3 Supplementary Methods

4 *Flow cytometry*

Fluorescently labeled antibodies were used to detect cell surface markers and intracellular proteins
(supplementary table 2). Cells were stained as previously described¹. In short: cells were harvested and
stained on ice for 20 minutes with fluorescently labeled antibodies in PBA; a solution of 0.5% bovine serum
albumin and 0.02% sodium azide in PBS. Cells were then washed in PBA, resuspended in an appropriate
volume of PBA and acquired on an LSR Fortessa (BD Biosciences).

10

11 Cell culture

12 PBMCs from CLL patients and HD were thawed and either directly analyzed or cultured for 1-29 days as 13 indicated. PBMCs, CAR-T cells, the mantle cell lymphoma (MCL) cell line JeKo-1 (CRL-3006; ATCC), and the 14 NIH3T3 fibroblast (3T3) and CD40L-transfected NIH3T3 fibroblast (3T40) cell lines were cultured in RPMI 15 1640 (#22400089; Gibco) supplemented with 10% FCS by volume and supplemented with Penicillin and Streptomycin (#15140-122; ThermoFisher Scientific) at 37°C and 5% CO₂. All final PBMC concentrations 16 17 were adjusted to 3*10⁶ cells per ml. T cells were stimulated using soluble anti-CD3 IgM (91 ng/µl, clone 18 1XE; Sanquin) and anti-CD28 IgG (3 µg/ml, clone 15E8; Sanquin). CLL cells were co-cultured with 3T3 or 19 3T40 cells as previously described^{23,24}. After 2 days of culturing CLL cells with either 3T3 or 3T40 cells with or without ibrutinib (S2680, Selleckchem; 0.1 μM, or 1 μM), imatinib (13139, Cayman Chemical) (1 μM),
dasatinib (S1021, Selleckchem) (1 μM), and Bay 11-7082 (196870, Calbiochem) (250 nM), CLL cells were
detached by gently resuspending the cell culture medium. The kinase inhibitors were washed away
thoroughly before proceeding an autologous T cell co-culture. The treated or untreated CLL cells were
then co-cultured in a 1:1 ratio with autologous PBMCs.

25

26 CAR T-cell production

27 To generate CAR-T cells, 293T cells (CRL-3216, ATCC) were transfected at 80% confluency with 15 ug of the lentiviral vector encoding the anti-CD19 4-1BB CAR (CAR19, Tisagenlecleucel; Novartis)⁷, and 28 29 packaging plasmids pRSV REV (18 ug, Rev expression plasmid; plasmid #12253, Addgene), pMDLg/p RRE 30 (18 ug, Gag/Pol expression plasmid; plasmid #12251, Addgene), and pVSV-G (7 ug, VSV glycoprotein 31 expression plasmid; plasmid #138479, Addgene) using Lipofectamine 20000 (11668019, Thermofisher). 32 The lentivirus was harvested after 24 hours, and concentrated by ultracentrifugation. Prior to transduction 33 with the CAR19 encoding lentivirus, T cells were purified from PBMCs from HD or CLL patients using a 34 negative T-cell selection kit following manufacturer's instructions (17951; StemCell). T cells were 35 stimulated using CD3/CD28 coated beads according to manufacturer's instructions (11131D; ThermoFisher Scientific), and supplemented with 100 U/ml recombinant human IL-2 (200-02; Peprotech). 36 37 24h post activation, the T cells were transduced with the lentiviral particles encoding CAR19. The CAR-T cells were subsequently expanded for 2 weeks to obtain sufficient CAR-T cells while the cell culture media 38

was refreshed every 3-4 days. Purified CAR-T cells were obtained by staining CAR-T cells with biotinylated
protein L (29997, ThermoFisher Scientific), and Streptavidin (554061, BD Biosciences), and subsequently
cell sorting using a BD FACSAria[™] II.

42

43 RNA sequencing

44 FACS sorted CLL cells (based on CD19 positivity and cell viability using the SH800 Cell Sorter (Sony)) were 45 cultured for 48 hours on 3T3 fibroblasts, 3T40 fibroblasts or 3T40 fibroblasts with Dasatinib (100 nM). The 46 cells were pelleted and total RNA was isolated using the RNeasy Mini kit (Qiagen) according to the 47 manufacturer's protocol. RNA quality was assessed using the High Sensitivity RNA ScreenTape (Agilent 48 Technologies). Sequencing libraries were prepared with the KAPA mRNA HyperPrep kit (Roche), all 49 samples were amplified for 14 cycles. Barcoded samples were pooled based on Qubit DNA HS 50 (ThermoFisher Scientific) measurement and sequenced on Illumina HiSeq 4000 (Illumina) using a single-51 read 50 bp standard protocol. Sequencing depth was approximately 20M reads per sample. Raw FASTQ 52 files were subjected to quality control using FastQC and trimmed using Trimmomatic (v0.32). Reads were 53 aligned to the human reference genome (GRCh38/hg38) using HISAT2(v2.1.0)². Gene level counts were 54 obtained using HTSeq (v0.11.0) and the human GTF (gene transfer format) file from Ensembl (release 94). X and Y chromosomal genes were removed prior to differential expression analysis due to a large sex-55 specific effect. Differential expression was assessed with DESeq2³, using an FDR cut-off of 0.05. 56 57 Differentially expressed genes (DEGs) between the different conditions were used for retrieving the

58	inversely regulated genes, which were defined as genes that changed in opposite directions comparing
59	the 3T40 vs 3T3 DEGs with the 3T40 + dasatinib vs 3T40 DEGs. From this set of genes, those involved in
60	contact-dependent cell-cell interactions were extracted using the publicly available ligand-receptor pair
61	repository curated by Armingol et al. 2021 (<u>https://github.com/LewisLabUCSD/Ligand-Receptor-Pairs</u>) ^{4,5} .
62	Plots were generated with ggplot2 (Bioconductor) ^{6} and gplots (CRAN) using R ⁷ , Bioconductor and
63	Rstudio ^{8,9} .

64	Supplementary table	1 Characteristics of treatment-naive	CLL patients included in this study
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	Sex	٨٥٥	Rai	Mutation	Leuco	% CD5+	% CD3+	CMV
<u> </u>		Age	Stage	Status	*10 ⁹ /L	CD19+		Status
1	Male	72	0	Mutated	71.4	96.7	1.7	+
2	Female	74	0	Mutated	39.6	96.9	7.1	+
3	Male	66	I	Mutated	36.2	89.9	6.7	+
4	Female	69	I	Mutated	30.1	85.7	6.9	N.D.
5	Male	65	0	N.D.	127	55.7	1.6	N.D.
6	Male	68	I	Mutated	39	19.5	0.4	N.D.
7	Male	27	N.D.	Unmutated	286	65.4	0.6	+
8	Female	55	N.D.	Mutated	92.6	91.9	5.4	N.D.
9	Male	73	0	N.D.	129.7	91.7	0.3	+
10	Female	60	0	Mutated	152	91.8	5.2	+
11	Male	56	0	Mutated	123.33	92.9	2.4	+
12	Male	74	II	Mutated	69.67	96.8	2.3	+
13	Female	74	0	Mutated	59.6	91	3.1	+
14	Male	72	0	Unmutated	77.8	93.08	4.55	+
15	Female	62	I	Mutated	139	91.7	9.1	N.D.
16	Male	66	I	N.D.	90.92	96.14	2.94	N.D.
17	Male	66	IV	Mutated	41.06	82.7	15.86	N.D.
18	Male	66	0	N.D.	51.1	88.45	9.67	N.D.
19	Female	70	N.D.	N.D.	24.87	90.68	7.59	N.D.
20	Male	55	0	N.D.	69.64	92.33	6.05	N.D.
21	Female	57	0	Mutated	89.9	95.89	3.55	N.D.
22	Male	58	II	Mutated	116.93	94.81	4.73	+
23	Female	79	0	N.D.	50.39	90.91	7.64	N.D.
24	Male	61	III	Mutated	200.68	94.82	4.43	-

Female	75	N.D.	Unmutated	85.54	87.45	10.21	N.D.
Male	64	0	Mutated	52.26	94	4.69	+
Female	69	1	Mutated	76.82	90.29	7.49	N.D.
Female	63	II	Mutated	60.37	86.44	12.02	N.D.
Female	70	N.D.	Mutated	223.94	94.98	4.34	N.D.
Male	66	N.D.	Mutated	221.75	95.62	3.66	+
Female	62	0	Mutated	91.81	91.67	7.34	+
Female	69	1	Mutated	91.17	93.59	5.29	N.D.
Male	67	0	Mutated	118.03	98.09	1.77	N.D.
Male	51	N.D.	Mutated	167.31	96.05	3.06	+
Female	60	N.D.	N.D.	124.82	96.16	3.19	N.D.
Male	71	0	N.D.	19.89	89.18	8.64	N.D.
Female	68	0	Mutated	24.5	90.1	6.8	-
Male	73	N.D.	Mutated	29.5	89.3	3.8	N.D.
Female	83	I	Mutated	25.05	85.25	11.75	+
Male	79	I	Mutated	44.9	74	2.4	-
Male	59	111	Mutated	58.7	93	4.4	-
Male	75	II	Mutated	58.4	92.7	1.7	+
Female	77	0	Unmutated	55.87	88.68	3.65	N.D.
Male	81	1	Mutated	183.48	78	1.2	-
Male	60		Mutated	85.2	93.7	5.7	-
Male	81	N.D.	Mutated	85.2	98.23	1.42	+
	FemaleMaleFemaleFemaleFemaleMaleFemaleMaleFemaleMaleFemaleMaleFemaleMaleFemaleMaleFemaleMaleFemaleMaleFemaleMale	Female75Male64Female69Female63Female70Male66Female62Female69Male67Male51Female60Male71Female68Male73Female83Male79Male59Male75Female81Male81Male81	Female 75 N.D. Male 64 0 Female 69 I Female 63 II Female 70 N.D. Male 66 N.D. Female 62 0 Female 69 I Male 67 0 Male 67 0 Male 51 N.D. Female 60 N.D. Female 60 N.D. Female 60 N.D. Female 63 0 Male 71 0 Female 68 0 Male 73 N.D. Female 83 I Male 79 I Male 59 III Male 75 I Female 77 0 Male 81 I Male 60 III Male 81 N.D.	Female75N.D.UnmutatedMale640MutatedFemale69IMutatedFemale63IIMutatedFemale70N.D.MutatedMale66N.D.MutatedFemale620MutatedFemale69IMutatedMale670MutatedMale51N.D.MutatedMale51N.D.MutatedFemale60N.D.N.D.Male710N.D.Female680MutatedMale73N.D.MutatedMale79IMutatedMale59IIIMutatedMale75IMutatedMale81IMutatedMale81N.D.Mutated	Female 75 N.D. Unmutated 85.54 Male 64 0 Mutated 52.26 Female 69 I Mutated 76.82 Female 63 II Mutated 60.37 Female 63 II Mutated 223.94 Male 66 N.D. Mutated 221.75 Female 62 0 Mutated 91.81 Female 62 0 Mutated 91.17 Male 67 0 Mutated 118.03 Male 51 N.D. Mutated 167.31 Female 60 N.D. N.D. 124.82 Male 71 0 N.D. 19.89 Female 68 0 Mutated 24.5 Male 73 N.D. Mutated 25.05 Male 79 I Mutated 58.7 Male 59 III Mutated<	Female 75 N.D. Unmutated 85.54 87.45 Male 64 0 Mutated 52.26 94 Female 69 I Mutated 76.82 90.29 Female 63 II Mutated 60.37 86.44 Female 70 N.D. Mutated 223.94 94.98 Male 66 N.D. Mutated 221.75 95.62 Female 62 0 Mutated 91.81 91.67 Female 69 I Mutated 91.81 93.59 Male 67 0 Mutated 91.17 93.59 Male 67 0 Mutated 167.31 96.05 Female 60 N.D. N.D. 124.82 96.16 Male 71 0 N.D. 19.89 89.18 Female 68 0 Mutated 24.5 90.1 Male 73	Female75N.D.Unmutated85.5487.4510.21Male640Mutated52.26944.69Female69IMutated76.8290.297.49Female63IIMutated60.3786.4412.02Female70N.D.Mutated223.9494.984.34Male66N.D.Mutated221.7595.623.66Female620Mutated91.8191.677.34Female69IMutated91.1793.595.29Male670Mutated118.0398.091.77Male51N.D.Mutated167.3196.053.06Female60N.D.N.D.124.8296.163.19Male710N.D.19.8989.188.64Female680Mutated29.589.33.8Female681Mutated29.585.2511.75Male73N.D.Mutated25.0585.2511.75Male75IIMutated58.7934.4Male75IIMutated58.788.683.65Male81IMutated183.48781.2Male60IIIMutated85.293.75.7Male60IIIMutated85.293.75.7

65 N.D.: Not determined, +: Positive, -: Negative

66

67 Supplementary table 2

Marker	Manufacturer	Product
	manaractarer	ID
CD3	eBioscience	56-0038-82
CD4	BD Biosciences	555349
CD4	Biolegend	317442
CD5	eBioscience	12-0059-42
CD8	BD Biosciences	580347
CD8	BD Biosciences	563823
CD19	BD Biosciences	555415
CD19	Beckman	IM3628
CD24	Biolegend	311120
CD25	BD Biosciences	340907
CD25	BD Biosciences	563701
CD27	BD Biosciences	563816
CD45RA	BD Biosciences	563953
CD45RA	Biolegend	304135
CD52	Biolegend	316004
CD54	Biolegend	322720

CD58	Biolegend	330916
CD70	Biolegend	355111
CD71	BD Biosciences	563768
CD71	eBioscience	11-0719-41
CD80	eBioscience	11-0809-41
CD86	BD Biosciences	555660
CD95	BD Biosciences	564710
CD107a	Biolegend	561348
PD-1	BD Biosciences	561272
PD-L1	Biolegend	329731
4-1BBL	Biolegend	311507
OX-40L	Biolegend	326307
MHC-I	Biolegend	311438
MHC-II	Biolegend	361716
Siglec-10	BD Biosciences	566588
Siglec-10	Biolegend	347603
IFNγ	BD Biosciences	563563
IL-2	BD Biosciences	340450
ΤΝFα	BD Biosciences	557996
Granzyme B	BD Biosciences	562462
Perforin	Antibodychain	2140540

69 Supplementary references

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94 (A) PBMCs from HD and CLL patients were stimulated with a single dose of soluble CD3/CD28 antibodies
95 and kept in culture for 14 days. Expression of CD25 was measured during T-cell activation over a period
96 of 14 days (n=3-5). (B) Additionally, after an initial 14 days of stimulation, the T cells were re-stimulated
97 for 2 days and degranulation (CD107a), IFNγ, IL-2, and TNFα were measured on CD4 T cells (HD, n=4; CLL,
98 n=3). *P* values were calculated by a 1-way ANOVA, followed by a Šídák's test for multiple comparisons (B).
99 Data are presented as mean ± SEM, *p≤0.05, **p≤0.01, ***p≤0.001.

Transwell system set-up



100

101 Supplemental figure 2:

- 102 Schematic overview of a transwell experiment to determine the relevance of cell-cell contact of CD40-
- stimulated cells on T-cell activation. Red cells indicate CD40-primed CLL cells and blue cells indicate fresh
- 104 CLL PBMCs labelled with CTV, these cells are mixed either allowing cell-cell contact or preventing cell-cell
- 105 contact due to the transwell insert.





120 Supplemental figure 4:

121 (A) PBMCs from 4 CLL patients were thawed and cultured on a layer of CD40L expressing fibroblasts for 2 122 days with or without 1 uM dasatinib. Heat map showing DESeq2's normalized counts for each patient 123 (column) of genes (rows) that are inversely correlated between the 3T40 vs 3T3 comparison and the 3T40 124 + DAS vs 3T40 comparison. Genes known to be involved in contact-dependent cell-cell interaction were 125 selected. CD24 and CD52 were identified as potential targets of interest. (B) Variation in CD24 expression 126 on CLL cells from patients in different disease stages. PBMCs from patients in different disease stages 127 indicated by the WBC/leucocyte count in the blood, were thawed and CD24 expression on CLL cells 128 (CD5+CD19+) was measured using flow cytometry. (C) Geometric Mean fluorescence intensity of CD24 on 129 CLL cells from patients in different disease stages



131

(A) PBMCs derived from CLL patients and HD were incubated with 1 μg/ml alemtuzumab for 1 hour after
which T cells were stimulated. T cells were measured for expression of CD25 (HD, n=4; CLL, n=5). (B)
PBMCs from CLL patients were stimulated using soluble CD3/CD28 antibodies in presence or absence of
CD24 and CD52 blocking antibodies. Five minutes after activation, the T cells were stained and analyzed
for phosphorylation of tyrosine residue 493 in ZAP70 (n=4). (C and D) PBMCs from CLL patients were preincubated for 1 hour with CD24 and CD52 blocking antibodies or without. Next, T-cell stimulation was

¹³² Supplemental figure 5:

139 performed using soluble CD3/CD28 antibodies (baseline and 5 minutes) and CD3ζ (C) and ZAP70 (D) 140 phosphorylation was measured (n=2). (E-H) PBMCs from CLL patients were cultured for 16 days in 141 presence of a single dose of soluble CD3/CD28 antibodies with or without CD24 and CD52 blocking 142 antibodies. During the culturing period, T-cell activation (E: CD69, F: CD52, and G: CD71), as well as 143 expression of PD-1 (H) was measured. Single arrows denote days on which CD24 and CD52 blocking 144 antibodies were re-added, and double arrows indicate days on which both cell culture medium was 145 refreshed as well as the addition of fresh CD24 and CD52 blocking antibodies. P values were calculated by 146 an unpaired or paired t-test (A and B). Data are presented as mean \pm SEM, $p \leq 0.05$, $****p \leq 0.0001$.