

Clonal expansion of CD8⁺ T cells in acute myeloid leukemia patients

Table S1. AML Patients and Donors characteristics

Domain	Patients Total (n = 31)	Donors Total (n = 10)
Age (y)		
Median	47	40
Range	23-74	34-46
Gender		
Male	17	5
Female	14	5
WBC ($\times 10^9/L$)		
Mean	27.91	6.17
Range	6.38-63.72	5.24-7.72
PB blasts (%)		
Mean	33.29	
Range	21-56	
PB Absolute blasts count ($\times 10^9/L$)		
Mean	9.94	
Range	1.54-29.94	
BM blasts (%)		
Mean	66.23	
Range	27-95	
BM Absolute blasts count ($\times 10^9/L$)		
Mean	18.76	
Range	3.08-47.71	
Moleculars		
FLT3-ITD	16.13%	
NPM1	19.35%	
TP53	6.45%	
Cytogenetics		
Favorable	22.58%	
Intermediate	58.07%	
Adverse	19.35%	

WBC, white blood cell; PB, peripheral blood; BM, bone marrow. AML type accords to WHO (World Health Organization) 2016.

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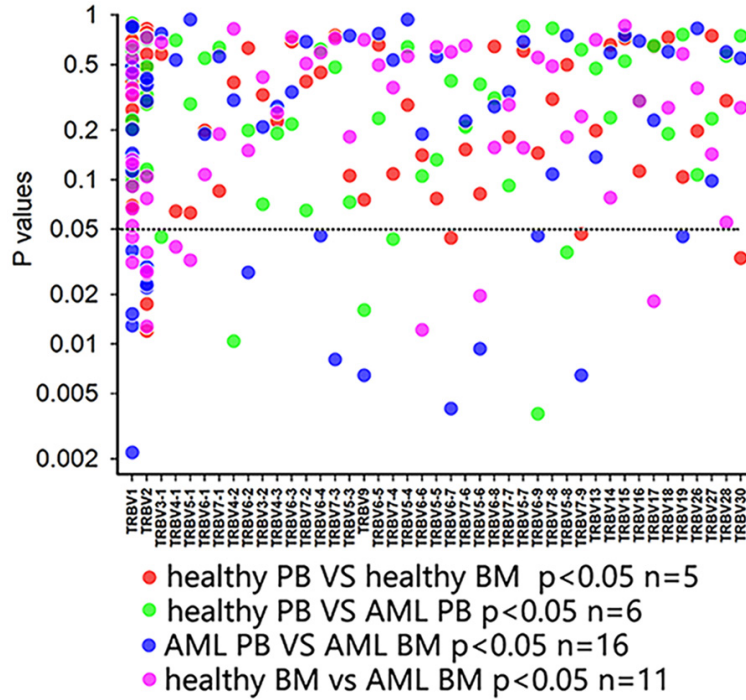


Figure S1. Comparison of overall usage of TCR β V gene segments in AML patients and healthy donors. Differences in the frequencies of TR β V gene segments in normal PB vs. normal BM, AML PB vs. AML BM, AML BM vs. normal BM, and AML PB vs. normal PB. Four study groups containing BM ($n = 31$) and PB ($n = 31$) samples obtained from AML patients and BM ($n = 10$) and PB ($n = 10$) samples obtained from healthy donors.

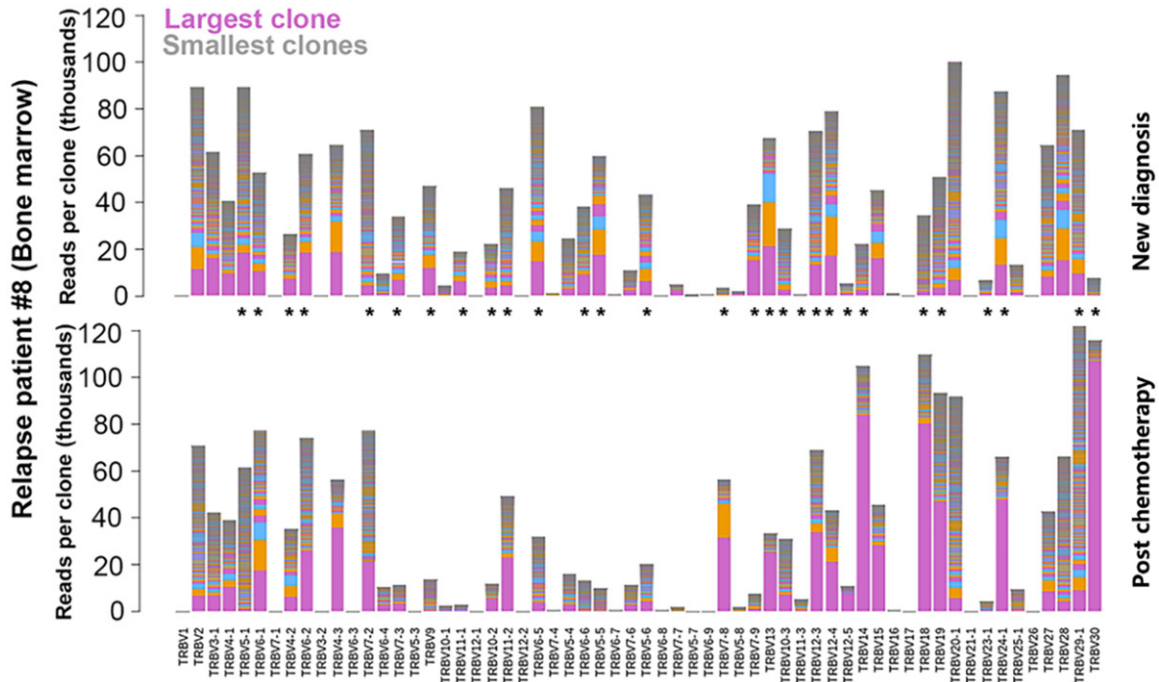


Figure S2. The usage pattern of V gene segments in the relapsed patient (#8) at new diagnosis and post chemotherapy. Color segments within each bar indicate the contribution of individual clones, arranged from the smallest clones (gray, top) to the largest clones (purple, bottom). The Mann-Whitney U-test was used for comparisons between two groups. * indicates $P < 0.01$.

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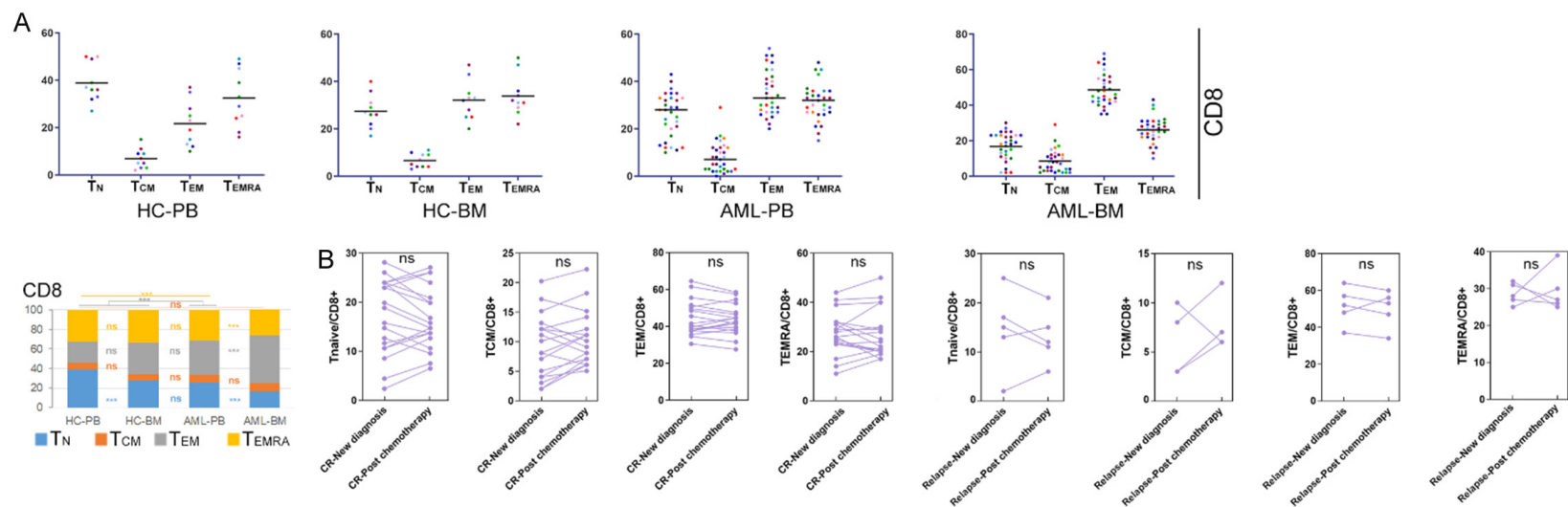


Figure S3. Phenotypical analysis of CD8⁺ T cells from healthy donors and AML patients. CD8⁺ T cell subsets were analyzed by multiparameter flow cytometry according to the expression of CD45RA and CCR7. A. Phenotypical features of BM and PB T cells from newly diagnosed AML patients (n = 31) and healthy controls (HCs) (n = 10). B. Phenotypical features of BM T cells from patients before and after chemotherapy. Samples collected from patients who relapsed (n = 5) and patients who achieved CR (n = 19) after chemotherapy. The Mann-Whitney U-test was used for comparisons between two groups. The Wilcoxon signed-rank test was used for matched paired comparisons. *** indicates P < 0.01.

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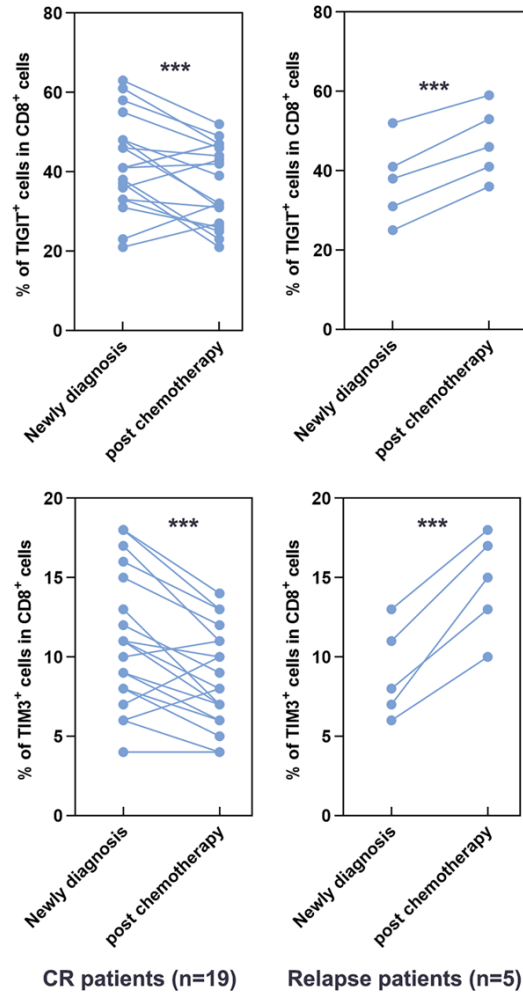


Figure S4. Expression levels of TIGIT and TIM3 in BM CD8⁺ T cells from patients before and after chemotherapy. Samples collected from patients who relapsed (n = 5) and patients who achieved CR (n = 19) after chemotherapy and analyzed by flow cytometry. The Wilcoxon signed-rank test was used for matched paired comparisons. *** indicates P < 0.01.

Clonal expansion of CD8⁺ T cells in acute myeloid leukemia patients

Table S2. The top 50 clonotypes in CD8⁺ T cells were frequently distributed in CD8⁺ PD-1⁺ populations and CD8⁺ PD-1⁻ populations

Variable Gene	Diversity Gene	Joining Gene	Constant	CDR3 AA	V Gene Allele	D Gene Allele	J Gene Allele	PD-1 ⁺ Freq. (%)	PD-1 ⁻ Freq. (%)
TRBV6-2	TRBD2	TRBJ2-7	TRBC2	ASSGLAGANDEQY	1	2	1	6.828	0.806
TRBV24-1	TRBD2	TRBJ2-1	TRBC2	ATSAQMDYNEQF	1	1	1	3.252	0.155
TRBV6-2	TRBD2	TRBJ2-1	TRBC2	ASSYKTRRNEQF	1	2	1	2.035	0.000
TRBV7-8		TRBJ2-1	TRBC2	ASSPSPSYNEQF	1		1	3.181	0.069
TRBV4-3	TRBD1	TRBJ2-3	TRBC2	ASSQANQGNTQY	1	1	1	2.150	0.086
TRBV6-2	TRBD2	TRBJ2-5	TRBC2	ATMGLAGVETQY	1	2	1	1.947	0.083
TRBV4-1		TRBJ1-5	TRBC1	ASSQSAVSNQPQH	1		1	3.737	0.056
TRBV19	TRBD1	TRBJ1-2	TRBC1	ASSFGTSDGYT	1	1	1	1.696	0.000
TRBV29-1	TRBD2	TRBJ2-3	TRBC2	SVRTTSTDTQY	1	1	1	1.794	0.413
TRBV19	TRBD1	TRBJ2-1	TRBC2	ASSYSDSNNEQF	1	1	1	0.856	0.338
TRBV11-2	TRBD1	TRBJ2-7	TRBC2	ASGPPTVFEQY	3	1	1	0.787	0.276
TRBV2	TRBD1	TRBJ2-7	TRBC2	ASKDRGYEQY	1	1	1	0.456	0.200
TRBV6-2	TRBD1	TRBJ1-5	TRBC1	ASSYSYGTGGTSGQPQH	1	1	1	0.450	0.178
TRBV28		TRBJ2-7	TRBC2	ASTAAEQY	1		1	0.210	0.000
TRBV4-3	TRBD2	TRBJ2-5	TRBC2	ASSQEPPGSKVETQY	1	2	1	0.402	0.190
TRBV5-1		TRBJ2-7	TRBC2	ASRLPGGNEQY	1		1	0.400	0.011
TRBV15	TRBD2	TRBJ2-3	TRBC2	ATSGTSGTPDTQY	2	2	1	0.998	0.846
TRBV12-4		TRBJ1-5	TRBC1	ASSLGVSNQPQH	1		1	0.880	0.036
TRBV11-2	TRBD1	TRBJ2-3	TRBC2	ASSLEGQNTQY	1	1	1	0.862	0.261
TRBV19		TRBJ1-1	TRBC1	ASSISQDTEAF	1		1	0.761	0.526
TRBV5-1	TRBD1	TRBJ2-3	TRBC2	ASSLEQGARTDTQY	1	1	1	0.850	0.058
TRBV18		TRBJ2-3	TRBC2	ASSVTDQY	1		1	0.399	0.000
TRBV5-4	TRBD1	TRBJ2-3	TRBC2	ASSPTGQGARDTQY	1	1	1	0.765	0.000
TRBV5-1		TRBJ1-1	TRBC1	ASSLELNTEAF	1		1	0.725	0.448
TRBV12-3	TRBD1	TRBJ1-1	TRBC1	ASSWTGGRAF	1	1	1	0.024	0.000
TRBV24-1	TRBD2	TRBJ2-7	TRBC2	ATSDLLYGEQY	1	2	1	0.023	0.080
TRBV20-1		TRBJ2-1	TRBC2	SARAPAGDEQF	1		1	0.023	0.131
TRBV18	TRBD2	TRBJ2-1	TRBC2	ASSLEGPYNEQF	1	2	1	0.219	1.247
TRBV20-1	TRBD1	TRBJ1-1	TRBC1	SARTGELEAF	1	1	1	0.216	1.140
TRBV20-1	TRBD1	TRBJ1-5	TRBC1	SAPLGGLDGQPQH	1	1	1	0.213	2.109
TRBV27	TRBD2	TRBJ2-1	TRBC2	ASIPGTSGSLYNEQF	1	2	1	0.208	0.109
TRBV5-1	TRBD2	TRBJ1-1	TRBC1	ASSLEAGYTEAF	1	2	1	0.203	0.103
TRBV11-1	TRBD2	TRBJ2-1	TRBC2	ASSLEAGVYNEQF	1	2	1	0.200	0.100
TRBV29-1	TRBD2	TRBJ2-1	TRBC2	SVGGISNEQF	1	1	1	0.195	0.000
TRBV5-8	TRBD2	TRBJ2-5	TRBC2	ASSHPATRYIPETQY	1	1	1	0.193	0.094
TRBV9	TRBD1	TRBJ1-5	TRBC1	ASSPRTGPFNQPQH	1	1	1	0.178	0.092
TRBV7-6	TRBD1	TRBJ2-1	TRBC2	ASSRGDEQF	1	1	1	0.177	0.086
TRBV7-2		TRBJ1-2	TRBC1	ASSLAMAGYT	1		1	0.176	0.000
TRBV7-6		TRBJ2-5	TRBC2	ASSSGETQY	1		1	0.175	0.084
TRBV4-1		TRBJ1-3	TRBC1	ASSQAQISGNTIY	1		1	0.170	0.083
TRBV12-3	TRBD2	TRBJ2-1	TRBC2	ASSSTSGRSEQF	1	2	1	0.200	0.313
TRBV2	TRBD2	TRBJ2-1	TRBC2	AGGTPVVDQF	1	1	1	0.354	0.060
TRBV20-1		TRBJ1-6	TRBC1	SATDHNSPLH	1		1	0.451	0.178
TRBV6-5	TRBD1	TRBJ1-1	TRBC1	ASSYSRQGVTEAF	1	1	1	0.167	0.000
TRBV3-1	TRBD2	TRBJ1-3	TRBC1	ASGGRLSGNTIY	1	1	1	0.548	0.043
TRBV7-6	TRBD1	TRBJ2-7	TRBC2	ASSFRGTALDEQY	1	1	1	0.277	0.247
TRBV7-3		TRBJ2-7	TRBC2	ATRLASYEQY	1		1	0.125	0.072
TRBV5-4		TRBJ2-1	TRBC2	ASSPGPLYLGEQF	1		1	0.125	0.072
TRBV7-2		TRBJ2-5	TRBC2	ASSFDIETQY	2		1	0.123	0.071
TRBV3-1	TRBD2	TRBJ2-5	TRBC2	ASSQAGGPEPETQY	1	2	1	0.120	0.204

Samples were collected at new diagnosis from patient (Patient #8) who relapsed post chemotherapy.

Clonal expansion of CD8⁺ T cells in acute myeloid leukemia patients

Table S3. The top 50 clonotypes in CD8⁺ T cells were frequently distributed in CD8⁺ PD-1⁺ populations and CD8⁺ PD-1⁻ populations

Variable Gene	Diversity Gene	Joining Gene	Constant	CDR3 AA	V Gene Allele	D Gene Allele	J Gene Allele	PD-1 ⁺ Freq. (%)	PD-1 ⁻ Freq. (%)
TRBV10-3	TRBD1	TRBJ2-3	TRBC2	AIGEVEQGNADTQY	2	1	1	15.324	1.253
TRBV4-1	TRBD2	TRBJ2-1	TRBC2	ASSQTLRGGVNEQF	1	2	1	2.091	0.499
TRBV29-1	TRBD1	TRBJ2-5	TRBC2	SVEDDRGRGETQY	1	1	1	1.140	1.062
TRBV29-1	TRBD1	TRBJ2-5	TRBC2	SVESDRGRGETQY	1	1	1	3.927	0.019
TRBV5-1		TRBJ2-1	TRBC2	ASSLDATALNEQF	1		1	2.890	0.000
TRBV13		TRBJ2-7	TRBC2	ASSLVGYEQY	1		1	1.878	0.036
TRBV6-1	TRBD2	TRBJ1-5	TRBC1	ASSGRAVNQPQH	1	2	1	4.798	0.030
TRBV20-1		TRBJ2-5	TRBC2	SASGWSGETQY	1		1	1.779	0.336
TRBV15	TRBD1	TRBJ2-7	TRBC2	ATSLKGTGEQY	2	1	1	1.138	0.041
TRBV28		TRBJ2-7	TRBC2	ASSLDGYEQY	1		1	0.734	0.111
TRBV30	TRBD2	TRBJ2-7	TRBC2	AWSAGEGYEQY	1	2	1	0.634	0.106
TRBV20-1		TRBJ2-1	TRBC2	SARAPAGDEQF	1		1	0.607	0.105
TRBV6-5	TRBD1	TRBJ1-2	TRBC1	ASSYLGQSFHYGYT	1	1	1	0.020	0.518
TRBV2	TRBD2	TRBJ2-7	TRBC2	ASRRSSPEQY	1	1	1	0.567	0.311
TRBV6-5	TRBD2	TRBJ2-1	TRBC2	ASSYSPLAGEQF	1	1	1	0.421	0.111
TRBV7-6	TRBD2	TRBJ2-1	TRBC2	ASSPEGAGNAYNEQF	1	1	1	0.019	0.285
TRBV4-1		TRBJ2-3	TRBC2	ASSQESPHDTQY	1		1	0.351	0.138
TRBV6-4		TRBJ1-1	TRBC1	ASSESANTEAF	1		1	0.811	0.148
TRBV4-3	TRBD1	TRBJ2-3	TRBC2	ASSQANQGNTOY	1	1	1	0.794	0.000
TRBV20-1	TRBD2	TRBJ2-1	TRBC2	SAATSSGYNEQF	5	1	1	0.680	0.000
TRBV7-9		TRBJ1-1	TRBC1	ASSLLHGKNTAF	1		1	0.969	0.020
TRBV12-3	TRBD2	TRBJ1-2	TRBC1	ASSLIAGAGYGYT	1	2	1	0.363	0.000
TRBV7-8		TRBJ2-7	TRBC2	ASSLDGPVQY	1		1	1.257	0.021
TRBV20-1		TRBJ2-3	TRBC2	SASHGNSDTQY	5		1	0.143	0.004
TRBV6-5		TRBJ1-5	TRBC1	ASSLKPPGEGQPQH	1		1	0.736	0.011
TRBV7-8		TRBJ2-2	TRBC2	ASSPGELF	1		1	0.227	0.008
TRBV6-1	TRBD1	TRBJ1-5	TRBC1	ASRDWGYPPQPQH	1	1	1	0.223	0.058
TRBV13	TRBD2	TRBJ2-7	TRBC2	ASSSHGVSYEQY	1	1	1	0.210	0.122
TRBV4-3	TRBD1	TRBJ2-1	TRBC2	ASSQDAAGQVYNEQF	1	1	1	0.208	3.503
TRBV6-1	TRBD2	TRBJ1-2	TRBC1	ASSDPGGRGYGYT	1	2	1	0.874	2.831
TRBV4-1	TRBD1	TRBJ2-7	TRBC2	ASSQTGGSSLSYEQY	1	1	1	0.202	0.623
TRBV4-1	TRBD2	TRBJ2-4	TRBC2	ASSQGGRALFAIQY	1	2	1	0.020	0.537
TRBV27	TRBD2	TRBJ2-3	TRBC2	ASSSRLAGGTDQY	1	2	1	0.118	0.528
TRBV9	TRBD1	TRBJ2-1	TRBC2	ASSPQGSYNEQF	1	1	1	0.185	0.657
TRBV7-2		TRBJ2-5	TRBC2	ASSDQETQY	1		1	0.180	0.789
TRBV28		TRBJ2-7	TRBC2	ASTAAEQY	1		1	0.172	0.253
TRBV20-1		TRBJ2-5	TRBC2	SARDGKGSETQY	5		1	0.172	0.253
TRBV4-1		TRBJ2-1	TRBC2	ASSHGRLTDEQF	1		1	0.078	0.384
TRBV27		TRBJ2-2	TRBC2	ASSYGSGELF	1		1	0.071	0.314
TRBV6-2	TRBD1	TRBJ1-5	TRBC1	ASTLDTYSNQPPQH	1	1	1	0.018	0.105
TRBV20-1	TRBD1	TRBJ2-1	TRBC2	SAPPRGLGNEQF	1	1	1	0.334	0.072
TRBV20-1	TRBD2	TRBJ1-2	TRBC1	SVVGGAGGYT	5	1	1	0.230	0.024
TRBV4-1	TRBD2	TRBJ2-1	TRBC2	ASSWELGEQF	1	1	1	0.320	0.037
TRBV27	TRBD1	TRBJ2-1	TRBC2	ASSPTPGTVYNEQF	1	1	1	0.207	0.017
TRBV12-4	TRBD2	TRBJ2-1	TRBC2	ASSFDYFYPSSGSSNEQF	1	2	1	0.638	0.010
TRBV10-3	TRBD2	TRBJ1-6	TRBC1	AIRGGDPPDPLH	2	1	1	0.738	0.010
TRBV29-1	TRBD2	TRBJ2-5	TRBC2	SASPGLSGETQY	1	1	1	0.104	0.099
TRBV5-1	TRBD1	TRBJ2-3	TRBC2	ASSLEQGARTDTQY	1	1	1	0.102	0.097
TRBV29-1	TRBD2	TRBJ2-1	TRBC2	SVVPSGRNNEQF	1	2	1	0.099	0.096
TRBV6-2		TRBJ2-3	TRBC2	ASSTSSVDQY	1		1	0.099	0.094

Samples were collected after treatment from patient (Patient #8) who relapsed post chemotherapy.

Clonal expansion of CD8⁺ T cells in acute myeloid leukemia patients

Table S4. The top 50 clonotypes in CD8⁺ T cells were frequently distributed in CD8⁺ PD-1⁺ populations and CD8⁺ PD-1⁻ populations

Variable Gene	Diversity Gene	Joining Gene	Constant	CDR3 AA	V Gene Allele	D Gene Allele	J Gene Allele	PD-1 ⁺ Freq. (%)	PD-1 ⁻ Freq. (%)
TRBV6-6	TRBD1	TRBJ1-1	TRBC1	ASSSSGTGNTAEAF	1	1	1	6.013	0.157
TRBV5-1	TRBD1	TRBJ2-7	TRBC2	ASSFETEIDEQY	1	1	1	3.878	0.120
TRBV24-1	TRBD1	TRBJ2-1	TRBC2	ATSEGDYSYNEQF	1	1	1	1.684	0.367
TRBV11-1	TRBD1	TRBJ2-7	TRBC2	ASSLEGPTYEQY	1	1	1	2.667	0.098
TRBV11-2	TRBD1	TRBJ2-5	TRBC2	ASSSQVQVETQY	1	1	1	2.519	0.029
TRBV20-1	TRBD1	TRBJ1-2	TRBC1	SARGLTVADGYT	5	1	1	3.390	0.257
TRBV9		TRBJ1-6	TRBC1	ASSGPN SPLH	1		1	1.691	1.676
TRBV9	TRBD2	TRBJ1-2	TRBC1	ASSGKPGTPHYGYT	1	2	1	1.661	0.059
TRBV7-2	TRBD2	TRBJ2-5	TRBC2	ASSLGGFQETQY	1	2	1	2.638	0.050
TRBV28	TRBD1	TRBJ2-1	TRBC2	ASSYRLLSNNEQF	1	1	1	0.624	0.049
TRBV27		TRBJ1-5	TRBC1	ASSLDVRSNQPQH	1		1	0.589	0.048
TRBV28	TRBD2	TRBJ2-1	TRBC2	ASTLTSGSTDEQF	1	2	1	0.536	0.042
TRBV7-2	TRBD1	TRBJ2-5	TRBC2	ASSLAPGLDEKTQY	1	1	1	0.533	0.041
TRBV14	TRBD2	TRBJ2-7	TRBC2	ASSLLAENEQY	2	1	1	0.474	0.040
TRBV6-6		TRBJ2-1	TRBC2	ASSYIQVGEQF	1		1	0.452	0.393
TRBV20-1		TRBJ2-7	TRBC2	SARTTESYEQY	5		1	0.020	0.367
TRBV12-4		TRBJ2-7	TRBC2	ASSLNGYVHEQY	1		1	0.403	0.035
TRBV27	TRBD2	TRBJ2-1	TRBC2	ASSLTPSGNNEQF	1	2	1	0.598	0.024
TRBV9	TRBD2	TRBJ2-2	TRBC2	ASSGSR LAGGKHAGELF	1	2	1	0.564	0.260
TRBV13		TRBJ1-1	TRBC1	ASSLADMNTEAF	1		1	0.764	0.000
TRBV10-3	TRBD2	TRBJ1-4	TRBC1	AISGGPGEKLF	3	1	1	0.897	0.000
TRBV28	TRBD2	TRBJ2-3	TRBC2	ASSYHWSGAGVTDTOY	1	2	1	0.358	0.474
TRBV4-1	TRBD2	TRBJ2-7	TRBC2	ASSQEFGLAGGAYEQY	1	2	1	0.345	0.049
TRBV14	TRBD1	TRBJ1-5	TRBC1	ASSQDRTGPRH	2	1	1	0.080	0.000
TRBV7-2		TRBJ1-5	TRBC1	ASSLPETVTRQPQH	2		1	0.127	0.036
TRBV7-6	TRBD1	TRBJ1-2	TRBC1	ASSMTGLYGYT	1	1	1	0.023	0.259
TRBV12-4		TRBJ2-3	TRBC2	ASSLDTQY	1		1	0.225	0.248
TRBV7-2	TRBD1	TRBJ1-1	TRBC1	ASSLVGNTEAF	2	1	1	0.022	0.227
TRBV4-1	TRBD1	TRBJ2-5	TRBC2	ASSQSGTSQETQY	1	1	1	0.022	0.225
TRBV6-2	TRBD2	TRBJ2-1	TRBC2	ASTPPGLAGGRGEQF	1	2	1	0.208	0.139
TRBV18	TRBD2	TRBJ2-7	TRBC2	ASSPSSGGGREQY	1	2	1	0.208	0.138
TRBV16	TRBD1	TRBJ1-2	TRBC1	ASSHRTGGFYGYT	1	1	1	0.201	0.133
TRBV20-1	TRBD1	TRBJ2-7	TRBC2	SARDPGQGSYEQY	5	1	1	0.192	0.210
TRBV5-6	TRBD1	TRBJ1-2	TRBC1	ASSLTGVHGYT	1	1	1	0.185	0.089
TRBV5-4		TRBJ2-1	TRBC2	ASSLESVWSYNEQF	1		1	0.174	0.089
TRBV6-1	TRBD1	TRBJ2-2	TRBC2	ASQFQGRITGELF	1	1	1	0.173	0.172
TRBV19		TRBJ1-1	TRBC1	ASSIRYTEAF	1		1	0.172	0.113
TRBV28	TRBD1	TRBJ1-6	TRBC1	ASSDSLSTGYN SPLH	1	1	1	0.162	0.162
TRBV9		TRBJ1-6	TRBC1	ASSGNS SPLH	1		1	0.160	0.101
TRBV7-2	TRBD2	TRBJ2-7	TRBC2	ASSPTSGSSYEQY	1	1	1	0.157	0.098
TRBV14	TRBD2	TRBJ2-1	TRBC2	ASSLTPGSEQF	2	2	1	0.855	0.000
TRBV9	TRBD2	TRBJ2-2	TRBC2	ASSGPTSGRAHTGELF	1	2	1	0.744	0.194
TRBV30	TRBD2	TRBJ2-1	TRBC2	AWTLAGDYNEQF	1	2	1	0.738	0.050
TRBV29-1	TRBD1	TRBJ2-1	TRBC2	SVEQALGDRVNEQF	1	1	1	0.590	0.000
TRBV9	TRBD2	TRBJ2-7	TRBC2	ASSPPGLGYEQY	1	1	1	0.627	0.091
TRBV29-1		TRBJ2-3	TRBC2	SVEFGDTQY	1		1	0.942	0.000
TRBV7-2		TRBJ2-7	TRBC2	ASSSGLGTYEQY	1		1	0.764	0.142
TRBV6-1	TRBD2	TRBJ2-5	TRBC2	ASSQGLDLETQY	1	1	1	0.622	0.134
TRBV20-1	TRBD2	TRBJ2-2	TRBC2	SASSGREFGELF	1	2	1	0.895	0.130
TRBV20-1	TRBD2	TRBJ2-3	TRBC2	SASPSRGP SGISDTQY	5	2	1	0.418	0.129

Samples were collected at new diagnosis from patient (Patient #19) with sustained CR post chemotherapy.

Clonal expansion of CD8⁺ T cells in acute myeloid leukemia patients

Table S5. The top 50 clonotypes in CD8⁺ T cells were frequently distributed in CD8⁺ PD-1⁺ populations and CD8⁺ PD-1⁻ populations

Variable Gene	Diversity Gene	Joining Gene	Constant	CDR3 AA	V Gene Allele	D Gene Allele	J Gene Allele	PD-1 ⁺ Freq. (%)	PD-1 ⁻ Freq. (%)
TRBV29-1	TRBD1	TRBJ2-3	TRBC2	SVEWGREGASTDTQY	1	1	1	8.169	0.734
TRBV29-1	TRBD2	TRBJ2-1	TRBC2	SVPQTLSSGPEHEQF	1	1	1	2.272	0.362
TRBV28	TRBD1	TRBJ2-3	TRBC2	ASSRDGRTDTQY	1	1	1	0.910	0.131
TRBV5-6	TRBD1	TRBJ2-3	TRBC2	ASSLAPTGSTDTQY	1	1	1	1.742	0.000
TRBV3-1	TRBD2	TRBJ2-1	TRBC2	ASSQGRDYPYNEQF	1	1	1	1.736	0.172
TRBV14	TRBD2	TRBJ2-7	TRBC2	ASSREYEQY	1	2	1	1.772	0.000
TRBV28	TRBD1	TRBJ1-1	TRBC1	ASSLPGQNTAEF	1	1	1	1.419	0.098
TRBV28	TRBD1	TRBJ1-5	TRBC1	ASSRQGPQH	1	1	1	1.417	0.061
TRBV7-2	TRBD2	TRBJ2-7	TRBC2	ASSFSLGLYEQY	1	1	1	1.399	0.056
TRBV2	TRBD1	TRBJ2-1	TRBC2	ASSRGGAVDEQF	1	1	1	0.335	0.050
TRBV9	TRBD2	TRBJ2-5	TRBC2	ASSPEETSGQETQY	1	1	1	0.589	0.048
TRBV30	TRBD2	TRBJ2-1	TRBC2	AWTLAGDYNEQF	1	2	1	0.670	0.043
TRBV9	TRBD2	TRBJ2-1	TRBC2	ASSVGTFINEQF	1	1	1	0.276	0.043
TRBV29-1		TRBJ2-7	TRBC2	SVELYRVGQYVNEQY	1		1	0.874	0.043
TRBV29-1		TRBJ1-1	TRBC1	SVAPVNTEAF	1		1	0.226	0.042
TRBV29-1		TRBJ1-1	TRBC1	SVETTQNTAEF	1		1	0.226	0.000
TRBV20-1	TRBD2	TRBJ2-2	TRBC2	SASSGREFGELF	1	2	1	0.207	0.038
TRBV23-1	TRBD1	TRBJ2-5	TRBC2	ASSARGLTQETQY	1	1	1	0.896	0.031
TRBV4-3	TRBD2	TRBJ2-5	TRBC2	ASSYGTAGAQY	1	1	1	0.695	0.030
TRBV29-1		TRBJ2-1	TRBC2	SVEEPRSNEQF	1		1	0.781	0.030
TRBV29-1	TRBD1	TRBJ2-5	TRBC2	SVGGHKETQY	1	1	1	0.679	0.000
TRBV6-2		TRBJ2-5	TRBC2	ASSSSQETQY	1		1	0.578	0.029
TRBV7-2	TRBD2	TRBJ2-5	TRBC2	ASSSLGGFQETQY	1	2	1	0.876	0.029
TRBV5-6		TRBJ2-7	TRBC2	ASSLDRSIEQY	1		1	0.466	0.018
TRBV6-2	TRBD2	TRBJ2-5	TRBC2	ASSYPGIRDSIVLQETQY	1	2	1	0.963	0.000
TRBV14	TRBD1	TRBJ1-2	TRBC1	ASRGLTDGYT	1	1	1	0.137	0.017
TRBV29-1	TRBD2	TRBJ2-3	TRBC2	SVEDEVAGVFSTDTQY	1	1	1	0.137	0.016
TRBV12-4		TRBJ2-7	TRBC2	ASSLNGYVHEQY	1		1	0.135	0.000
TRBV7-6	TRBD2	TRBJ2-3	TRBC2	ASTPNQRGVTDQY	1	1	1	0.108	1.160
TRBV11-3	TRBD2	TRBJ2-1	TRBC2	ASSLLAGDNEQF	1	1	1	0.107	1.154
TRBV5-4	TRBD1	TRBJ1-2	TRBC1	ASSLLGDDGYT	1	1	1	0.020	0.878
TRBV14		TRBJ2-1	TRBC2	ASSLTHNEQF	1		1	0.073	0.605
TRBV29-1		TRBJ2-3	TRBC2	SVGGKLLTDTQY	1		1	0.064	0.417
TRBV14	TRBD1	TRBJ1-2	TRBC1	ASSQGPQEGFNQYGT	1	1	1	0.089	0.482
TRBV14		TRBJ2-2	TRBC2	ASSPIVFDGELF	2		1	0.087	0.206
TRBV29-1	TRBD2	TRBJ2-7	TRBC2	SVGLADAYEQY	1	1	1	0.041	0.197
TRBV29-1	TRBD1	TRBJ2-3	TRBC2	SVSSLQKQGTQY	1	1	1	0.031	0.190
TRBV29-1	TRBD2	TRBJ2-3	TRBC2	SVRLAGGPGTQY	1	2	1	0.020	0.168
TRBV7-2	TRBD2	TRBJ2-2	TRBC2	ASSLLPQLAGGSPDGELF	1	2	1	0.083	0.165
TRBV29-1	TRBD1	TRBJ1-4	TRBC1	SAAGHLNEKLF	1	1	1	0.028	0.165
TRBV28	TRBD1	TRBJ1-1	TRBC1	ASSFQGTEAF	1	1	1	0.973	0.000
TRBV18	TRBD2	TRBJ2-7	TRBC2	ASSPPSSGGGREQY	1	2	1	0.771	0.159
TRBV2	TRBD1	TRBJ1-1	TRBC1	ARGDRDTEAF	1	1	1	0.978	0.156
TRBV23-1	TRBD2	TRBJ2-7	TRBC2	ASSQPRGGQRYEQY	1	2	1	0.477	0.000
TRBV23-1	TRBD2	TRBJ2-1	TRBC2	ASSHLTSGGSYNEQF	1	1	1	0.477	0.000
TRBV28	TRBD2	TRBJ2-7	TRBC2	ASTIKGSTPYEQY	1	2	1	0.367	0.148
TRBV28	TRBD2	TRBJ2-3	TRBC2	ASSYHWSGAGVTDQY	1	2	1	0.199	0.147
TRBV14	TRBD2	TRBJ2-1	TRBC2	ASSRLAGGPIDEQF	1	1	1	0.074	0.145
TRBV7-9	TRBD2	TRBJ2-4	TRBC2	ASSPLMTGGNIQY	1	2	1	0.164	0.136
TRBV7-2	TRBD2	TRBJ2-2	TRBC2	ASSLDNSVRTGELF	1	1	1	0.255	0.129

Samples were collected after treatment from patient (Patient #19) with sustained CR post chemotherapy.

Clonal expansion of CD8⁺ T cells in acute myeloid leukemia patients

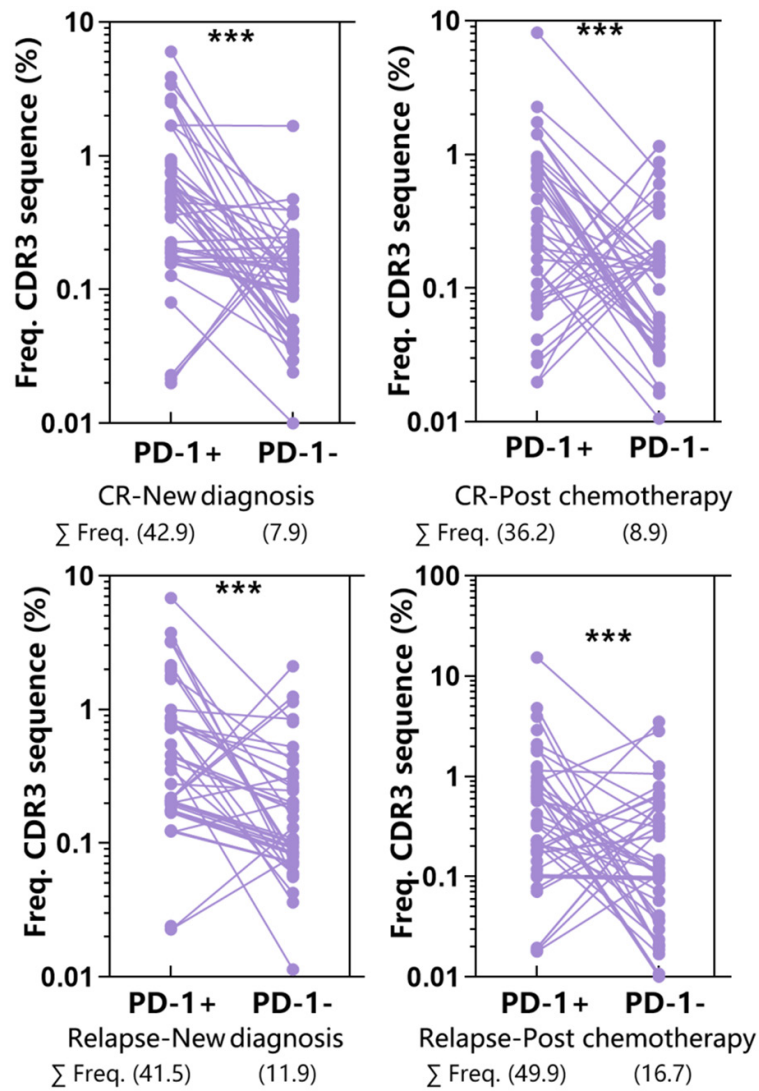


Figure S5. The top 50 clonotypes in CD8⁺ PD-1⁺ T cells were frequently distributed in CD8⁺ PD-1⁻ populations. A dot is used to represent one patient or one donor sample. CR: patients who were newly diagnosed with AML and remained in complete remission after chemotherapy. Relapse: patients who were newly diagnosed with AML and relapsed post chemotherapy. The Wilcoxon signed-rank test was used for matched paired comparisons. *** indicates P < 0.01.