Peripheral T-cell lymphoma cell line T8ML-1 highlights conspicuous targeting of PVRL2 by t(14;19)(q11.2;q13.3)

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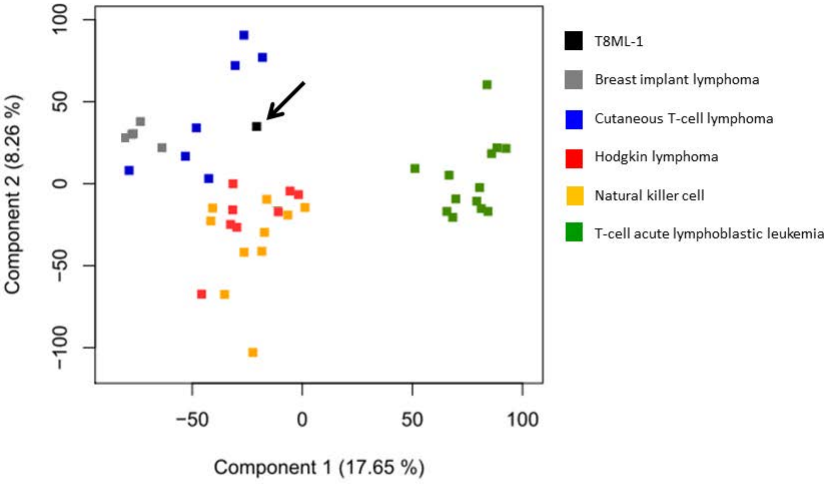
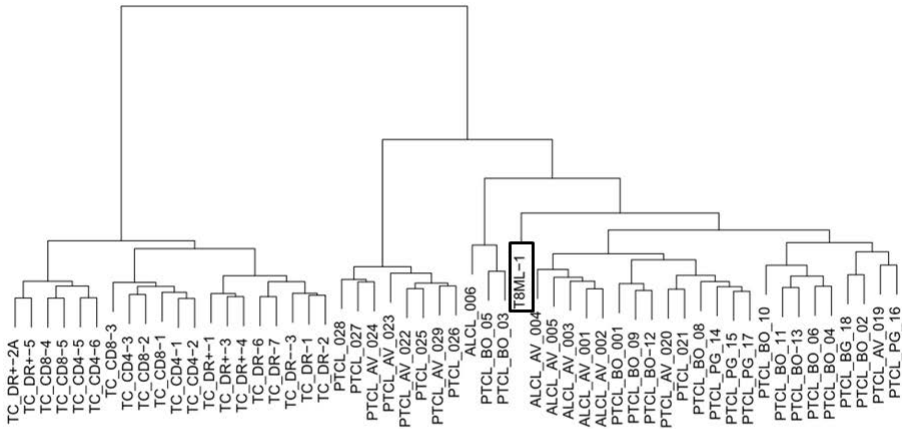
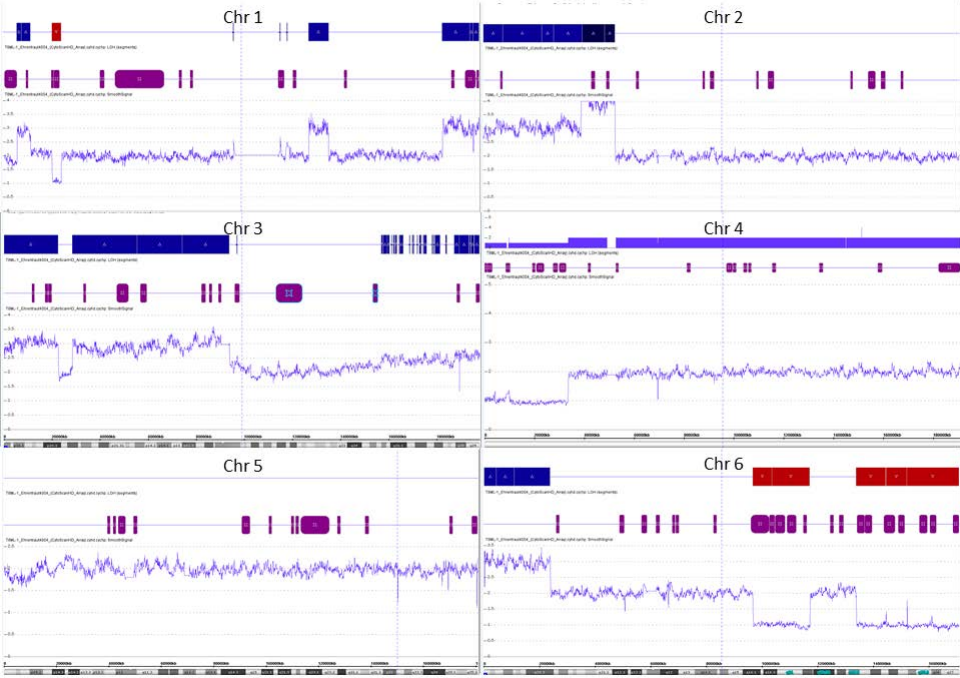
S1A


Component 2 (8.26 %)
100
50
0
−50
−100
−50
0
50
100
Component 1 (17.65 %)
T8ML-1
Breast implant lymphoma
Cutaneous T-cell lymphoma
Hodgkin lymphoma
Natural killer cell
T-cell acute lymphoblastic leukemia

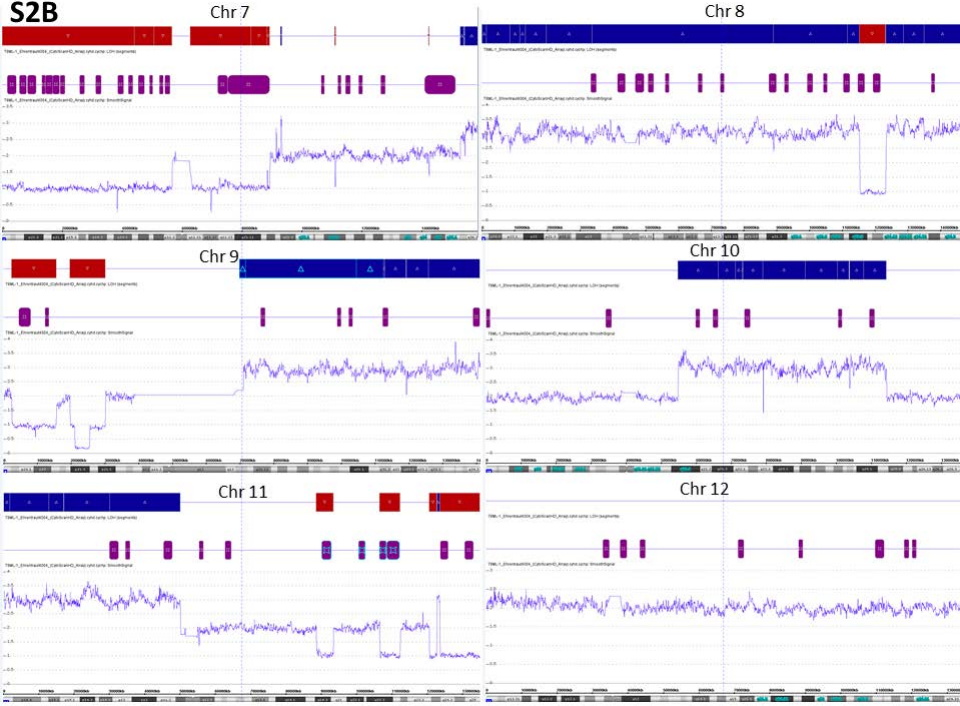
S1B


TC_DR+-2A
TC_DR+-5
TC_CD8-4
TC_CD8-5
TC_CD4-5
TC_CD4-6
TC_CD8-3
TC_CD4-3
TC_CD8-2
TC_CD8-1
TC_CD4-1
TC_CD4-2
TC_DR+-1
TC_DR+-3
TC_DR+-4
TC_DR-6
TC_DR-7
TC_DR--3
TC_DR-1
TC_DR-2
PTCL_028
PTCL_027
PTCL_AV_024
PTCL_AV_023
PTCL_AV_022
PTCL_025
PTCL_AV_029
PTCL_026
ALCL_006
PTCL_BO_05
PTCL_BO_03
T6ML-1
ALCL_AV_004
ALCL_AV_005
ALCL_AV_003
ALCL_AV_001
ALCL_AV_002
PTCL_BO_001
PTCL_BO_09
PTCL_BO-12
PTCL_AV_020
PTCL_021
PTCL_BO_08
PTCL_PG_14
PTCL_PG_15
PTCL_PG_17
PTCL_BO_10
PTCL_BO_11
PTCL_BO-13
PTCL_BO_06
PTCL_BO_04
PTCL_BG_18
PTCL_BO_02
PTCL_AV_019
PTCL_PG_16

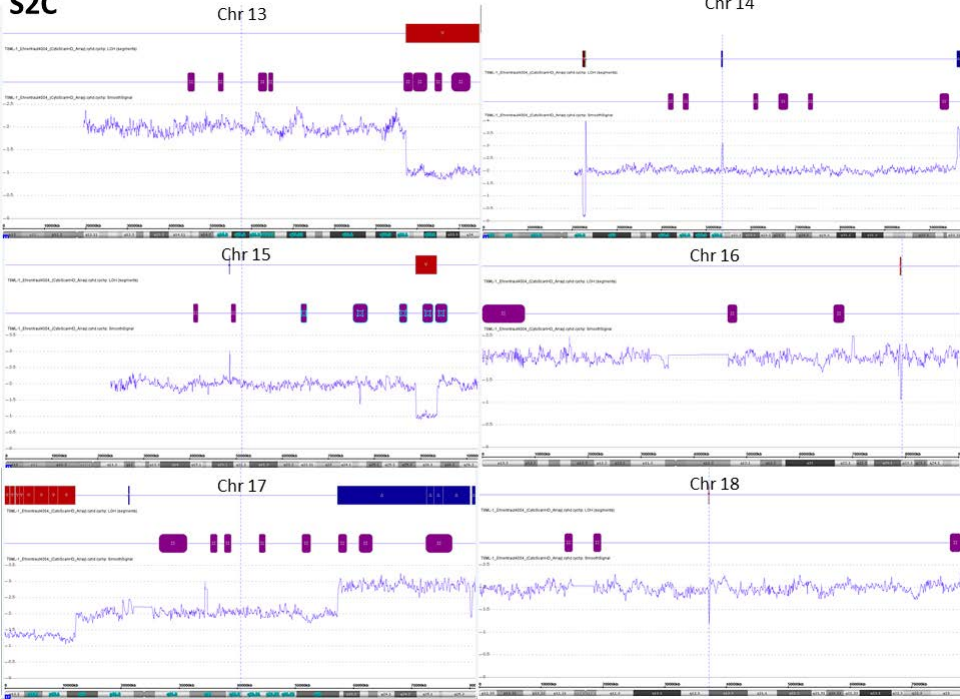
S2A



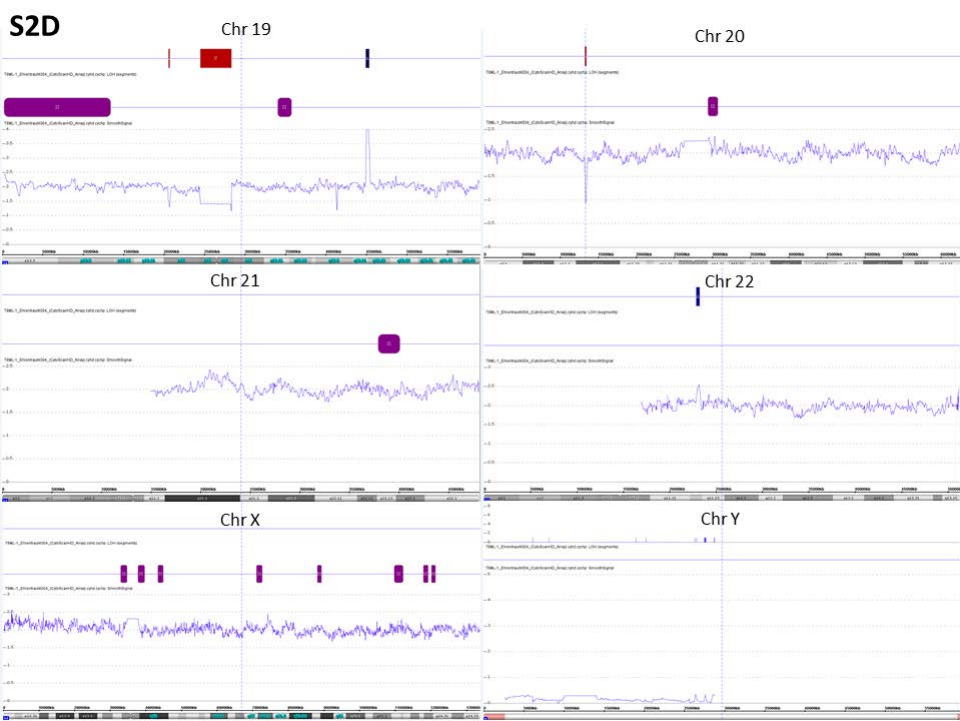
S2B



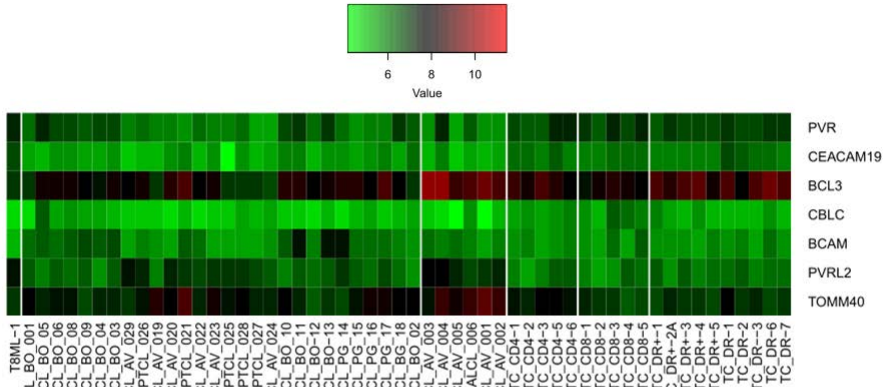
S2C



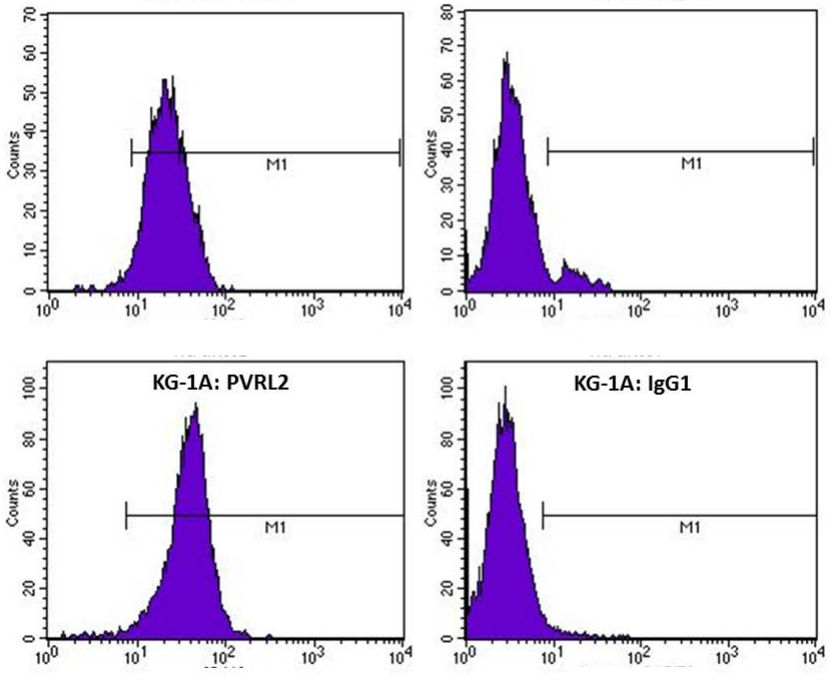
S2D



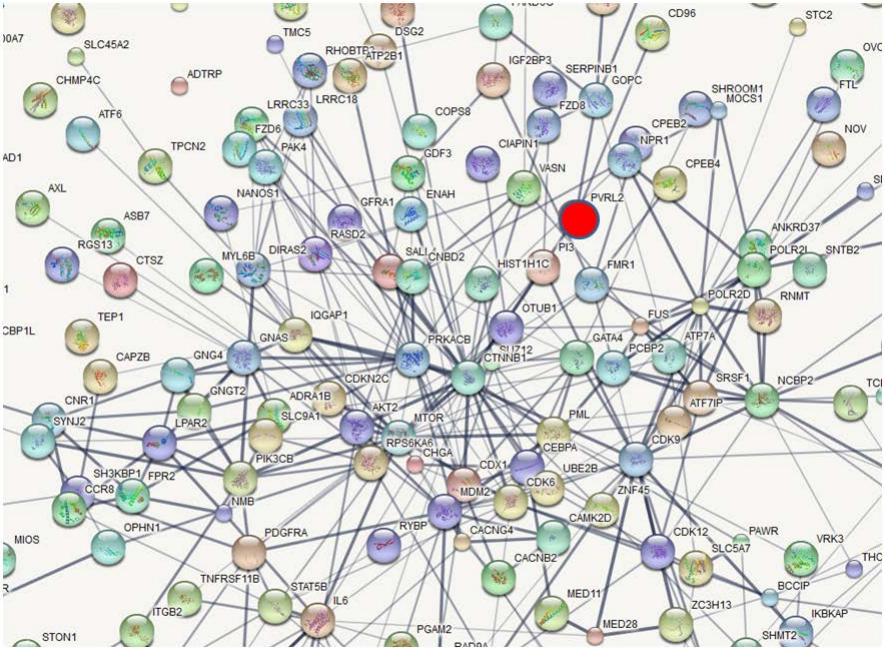
S3


6
8
10
Value
PVR
CEACAM19
BCL3
CBLC
BCAM
PVRL2
TOMM40
T4ML−1
PTCL_BO_001
PTCL_BO_05
PTCL_BO_06
PTCL_BO_08
PTCL_BO_09
PTCL_BO_04
PTCL_BO_03
PTCL_AV_029
PTCL_026
PTCL_AV_019
PTCL_AV_020
PTCL_021
PTCL_AV_022
PTCL_AV_023
PTCL_025
PTCL_028
PTCL_027
PTCL_AV_024
PTCL_BO_10
PTCL_BO_11
PTCL_BO−12
PTCL_BO−13
PTCL_PG_14
PTCL_PG_15
PTCL_PG_16
PTCL_PG_17
PTCL_BG_18
PTCL_BO_02
ALCL_AV_003
ALCL_AV_004
ALCL_AV_005
ALCL_006
ALCL_AV_001
ALCL_AV_002
TC_CD4−1
TC_CD4−2
TC_CD4−3
TC_CD4−5
TC_CD4−6
TC_CD8−1
TC_CD8−2
TC_CD8−3
TC_CD8−4
TC_CD8−5
TC_DR+−1
TC_DR+−2A
TC_DR+−3
TC_DR+−4
TC_DR+−5
TC_DR−1
TC_DR−2
TC_DR−−3
TC_DR−6
TC_DR−7

S4



S5


CD96
STC2
SLC45A2
TMC5
DSG2
RHOBTB3
ATP2B1
IGF2BP3
SERPINB1
GOPC
CHMP4C
ADTRP
LRRC33
LRRC18
SHROOM1
MOCS1
FTL
ATF6
COPS8
FZD8
CPEB2
NOV
FZD6
PAK4
NPR1
TPCN2
GDF3
CIAPIN1
CPEB4
VASN
AXL
NANOS1
ENAH
PVRL2
ASB7
GFRA1
RASD2
ANKRD37
RGS13
CTSZ
MYL6B
DIRAS2
SALL4
CNBD2
PI3
HIST1H1C
FMR1
POLR2L
SNTB2
POLR2D
RNMT
TEP1
IQGAP1
OTUB1
FUS
GNAS
PRKACB
CTNNB1
GATA4
PCBP2
ATP7A
CAPZB
GNG4
CDKN2C
SRSF1
NCBP2
GNGT2
ADRA1B
ATF7IP
CNR1
AKT2
MTOR
PML
SYNJ2
SLC9A1
LPAR2
RPS6KA5
CHGA
CEBPA
CDK9
PIK3CB
CDX1
UBE2B
SH3KBP1
FPR2
CCR8
CDK6
ZNF45
MDM2
NMB
CAMK2D
OPHN1
RYBP
CACNG4
PDGFRA
CDK12
PAWR
VRK3
SLC5A7
CACNB2
TNFRSF11B
STAT5B
IL6
BCCIP
MED11
ZC3H13
ITGB2
IKBKAP
MED28
PGAM2
SHMT2
STON1

Supplementary Figure Legends

Supplementary Figure S1: Gene expression profiling (GEP) of T-cell lymphoma cell lines. Principal component analysis was performed on GEP data. Note isolation of T8ML-1. Names of cell lines are available on request. **B**: **Cluster diagram of T8ML-1 and PTCL patients:** GEP clustering shows that T8ML-1 consorts with PTCL patient profiles. Primary lymphoma and normal T cells expression data were obtained from the public GEO dataset GSE3668 (**9**). After RMA-background correction and quantile normalization of the spot intensities via R/Bioconductor using limma and affy packages (http://www.bioconductor.org), hierarchical clustering was calculated on basis of Ward's method.

Supplementary Figure S2: Copy number alterations and zygosity in T8ML-1. Figure summarizes genomic array data for chromosomes 1-6 (A), 7-12 (B), 13-18 (C), and 19-22, X and Y (D). Note gross changes in copy number associated with cytogenetic breakpoints (**Fig. 1A**). For technical details see legend to Fig. 1.

Supplementary Figure S3: PTCL patient gene expression at 19q13.3: Shows GEP incorporating public GEP data (GEO-GSE6338) from ref. 9. Note moderate upregulation of *PVRL2* in PTCL patient PTCL-026 only and in two ALCL patients, while *BCL3* is usually downregulated in PTCL patients, when compared to primary T-cells. For data source see Supplementary Figure 1.

Supplementary Figure S4: Surface expression of PVRL2 in T8ML-1 cells. Flow cytometric plots for PVRL2 and (reference) IgG1 on T8ML-1 and (positive) control KG-1A cells. Cell surface expression of PVRL2 closely matches that of positive control cells. Cells were analyzed by flow cytometry on a FACSCalibur (BD Biosciences, Heidelberg/Germany) using CellQuest Pro software.

Supplementary Figure S5: Protein interactogram. Shows STRING analysis results of interactions predicted among top 500 expressed protein coding genes in T8ML-1 versus congener T-cell lymphoma cell lines. PVRL2 (shown red) is connected to CD96, CTNNB1, GOPC based on co-citation evidence. Functional associations remain to be determined.