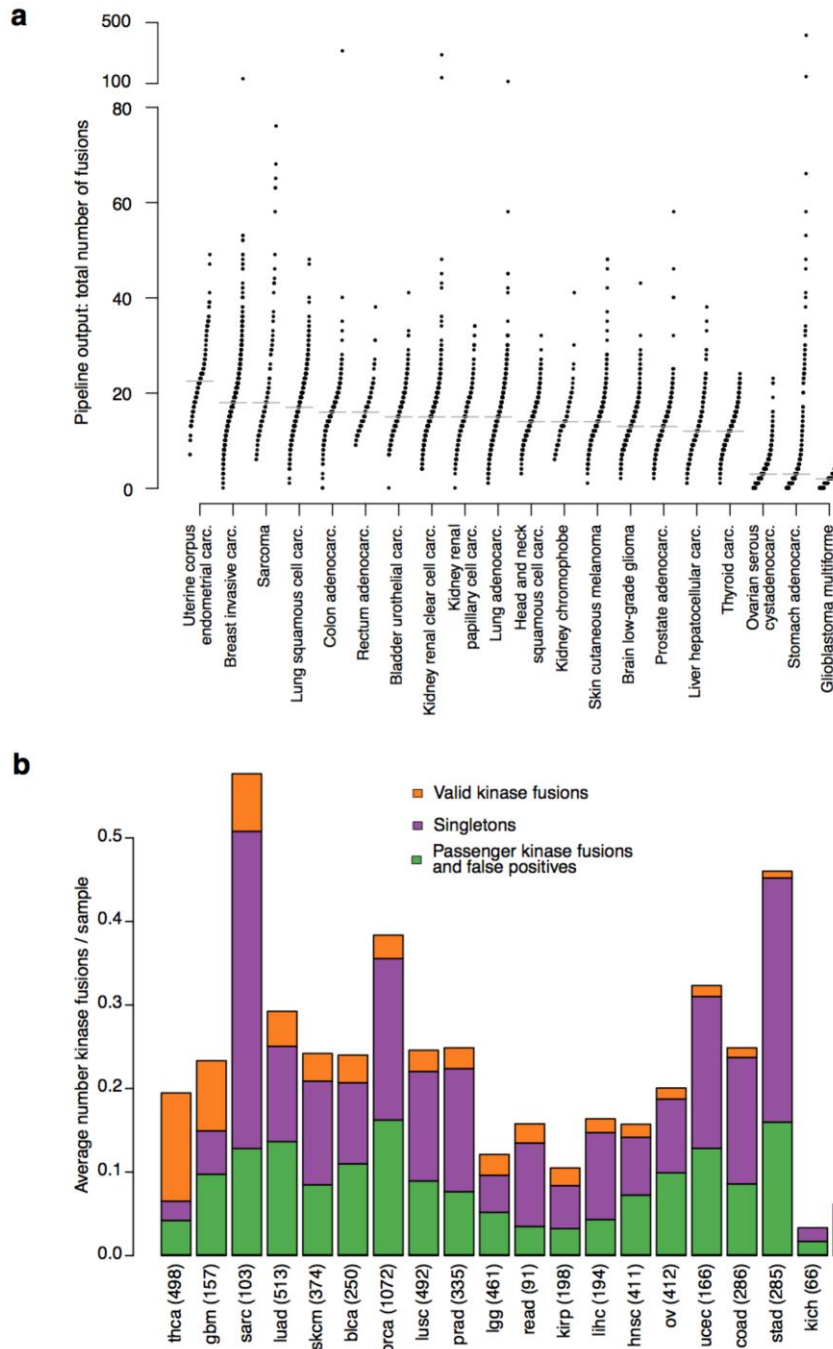


Supplementary Figures

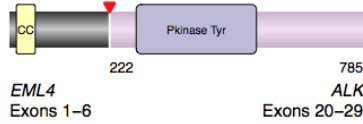


Supplementary Figure 1: Output of pipeline

a, Each dot corresponds to a tumor, with vertical position indicating the total number of fusions identified. Tumor types are ordered by their median number of fusions per sample, indicated by a grey horizontal line. **b**, For each tumor type, the average number of kinase fusions per sample is indicated and color-coded by category.

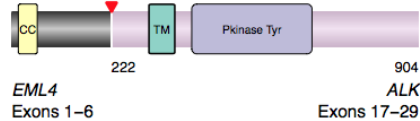
participant ID: 5c631aef-0d24-4497-83b9-3f71675e90e8
 2cdaa358-cba5-4c7c-bd9a-6a459f0c7ee
 03570ba4-236b-4ec2-8212-d7341eb09c19
 d025f4ee-468c-417f-94e2-4a8212f712c0
 c5ebb089-2c71-44bf-8af0-75f14195aae1
 cancer type: lung adenocarcinoma

...GTCATCATCAACCAAGTGTACCGCCGGAAGCA...
 . V I I N Q Y Y R R K .



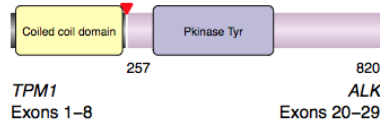
participant ID: 100f3512-7a98-412e-8a20-12f547fa3d65
 cancer type: thyroid carcinoma

...GTCATCATCAACCAAGGCGGCAATGCAGCCTC...
 . V I I N Q G G N A A .



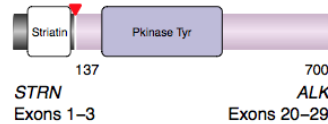
participant ID: 78b55924-02ae-49d2-98f5-48c7a6e3542
 cancer type: bladder cancer

...ATTGATGACTTAGAAGTGTACCGCCGGAAGCA...
 . I D D L E Y Y R R K .



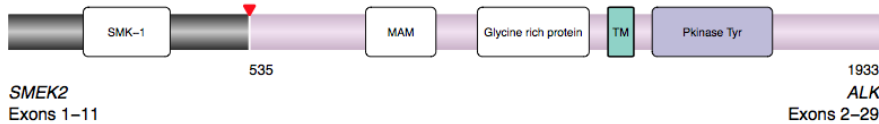
participant ID: 0d29200e-946b-4ec1-990f-ddb7443b5c9e (thyroid carcinoma)
 34d1f767-ce01-44b6-9b7e-f5014ed52a0e (kidney papillary)

...CCAAGCTATGATTCTGTGTACCGCCGGAAGCA...
 . P S Y D S Y Y R R K .



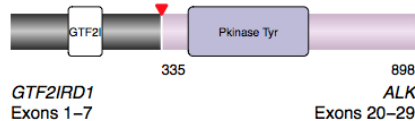
participant ID: a304de25-4fd0-475e-8fd9-65f0b0f77068
 cancer type: rectum adenocarcinoma

...AACACAATTGTCCCGTTCATAGCTCCTTGG...
 . N T I C P G H S S L .



participant ID: 4f3d2561-fc5d-4fcf-8688-96eade990f83
 cancer type: thyroid carcinoma

...GTCCATGACAAGTCAGTGTACCGCCGGAAGCA...
 . V H D K S Y Y R R K .

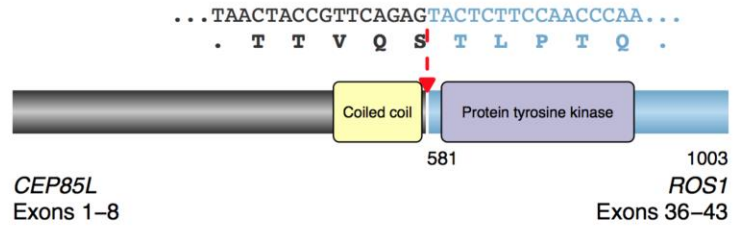


Pkinase Tyr: Protein tyrosine kinase
 SMK-1: Component of IIS longevity pathway SMK-1
 MAM: MAM domain
 GTF2I: GTF2I-like repeat
 CC: Coiled-coil domain
 TM: Transmembrane domain

Supplementary Figure 2: ALK fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domains are colored in purple, the transmembrane domains (TM) are indicated in teal, coiled-coil (CC) dimerization domains are indicated in yellow, whereas other domains are left in white. Fusion breakpoints are delineated by red arrows.

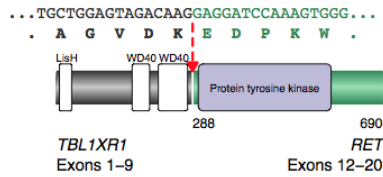
participant ID: 3ac69d4b-68f7-4d85-88e9-191a3d195047
cancer type: glioblastoma



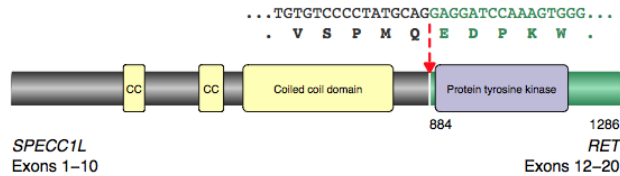
Supplementary Figure 3: *ROS1* fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domain is colored in purple, the coiled-coil (CC) dimerization domain is indicated in yellow. Fusion breakpoint is delineated by a red arrow.

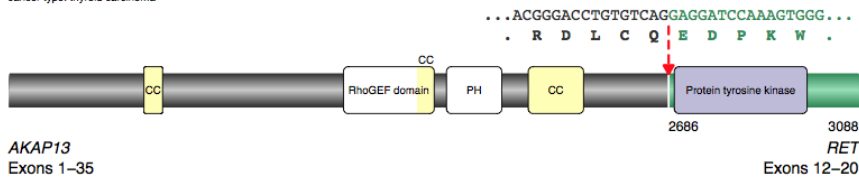
participant ID: 47ad3d2e-9096-4e6d-864f-83507fd8e970
cancer type: thyroid carcinoma



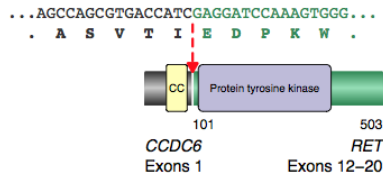
participant ID: 3d114411-0215-4870-87d6-7f08ca8f771
cancer type: thyroid carcinoma



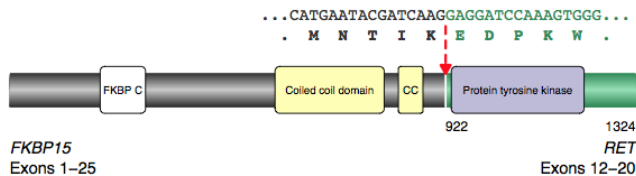
participant ID: 494fec2d-a439-4b21-903c-6ef07b08fe4
cancer type: thyroid carcinoma



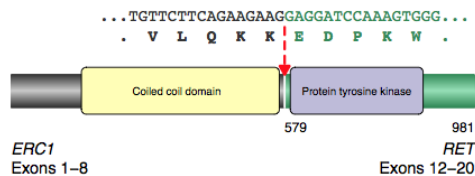
participant ID: cb87eb0f-2502-4277-a8ef-435b08f3c863
cancer type: colon adenocarcinoma



participant ID: 449ee008-36eb-4cb8-8717-be79a568481f
cancer type: thyroid carcinoma



participant ID: 8a209c68-bef9-4191-b6ec-7a1a9258b3bd
cancer type: breast invasive carcinoma

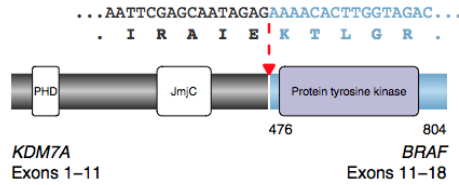


CC: Coiled coil domain
 LisH: LisH
 WD40: WD domain, G-beta repeat
 FKBP C: FKBP-type peptidyl-prolyl cis-trans isomerase
 PH: PH domain

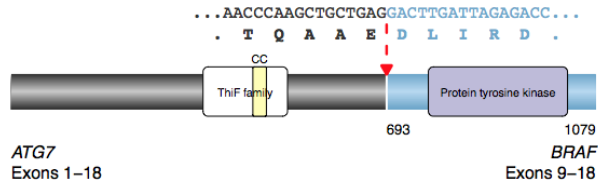
Supplementary Figure 4: *RET* fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domains are colored in purple, the transmembrane domains (TM) are indicated in teal, coiled-coil (CC) dimerization domains are indicated in yellow, whereas other domains are left in white. Fusion breakpoints are delineated by red arrows.

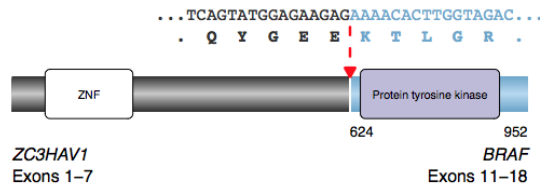
participant ID: 922e54e-7c0b-4261-97b2-344da6abc267
 cancer type: prostate adenocarcinoma



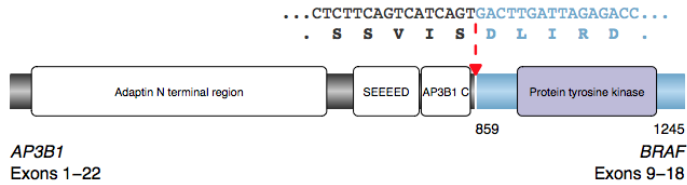
participant ID: 60e574aa-167a-442d-8642-e8426d5bb24b
 cancer type: skin cutaneous melanoma



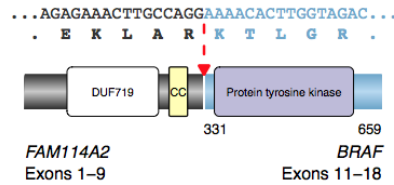
participant ID: 6f7b7201-31bd-4647-86fc-85dbb40f02e3
 cancer type: thyroid carcinoma



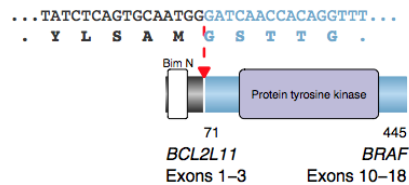
participant ID: ba92c434-3604-4b85-bc76-3bbe5c44253f
 cancer type: thyroid carcinoma



participant ID: 117a21dd-d717-4320-abe3-08c2d5041fc5
 cancer type: thyroid carcinoma



participant ID: 719b0041-becc-45a0-b5be-059426574e90
 cancer type: thyroid carcinoma



AP3B1_C: Clathrin-adaptor complex-3 beta-1 subunit C-terminal
 SEEEEED: Serine-rich region of AP3B1, clathrin-adaptor complex
 DUF719: Protein of unknown function (DUF719)
 PHD: PHD-finger
 JmjC: JmjC domain, hydroxylase
 CC: Coiled_Coil
 Bim N: Bim protein N-terminus

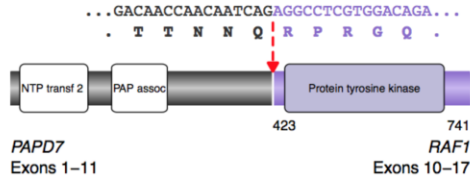
Supplementary Figure 5: BRAF fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domains are colored in purple, the transmembrane domains (TM) are indicated in teal, coiled-coil (CC) dimerization domains are indicated in yellow, whereas other domains are left in white. Fusion breakpoints are delineated by red arrows.

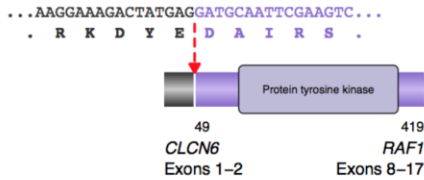
participant ID: 5fa9190-c423-4193-800d-1b38c4e9a810 (thyroid carcinoma)
 7981ceb4-3f67-4060-9deb-54288cb1c5cb (thyroid carcinoma)
 9b585da2-52b5-4885-b063-d40992649bb9 (thyroid carcinoma)
 6fa50314-44cf-4545-9160-452170ea47e9 (thyroid carcinoma)
 fa0b5119-7406-49e1-a853-51ceade839ffa (thyroid carcinoma)
 d2d8257d-2763-4538-93a7-192d4923c2ef (thyroid carcinoma)
 2b16f848-9038-413f-8ae1-a27ac0e029a2 (thyroid carcinoma)
 922e5a4e-7c0b-4261-97b2-344da6abc267 (prostate adenocarcinoma)



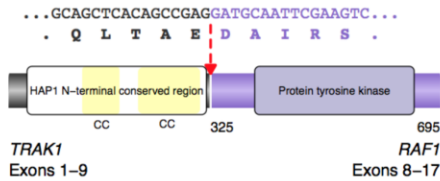
participant ID: 238589a3-17d7-49d5-bdc3-b561d5a1ef3b
 cancer type: prostate adenocarcinoma



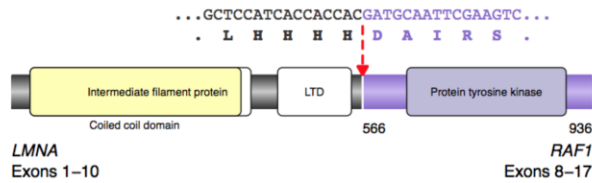
participant ID: b10a88d5-3469-4e19-956a-09d83e04149d
 cancer type: skin cutaneous melanoma



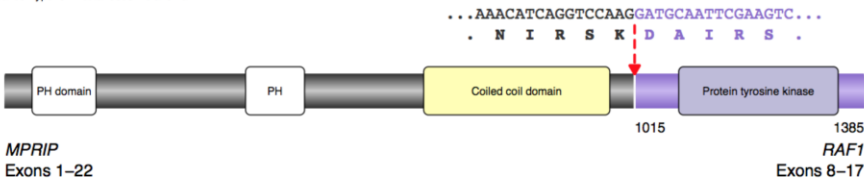
participant ID: 8cb1790f-9139-4617-8315-fefdf57de8d1
 cancer type: skin cutaneous melanoma



participant ID: 8e2cd8f4-b121-403b-bf83-66f8da646776
 cancer type: skin cutaneous melanoma



participant ID: b28c3eb9-7970-42a7-9641-9209213e9042
 cancer type: skin cutaneous melanoma

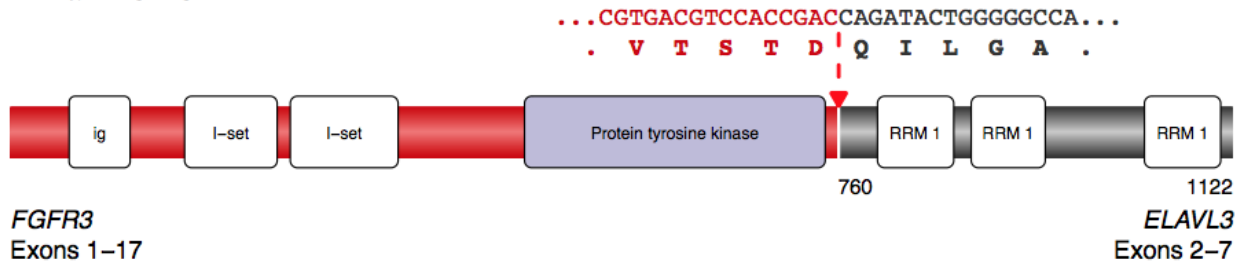


CC: Coiled coil domain NTP transf 2: Nucleotidyltransferase domain
 PAP assoc: Cid1 family poly A polymerase LTD: Lamin Tail Domain

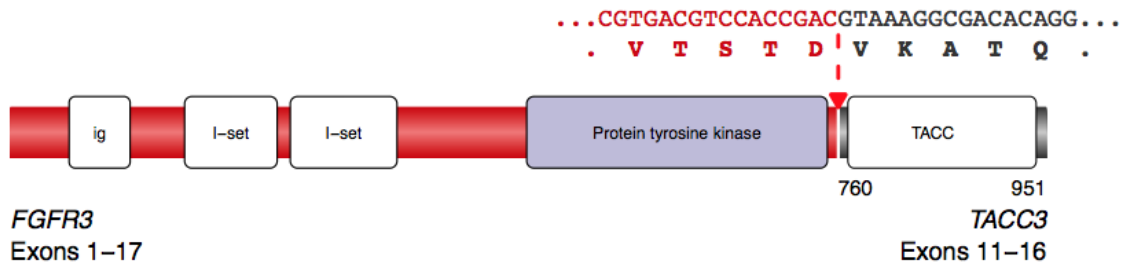
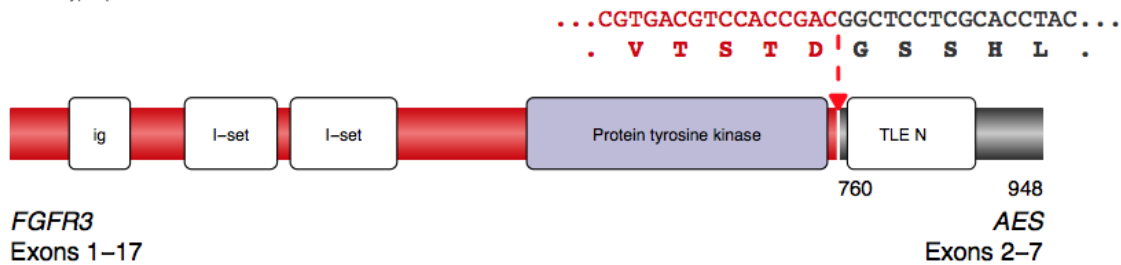
Supplementary Figure 6: RAF1 fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domains are colored in purple, the transmembrane domains (TM) are indicated in teal, coiled-coil (CC) dimerization domains are indicated in yellow, whereas other domains are left in white. Fusion breakpoints are delineated by red arrows.

participant ID: 1b4388e8-0ff1-46f2-9396-2cc8f2f11ceb
 cancer type: low grade glioma



participant ID: 6d78186c-ca8d-4fe2-befc-a14949a84c38
 cancer type: prostate adenocarcinoma

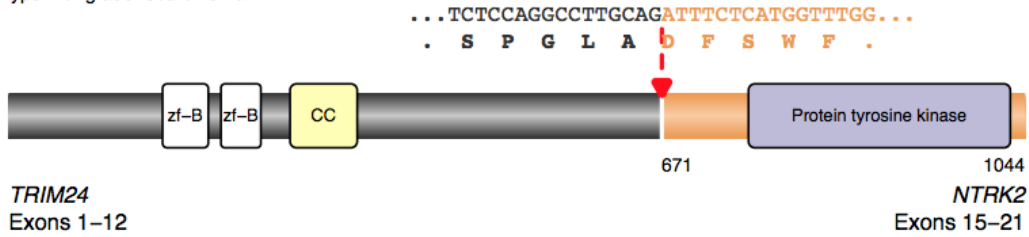


I-set: Immunoglobulin I-set domain	TLE N: Groucho/TLE N-terminal Q-rich domain
ig: Immunoglobulin domain	TACC: Transforming acidic coiled-coil-containing protein (TACC)
RRM 1: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	

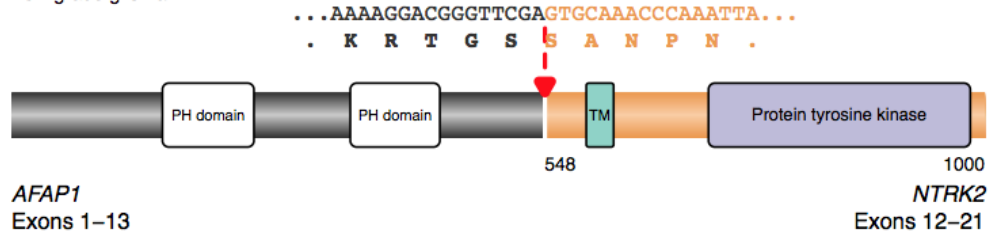
Supplementary Figure 7: *FGFR3* fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domains are colored in purple, the transmembrane domains (TM) are indicated in teal, coiled-coil (CC) dimerization domains are indicated in yellow, whereas other domains are left in white. Fusion breakpoints are delineated by red arrows.

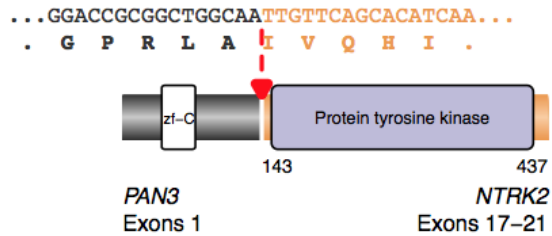
participant ID: f6f2d86e-fa34-43bd-a89b-09add6995833
 cancer type: Lung adenocarcinoma



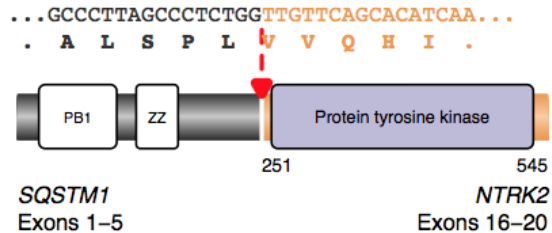
participant ID: b2e0a631-c703-4601-945b-6fadf2f30656
 cancer type: Low grade glioma



participant ID: 01c9c486-321f-4ebc-ade7-bbe6ea5c4a6e
 cancer type: Head and neck squamous cell carcinoma



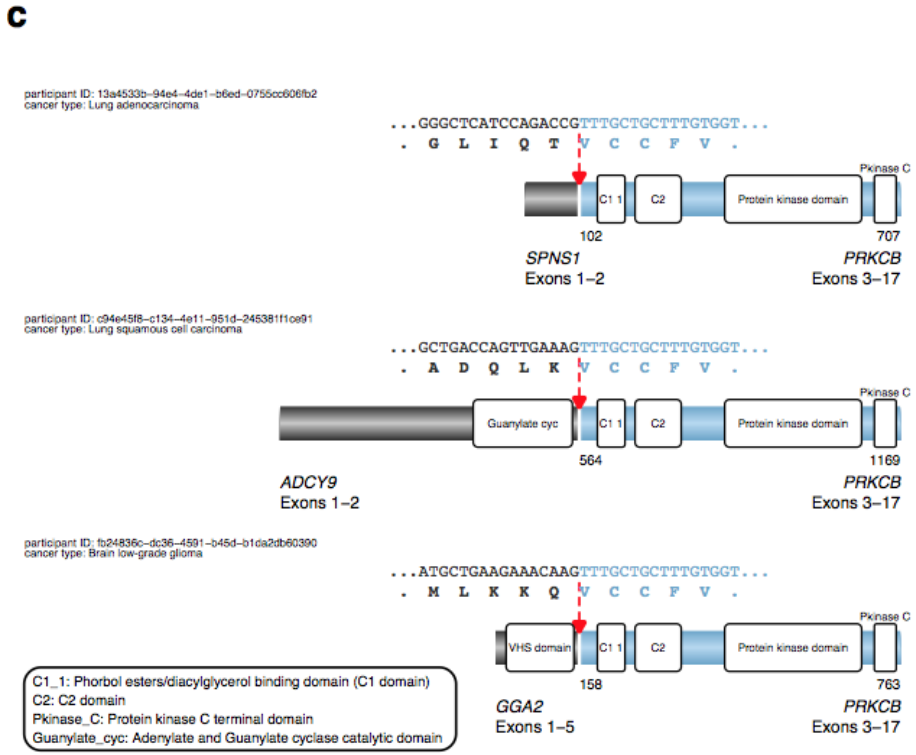
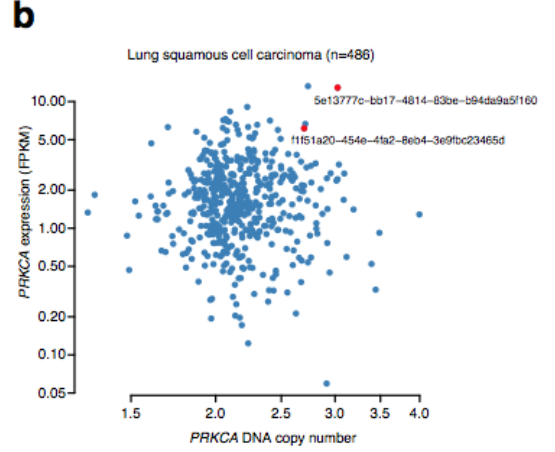
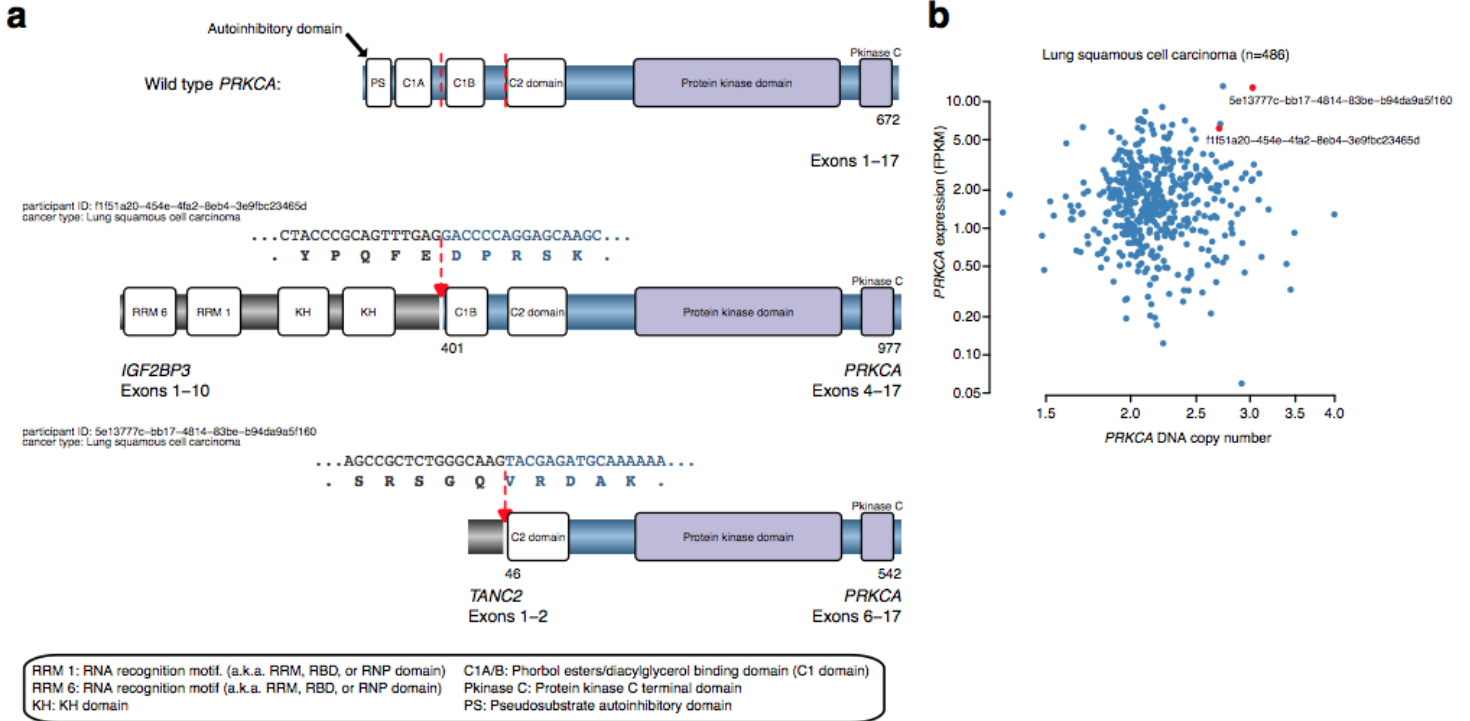
participant ID: e4e84c27-69c6-4972-ac64-aa78ff6d6f02
 cancer type: Lower grade glioma



CC: Coiled_Coil
 PB1: PB1 domain
 TM: Transmembrane domain
 zf-B_box: B-box zinc finger
 zf-CCCH: Zinc finger C-x8-C-x5-C-x3-H type (and similar)
 ZZ: Zinc finger, ZZ type

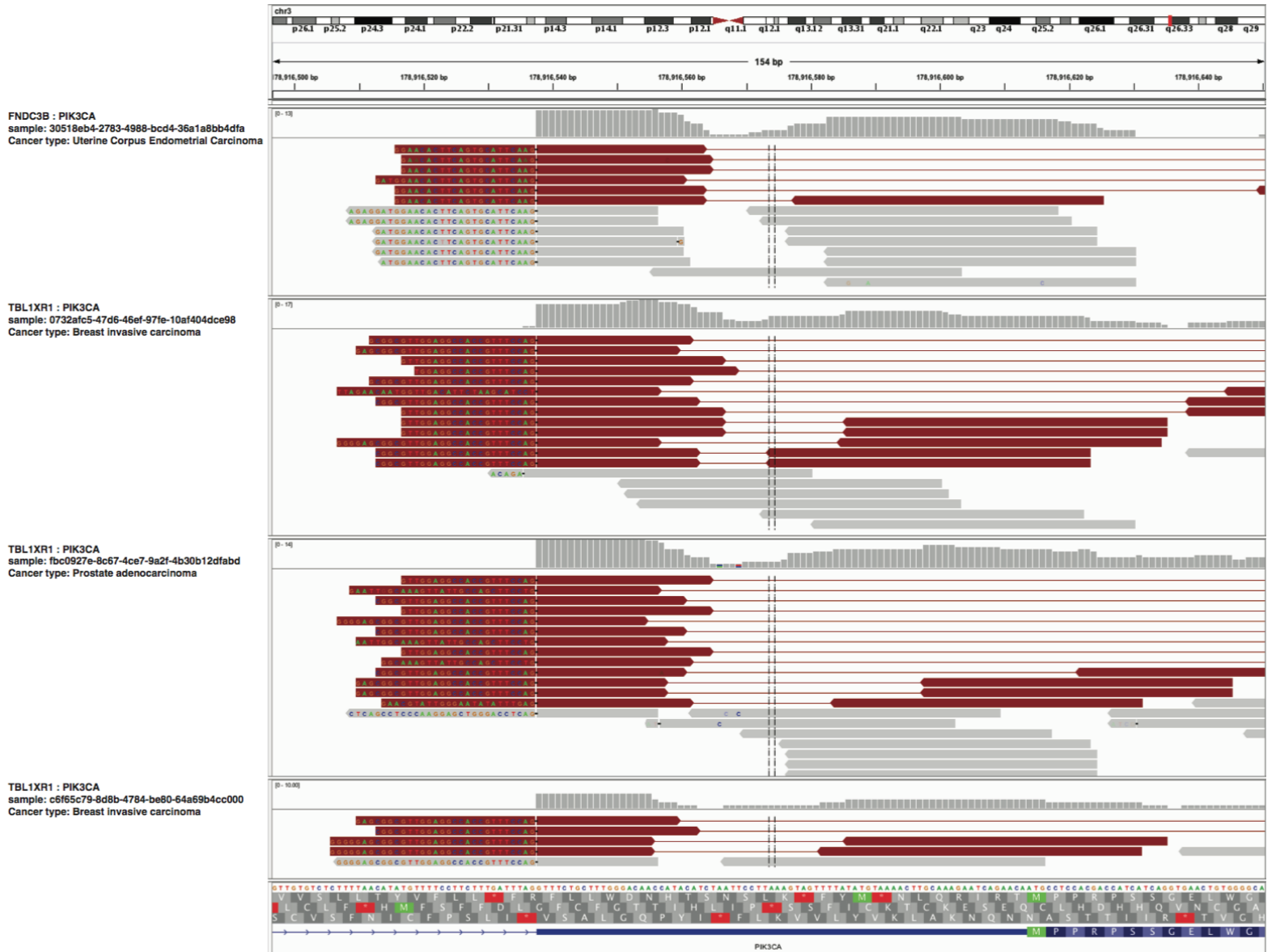
Supplementary Figure 8: *NTRK2* fusions

Protein domains, sample details, cancer type, gene partners, as well as genomic and amino acid sequence are indicated for each predicted kinase fusion proteins. In addition, the protein coordinates of the fusion breakpoints and the total amino acid length of the fusion protein are noted under each protein structure. The protein tyrosine kinase domains are colored in purple, the transmembrane domains (TM) are indicated in teal, coiled-coil (CC) dimerization domains are indicated in yellow, whereas other domains are left in white. Fusion breakpoints are delineated by red arrows.



Supplementary Figure 9: PRKCA/PRKCB fusions

a, Structure of PRKCA wild-type (top) and of the two PRKCA fusion proteins. **b**, Scatter plot of the PRKCA copy number versus mRNA expression. Each dot represents a sample with the red dots representing the samples harboring PRKCA fusions. **c**, Structure of the three PRKCB fusion proteins.



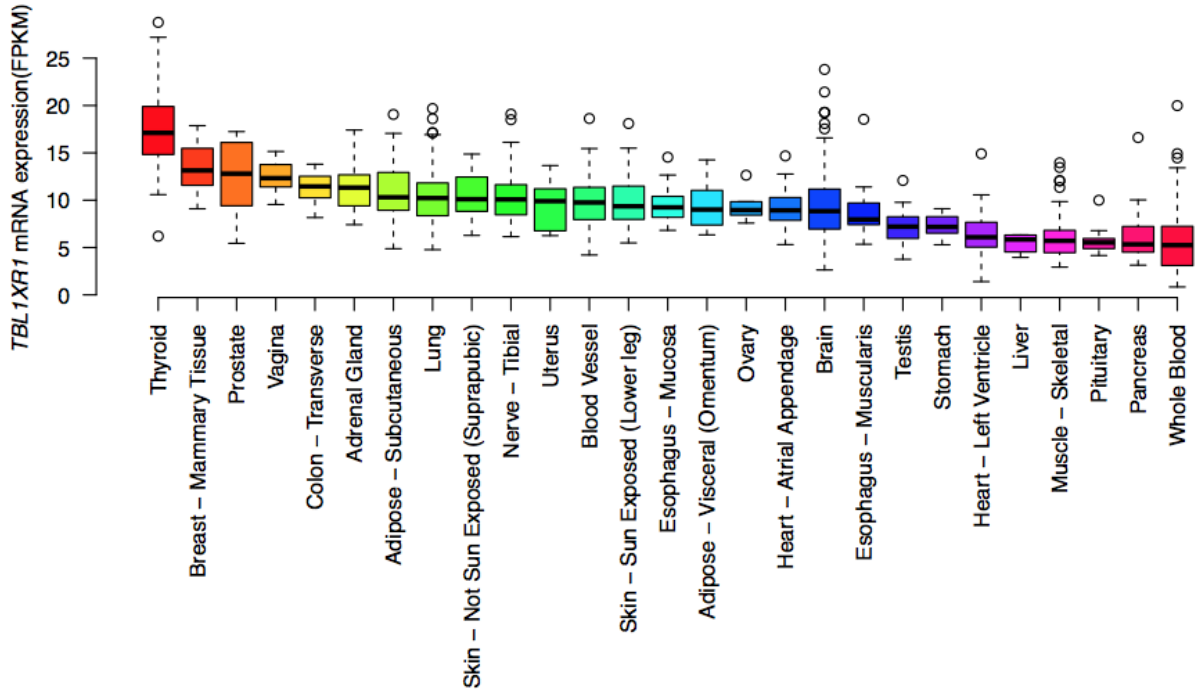
Supplementary Figure 10: *PIK3CA* fusions sequencing reads (1/2)

Sequencing reads mapping to *PIK3CA* (screenshots from the integrative genome viewer) supporting the presence of *PIK3CA* fusions in four TCGA samples. All reads are either chimeric (one end maps to *PIK3CA* and the other end maps to the partner gene) or split between both genes, with soft-clipped bases shown.



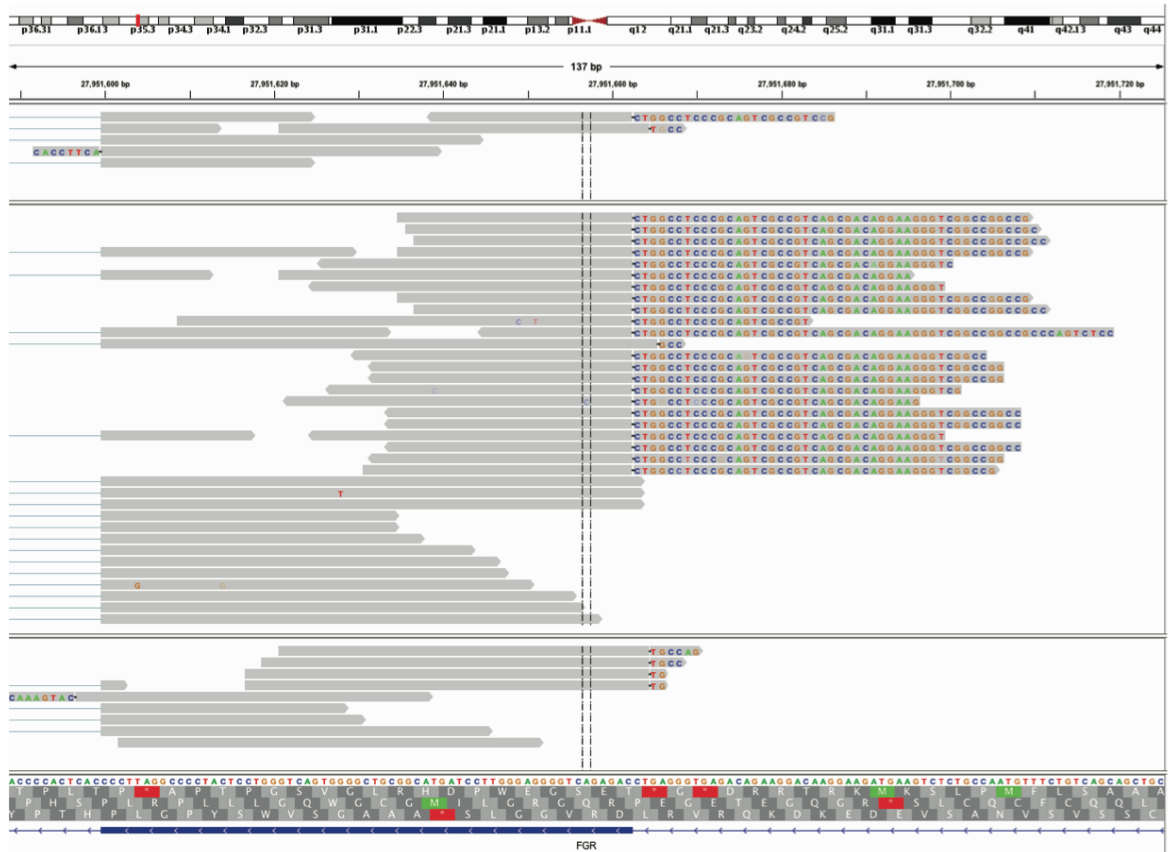
Supplementary Figure 11: *TBL1XR1-PIK3CA* fusions sequencing reads (2/2)

Sequencing reads mapping to *TBL1XR1* (screenshots from the integrative genome viewer) supporting the presence of *TBL1XR1-PIK3CA* fusions in three TCGA samples. All reads are either chimeric (one end maps to *PIK3CA* and the other end maps to the partner gene) or split between both genes, with soft-clipped bases shown.



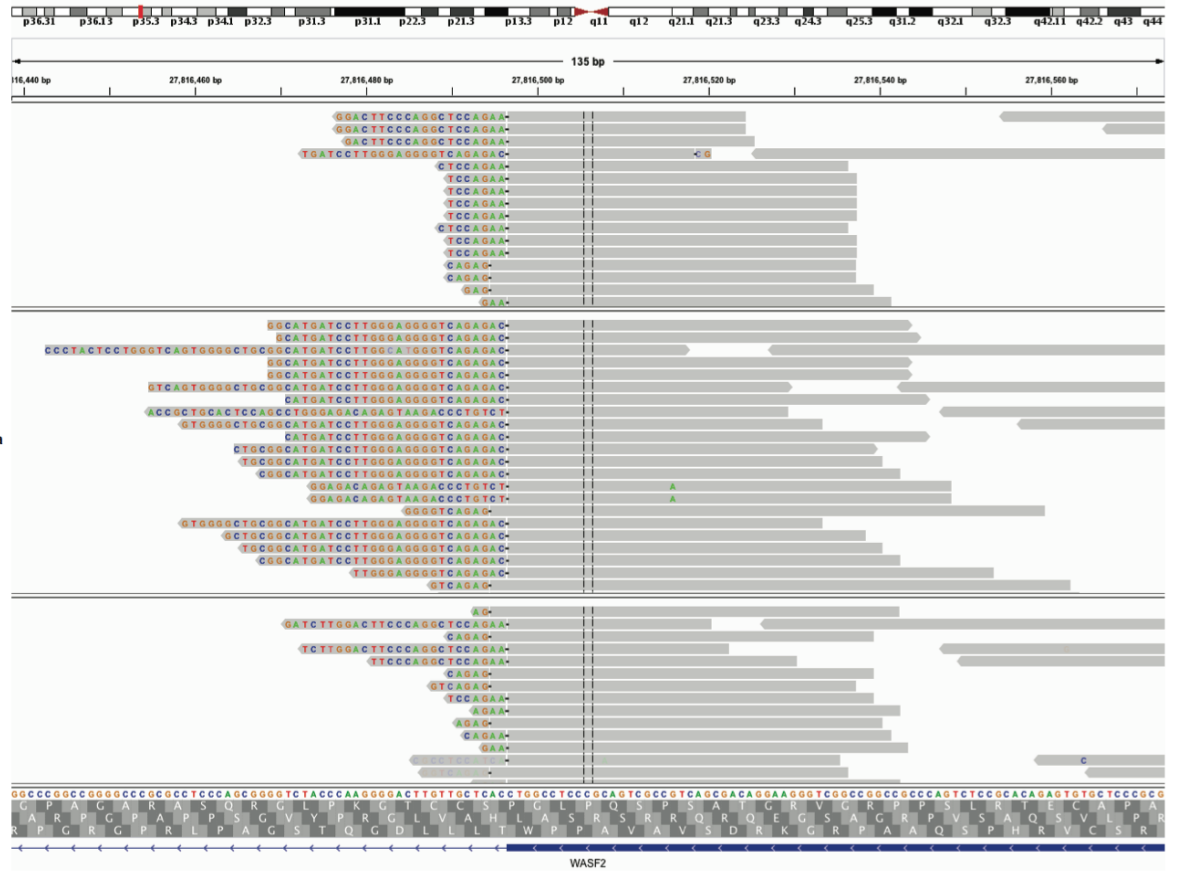
Supplementary Figure 12: *PIK3CA* expression in normal samples.

PIK3CA expression across 1,750 normal samples from the GTEx project, in 27 tissue types, ordered by their median expression (bold horizontal line). Boxplot whiskers extend to the most extreme data point which is no more than 1.5 times the interquartile range from the box (first and third quartiles). Outlier values are indicated with circles.



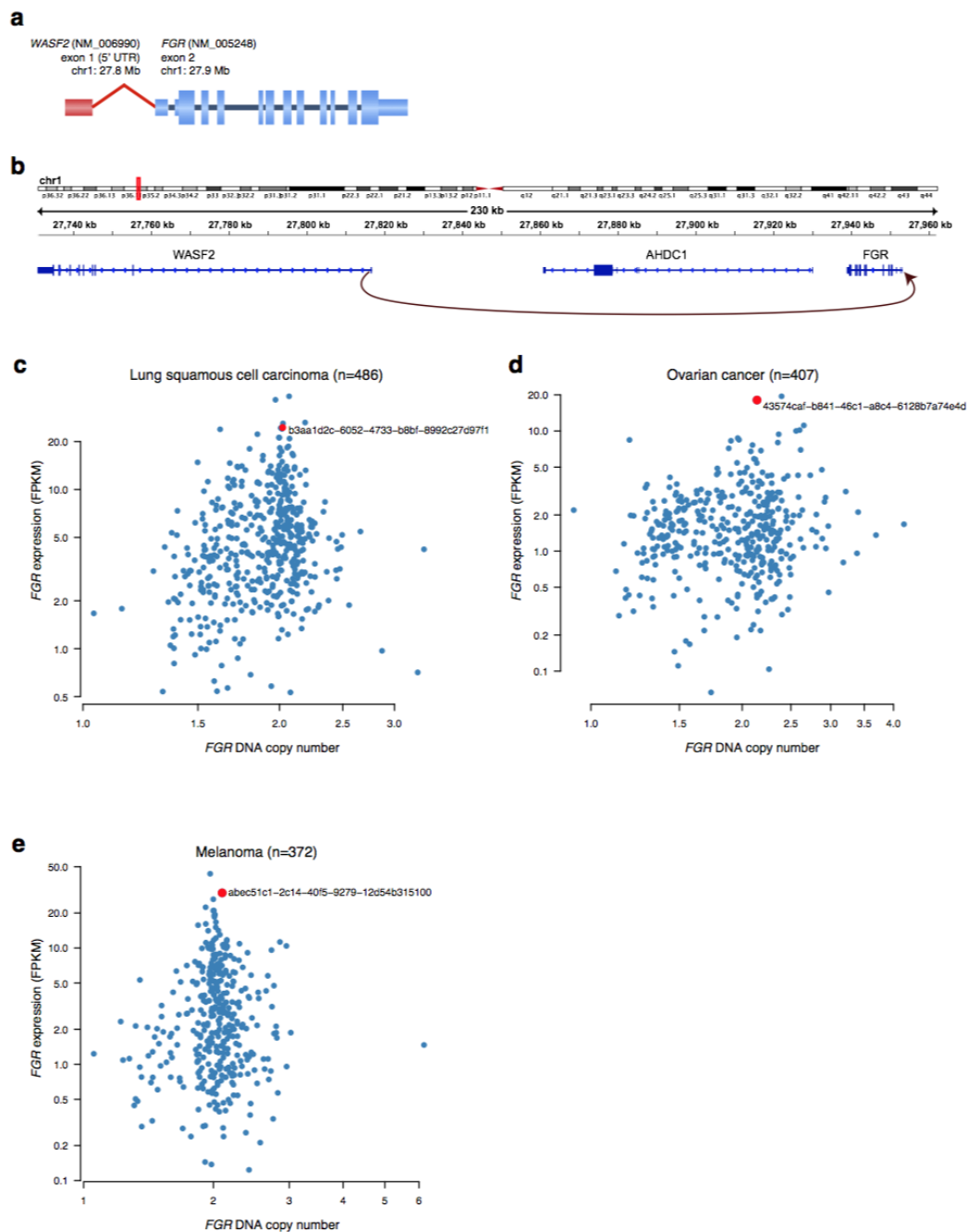
Supplementary Figure 13: *FGR* fusions (1/2)

Sequencing reads mapping to *FGR* (screenshots from the integrative genome viewer) supporting the presence of *WASF2-FGR* fusions in three TCGA samples. All reads are either chimeric (one end maps to *FGR* and the other end maps to *WASF2*) or split between both genes, with soft-clipped bases shown.



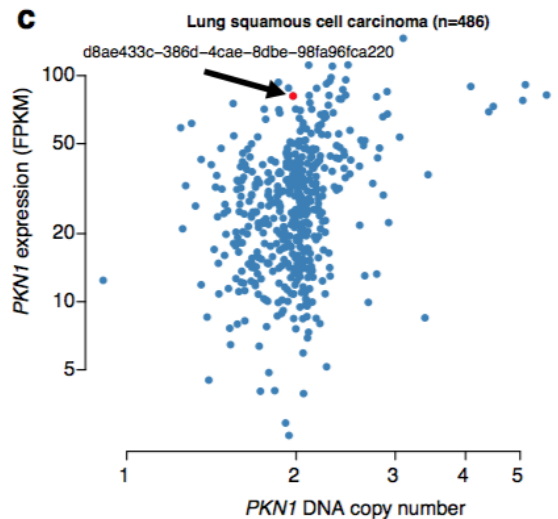
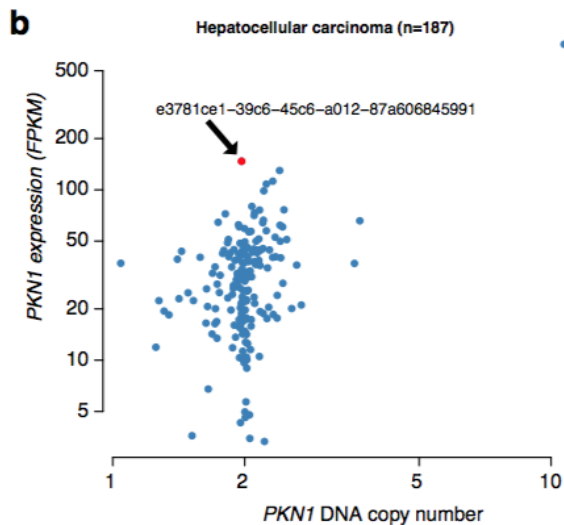
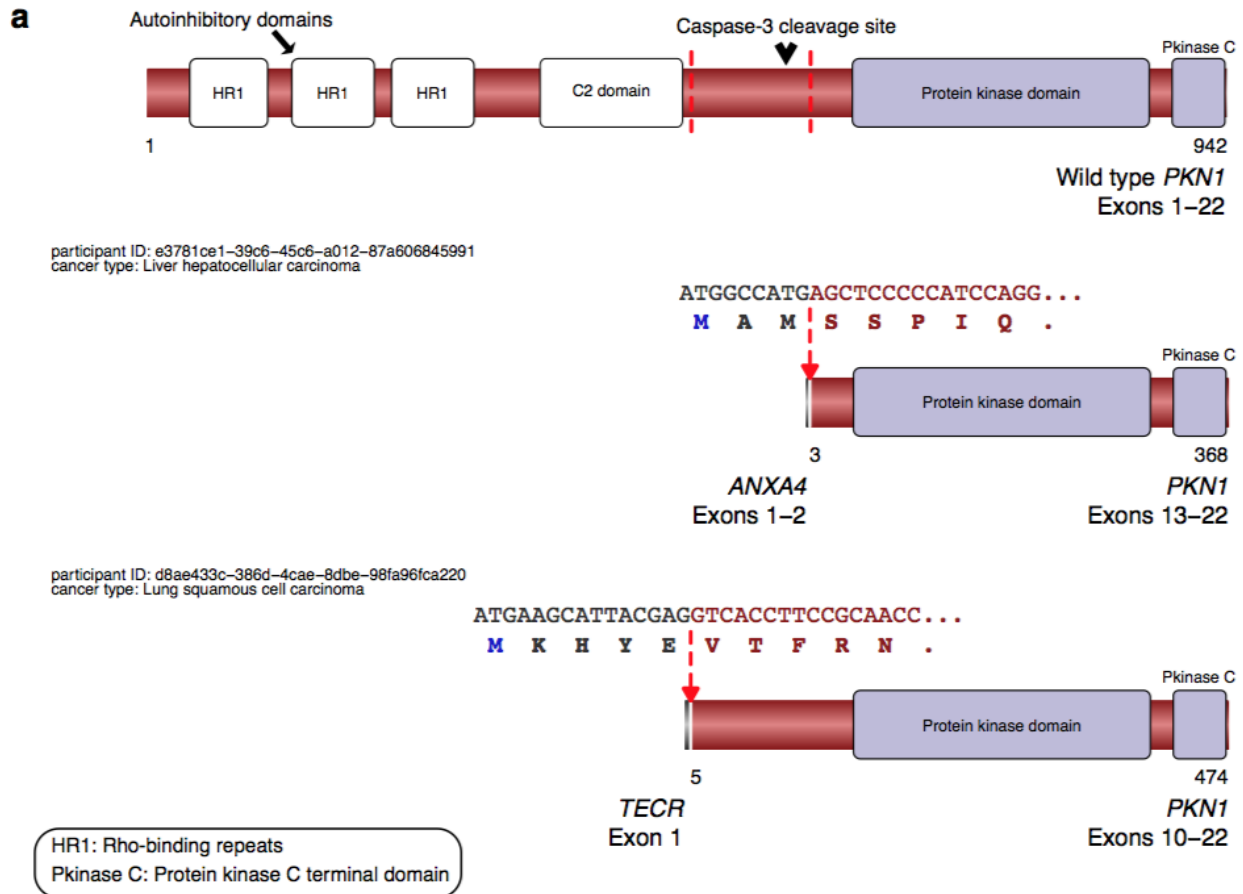
Supplementary Figure 14: *FGR* fusions (2/2)

Sequencing reads mapping to *WASF2* (screenshots from the integrative genome viewer) supporting the presence of *WASF2-FGR* fusions in three TCGA samples. All reads are either chimeric (one end maps to *FGR* and the other end maps to *WASF2*) or split between both genes, with soft-clipped bases shown.



Supplementary Figure 15: *FGR* fusions

a, b, Genomic structure of *WASF2-FGR* fusions. In all cases the entire coding sequence of *FGR* is present in the predicted fusion sequence. RefSeq IDs, exon numbers, and genomic coordinates are indicated. Exon 1 of *WASF2* (5-prime UTR) is fused to exon 2 of *FGR* (5-prime UTR). **c-e**, Scatter plots of *FGR* DNA copy number versus mRNA expression across all TCGA samples for which both data types are available. Samples harboring a *FGR* fusion are depicted in red (along with TCGA sample ID) and show a high expression of *FGR* relative to the other samples. FPKM: Fragments per kilobase of transcript per million mapped reads.



Supplementary Figure 16: *PKN1* fusions

a, Protein structure of *PKN1* wild-type (top) and *PKN1* fusions. **b**, **c**, Scatter plots of *PKN1* DNA copy number versus mRNA expression across all TCGA samples for which both data types are available. Samples harboring a *PKN1* fusion are depicted in red, along with TCGA sample ID.

Supplementary table 1: TCGA cancer types summary

Study		
Abbreviation	Study Name	n samples
blca	Bladder Urothelial Carcinoma	250
lgg	Brain Lower Grade Glioma	461
brca	Breast invasive carcinoma	1072
coad	Colon adenocarcinoma	286
gbm	Glioblastoma multiforme	157
hnsc	Head and Neck squamous cell carcinoma	411
kich	Kidney Chromophobe	66
kirc	Kidney renal clear cell carcinoma	529
kirp	Kidney renal papillary cell carcinoma	198
lihc	Liver hepatocellular carcinoma	194
luad	Lung adenocarcinoma	513
lusc	Lung squamous cell carcinoma	492
ov	Ovarian serous cystadenocarcinoma	412
prad	Prostate adenocarcinoma	335
read	Rectum adenocarcinoma	91
sarc	Sarcoma	103
skcm	Skin Cutaneous Melanoma	374
stad	Stomach adenocarcinoma	285
thca	Thyroid carcinoma	498
ucec	Uterine Corpus Endometrial Carcinoma	166