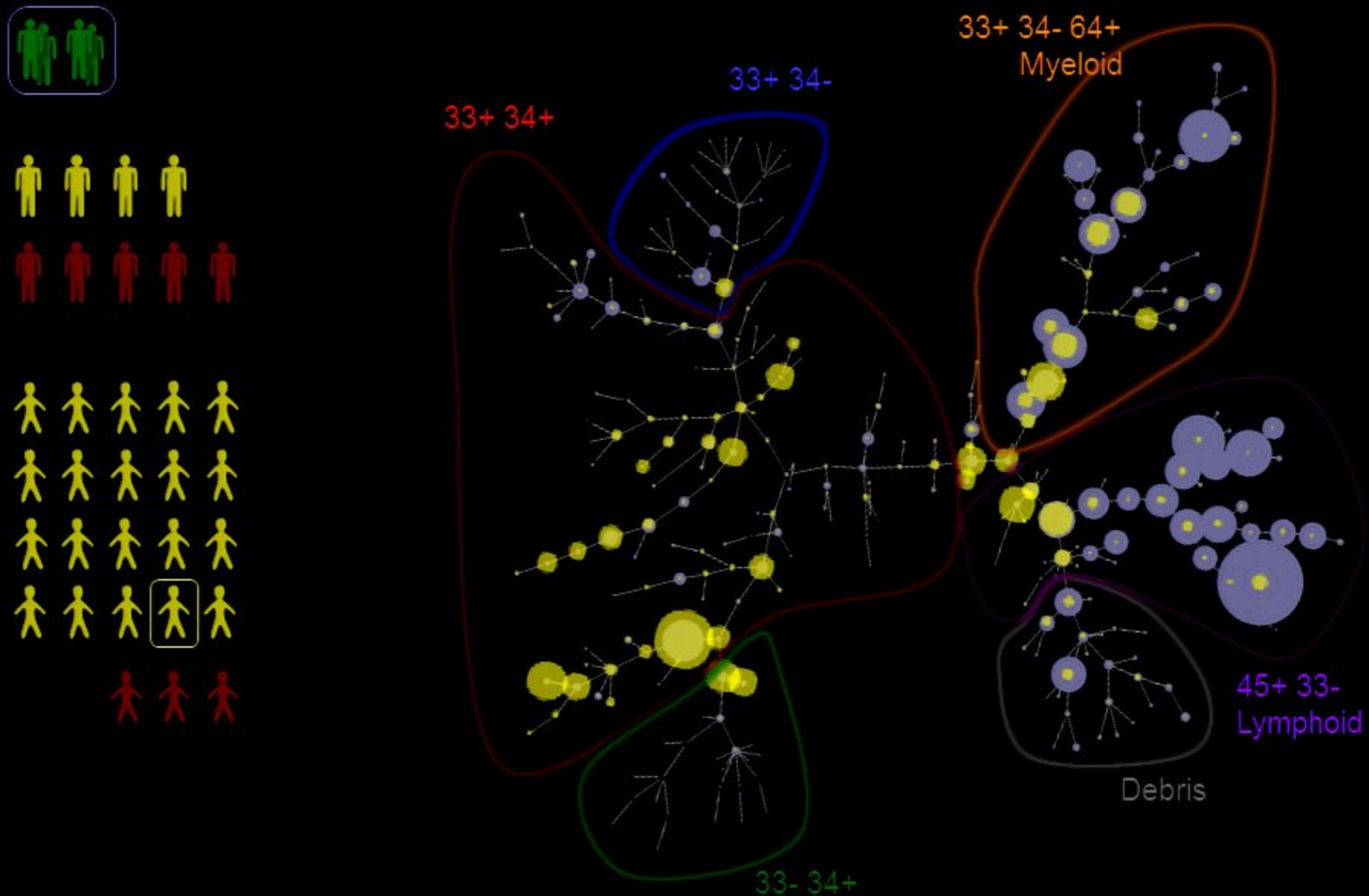
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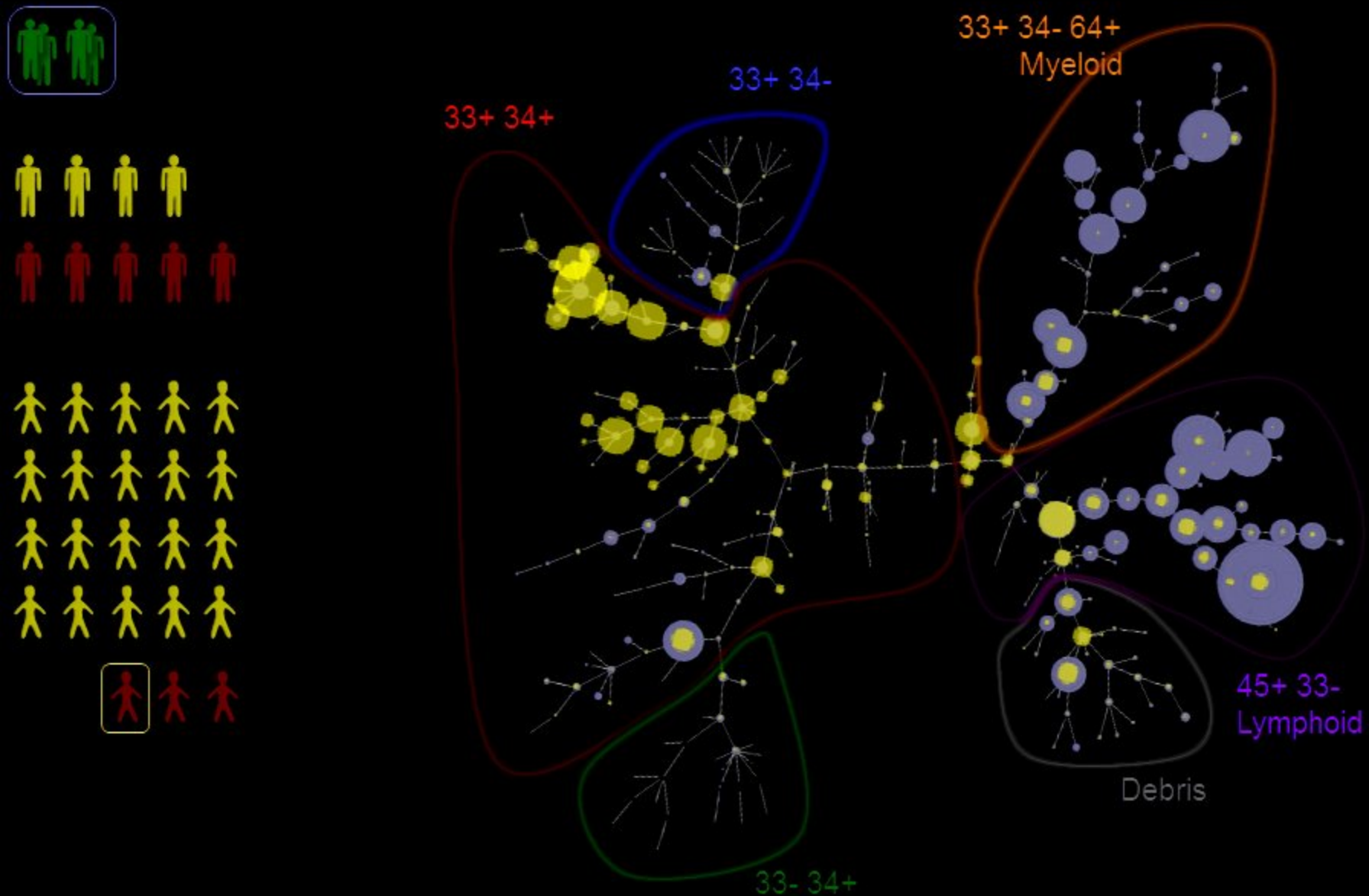
Phenotypic landscape of AML is diverse, but constrained...



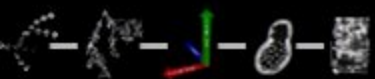
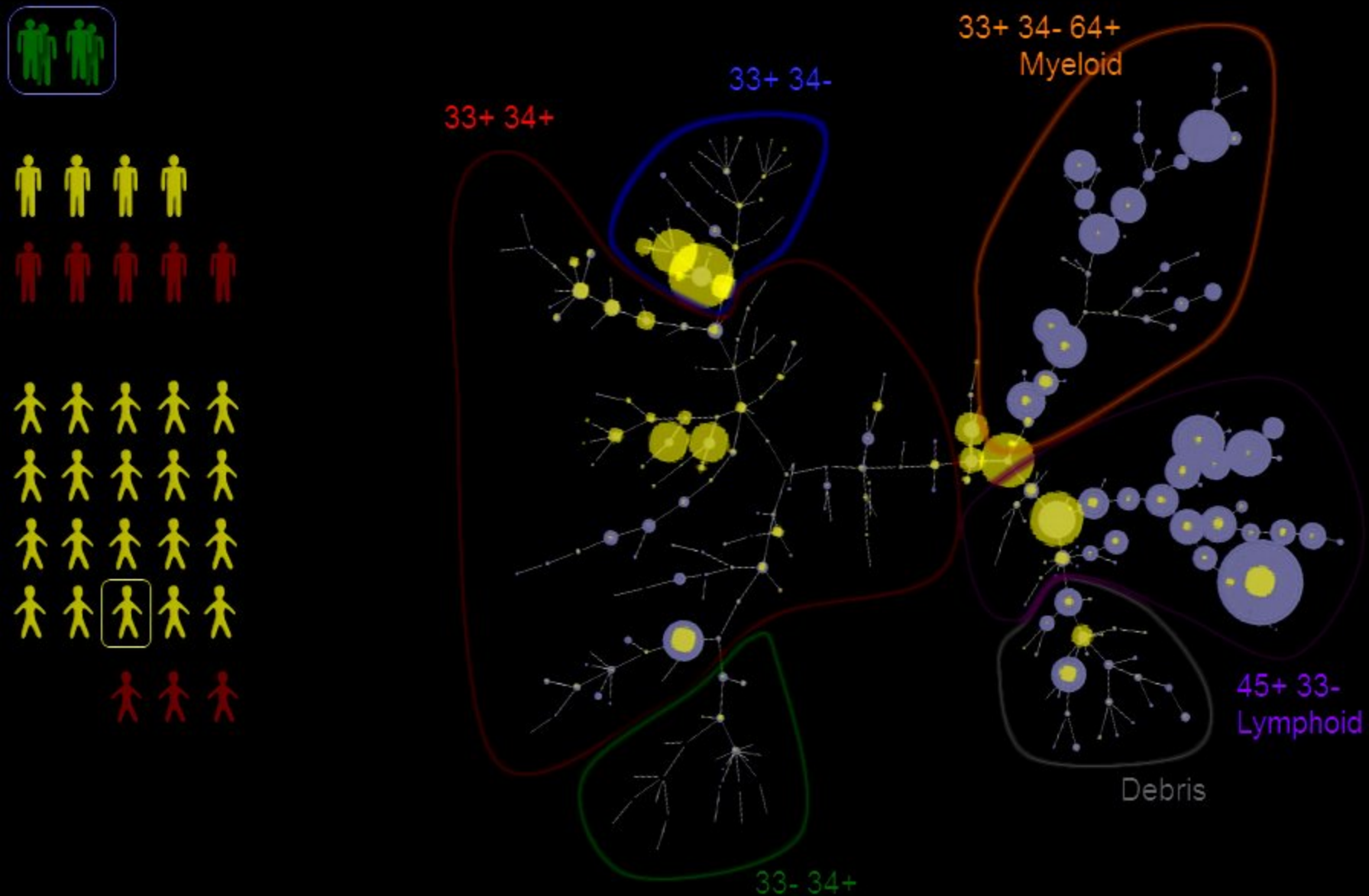
Phenotypic landscape of AML is diverse, but constrained...



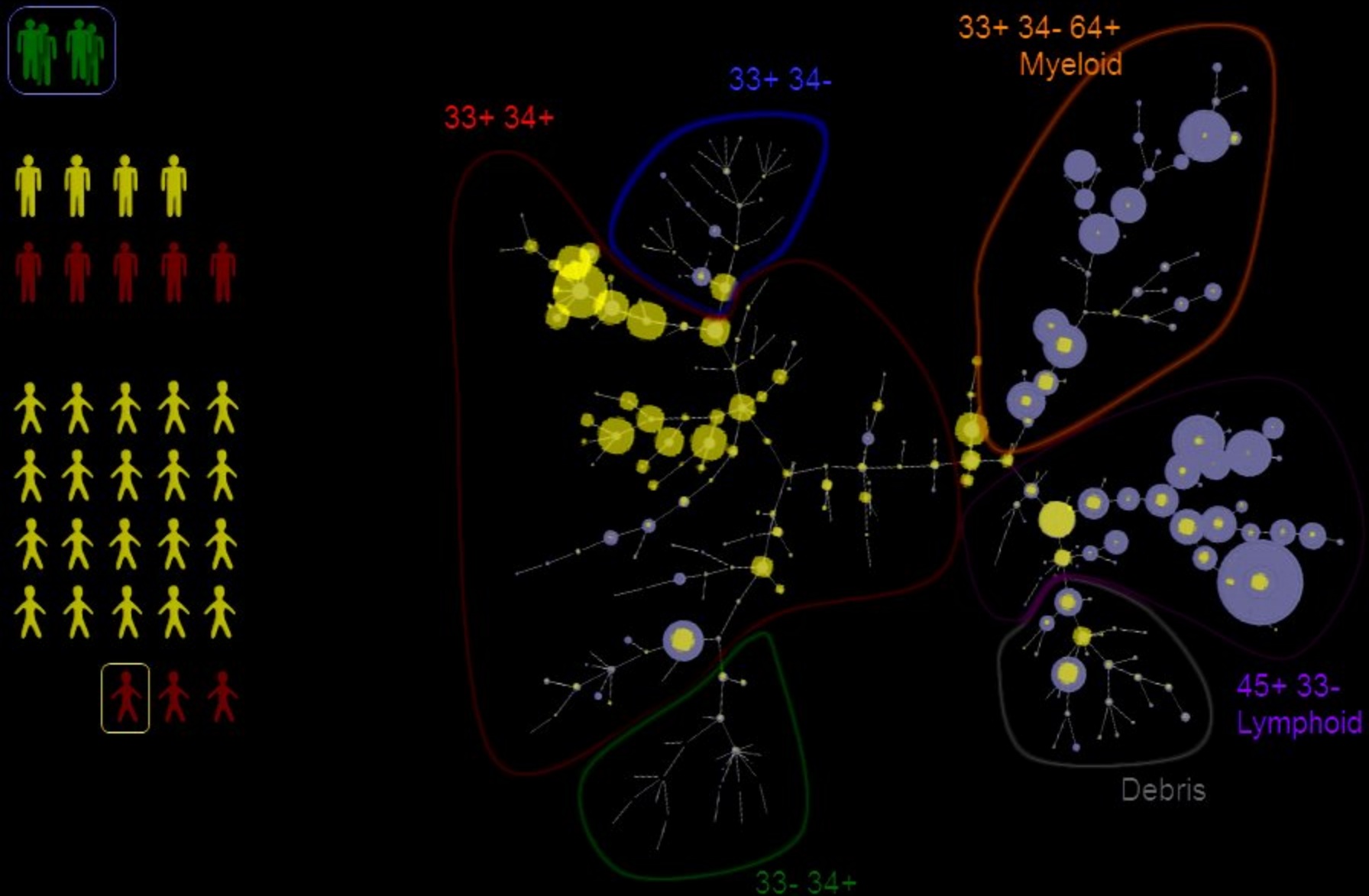
Phenotypic landscape of AML is diverse, but constrained...



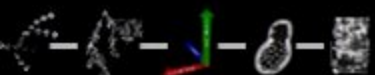
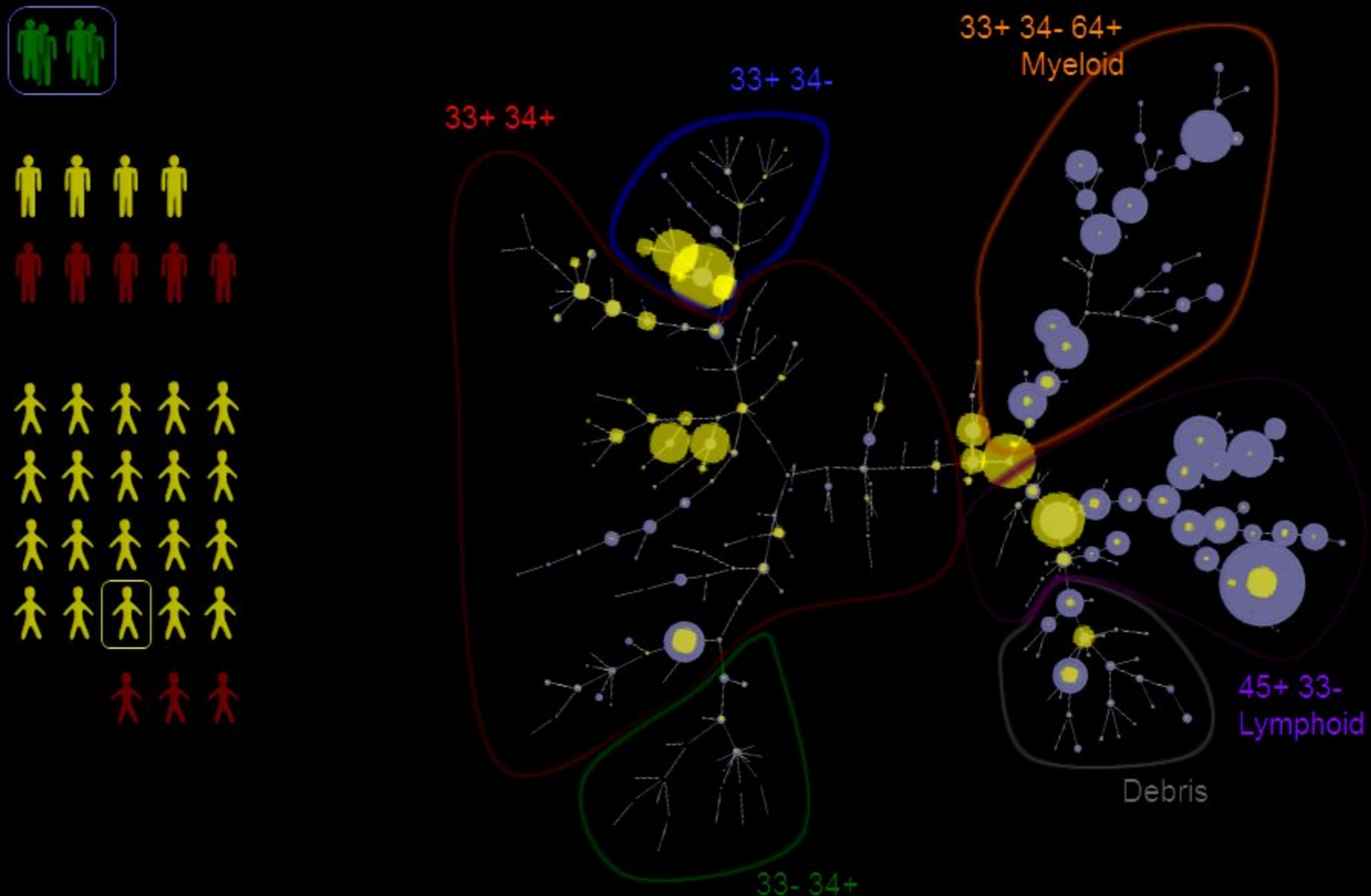
Phenotypic landscape of AML is diverse, but constrained...



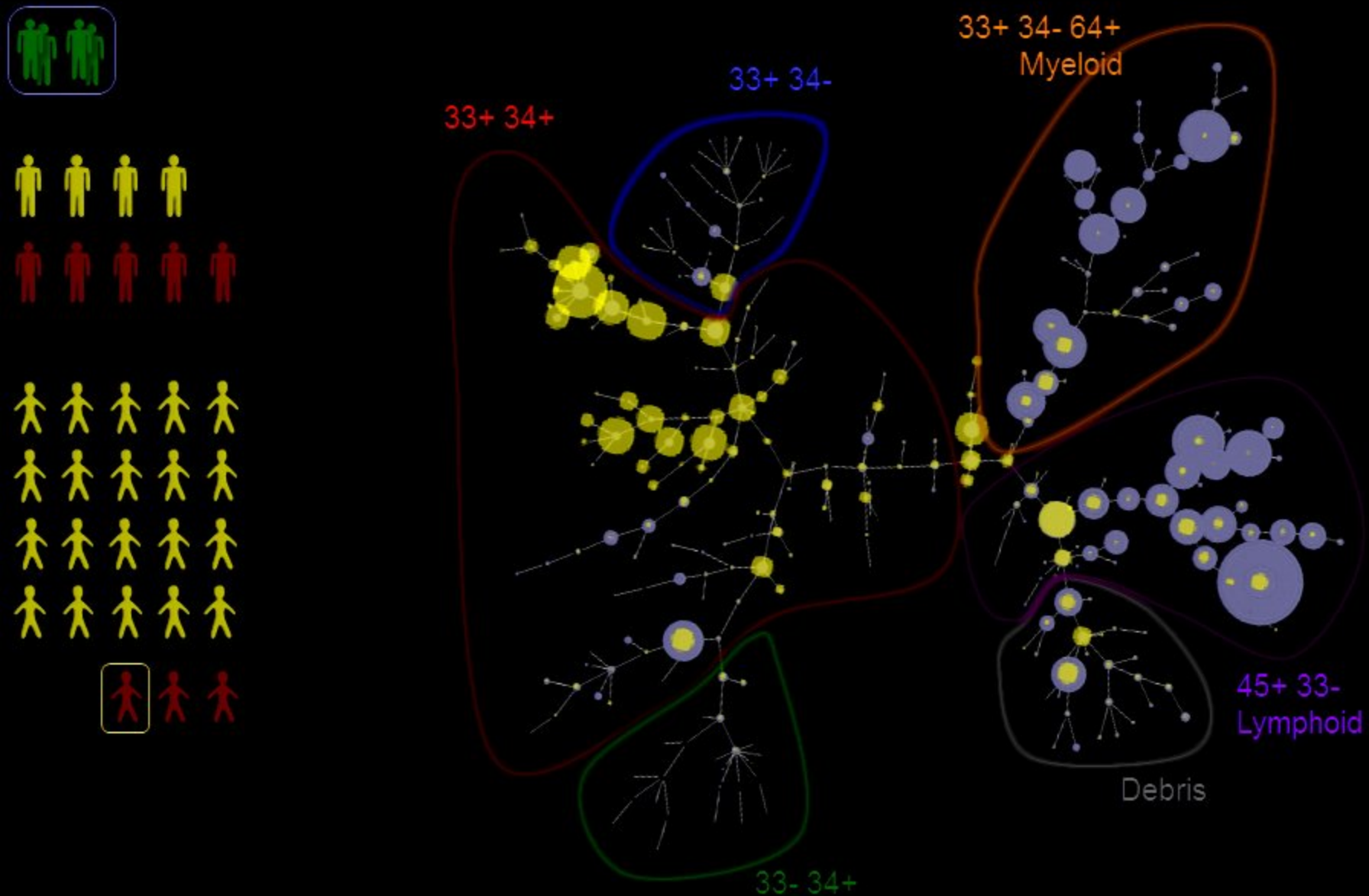
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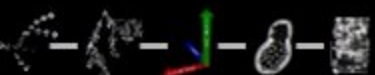
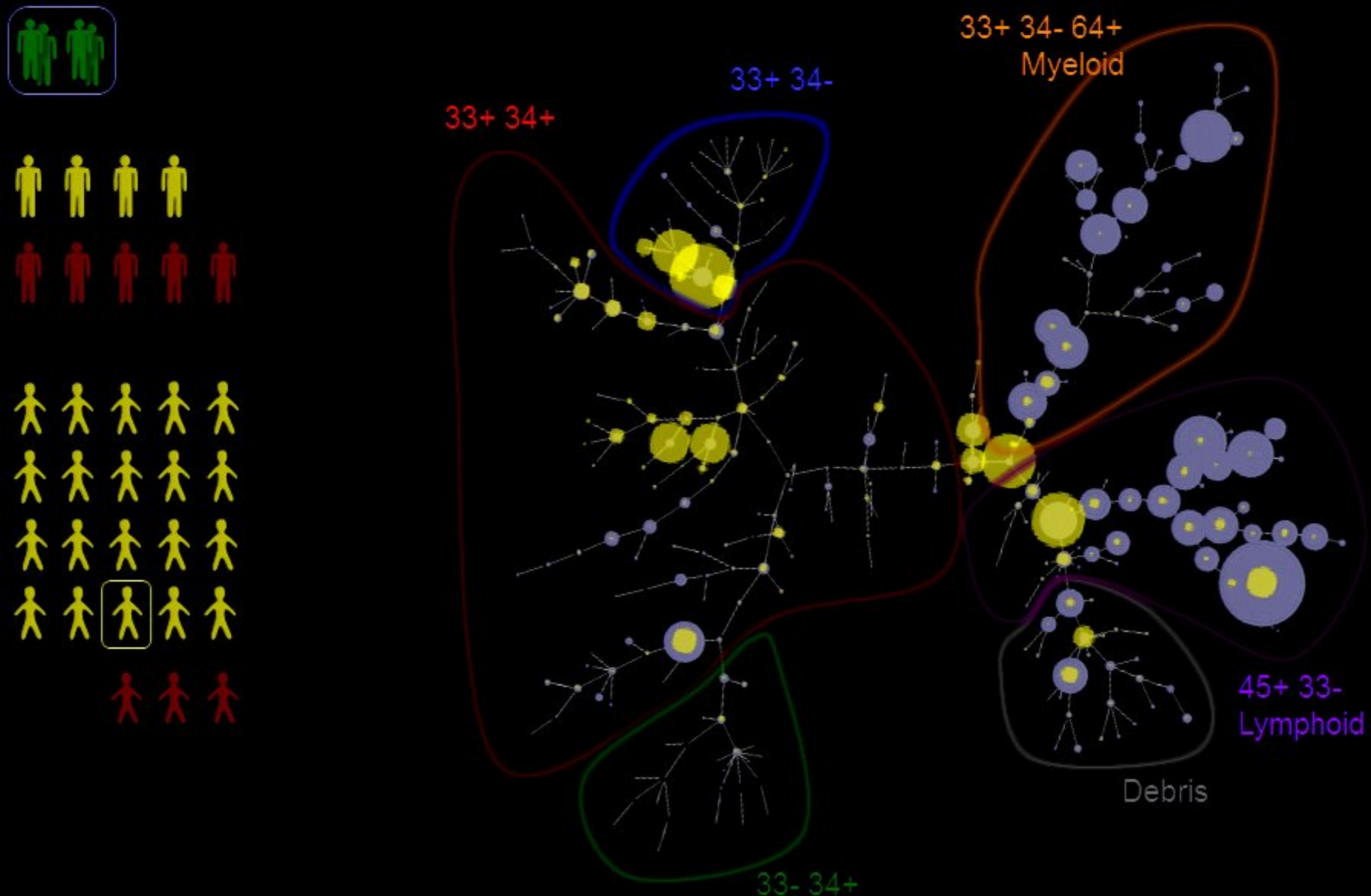
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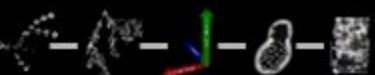
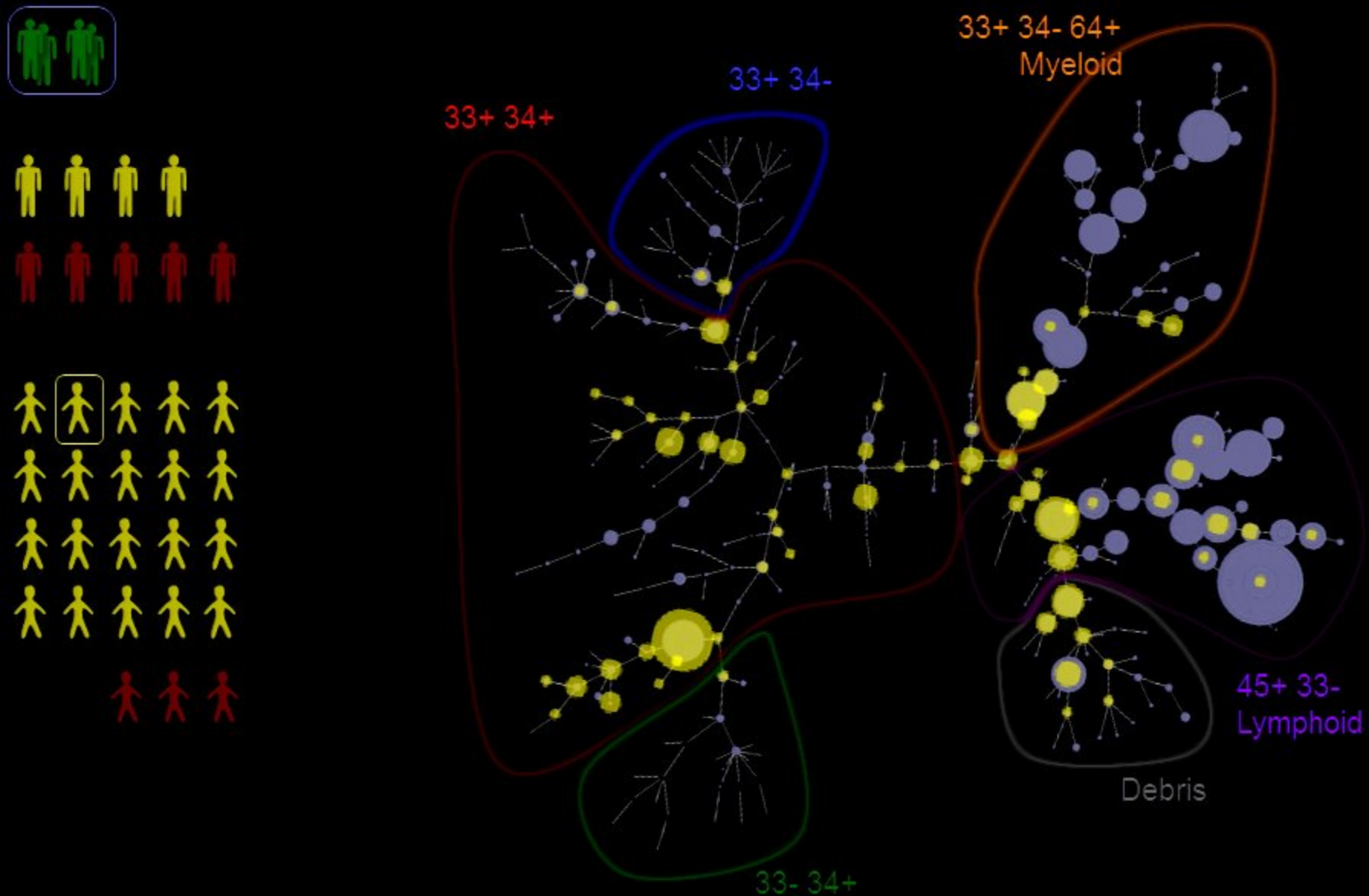
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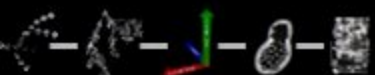
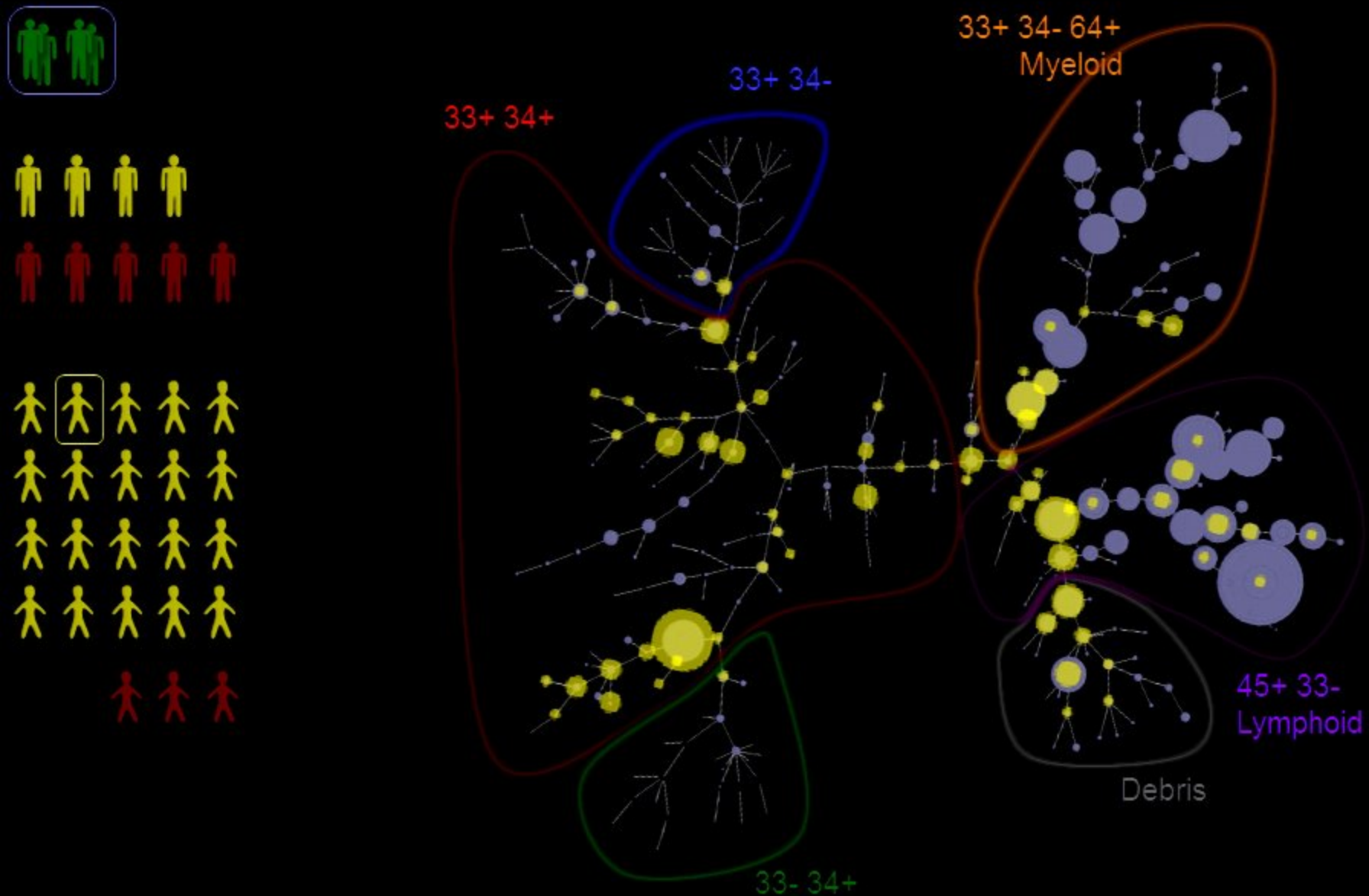
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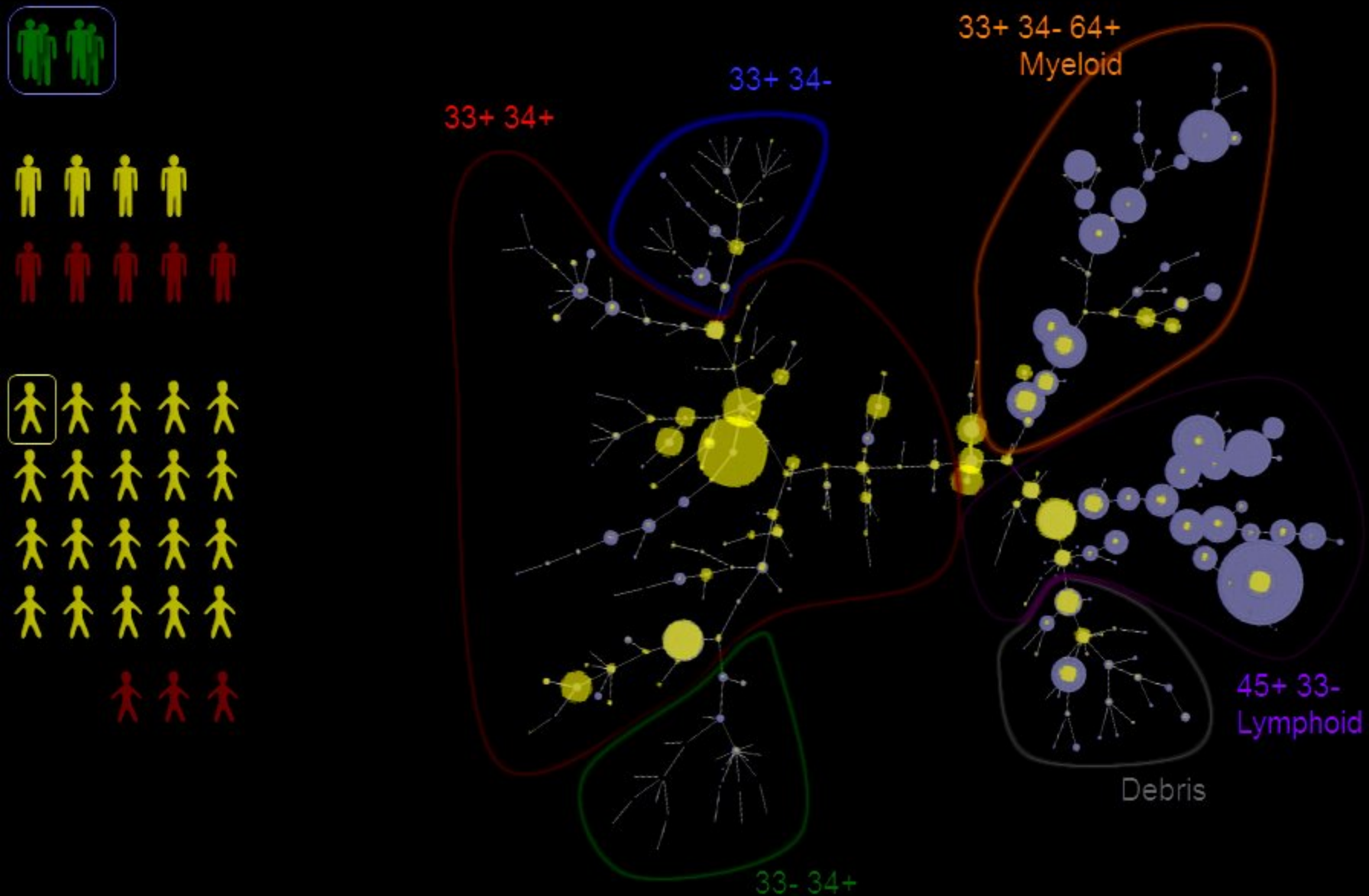
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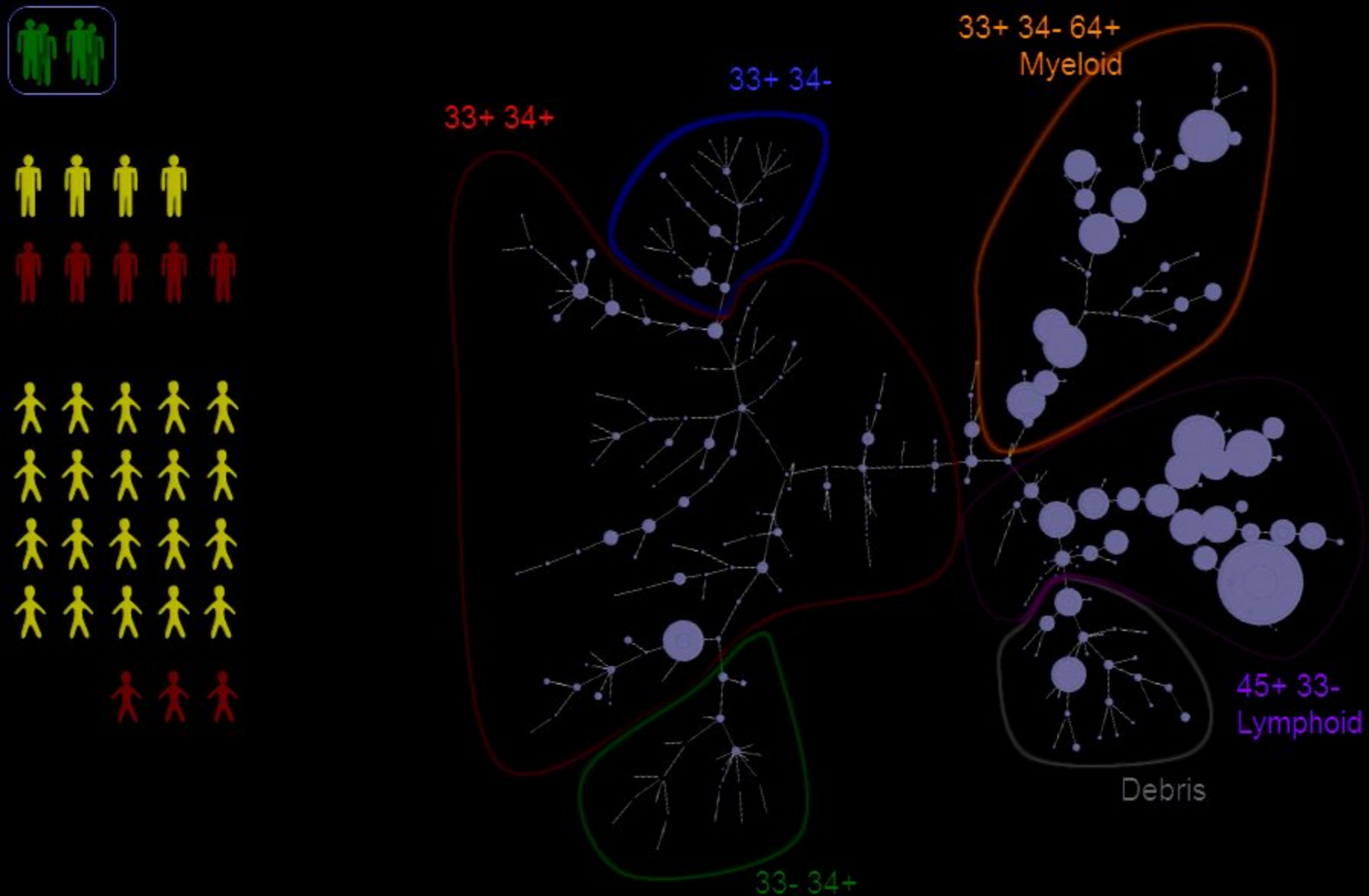
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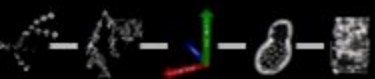
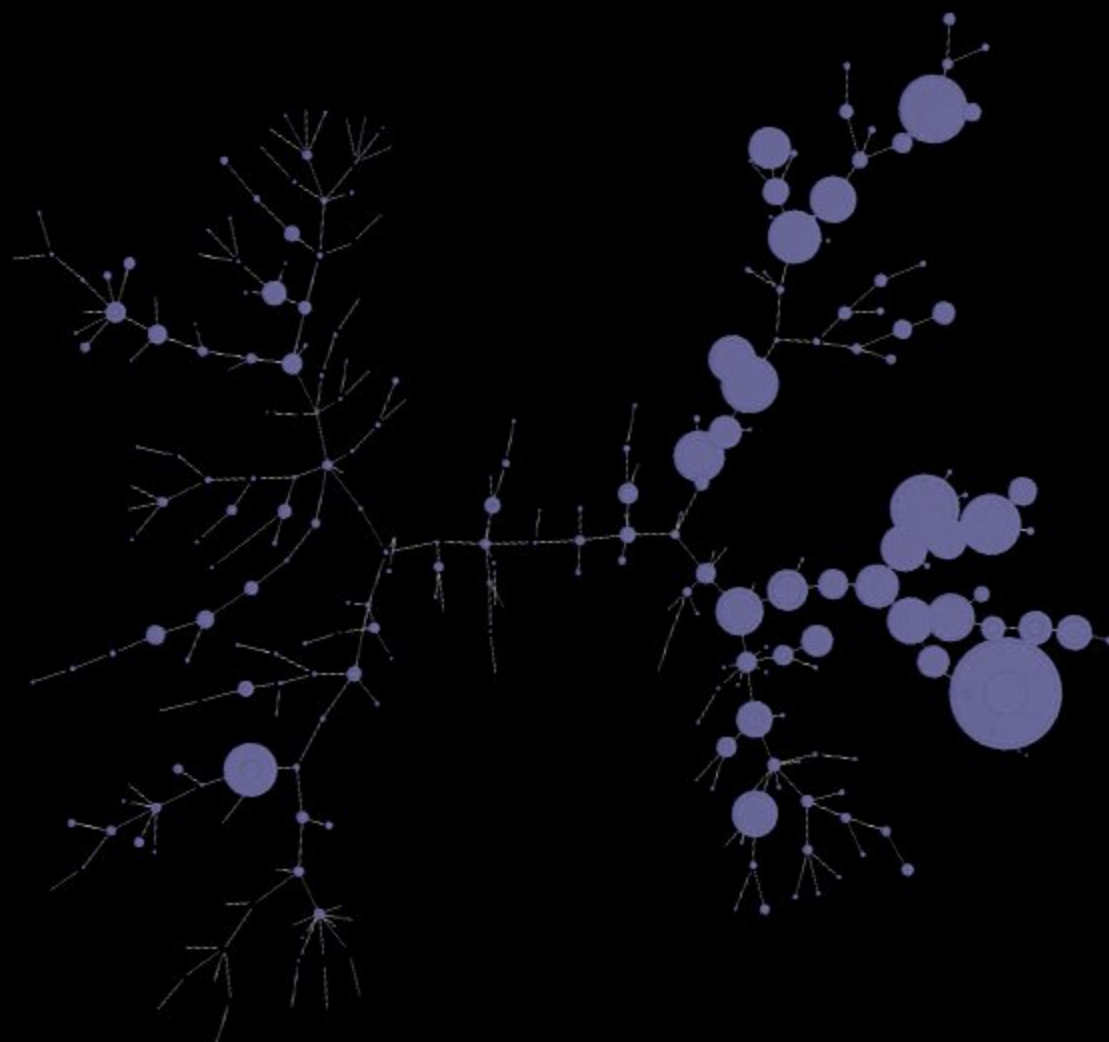
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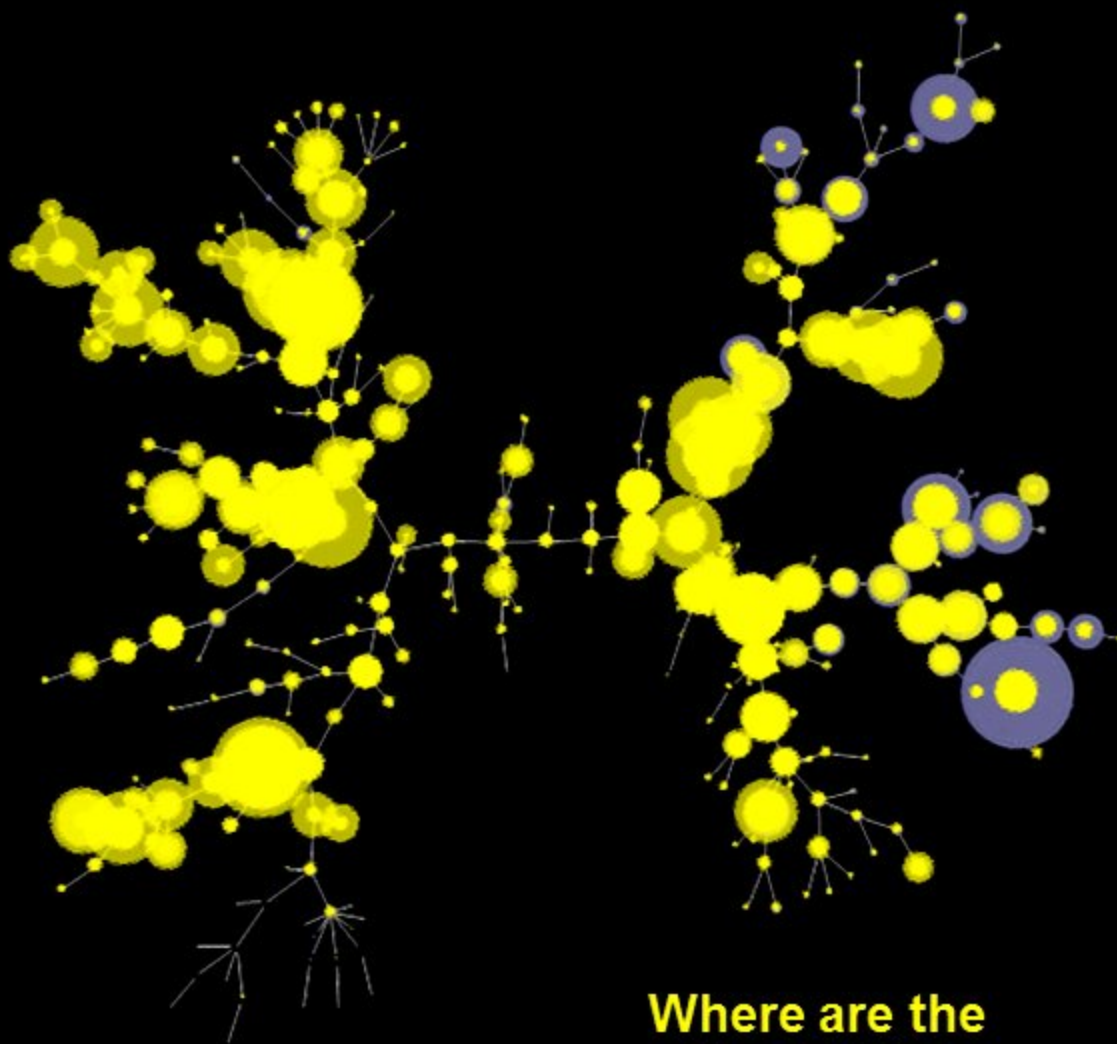
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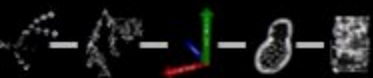
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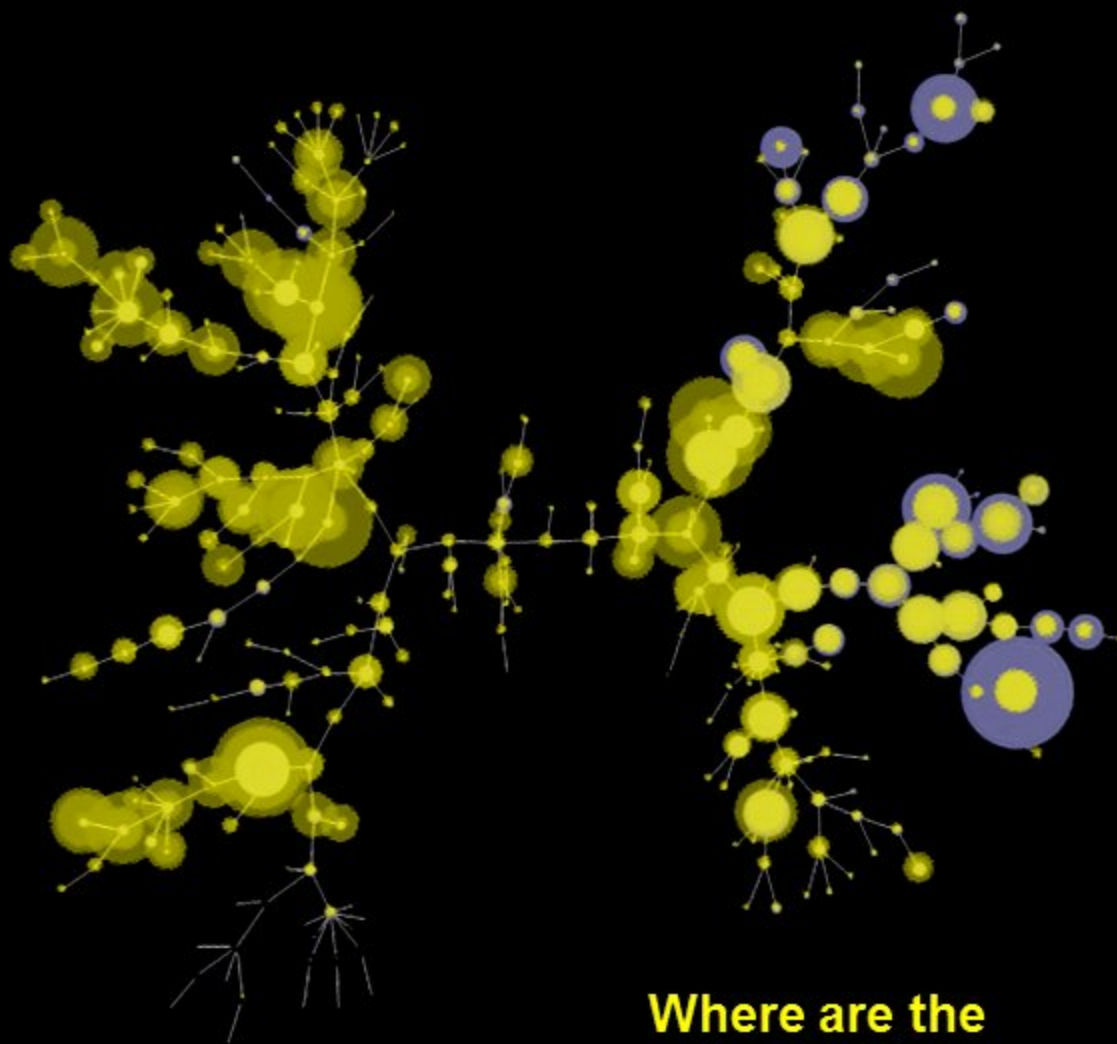
Relandscaping by Tumor Niche Filling



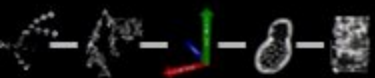
Where are the
“invisible”
leukemia cells?



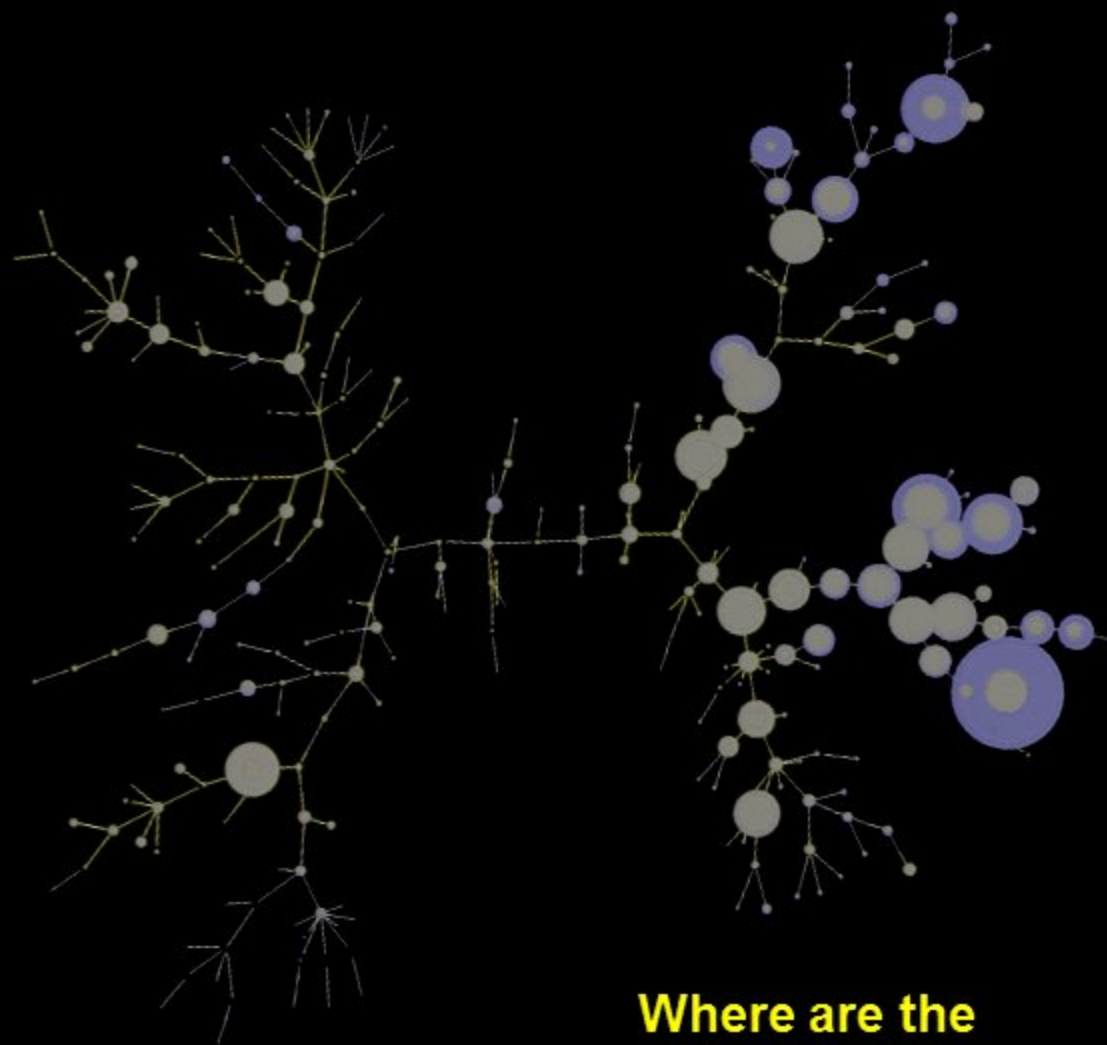
Relandscaping by Tumor Niche Filling



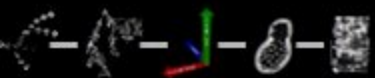
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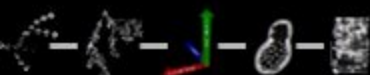
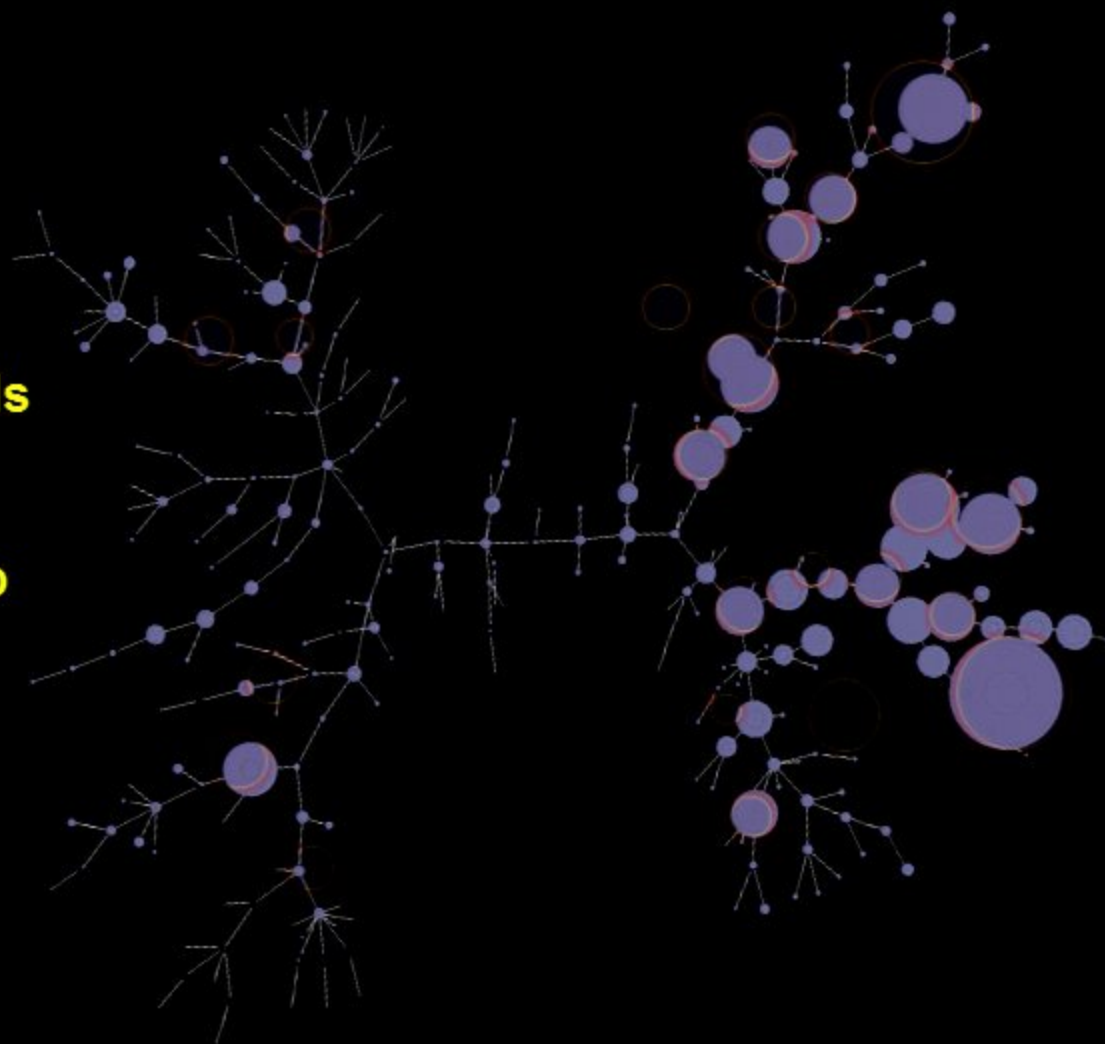
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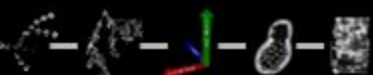
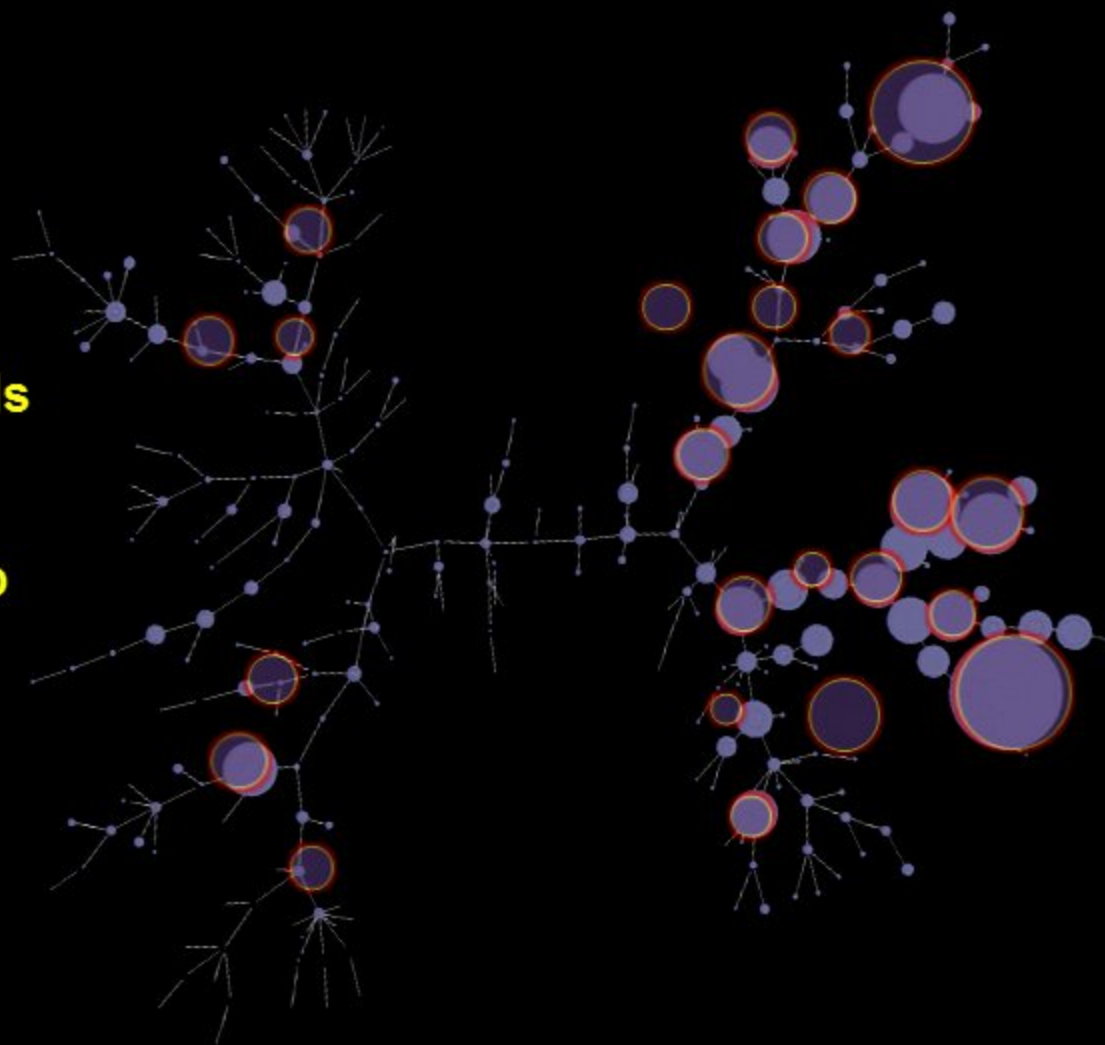
**Add
“invisible”
leukemia cells
from all
Patients &
redraw map**



Relandscaping by Tumor Niche Filling



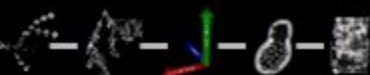
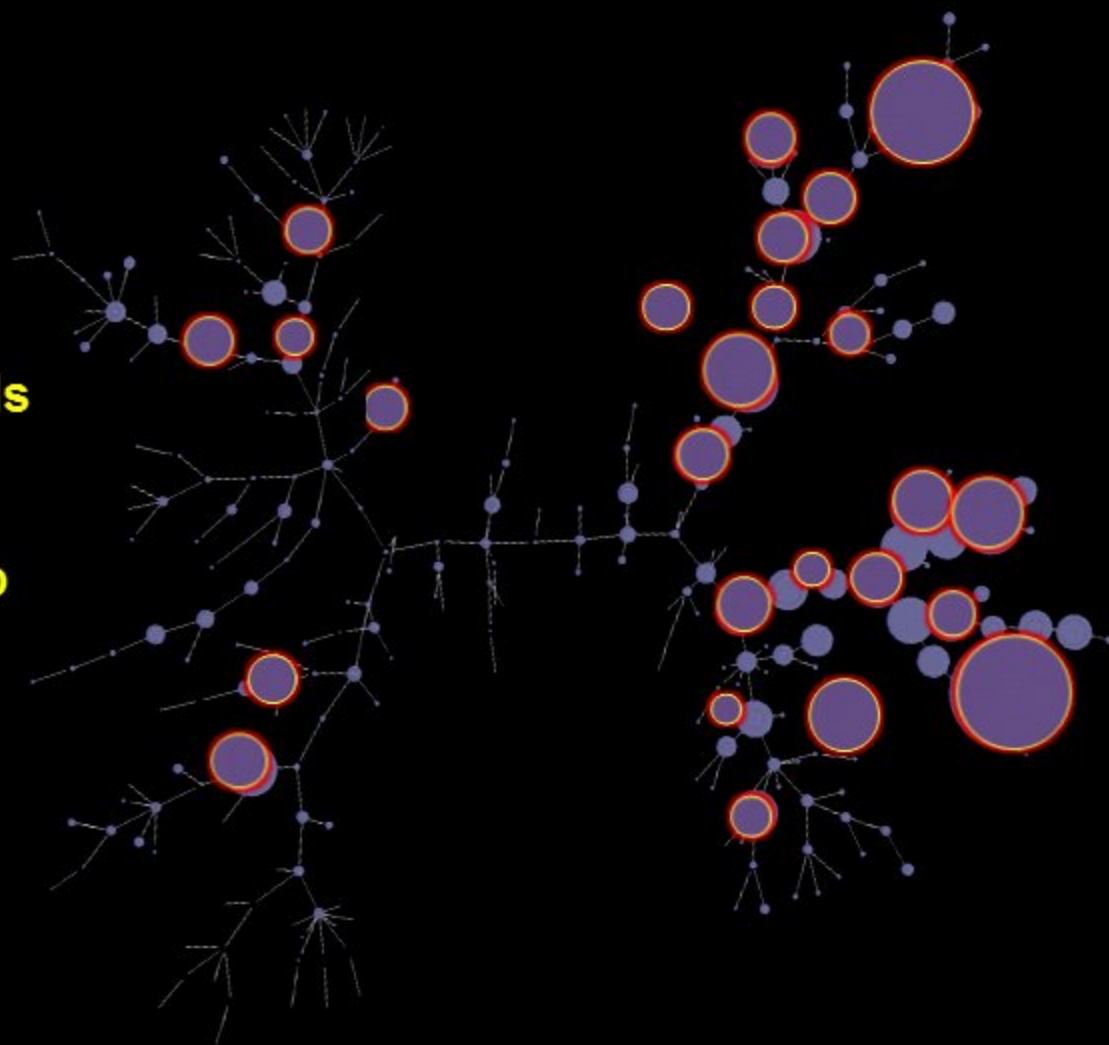
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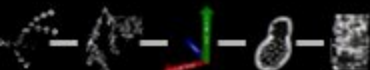
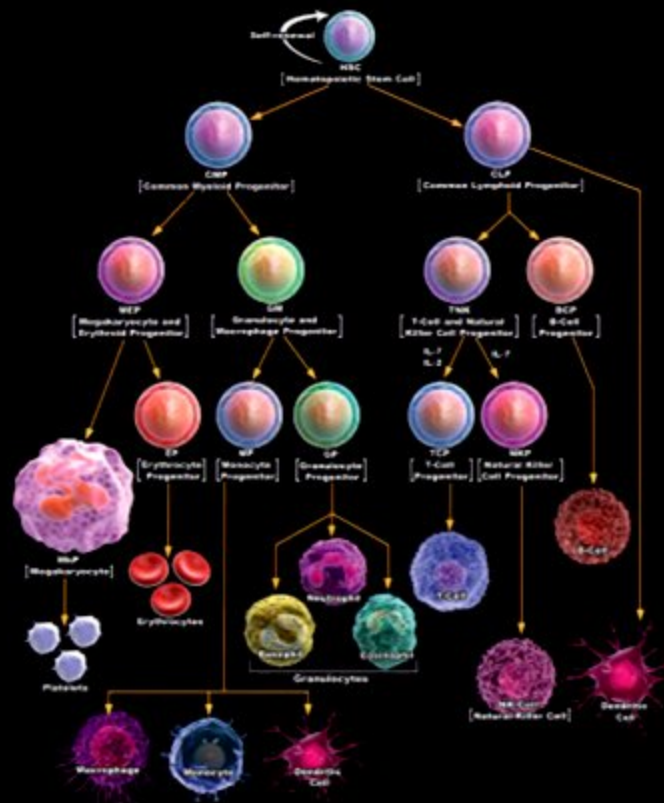
**Add
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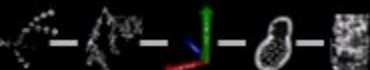
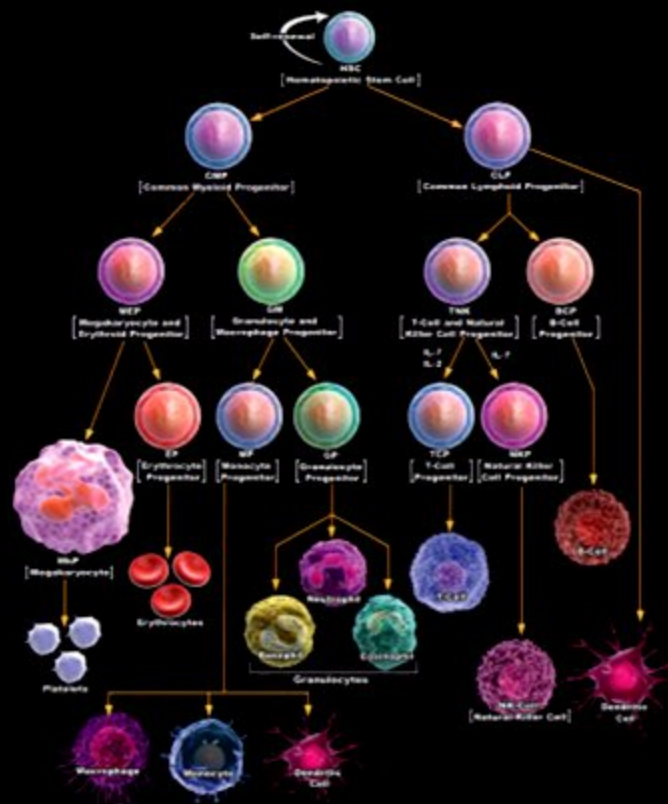
Relandscaping by Tumor Niche Filling



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Relandscaping by Tumor Niche Filling



Deep profiling of AML signaling in oligoclonal AML

Pediatric AML
diagnosis
bone marrow
(n = 1)

Perturbations (19)

No inhibitor

Basal (unstim.)
AICAR
Flt3 ligand
G-CSF
GM-CSF
IFN α
IFN γ
IL-3
IL-6
IL-10
IL-27
PMA + ionomycin
PVO₄
SCF
TNF α
TPO

PI3K/mTOR inhib.

Inhibitor alone
PMA/ionomycin
PVO₄

Staining panel

15 Functional Markers

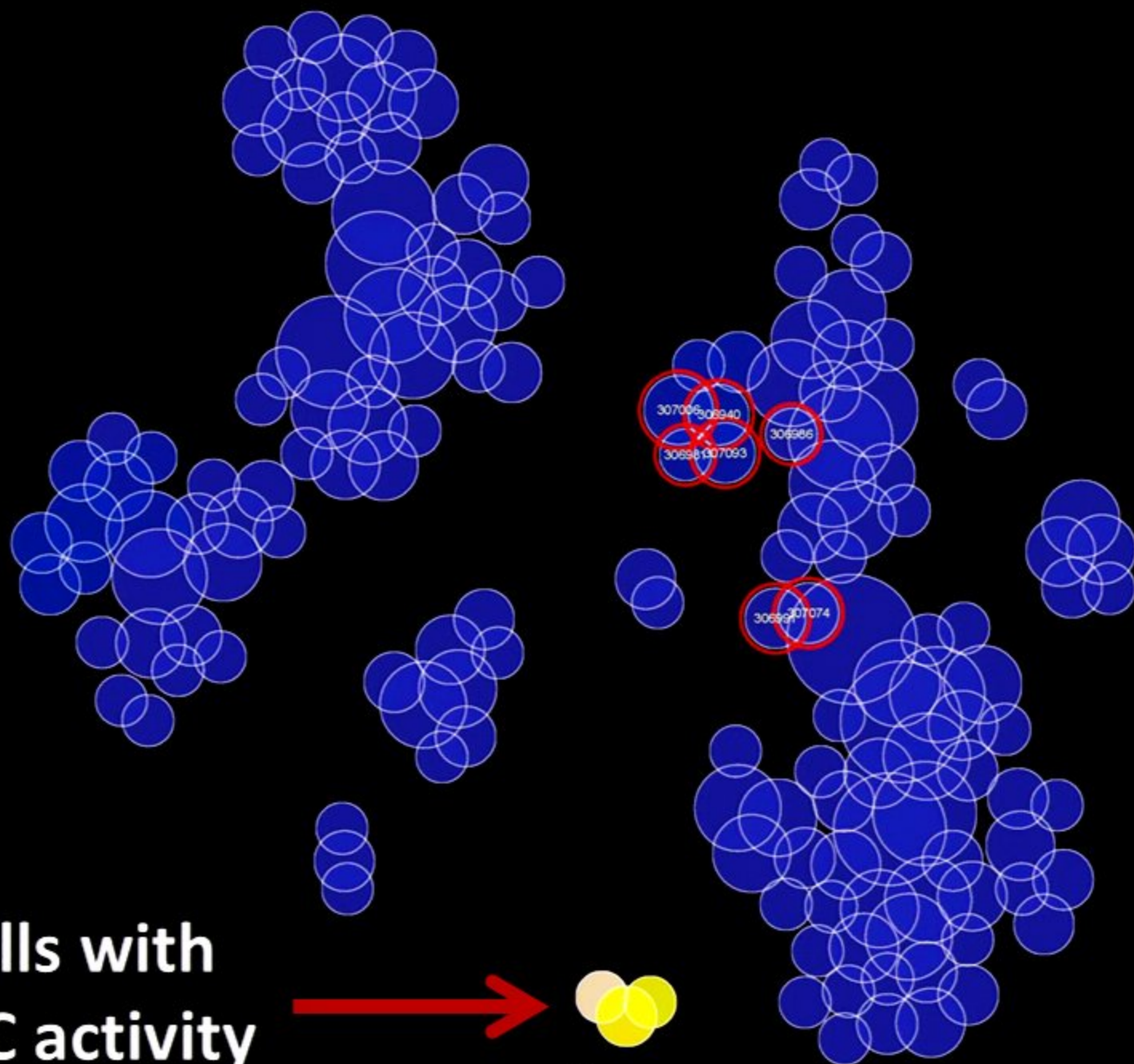
p4EBP1	pS6
pAkt	pSTAT1
pAMPK	pSTAT3
pCbl	pSTAT5
pCREB	pSyk
pERK1/2	
p-p38 MAPK	
cleaved Casp3	
pPLCgamma2	
pRb	

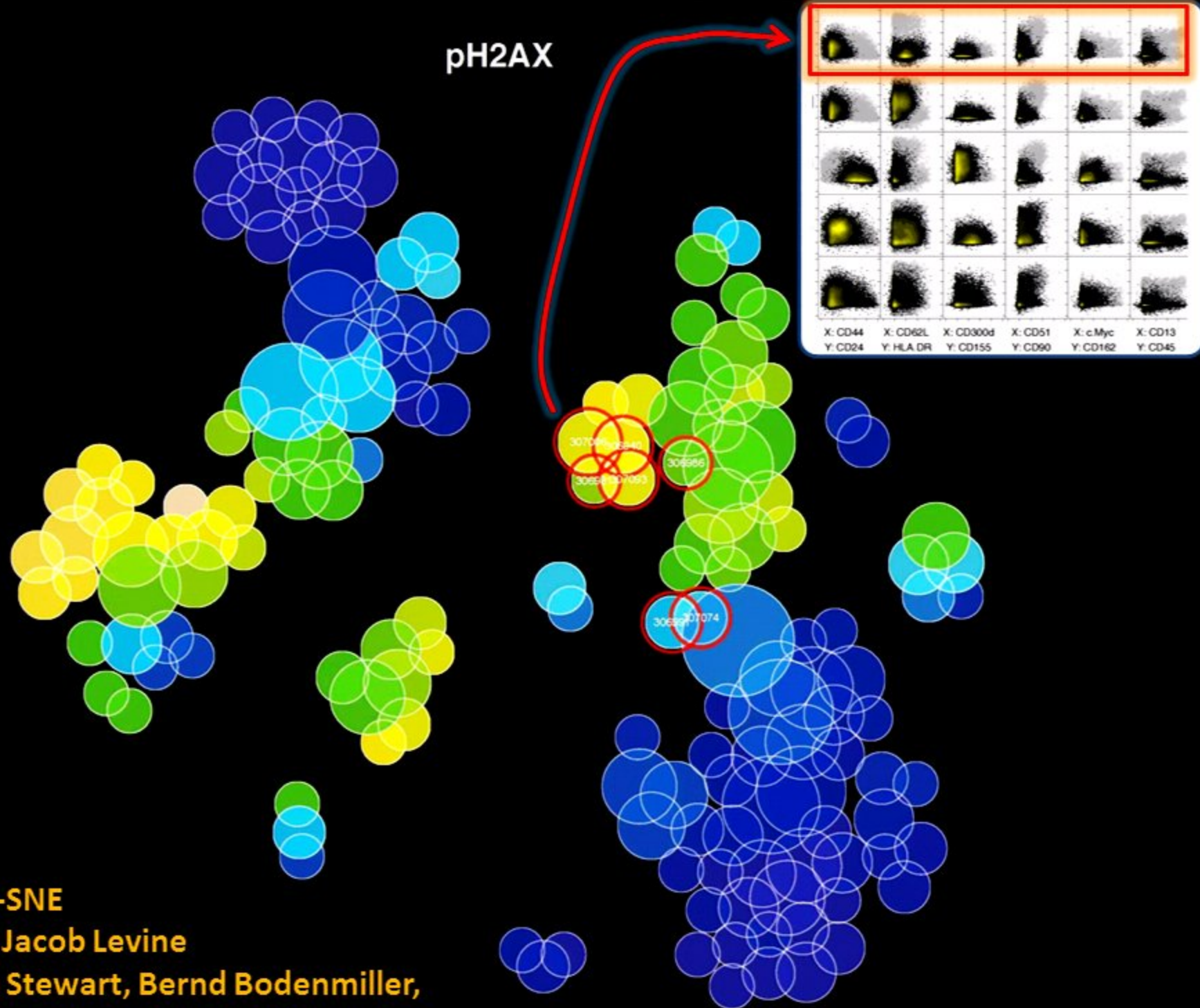
16 Surface Markers

CD3	CD45
CD7	CD47
CD11b	CD64
CD15	CD117
CD19	CD123
CD33	HLADR
CD34	
CD38	
CD41	
CD44	



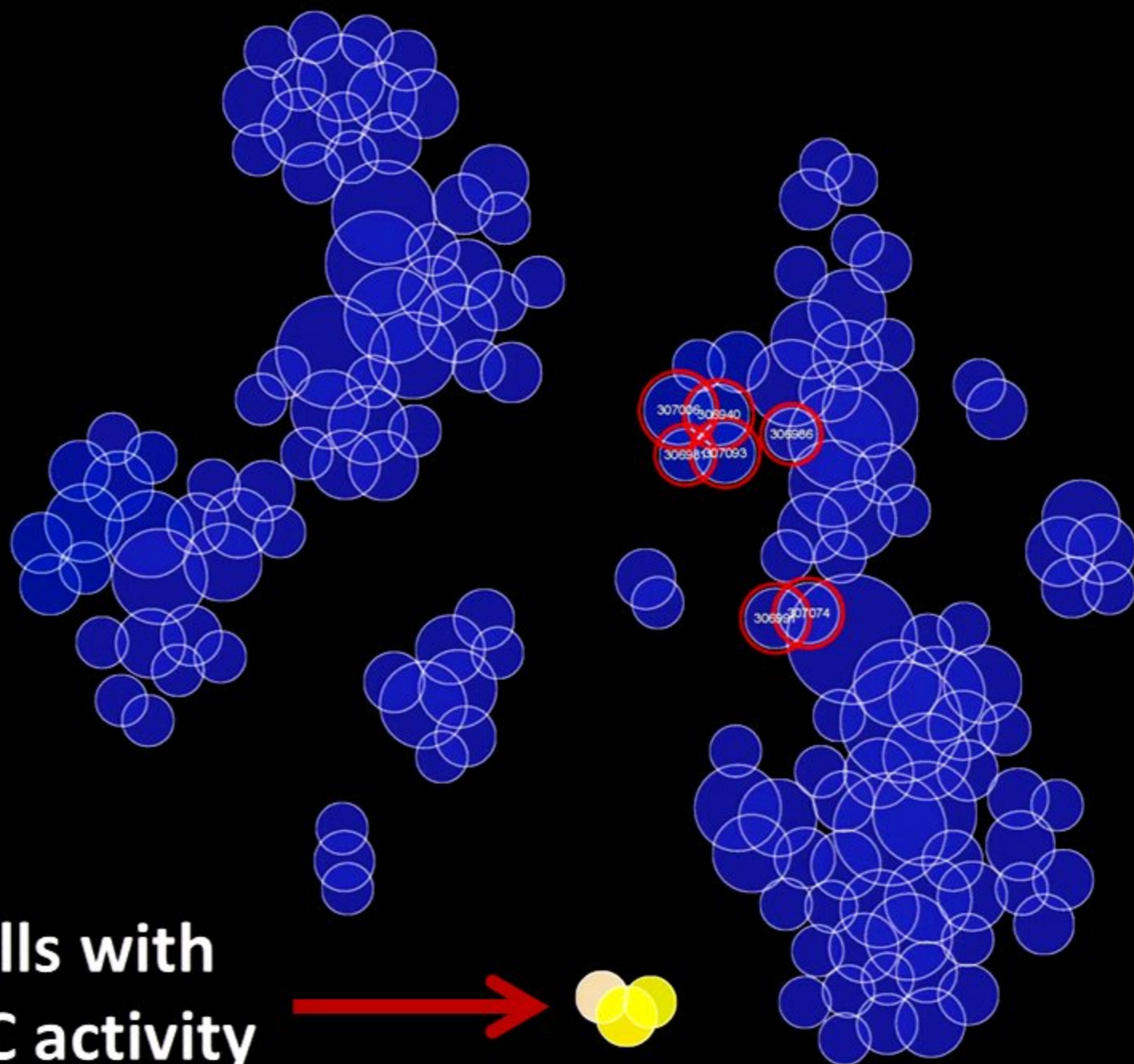
CD133

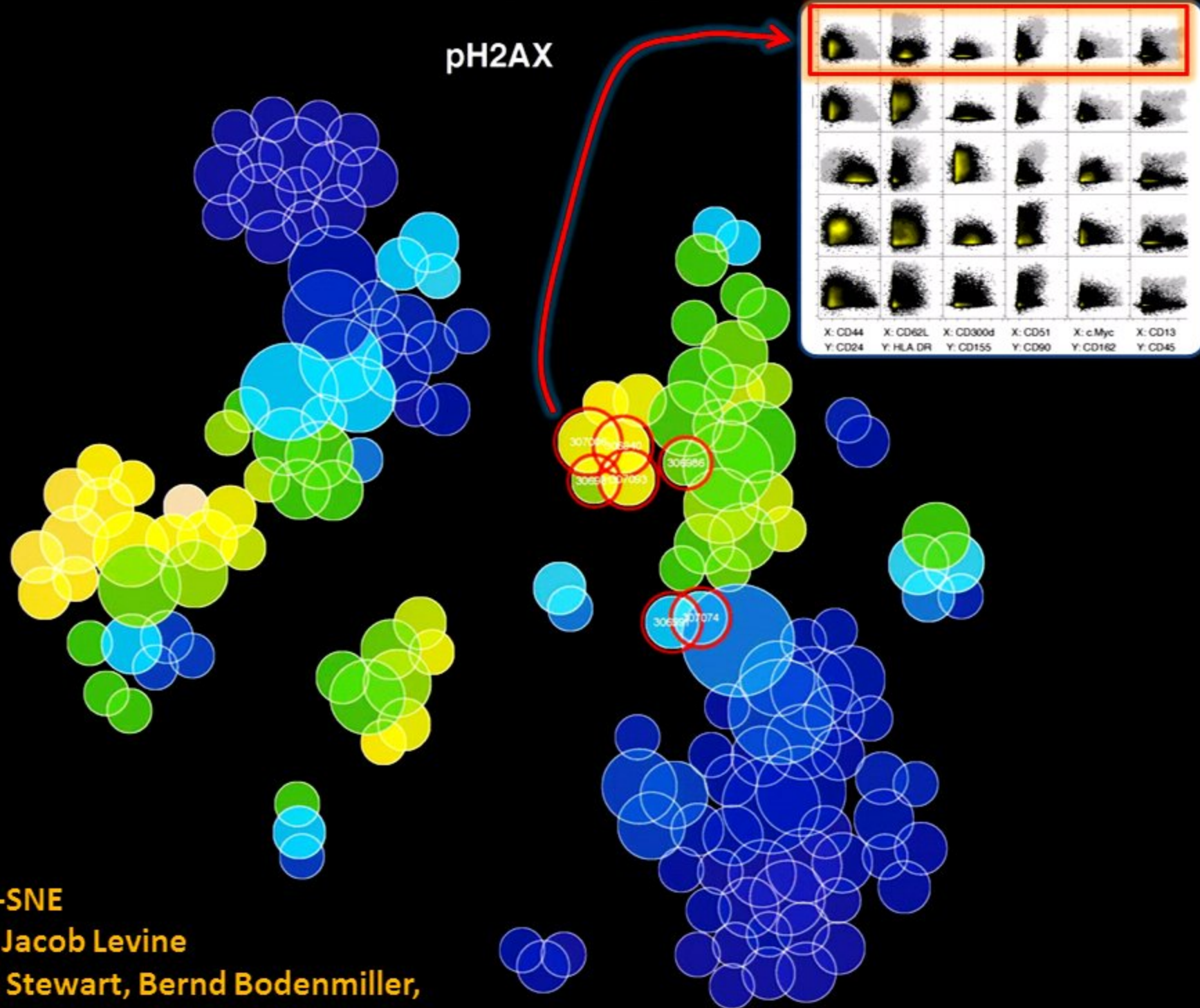




Based on cell-SNE
 Dana Pe'er & Jacob Levine
 Data: Jocelyn Stewart, Bernd Bodenmiller,
 Rob Bruggner, Ben Neel, GPN

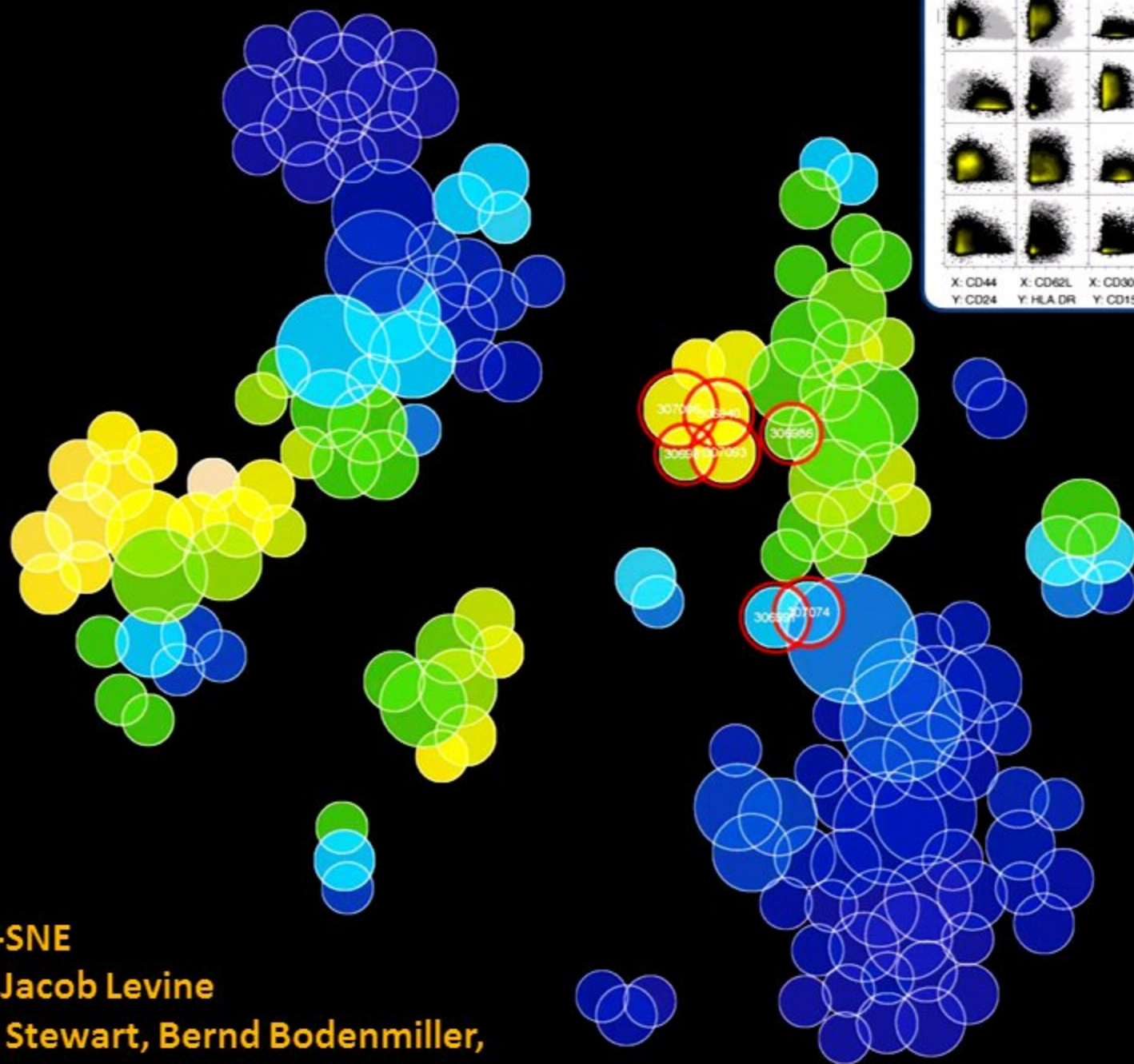
CD133





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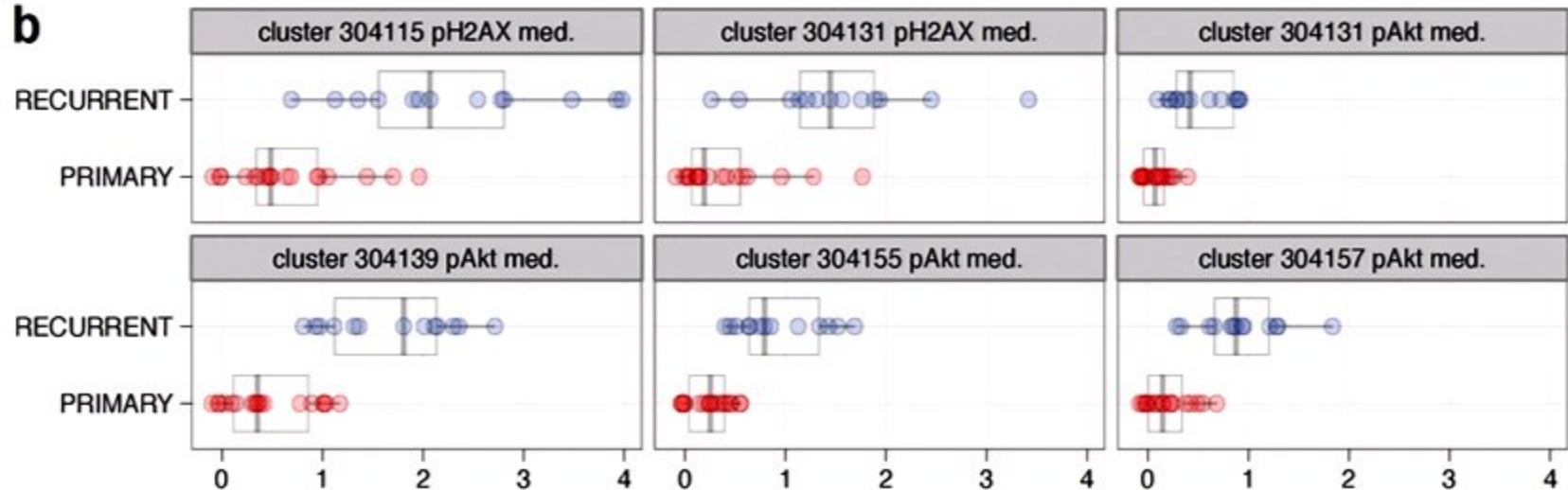
pH2AX



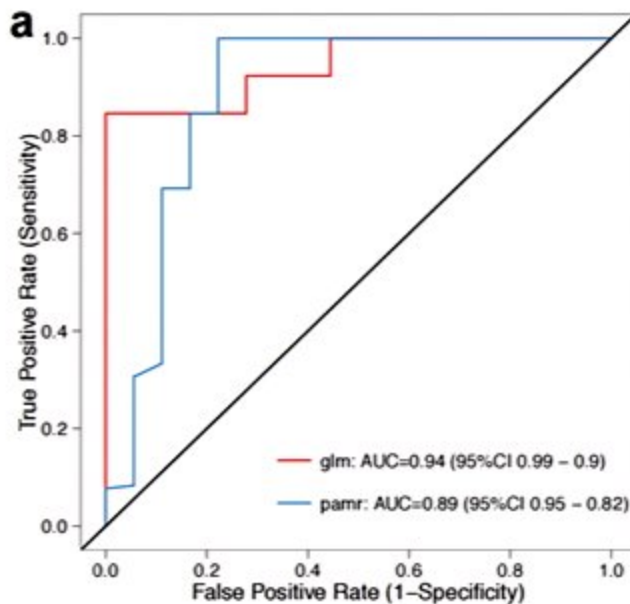
Based on cell-SNE
 Dana Pe'er & Jacob Levine
 Data: Jocelyn Stewart, Bernd Bodenmiller,
 Rob Bruggner, Ben Neel, GPN

Cellular clusters stratify outcome for primary and recurrent forms of ovarian cancer

b

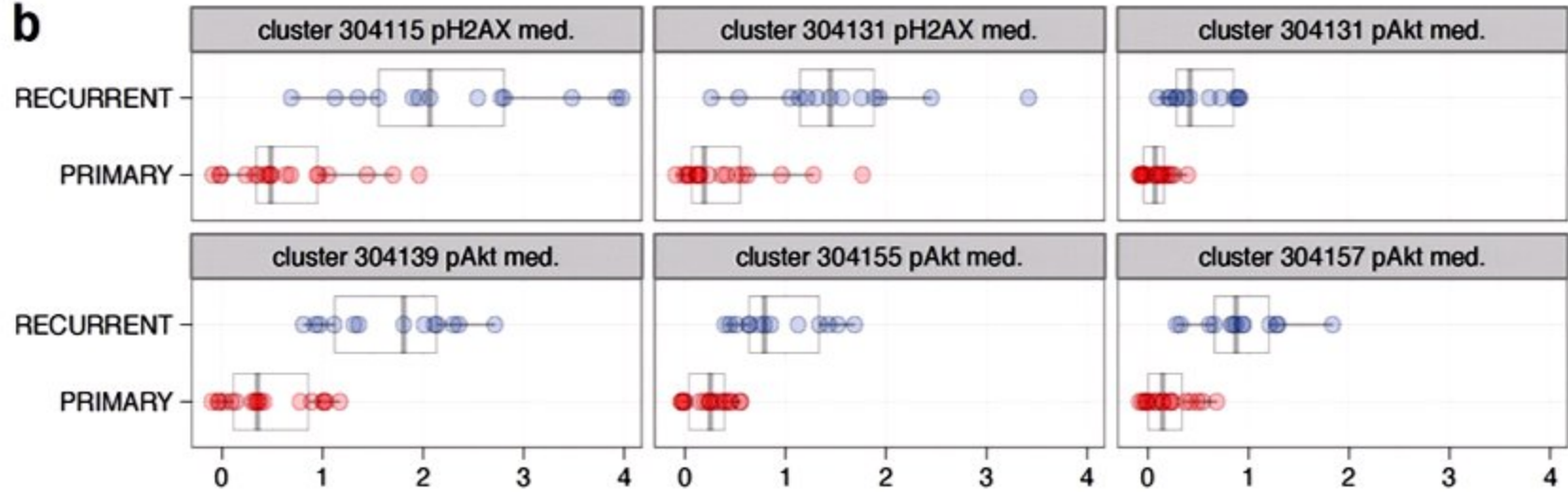


a

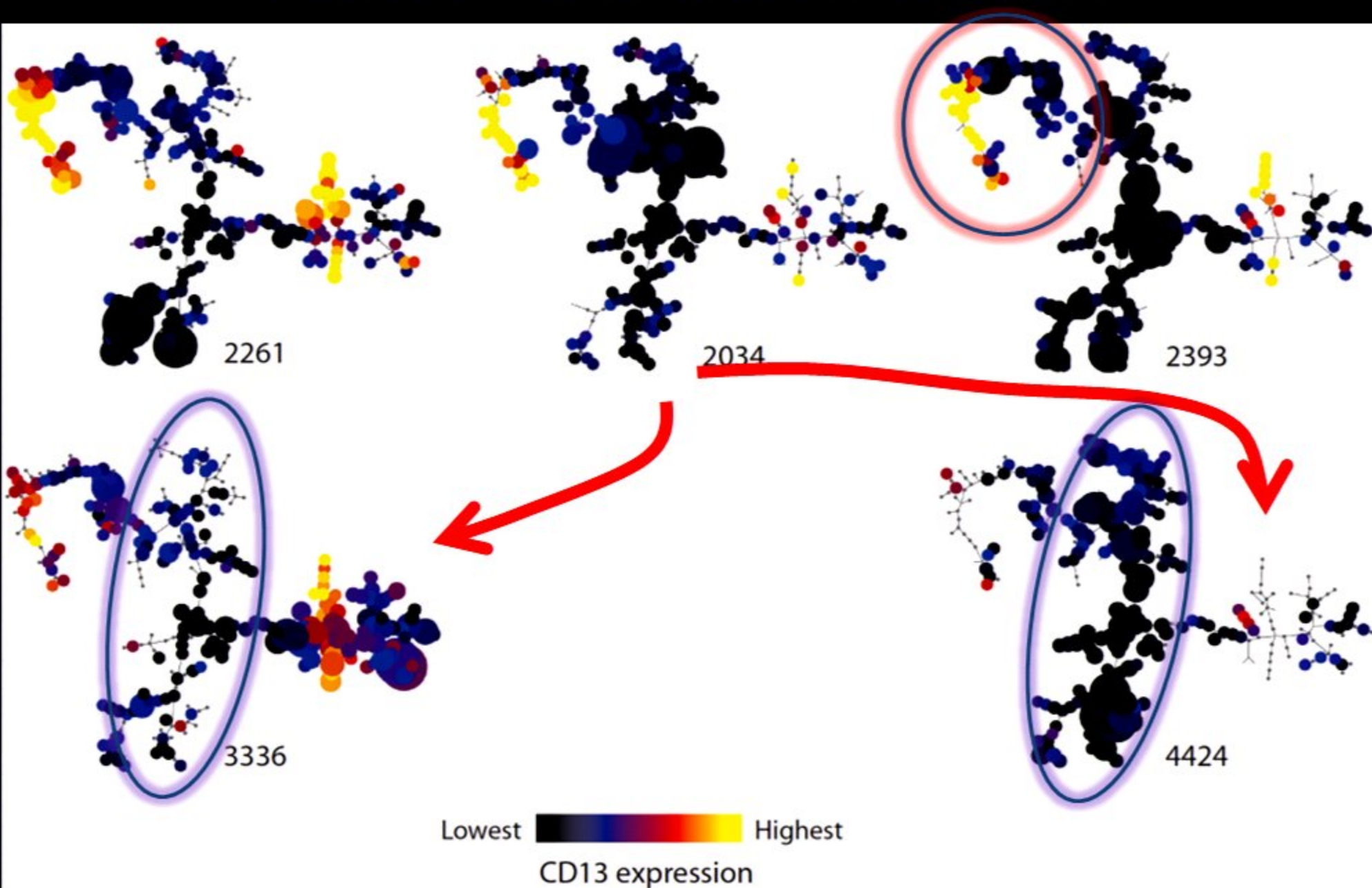


Cellular clusters stratify outcome for primary and recurrent forms of ovarian cancer

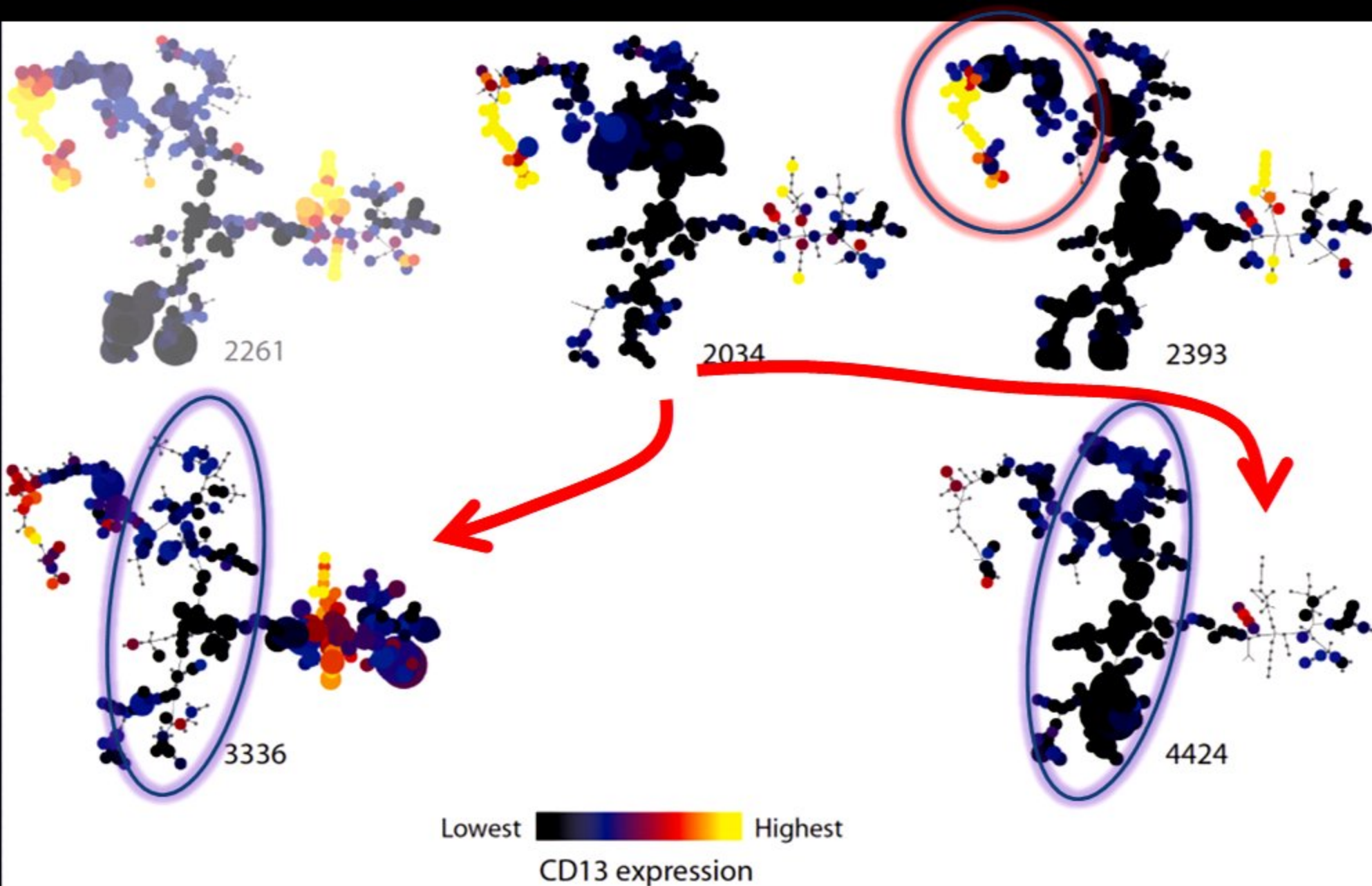
b



SOC Cell Subset Differences Within & Across Patients – Surface Markers CD13

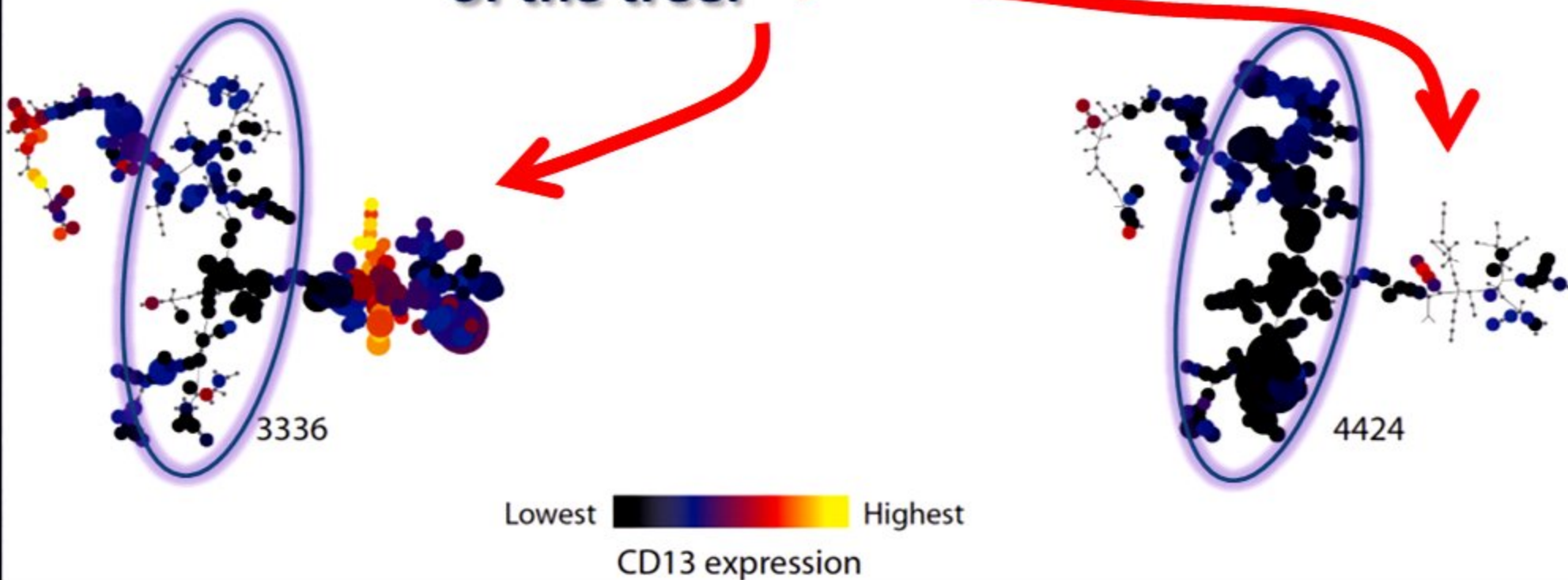


SOC Cell Subset Differences Within & Across Patients – Surface Markers CD13



SOC Cell Subset Differences Within & Across Patients – Surface Markers CD13

**Different Patients
Populate different branches
of the tree.**



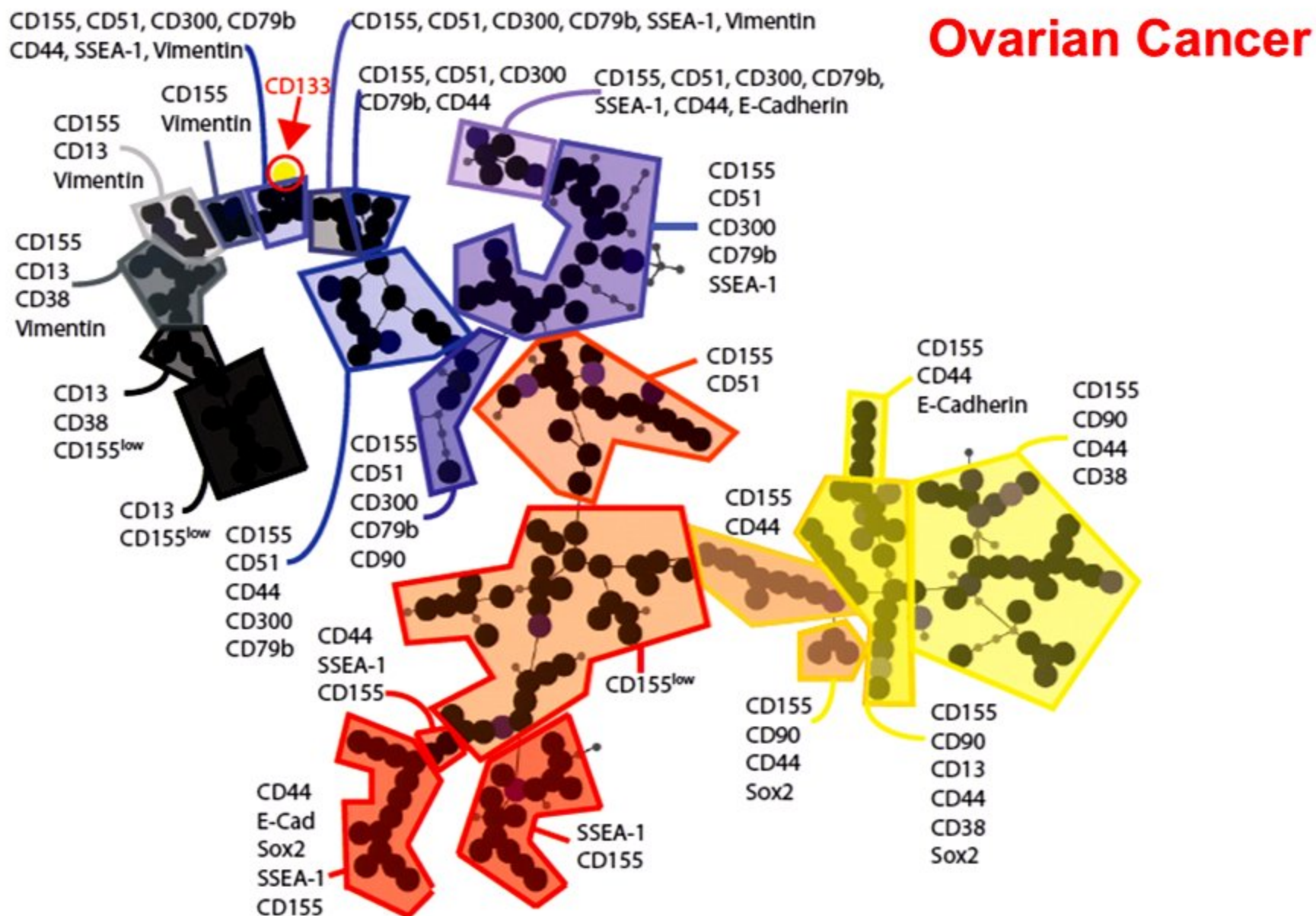
SOC Cell Subset Differences Within & Across Patients – Surface Markers CD13

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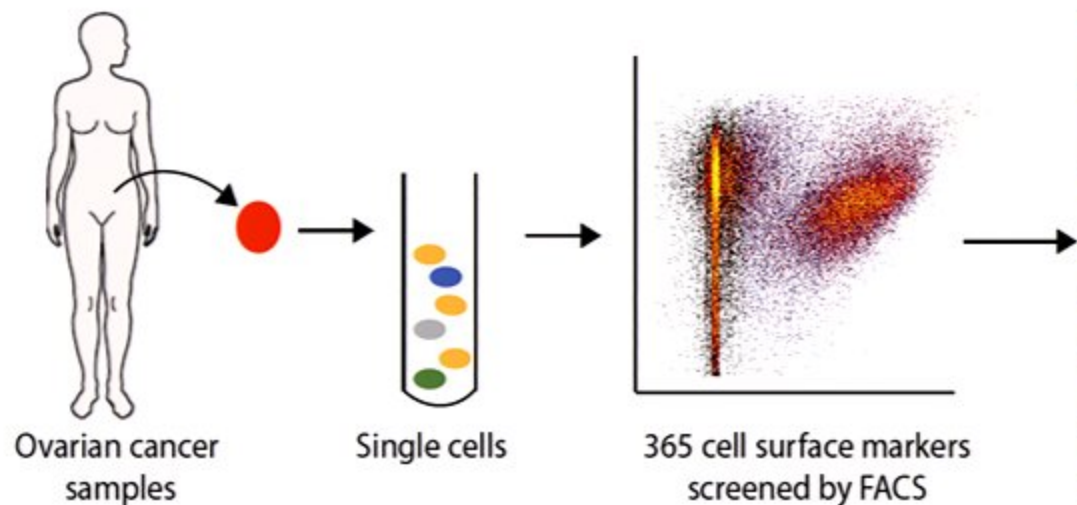


Lowest  Highest
CD13 expression

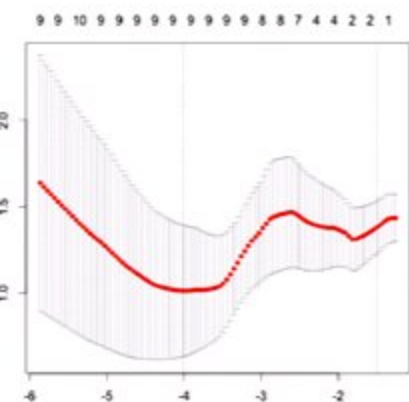
Meta-clusters Based on Expression of Surface & Stem Cell Markers in Ovarian Cancer



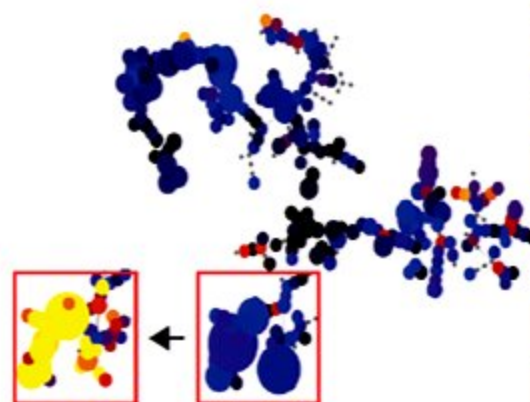
Extending Approach to Disease



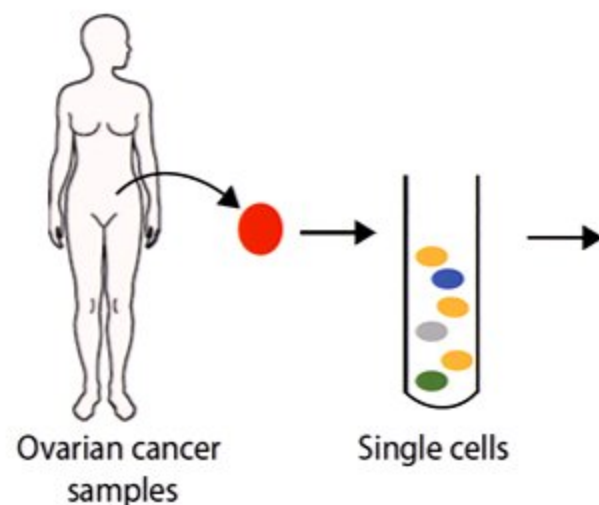
Isotope Channel	Marker	Isotope Channel	Marker
115	CD45	158	E-Cadherin
139	p-S6	159	p-Akt
141	CD133	160	Sox2
142	CD51	162	SSEA-1
143	p-H2AX	164	p-Stat5
144	CD90	165	CD162
145	CD79B	166	CD44
146	p-ATM	167	CD38
147	c-Myc	168	CD13
148	CD34	169	p-p53
149	p-NFkb	170	CD49A
150	CD117	171	CD24
151	p-Erk	172	c-Casp 3
152	CD155	174	HLA-DR
153	CD62L	175	CD300d
154	Vimentin	176	p-HH3
156	CD10		



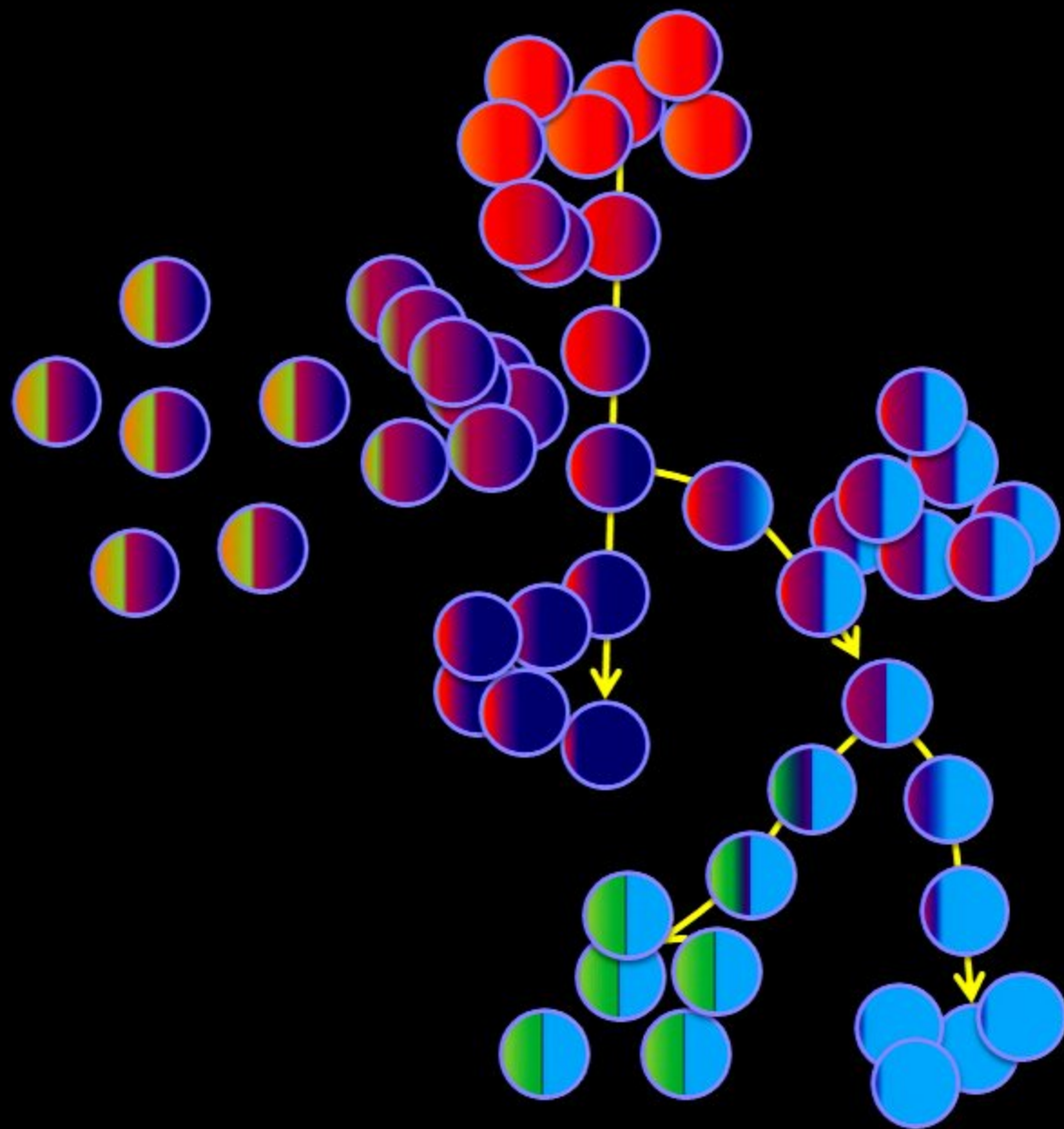
Patient stratification

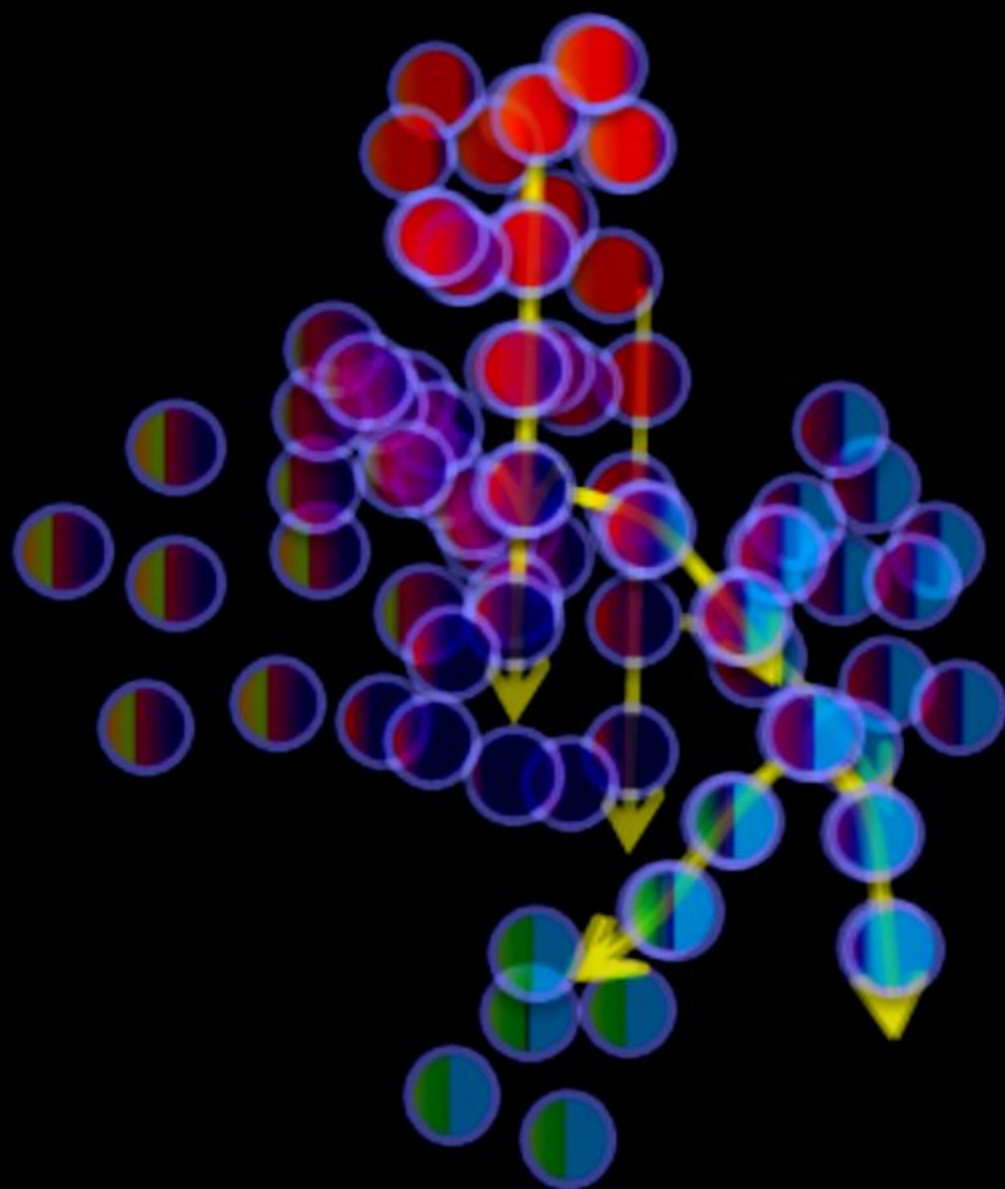


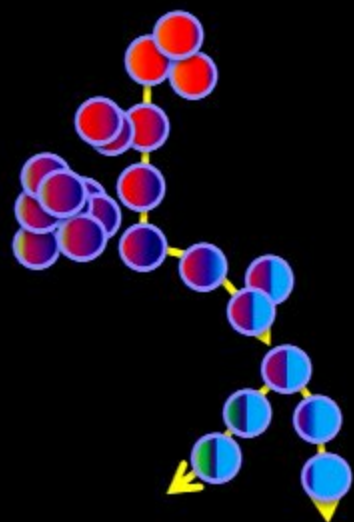
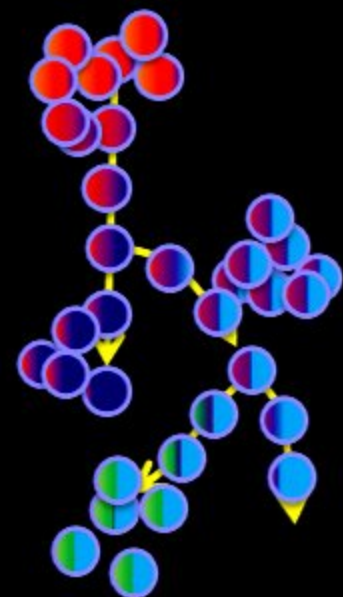
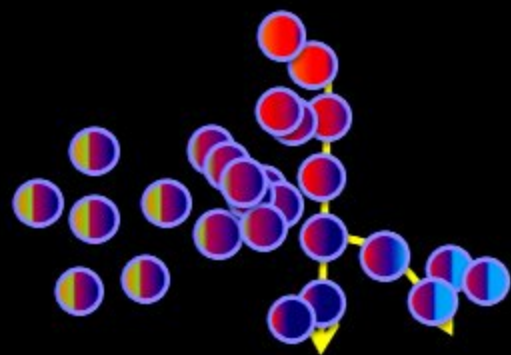
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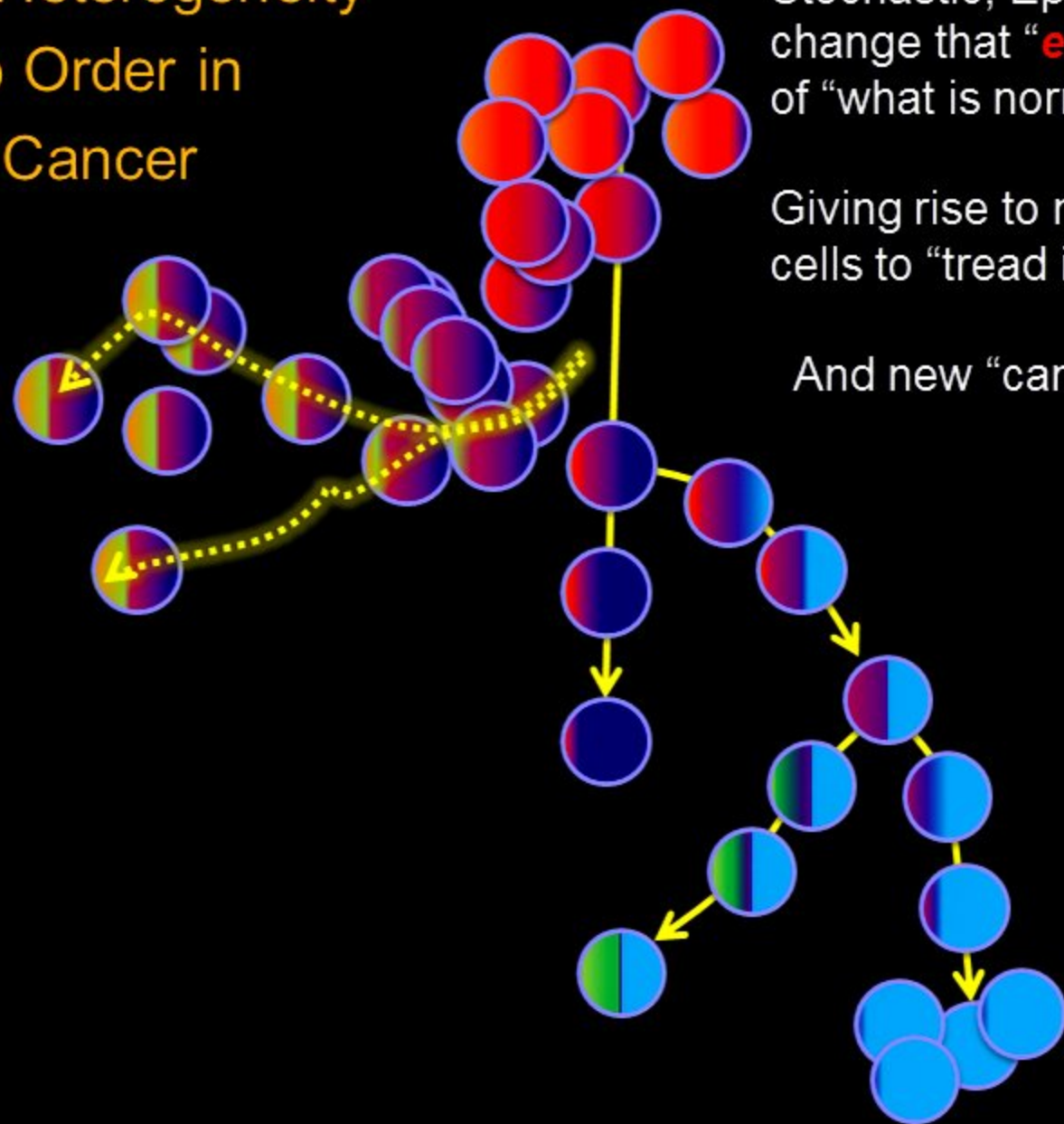
Isotope		Isotope	
Channel	Marker	Channel	Marker
115	CD45	158	E-Cadherin
139	p-S6	159	p-Akt
141	CD133	160	Sox2
142	CD51	162	SSEA-1
143	p-H2AX	164	p-Stat5
144	CD90	165	CD162
145	CD79B	166	CD44
146	p-ATM	167	CD38
147	c-Myc	168	CD13
148	CD34	169	p-p53
149	p-NFkb	170	CD49A
150	CD117	171	CD24
151	p-Erk	172	c-Casp 3
152	CD155	174	HLA-DR
153	CD62L	175	CD300d
154	Vimentin	176	p-HH3
156	CD10		







From Heterogeneity to Order in Cancer

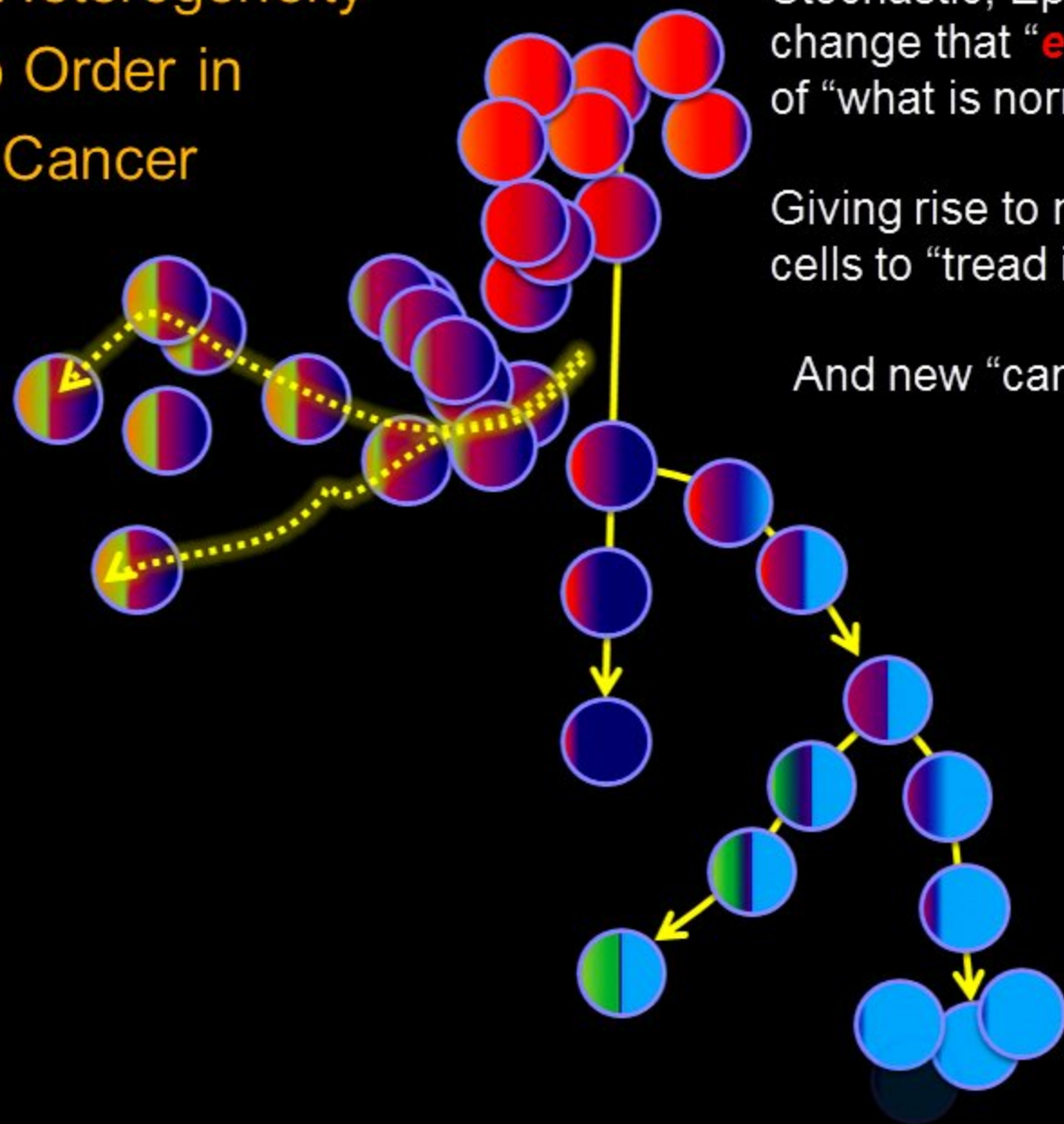


Stochastic, Epigenetic, or Genetic change that “**expands the boundary**” of “what is normal”...

Giving rise to new opportunities for cells to “tread into” new regulatory terrain.

And new “cancer” lineages...

From Heterogeneity to Order in Cancer



Stochastic, Epigenetic, or Genetic change that “**expands the boundary**” of “what is normal”...

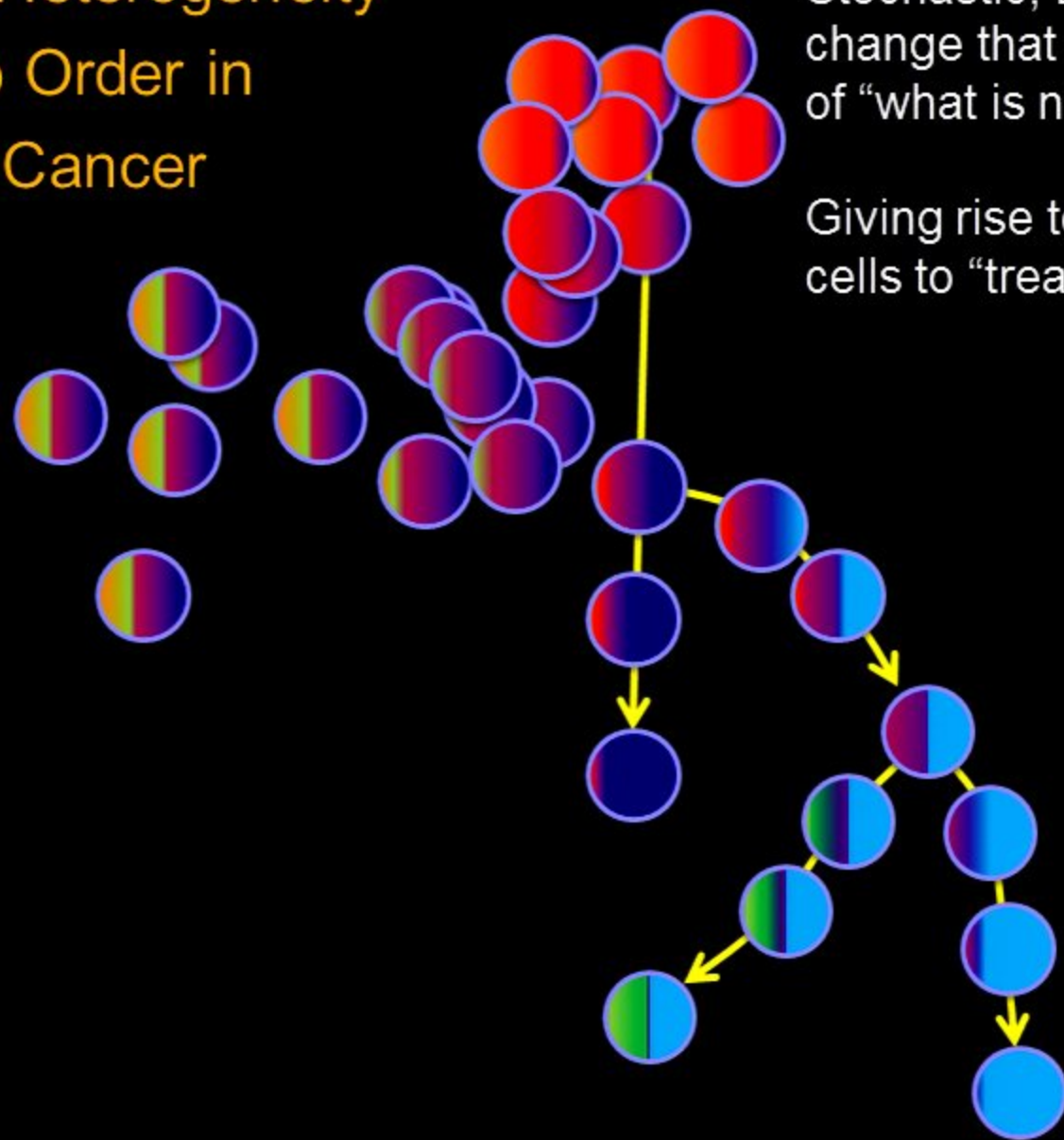
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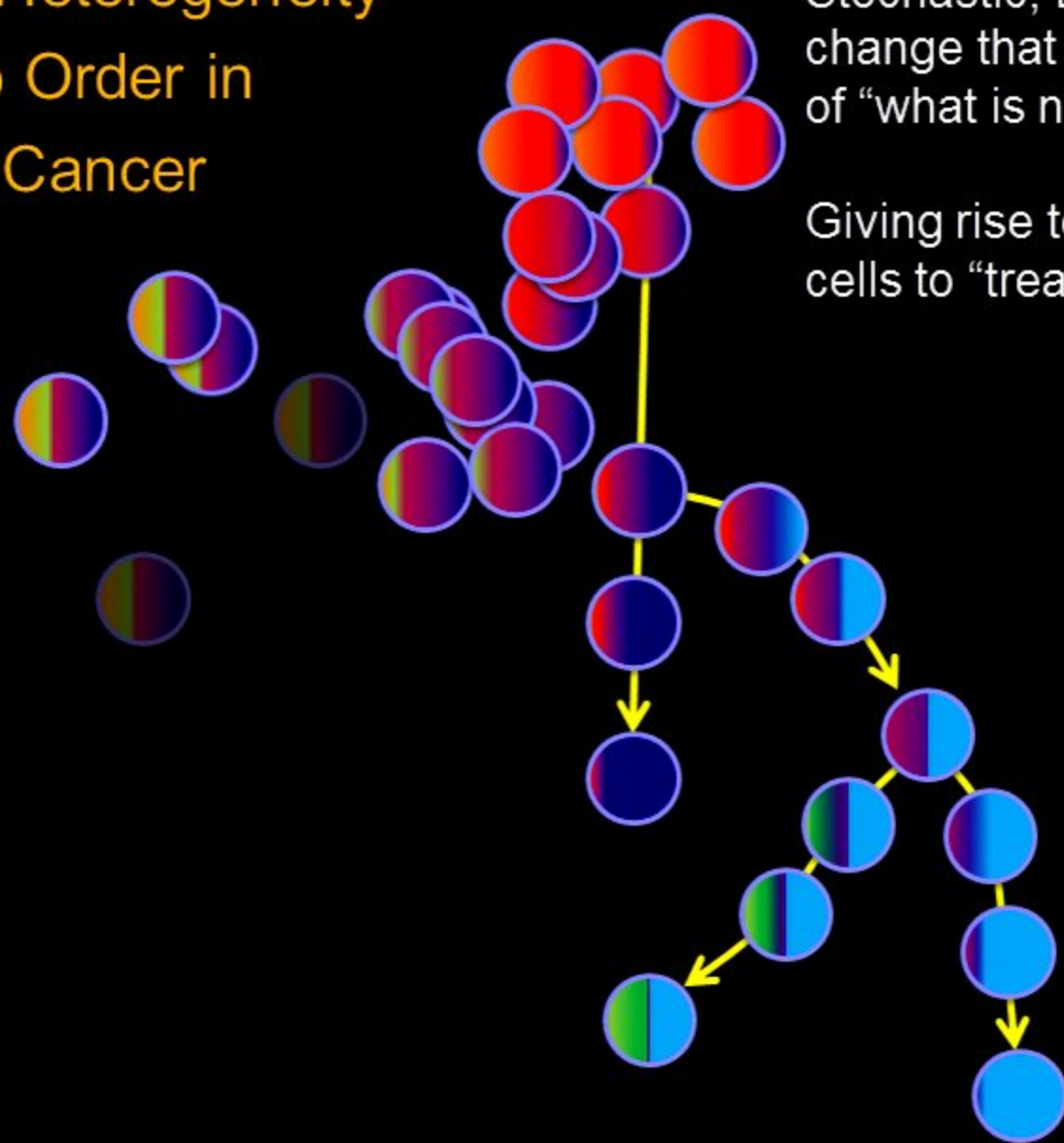
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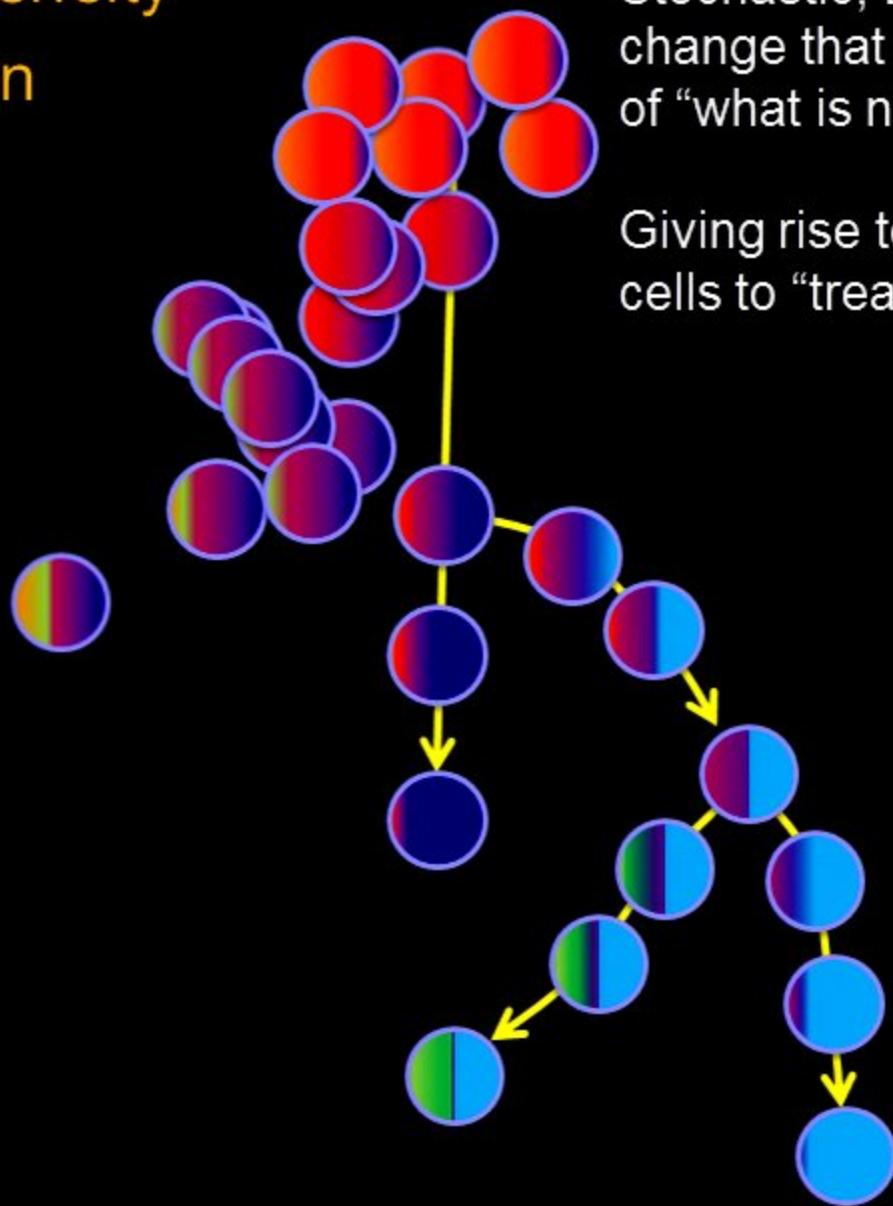
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From Heterogeneity to Order in Cancer

Stochastic, Epigenetic, or Genetic
change that “**expands the boundary**”
of “what is normal”...

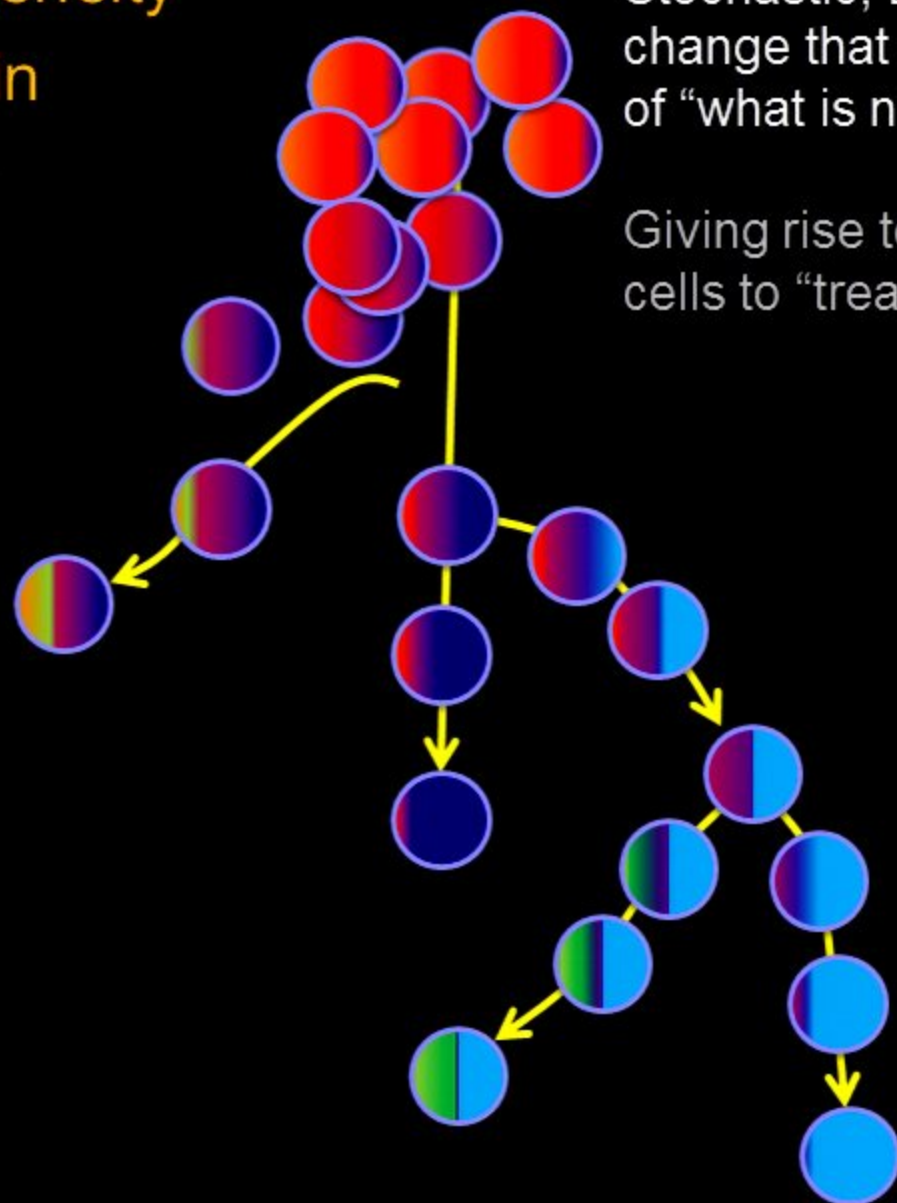
Giving rise to new opportunities for
cells to “tread into” new regulatory terrain.



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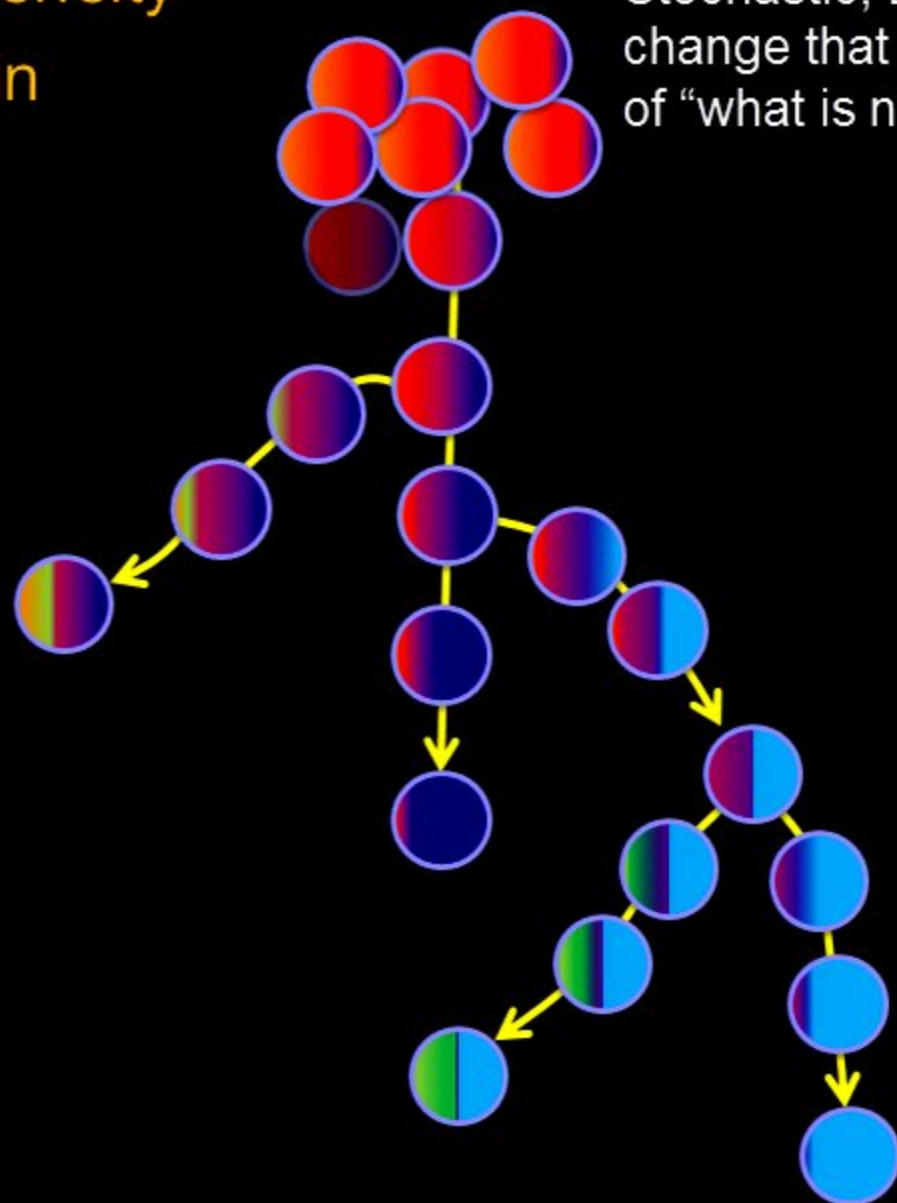
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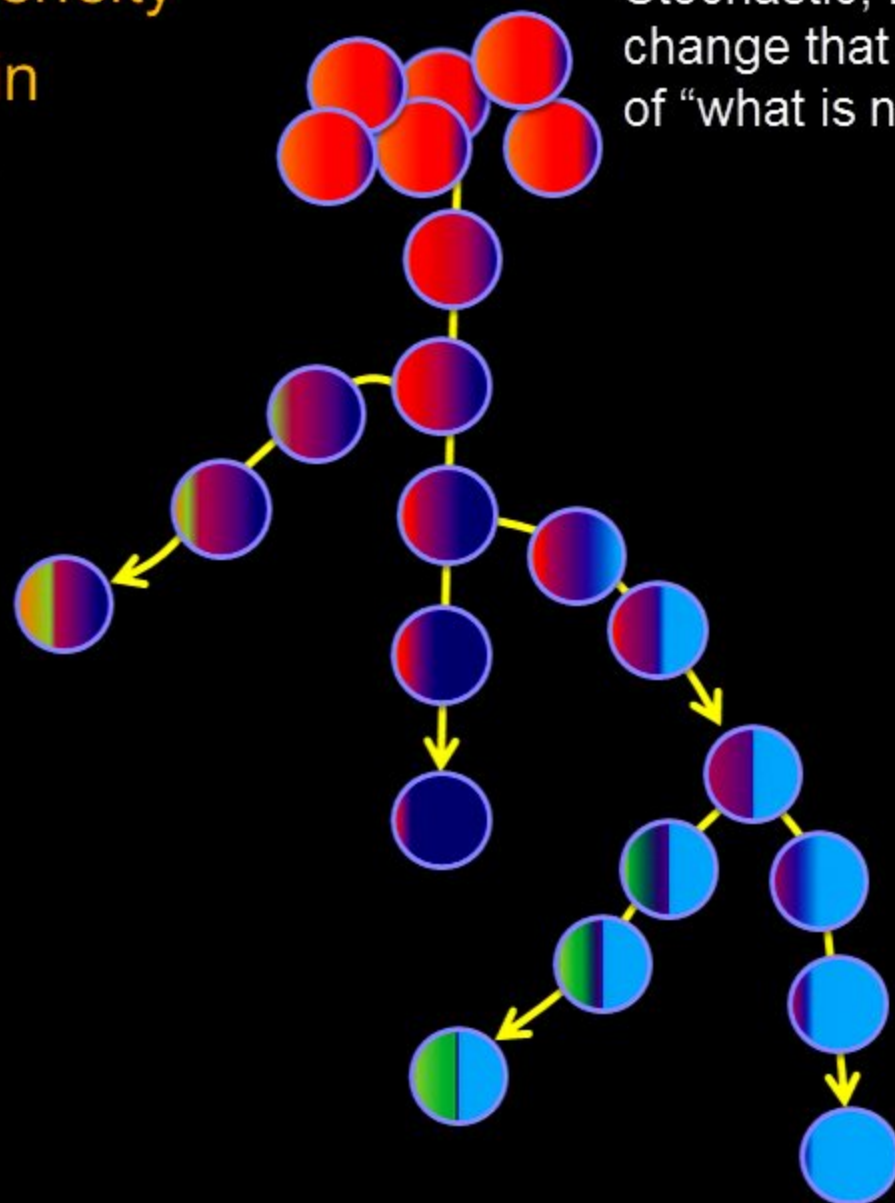
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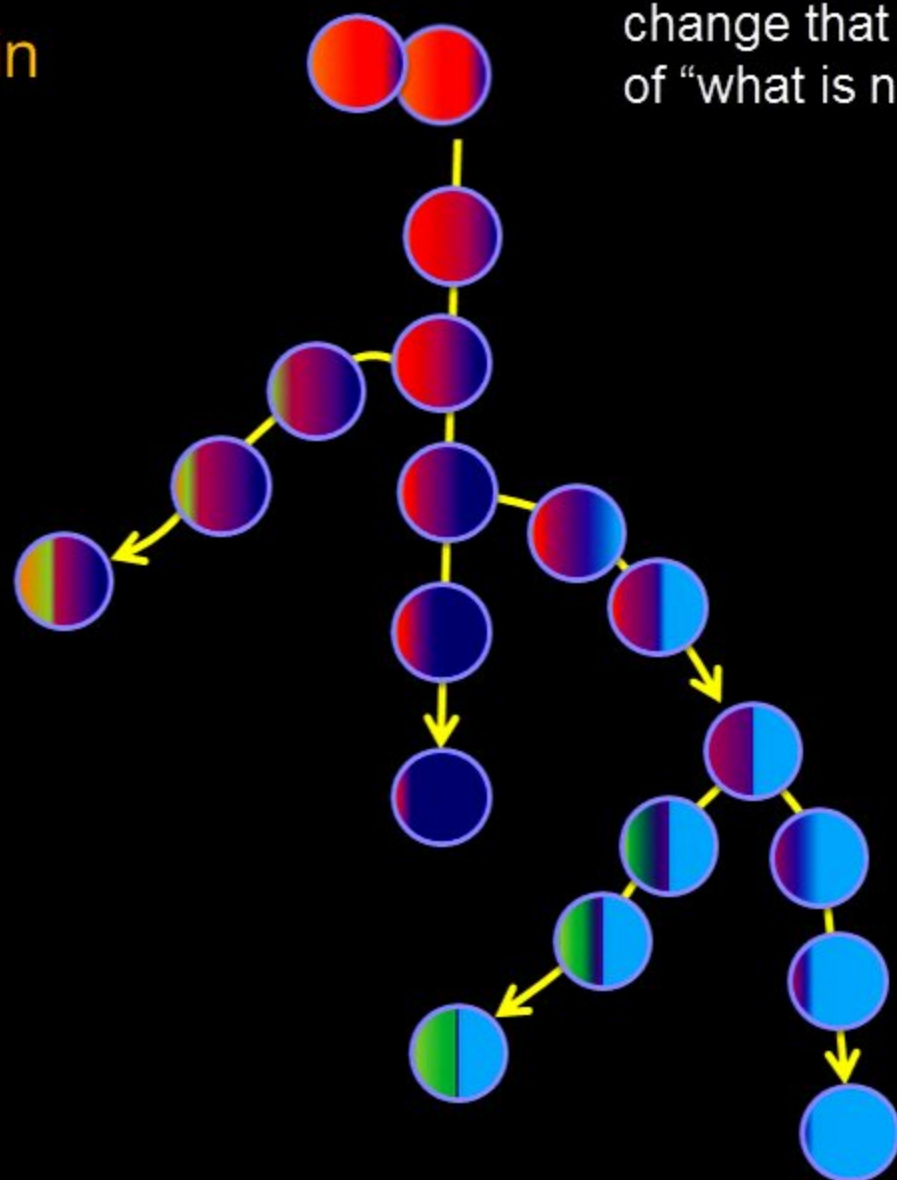
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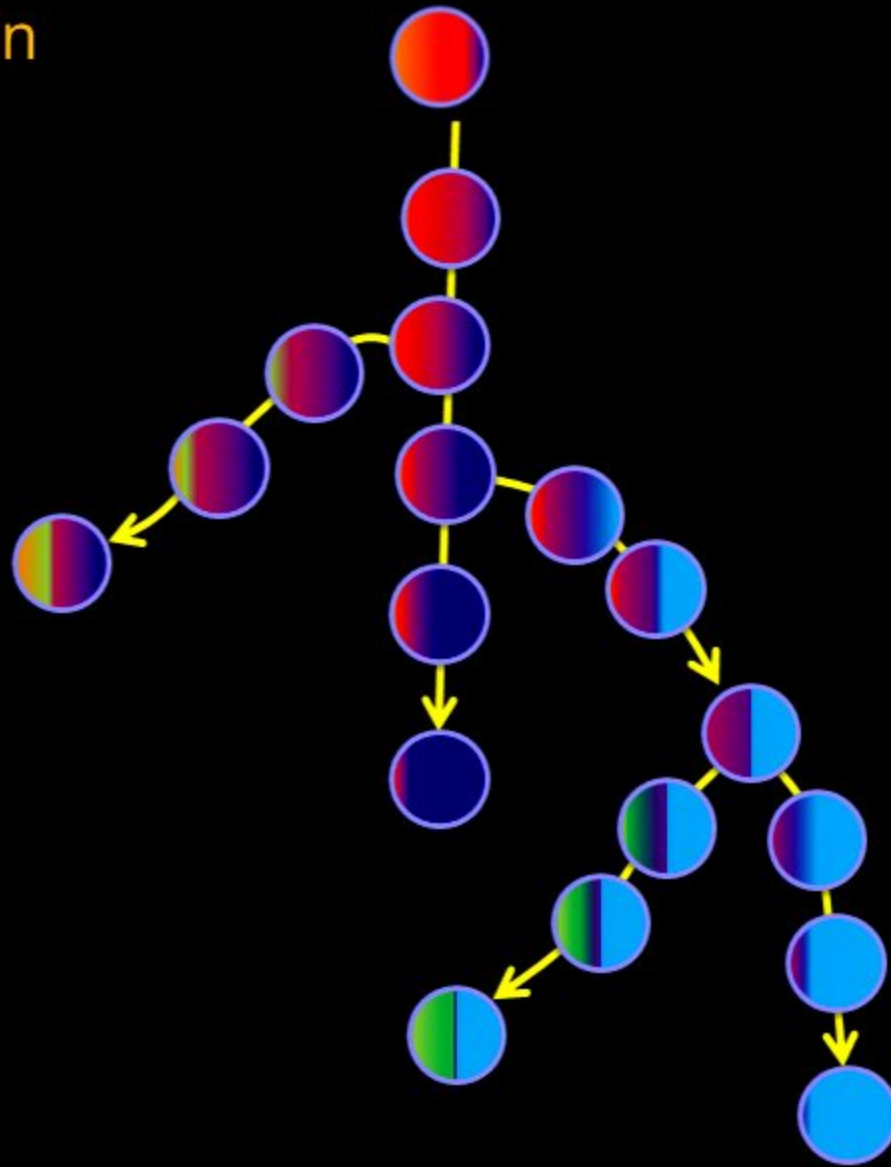


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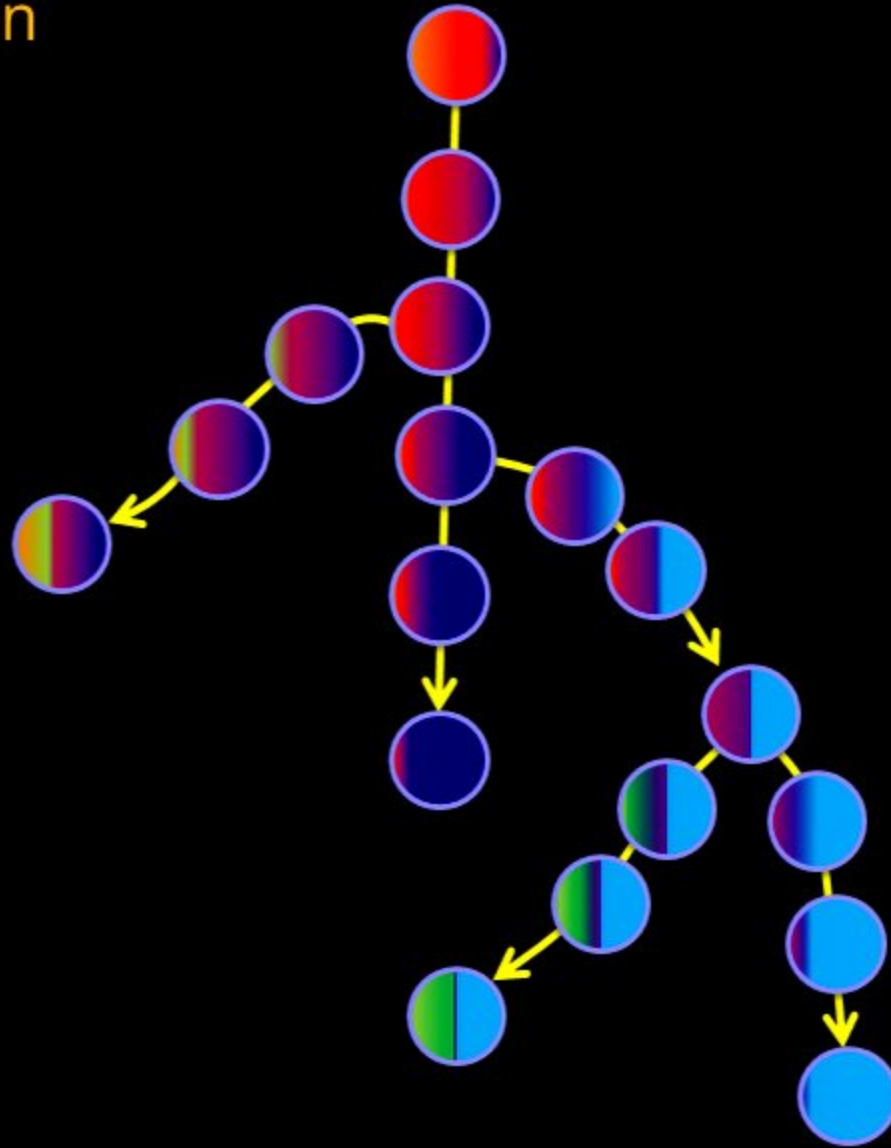
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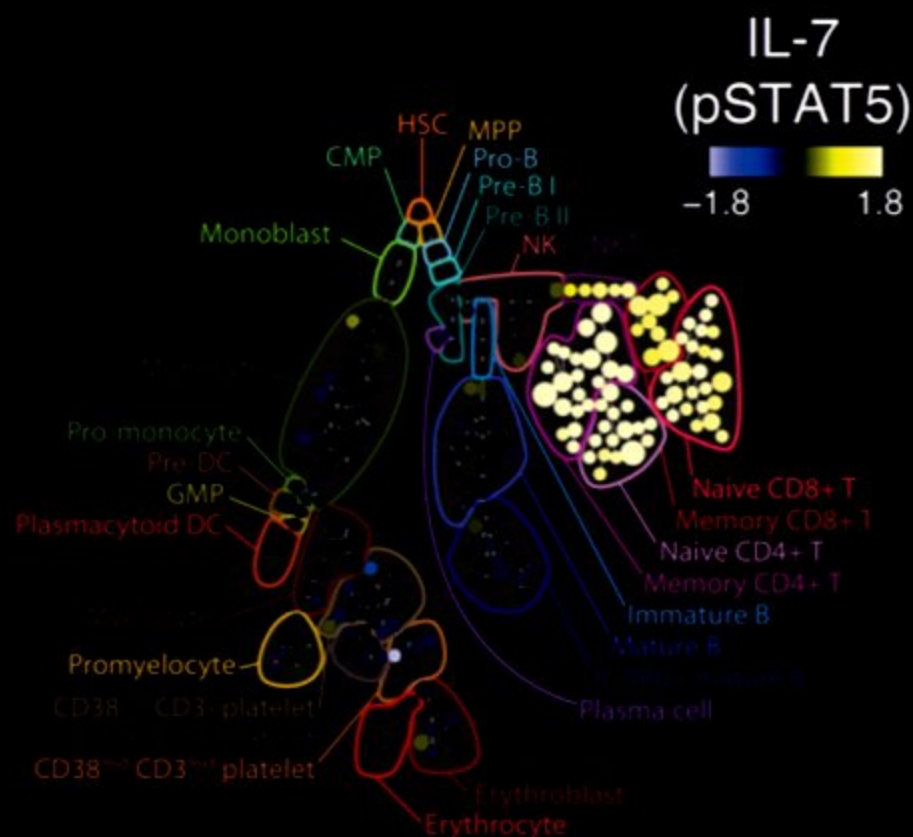
From Heterogeneity to Order in Cancer



Bodenmiller et al
Nature Biotechnology, August, 2012



Single cell signaling on an immune system wide basis

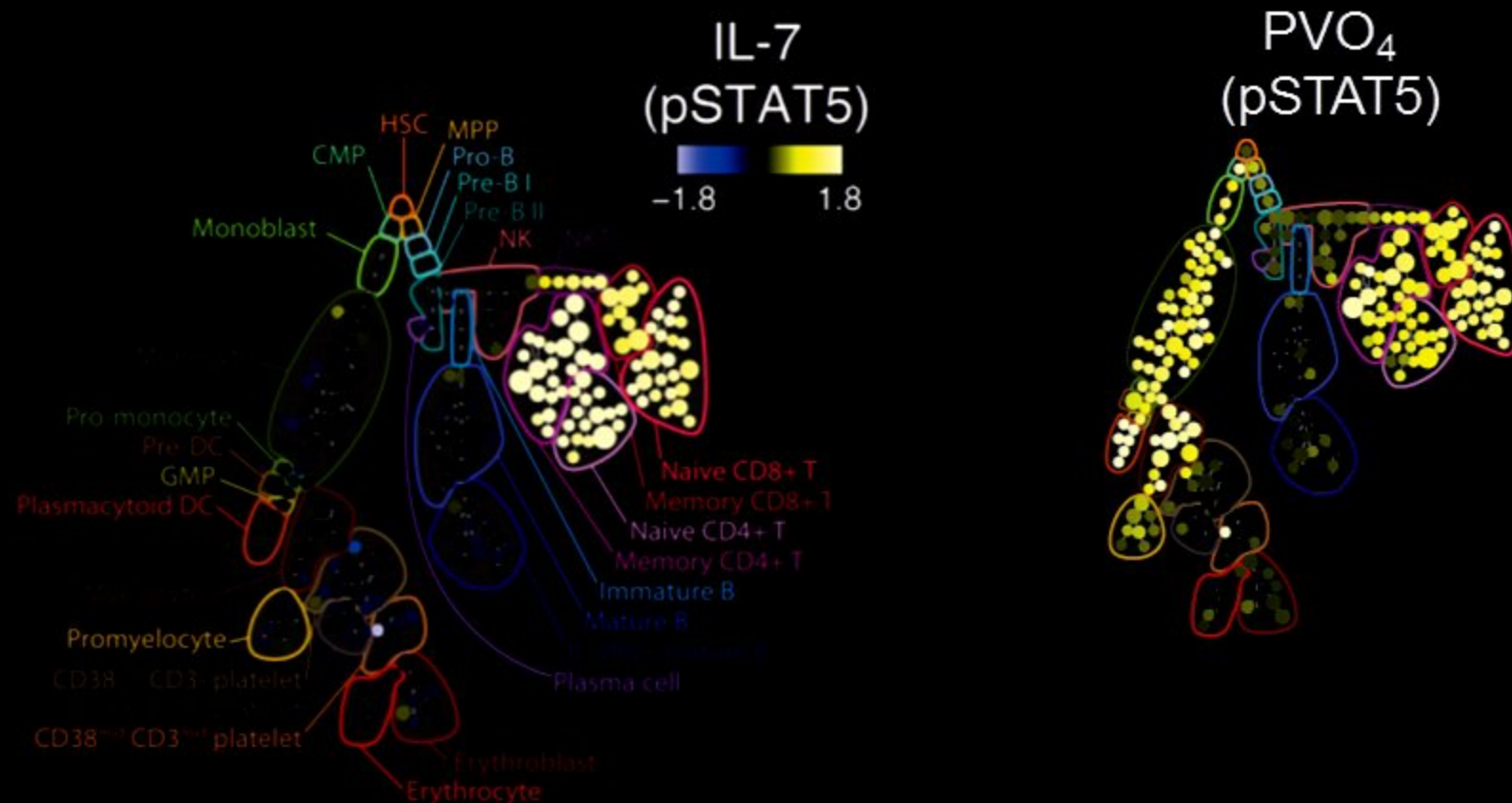


+ Dasatinib

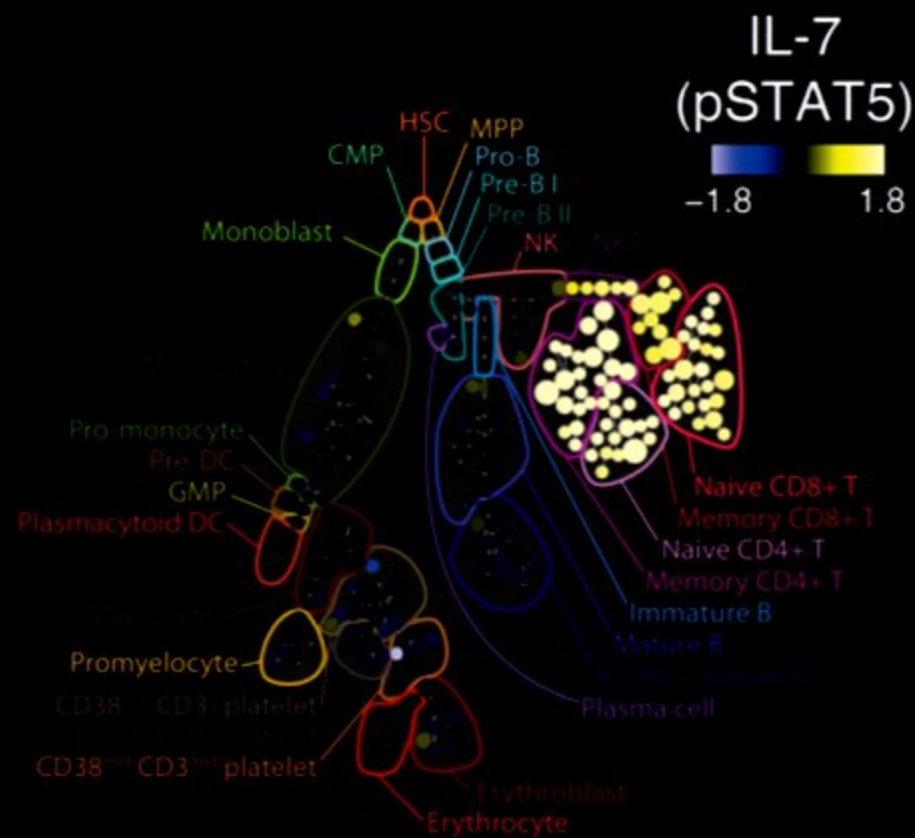
Abl / Src-family
kinase inhibitor



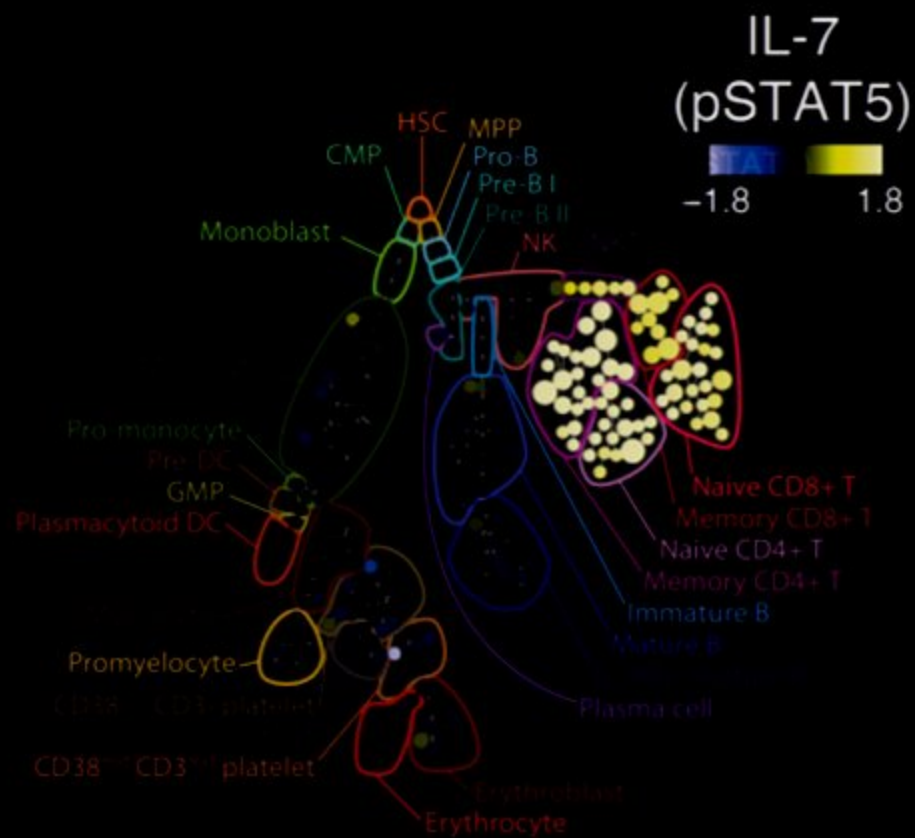
Single cell signaling on an immune system wide basis



Single cell signaling on an immune system wide basis

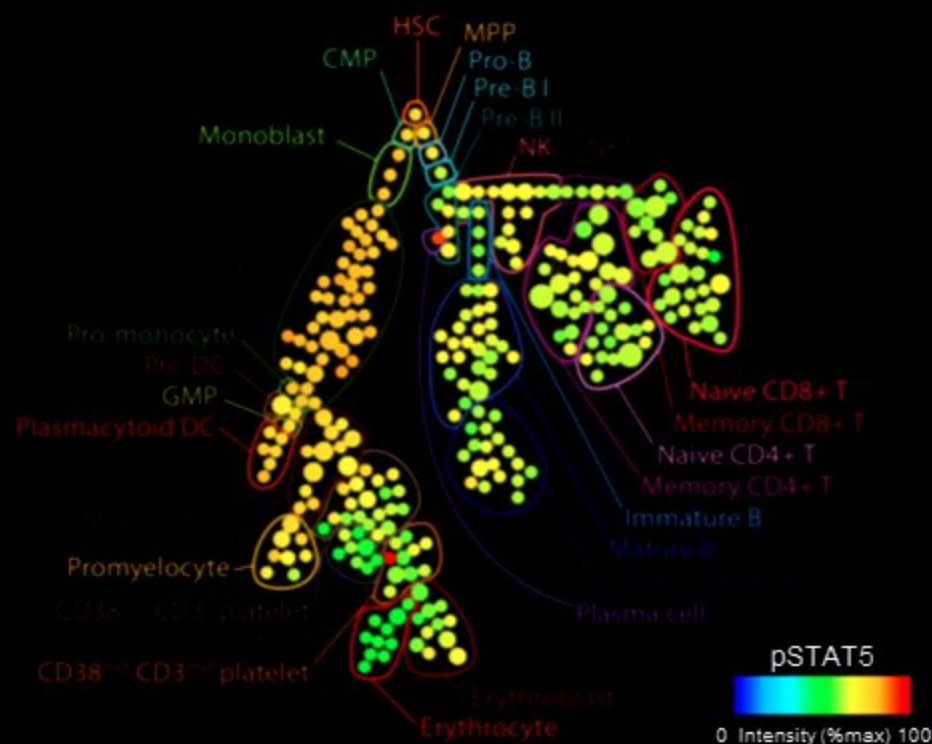


Single cell signaling on an immune system wide basis

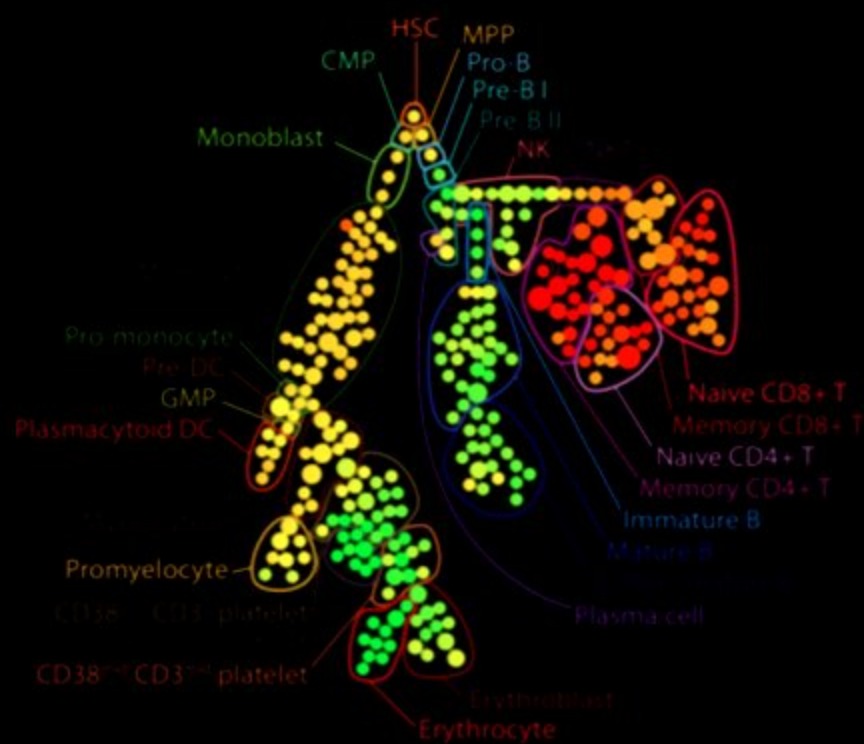


Single cell signaling on an immune system wide basis

Basal

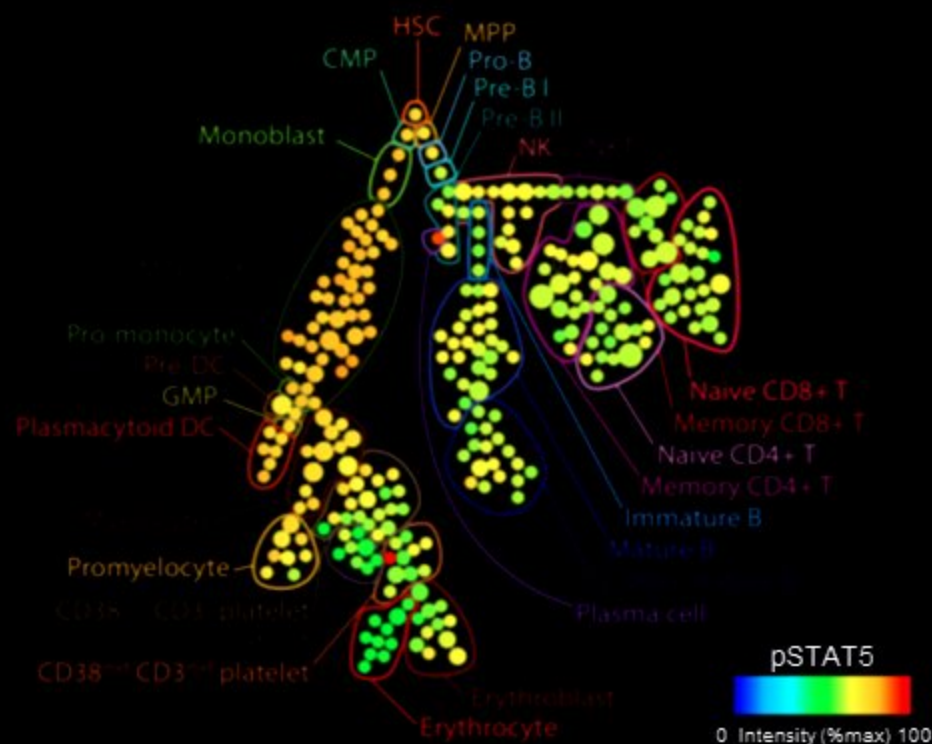


IL-7



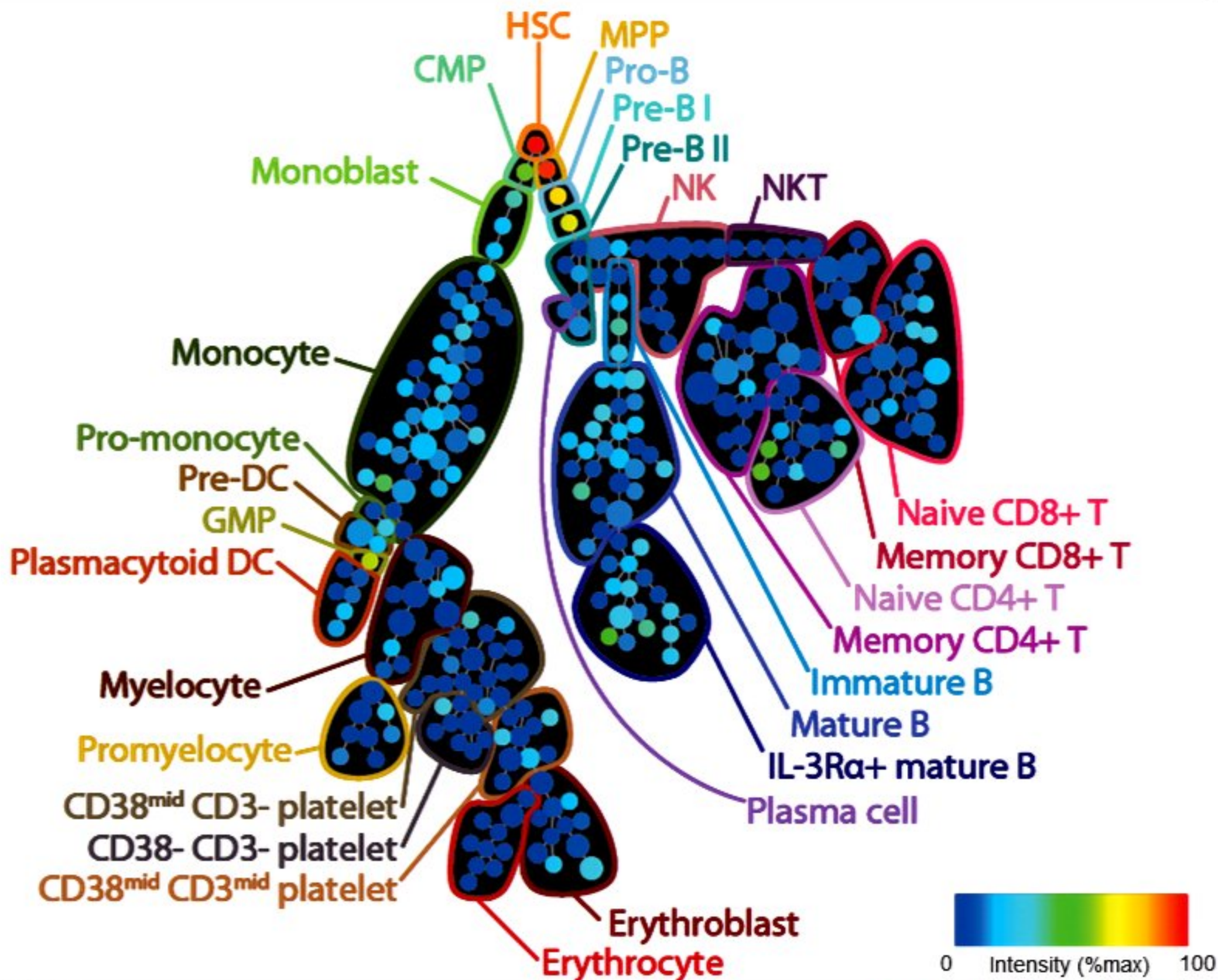
Single cell signaling on an immune system wide basis

Basal

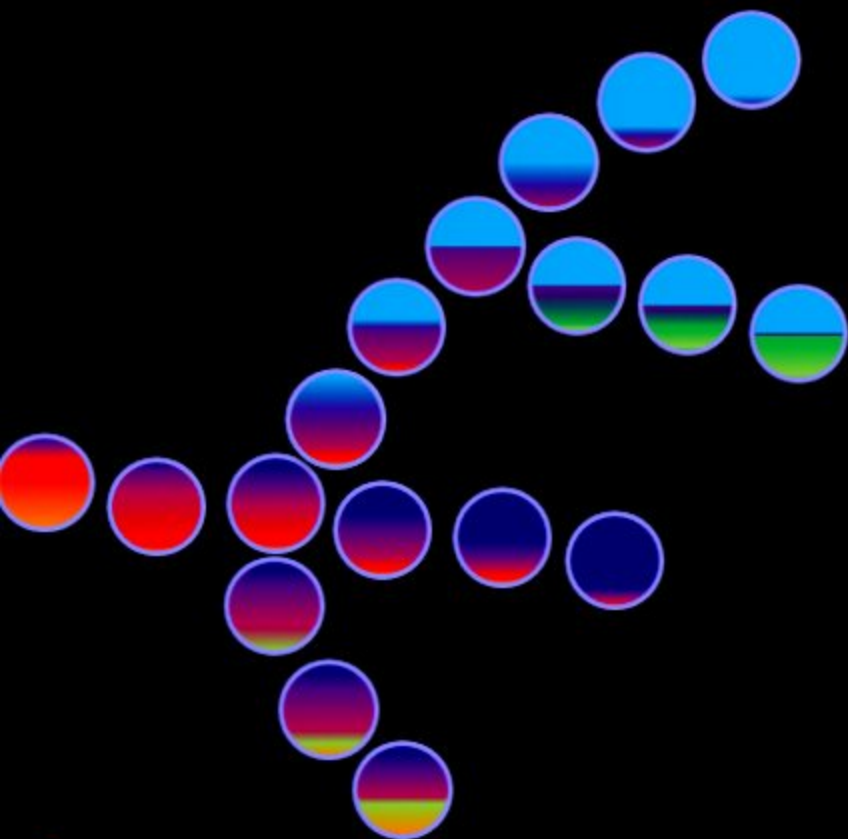


SPADE projects bone marrow as a continuum of phenotypes

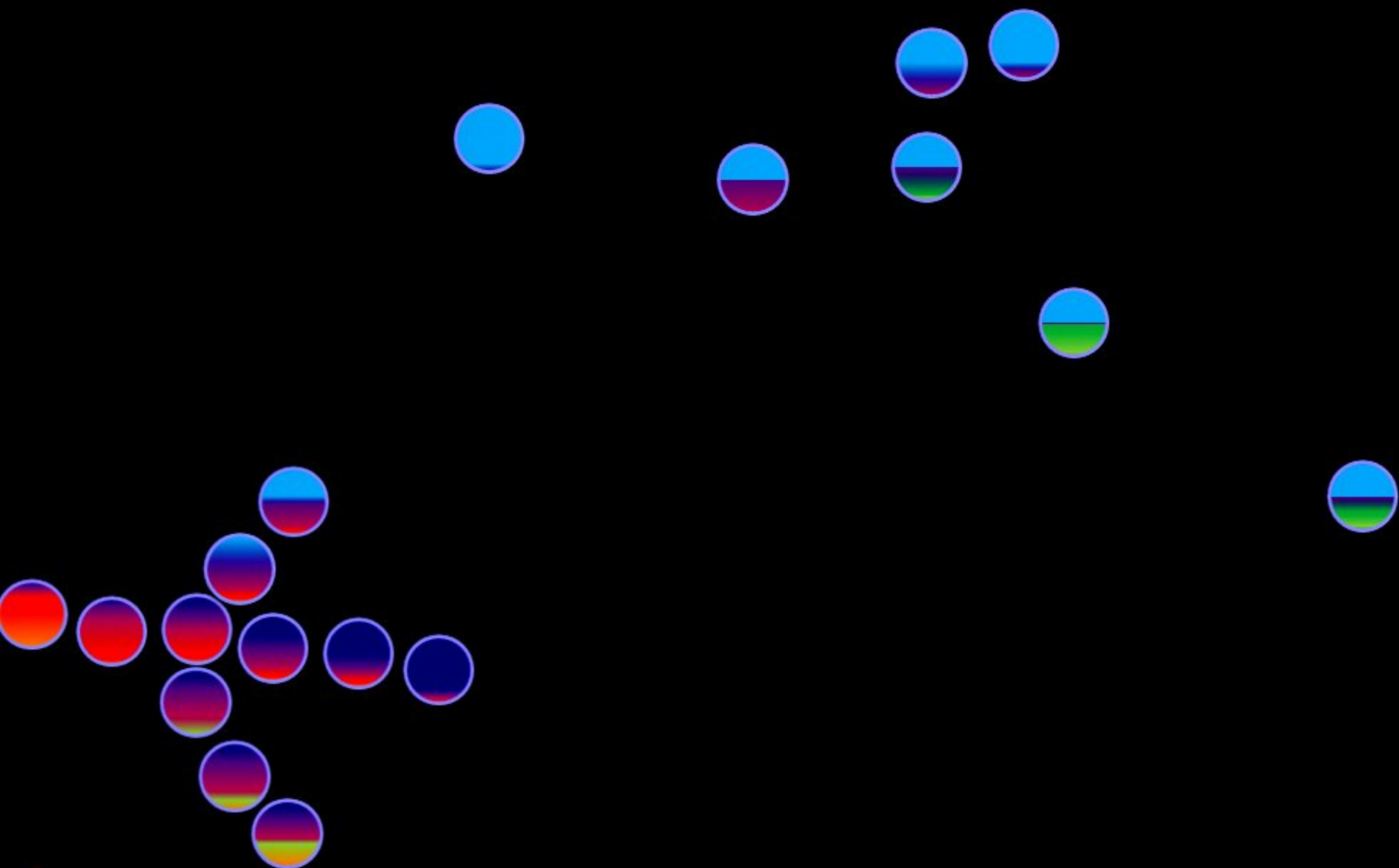
CD34



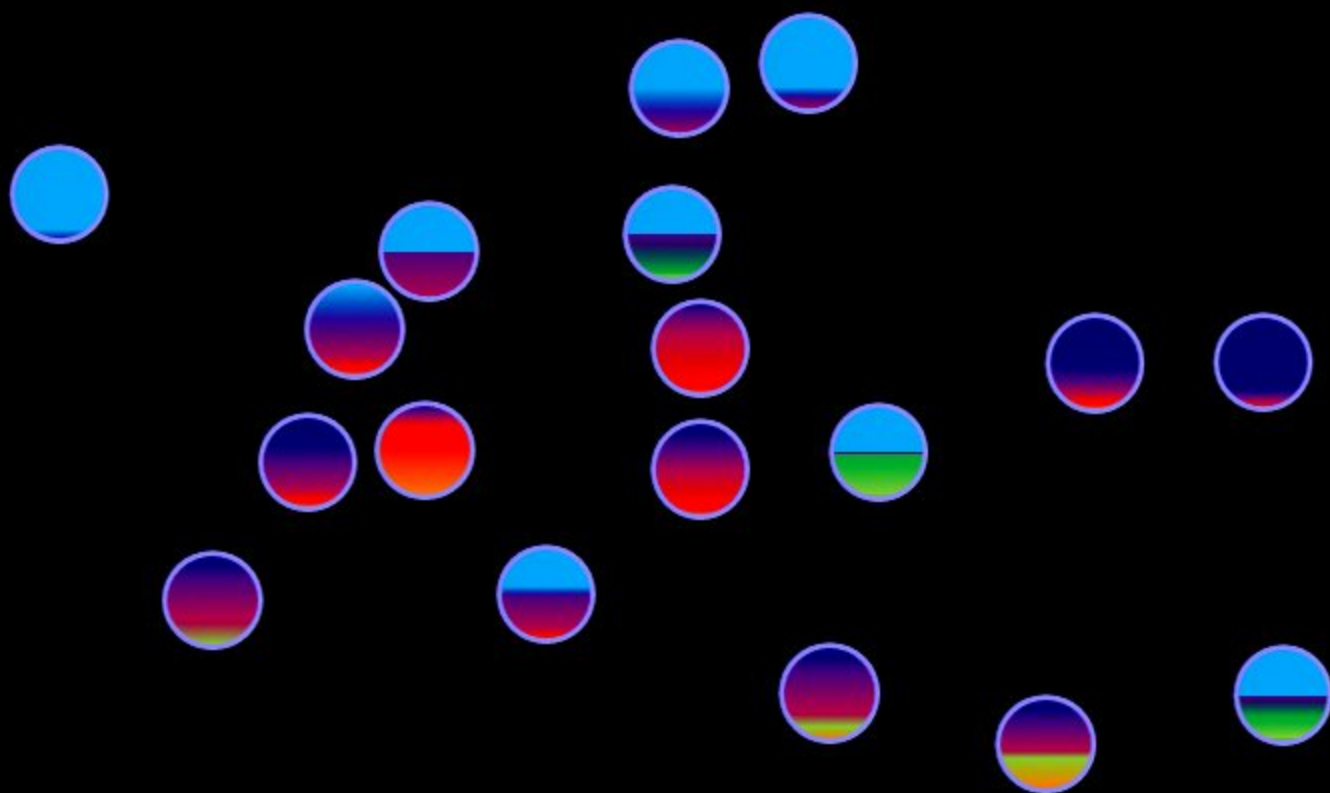
Can we reconstruct the lineages by aligning “Like near Like”?



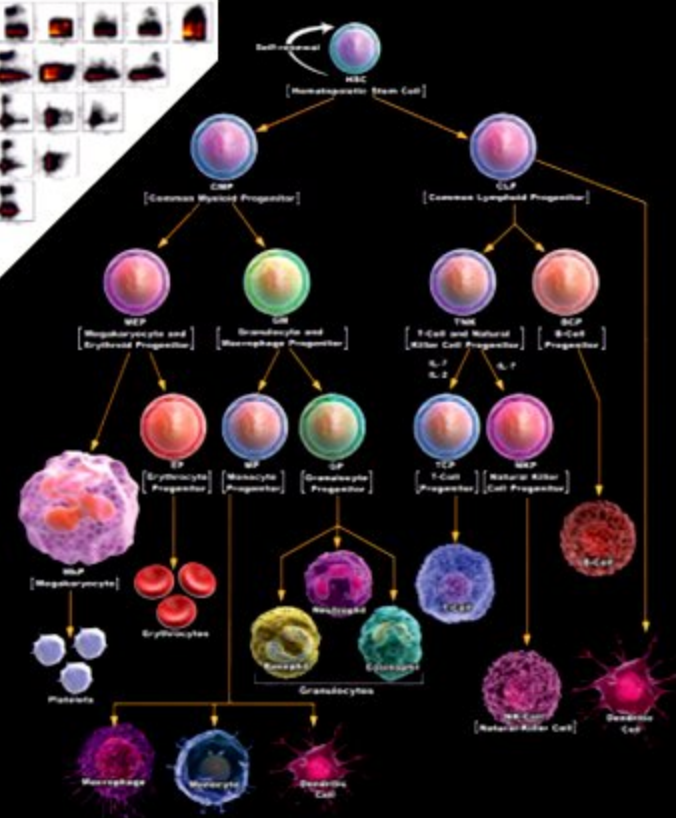
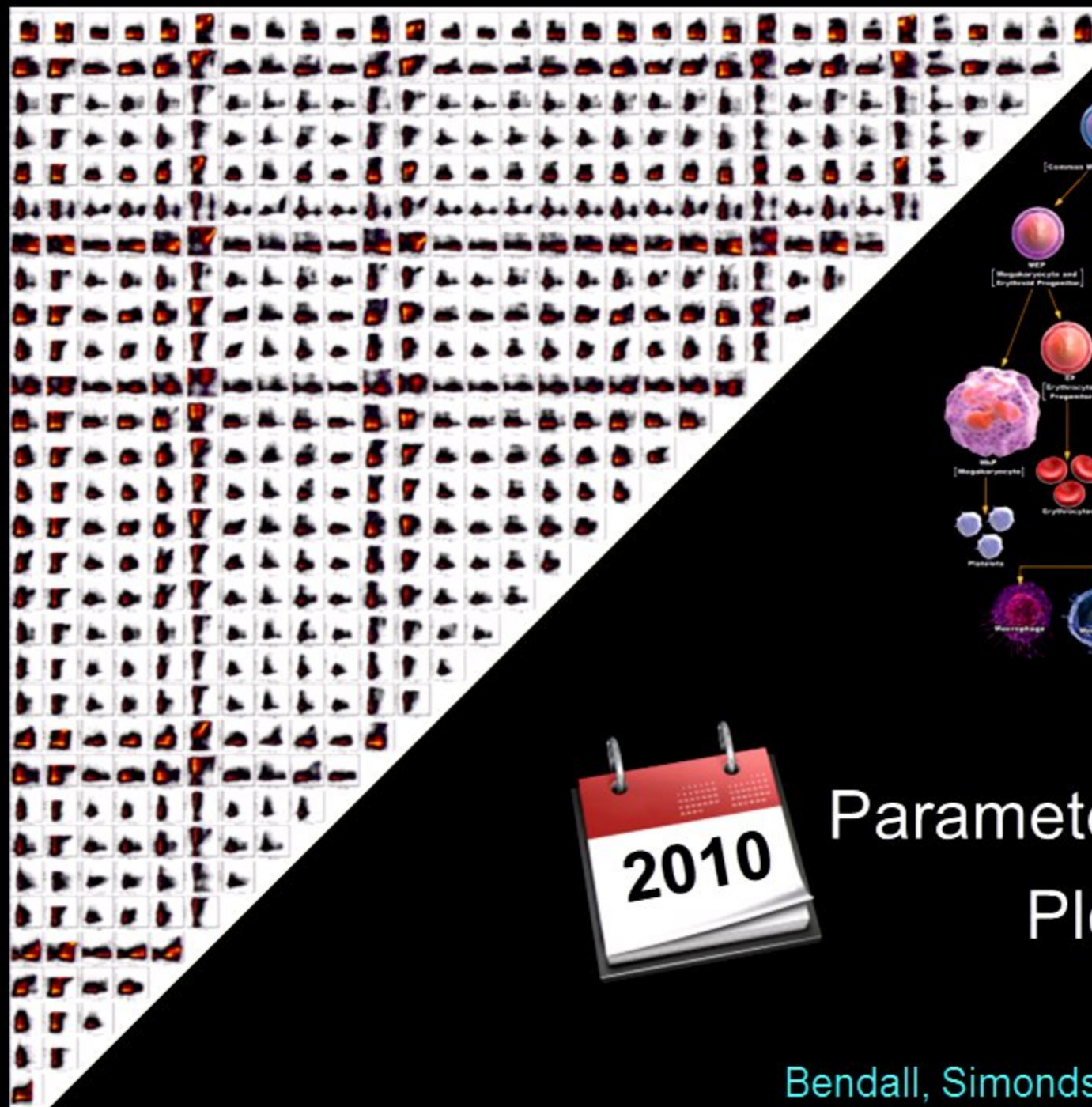
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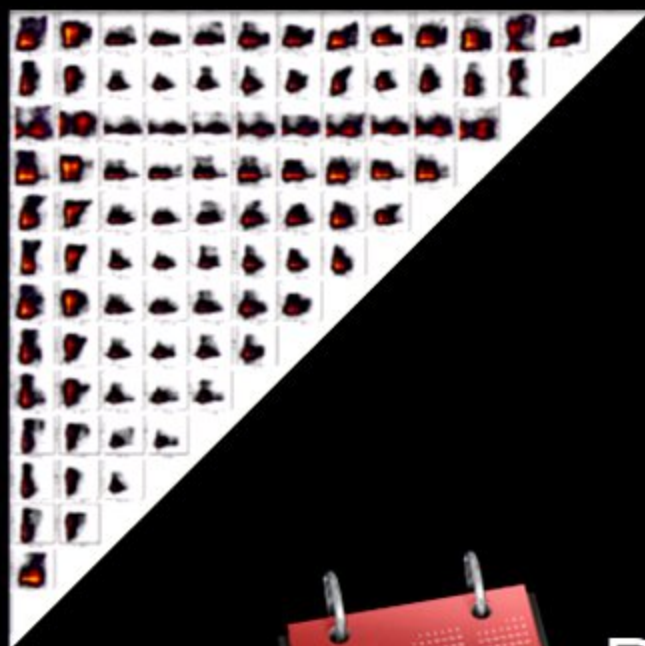
Biaxial plots are not a scalable solution



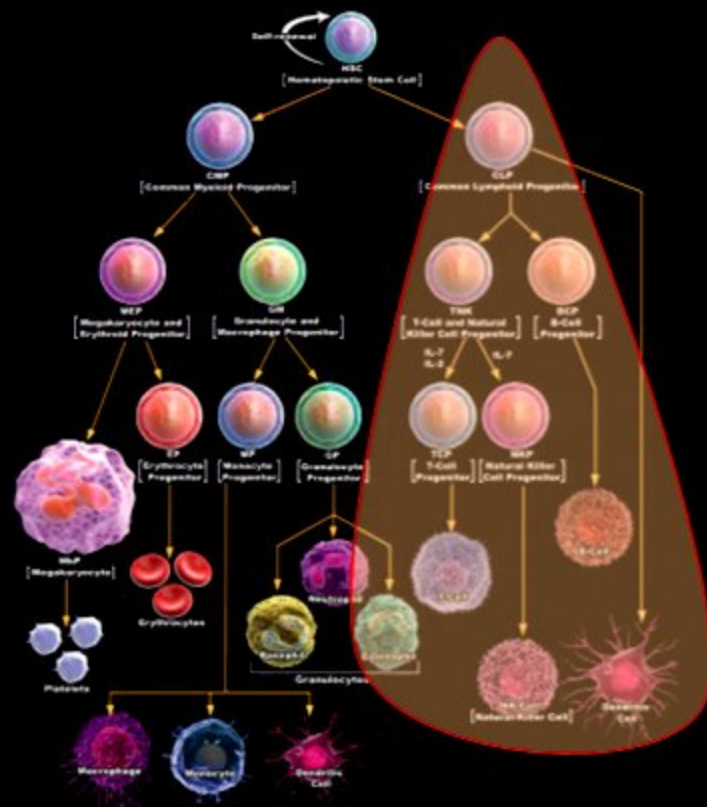
Parameters: 32

Plots: 496

Biaxial plots are not a scalable solution



Parameters: 14
Plots: 91

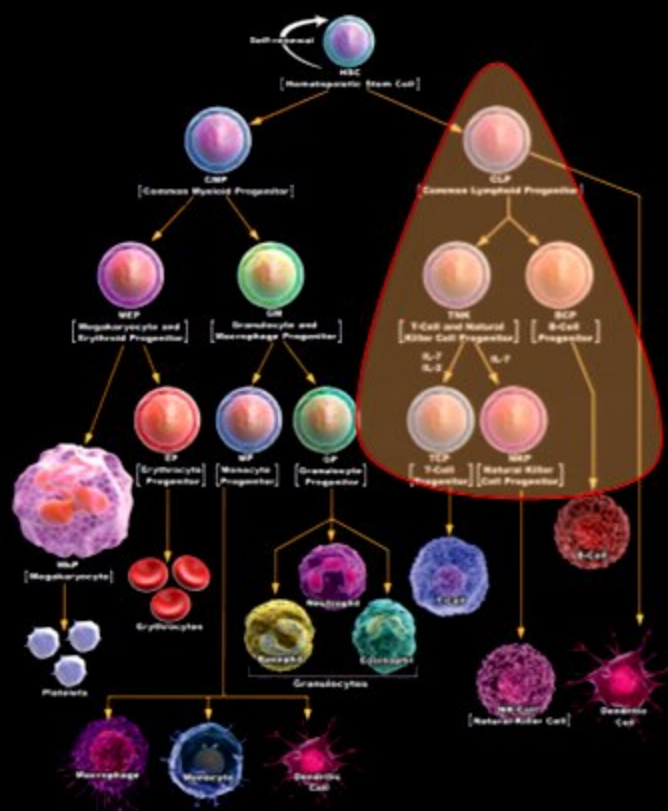


Biaxial plots are not a scalable solution

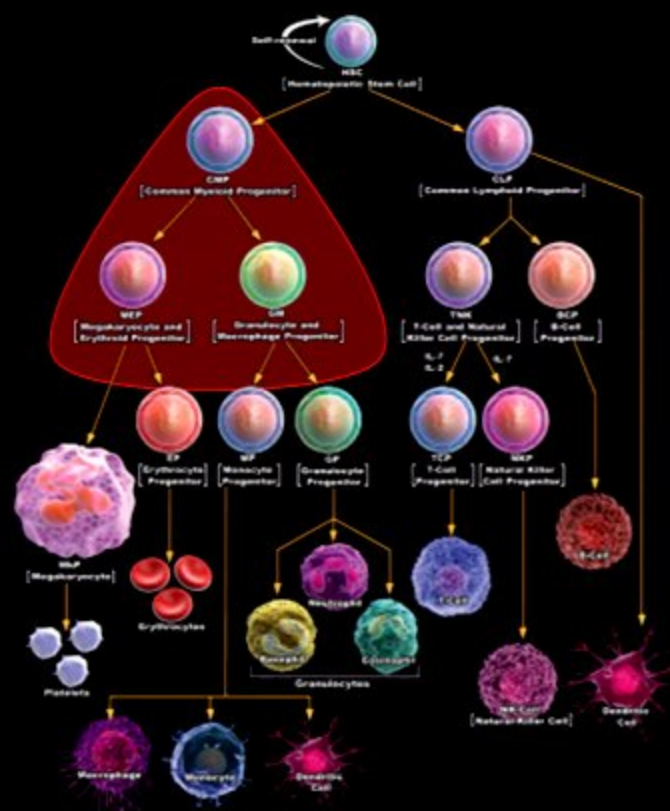


Parameters: 8

Plots: 28



Biaxial plots are not a scalable solution



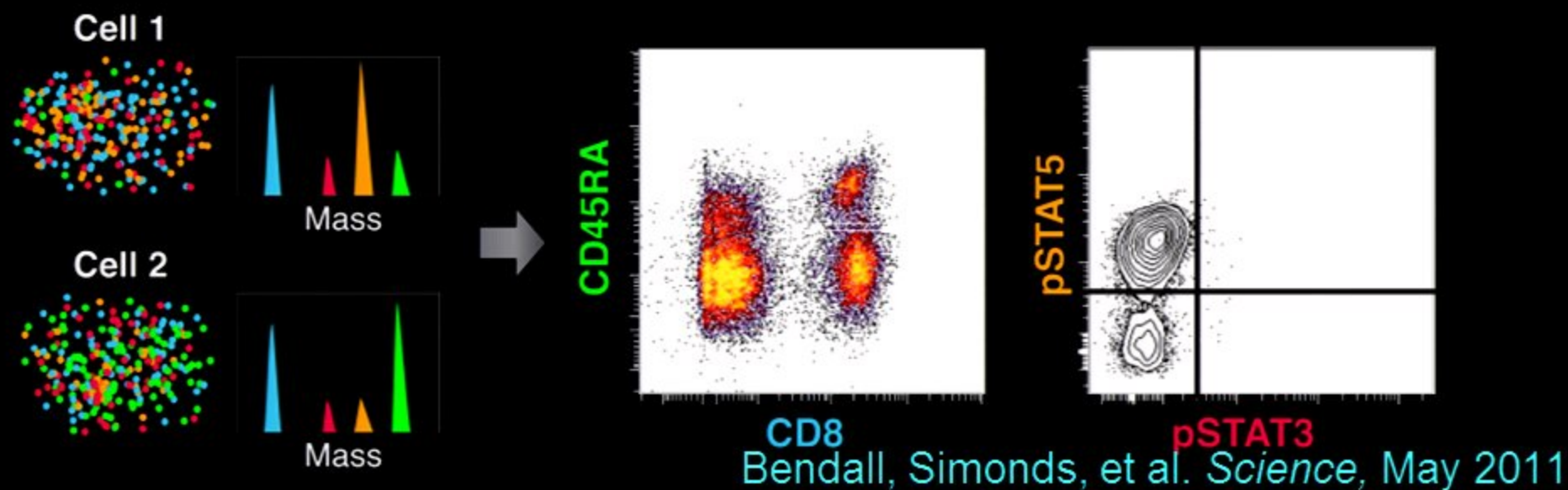
Parameters: 4
Plots: 6

CyTOF Phenotyping & Mechanism Panels

- >100 Human surface:
- > 60 Murine surface:
- > 20 murine & human cytokines

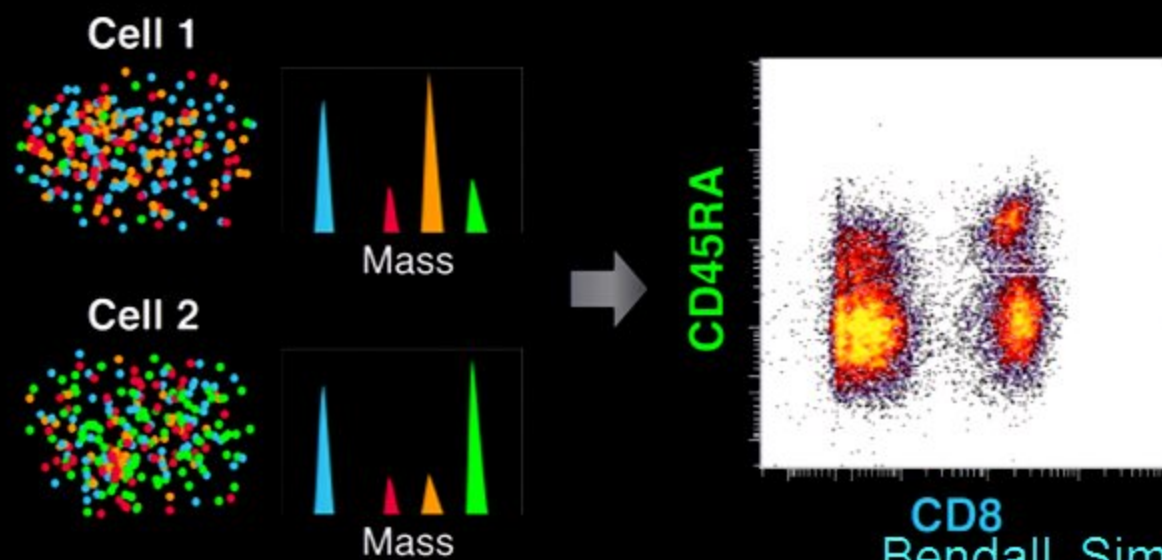
- ~ 100 intracellular mechanism targets for panels
 - ‘total’ protein
 - Phospho epitopes- kinases and targets of kinases
 - Apoptosis: Bad, Bax, Bcl2, Bid, Akt, CytC, caspases
 - Epigenetic panels: pH3, pH2AX,
 - DNA Damage: pATM, pRb, p53, p16, p21, ATR, pChk1, 2, etc.
 - Stem cell: Sox2, c-Myc, nanog, Gata, surface markers
 - Cell cycle: CyclinA/B/D1,2,3/E, Rb, Ki67,
 - Wnt, Bmp pathways panels

Mass cytometry enables single-cell phosphoproteomics



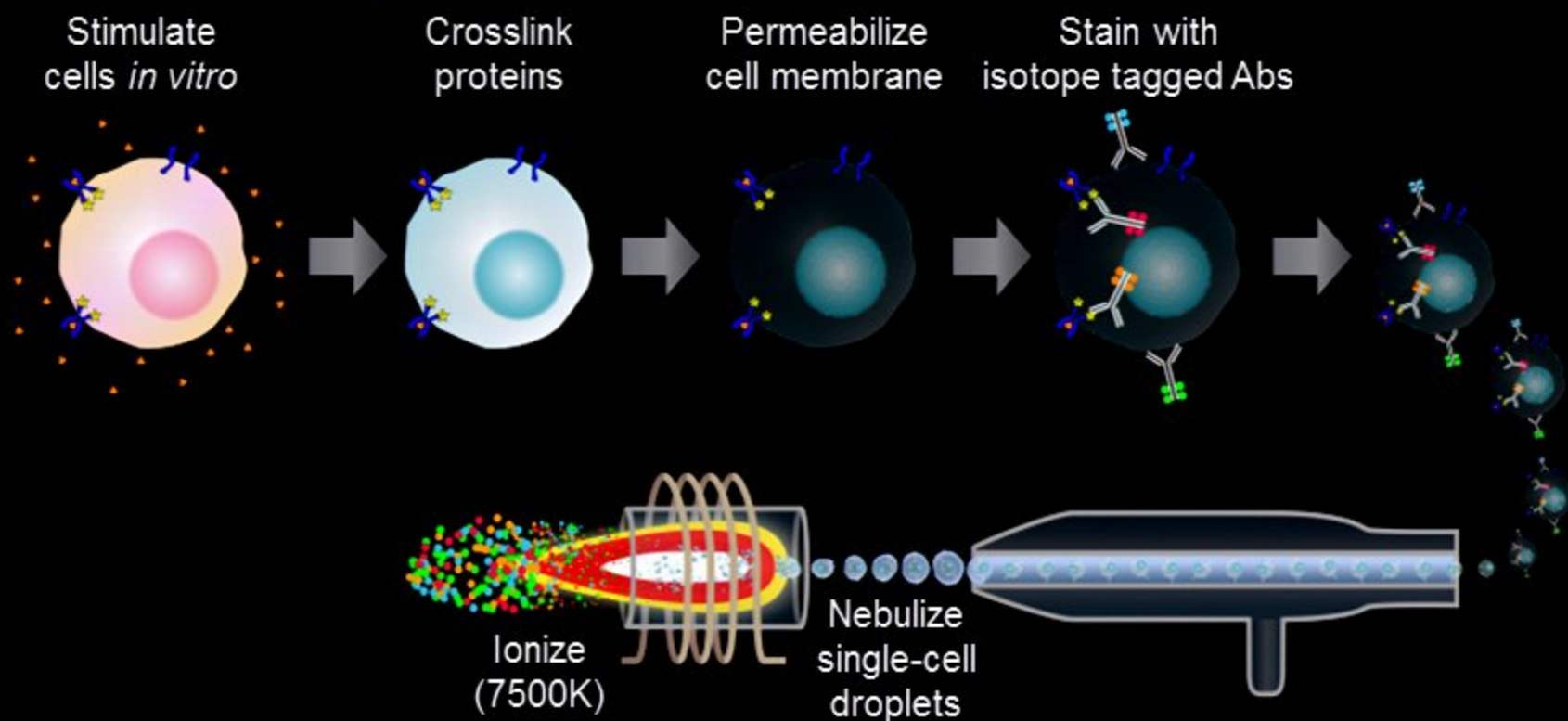
Mass cytometry enables single-cell phosphoproteomics

Simons, D. J., Bendall, S. C., Bratton, R. L., et al. (2011) Single-cell phosphoproteomics by mass cytometry. *Science*, 334(6060), 1235-1240.

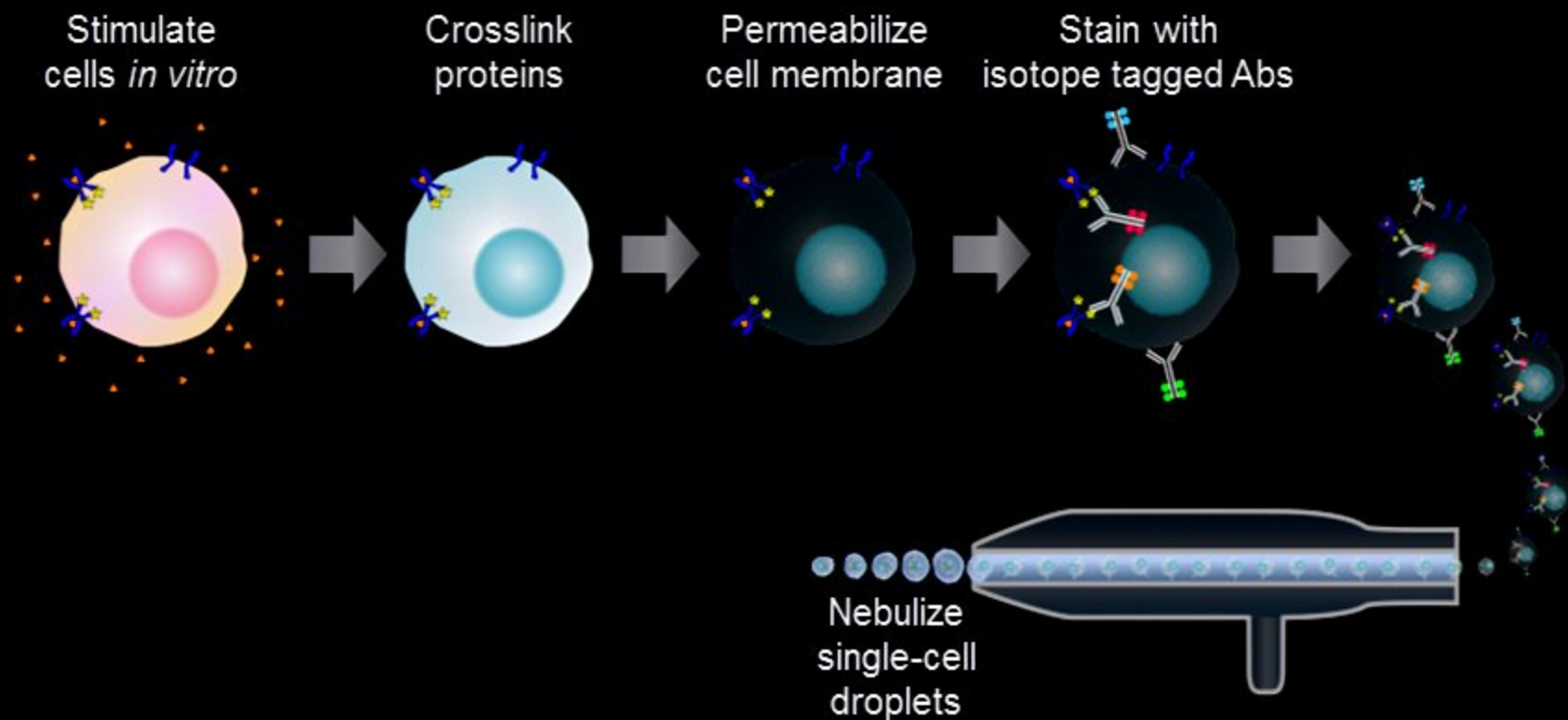


Bendall, Simonds, et al. *Science*, May 2011

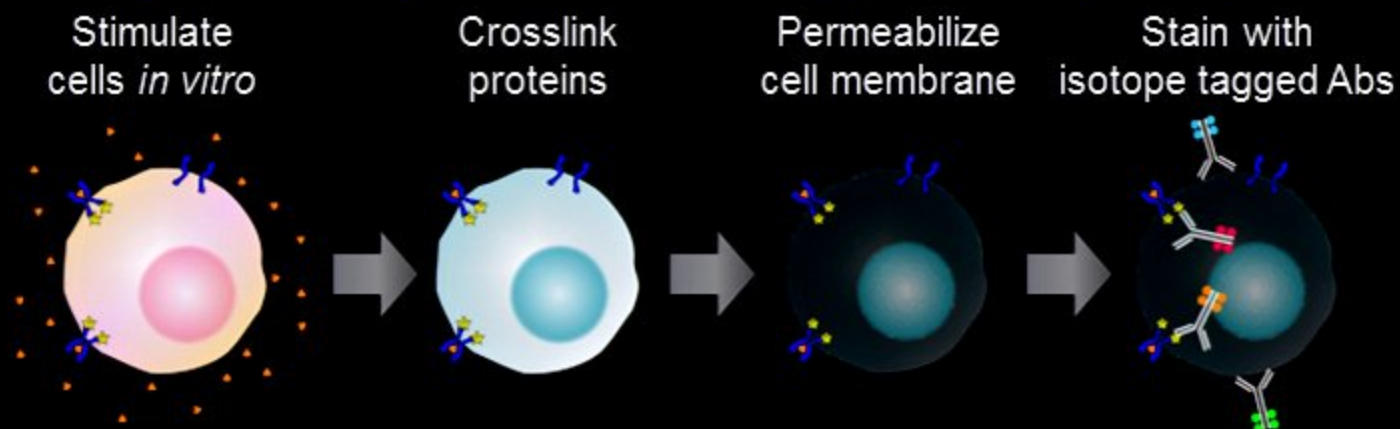
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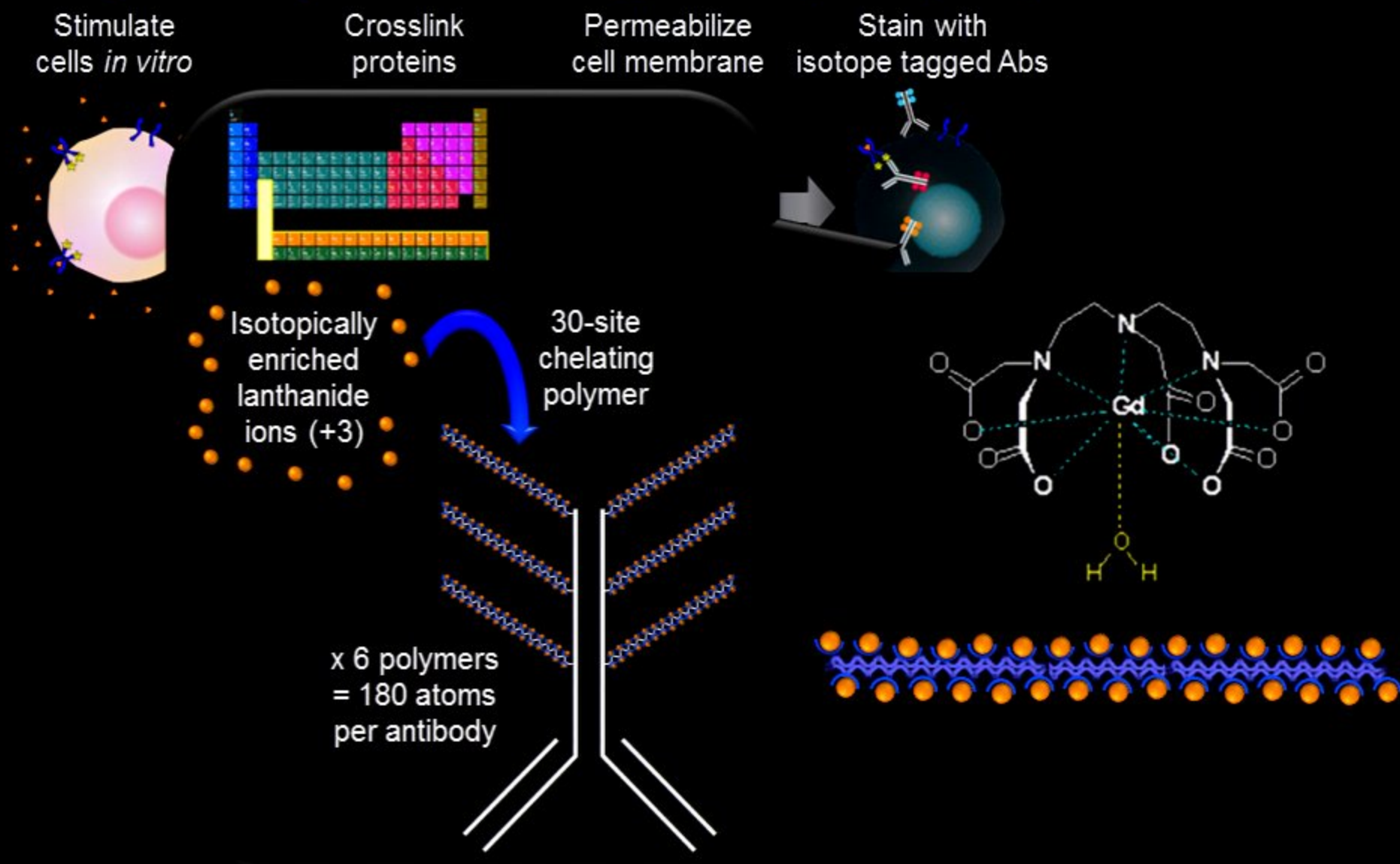
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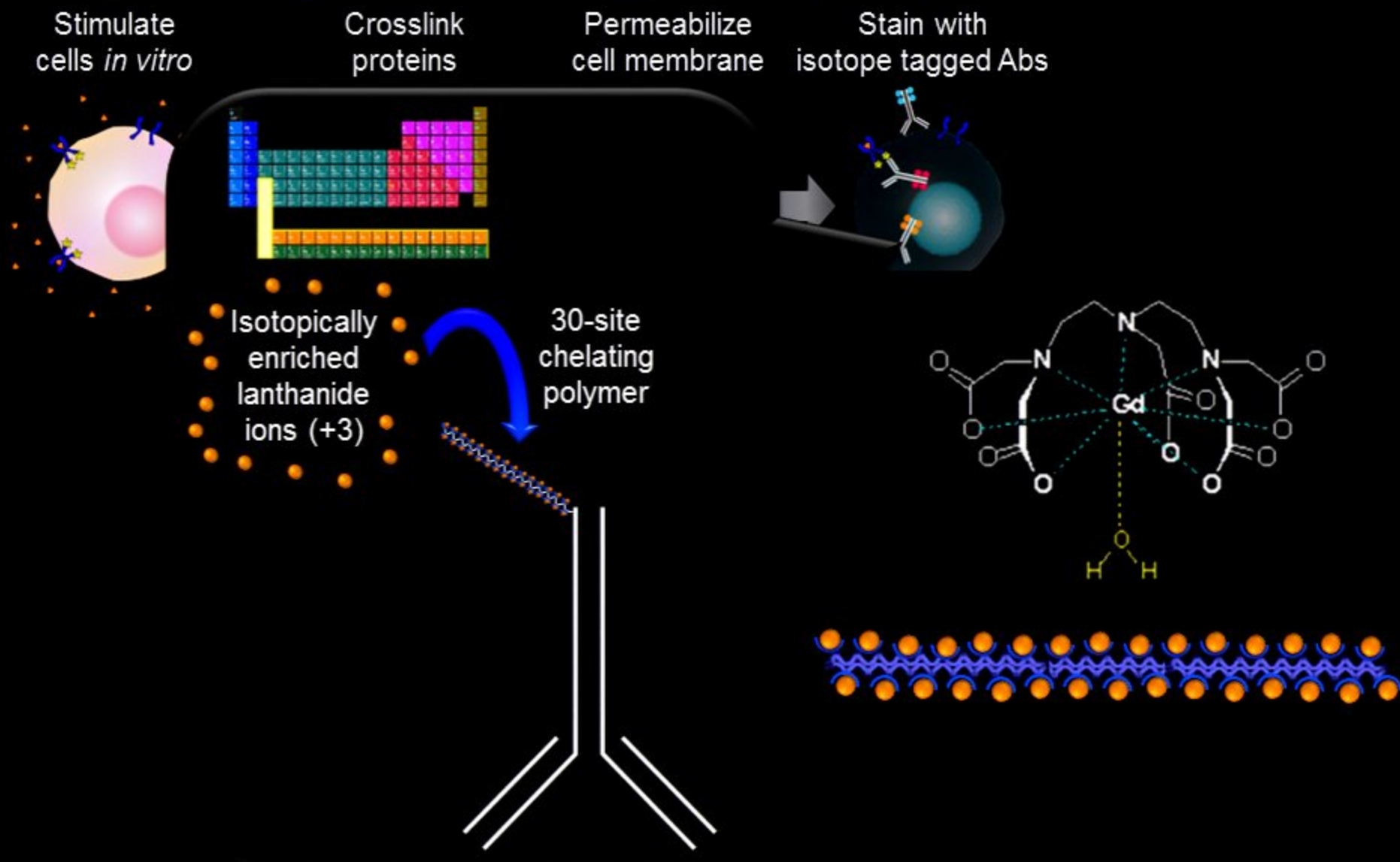
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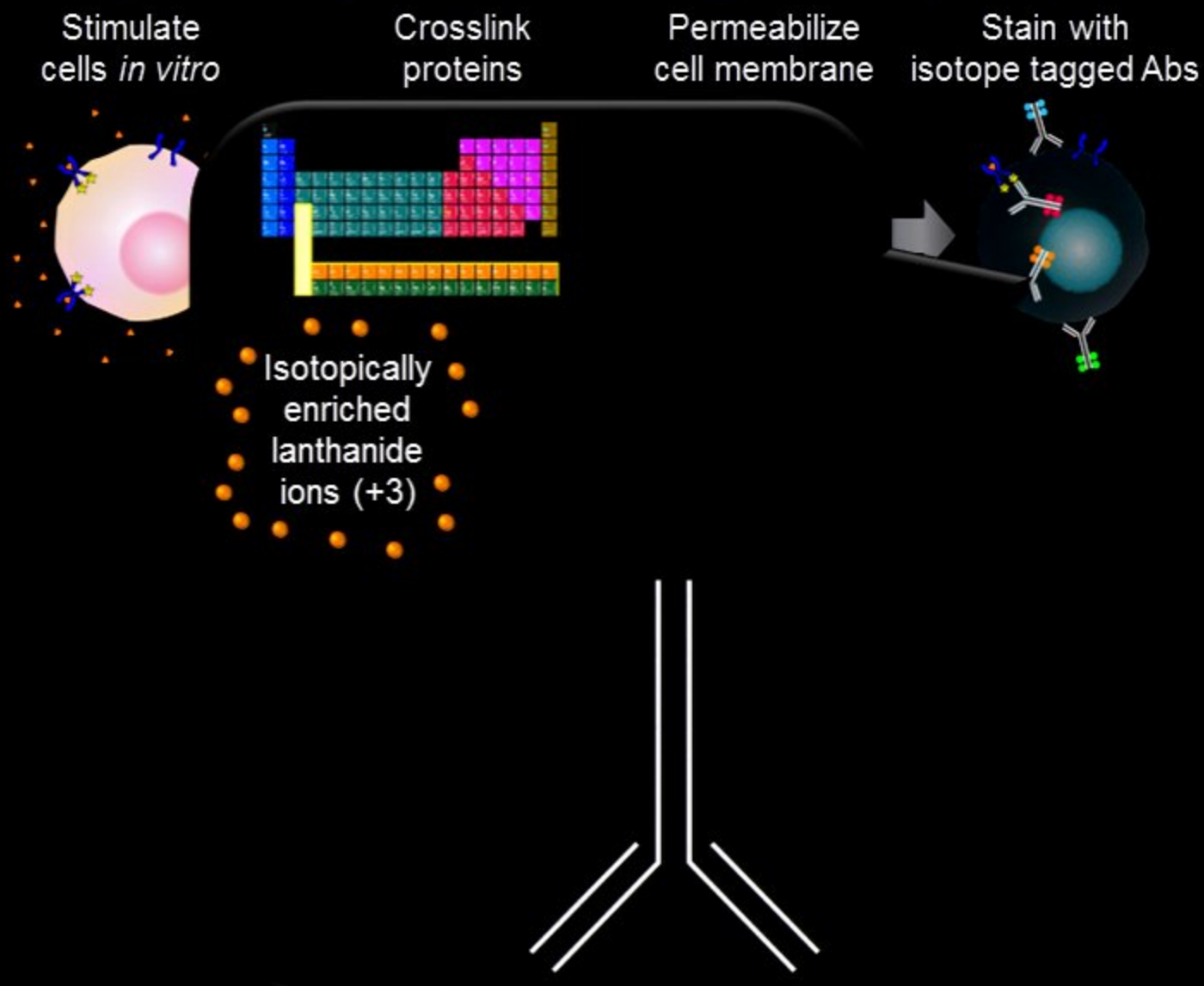
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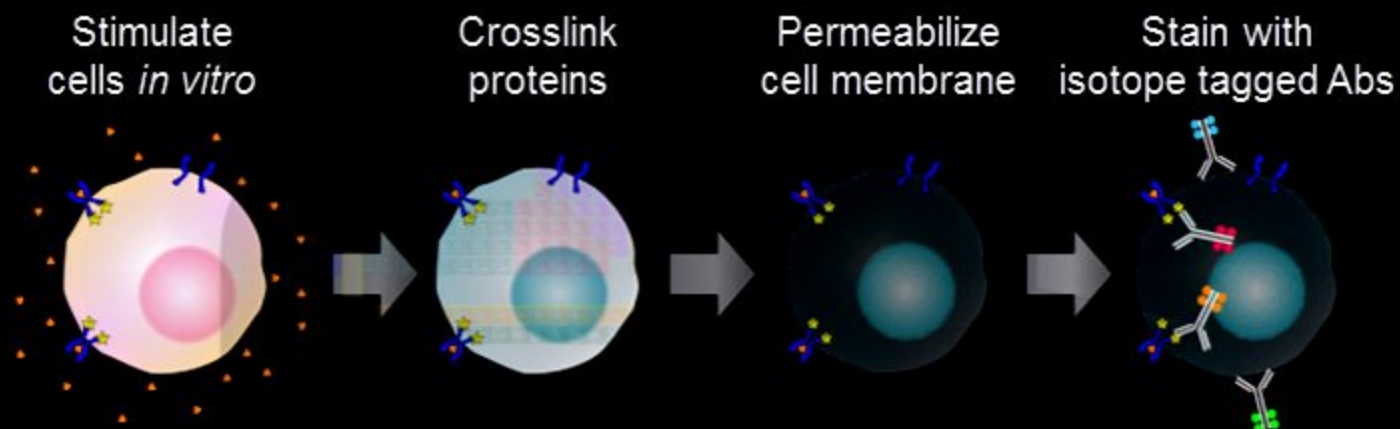
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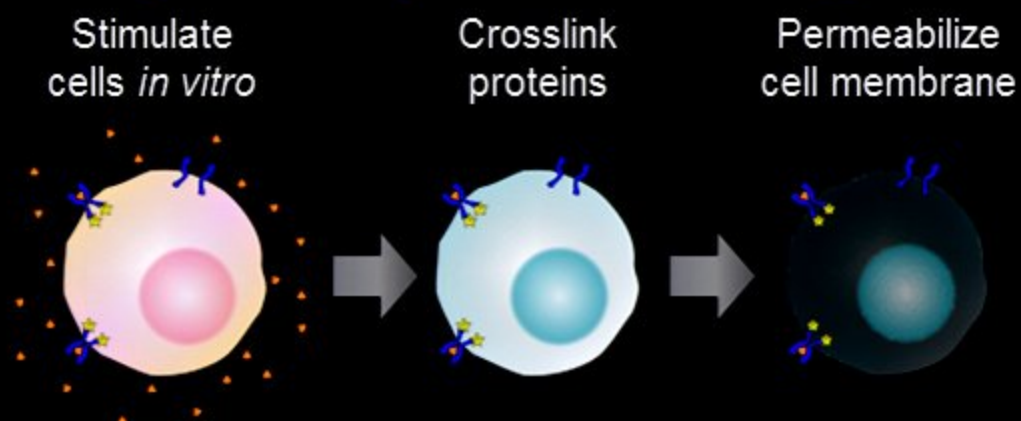
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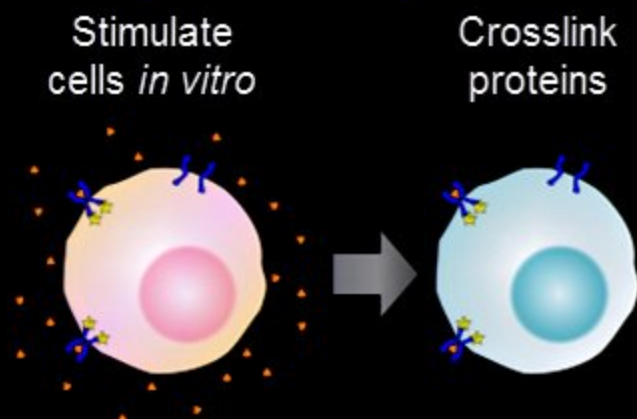
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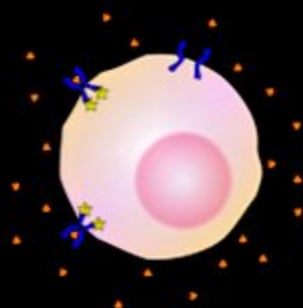


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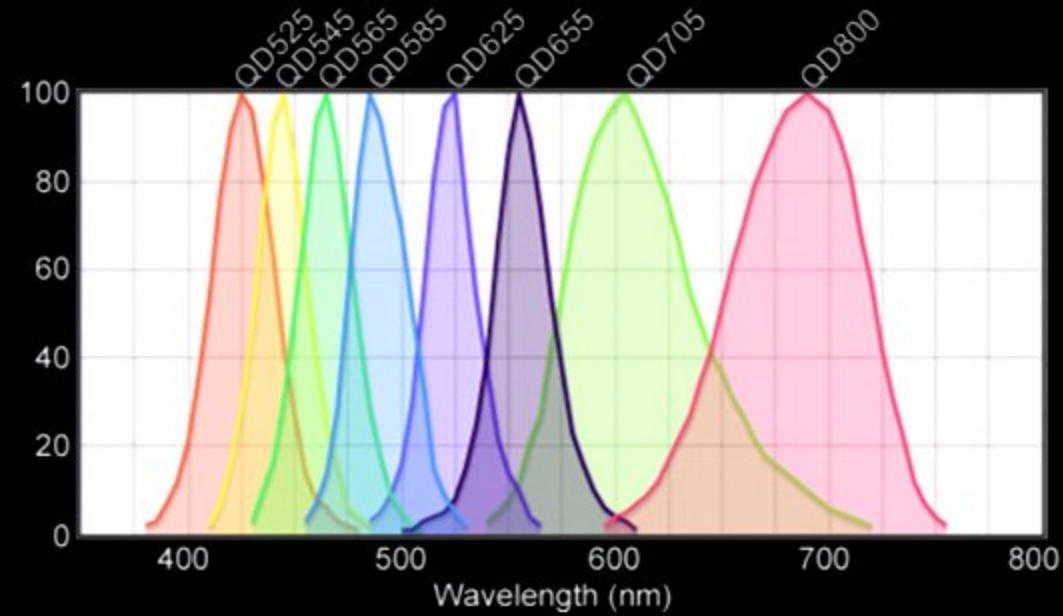
Stimulate
cells *in vitro*



The fluorescence spectrum is crowded

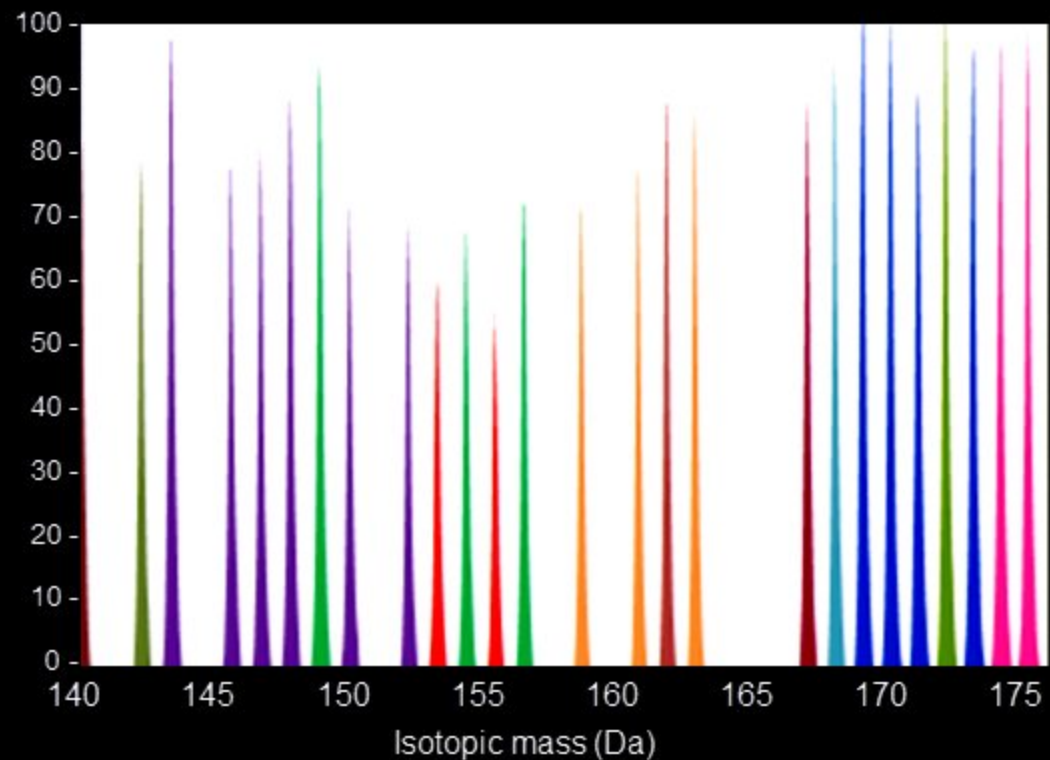
Fluorescent cytometry

- Up to 12 colors can be “routine”
- 17 colors have been reported
- 17? Forgedda bowdid...
- High background



Mass cytometry

- Up to 100 non-biological elemental mass channels
- No compensation required
- No autofluorescence



The fluorescence spectrum is crowded

Fluorescent cytometry

- Up to 12 colors can be “routine”
- 17 colors have been reported
- 17? Forgedda bowdid...
- High background

