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# Disruption of *TET2* promotes the therapeutic efficacy of CD19-targeted T cells

Joseph A. Fraietta<sup>1,2,3,4</sup>, Christopher L. Nobles<sup>5</sup>, Morgan A. Sammons<sup>6,10</sup>, Stefan Lundh<sup>1,2</sup>, Shannon A. Carty<sup>2,11</sup>, Tyler J. Reich<sup>1,2</sup>, Alexandria P. Cogdill<sup>1,2</sup>, Jennifer J. D. Morrisette<sup>3</sup>, Jamie E. DeNizio<sup>7,8</sup>, Shantanu Reddy<sup>5</sup>, Young Hwang<sup>5</sup>, Mercy Gohil<sup>1,2</sup>, Irina Kulikovskaya<sup>1,2</sup>, Farzana Nazimuddin<sup>1,2</sup>, Minnal Gupta<sup>1,2</sup>, Fang Chen<sup>1,2</sup>, John K. Everett<sup>5</sup>, Katherine A. Alexander<sup>6</sup>, Enrique Lin-Shiao<sup>6</sup>, Marvin H. Gee<sup>9</sup>, Xiaojun Liu<sup>1,2</sup>, Regina M. Young<sup>1,2</sup>, David Ambrose<sup>1,2</sup>, Yan Wang<sup>1,2</sup>, Jun Xu<sup>1,2</sup>, Martha S. Jordan<sup>2,3</sup>, Katherine T. Marcucci<sup>1,2</sup>, Bruce L. Levine<sup>1,2,3</sup>, K. Christopher Garcia<sup>9</sup>, Yangbing Zhao<sup>1,2</sup>, Michael Kalos<sup>1,2,3</sup>, David L. Porter<sup>1,2,7</sup>, Rahul M. Kohli<sup>5,7,8</sup>, Simon F. Lacey<sup>1,2,3</sup>, Shelley L. Berger<sup>6</sup>, Frederic D. Bushman<sup>5</sup>, Carl H. June<sup>1,2,3,4\*</sup> & J. Joseph Melenhorst<sup>1,2,3,4\*</sup>

<sup>1</sup>Center for Cellular Immunotherapies, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>2</sup>Abramson Cancer Center, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>3</sup>Pathology and Laboratory Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>4</sup>Parker Institute for Cancer Immunotherapy, University of Pennsylvania, Philadelphia, PA, USA. <sup>5</sup>Department of Microbiology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>6</sup>Department of Cell and Developmental Biology, Epigenetics Program, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>7</sup>Department of Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>8</sup>Department of Biochemistry and Biophysics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. <sup>9</sup>Department of Molecular and Cellular Physiology, Stanford University School of Medicine, Stanford, CA, USA. <sup>10</sup>Present address: Department of Biology, University at Albany, State University of New York, Albany, NY, USA. <sup>11</sup>Present address: Department of Internal Medicine and Rogel Cancer Center, University of Michigan, Ann Arbor, MI, USA. \*e-mail: [cjune@upenn.edu](mailto:cjune@upenn.edu); [mej@upenn.edu](mailto:mej@upenn.edu)

**Supplementary Table 1: Patient-10 baseline characteristics and CTL019 treatment information.**

Age/Sex	CLL Characteristics	CLL Involvement at Baseline	Previous Therapies	CTL019 Treatment Information
78/Male	ATM deletion (del); del11q; del17p	85% of marrow; bulky adenopathy with the largest mass in the mesentary measuring 13.5 × 6.8 cm	Rituxan-CVP* ×6 cycles Rituxan Alone Fludarabine/Rituxan; Excellent Partial Response Chlorambucil; Progression Bendamustine ×1 cycle; Progression CHOP** ×8 cycles PCR <sup>±</sup> with stable to mild progression on PET/CT <sup>‡</sup> 2 weeks later	Lymphodepleting chemotherapy given prior to CTL019 cell infusion: pentostatin/cyclophosphamide  2 adoptive transfers of 3.75 × 10 <sup>8</sup> and 5.61 × 10 <sup>8</sup> autologous CTL019 cells (82% CD4+; 18% CD8+)
<p>*cyclophosphamide, vincristine and prednisolone</p> <p>**cyclophosphamide, doxorubicin, vincristine and prednisone</p> <p><sup>±</sup>pentostatin, cyclophosphamide and rituximab</p> <p><sup>‡</sup>positron emission tomography–computed tomography</p>				

**Supplementary Table 2: Tumor burden evaluated by IgH deep sequencing analysis of peripheral blood and bone marrow from Patient-10.**

Sample Information			IgH Repertoire Assessment					Tumor Clone		
Sample Type	First Infusion <sup>1</sup>	Second Infusion <sup>2</sup>	Entropy <sup>3</sup>	Clonality <sup>4</sup>	Max Frequency (%) <sup>5</sup>	Gene Rearrangements <sup>6</sup>	Fraction of Nucleated <sup>7</sup>	Estimated # of Genomes <sup>8</sup>	Log Reduction (First Infusion) <sup>9</sup>	Log Reduction (Second Infusion) <sup>10</sup>
Peripheral Blood	-29		0.078583	0.990387	99.4	110710	0.343804	109271		
	14		0.067824	0.991416	99.46	157699	0.321995	156371	0.028	
	28		0.164639	0.967638	98.13	10303	0.025852	10034	1.124	
	63	-7	0.154459	0.973519	98.33	60725	0.11781	59601	0.465	
	69	-1	0.149261	0.971558	98.31	47691	0.132377	46809	0.415	
	84	14	0.152248	0.97316	98.34	115697	0.176816	113715	0.289	-0.176
	121	51	0.096938	0.978857	98.93	5126	0.014364	5011	1.379	0.965
	147	77	1.479932	0.260034	15.07	22	0	0	5.499	5.084
	259	189	2.613258	0.175609	14.98	40	0	0	5.532	5.117
	351	281	2.613371	0.213297	15.02	60	0	0	5.532	5.117
	526	456	2.278436	0.240522	16.07	39	0	0	5.503	5.088
	619	549	1.829257	0.348405	13.84	54	0	0	5.491	5.076
	710	640	NA	NA	38.33	12	0	0	5.528	5.113
1177	1107	2.611971	0.213718	12.09	69	0	0	5.479	5.065	
Bone Marrow	101	31	0.015523	0.997597	99.79	139042	0.301654	138663	NA	
	442	372	2.336592	0.167689	11.21	31	0	0	5.458	
	801	731	1.351141	0.32443	17.71	16	0	0	5.247	

<sup>1</sup>Day relative to first infusion; <sup>2</sup>Day relative to second infusion; <sup>3</sup>Shannon's entropy, a measure of the shape of the distribution of the read counts with a low entropy denoting a clonal sample composition; <sup>4</sup>Clonality= 1-(entropy/Log<sub>2</sub> productive unique rearrangements). Clonality ranges from 0-1 with 1 denoting a clonal and 0 a polyclonal sample; <sup>5</sup>Maximum frequency for each sample; <sup>6</sup>The number of unique IgH rearrangements; <sup>7</sup>The proportion the leukemic clone makes up of the total genomic mass of all input B-cells; <sup>8</sup>The estimated number of diploid genomes (or cells) with this leukemia rearrangement; <sup>9</sup>Log<sub>10</sub> reduction of the leukemic clonotype relative to the baseline sample; <sup>10</sup>Log<sub>10</sub> reduction relative to the second infusion baseline sample; NA, Not available

**Supplementary Table 3: Summary statistics for ATAC-seq of Patient-10 CD8+ CAR+ and CD8+ CAR- T-cells.**

<b>Sample Name</b>	<b>Nextera Index</b>	<b>Total Reads (paired-end 2 × 75 bp)</b>	<b>Unique Concordant Alignment #</b>	<b>% Aligned Concordantly</b>
CD8+ CAR+ T-cells (Replicate 1)	CAGAGAGG	98,139,264	89,411,351	91.1
CD8+ CAR+ T-cells (Replicate 2)	CTCTCTAC	78,513,260	75,702,498	96.4
CD8+ CAR- T-cells (Replicate 1)	GGACTCCT	220,099,187	204,644,381	93.0
CD8+ CAR- T-cells (Replicate 2)	TAGGCATG	98,975,732	91,325,785	92.3