Figure S1) RTK inhibitors selectively target RT CCLs, related to Figure 1.

a) Related to Figure 1a. Heatmap visualization of *z*-scored AUCs of RTK inhibitors and downstream components of RTK signaling in RT CCLs. b) Related to Figure 1a. Comparison of FDA-approved RTK inhibitors in CCLs best matching the approved indication(s) to RT CCLs. Abbreviations: ALL, acute lymphoblastic leukemia; CML, chronic myeloid leukemia; STS, soft tissue sarcoma; NSCLC, non-small cell lung cancer; RCC, renal cell carcinoma. c) Related to Figure 1b. Western blot analysis of SMARCB1 deficiency in 16 rhabdoid cell lines used in this study. The SMARCB1-wild-type lung cancer cell line, LUDLU1, was used as a positive control, and uniqueness was confirmed by SNP fingerprinting. d) Related to Figure 1a. Activity of RTK inhibitors in select non-RT CCLs. AUC values are shown, along with genomic features underlying each RTK dependency. e) Related to Figure 1c, see also Table S3. Heatmap of CRISPR CERES scores for genes encoding RTK pathway members in RT and non-RT CCLs. Median score for each gene in RT CCLs and non-RT CCLs shown. f) Clustering of DNA methylation data at RTK gene promoters (defined as < 5 kb from transcription start site, TSS) of RTK genes. Rhabdoid cell lines show selective low levels for specific RTKs relevant in each cell line.

Figure S1) RTK inhibitors selectively target RT CCLs, related to Figure 1.

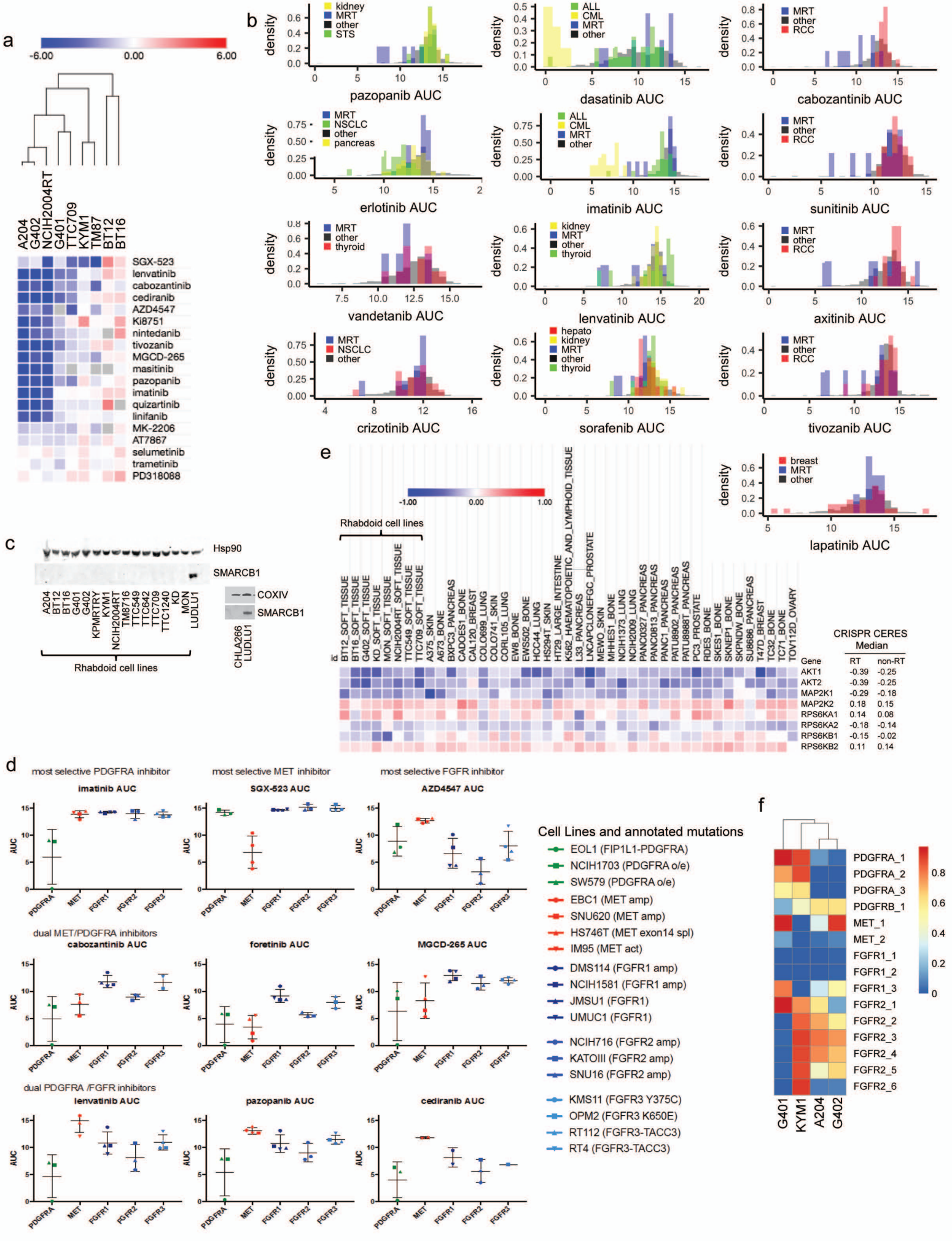

Figure S2) RT CCLs express and phosphorylate different RTKs, related to Figure 2.
a) Related to Figure 2b. Western blots of untreated RT CCLs. b) Related to Figure 2d. SMARCB1 expression in G402 cells decreases RTK activation. Western blots to RTK pathway in three biological replicates of G402 cell line infected with pBABE-PURO-SMARCB1 or empty vector (EV) and selected with puromycin for 72 hr. c) Related to Figure 2e. Western blots of RT CCLs treated with PDGFR-inhibiting small molecules for indicated times. d) i) Related to Figure 2f. Western blots of RT CCLs treated with MET-inhibiting small molecules for indicated times. ii) Related to Figure 3a-b.Western blots of TTC642 treated with RTK-inhibiting small molecules for indicated times. Relative phospho-protein expression was quantified in ImageJ. iii) Related to Figure 3a. TTC549 cells were treated for three hours with indicated inhibitors then prepared for phospho-RTK arrays. Relative phospho-protein expression was quantified in ImageJ. e) Related to Figure 2e-f. Western blots of RT CCLs treated with FGFR-inhibiting small molecules for indicated times. Compound abbreviations: Ax, axitinib; AZD, AZD4547; Cabo, cabozantinib; Ced, cediranib; Cren, crenolanib; Criz, crizotinib; Imat, imatinib; Lenv, lenvatinib; PD, PD173034; SGX, SGX523.

Figure S2) RT CCLs express and phosphorylate different RTKs, related to Figure 2.

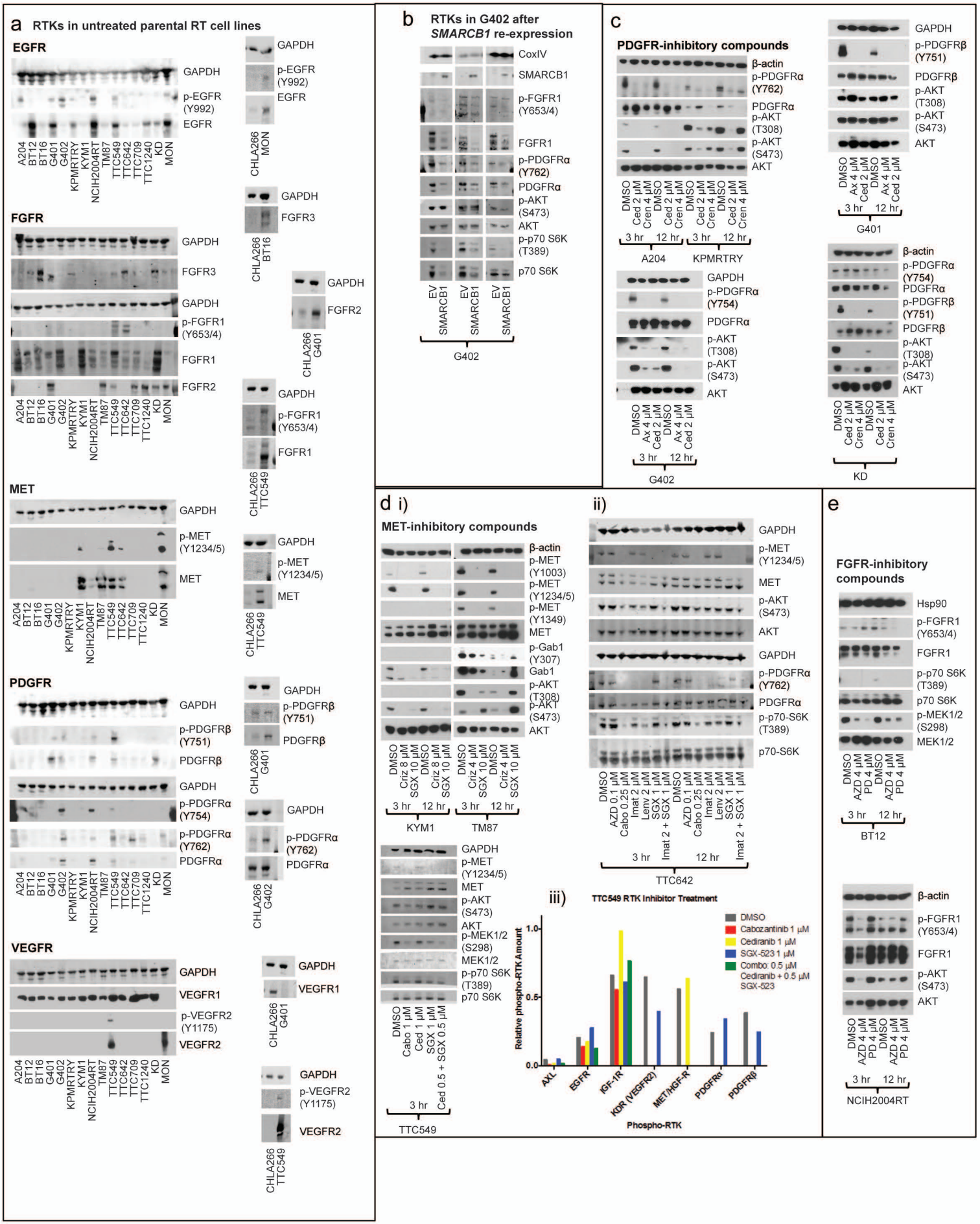

Figure S3) Co-treatment with RTK inhibitors targeting multiple RTK dependencies is synergistic, related to Figure 3.
a) Related to Figure 3c-d. Full co-treatment concentration matrices of AZD4547 + crizotinib in TTC642 cells, and AZD4547 + cabozantinib and AZD4547 + cediranib in G402 cells. b) Pairwise combination treatments of 13 RTK inhibitors, and full co-treatment concentration matrix of AZD4547 + crizotinib and cediranib + crizotinib, in TTC549 cells. c) Pairwise combination treatments of 12 RTK inhibitors in A204, KD, and NCIH2004RT cells, and full co-treatment concentration matrix of cabozantinib + AZD4547, in NCIH2004RT cells. Concentration-response curves are normalized to the appropriate concentration of the second compound alone. d) Pairwise combination treatments in BT12, BT16, and TM87 cells.
For all full co-treatment matrices, the lowest concentrations (12.2 nM for all compounds, except 6.1 nM crizotinib in TTC642 cells) are in red, with increasing twofold concentrations shown by increasing blue color. The first compound alone is shown in black.
For Corrplot diagrams, FGFR inhibitors are highlighted in yellow, and MET inhibitors are highlighted in blue. Red circles indicate synergistic interactions, and inert combinations are indicated with black dots.
Visualization was performed using the Corrplot package in R.

Figure S3) Co-treatment with RTK inhibitors targeting multiple RTK dependencies is synergistic, related to Figure 3.

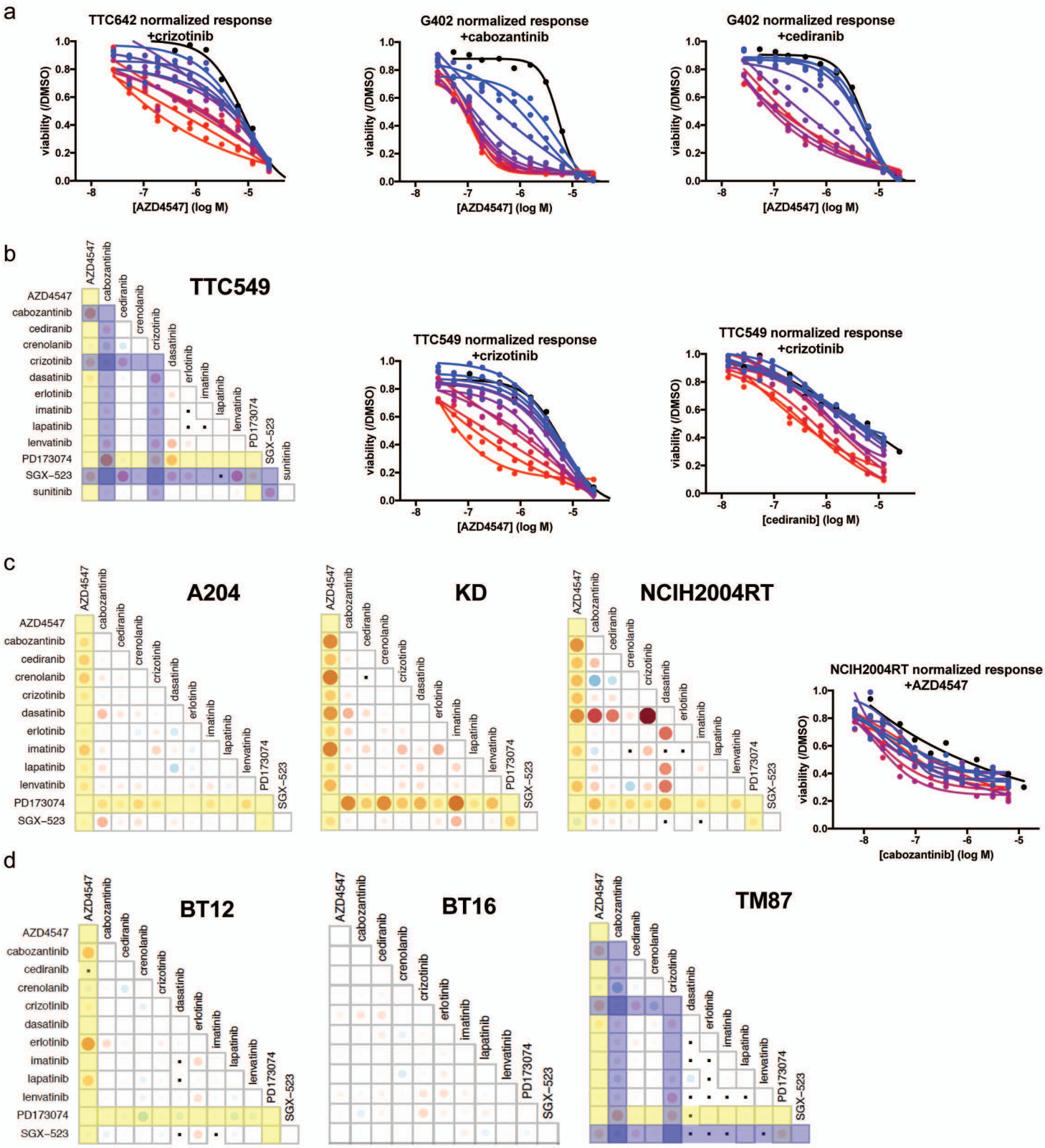

Figure S4) Expression levels of 58 RTK transcripts in human RT samples, related to Figure 2.

a) Related to Figure 2b, Figure S2a. RNA-sequencing data (log2 RPKM) from the TARGET study, consisting of 57 kidney, 2 liver, and 6 soft tissue RT samples. b) gcrma-normalized microarray expression from Birks *et al.* (GSE35493), consisting of 20 AT/RT samples. c) gcrma-normalized microarray expression from Bourdeaut *et al.* (GSE64019), consisting of 19 AT/RT samples and 31 soft tissue RT samples. d) gcrma-normalized microarray expression from Gadd *et al.* (GSE11482), consisting of 10 RT samples. e) gcrma-normalized microarray expression from Johann *et al.* (GSE70678), consisting of 49 AT/RT samples. f) Microarray expression from Torchia *et al.* (EGAD00010000789-90), consisting of 45 AT/RT samples. Each plot is ordered by median expression value in RT samples.

Figure S4) Expression levels of 58 RTK transcripts in human RT samples, related to Figure 2.

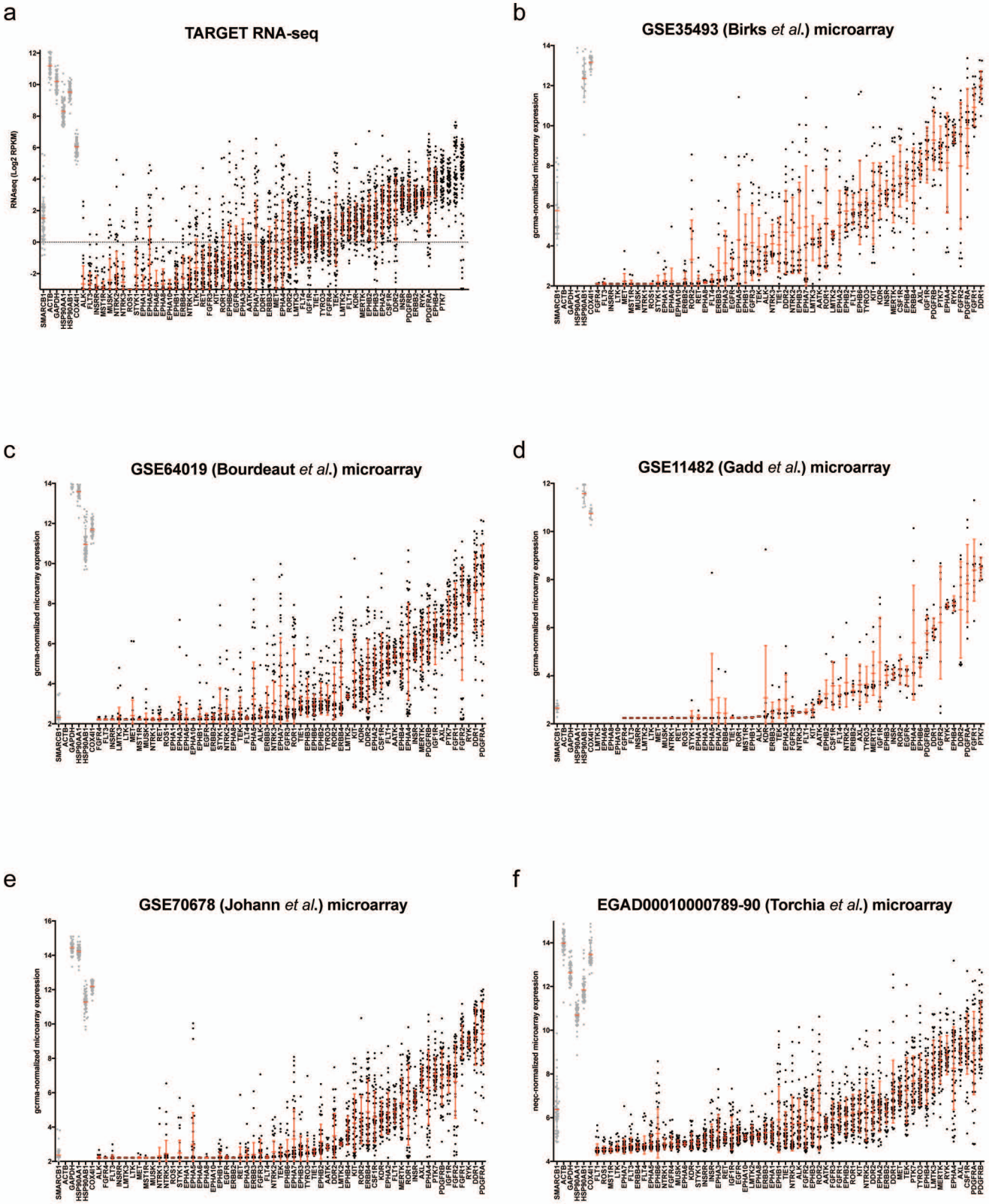

Figure S5) SHP2/PTPN11 inhibition is an RTK-dependent vulnerability shared across rhabdoid cell lines, related to Figure 5.

a) Related to Figure 5c. SHP099 treatment in rhabdoid cell lines does not cause an increase in RTK proteins. Representative replicate (of n=2) shown. b) Related to Figure 5c. Rhabdoid cell lines and selected controls express SHP2 (*PTPN11*) and ERK protein. c) Related to Figure 5a. *PTPN11* is ubiquitously expressed across cancer cell lines and RT patient samples from the TARGET study. RTK genes (rows) are ordered (top to bottom) by their median expression in TARGET samples, while additional pathway genes are shown below. TARGET samples (columns) are ordered by hierarchical clustering (1-Pearson correlation; average linkage), while cell-line samples are ordered (most to least) according to senstivity to SHP099.

Figure S5) SHP2/PTPN11 inhibition is an RTK-dependent vulnerability shared across rhabdoid cell lines, related to Figure 5.

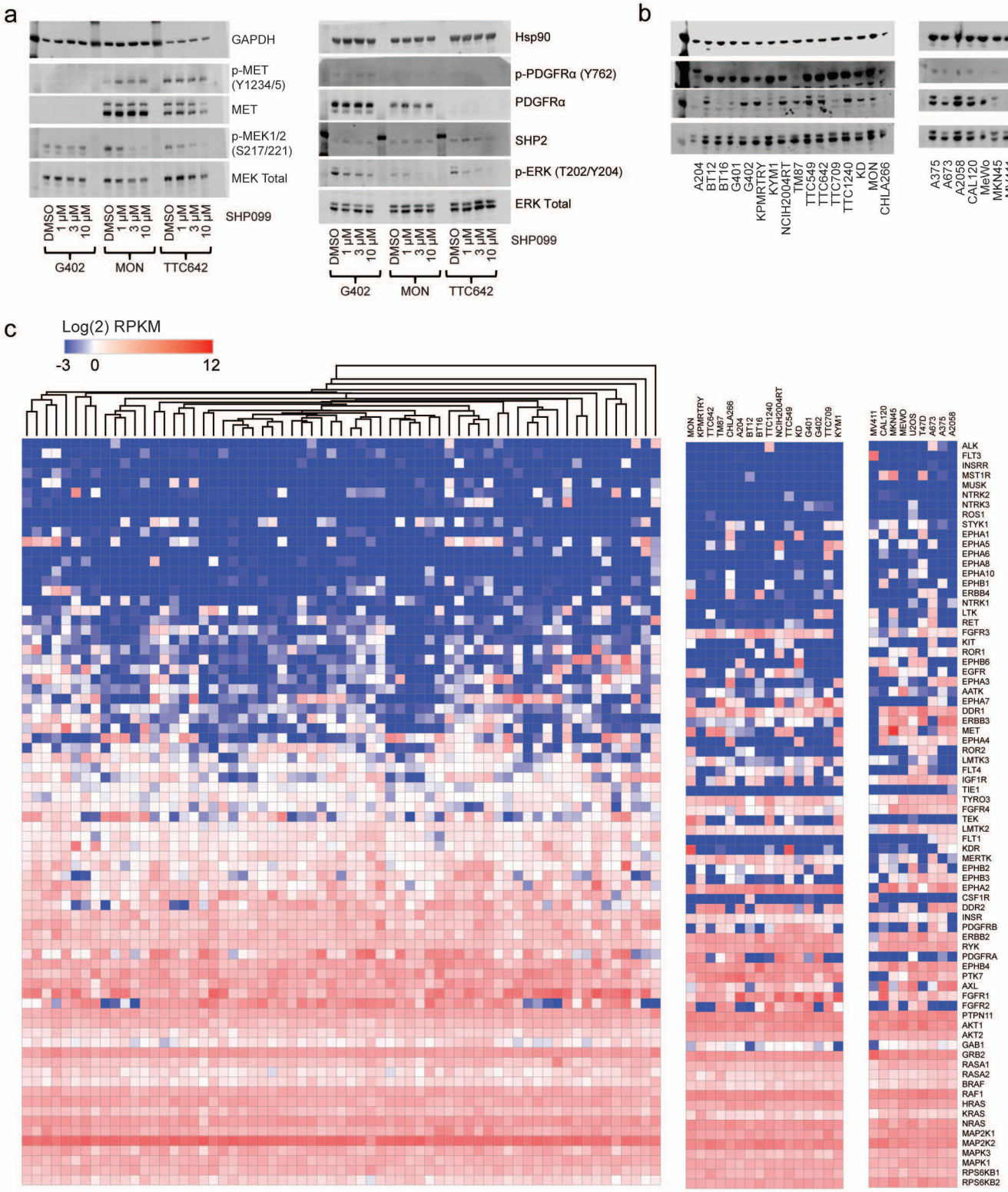

Table S1. Related to Figure 1b. *Z*-scored AUC values for 30 RTK inhibitors across 16 RT CCLs.

Compound name	A204	BT12	BT16	CHLA266	G401	G402	KD	KPMRTRY	KYM1	MON	NCIH2004RT	TM87	TTC1240	TTC549	TTC642	TTC709
allitinib	1.01	1.32	-1.92	-0.27	-0.89	-0.32	1.89	-0.93	0.10	-0.36	0.05	1.12	-0.40	-0.05	1.92	0.46
axitinib	-1.60	0.76	1.09	0.35	-0.11	-2.18	-1.42	-0.35	0.87	0.59	-1.13	0.84	-0.16	0.41	-0.15	0.11
AZD4547	0.01	-1.04	0.71	0.40	-0.33	0.24	-1.27	-0.77	1.16	1.22	-0.83	0.23	-0.01	0.61	-0.64	-1.03
cabozantinib	-0.98	1.10	1.18	0.11	0.75	-0.68	-0.67	-0.28	1.27	-2.47	-0.98	-0.23	0.12	-0.01	0.01	0.67
cediranib	-1.33	0.36	0.64	0.75	-0.30	-1.42	-1.21	-0.64	0.70	1.60	-1.13	0.78	-0.01	0.65	-0.20	0.01
CP-673451	-2.12	-0.82	-0.88	-0.02	0.66	-2.73	-0.91	-0.77	0.02	0.48	0.48	0.54	0.79	0.62	-0.54	0.69
crenolanib	-3.42	-0.70	0.05	0.47	0.59	-4.78	-1.69	-0.72	-1.18	0.48	0.65	-0.05	0.58	0.55	-1.24	1.31
crizotinib	0.81	0.61	0.85	-0.20	0.05	-0.33	1.38	0.24	0.24	-2.92	-0.16	-1.53	-0.05	-0.74	-1.27	1.13
dasatinib	-0.79	0.66	-0.88	-0.08	0.33	-1.47	-0.69	-0.75	0.74	0.75	-0.42	0.72	0.08	0.34	-0.31	0.20
erlotinib	-0.65	-0.52	-4.20	-0.81	-0.04	0.04	-0.64	-1.02	1.21	0.50	-0.97	0.91	0.57	0.70	0.13	1.07
foretinib	-1.33	2.66	1.94	0.10	0.59	-0.12	-0.28	-0.38	3.65	-4.01	-1.59	-0.73	0.00	0.62	0.00	1.56
glesatinib	-2.41	0.39	0.80	-0.23	0.44	-1.16	-1.45	-0.88	0.72	-2.97	-2.15	0.00	0.29	0.09	0.00	0.63
imatinib	-3.72	-0.27	0.27	0.02	0.88	-4.43	-1.91	-0.88	0.84	0.92	-0.85	0.43	-0.02	0.51	-0.38	0.06
infigratinib	-0.60	0.24	1.16	-0.28	0.06	0.75	-0.41	-1.20	0.30	1.32	-0.86	-0.08	-0.06	1.01	0.75	-1.73
Ki8751	-2.69	-0.71	0.12	0.31	0.41	-3.49	-1.34	-1.18	1.09	1.23	-0.92	0.64	-0.12	0.51	-0.46	0.42
KW-2449	-0.37	0.73	-0.23	-0.48	0.12	-1.15	0.18	-1.58	1.54	0.78	-0.62	1.16	0.05	-0.05	-1.56	0.88
lapatinib	3.00	0.63	-5.01	-0.41	-1.16	-0.46	4.50	-0.84	0.32	-0.19	0.12	2.46	-0.72	-0.12	3.57	0.24
lenvatinib	-1.61	0.33	0.86	-0.10	-0.35	-1.49	-1.40	-1.17	0.76	0.70	-1.29	0.50	0.38	0.64	0.10	-0.27
masitinib	-6.99	0.02	0.40	0.06	-0.02	-6.42	-3.68	-1.68	0.67	0.13	-4.08	0.65	-0.68	0.82	-0.16	1.06
nintedanib	-2.09	0.91	0.72	-0.42	-0.48	-1.62	-1.36	-0.32	1.37	0.97	-1.57	0.25	-0.25	0.63	0.44	0.27
OSI-930	-0.33	1.06	1.18	-0.84	-1.04	-0.11	0.01	0.05	0.77	-0.01	-0.01	0.63	-0.87	-0.57	0.91	0.71
pazopanib	-2.28	0.13	0.96	-0.04	-0.22	-2.16	-3.16	-0.64	0.82	0.73	-1.29	0.55	0.17	0.71	0.04	-0.20
PD173074	-0.07	-1.24	0.67	0.67	-0.68	0.20	-0.80	-0.78	0.55	1.59	-0.97	0.41	0.07	1.38	-0.29	-0.86
ponatinib	-1.00	-0.18	0.00	1.37	0.00	-1.15	-0.53	-0.18	0.85	1.14	-0.60	1.06	0.75	0.78	0.25	-0.07
quizartinib	-1.11	0.96	-0.46	1.01	-0.06	-0.56	-0.88	-0.23	1.24	0.44	-0.51	0.71	0.06	0.94	-1.27	0.64
SGX-523	0.14	-1.22	0.84	3.44	0.51	0.07	0.17	0.25	-0.33	-15.83	-0.27	-4.14	-0.07	-3.43	-5.74	1.40
sunitinib	-4.04	0.28	-0.01	-0.36	0.01	-3.49	-2.08	-1.11	1.15	0.13	-2.17	0.59	-0.38	0.76	0.15	1.27
tandutinib	-5.91	0.60	0.69	-0.02	0.28	-3.73	-2.30	-1.38	0.77	0.66	-3.73	0.88	-0.05	0.02	-0.26	0.39
tivozanib	-5.13	0.38	0.64	0.30	-0.21	-3.94	-4.02	0.02	1.04	0.04	-2.92	1.12	-0.71	0.82	-0.02	-0.37
vandetanib	-1.68	1.09	-1.51	-0.10	-0.67	-0.68	-1.24	-0.64	1.07	0.57	-0.58	1.09	0.10	0.61	0.58	0.90

Table S2. Related to Figure 1b. Published inhibitory profiles of RTK inhibitors in Table S1.

Compound	ERBB2	ERBB4	FGFR1	FGFR2	MET	PDGFRA	PDGFRB	Study
axitinib	-5%	4%	380 nM 98%	110 nM 100%	820 nM 36%	0.51 nM 102%	0.57 nM 101%	(Davis et al., 2011, Uitdehaag et al., 2014)
cabozantinib	10%	23%	16%	32%	101%	100%	84%	(Uitdehaag et al., 2014)
cediranib	3000 nM	1400 nM	53 nM	35 nM	370 nM	0.41 nM	0.32 nM	(Davis et al., 2011)
crizotinib	-1%	-18%	17%	27%	2.1 nM 100%	49%	18%	(Davis et al., 2011, Uitdehaag et al., 2014)
dasatinib	1400 nM 21%	55 nM 103%	3700 nM 47%	1400 nM 73%	3%	0.47 nM 100%	0.63 nM 99%	(Davis et al., 2011, Uitdehaag et al., 2014)
erlotinib	2900 nM 14%	230 nM 97%	24%	58%	3800 nM 13%	1800 nM 52%	1400 nM 56%	(Davis et al., 2011, Uitdehaag et al., 2014)
imatinib	7%	52%	-1%	3%	-5%	31 nM 98%	14 nM 91%	(Davis et al., 2011, Uitdehaag et al., 2014)
KW-2449			370 nM	850 nM	170 nM	130 nM	30 nM	(Davis et al., 2011)
lapatinib	7 nM 85%	54 nM 102%	-1%	0%	0%	40%	3%	(Davis et al., 2011, Uitdehaag et al., 2014)
masitinib	1200 nM					25 nM	8.4 nM	(Davis et al., 2011)
nintedanib			92 nM	350 nM	200 nM	16 nM	15 nM	(Davis et al., 2011)
pazopanib	1%	16%	990 nM 91%	210 nM 97%	2000 nM 35%	4.9 nM 99%	2 nM 96%	(Davis et al., 2011, Uitdehaag et al., 2014)
ponatinib	88%	101%	101%	100%	17%	103%	102%	(Uitdehaag et al., 2014)
quizartinib						11 nM	7.7 nM	(Davis et al., 2011)
SGX-523					0.19 nM			(Davis et al., 2011)
sunitinib	8%	26%	520 nM 93%	570 nM 97%	7200 nM 28%	0.79 nM 98%	0.075 nM 99%	(Davis et al., 2011, Uitdehaag et al., 2014)
tandutinib						2.4 nM	4.5 nM	(Davis et al., 2011)
vandetanib	2600 nM 67%	480 nM 93%	560 nM 87%	1100 nM 103%	5700 nM 8%	230 nM 101%	88 nM 89%	(Davis et al., 2011, Uitdehaag et al., 2014)

Assays: Uitdehaag et al. % inhibition at 1 μM; Davis et al. Kd values of binding.

Table S3. Related to Figure 2a. *Z*-scored CERES scores and log2 RPKM gene expression values in 8 RT CCLs for 7 RTK genes with dependency score < -0.5 and relative dependency score (zmad) < -2 in at least 1 RT CCL.

	Cell line	PDGFRA	FGFR1	FGFR2	MET	ERBB4	EPHB2	PDGFRB
Z-scored CERES scores	G402	-8.02	-4.09	-0.45	1.08	-0.03	1.57	-2.58
	NCIH2004RT	-8.07	-6.25	0.00	-0.38	0.14	-0.95	-1.60
	BT12	1.14	-5.54	0.04	0.22	0.68	0.64	0.16
	KD	-0.65	-3.92	-0.12	2.90	1.11	-0.65	-4.69
	TTC709	-0.63	-0.67	-10.3	0.32	-0.87	0.03	0.92
	MON	-1.99	0.02	-0.74	-10.3	0.01	1.02	-1.33
	TTC549	-1.81	-0.20	-1.20	-4.08	0.40	0.05	-0.86
	BT16	-0.24	-2.68	0.27	0.14	-2.05	-2.70	-0.93
CERES scores	G402	-1.09	-0.95	-0.09	0.21	-0.57	0.01	-0.31
	NCIH2004RT	-1.09	-1.27	-0.05	0.06	-0.54	-0.30	-0.20
	BT12	-0.16	-1.17	-0.04	0.12	-0.45	-0.10	-0.01
	KD	-0.34	-0.93	-0.06	0.39	-0.37	-0.26	-0.54
	TTC709	-0.34	-0.45	-1.04	0.13	-0.72	-0.18	0.08
	MON	-0.48	-0.34	-0.12	-0.94	-0.57	-0.06	-0.17
	TTC549	-0.46	-0.38	-0.16	-0.31	-0.50	-0.18	-0.12
	BT16	-0.30	-0.74	-0.02	0.14	-0.92	-0.52	-0.13
log2 RPKM	G402	6.19	7.51	-3.00	-2.53	-0.95	-3.00	2.75
	NCIH2004RT	6.25	7.08	2.52	3.96	-1.56	-0.20	3.69
	BT12	-3.00	5.03	-3.00	-1.35	-3.00	-3.00	-0.67
	KD	4.00	7.64	4.49	-3.00	-3.00	-3.00	5.00
	TTC709	-3.00	3.95	5.75	-2.88	-3.00	3.51	1.49
	MON	5.22	1.53	4.70	5.61	4.92	-3.00	-3.00
	TTC549	4.90	5.14	4.16	4.26	-3.00	-3.00	5.01
	BT16	-3.00	5.37	0.90	-3.00	3.93	2.33	-3.00

Table S4. Related to Figure 2c. H3K27Ac changes at RTK genes (SMARCB1+/-) in G401 and TTC549 RT CCLs (data from Wang et al., 2016). Average bigWig scores were calculated across a +/- 5 kb interval centered on transcription start sites and a SMARCB1(+) over SMARCB1(-) fold change was computed for each cell line.

gene	chrom	strand	txStart	G401 SMARCB1/Ctrl	TTC549 SMARCB1/Ctrl
FGFR1	chr8	-	38268655	1.2	0.9
FGFR1	chr8	-	38280850	1.2	0.8
FGFR1	chr8	-	38283639	1.6	0.8
FGFR1	chr8	-	38277050	1.3	0.8
FGFR1	chr8	-	38277056	1.3	0.8
FGFR1	chr8	-	38279165	1.2	0.7
FGFR2	chr10	-	123237843	1.0	1.0
FGFR2	chr10	-	123239353	1.0	1.1
FGFR2	chr10	-	123276832	1.3	1.4
FGFR2	chr10	-	123276725	1.3	1.4
FGFR2	chr10	-	123279477	1.2	1.2
FGFR2	chr10	-	123298052	0.9	1.0
FGFR2	chr10	-	123241366	1.0	1.0
FGFR2	chr10	-	123243211	1.1	0.9
IGF1R	chr15	+	99192760	1.4	1.3
IGF1R	chr15	+	99467753	0.9	1.4
IGF1R	chr15	+	99454543	0.9	1.1
KDR	chr4	-	55944425	0.9	0.7
KDR	chr4	-	55945925	1.1	0.8
KDR	chr4	-	55970759	0.6	0.7
MET	chr7	+	116312458	1.0	0.7
MET	chr7	+	116339124	0.7	0.7
MET	chr7	+	116364175	0.8	0.6
PDGFRA	chr4	+	54243819	1.5	1.0
PDGFRA	chr4	+	55095263	1.2	0.9
PDGFRA	chr4	+	55143342	0.7	1.3
PDGFRB	chr5	-	149493401	1.6	1.3
PDGFRB	chr5	-	149512312	1.6	1.3

Table S5. Related to Figure S4. RTK genes with significant differential expression between tissue types.

RTK gene	Adjusted P Value	P Value	logFC	Comparison	Study
AXL	9.24E-03	1.34E-03	-0.655	Brain vs. Soft Tissue	(Han et al., 2016)
DDR1	5.80E-07	2.54E-09	2.793	Brain vs. Soft Tissue	(Han et al., 2016)
DDR2	4.13E-03	4.78E-04	-2.238	Brain vs. Soft Tissue	(Han et al., 2016)
IGF1R	4.55E-02	1.06E-02	0.954	Brain vs. Soft Tissue	(Han et al., 2016)
KIT	5.68E-03	7.19E-04	1.676	Brain vs. Soft Tissue	(Han et al., 2016)
NTRK3	4.76E-02	1.12E-02	0.862	Brain vs. Soft Tissue	(Han et al., 2016)
PDGFRB	2.94E-03	3.04E-04	1.358	Brain vs. Soft Tissue	(Han et al., 2016)
PTK7	6.55E-03	8.66E-04	-0.848	Brain vs. Soft Tissue	(Han et al., 2016)
ROR1	4.01E-02	8.99E-03	0.904	Brain vs. Soft Tissue	(Han et al., 2016)
EPHB4	2.28E-07	6.13E-10	-1.541	Brain vs. Soft Tissue	(Han et al., 2016)
ERBB4	1.67E-03	1.48E-04	1.637	Brain vs. Soft Tissue	(Han et al., 2016)
MET	4.84E-02	1.03E-03	-2.511	Kidney vs. Soft Tissue	TARGET
PDGFRA	2.65E-04	6.21E-07	3.452	Kidney vs. Soft Tissue	TARGET
ROR2	2.79E-02	4.41E-04	2.291	Kidney vs. Soft Tissue	TARGET
MET	5.36E-03	5.86E-05	-4.482	Kidney vs. Liver	TARGET
FLT3	9.31E-03	5.26E-05	4.708	Liver vs. Soft Tissue	TARGET

RTK genes with adjusted p values < 0.05 are shown. Adjusted P Values were calculated using GEO2R (Han et al. study) or the DESeq2 R package (TARGET study).

Table S6. Related to Figure 5. *PTPN11* CRISPR CERES scores, *z*-scored CERES scores and SHP099 AUC values across RT CCLs and non-RT control lines. AUCs averaged across at least two biological replicates.

Cell line		*PTPN11* CERES scores	*PTPN11* *z*-scored CERES scores	SHP099 AUC Mean	*PTPN11* log2 RPKM
Rhabdoid Cell Lines	A204			10.94	4.98
	BT12	-0.96	-0.58	11.12	5.26
	BT16	-1.28	-1.76	11.29	5.49
	CHLA266			7.38	5.06
	G401			11.73	5.89
	G402	-1.07	-1.01	12.03	5.37
	KD	-1.30	-1.83	11.60	5.16
	KPMRTRY			10.08	5.44
	KYM1			12.78	5.17
	MON	-1.19	-1.46	8.53	5.88
	NCIH2004RT	-1.15	-1.31	11.52	4.86
	TM87			10.83	4.82
	TTC549	-1.06	-0.97	11.52	5.29
	TTC642			10.47	5.59
	TTC709	-1.33	-1.95	12.03	5.38
	TTC1240			11.42	5.66
Control Cell Lines	A375	-0.45	1.31	13.01	5.83
	A673	-0.66	0.54	12.90	5.41
	A2058			13.40	5.41
	CAL120	-1.31	-1.88	11.54	5.52
	MEWO	-0.98	-0.65	12.46	5.69
	MKN45			12.04	4.71
	MV411			8.16	4.62
	T47D	-0.69	0.43	12.84	5.72
	U2OS			11.90	5.41

Table S7. Related to Figure 5e-f. Methylation profiling reveals that rhabdoid cell lines classify as "MYC" (high or low confidence) or "not defined" based on methylation status.

Cell Line Name	Tissue of Tumor location	Tumor Type	Methylation Subtype
A204	Muscle	Rhabdoid tumor	MYC
BT12	Brain	AT/RT	Not Defined
BT16	Brain	AT/RT	Low confidence MYC
CHLA266	Brain	AT/RT	Not Defined
G401	Kidney	Rhabdoid tumor	Low confidence MYC
G402	Kidney	Rhabdoid tumor	Low confidence MYC
KD	Soft Tissue (abdomen)	Rhabdoid tumor	MYC
KPMRTRY	Kidney	Rhabdoid tumor	MYC
KYM1	Soft Tissue (neck)	Rhabdoid tumor	Not Defined
MON	Soft Tissue (abdomen)	Rhabdoid tumor	Not Defined
NCIH2004RT	Kidney	Rhabdoid tumor	Low confidence MYC
TM87	Striated muscle; retroperitoneum	Rhabdoid tumor	MYC
TTC549	Extra-renal primary tumor, hepatic	Rhabdoid tumor	Low confidence MYC
TTC642	Extra-renal primary tumor	Rhabdoid tumor	Low confidence MYC
TTC709	Striated muscle	Rhabdoid tumor	Not Defined
TTC1240	Kidney metastasis found in brain	Rhabdoid tumor	Not Defined

Supplementary References for Supplementary Tables:

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