

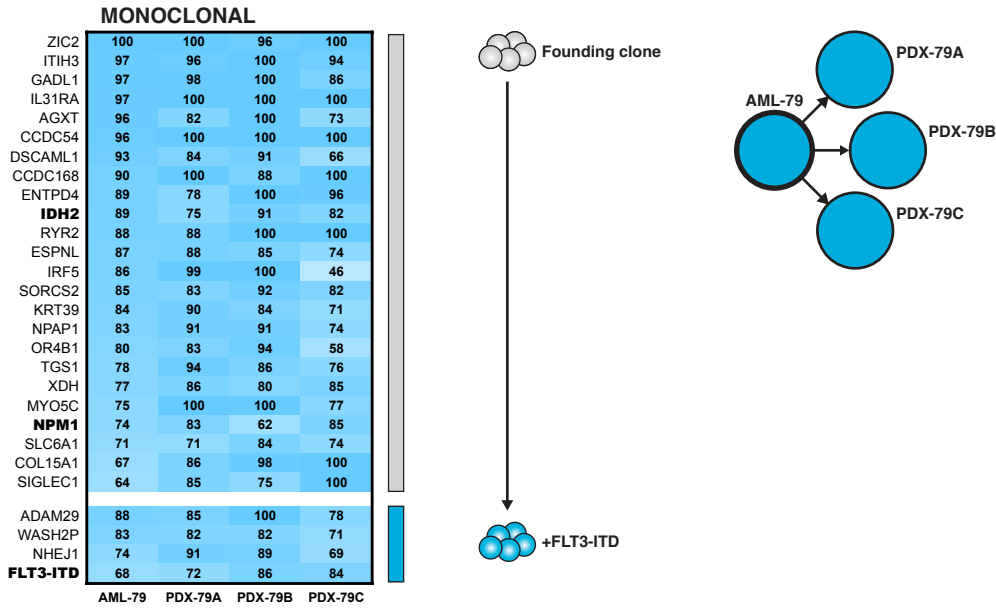
**Supplementary Information**

**Clonal competition within complex evolutionary hierarchies shapes AML over time**

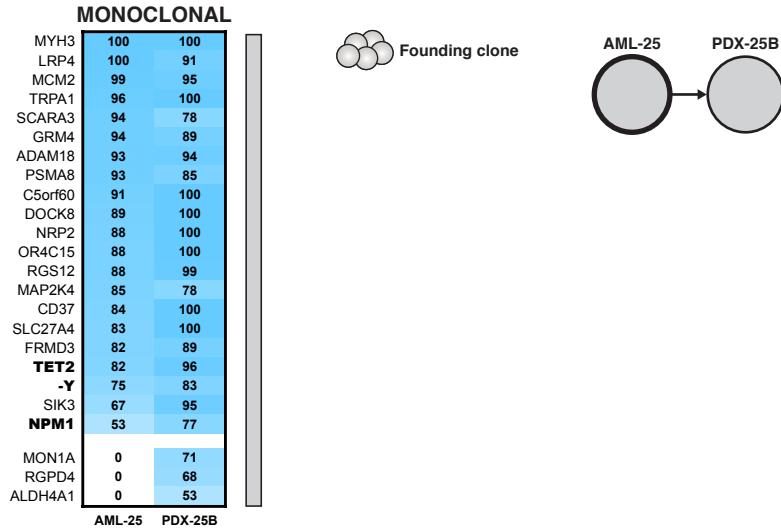
Sandén et al.

# Supplementary Figures

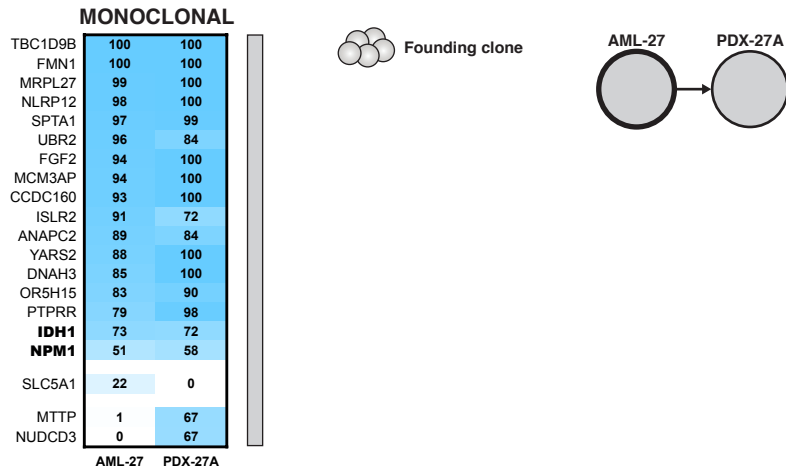
**a**

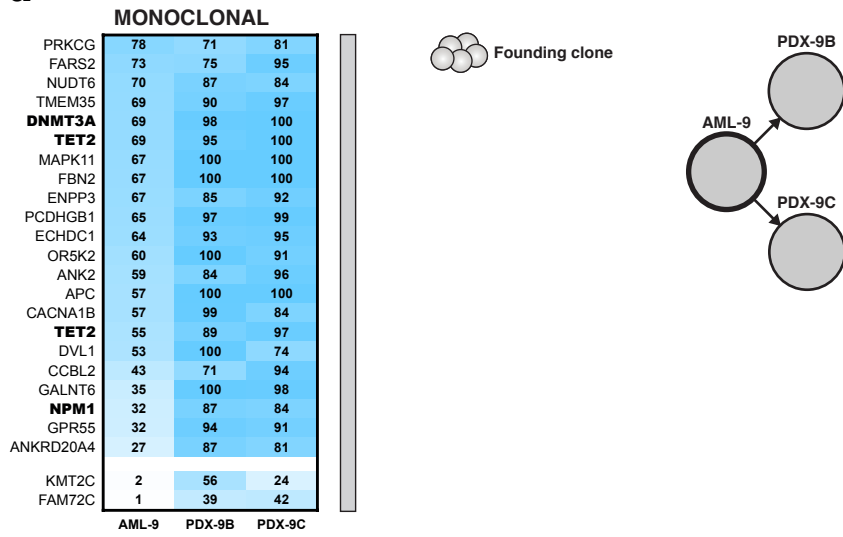


**b**

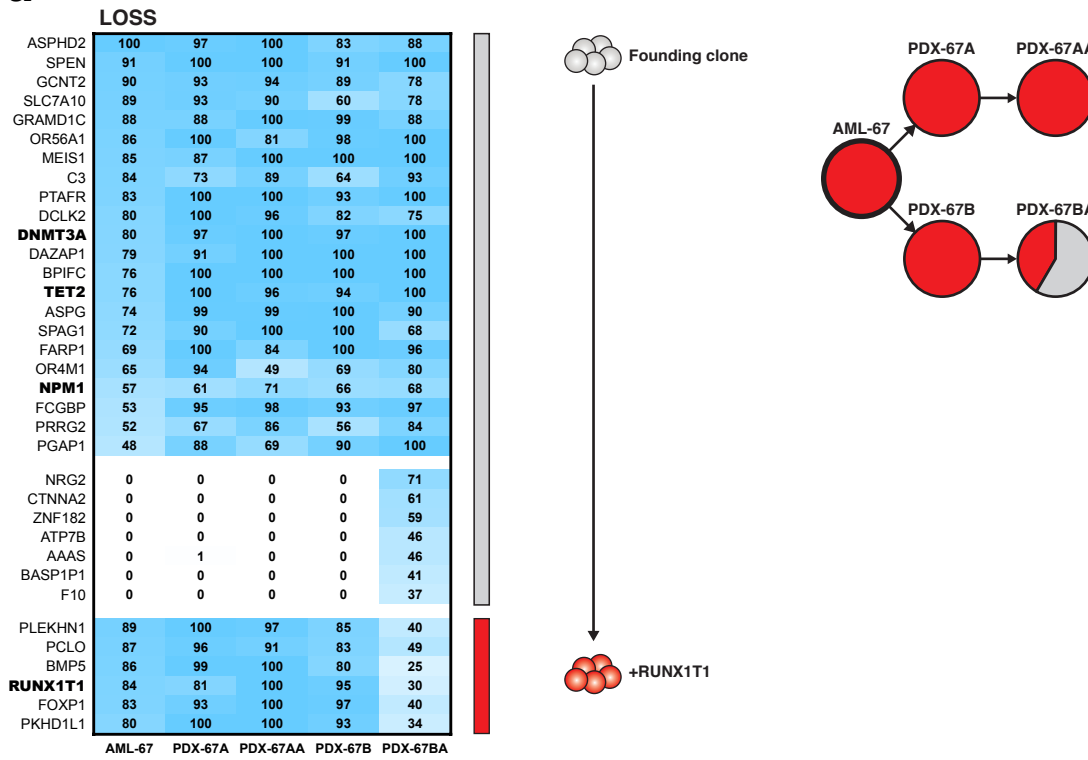
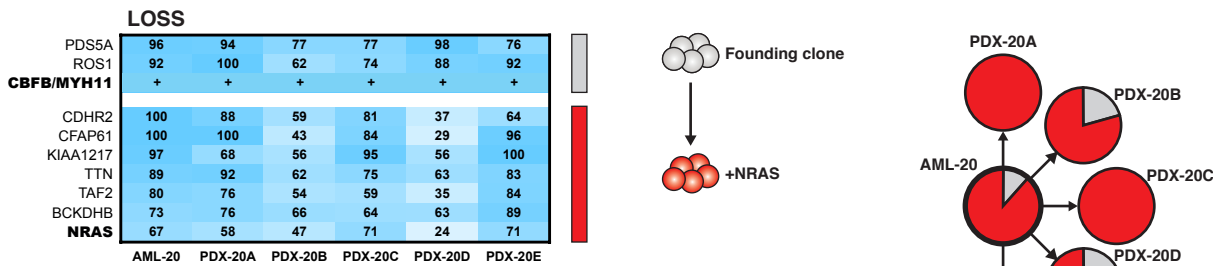
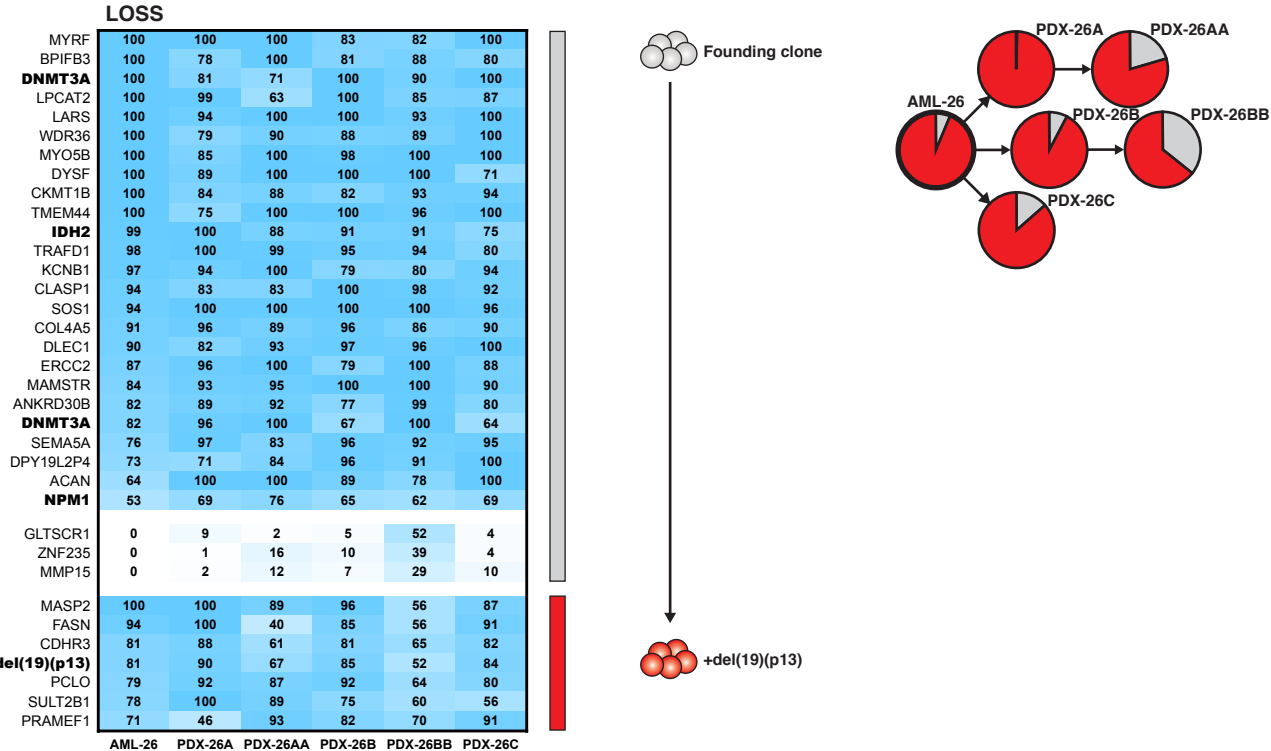


**c**



**d**

**Supplementary Figure 1. Additional xenografts with the Monoclonal pattern.** (a-d) Four additional cases with the Monoclonal pattern of clonal dynamics.

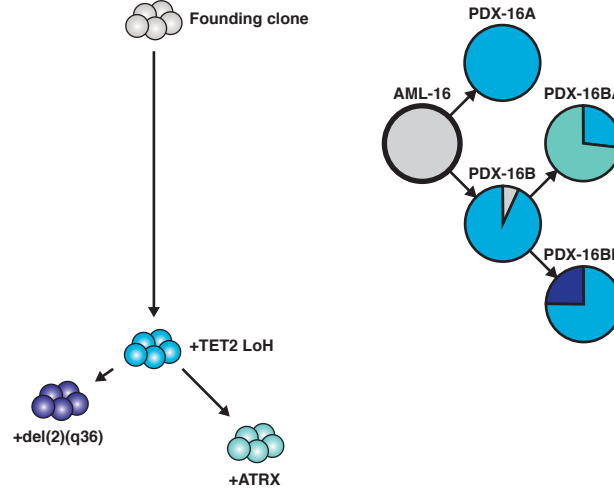
**a****b****c**

**Supplementary Figure 2. Additional xenografts with the Loss pattern. (a-c) Three additional cases with the Loss pattern of clonal dynamics.**

**a**

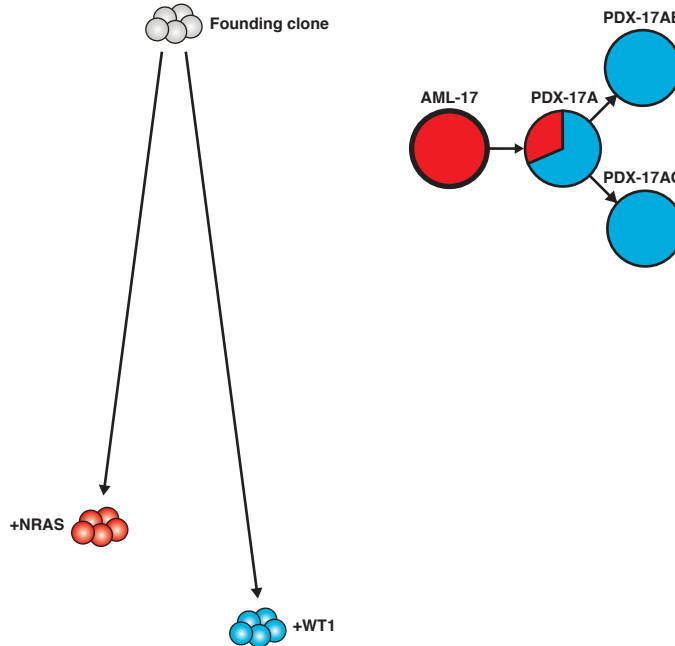
**EXPANSION**

THADA	100	100	100	100	100
MYT1L	100	88	78	100	100
<b>FLT3</b>	98	85	100	93	100
<b>STAG2</b>	93	100	100	100	100
GGT8P	92	78	88	100	90
IGSF9B	92	100	90	84	74
<b>TET2</b>	86	100	93	100	100
EVPL	85	100	92	100	83
MYO3A	85	100	91	70	97
ABC4	80	100	100	79	100
ZFYVE9	79	61	60	83	97
NRP2	67	80	85	100	78
WDR17	58	100	98	99	100
HMCN2	58	94	94	85	88
<b>NPM1</b>	47	47	62	57	63
MANF	21	61	100	98	78
<b>LOH(4)(q21-35)</b>	0	94	92	100	100
PCDHB7	0	0	10	77	15
<b>del(2)(q36)</b>	0	0	0	0	89
SCRN1	0	0	0	74	7
<b>ATRX</b>	0	0	0	72	1

**b**

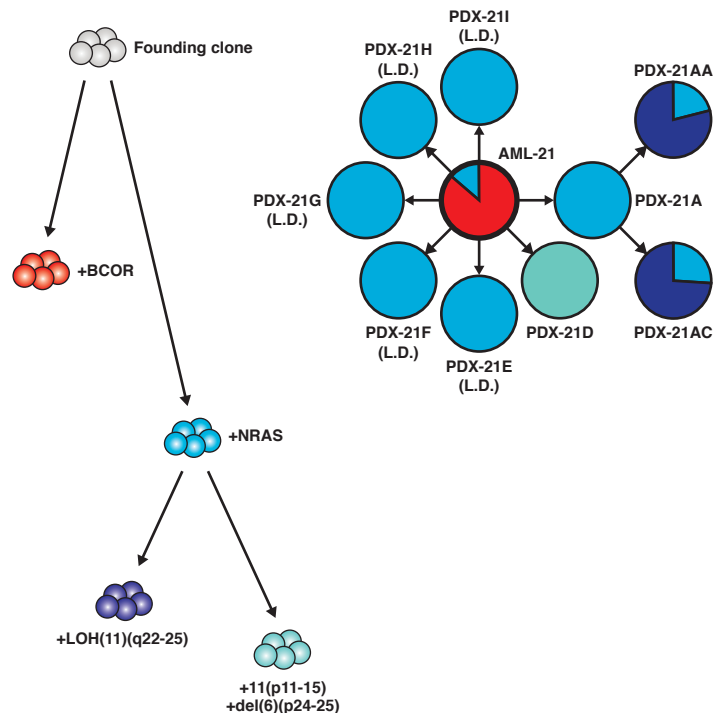
**EXPANSION**

PCDH11Y	86	100	100	100
ACOT1	73	83	97	100
LOC101928697	100	74	100	100
WBSCR17	100	83	100	100
PSMB7	100	71	90	85
ADGRV1	96	99	94	74
MMP16	96	45	52	89
MEGF10	95	91	95	100
<b>DNMT3A</b>	92	100	96	81
KIAA0226	91	97	96	99
FLT3	89	100	100	84
ZNF366	89	79	89	90
DSC3	89	85	99	89
HMCN1	85	90	100	95
PEPD	82	85	100	100
PEX16	81	85	94	100
AKAP13	79	85	63	92
SPTA1	76	69	100	100
EPHA7	73	99	97	83
DNAH3	73	100	100	100
PATL1	70	89	92	100
<b>GATA2</b>	59	64	72	100
NMUR2	51	80	74	99
<b>NPM1</b>	50	58	74	80
KRT28	49	63	100	90
KIAA0922	87	38	1	0
<b>NRAS</b>	82	30	0	0
KIF2B	74	27	0	0
<b>WT1</b>	0	52	88	100
WDR62	1	50	87	99
CCT6B	0	0	100	2
PAPPA	0	0	89	0
PDE2A	0	0	3	96

**c**

**EXPANSION**

EDAR	100	94	100	91	100	92	62	85	92	74
ANXA2P2	100	91	89	100	100	100	100	98	95	89
TTN	100	100	90	92	86	99	95	100	89	94
TUBB3	90	94	96	79	99	100	100	100	100	100
<b>STAG2</b>	89	97	89	95	100	100	94	98	99	98
SH2B3	87	100	86	97	93	99	80	100	88	92
<b>IDH2</b>	84	100	90	99	77	96	96	90	91	86
MPP4	79	86	100	82	100	87	100	92	100	100
HNF1A	77	87	100	90	93	100	100	91	92	100
<b>SRSF2</b>	72	100	87	100	86	NA	NA	100	90	98
SERPINB4	71	100	91	84	100	91	100	95	100	94
TGM4	67	100	78	100	100	101	92	100	95	97
<b>BCOR</b>	78	0	0	0	0	0	0	3	0	0
USP9X	38	0	0	0	0	0	2	0	0	1
SARS	25	100	81	100	84	100	85	100	100	90
GRIA4	18	100	100	91	100	88	99	100	83	82
DRD5	16	87	91	65	67	100	79	85	100	100
MMP13	12	100	77	90	91	91	81	88	100	93
<b>NRAS</b>	6	94	94	98	89	89	74	79	80	100
TGFBR3	4	75	80	84	72	73	54	100	72	95
PROX1	4	97	91	100	99	100	98	86	93	71
TANGO6	4	69	32	57	36	84	57	74	95	65
DNM3	0	0	0	0	0	0	80	0	1	0
NOTCH3	0	0	0	0	0	0	3	74	0	0
DHRS7C	0	0	0	0	0	0	0	0	41	0
ZNF322	0	0	0	0	0	0	0	0	31	0
SMG1	4	0	0	0	3	1	0	2	1	84
<b>LOH(11)(q22-25)</b>	0	0	79	74	0	0	0	0	0	0
<b>+11(p11-15)</b>	0	0	0	0	96	0	0	0	0	0
<b>del(6)(p24-25)</b>	0	0	0	0	67	0	0	0	0	0
ORTD4	0	0	0	0	54	0	0	0	0	0

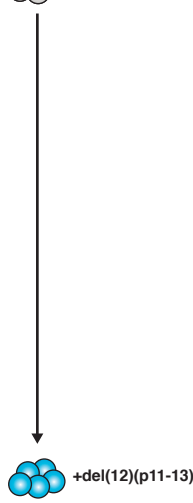


**d****EXPANSION**

ANKRD44	92	96	100	100
ZNF45	78	99	75	99
AKAP8	75	78	76	94
MIR5684	75	67	94	88
LHFPL3	74	75	100	100
XDH	73	100	77	92
TDRD5	65	100	100	95
APLN	64	100	100	97
<b>IDH1</b>	62	66	91	83
ACE	62	100	100	100
TJP1	61	83	100	94
SSPO	59	68	87	59
COL6A3	56	82	100	82
SLC35E3	56	63	92	100
KCNH1	54	99	75	81
CRELD2	54	100	100	100
CNTNAP5	54	98	97	93
CHD9	53	88	100	90
SCAMP2	53	75	80	100
TUSC3	50	100	100	80
STX11	41	0	0	0
<b>del(12)(p11-13)</b>	9	92	100	100
DIP2B	8	79	100	86
CTNNA2	5	100	53	100
NUPR1L	2	59	84	78
RPL5	0	28	92	100
SOST	0	0	62	0
ZNF503-AS2	0	0	0	88

AML-74 PDX-74A PDX-74AA PDX-74AB

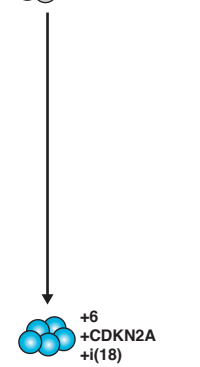
Founding clone

**e****EXPANSION**

CCDC26	80	100	99	100
<b>TP53</b>	76	100	95	97
DNTTIP1	67	100	97	89
IL12A-AS1	66	100	100	95
SPR	66	100	100	100
SLC25A26	63	69	100	86
DRD2	62	100	95	76
SPG20	60	88	94	79
ERBB4	60	100	94	100
<b>i(22)</b>	60	100	98	100
<b>i(8)</b>	59	94	90	97
SEC61B	58	93	94	85
CRAMP1L	58	96	92	90
KIF21A	56	97	99	86
<b>FLT3</b>	55	101	96	88
<b>LOH(17)(p12-13)</b>	51	100	99	96
CNGB1	35	89	92	72
<b>+6</b>	17	76	76	100
<b>CDKN2A</b>	16	71	55	73
<b>i(18)</b>	7	49	52	90

AML-37 PDX-37C PDX-37D PDX-37E

Founding clone

**f****EXPANSION**

SPTBN2	98	100	100	100	78
MRPL52	96	100	100	82	100
ANAPC2	96	100	79	100	73
ZNF644	91	100	100	100	100
NPHP4	90	100	98	100	88
ADGRV1	90	100	94	100	88
BMPR1A	89	85	95	94	89
EPHA3	87	97	100	92	100
<b>IDH1</b>	87	86	53	100	70
PKD1L2	87	90	96	100	89
C15orf41	85	62	80	83	100
CLSTN3	84	75	100	82	100
MGAM	80	100	72	95	100
TYRO3	78	100	100	100	100
SLC6A19	77	94	91	100	84
<b>DNMT3A</b>	77	95	99	100	100
TTYH1	77	100	98	100	100
TTN	76	79	19	78	48
IARS	74	85	93	100	100
LMAN1	52	74	24	78	43
<b>NPM1</b>	49	74	34	68	51
<b>FLT3-ITD</b>	+	+	+	+	+
<b>LOH(13)</b>	35	96	97	96	100
ZNF845	4	1	49	0	35
TFAM	0	0	48	0	50
PLBD1	0	3	64	0	14
MAGEA4	0	0	56	0	24

AML-33 PDX-33B PDX-33BA PDX-33C PDX-33CA

Founding clone



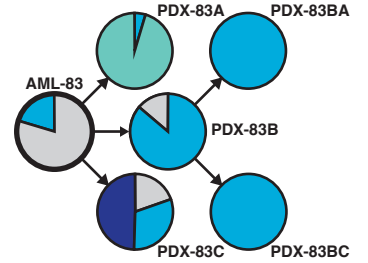
**g**

**EXPANSION**

MCM4	100	100	96	100	81	100
CPNE4	100	100	100	91	100	100
PTPRB	100	100	100	100	100	99
GOT2	97	58	53	77	90	100
OSBPL8	97	100	100	97	100	100
RIMS2	95	92	100	100	90	94
KIF14	94	100	85	100	100	95
ITGBL1	92	80	81	100	100	88
<b>+11(q23-25)</b>	92	100	100	100	100	100
RNF217-AS1	91	89	82	100	82	84
CODC67	89	95	76	65	70	100
SNORD80	88	78	97	100	100	100
<b>TP53</b>	88	98	100	100	97	100
IMPG2	87	86	100	92	100	110
<b>NF1</b>	87	100	100	97	99	98
SURF1	86	78	100	100	82	100
HAL	84	93	91	100	99	94
MYO6	84	100	98	95	99	100
SNAP91	83	50	87	100	89	100
<b>-5q</b>	83	100	100	100	100	100
<b>del(10)(p13-15)</b>	83	100	100	100	100	100
<b>del(20)(q12-13)</b>	83	100	100	100	100	100
<b>-16p</b>	83	100	100	100	100	100
ERBB3	82	100	100	92	99	100
<b>LOH(17)</b>	82	100	100	100	100	100
PRPF8	82	97	100	95	100	98
UNC5A	81	100	100	100	100	100
CLTCL1	80	98	97	83	85	100
<b>TET2</b>	80	75	92	78	76	87
<b>del(9)(p23-q22)</b>	79	100	100	100	100	100
FBN2	79	98	97	100	100	99
SEP15	79	100	100	100	100	100
<b>-7q</b>	78	96	95	96	97	95
C19orf80	77	65	100	83	100	100
PPFIA2	76	97	100	100	100	100
DSG1	76	100	100	93	91	100
MIA-RAB4B	75	95	80	88	96	94
SPATA5	74	84	99	65	100	98
APOB	73	77	87	100	85	84
FGF20	66	99	94	99	90	100
<b>del(10)(p11-12)</b>	64	100	100	100	100	100
FAM208B	63	100	100	100	100	98
ARHGEF33	63	65	100	81	79	68
ERBB2IP	58	85	86	90	76	89
SULT1B1	50	61	100	100	90	100
C2orf71	50	80	92	60	74	57
A1CF	79	0	55	0	0	72
HTN1	1	0	21	0	0	52
MVK	0	0	12	0	0	65
<b>del(13)(q13-31)</b>	0	0	0	0	0	41
<b>del(14)(q12-31)</b>	0	0	0	0	0	39
<b>del(10)(q11-21)</b>	17	73	65	97	98	32
CTNBN1	33	99	39	0	0	23
FMN2	25	79	30	0	3	22
NFATC4	18	100	51	0	0	22
GNAI2	7	83	19	0	0	11
MYH1	5	92	12	0	0	19
ZNF385D	4	100	16	3	4	27
DSP	3	100	30	0	0	13
CDH6	3	89	58	4	0	14
PLCE1	0	29	0	0	1	0
WDR33	31	0	65	100	98	25
CHD4	10	0	41	93	80	14
KIF5B	5	0	47	78	96	18
HJURP	2	0	73	30	90	6
LOC644145	0	0	66	54	100	0
NDUFS5	0	0	3	65	5	0
<b>del(10)(q21-23)</b>	0	86	0	0	0	0
PSIP1	0	22	0	0	0	0

AML-83 PDX-83A PDX-83B PDX-83BA PDX-83BC PDX-83C

Founding clone



+del(13)(q13-31)

+del(10)(q11-21)

+del(10)(q21-23)

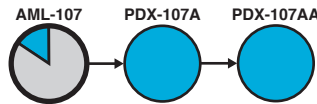
**h**

**EXPANSION**

SCAF8	51	100	77
NECAB1	49	83	100
ADCY2	49	100	100
<b>del(7)(q33-35)</b>	45	100	100
<b>-5q</b>	42	100	100
<b>+11(q22-25)</b>	42	100	100
<b>-17(p12-13)</b>	41	100	100
ODF2	38	82	96
<b>TP53</b>	37	96	94
<b>-12(p12-13)</b>	37	100	100
BPIFB2	37	71	96
ZCCHC12	36	79	88
NAPB	34	100	77
TBX22	30	70	82
SALL3	27	100	100
DIAPH3	25	100	100
<b>-15q</b>	21	100	100
TYR	30	1	1
PHF3	10	96	73
<b>CBL</b>	7	100	100
CTSS	1	100	88
<b>-19(p12-q13)</b>	0	100	100
PCDH17	0	98	37
SLC24A1	0	75	39
TPTE	1	31	28

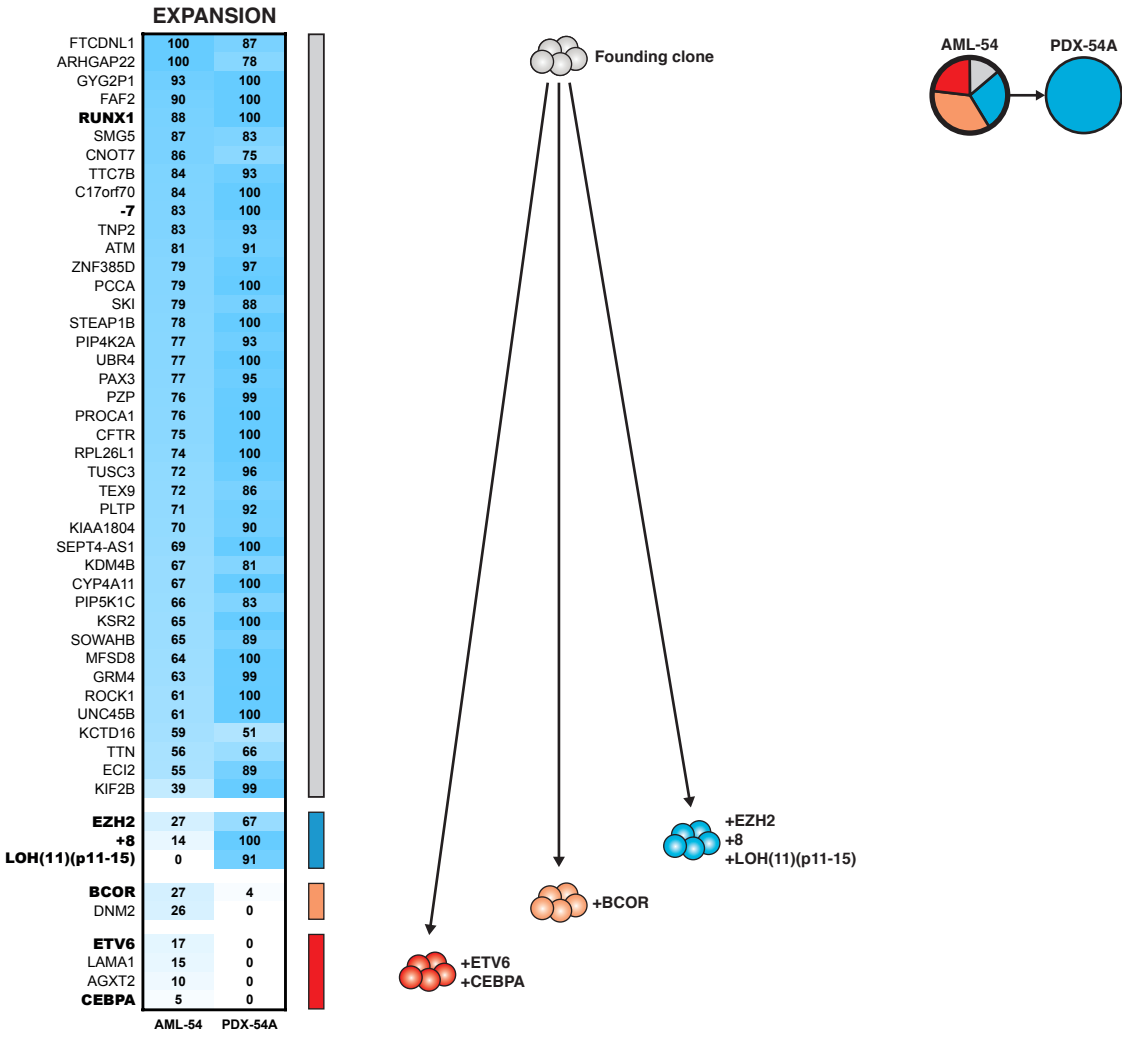
AML-107 PDX-107A PDX-107AA

Founding clone

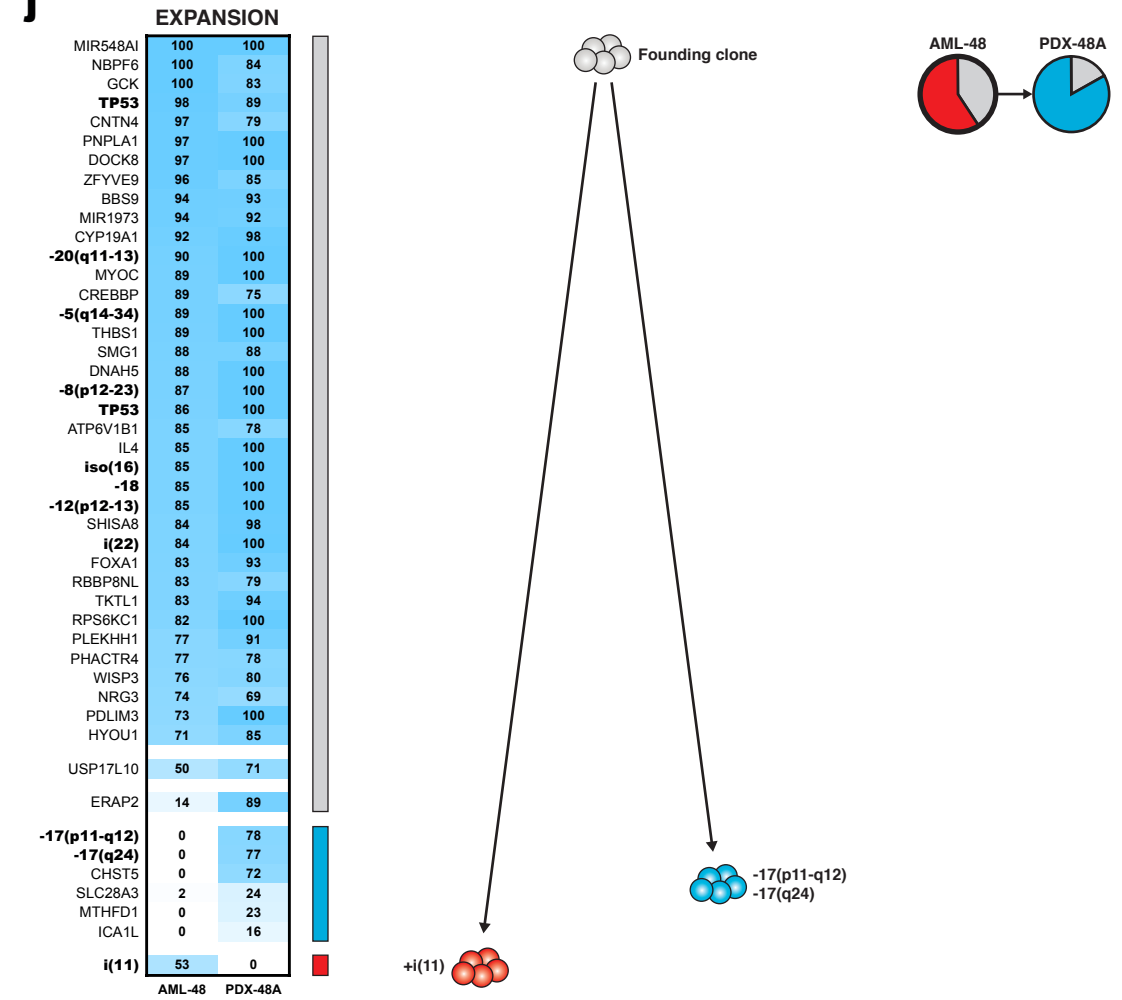


+CBL  
-19(p12-q13)

**i**

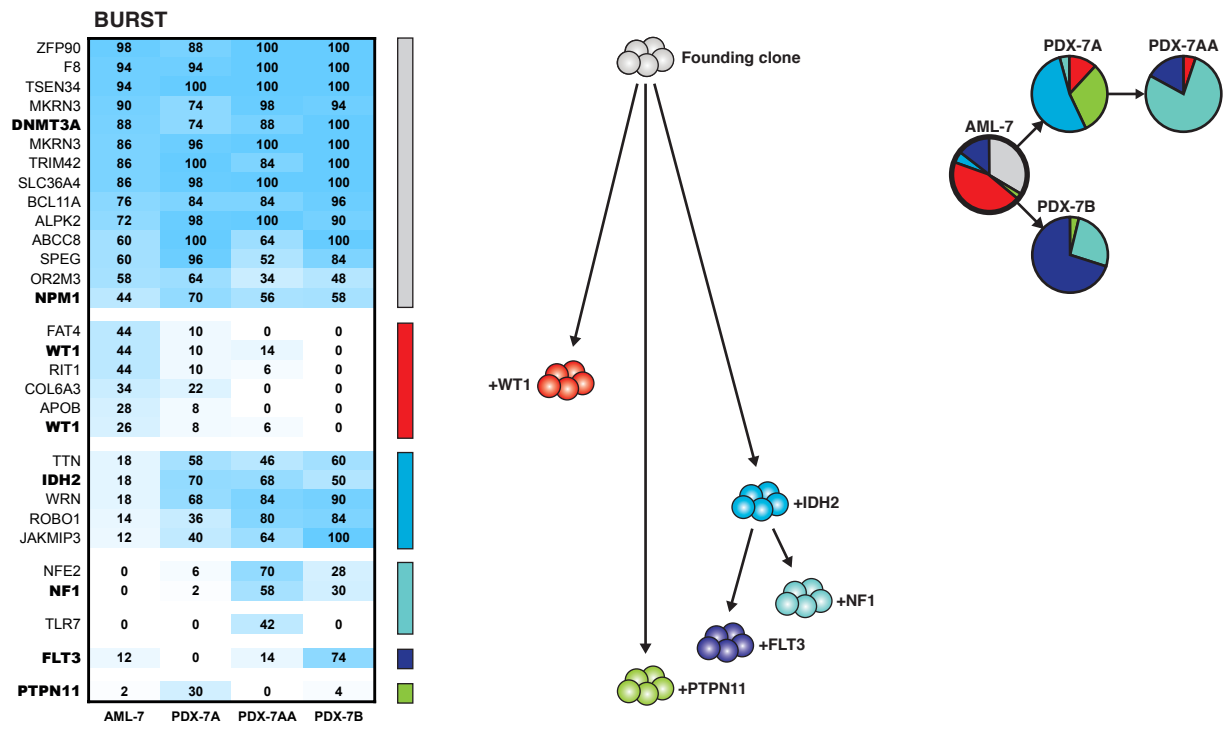


**j**

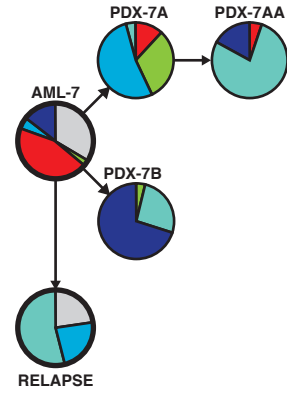
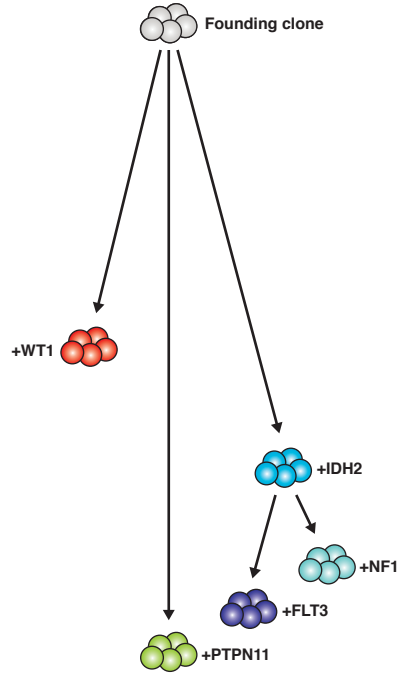
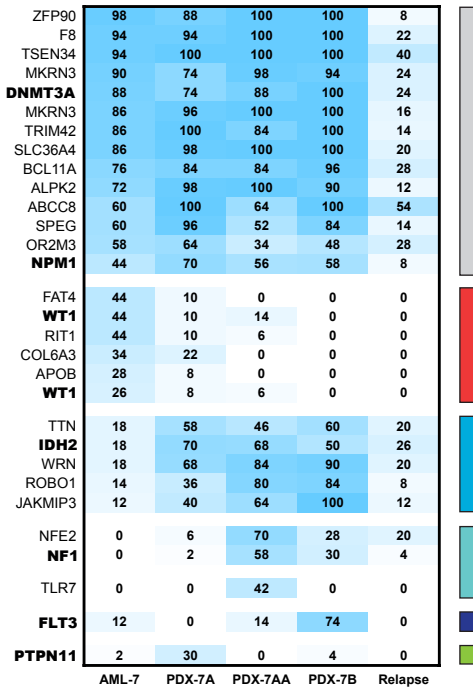
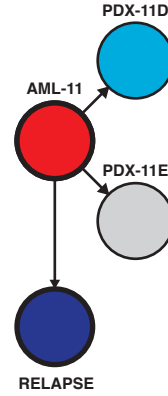
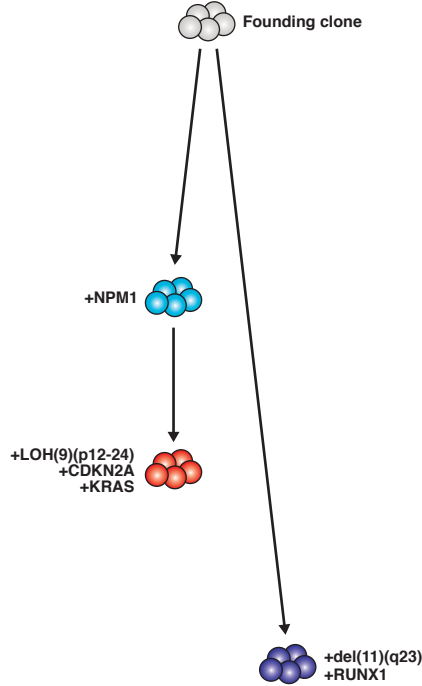
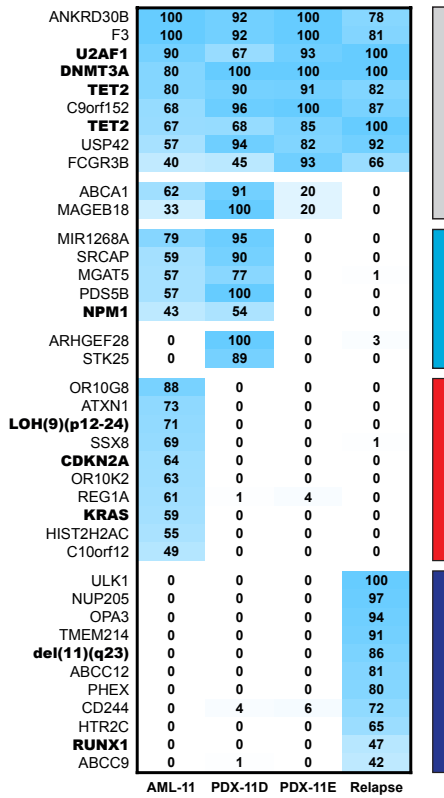
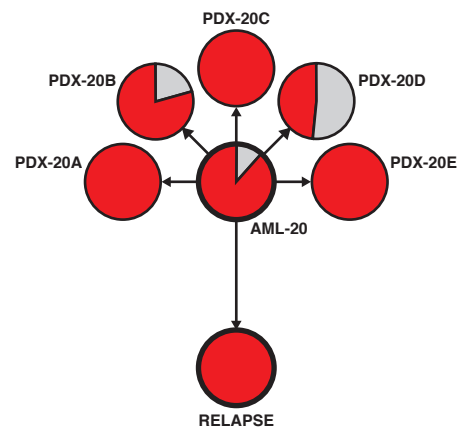
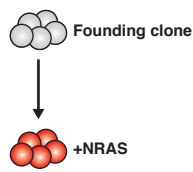
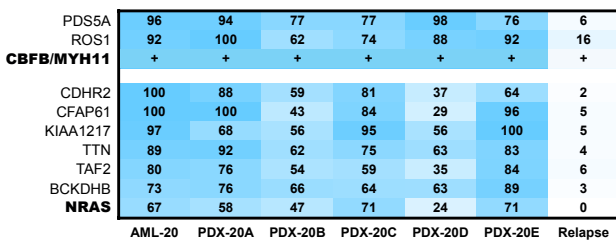


**Supplementary Figure 3. Additional xenografts with the Expansion pattern. (a-j) Ten additional cases with the Expansion pattern of clonal dynamics.**

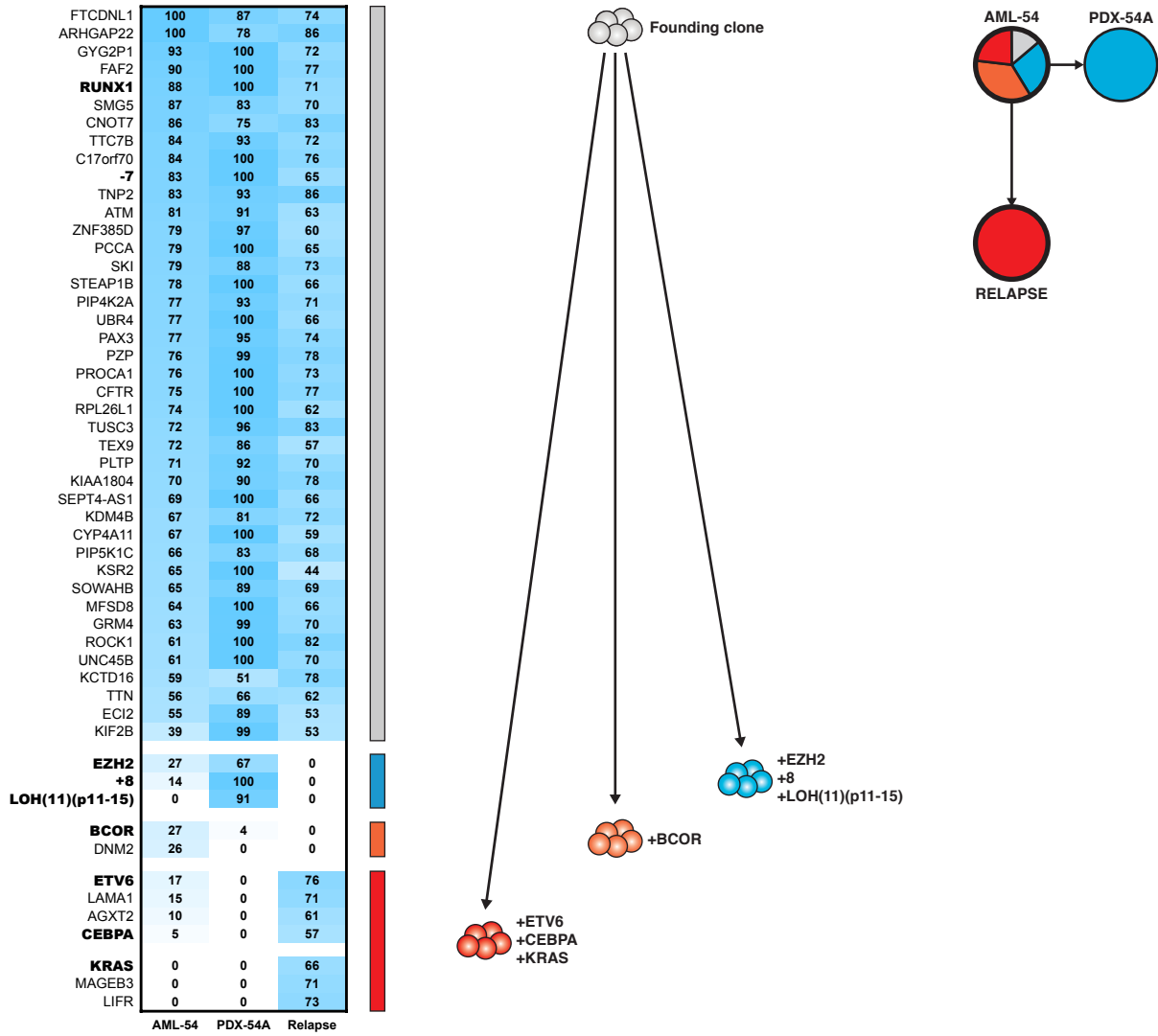




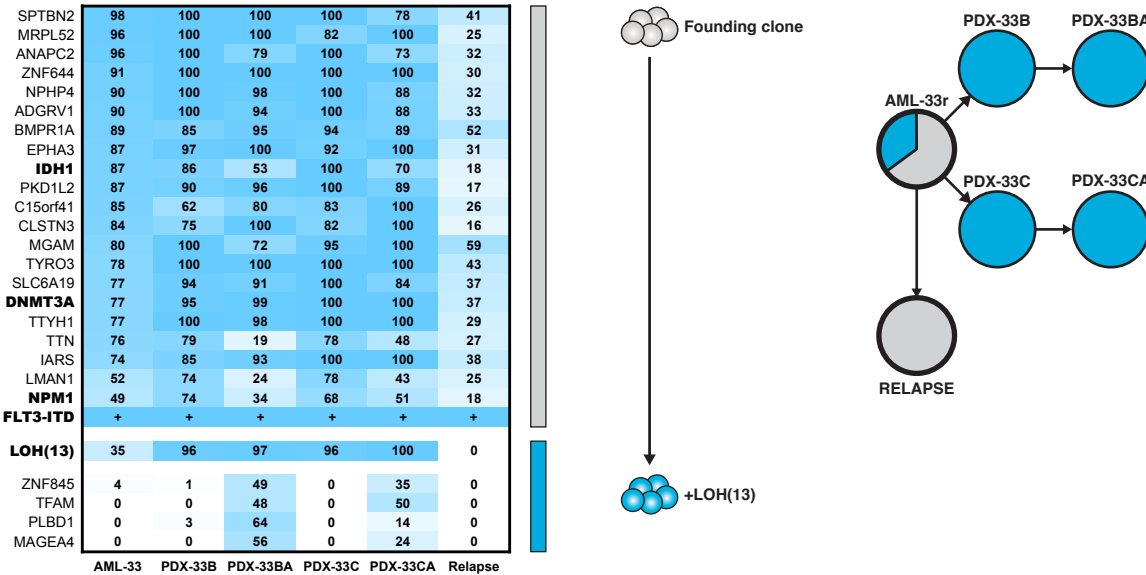
**Supplementary Figure 4. Additional xenografts with the Burst pattern.** One additional case with the Burst pattern of clonal dynamics.

**a****b****c**

**d**

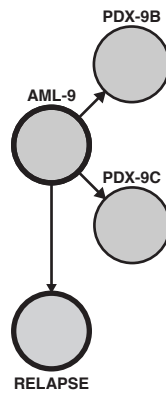


**e**



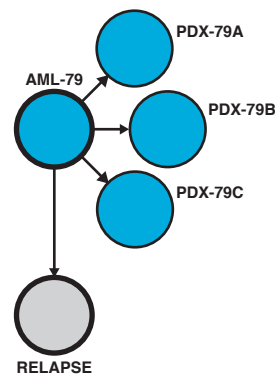
f

PRKCG	78	71	81	78
FARS2	73	75	95	59
NUDT6	70	87	84	75
TMEM35	69	90	97	75
<b>DNMT3A</b>	69	98	100	81
<b>TET2</b>	69	95	100	74
MAPK11	67	100	100	73
FBN2	67	100	100	77
ENPP3	67	85	92	76
PCDHGB1	65	97	99	73
ECHDC1	64	93	95	74
OR5K2	60	100	91	68
ANK2	59	84	96	63
APC	57	100	100	80
CACNA1B	57	99	84	73
<b>TET2</b>	55	89	97	58
DVL1	53	100	74	62
CCBL2	43	71	94	65
GALNT6	35	100	98	69
<b>NPM1</b>	32	87	84	44
GPR55	32	94	91	74
ANKRD20A4	27	87	81	34
KMT2C	2	56	24	8
FAM72C	1	39	42	14
PLEKHG4B	0	0	0	89
GSAP	0	0	0	68
PLEC	0	0	0	62

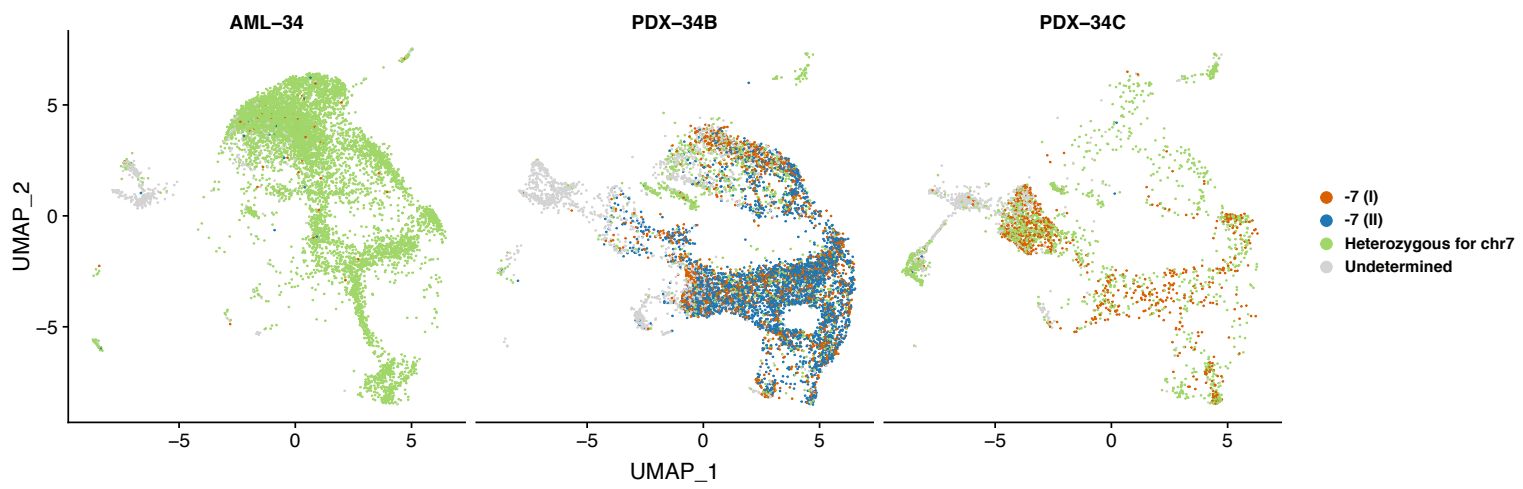
 Founding clone


g

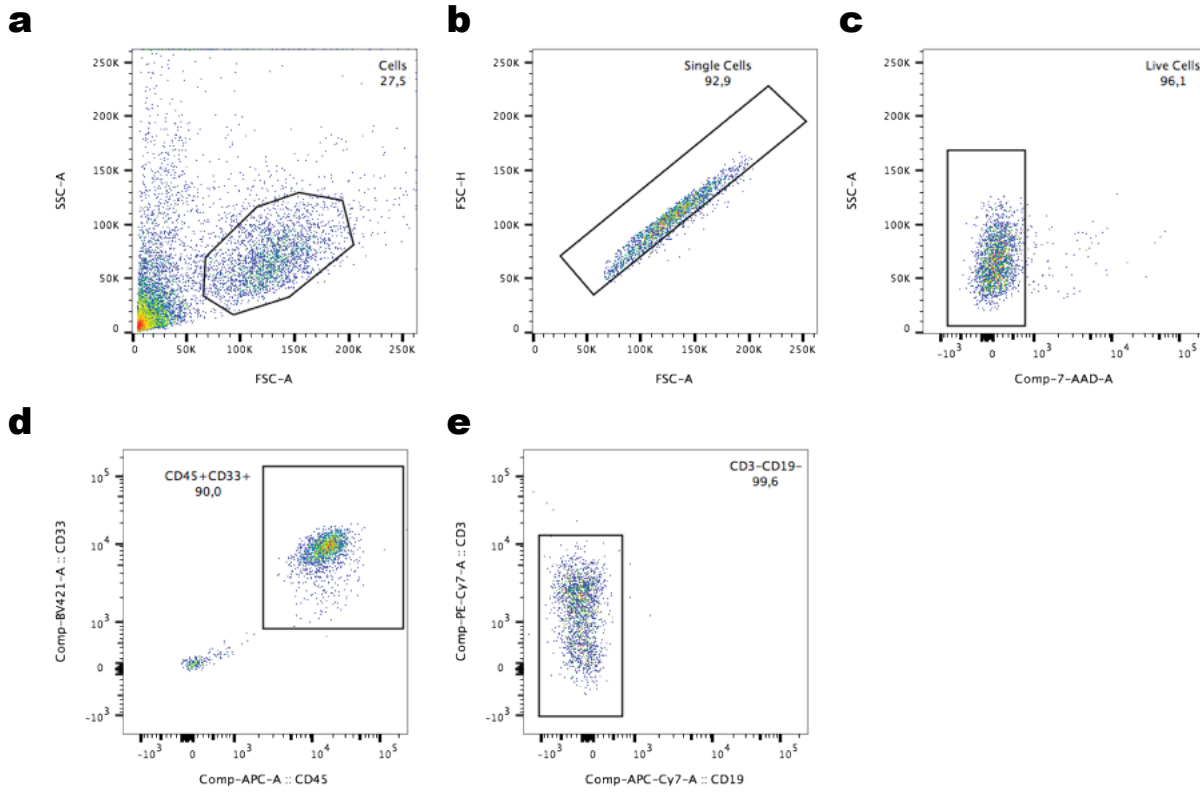
ZIC2	100	100	96	100	44
ITIH3	97	96	100	94	15
GADL1	97	98	100	86	40
IL31RA	97	100	100	100	24
AGXT	96	82	100	73	38
CCDC54	96	100	100	100	31
DSCAML1	93	84	91	66	36
CCDC168	90	100	88	100	36
ENTPD4	89	78	100	96	40
<b>IDH2</b>	89	75	91	82	36
RYR2	88	88	100	100	42
ESPNL	87	88	85	74	26
IRF5	86	99	100	46	33
SORCS2	85	83	92	82	33
KRT39	84	90	84	71	32
NPAP1	83	91	91	74	35
OR4B1	80	83	94	58	34
TGS1	78	94	86	76	19
XDH	77	86	80	85	30
MYO5C	75	100	100	77	25
<b>NPM1</b>	74	83	62	85	18
SLC6A1	71	71	84	74	27
COL15A1	67	86	98	100	25
SIGLEC1	64	85	75	100	32
C14orf180	1	0	0	0	29
SNORD116-25	0	0	0	0	44
ADAM29	88	85	100	78	1
WASH2P	83	82	82	71	0
NHEJ1	74	91	89	69	0
<b>FLT3-ITD</b>	68	72	86	84	0

 Founding clone

 +FLT3-ITD

**Supplementary Figure 5. AML Xenografts can reveal relapse clones but not predict clonal evolution from diagnosis to relapse.** AML xenografts identified the relapsing clone in the diagnostic sample from AML-7 (a) and partially recapitulated the clonal dynamics from diagnosis to relapse in AML-11 (b) but did not predict the evolution from diagnosis to relapse in AML-20 (c), AML-54 (d), AML-33 (e) and AML-79 (g). AML-9 (f) contained the same clone at diagnosis and relapse. The presence of FLT3-ITD in AML-33 and corresponding xenografts is denoted by "+", as the rearrangement in this case is detectable but not quantifiable by WES.



**Supplementary Figure 6. Validation of clonal dynamics by single cell sequencing.** Identification of monosomy 7 by single cell RNA sequencing through detection of SNVs in expressed transcripts from chromosome 7, confirming the expansion of clones with losses of either allele of chromosome 7 in two independent xenografts.



**Supplementary Figure 7. Gating strategy for flow cytometry.** Leukemic engraftment was assessed as the percentage of hCD45+CD33+CD3-CD19- cells within the live cell compartment through sequential gating from (a) to (e).

## Supplementary Methods

### Algorithmic clone calling

Manual clone calling was validated by clone calling using the PyClone software.<sup>1</sup> The PyClone results confirmed the original clone calling, except in three instances where the algorithm produced less credible clonal structures, thus validating the manual approach. First, in four samples with insertions in *NPM1* (AML-7, AML16, AML-26 and AML-28), PyClone separated the *NPM1* alteration from the other founding clone mutations due to well-known systematic underestimation of insertions and deletions in sequencing data. Second, PyClone failed to separate the *NRAS* (G12V) mutation from the founding clone mutations in AML-34, despite the mutation being present in virtually all cells in eight of the nine samples but completely absent from the xenograft which instead carried the *NRAS* (G12S) mutation. Third, in AML-7, PyClone combined the *PTPN11* and *WT1* mutations into a single clone despite the presence of samples containing the *WT1* mutation but not the *PTPN11* mutation and vice versa. The same was done for the *NF1* and *FLT3* clones, which were anticorrelated, with PDX-7AA containing the *FLT3* clone at 14% and the *NF1* clone at 64% but PDX-7B containing the *FLT3* clone at 74% and the *NF1* clone at 29%.

## Supplementary References

- 1 Roth, A. *et al.* PyClone: statistical inference of clonal population structure in cancer. *Nature methods* **11**, 396-398, doi:10.1038/nmeth.2883 (2014).