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Supplemental Information

Antiviral treatment causes a unique mutational signature in cancers of transplantation recipients

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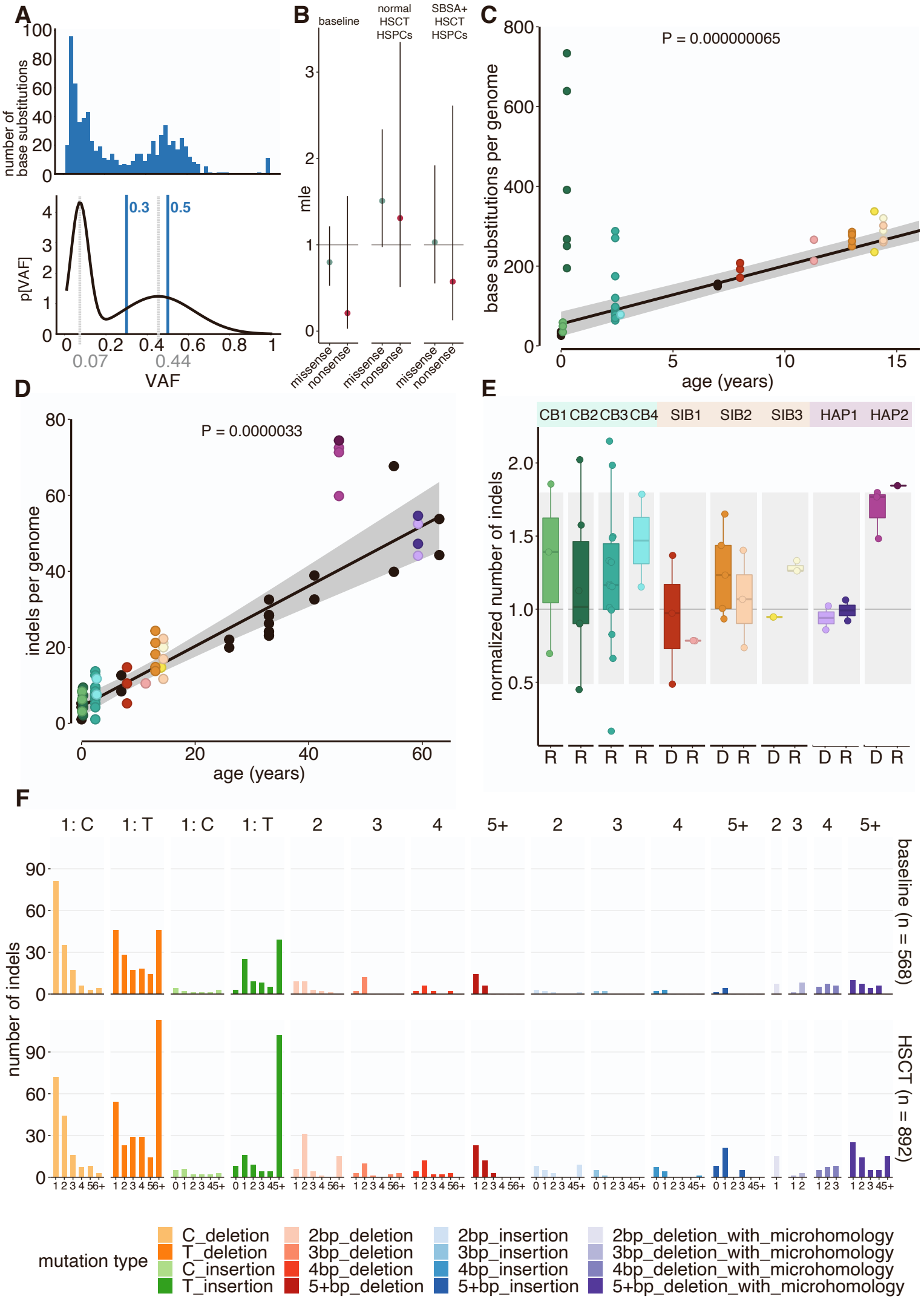
A
number of base substitutions
p[VAF]
0.3
0.5
0.07
0.44
VAF
B
baseline
normal HSCT HSPCs
SBSA+ HSCT HSPCs
mle
missense
nonsense
C
P = 0.000000065
base substitutions per genome
age (years)
D
P = 0.0000033
indels per genome
age (years)
E
CB1 CB2 CB3 CB4 SIB1 SIB2 SIB3 HAP1 HAP2
normalized number of indels
R R R R D R D R D R D R D R
F
1: C
1: T
2
3
4
5+
number of indels
baseline (n = 568)
HSCT (n = 892)
mutation type
C_deletion
T_deletion
C_insertion
T_insertion
2bp_deletion
3bp_deletion
4bp_deletion
5+bp_deletion
2bp_insertion
3bp_insertion
4bp_insertion
5+bp_insertion
2bp_deletion_with_microhomology
3bp_deletion_with_microhomology
4bp_deletion_with_microhomology
5+bp_deletion_with_microhomology

Figure S1. The number of indels in HSCT donor and recipient HSPCs is variable but not consistently altered after transplantation, related to Figure 1.

(A) A representative VAF plot of a HSPC clone. Above, a histogram of the variant allele frequency (VAF). Below, the probability distribution of these VAFs is shown, with the peaks of the subclonal (0.07) and clonal mutations (0.44) highlighted. (B) dn/ds analysis of nonsynonymous (either missense or nonsense) versus synonymous mutations. “mle” is the maximum likelihood estimate of the ratio between the nonsynonymous and synonymous mutations. (C) Similar to Figure 1B, but zoomed into the HSPC clones of pediatric donors and recipients. The corresponding P value of the linear mixed-effects model of the baseline is depicted above the baseline. (D) Similar to Figure 1B, but the number of indels are shown instead of the number of base substitutions for all samples and the baseline. (E) The number of indels per clone normalized to the indel baseline, similar to Figure 1C. (F) Indel context profiles from the baseline and the HSCT clones.

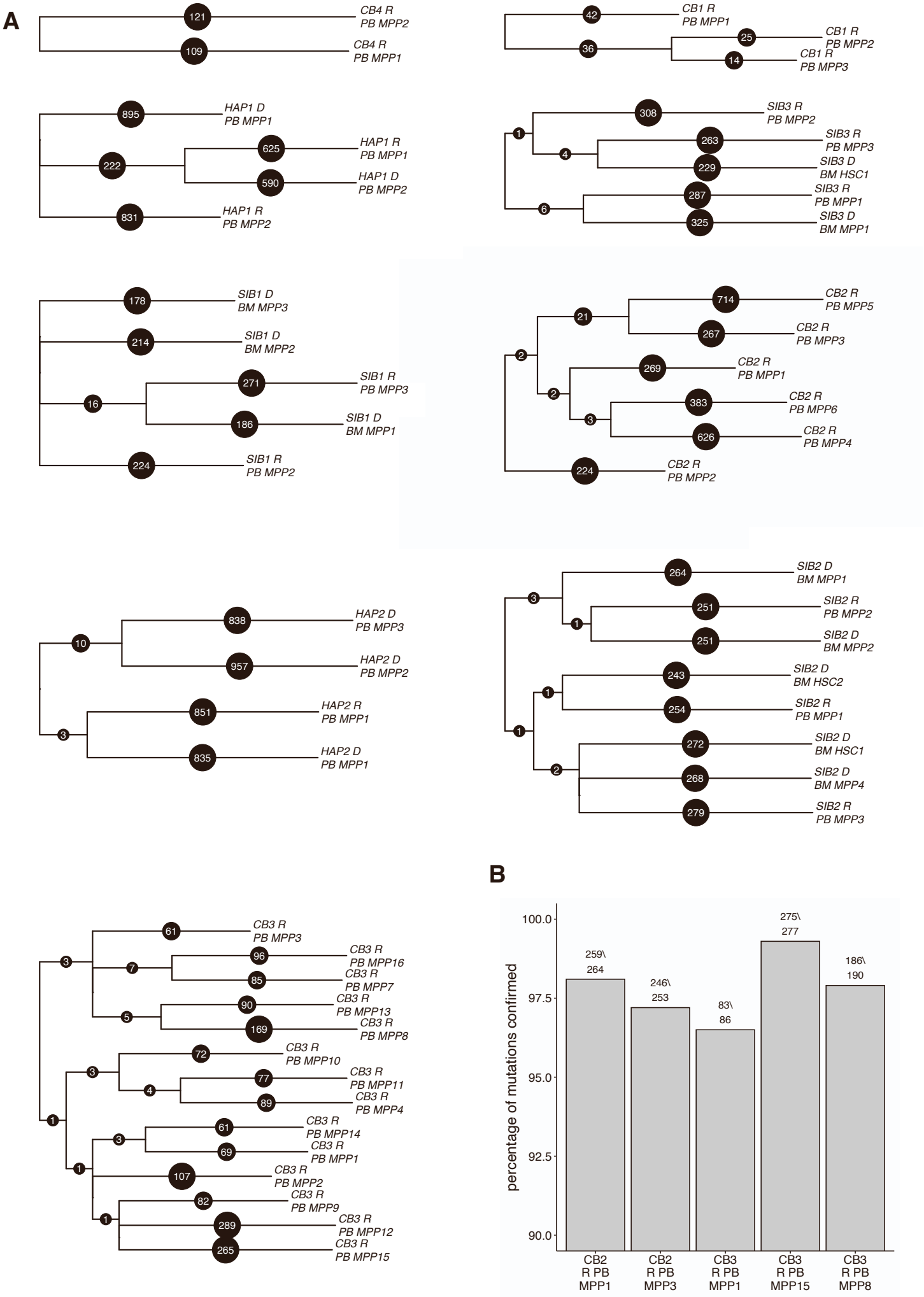
A
121
CB4 R
PB MPP2
109
CB4 R
PB MPP1
42
CB1 R
PB MPP1
25
CB1 R
PB MPP2
36
14
CB1 R
PB MPP3
895
HAP1 D
PB MPP1
625
HAP1 R
PB MPP1
222
590
HAP1 D
PB MPP2
831
HAP1 R
PB MPP2
308
SIB3 R
PB MPP2
1
263
SIB3 R
PB MPP3
4
229
SIB3 D
BM HSC1
287
SIB3 R
PB MPP1
6
325
SIB3 D
BM MPP1
178
SIB1 D
BM MPP3
214
SIB1 D
BM MPP2
271
SIB1 R
PB MPP3
16
186
SIB1 D
BM MPP1
224
SIB1 R
PB MPP2
714
CB2 R
PB MPP5
21
267
CB2 R
PB MPP3
2
269
CB2 R
PB MPP1
2
383
CB2 R
PB MPP6
3
626
CB2 R
PB MPP4
224
CB2 R
PB MPP2
838
HAP2 D
PB MPP3
10
957
HAP2 D
PB MPP2
851
HAP2 R
PB MPP1
3
835
HAP2 D
PB MPP1
264
SIB2 D
BM MPP1
3
251
SIB2 R
PB MPP2
1
251
SIB2 D
BM MPP2
243
SIB2 D
BM HSC2
1
254
SIB2 R
PB MPP1
1
272
SIB2 D
BM HSC1
2
268
SIB2 D
BM MPP4
279
SIB2 R
PB MPP3
61
CB3 R
PB MPP3
3
96
CB3 R
PB MPP16
7
85
CB3 R
PB MPP7
90
CB3 R
PB MPP13
5
169
CB3 R
PB MPP8
72
CB3 R
PB MPP10
3
77
CB3 R
PB MPP11
4
89
CB3 R
PB MPP4
1
61
CB3 R
PB MPP14
3
69
CB3 R
PB MPP1
1
107
CB3 R
PB MPP2
82
CB3 R
PB MPP9
1
289
CB3 R
PB MPP12
265
CB3 R
PB MPP15
B
percentage of mutations confirmed
100.0
97.5
95.0
92.5
90.0
259\
264
246\
253
83\
86
275\
277
186\
190
CB2
R PB
MPP1
CB2
R PB
MPP3
CB3
R PB
MPP1
CB3
R PB
MPP15
CB3
R PB
MPP8

Figure S2. Verification of WGS results by phylogenetic analyses and re-sequencing, related to Figure 2.
(A) Phylogenetic analysis of the clones per patient. The trees indicate which mutations are shared between clones, and which mutations are only present in individual mutations. Most mutations are acquired in single clones. (B) Re-sequencing of DNA of five HSPC clones from two patients, CB2 (n=2) and CB3 (n=3). Above each bar, the number of mutations identified in the original sequencing of the clone and the number of these mutations that are found at a VAF of 0.15 or higher in the re-sequenced sample are shown.

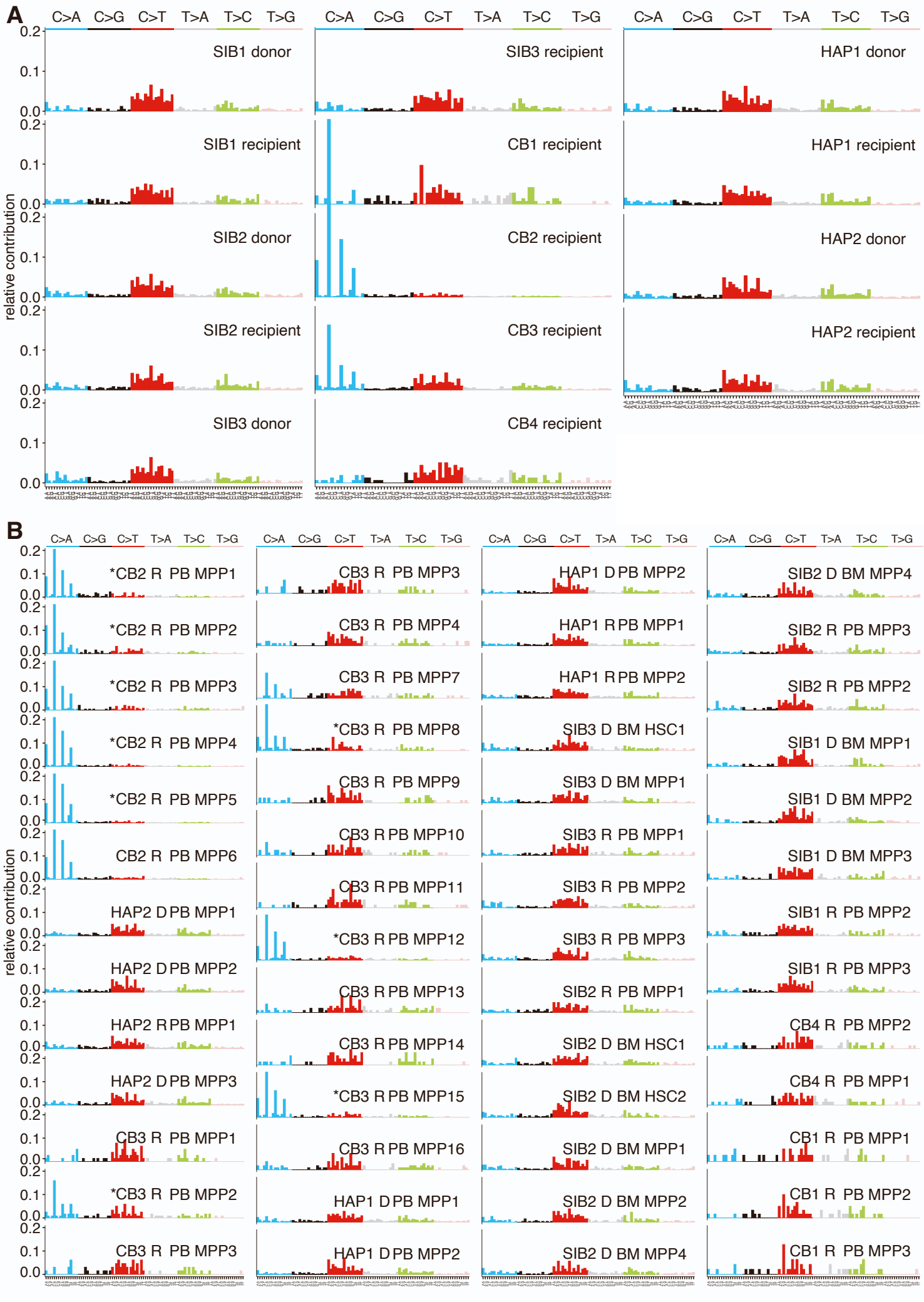
A
C>A C>G C>T T>A T>C T>G
relative contribution
0.2
0.1
0.0
SIB1 donor
SIB1 recipient
SIB2 donor
SIB2 recipient
SIB3 donor
SIB3 recipient
CB1 recipient
CB2 recipient
CB3 recipient
CB4 recipient
HAP1 donor
HAP1 recipient
HAP2 donor
HAP2 recipient
B
*CB2 R PB MPP1
*CB2 R PB MPP2
*CB2 R PB MPP3
*CB2 R PB MPP4
*CB2 R PB MPP5
CB2 R PB MPP6
HAP2 D PB MPP1
HAP2 D PB MPP2
HAP2 R PB MPP1
HAP2 D PB MPP3
CB3 R PB MPP1
*CB3 R PB MPP2
CB3 R PB MPP3
CB3 R PB MPP4
CB3 R PB MPP7
*CB3 R PB MPP8
CB3 R PB MPP9
CB3 R PB MPP10
CB3 R PB MPP11
*CB3 R PB MPP12
CB3 R PB MPP13
CB3 R PB MPP14
*CB3 R PB MPP15
CB3 R PB MPP16
HAP1 D PB MPP1
HAP1 D PB MPP2
HAP1 D PB MPP2
HAP1 R PB MPP1
HAP1 R PB MPP2
SIB3 D BM HSC1
SIB3 D BM MPP1
SIB3 R PB MPP1
SIB3 R PB MPP2
SIB3 R PB MPP3
SIB2 R PB MPP1
SIB2 D BM HSC1
SIB2 D BM HSC2
SIB2 D BM MPP1
SIB2 D BM MPP2
SIB2 D BM MPP4
SIB2 D BM MPP4
SIB2 R PB MPP3
SIB2 R PB MPP2
SIB1 D BM MPP1
SIB1 D BM MPP2
SIB1 D BM MPP3
SIB1 R PB MPP2
SIB1 R PB MPP3
CB4 R PB MPP2
CB4 R PB MPP1
CB1 R PB MPP1
CB1 R PB MPP2
CB1 R PB MPP3

Figure S3. HSCT recipient clones with increased mutational burden have higher contribution of NpC>ApA mutations, related to Figure 3.

(A) SBS 96-trinucleotide profiles of HSPC clones, summed per patient and donor and recipient origin. (B) SBS 96-trinucleotide profiles of all 51 individual HSCT HSPC clones in this study. Names of clones with increased mutation burden are indicated by a "*".


A
SBSA+ HSCs
OGG1KO
KBrO3
mutated
B
C>A
C>G
C>T
T>A
T>C
T>G
SBSA+ HSPC
OGG1KO
KBrO3
relative contribution
strand
transcribed
untranscribed
C
SBS4
SBS18
SBS29
SBS38
KBrO3 260uM
KBrO3 875uM
Benzidine
MX+S9
SBSA
D
leading
lagging
E
chromosomal strand
baseline sample 1 C>A
baseline sample 2 C>A
F
fraction of C>A
genomic region
exon
gene
intron
splicesite
tss

Figure S4. SBSA has a distinct nucleotide context and other characteristics that are distinct from previously reported signatures, related to Figure 4.

(A) Riverplots indicating the order of the -4:+4 nucleotide context of C>ApA mutations of SBSA positive HSPCs, a knock-out of OGG1 and exposure to potassium bromate (KBrO3). The mutated C is present on position 0. SBSA C>A mutations have increased G-2 preceding G-1 (*1), C-2 following C-3 (*2) and decreased A-3 preceding C-2 (*3). (B) The 96-trinucleotide context separated by the transcribed and untranscribed strand op protein-coding genes. Samples are the same as those depicted in A. (C) The 96-trinucleotide context of COSMIC and environmental agent mutational signatures with the highest correlation to SBSA as shown in Figure 2E. (D) The 96-trinucleotide context separated by the leading and lagging strand of replication for the same samples as those depicted in A. (E) The chromosomal strand of C>A mutations of HSCT recipient HSPC clones with increased mutational burden not shown in Figure 3C, and of two baseline HSPC clones. (F) The distribution of C>A mutations over functional genomic regions of HSCT recipient clones with increased mutation burden, a knock-out of OGG1 and KBrO3 treated cells.

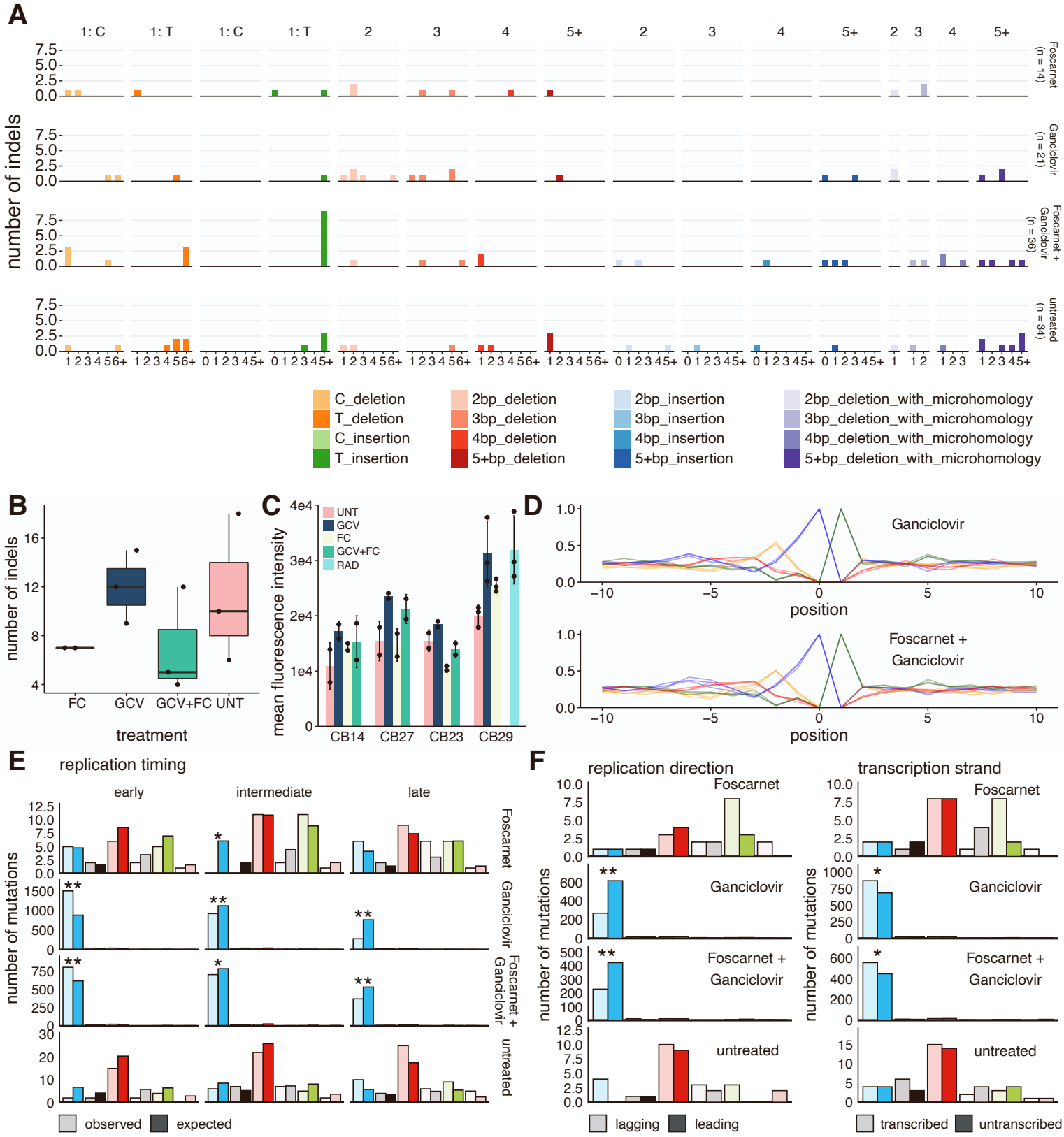
A
number of indels
1: C
1: T
2
3
4
5+
Foscarnet (n = 14)
Ganciclovir (n = 21)
Foscarnet + Ganciclovir (n = 36)
untreated (n = 34)
C_deletion
T_deletion
C_insertion
T_insertion
2bp_deletion
3bp_deletion
4bp_deletion
5+bp_deletion
2bp_insertion
3bp_insertion
4bp_insertion
5+bp_insertion
2bp_deletion_with_microhomology
3bp_deletion_with_microhomology
4bp_deletion_with_microhomology
5+bp_deletion_with_microhomology
B
number of indels
FC
GCV
GCV+FC
UNT
treatment
C
mean fluorescence intensity
UNT
GCV
FC
GCV+FC
RAD
CB14
CB27
CB23
CB29
D
Ganciclovir
Foscarnet + Ganciclovir
position
E
replication timing
early
intermediate
late
number of mutations
observed
expected
F
replication direction
transcription strand
lagging
leading
transcribed
untranscribed
G
lesion segregation
−log10 FDR
H
chromosomal strand

Figure S5. Mutations induced *in vitro* by ganciclovir have similar molecular characteristics as SBSA, related to Figure 5.
Molecular characterization of *in vitro* treatment of umbilical human cord blood cells with 5 µM Ganciclovir, 200µM Foscarnet, or a combination of both. * = FDR <0.05, ** = FDR < 10-7. (A) The indel context profiles of the clones of each treatment condition. (B) The number of indels per treatment condition. Each dot represents a single clone. (C) The mean fluorescence intensity, similar to figure 4C, but grouped per cord blood sample, and including CB29, for which radiation treatment was available, but not the combined treatment of foscarnet and ganciclovir. (D) The -10:+10 nucleotide context of ganciclovir and a combination of ganciclovir and foscarnet. (E) Enrichment/depletion of the clones from each treatment condition divided in early, intermediate and late replicating regions. Data from clones of one condition were pulled. (F) Replication strand bias and transcription strand bias of the same data as depicted in E. (G) FDR-corrected p-values of Wald-Wolfowitz runs test on summed numbers of mutations and runs in each treatment condition. (H) The chromosomal strand and position of the cytosine of C>A mutations for all clones of all treatment conditions. Abbreviations: FC = foscarnet, GCV = ganciclovir, UNT = untreated, RAD = radiation.

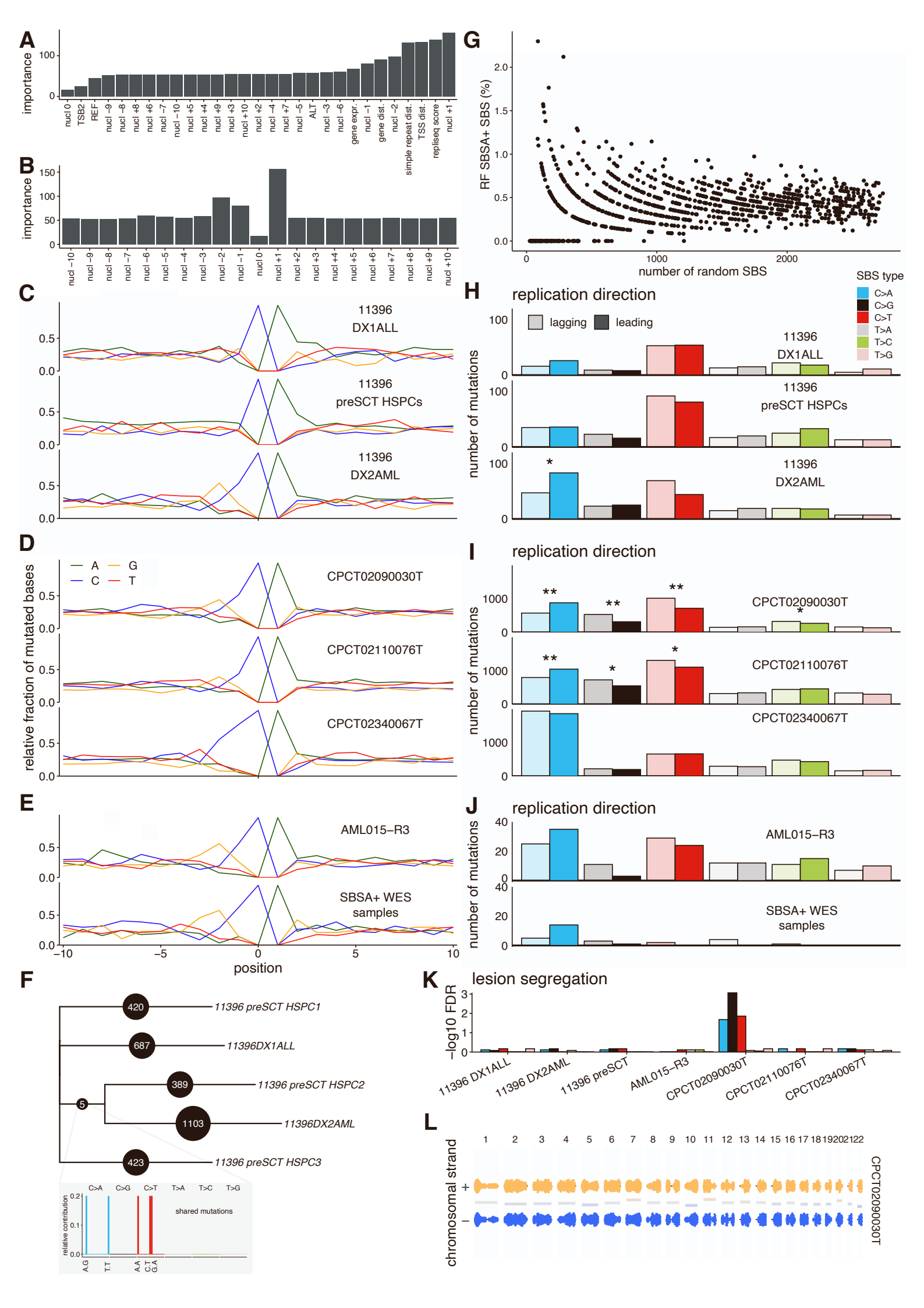
A
importance
nucl 0
TSB2
REF
nucl −9
nucl −8
nucl +8
nucl +6
nucl −7
nucl −10
nucl +5
nucl +4
nucl +9
nucl +3
nucl +10
nucl +2
nucl −4
nucl +7
nucl −5
ALT
nucl −3
nucl −6
gene expr.
nucl −1
gene dist.
nucl −2
simple repeat dist.
TSS dist.
repliseq score
nucl +1
B
importance
nucl −10
nucl −9
nucl −8
nucl −7
nucl −6
nucl −5
nucl −4
nucl −3
nucl −2
nucl −1
nucl 0
nucl +1
nucl +2
nucl +3
nucl +4
nucl +5
nucl +6
nucl +7
nucl +8
nucl +9
nucl +10
G
RF SBSA+ SBS (%)
number of random SBS
SBS type
C>A
C>G
C>T
T>A
T>C
T>G
C
11396
DX1ALL
11396
preSCT HSPCs
11396
DX2AML
H
replication direction
lagging
leading
number of mutations
11396
DX1ALL
11396
preSCT HSPCs
11396
DX2AML
D
A
C
G
T
relative fraction of mutated bases
CPCT02090030T
CPCT02110076T
CPCT02340067T
I
replication direction
number of mutations
CPCT02090030T
CPCT02110076T
CPCT02340067T
E
AML015−R3
SBSA+ WES
samples
position
J
replication direction
number of mutations
AML015−R3
SBSA+ WES
samples
F
420
11396 preSCT HSPC1
687
11396DX1ALL
389
11396 preSCT HSPC2
5
1103
11396DX2AML
423
11396 preSCT HSPC3
C>A
C>G
C>T
T>A
T>C
T>G
relative contribution
shared mutations
A:G
T:T
A:A
C:T
G:A
K
lesion segregation
−log10 FDR
11396 DX1ALL
11396 DX2AML
11396 preSCT
AML015−R3
CPCT02090030T
CPCT02110076T
CPCT02340067T
L
chromosomal strand
CPCT02090030T

Figure S6. A random forest-based approach identifies tumors with contribution of SBSA to their mutational profile, related to Figure 6.

(A) The importance given by the random forest to the mutation characteristics sorted from low to high. For each mutation the +10:-10 nucleotide context was used, the Repliseq score, distance to the closest TSS, gene body, and simple repeat, reference (REF) and alternative (ALT) allele and transcriptional strand bias (TSB2). (B) Similar to A, but only the importance of the nucleotide context is shown, sorted by position. (C) The -10:+10 nucleotide context of the C>ApA mutations of the primary (DX1) ALL, pre-HSCT HSPC clones (pulled) and therapy-related (DX2) AML of patient PMC11396. (D) Similar to C, but for the three samples classified SBSA positive by the random forest of the Dutch solid tumor metastases dataset. (E) Similar to C, but for AML015-R3, an AML relapse after allogeneic-HSCT, and the merged data of four SBSA+ classified WES samples. (F) The developmental lineage tree of the samples of patient PMC11396, based on shared mutations. The nucleotide context of mutations shared between the secondary (DX2) AML and HSPC3 is shown. (G) The number of SBS and percentage of random forest SBSA-positively classified SBS of 1000 sets of randomly sampled mutations. The highest percentage (2.3%) was used as a cut-off for expected false-positive rates for input samples. (H), (I), (J) The replication strand bias of the samples in C,D and E respectively. * = FDR <0.05, ** = FDR < 10-7. (K) FDR-corrected p-values for Wald-Wolfowitz runs test for the same samples as C, D and E, similar to Figure 3D. (L) The chromosomal strand of the cytosines of C>A mutations for CPCT02090030T.

	CB1	CB2	CB3	CB4	SIB1	SIB2	SIB3	HAP1	HAP2
Diagnosis	MDS-EB	ALL-HR	AML-HR	ALCL-relapse	ALL-relapse	ALL-HR	ALL-relapse	CML	SCID
Stem cell source	UCB	UCB	UCB	UCB	BM	BM	BM	PB	BM
Conditioning regimen	BuCyMel	BuFluCy	CloFluBu	TBI, TT, VP16	CloFluBu	CloFluBu	CloFluBu	TBI/Cy	BuCy
Serotherapy	ATG	ATG	None	None	None	None	None	ATG	None
G-CSF	Yes	Yes	Yes	Yes	No	No	No	No	No
$CD34^+$ cell dose (10^6/kg)	0.23	0.48	0.21	0.23	2.4	2.2	5.6	7.8	N.A.
TNC dose (10^8/kg)	0.56	1.22	0.44	0.88	3.2	3.1	2.7	0.1	0.59
Donor chimerism (%)	100	100	100	96	100	99	100	100	100
Sample (months after HSCT)	1	3	29	30	40	17	5	195	295
GvHD prophylaxis	Pred, CsA	Pred, CsA	Pred, CsA	Pred, CsA	MTX, CsA	MTX, CsA	MTX, CsA	MTX, CsA	MTX, CsA
Viral reactivations	None	CMV,Adenovirus	HHV6	None	None	None	None	None	None
Antiviral therapy	None	cidofovir, foscarnet, valganciclovir	foscarnet, ganciclovir	None	None	None	None	None	None
GvHD	None	None	None	None	None	None	None	None	None

Table S1. An overview of the clinical data, related to Figure 1

Abbreviations: MDS-EB: myelodysplastic syndrome with excess of blasts; ALL: acute lymphoblastic leukemia; AML: acute myeloid leukemia; ALCL: anaplastic large cell lymphoma; HR: high risk; BM: bone marrow; PB: peripheral blood; UCB: umbilical cord blood; M: male; F: female; Bu: busulfan; Cy: Cyclophosphamide; Mel: Melphalan; Flu: Fludarabine; TBI: Total body irradiation; TT: Thiotepa; VP16: Etoposide; TNC: Total nucleated cell; Pred: prednisolone; MTX: methotrexate; CsA: Ciclosporin A; CMV: cytomegalovirus.

Clone	Donor/ recipient	Sample source	Interval after HSCT (months)	Markers used for HSPC isolation	Cell type	Germline control	surveyed genome (%)	No. of SBS	No. of indels	Base Cov.
CB1_R_PB_MPP1	R	BM	1	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,954	37	9	30x
CB1_R_PB_MPP2	R	BM	1	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,955	60	8	30x
CB1_R_PB_MPP3	R	BM	1	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,954	47	3	30x
CB2_R_PB_MPP1	R	PB	3	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,954	262	2	30x
CB2_R_PB_MPP2	R	PB	3	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,955	191	9	30x
CB2_R_PB_MPP3	R	PB	3	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,954	245	4	30x
CB2_R_PB_MPP4	R	PB	3	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,950	628	4	15x
CB2_R_PB_MPP5	R	PB	3	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,953	729	5	15x
CB2_R_PB_MPP6	R	PB	3	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,954	383	7	15x
CB3_R_PB_MPP1	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,945	76	10	15x
CB3_R_PB_MPP10	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,947	83	8	15x
CB3_R_PB_MPP11	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,949	82	13	15x
CB3_R_PB_MPP12	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,949	297	6	15x
CB3_R_PB_MPP13	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,950	101	9	15x
CB3_R_PB_MPP14	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,950	70	3	15x
CB3_R_PB_MPP15	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,947	273	4	15x
CB3_R_PB_MPP16	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,952	105	9	15x
CB3_R_PB_MPP2	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,931	119	7	15x
CB3_R_PB_MPP3	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,943	65	8	15x
CB3_R_PB_MPP4	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,950	95	14	15x
CB3_R_PB_MPP7	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,939	94	7	15x
CB3_R_PB_MPP8	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,951	178	10	15x
CB3_R_PB_MPP9	R	PB	29	Lin$^-$CD34$^+$	MPP	other HSPC clones	0,948	87	6	15x
CB4_R_PB_MPP1	R	PB	32	Lin$^-$CD34$^+$	MPP	Bulk T-cells	0,939	78	11	15x
CB4_R_PB_MPP2	R	PB	32	Lin$^-$CD34$^+$	MPP	Bulk T-cells	0,926	80	9	15x
SIB1_D_BM_MPP1	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,953	195	6	15x
SIB1_D_BM_MPP2	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,953	212	10	30x

SIB1_D_BM_MPP3	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,949	173	15	30x
SIB1_R_PB_MPP2	R	PB	40	Lin$^-$CD34$^+$	MPP	MSCs	0,952	219	10	30x
SIB1_R_PB_MPP3	R	PB	40	Lin$^-$CD34$^+$	MPP	MSCs	0,951	276	10	30x
SIB2_D_BM_HSC1	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	HSC	MSCs	0,935	278	17	30x
SIB2_D_BM_HSC2	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	HSC	MSCs	0,945	249	15	30x
SIB2_D_BM_MPP1	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,945	269	22	30x
SIB2_D_BM_MPP2	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,945	258	13	30x
SIB2_D_BM_MPP4	D	BM	0	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,945	273	24	30x
SIB2_R_PB_MPP1	R	PB	17	Lin$^-$CD34$^+$	MPP	MSCs	0,944	258	21	30x
SIB2_R_PB_MPP2	R	PB	17	Lin$^-$CD34$^+$	MPP	MSCs	0,945	261	17	30x
SIB2_R_PB_MPP3	R	PB	17	Lin$^-$CD34$^+$	MPP	MSCs	0,942	291	11	30x
SIB3_D_BM_HSC1	D	BM	5	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	HSC	MSCs	0,953	228	16	30x
SIB3_D_BM_MPP1	D	BM	5	Lin$^-$CD11c$^-$CD16$^-$ CD34$^+$CD38$^-$ CD45RA$^-$	MPP	MSCs	0,952	337	14	30x
SIB3_R_PB_MPP1	R	PB	5	Lin$^-$CD34$^+$	MPP	MSCs	0,949	287	19	30x
SIB3_R_PB_MPP2	R	PB	5	Lin$^-$CD34$^+$	MPP	MSCs	0,947	305	20	30x
SIB3_R_PB_MPP3	R	PB	5	Lin$^-$CD34$^+$	MPP	MSCs	0,950	266	19	30x
HAP1_D_PB_MPP1	D	PB	195	Lin$^-$CD34$^+$	MPP	Granulocytes	0,952	868	43	15x
HAP1_D_PB_MPP2	D	PB	195	Lin$^-$CD34$^+$	MPP	Granulocytes	0,952	743	52	15x
HAP1_R_PB_MPP1	R	PB	195	Lin$^-$CD34$^+$	MPP	Granulocytes	0,952	791	52	15x
HAP1_R_PB_MPP2	R	PB	195	Lin$^-$CD34$^+$	MPP	Granulocytes	0,953	785	46	15x
HAP2_D_PB_MPP1	D	PB	295	Lin$^-$CD34$^+$	MPP	Granulocytes	0,951	807	71	15x
HAP2_D_PB_MPP2	D	PB	295	Lin$^-$CD34$^+$	MPP	Granulocytes	0,954	934	68	15x
HAP2_D_PB_MPP3	D	PB	295	Lin$^-$CD34$^+$	MPP	Granulocytes	0,953	826	60	15x
HAP2_R_PB_MPP1	R	PB	295	Lin$^-$CD34$^+$	MPP	Granulocytes	0,954	837	71	15x

Table S2. An overview of the samples and the number of mutations, related to Figure 1

Abbreviations: D; donor; R; recipient; MPP; multipotent progenitor cell; HSC; hematopoietic stem cell; MSCs; mesenchymal stromal cells.