Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

eMethods. Supplemental Methods

Patient data transfer

We obtained raw RNA-Seq data from clinical partners using AWS via Amazon S3 and external hard drives. For BCCH, a Canadian institution, due to international regulations that limit the transfer of raw genomic information, we packaged our analysis pipelines into Docker containers (www.docker.com) to ensure consistent reproducible execution of our process, and to alleviate the need to transfer raw data files internationally. The BCCH bioinformaticians ran the Docker-ized analysis pipeline on their servers and shared the resulting gene-level expression information (gene-level TPM) across the border.

RNA sequencing analysis pipeline

The RNA sequencing (RNA-Seq) analysis pipelines can be obtained with the following docker command: docker pull quay.io/ucsc_cgl/rnaseq-cgl-pipeline:3.2.1-1. Gene expression quantification was performed as follows: Adapters were removed with CutAdapt v1.9. Reads were then aligned by STAR v 2.4.2a using indices generated from the human reference genome GRCh38 and the human gene models GENCODE 23. RSEM Version 1.2.25 was used to quantify gene expression. Reference data sources: GRCh38 was downloaded from

ftp://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank/Eukaryotes/vertebrates_mammals/Homo_sapiens/ GRCh38/seqs_for_alignment_pipelines/ GCA_000001405.15_GRCh38_no_alt_analysis_set.fna.gz on July 22, 2016. GENCODE 23 was downloaded from

ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_23/gencode.v23.annotation.gtf.gz July 22, 2016. The source code of the pipeline is available at https://github.com/UCSC-Treehouse/pipelines.

For quality assessment, the genome-aligned reads that are output by our RNA-Seq pipeline¹ were sorted by name using sambamba v0.6.1, piped to Samblaster 0.1.22 for duplicate marking and then sorted by coordinate by sambamba v0.6.1. The tools geneBody_coverage.py and read_distribution.py from RSeQC v2.7.10 were run on all BAM files.

A quality metric, the number of mapped, exonic, non-duplicate (MEND) reads, was estimated from read_distribution.py output using the script parseReadDist.R to do the following 1) Calculate the number of reads per tag (from the top table, "Total Reads"/"Total Tags") 2) Calculate the number of exonic tags (from the bottom table, the sum of the Tag_count column for the rows "CDS_Exons", "5'UTR_Exons" and "3'UTR_Exons"). 3) Estimate the number of exonic tags" * "number of reads per tag" /2. The QC process is available as a stand-alone docker image at https://hub.docker.com/r/hbeale/treehouse_bam_qc/. The source code is at https://github.com/UCSC-Treehouse/bam_qc.

Datasets used for comparative RNA-Seq analysis

The RNA-Seq sample data with associated clinical metadata were managed using REDCap electronic data capture tools hosted at UCSC². Version 5 of the Treehouse Gene Expression Reference Compendium, used in this manuscript, comprises 11,340 samples derived from TCGA (n=9806), TARGET (n=784), 17 additional public repository datasets (n=586) and 164 from our partner clinical sites (eTable 2). The gene expression compendium is publicly available through the UCSC Xena Browser at https://treehousegenomics.ucsc.edu/p/vaske-2019-comparative-tumor-RNA.

Visualization of the reference compendium using TumorMap

To aid in the molecular classification of tumors, we used the previously published TumorMap method³. Briefly, we first computed pairwise Spearman correlations between RNA-Seq-derived gene expression profiles of the tumors in our reference cohort (n = 11,340). This produced a square correlation matrix with 11,340 columns and 11,340 rows. We initially measured the expression of 60,498 GENCODE 23 genes (58,581 of these had uique identifiers) and then filtered out 31,497 genes with low expression or variance from the original 60,498 for a final count of 27,084 genes retained for analysis. The correlation matrix is used as input for the TumorMap, which is available at https://tumormap.ucsc.edu/?p=vaske-2019-comparative-tumor-RNA.

Defining similar tumors for pan-disease outlier analysis

To identify compendium tumor samples most similar to each index sample, TPM values from each of the 144 samples were used to compute Spearman correlations between the index sample and all the tumors in our compendium. We used the correlations of the index sample to the compendium to identify samples most similar to the index case. For each case we defined the most similar tumors in four ways: (1) all samples with the same histopathological classification as the index sample ("diagnosed disease"), (2) all

samples with a disease shared with the top six most correlated samples (MCS) ("inferred disease"), (3) all MCS with a correlation to the index sample in the top 5th percentile of all correlations in the compendium (first degree MCS) ("high stringency correlation") and (4) all samples that are first degree MCS to the first degree MCS of the index samples (first and second degree MCS) ("low stringency correlation"). One hundred and thirty six samples (out of 144) shared a diagnosed disease with another sample in the compendium, and, as expected, for 129 of those 136 samples, the stringent correlation-based cohort included at least one sample with the diagnosed disease. In 119 of the 136, the stringent correlation-based cohort also included samples with other diseases, suggesting that comparative gene expression analysis can be useful for identifying tumors with similar expression signatures regardless of diagnoses. The cohorts of similar samples were used in the gene expression outlier analysis described below.

Gene	Category	Druggability	Available approved therapy
JAK1	JAK/STAT	directly druggable gene	ruxolitinib, tofacitinib
JAK2	JAK/STAT	directly druggable gene	ruxolitinib, tofacitinib
JAK3	JAK/STAT	directly druggable gene	tofacitinib
STAT1	JAK/STAT	indirectly actionable gene (JAK)	
STAT2	JAK/STAT	indirectly actionable gene (JAK)	
STAT3	JAK/STAT	directly druggable gene	
STAT5A	JAK/STAT	indirectly actionable gene (JAK)	
STAT5B	JAK/STAT	indirectly actionable gene (JAK)	
IL6	JAK/STAT	directly druggable gene	siltuximab
IL6R	JAK/STAT	directly druggable gene	tocilizumab
EGFR	Receptor Tyrosine Kinase (RTK)	directly druggable gene	cetuximab, erlotinib, afatinib, lapatinib
ERBB2	Receptor Tyrosine Kinase (RTK)	directly druggable gene	afatinib, lapatinib
ERBB3	Receptor Tyrosine Kinase (RTK)	directly druggable gene	lapatinib
ALK	Receptor Tyrosine Kinase (RTK)	directly druggable gene	crizotinib, ceritinib
MET	Receptor Tyrosine Kinase (RTK)	directly druggable gene	cabozantinib, crizotinib
ROS1	Receptor Tyrosine Kinase (RTK)	directly druggable gene	cabozantinib, crizotinib, ceritinib
FLT1	Receptor Tyrosine Kinase (RTK)	directly druggable gene	pazopanib, regorafenib
FLT3	Receptor Tyrosine Kinase (RTK)	directly druggable gene	ponatinib, sorafenib, sunitinib
KDR	Receptor Tyrosine Kinase (RTK)	directly druggable gene	sorafenib, sunitinib
FLT4	Receptor Tyrosine Kinase (RTK)	directly druggable gene	cabozantinib, axitinib
PDGFRA	Receptor Tyrosine Kinase (RTK)	directly druggable gene	dasatinib, pazopanib, sorafenib
PDGFRB	Receptor Tyrosine Kinase (RTK)	directly druggable gene	dasatinib, pazopanib, sorafenib, sunitinib
FGFR1	Receptor Tyrosine Kinase (RTK)	directly druggable gene	pazopanib, panopanib, regorafenib
KIT	Receptor Tyrosine Kinase (RTK)	directly druggable gene	imatinib, sunitinib, regorafenib
CSF1R	Receptor Tyrosine Kinase (RTK)	directly druggable gene	pazopanib
TEK	Receptor Tyrosine Kinase (RTK)	directly druggable gene	
CDK4	Cell Cycle	directly druggable gene	palbociclib, ribociclib
CDK6	Cell Cycle	directly druggable gene	palbociclib, ribociclib
CCND1	Cell Cycle	indirectly actionable gene (CDK)	
CCND2	Cell Cycle	indirectly actionable gene (CDK)	
CCND3	Cell Cycle	indirectly actionable gene (CDK)	
CCNE1	Cell Cycle	indirectly actionable gene (CDK)	
CDK2	Cell Cycle	directly druggable gene	
PIK3CA	PI3K/AKT/mTOR	directly druggable gene	idelalisib
PIK3CB	PI3K/AKT/mTOR	directly druggable gene	idelalisib

eTable 1. Directly and indirectly actionable genes used to prioritize gene expression outlier findings.

Gene	Category	Druggability	Available approved therapy
PIK3CG	PI3K/AKT/mTOR	directly druggable gene	idelalisib
PIK3CD	PI3K/AKT/mTOR	directly druggable gene	idelalisib
PIK3R1	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3R2	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3R3	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3R4	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3R5	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3R6	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3C2A	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3C2B	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3C2G	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
PIK3C3	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
AKT1	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
AKT3	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
TSC1	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
TSC2	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
MTOR	PI3K/AKT/mTOR	directly druggable gene	everolimus, temsirolimus
RPTOR	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
MLST8	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
DEPTOR	PI3K/AKT/mTOR	indirectly actionable gene (mTOR)	
NRAS	RAS/RAF/MEK	indirectly actionable gene (MEK)	
KRAS	RAS/RAF/MEK	indirectly actionable gene (MEK)	
HRAS	RAS/RAF/MEK	indirectly actionable gene (MEK)	
BRAF	RAS/RAF/MEK	directly druggable gene	dabrafenib
RAF1	RAS/RAF/MEK	directly druggable gene	dabrafenib, sorafenib, regorafenib
ARAF	RAS/RAF/MEK	indirectly actionable gene (MEK)	
MAP2K1	RAS/RAF/MEK	directly druggable gene	trametinib
MAP2K2	RAS/RAF/MEK	directly druggable gene	trametinib
PTCH1	Sonic Hedgehog (SHH)	indirectly actionable gene (SMO)	
GLI1	Sonic Hedgehog (SHH)	indirectly actionable gene (SMO)	
SMO	Sonic Hedgehog (SHH)	directly druggable gene	vismodegib
BCL2	BCL2/MDM2	directly druggable gene	venetoclax
BCL6	BCL2/MDM2	indirectly actionable gene (BCL2)	
MDM2	BCL2/MDM2	indirectly actionable gene (BCL2)	
HSP90AA1	Heat Shock Proteins	directly druggable gene	
HSP90AA2P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90N	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AA2	Heat Shock Proteins	directly druggable gene/gene family	

Gene	Category	Druggability	Available approved therapy
HSP90AA6P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AA3P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AA4P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AA5P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AB1	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AB3P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AB2P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AB6P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AB4P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90AB5P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90B1	Heat Shock Proteins	directly druggable gene/gene family	
HSP90B2P	Heat Shock Proteins	directly druggable gene/gene family	
HSP90B3P	Heat Shock Proteins	directly druggable gene/gene family	
BTK	B-cell receptor signaling	directly druggable gene/gene family	ibrutinib
MS4A1	B-cell receptor signaling	directly druggable gene/gene family	rituximab
AURKA	Aurora kinases	directly druggable gene/gene family	
AURKB	Aurora kinases	directly druggable gene/gene family	
AURKC	Aurora kinases	directly druggable gene/gene family	
PARP1	DNA repair	directly druggable gene/gene family	olaparib

eTable 2. Published repository datasets included in the Treehouse Compendium v5.

TH dataset	Accession	Repository	Project	Disease	N
TARGET	TARGET	dbGap	TARGET	multiple cancers	784
TCGA	TCGA	dbGap	TCGA	multiple cancers	9,806
THR08	EGAD00001001098	EGA	St Jude PCGP	ALL with MLL rearrangements	63
THR09	EGAD00001000356	EGA	ICGC	B-cell lymphoma	23
THR10	EGAD00001002680	EGA	St Jude PCGP	adrenocortical carcinoma	15
THR11	EGAD00001001666	EGA	St Jude PCGP	low grade glioma	32
THR13	phs000900.v1.p1	dbGap	PBTC (Monje Lab)	DIPG	10
THR14	CBTTC_HGG_PA_01	Cavatica	CBTTC	high grade glioma	29
THR15	phs000699.v1.p1	dbGap	Perry et al	osteosarcoma	29
THR17	EGAD00001000158	EGA	ICGC/MAGIC	medulloblastoma	17
THR18	EGAD00001000328	EGA	ICGC	medulloblastoma	6
THR19	EGAD00001000617	EGA	ICGC	pilocytic astrocytoma	69
THR20	EGAD00001001620	EGA	ICGC	medulloblastoma	39
THR22	EGAD00001000648	EGA	ICGC	germinal B-cell lymphoma	24
THR25	EGAD00001000826	EGA	ICGC	osteosarcoma	7
THR28	SRP040454	SRA	Kohsaka et al	rhabdomyosarcoma	3
THR29	phs000720.v2.p1	dbGap	Shern et al	rhabdomyosarcoma	83
THR30	phs000768.v2.p1	dbGap	Brohl et al	Ewing sarcoma	62
THR31	phs000673.v2.p1	dbGap	Peds Mi-OncoSeq/Met500	multiple cancers	75

A. Compendium v5 Repository Data

total 11,176

586

total - (TCGA+TARGET)

B. Compendium v5 Treehouse Partner Data

TH dataset	Treehouse Partner	N
TH02	Pacific Pediatric Neuro-Oncology Consortium (PNOC)	29
TH03	Stanford, Sweet-Cordero Lab	73
TH04	Memorial Sloan Kettering Cancer Center via Stanford, Sweet-Cordero Lab	1
TH06	British Columbia Personalized Onco-Genomics (POG) Program	31
TH26	Stanford, Merker Lab	6
TH27	UC San Francisco, Sweet-Cordero Lab	24
	total	164

C. Compendium v5 Repository Data By Consortium

Consortium	v5 (Feb 2018)
TCGA	9,806
TARGET	784
ICGC	168
ICGC/MAGIC	17
St Jude PCGP	110
CBTTC	29
PBTC	10
other	252
total	11,176

D. Repository Data Acknowledgments

Treehouse expression dataset (v5, February 2018)

Use of data available in public repositories allowed us to increase the number of pediatric cancer patients and pediatric cancer types included in our reference compendium, and we gratefully acknowledge the following data providers in the manner they have specified:

"International Cancer Genome Consortium. The following ICGC datasets were used in this work: EGAD00001000158, EGAD00001001620, EGAD00001000328, EGAD00001000648, EGAD00001000617, EGAD00001000826 and EGAD00001000356."

"St. Jude Children's Research Hospital – Washington University Pediatric Cancer Genome Project. The following datasets were accessed via EGA (https://www.ebi.ac.uk/ega/) and were used by permission:

EGAD00001001098: Andersson AK, Ma J, Wang J, et al. The landscape of somatic mutations in infant MLLrearranged acute lymphoblastic leukemias. Nat Genet. 2015;47(4):330-7. (PMC4553269). EGAD00001001666: Qaddoumi I, Orisme W, Wen J, et al. Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. Acta Neuropathol. 2016;131(6):833-45. (PMID 26810070). EGAD00001002680: Pinto EM, Chen X, Easton J, et al. Genomic landscape of paediatric adrenocortical tumours. Nat Commun. 2015;6:6302. (PMC4352712)."

"Provider(s) of the data under accession phs000178.v10.p8 at dbGap. The Cancer Genome Atlas Research Network

National Cancer Institute and National Human Genome Research Institute, Bethesda, MD, USA The results published here are in whole or part based upon data generated by The Cancer Genome Atlas managed by the NCI and NHGRI. Information about TCGA can be found at http://cancergenome.nih.gov/."

"Provider(s) of the data under accession phs000178.v10.p8 at dbGap: The Therapeutically Applicable Research to Generate Effective Treatments (TARGET) initiative managed by the NCI. The data used for this analysis are available at dbGap under accession phs000218. Information about TARGET can be found at http://ocg.cancer.gov/programs/target.

Children's Oncology Group (COG; Tissues for TARGET are collected as part of COG clinical and biological protocols) Peter C. Adamson, MD. Children's Hospital of Philadelphia, Philadelphia, PA, USA Principal Investigator (ALL Project Team) Stephen P. Hunger, MD. University of Colorado Cancer Center, Denver, CO, USA Principal Investigators (AML Project Team) Soheil Meshinchi, MD, PhD. Fred Hutchinson Cancer Research Center, Seattle, WA, USA Robert Arceci, MD, PhD. Children's Hospital, Phoenix, AZ, USA Principal Investigator (NBL Project Team) John M. Maris, MD. Children's Hospital of Philadelphia, Philadelphia, PA, USA Robert Seeger, MD. Children's Hospital of Los Angeles, Los Angeles, CA, USA Javed Khan, MD. National Cancer Institute, National Institutes of Health, Bethesda, MD, USA Principal Investigator (OS Project Team) Ching Lau, MD, PhD. Texas Children's Hospital, Houston, TX, USA Paul Meltzer, MD, PhD. National Cancer Institute, National Institutes of Health, Bethesda, MD, USA Principal Investigator (Kidney Project Teams - WT, CCSK, RT) Elizabeth J. Perlman, MD. Ann and Robert H. Lurie Children's Hospital of Chicago, Chicago, IL, USA Principal Investigator (Cell Lines and Xenografts - PPTP) Peter Houghton, PhD. The Research Institute at Nationwide Children's Hospital, Columbus, OH, USA"

Provider(s) of the data under accession phs000699.v1.p1 at dbGap: Todd Golub. Dana Farber Cancer Institute, Boston, MA, USA. This work was conducted as part of the Slim Initiative for Genomic Medicine in the Americas (SIGMA), a project funded by the Carlos Slim Health Institute in Mexico.

Provider(s) of the data under accession phs000900.v1.p1 at dbGap: Charles Keller. Children's Cancer Therapy Development Institute, Fort Collins, CO, USA. We thank the many patients and families who selflessly contributed to this study through tissue donations from surgery or autopsy and Amar Gajjar, for his guidance and vision throughout this study. We also thank Darren Hargrave, James Olson and Sarah Leary for selection of V.2 chemical screen agents. We are grateful for the critical questions and comments by Simone Cheetham and Nadim Nsouli. We also acknowledge important comments by other DIPG Preclinical Consortium member Oren Becher. We thank Gerald Grant for assistance in developing rodent CED techniques. Short read sequencing was performed by the OHSU Massively Parallel Sequencing Shared Resource. The first paper using this data was: Grasso CS, Tang Y, Truffaux N, et al. Functionally defined therapeutic targets in diffuse intrinsic pontine glioma. Nat Med. 2015;21(6):555-9. (PMID 25939062).

Provider(s) of the data under accession phs000720.v2.p1 at dbGap: Javed Khan, MD. National Institutes of Health, Bethesda, MD, USA. The authors thank the Children's Oncology Group Soft Tissue Sarcoma Committee and the BioPathology Center, for their careful collection of clinical samples. This research was supported by the Intramural Research Program of the National Institute of Health and National Cancer Institute.

Provider(s) of the data under accession phs000768.v2.p1 at dbGap. Javed Khan, MD. National Institutes of Health, Bethesda, MD, USA. This research was supported by the Intramural Research Program of the National Institute of Health and National Cancer Institute. The datasets have been accessed through the NIH database for Genotypes and Phenotypes (dbGaP) under accession # phs000768.v1.p1.

Provider(s) of the data under accession phs000673.v2.p1 at dbGap. Arul Chinnaiyan, MD PhD. Michigan Center for Translational Pathology, University of Michigan, MI, USA. The results published here are in whole or part based upon data generated by the Clinical Sequencing Exploratory Research (CSER) consortium

established by the NHGRI. Funding support was provided through cooperative agreements with the NHGRI and NCI through grant numbers U01 HG006508 (Exploring Cancer Medicine for Sarcoma and Rare Cancers). Information about CSER and the investigators and institutions who comprise the CSER consortium can be found at http://www.genome.gov/27546194

Provider(s) of the data under accession SRP040454 at SRA. Dataset was made available by Memorial Sloan Kettering Cancer Center.

This research was conducted using data made available by The Children's Brain Tumor Tissue Consortium (CBTTC).

Sample	Diagnosis Group	Diagnosis	Gender	Age at Diagnosis	Age Category
	Other				
	Neuroblastoma	neuroblastoma	male		
	Liver	hepatoblastoma	male		
	Bone sarcoma	osteosarcoma	female male not reported		
		sarcoma			
]. <u>.</u>	Soft tissue sarcoma	sarcoma	male		Age < 30 years
10 samples			female		
		diffuse intrinsic pontine glioma	male		
	CNS	glioblastoma multiforme	female		
			male		
		glioma			
			female		
	Hematopoietic	acute lymphoblastic	male		
		acute myeloid leukemia			
	Other	diffuse intrinsic pontine gli	oma	0 26	
	Neuroblastoma	neurofibroma		0 20	
	Wilms and other kidney	neurofibromatosis type 1	atypical teratoid/rha	abdoid tumor	
	Liver	fibromatosis	neuroblastoma		
	Bone sarcoma	lung adenocarcinoma	osteosarcoma		
	Soft tissue sarcoma	gliomatosis cerebri	wilms tumor		
	Germ cell tumor or teratoma	angiosarcoma	teratoma		
	CNS	NUT midline carcinoma	fibrolamellar hepat	ocellular carcinoma	
	Hematopoietic	glioblastoma multiforme	myoepithelial carci	noma of the liver	
		thyroid carcinoma	hepatoblastoma		
		craniopharyngioma	rhabdomyosarcom	a	
		nasopharyngeal carcinom	a acute leukemia of a	ambiguous lineage, CNS1	
		ependymoma	lymphoma		
		hepatocellular carcinoma	sarcoma		
		monocytic leukemia	germ cell tumor		
		adrenocortical	acute lymphoblasti	c	
		medulloblastoma	leukemia acute myeloid leuk	emia	

a.



eFigure 1. Treehouse reference compendium used for cross-tumor

COMPARISONS. The data and visualizations are publicly available at treehousegenomics.ucsc.edu/p/vaske-2019comparative-tumor-RNA. A. Treehouse prospective patient cohort (N=144) visualized using the UCSC Xena Browser (xena.ucsc.edu) B. Treehouse compendium (N=11,340) visualized using the TumorMap (eMethods). Each hexagon represents an individual sample and the samples are colored by disease as indicated in the legend.

b.

eTable 3. Findings from comparative RNA-Seq analysis and comparisons to mutation analysis.

Panel A, "DNA-RNA comparison", details comparisons of DNA and RNA findings for 74 samples with both types of data. Panel B contains results from comparative RNA-Seq analysis for all 144 samples.

A. DNA-RNA comparison for 74 samples with both types of data.

				Calid (DNA mutation call of	DNA mutation actoriony NCI		Outlier	Outlier not confirmed				
TH sample ID	Diagnosis	aberrantly expressed?	Utility of RNA sequencing	leukemia	clinical relevance	Pediatric MATCH	Treehouse category	by pathway	by pathway	gene	mutation	note	testVendor
in campion2	acute lymphoblastic		Prioritizing among multiple					a) pairiaj	paintay	90110			
TH01_0123_S01	leukemia	Yes	DNA findings	leukemia						new sample			
					FLT3 amplification	Receptor Tyrosine Kinase (RTK)	Receptor Tyrosine Kinase (RTK)	FLT3, FLT4		FLT3	Low-levelAmplification		NantOmics
					JAK2 p.R683S	JAK/STAT	JAK/STAT	JAK3		JAK2	p.R683S		NantOmics
							B-cell receptor signaling	MS4A1		JAK2	p.R683S		NantOmics
								PIK3CD,					
								PINJUG,					
TH01 0132 S01	acute myeloid leukemia	RNA only target	RNA only target	leukemia			FISRART/IIITOR	RETOR		new sample			
11101_0132_001	acute myeloid leukemia		RNA only target	leukeitiid						MITT10-			
					No druggable mutations		B-cell receptor signaling	втк		KMT2A	MLL rearrangement		NantOmics
							Cell cycle	CDK6					
							PI3K/AKT/mTOR	PIK3CG					
	acute lymphoblastic		Additional expression										
TH01_0129_S01	leukemia	No	support for DNA finding	leukemia						new sample			
					BCR-ABL1 fusion	Other							
							B-cell receptor signaling	MS4A1		BCR-ABL1			NantOmics
-							PI3K/AKT/mTOR	PIK3CG					
TH01_0120_S01	acute myeloid leukemia	RNA only target	RNA only target	leukemia				0.51/0		new sample	100/5		
					No druggable mutations			CDK6		GATA2	p.L321F		NantOmics
	aguta lymphoblastia						Receptor Tyrosine Kinase (RTK)	KII					
TH01 0121 S01		RNA only target	RNA only target	leukemia						new sample			
11101_0121_001				leakernia				IL6R JAK3		new sample			
					No druggable mutations		JAK/STAT	STAT5B					NantOmics
							B-cell receptor signaling	MS4A1					
								PIK3CD,					
								PIK3CG,					
							PI3K/AKT/mTOR	PIK3R5					
	acute lymphoblastic		Additional expression										
TH01_0122_S01	leukemia	No	support for DNA finding	leukemia						new sample			
					PAX5-JAK2 fusion	JAK/STAT		NO 44 4		PAX5-JAK2			NantOmics
							B-cell receptor signaling	MS4A1					
								PIK3CD,					
	acute lymphoblastic							1 11000					
TH01 0124 S01	leukemia	No		leukemia						new sample			
					KRAS p.G13D, NRAS								
					p.G12D	RAS/RAF/MEK				KRAS	p.G13D		NantOmics
							Receptor Tyrosine Kinase (RTK)	FLT3		NRAS	p.G12D		NantOmics
	acute lymphoblastic												
TH01_0125_S01	leukemia	RNA only target	RNA only target	leukemia				E I T 0		new sample	Receive		
					No druggable mutations		Receptor Tyrosine Kinase (RTK)	FLI3		CSF3R	p.D320N		NantOmics
								DIKACO		KMIZA-AFF1	n D2670	Donian	NantOmics
										1302		Denign	Nanionius
							B-cell receptor signaling	BTK					
	acute lymphoblastic												
TH01_0126 S01	leukemia	DNA only target	DNA only target	leukemia						new sample			
					NRAS p.G12D	RAS/RAF/MEK	No automated leads			NRAS	p.G12D		NantOmics
					CDKN2A deletion	Cell Cycle				CDKN2A	deletion		NantOmics
	acute lymphoblastic												
TH01_0128_S01	leukemia	RNA only target	RNA only target	leukemia						new sample			
					No druggable mutations		JAK/STAT	IL6R					NantOmics
								PIK3CD,					
								PINJUG,					
	acute lymphoblastic		Additional expression					LIV9K9					
TH01 0134 S01	leukemia	No	support for DNA finding	leukemia						new sample			
			copport of Driveniding	louitonnia	NRAS p.G13D	RAS/RAF/MEK				NRAS	p. G13D		NantOmics
<u> </u>							Cell cycle	CDK6					
	acute lymphoblastic												
TH01_0133_S01	leukemia	RNA only target	RNA only target	leukemia						new sample			
					No druggable mutations		Receptor Tyrosine Kinase (RTK)		FLT3				NantOmics
	acute lymphoblastic		DNA finding likely a										
TH01_0131_S01	leukemia	No	technical artifact	leukemia						new sample			

					14K2 p B692S						n P692S	NantOmics
				_	JAK2 P.R0035	JANSTAT		DTI		JAKZ	μ.κ	NantOmics
							B-cell receptor signaling	BIK				
							Cell cycle	CDK6				
							Receptor Tyrosine Kinase (RTK)	FLT3, FLT4				
							PI3K/AKT/mTOR	PIK3CG				
	acute lymphoblastic		Prioritizing among multiple									
TH01 0127 S01	leukemia	Yes	DNA findings	leukemia						new sample		
				louitonna	FLT3 p \/592D	Receptor Tyrosipe Kinase (RTK)	Receptor Tyrosine Kinase (RTK)	FLT3		FLT3	n \/592D	NantOmics
					1 E13 p. 0332D						p. 0332D	NantOmics
					KRAS p.G12D	RAS/RAF/MEK				KRAS	p.G12D	NantOmics
							B-cell receptor signaling	BTK				
							PI3K/AKT/mTOR	PIK3CG				
	acute lymphoblastic		Additional expression									
TH01_0130_S01	leukemia	No	support for DNA finding	leukemia						new sample		
11101_0100_001			support for Drivenhang	louitonnia	DAXE JAK2 fusion							NontOmico
					PAX5-JAK2 IUSION	JAN/STAT				PAX5-JAKZ		NantOmics
							Receptor Tyrosine Kinase (RTK)	FLT3				
							B-cell receptor signaling	MS4A1				
							PI3K/AKT/mTOR	PIK3CG				
	diffuse intrinsic pontine											
TH02 0082 S01	dioma	No DNA or RNA targets	No DNA or RNA targets	solid								
11102_0002_001	gioria	No DIA OF RIA algets		3010			No evitemente d'Ise de				- KOZM	Achien Anchetice
					No druggable mutations		No automated leads			НЗГЗА	p.K27W	Ashion Analytics
	diffuse intrinsic pontine		Prioritizing among multiple									
TH02_0083_S01	glioma	Yes	DNA findings	solid						new sample		
										CRKL	Gain	Ashion Analytics
								1		H3F3A	p.K27M	Ashion Analytics
					KDR gain	Receptor Tyrosine Kinase (PTK)		1		KDR	Gain	Ashion Analytics
						Receptor Tyrosine Kinase (KTK)						ASHION ANALYTICS
										MAPK1	Gain	Ashion Analytics
					MET gain	Receptor Tyrosine Kinase (RTK)				MET	Gain	Ashion Analytics
					PDGFRA gain	Receptor Tyrosine Kinase (RTK)	Receptor Tyrosine Kinase (RTK)	PDGFRA		PDGFRA	Gain	Ashion Analytics
					Ŭ					TP53	p.G245S	Ashion Analytics
	diffuse intrinsis ponting											
TU02 0004 C04				aalid								
TH02_0084_501	giloma	NO DNA OF RNA targets	NO DINA OF RINA targets	SOlid						new sample		
					No druggable mutations		No automated leads			TP53	p.A159P	Ashion Analytics
	diffuse intrinsic pontine		Prioritizing among multiple									
TH02_0085_S01	glioma	Yes	DNA findings	solid						new sample		
										H3F3A	p.K27M	Ashion Analytics
					KDR gain	Recentor Tyrosine Kinase (RTK)				KDR	Gain	Ashion Analytics
						Receptor Tyrosine Kinase (RTK)				KII	Gain	Ashion Analytics
					PDGFRA gain	Receptor Tyrosine Kinase (RTK)	Receptor Tyrosine Kinase (RTK)		PDGFRA	PDGFRA	Gain	Ashion Analytics
										TP53	p.A159P	Ashion Analytics
	diffuse intrinsic pontine											
TH02 0086 S01	glioma	RNA only target	RNA only target	solid						new sample		
	9				No druggable mutations		Sonic Hedgebog (SHH)		PTCH1	ATRX	n W/2001X	Ashion Analytics
									1 10111			
										RSF3A		
										PPM1D	p.S421X	Ashion Analytics
	diffuse intrinsic pontine											
TH02_0087_S01	glioma	No		solid						new sample		
										H3F3A	p.K27M	Ashion Analytics
					PIK3R1 unspecified							
					charration colled							
					uruggable by clinical					DUCCE		
					testing lab	PI3K/AKT/mTOR				PIK3R1	p.K567E	Ashion Analytics
										PPM1D	p.I546fs	Ashion Analytics
										TP53	p.R282W	Ashion Analytics
	diffuse intrinsic pontine											
TH02 0087 S02	glioma	DNA only target	DNA only target	solid						new sample		
	<u>g</u>									H3E2A	n K27M	Ashion Analytics
										погол		ASHIOIT Analytics
					PIK3R1 unspecified							
					aberration, called							
					druggable by clinical							
					testing lab	PI3K/AKT/mTOR	No automated leads			PIK3R1	p.K567E	Ashion Analytics
										PPM1D	p.1546fs	Ashion Analytics
	diffuse intrinsic pontine											
TH02 0000 004	alioma	No DNA or DNA torrete	No DNA or DNA torrete	colid						pour comple		
1102_0008_501	giona	NO DIVA OF KINA targets	NO DINA OF KINA targets	SUIU						new sample	Deletter	
				-	No druggable mutations		INO automated leads			AIKX	Deletion	Ashion Analytics
										H3F3A	p.K27M	Ashion Analytics
										TP53	p.S37Y	Ashion Analytics
										TP53	p.V157L	Ashion Analytics
	diffuse intrinsic ponting											
TH02 0000 004	alioma	No DNA or DNA torrete	No DNA or DNA torrete	colid						pour comple		
1102_0069_501	giona	NO DIVA OF KINA targets	NO DINA OF KINA targets	SUIU						new sample	110105	
					No druggable mutations		No automated leads			AIRX	p.A1812P	Ashion Analytics
										H3F3A	p.K27M	Ashion Analytics
										TP53	p.R248W	Ashion Analytics
	diffuse intrinsic pontine		Additional expression									-
TH02 0090 S01	glioma	Yes	support for DNA finding	solid						new sample		
	gioria		support for Drive infulling	Cond			Sonio Hodgobog (SUU)		DTCU4	now sample		
1	Ì	1	1	1				1		1	1 I I I I I I I I I I I I I I I I I I I	

										ATRX	p.E2279X	Ashion Analytics
					IGF1R gain	Receptor Tyrosine Kinase (RTK)				IGF1R	Gain	Ashion Analytics
										TP53	p.R110L	Ashion Analytics
	diffuse intrinsic pontine											
TH02_0091_S01	glioma	No		solid				00545		new sample		
							Receptor Tyrosine Kinase (RTK)	CSF1R				
					DRAF P.VOUUE	RAS/RAF/MER					p.v600E	Ashion Analytics
	diffuse intrinsic pontine		Additional expression								p.nz/iii	
TH02 0092 S01	dioma	No	support for DNA finding	solid						new sample		
	9									ATRX	p.K1357fs	Ashion Analytics
							RAS/RAF/MEK	MEK1		H3F3A	p.K27M	Ashion Analytics
					KDR gain	Receptor Tyrosine Kinase (RTK)				KDR	Gain	Ashion Analytics
					KIT gain	Receptor Tyrosine Kinase (RTK)				KIT	Gain	Ashion Analytics
					PDGFRA gain	Receptor Tyrosine Kinase (RTK)				PDGFRA	Gain	Ashion Analytics
										PTEN	Deletion	Ashion Analytics
										TP53	p.R196P	Ashion Analytics
TH02 0002 501	diffuse intrinsic pontine	DNA only torget	DNA only torget	aalid								
1802_0093_501	giloma			SOlia			No automated leads				p K27M	Ashion Analytics
					MET gain	Receptor Tyrosine Kinase (RTK)	No automateu leaus			MET	Gain	Ashion Analytics
					PDGFRA gain	Receptor Tyrosine Kinase (RTK)				PDGFRA	Gain	Ashion Analytics
										TP53	p.C242Y	Ashion Analytics
										TP53	p.K120E	
	diffuse intrinsic pontine		Additional expression									
TH02_0094_S01	glioma	Yes	support for DNA finding	solid						new sample		
										H3F3A	p.K27M	Ashion Analytics
					MET gain	Receptor Tyrosine Kinase (RTK)	Receptor Tyrosine Kinase (RTK)		MET	MET	Gain	Ashion Analytics
										TP53	p.R273C	Ashion Analytics
TU00 0005 004	diffuse intrinsic pontine	DNA anh tanat	DNM exhibitement	a a l'al								
TH02_0095_501	glioma	RNA only target	RNA only target	SOIID	No druggoble mutations		Sonia Hadgebag (SHH)			new sample	P P206H	Achien Analytics
									РІСПІ		p.R200H	
										TP53	p.R248Q	Ashion Analytics
	diffuse intrinsic pontine									11.00		
TH02_0096_S01	glioma	No DNA or RNA targets	No DNA or RNA targets	solid						new sample		
					No druggable mutations		No automated leads			DDX11	p.R167T	Ashion Analytics
										PPM1D	p.E405X	Ashion Analytics
										PPM1D H3F3A	p.E405X p.K27M	Ashion Analytics
TH03_0003_S01	sarcoma	DNA only target	DNA only target	solid						PPM1D H3F3A new sample	p.E405X p.K27M	Ashion Analytics Ashion Analytics
TH03_0003_S01	sarcoma	DNA only target	DNA only target	solid			No automated leads			PPM1D H3F3A new sample ATRX	p.E405X p.K27M LossExons13-35	Ashion Analytics Ashion Analytics Foundation Medicine
TH03_0003_S01	sarcoma	DNA only target	DNA only target	solid	CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A	p.E405X p.K27M LossExons13-35 CDKN2A_loss	Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma	DNA only target	DNA only target	solid	CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9	Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	Sarcoma	DNA only target	DNA only target	solid	CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 pew sample	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9	Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma	DNA only target DNA only target DNA only target	DNA only target DNA only target DNA only target	solid solid solid	CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35	Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma	DNA only target DNA only target DNA only target	DNA only target DNA only target DNA only target	solid solid solid solid	CDKN2A/2B deletion	Cell Cycle	No automated leads No automated leads No automated leads No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma	DNA only target DNA only target DNA only target	DNA only target DNA only target DNA only target	solid solid solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle Cell Cycle Cell Cycle Cell Cycle	No automated leads No automated leads No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A CDKN2A CDKN2B	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2B_loss	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma	DNA only target DNA only target DNA only target DNA only target	DNA only target DNA only target DNA only target	solid solid solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle Cell Cycle Cell Cycle Cell Cycle Cell Cycle	No automated leads No automated leads No automated leads No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A CDKN2B TP53	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma	DNA only target	DNA only target	solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle	No automated leads No automated leads No automated leads No automated leads			PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2BTP53new sampleATRXCDKN2BTP53new sample	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma	DNA only target	DNA only target	solid solid solid solid solid solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2B TP53 TP53 new sample ATRX	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma	DNA only target	DNA only target	solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma	DNA only target	DNA only target	solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2B TP53 new sample ATRX CDKN2B TP53 new sample ATRX CDKN2B	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine
TH03_0003_S01	Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma	DNA only target No DNA only target	DNA only target	solid solid solid solid solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2B TP53 new sample ATRX CDKN2B TP53 new sample ATRX CDKN2B TP53	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss TruncationExon9	Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma	DNA only target No DNA or RNA targets	DNA only target No DNA or RNA targets	solid	CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion CDKN2A/2B deletion	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2A CDKN2B TP53 new sample CDKN2B	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExon40 CDKN2A_loss	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine
TH03_0003_S01	Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma Sarcoma A A A A A A A A A A A A A A A A A A A	DNA only target No DNA or RNA targets No DNA or RNA targets	DNA only target No DNA or RNA targets	solid	CDKN2A/2B deletion No druggable mutations	Cell Cycle	No automated leads			PPM1D H3F3A new sample ATRX CDKN2A CDKN2B TP53 new sample ATRX CDKN2B TP53 new sample ATRX CDKN2B TP53 new sample ATRX CDKN2A CDKN2A CDKN2A CDKN2B TP53 new sample CTNNB1	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 D D D CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma hepatoblastoma	DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets	DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets	solid	CDKN2A/2B deletion No druggable mutations	Cell Cycle	No automated leads			PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2BTP53new sampleCTNNB1CTNNB1new sample	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss TruncationExon9 P.G34V p.G34V	Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma hepatoblastoma	DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets	DNA only target No DNA or RNA targets No DNA or RNA targets	solid	CDKN2A/2B deletion No druggable mutations No druggable mutations	Cell Cycle	No automated leads			PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleCDKN2BTP53new sampleCTNNB1CTNNB1CTNNB1New sampleCTNNB1	p.E405X p.K27M LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2B_loss TruncationExon9 LossExons13-35 CDKN2A_loss CDKN2A_loss DKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss CDKN2A_loss TruncationExon9 J J J J J J J J J J J J J J J J J J <th>Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine</th>	Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma hepatoblastoma	DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets	DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets	solid	CDKN2A/2B deletion No druggable mutations No druggable mutations	Cell Cycle	No automated leads			PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2ACDKN2ACDKN2ACDKN2ACDKN2BTP53new sampleCTNNB1new sampleCTNNB1new sampleCTNNB1CTNNB1CTNNB1	p.E405Xp.K27MLossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExon9DLossExon9LossExon9DDD<	Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine
TH03_0003_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma hepatoblastoma hepatoblastoma hepatoblastoma	DNA only target DNA only target DNA only target DNA only target DNA only target DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets	DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets RNA only target	solid	CDKN2A/2B deletion No druggable mutations No druggable mutations	Cell Cycle	No automated leads			PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2BTP53new sampleCTNNB1new sampleCTNNB1new sampleCTNNB1new sampleCTNNB1new sampleCTNNB1new sample	p.E405Xp.K27MLossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2A_lossCDKN2A_lossTruncationExon9LossExons13-35CDKN2A_loss <th>Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine</th>	Asnion Analytics Ashion Analytics Ashion Analytics Foundation Medicine
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TH03_0003_S01 TH03_0003_S03 TH03_0003_S04 TH03_0003_S04 TH03_0004_S02 TH03_0004_S03 TH03_0004_S03 TH03_0004_S04 TH03_0005_S01 TH03_0005_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma hepatoblastoma nasopharyngeal carcinoma rhabdomyosarcoma rhabdomyosarcoma	DNA only target DNA only target DNA only target DNA only target DNA only target DNA only target DNA only target No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets No DNA or RNA targets RNA only target RNA only target RNA only target	DNA only target NO DNA or RNA targets RNA only target	solid	 CDKN2A/2B deletion No druggable mutations 	Image: Cell Cycle Image: Cell Cycle <t< th=""><th>No automated leads No automated leads JAK/STAT Heat Shock Proteins Heat Shock Proteins Heat Shock Proteins</th><th>I <td< th=""><th>Image: Control of the second secon</th><th>PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleCTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1New sampleCTNNB1Rew sampleCTNNB1New sampleCTNNB1REM4CREBBPIKZF2MYCTP53</th><th>p.E405Xp.K27MLossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9D</th><th>Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine</th></td<></th></t<>	No automated leads JAK/STAT Heat Shock Proteins Heat Shock Proteins Heat Shock Proteins	I I <td< th=""><th>Image: Control of the second secon</th><th>PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleCTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1New sampleCTNNB1Rew sampleCTNNB1New sampleCTNNB1REM4CREBBPIKZF2MYCTP53</th><th>p.E405Xp.K27MLossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9D</th><th>Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine</th></td<>	Image: Control of the second secon	PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleATRXCDKN2BTP53new sampleCTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1New sampleCTNNB1Rew sampleCTNNB1New sampleCTNNB1REM4CREBBPIKZF2MYCTP53	p.E405Xp.K27MLossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9DupliCationExon9D	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine
TH03_0003_S01 TH03_0003_S03 TH03_0003_S03 TH03_0003_S04 TH03_0004_S02 TH03_0004_S02 TH03_0004_S03 TH03_0004_S04 TH03_0005_S01 TH03_0005_S01 TH03_0005_S01 TH03_0005_S01	sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma sarcoma hepatoblastoma hepatoblastoma nasopharyngeal carcinoma rhabdomyosarcoma rhabdomyosarcoma rhabdomyosarcoma	Image: Provide the structure of the structu	 DNA only target No DNA or RNA targets RNA only target No DNA or RNA targets RNA only target No DNA or RNA targets RNA only target RNA only target 	Solid	 CDKN2A/2B deletion No druggable mutations 	Image: Section of the section of th	No automated leads Heat Shock Proteins Heat Shock Proteins Heat Shock Proteins Heat Shock Proteins	 	Image: state stat	PPM1DH3F3Anew sampleATRXCDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2ACDKN2ACDKN2ACDKN2BTP53new sampleATRXCDKN2ACDKN2BTP53new sampleCTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1CTNNB1TP53TP53TP53TP53New sampleCTNNB1CTNNB1KZF2MYCTP53new sample	p.E405Xp.K27MLossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9LossExons13-35CDKN2A_lossCDKN2B_lossTruncationExon9p.G34Vp.G34Vp.G34Vp.G34Vp.G34VDuplicationExon9-13DuplicationExon99-13DuplicationExon99-13DuplicationExon99-13DuplicationExon99-13DuplicationExon99-13DuplicationExon90-13Duplication[Equivoca]p.R282W	Ashion Analytics Ashion Analytics Ashion Analytics Foundation Medicine Foundation Medicine

									CRE	EBBP	s894fs*64	Foundation Medicine
									IKZI	F2	DeletionExon 4	Foundation Medicine
									MYC	С	Amplification(Equivocal)	Foundation Medicine
									TP5	53	p.R282W	Foundation Medicine
TH03_0008_S01	neuroblastoma	RNA only target	RNA only target	solid					new	v sample		
11103_0000_001	neuroblastoma	Rive only target	True only target	3010	No druggable mutations							Equipation Medicine
										\ <u>\</u>	2033EX0132-3	
							JAN/STAT	STATS		,		Foundation Medicine
									MYC	C	SingleCopy	Foundation Medicine
	acute leukemia of		Additional expression									
TH03_0010_S01	ambiguous lineage, CNS1	No	support for DNA finding	leukemia					new	v sample		
							B-cell receptor signaling	BTK	CRE	EBBP	SpliceSite5173-1G>A	Foundation Medicine
							Cell cycle	CDK6				
							JAK/STAT	STAT5A	JAK	(3	p.A573T	Foundation Medicine
					NRAS p Q61H	RAS/RAF/MEK			NRA	AS	p Q61H	Eoundation Medicine
										53	p.Q0111	Foundation Medicine
	agute laukamia of		Additional expression						113		p.01001	T oundation medicine
TU00 0040 000		Ne	Additional expression	la di anche								
TH03_0010_502	ambiguous lineage, CNST	INO	support for DNA finding	leukemia					new	vsampie		
							B-cell receptor signaling	BIK	CRE	EBBD	SpliceSite51/3-1G>A	Foundation Medicine
							BCL2/MDM2	MDM2	JAK	(3	p.A573T	Foundation Medicine
							JAK/STAT	STAT5A				
					NRAS p.Q61H	RAS/RAF/MEK			NRA	AS	p.Q61H	Foundation Medicine
									TP5	53	p.C135F	Foundation Medicine
	acute lymphoblastic		Additional expression									
TH03_0011_S01	leukemia	No	support for DNA finding	leukemia					new	v sample		
				louitonna			B-cell receptor signaling	BTK	BCC		p C1572E	Equindation Medicine
											p.010721	
									BCC			
							Receptor Tyrosine Kinase (RTK)	FLI3	CPS	51	p.K1281	Foundation Medicine
							JAK/STAT	IL6R	EXC	DSC6	p.G10C	Foundation Medicine
									EXC	DSC6	p.G10C	Foundation Medicine
									MAF	P3K1	p.S939C	Foundation Medicine
									MAF	P3K1	p.S939C	Foundation Medicine
									MLI	2	p.V4305l	Foundation Medicine
									MLI	2	p V/43051	Eoundation Medicine
										2	p.01582V	Foundation Medicine
									IVILL		p.G1562V	
									MLL	_3	p.G1582V	Foundation Medicine
									MLL	_3	p.L804V	Foundation Medicine
									NCC	OR2	p.K1405R	Foundation Medicine
									NOT	TCH1	p.T859M	Foundation Medicine
					NRAS p.Q61K	RAS/RAF/MEK			NRA	AS	p.Q61K	Foundation Medicine
					•				NTE	RK1	p.R744H	Foundation Medicine
									PCI	0	n S4289 S4292del	Eoundation Medicine
TH02 0012 S01	wilms tumor	PNA only target	PNA only target	colid					1 01		p.0+200_0+202001	
11103_0012_301		KINA Ulily target	KINA OIIIy target	SUIU				DIKO			- T07414	Formulation Mariaina
					No druggable mutations		PI3K/AKT/mTOR	PIK3	R1 ABL	_2	p.16/1M	Foundation Medicine
									ALK	K	p.E1435K	Foundation Medicine
									AR		p.G457_G468del	Foundation Medicine
									ASX	XL1	p.G645fs*58	Foundation Medicine
									SPE	EN	p.S2306del	Foundation Medicine
									TP5	53	p.C176S	Foundation Medicine
TH03 0012 S02	wilms tumor	RNA only target	RNA only target	solid					new	v sample		
					No druggable mutations		ΙΔΚ/STΔΤ	STAT3	ABI	2	p T671M	Equindation Medicine
							GARGUTAT	UIAIO		_ <u>_</u>		Foundation Medicine
								+		`		
									AR			Foundation Medicine
									ASX	XL1	p.G645ts*58	Foundation Medicine
									SPE	=N	p.S2306del	Foundation Medicine
									TP5	53	p.C176S	Foundation Medicine
	atypical teratoid/rhabdoid		Additional expression									
TH03_0016 S01	tumor	No	support for DNA finding	solid					new	v sample		
							Receptor Tyrosine Kinase (RTK)	ERBB2	SMA	ARCB1	p.P383fs*4+	Foundation Medicine
							Receptor Tyrosine Kinase (RTK)	EGER1				
	1										<u> </u>	
							JANSTAT	ILO				
					SMARCB1 p.P383fs^4+	Chromatin remodeling						
	fibrolamellar hepatocellular											
TH03_0019_S01	carcinoma	RNA only target	RNA only target	solid					new	v sample		
					No druggable mutations				FAN	NCG	p.A607T	Foundation Medicine
							Receptor Tyrosine Kinase (RTK)	FLT1	1			
							Receptor Tyrosine Kinase (RTK)	KDR			1	
	fibrolamellar hepatocellular											
TH03 0114 S01	carcinoma	RNA only target	RNA only target	solid					new	sample		
	Saronoma		the start only target	3010	No druggable mutations		No automated loads			3	p C310S	Equindation Medicine
											p.00100	
THORADA									IER	T I	promoter 1240>1	Foundation Medicine
TH03_0143_S01	osteosarcoma	RNA only target	RNA only target	solid					new	vsample		
					No druggable mutations		JAK/STAT	IL6	FAN	NCL	p.S351fs*2	Foundation Medicine
									MLL	_3	p.Y306*	Foundation Medicine
TH03_0143_S02	osteosarcoma	No DNA or RNA targets	No DNA or RNA targets	solid					new	v sample		
					No druggable mutations		No automated leads		FAN	NCL	p.S351fs*2	Foundation Medicine
<u> </u>	1					1		+	MII	_3	p.Y306*	Foundation Medicine
				1		1						

			A LIPPE I L									
			Additional expression									
TH03_0149_S01	acute myeloid leukemia	Yes	support for DNA finding	leukemia						new sample		
					FLT3-ITD	Receptor Tyrosine Kinase (RTK)	Receptor Tyrosine Kinase (RTK)	FLT3		FLT3	FLT3-ITD Y597-E598ins15	Foundation Medicine
							B-cell receptor signaling	BTK		WT1	p.\$381fs*67	Foundation Medicine
TH03 0286 S01	benatocellular carcinoma	RNA only target	RNA only target	solid						new sample	F	
11103_0200_001				30110			Decenter Turceire Kinese (DTK)	DDOEDD				Foundation Madiaina
					No druggable mutations		Receptor Tyrosine Kinase (RTK)	PDGFRD		CININDI	SpliceSite14-59_241+790e1366	Foundation Medicine
TH03_0288_S01	neuroblastoma	RNA only target	RNA only target	solid						new sample		
					No druggable mutations		Cell cycle	CDK6		ATRX	LossExons2-12	Foundation Medicine
			No expression evidence for									
TH03 0290 S01	glioma	No	DNA target	solid						new sample		
					BRAE n V600E	RAS/RAF/MEK				BRAF	n V600E	Eoundation Medicine
												Foundation Medicine
							JAN/STAT	IL6		CDKNZA	CDKNZA/B LOSS	Foundation Medicine
	acute lymphoblastic											
TH03_0013_S02	leukemia	RNA only target	RNA only target	leukemia						new sample		
												chromosomal
					No druggable mutations		Cell cvcle	CDK6		t(14:19)	translocation	analysis
							PI3K/AKT/mTOR	PIK3CD				
	+										possible rearrangement	
							FISR/ART/IIITOR	FINOND		IGH	possible realitaligement	FIGH
	acute lymphoblastic											
TH03_0013_S01	leukemia	RNA only target	RNA only target	leukemia						new sample		
					No druggable mutations		Cell cycle	CDK6				
							PI3K/AKT/mTOR	PIK3CD				
							PI3K/AKT/mTOR	PIK3R5		IGH	possible rearrangement	FISH
TH02 0014 S01	corcomo	PNIA only target	PNA only target	colid							peccipie realitaligement	
11103_0014_301	Sarcoma			SUIU	No durante la contra d				10124			
					INO GRUGGADIE MUTATIONS		JAKISTAT		JAK1	EVVSR1	EVVSK1-FL1 rearrangement	Foundation Medicine
										FLI1	EWSR1-FL1 rearrangement	Foundation Medicine
TH03_0018_S01	sarcoma	RNA only target	RNA only target	solid						new sample		
					No druggable mutations		Receptor Tyrosine Kinase (RTK)	FLT4		EWSR1	negative for rearrangement	Foundation Medicine
										SS18	negative for rearrangement	Eoundation Medicine
	+	+									negative for realitangement	
										performed, no		
										alterations		
										identified	none	Foundation Medicine
TH03_0020_S01	medulloblastoma	RNA only target	RNA only target	solid						new sample		
					No druggable mutations		Sonic Hedgehog (SHH)	PTCH1		MYC	High amplification	FISH
TH02 0112 S01	corcomo	PNIA only target	PNA only torget	colid							i iigii airipiirioaliori	
1005_0112_301	Sarcoma	KINA ONIY target	KINA ONLY LAIGEL	Solid				50000				
					No druggable mutations		Receptor Tyrosine Kinase (RTK)	ERBB2		5518	SS18-SSX translocation	Foundation Medicine
							PI3K/AKT/mTOR	MLST8		SSX	SS18-SSX translocation	Foundation Medicine
TH03_0112_S02	sarcoma	RNA only target	RNA only target	solid						new sample		
					No druggable mutations		Sonic Hedgehog (SHH)	GLI1		SS18	SS18-SSX translocation	Foundation Medicine
							Sonic Hedgebog (SHH)	PTCH1		SSX	SS18-SSX translocation	Foundation Medicine
										00/1		
	myconithalial caroinama of	+	Additional expression									
T100 0440 004	myoepithelial carcinoma of		Additional expression									
TH03_0113_S01	myoepithelial carcinoma of the liver	No	Additional expression support for DNA finding	solid						new sample		
TH03_0113_S01	myoepithelial carcinoma of the liver	No	Additional expression support for DNA finding	solid	INI1 loss of expression	Chromatin remodeling	Receptor Tyrosine Kinase (RTK)	FGFR1		new sample	Loss of expression	IHC
TH03_0113_S01 TH03_0115_S01	myoepithelial carcinoma of the liver teratoma	No No DNA or RNA targets	Additional expression support for DNA finding No DNA or RNA targets	solid	INI1 loss of expression	Chromatin remodeling	Receptor Tyrosine Kinase (RTK)	FGFR1		new sample INI1 new sample	Loss of expression	IHC
TH03_0113_S01 TH03_0115_S01	myoepithelial carcinoma of the liver teratoma	No No DNA or RNA targets	Additional expression support for DNA finding No DNA or RNA targets	solid	INI1 loss of expression No druggable mutations	Chromatin remodeling	Receptor Tyrosine Kinase (RTK)	FGFR1		new sample INI1 new sample MLL3	Loss of expression C310S	IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01	myoepithelial carcinoma of the liver teratoma	No No DNA or RNA targets	Additional expression support for DNA finding No DNA or RNA targets	solid solid	INI1 loss of expression No druggable mutations	Chromatin remodeling	Receptor Tyrosine Kinase (RTK) No automated leads	FGFR1		new sample INI1 new sample MLL3	Loss of expression C310S	IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01	myoepithelial carcinoma of the liver teratoma	No No DNA or RNA targets Ves	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid	INI1 loss of expression No druggable mutations	Chromatin remodeling	Receptor Tyrosine Kinase (RTK) No automated leads	FGFR1		new sample INI1 new sample MLL3	Loss of expression C310S	IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid	INI1 loss of expression No druggable mutations	Chromatin remodeling	Receptor Tyrosine Kinase (RTK) No automated leads	FGFR1		new sample INI1 new sample MLL3 new sample	Loss of expression C310S	IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid	INI1 loss of expression INO druggable mutations CCND3 amplification	Chromatin remodeling Cell Cycle	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle	FGFR1 CCND3		new sample INI1 new sample MLL3 new sample CSK4	Loss of expression C310S Amplification	IHC Foundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid	INI1 loss of expression INO druggable mutations CCND3 amplification	Chromatin remodeling Cell Cycle	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle	FGFR1 CCND3 CDK4		new sampleINI1new sampleMLL3new sampleCSK4MDM2	Loss of expression C310S Amplification Amplification	IHC IHC Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid	INI1 loss of expression IN0 druggable mutations CCND3 amplification INDM2 amplification	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2	FGFR1 CCND3 CDK4 MDM2		new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3	Loss of expression C310S Amplification Amplification Amplification	IHC IHC Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid	INI1 loss of expression INO druggable mutations CCND3 amplification MDM2 amplification	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2	FGFR1 CCND3 CDK4 MDM2		new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2	Loss of expression C310S Amplification Amplification Amplification Amplification Amplification Amplification	IHC IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid	INI1 loss of expression No druggable mutations CCND3 amplification MDM2 amplification	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2	FGFR1 CCND3 CDK4 MDM2		new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sample	Loss of expression C310S Amplification Amplification Amplification Amplification	IHC IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma	No No DNA or RNA targets Yes RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings	solid solid solid solid solid solid	INI1 loss of expression INO druggable mutations CCND3 amplification MDM2 amplification INO druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 Pl3K/AKT/mTOR	FGFR1 CCND3 CDK4 MDM2		new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sample	Loss of expression C310S Amplification Amplification Amplification Amplification Amplification	IHC IHC Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor	No No DNA or RNA targets Yes	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target	solid solid solid solid solid solid	INI1 loss of expression IN0 druggable mutations CCND3 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR IAK/STAT	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1		new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleOKInew sample	Loss of expression C310S Amplification Amplification Amplification Amplification	IHC IHC Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor	No No DNA or RNA targets Yes Yes RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target	solid solid solid solid solid	INI1 loss of expression IN0 druggable mutations CCND3 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1		new sample INI1 new sample MLL3 new sample CSK4 MDM2 CCND3 FRS2 new sample	Loss of expression C310S Amplification Amplification Amplification Amplification	IHC IHC IFoundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target	solid solid solid solid solid solid solid	INI1 loss of expression IN0 druggable mutations CCND3 amplification MDM2 amplification No druggable mutations IN0 druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1		new sample INI1 new sample MLL3 new sample CSK4 MDM2 CCND3 FRS2 new sample	Loss of expression C310S Amplification Amplification Amplification Amplification	IHC IHC IFoundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target	solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations No druggable mutations No druggable mutations No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleImage: sample	Loss of expression C310S C310S Amplification Amplification Amplification Amplification CIC-DUX4 translocation	IHC IHC IFoundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target	solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations No druggable mutations No druggable mutations No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK)	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleCCND3FRS2new sampleCUCDUX4	Loss of expression C310S Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation CIC-DUX4 translocation	IHC IHC IFoundation Medicine Foundation Medicine FISH FISH
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target RNA only target No No DNA or RNA targets	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target No DNA or RNA targets	solid solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK)	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleCICDUX4new sample	Loss of expression C310S C310S Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation	IHC IHC IFoundation Medicine Foundation Medicine Fish Fish Fish Fish Fish
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target RNA only target No DNA or RNA targets	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings Image: Prioritizing among multiple	solid solid solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK) No automated leads	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleImage: CICDUX4new sampleMSH3	Loss of expression C310S C310S Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation CIC-DUX4 translocation Splice site 580-2a>q	IHC IHC IFoundation Medicine Foundation Medicine FISH FISH FISH FISH FISH FISH
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01 TH03_0296_S02	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target RNA only target No DNA or RNA targets RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target No DNA or RNA targets	solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK) No automated leads	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleImage: CICDUX4new sampleMSH3paye sample	Loss of expression C310S C310S Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation CIC-DUX4 translocation	IHCIHCFoundation MedicineFoundation MedicineFISHFISHFISHFOUNDATION MedicineFOUNDATION Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01 TH03_0296_S02	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma osteosarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target No DNA or RNA targets RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target No DNA or RNA targets RNA only target RNA only target RNA only target RNA only target	solid solid solid solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK) No automated leads	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleCCICDUX4new sampleMSH3new sample	Loss of expression C310S C310S Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocatiO CIC-DUX4 translocatiO CIC-DUX4 translocatiO CIC-DUX	IHC IHC Foundation Medicine Fish FISH Fish Foundation Medicine Foundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01 TH03_0296_S02	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma osteosarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target No DNA or RNA targets RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings RNA only target RNA only target No DNA or RNA targets RNA only target RNA only target RNA only target RNA only target	solid solid solid solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK) No automated leads Receptor Tyrosine Kinase (RTK)	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4 TEK	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleCCICDUX4new sampleMSH3new sampleMSH3	Loss of expression C310S C310S Amplification Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation Splice site 580-2a>g Splice site 580-2a>g	IHCIHCFoundation MedicineFoundation MedicineFISHFISHFOUNDATION MedicineFoundation MedicineFoundation Medicine
TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01 TH03_0296_S02	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma osteosarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target No DNA or RNA targets RNA only target	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings Image: Prioritizing among multiple	solid solid solid solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK) No automated leads Receptor Tyrosine Kinase (RTK)	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1	CCNE1 FLT4 FLT4 TEK	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleCCICDUX4new sampleMSH3new sampleMSH3NSH3	Loss of expression C310S Amplification Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation CIC-DUX4 translocation Splice site 580-2a>g Splice site 580-2a>g	IHCIHCFoundation MedicineFoundation MedicineFISHFISHFoundation MedicineFoundation MedicineFoundation MedicineFoundation Medicine
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TH03_0113_S01 TH03_0115_S01 TH03_0141_S01 TH03_0144_S01 TH03_0146_S01 TH03_0296_S01 TH03_0296_S02 TH06_0645_S01	myoepithelial carcinoma of the liver teratoma osteosarcoma wilms tumor sarcoma osteosarcoma osteosarcoma sarcoma	No No DNA or RNA targets Yes Yes RNA only target RNA only target No DNA or RNA targets RNA only target RNA only target No DNA or RNA targets No DNA or RNA targets No No No	Additional expression support for DNA finding No DNA or RNA targets Prioritizing among multiple DNA findings Image: Prioritizing among multiple DNA finding	solid solid solid solid solid solid solid solid solid solid solid solid solid	INI1 loss of expression INI1 loss of expression No druggable mutations CCND3 amplification MDM2 amplification MDM2 amplification No druggable mutations	Chromatin remodeling Cell Cycle BCL2/MDM2	Receptor Tyrosine Kinase (RTK) No automated leads Cell cycle Cell cycle BCL2/MDM2 PI3K/AKT/mTOR JAK/STAT Cell cycle Receptor Tyrosine Kinase (RTK) Receptor Tyrosine Kinase (RTK) Receptor Tyrosine Kinase (RTK)	FGFR1 CCND3 CDK4 MDM2 MLST8 STAT1 MLST8 STAT1 COM COM COM COM COM COM COM COM	CCNE1 FLT4 FLT4 TEK	new sampleINI1new sampleMLL3new sampleCSK4MDM2CCND3FRS2new sampleCICDUX4new sampleMSH3new sampleMSH3new sampleNF1POTEIMUC17LUERCO	Loss of expression C310S C310S Amplification Amplification Amplification Amplification Amplification CIC-DUX4 translocation CIC-DUX4 translocation CIC-DUX4 translocation Splice site 580-2a>g Splice site 580-2a>g Splice site 580-2a>g	IHCIHCFoundation MedicineFoundation MedicineFISHFISHFISHFOUNDATION MedicineFoundation MedicineBC POG DNA resultsBC POG DNA resultsBC POG DNA resultsBC POG DNA results
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				CDKN2A homozygous loss	Cell Cycle	CCND3, Cell cycle		IGHJ6 IGHM KLF9 NCOR1 NUP160 SLC29A1 SUZ12 ZBTB44 ZCCHC7 ETV6 CDKN2A CNR2 CNTNAP3B	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous losshomozygous losshomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Cell cycle CCND3, CDK6		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous losshomozygous losshomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Cell cycle CCND3, CDK6 Contact CDK6		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAP	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Cell cycle CCND3, CDK6 Contact CCND3, CDK6		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5DWR74	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		Idew SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous loss	BC POG DNA resultsBC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second state of the second sta		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TUP2	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second state of the second sta		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationhomozygous losshomozygous loss	BC POG DNA resultsBC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous loss	BC POG DNA resultsBC POG DNA results
				CDKN2A homozygous loss		Image: Constraint of the second se		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3PAS	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous loss	BC POG DNA results
				CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RAS	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous loss	BC POG DNA resultsBC POG DNA results
			Divertimentings Decementing	CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASRAS	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossfor datafor datafor datag12Ag13D	BC POG DNA resultsBC POG DNA results
			Divertimentings Dediction of the second	CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second state of the second sta		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASRASPCNT	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossfor dataG12AG13DR3232l	BC POG DNA resultsBC POG DNA results
			Divertimentings Decementing	CDKN2A homozygous loss	Cell Cycle	Image: Constraint of the second se		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPONT	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous losshomoz	BC POG DNA results
			Divertimentings Decementing	CDKN2A homozygous loss loss	Cell Cycle	Image: state of the state		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNT	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossR3232LR3232R	BC POG DNA resultsBC POG DNA results
			Divertimitings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	Cell Cycle	Image: state of the state		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossRomozygous losshomozygous losshomozyg	BC POG DNA resultsBC POG DNA results
			Divertimentings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	Cell Cycle	Image: state of the state		Idew SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V(10)	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous losshomoz	BC POG DNA results B
			Divertimentings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	Cell Cycle	Image: Section of the section of th		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNR1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48L	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous losshomoz	BC POG DNA resultsBC POG DNA results
			Divertimentings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	Cell Cycle	Image: state of the state		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossKatalG12AG13DR3232LR3232RQ185KV48L – not characterizedV574I	BC POG DNA resultsBC POG DNA results
			Divertimitings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Section of the section of th		IGW SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGE1P	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous losshomoz	BC POG DNA resultsBC POG DNA results
			Divertimentings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Section of the section of th		IGW Sample IGHJ6 IGHM KLF9 NCOR1 NUP160 SLC29A1 SUZ12 ZBTB44 ZCCHC7 ETV6 CDKN2A CNR2 CNTNAP3B DMRTA1 MTAP PGBD4P5 PNRC2 RBM17P3 TJP2 FLT3 RAS PCNT PCNT NTRK3 KIT V48L ZNF521 IGF1R	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203F	BC POG DNA resultsBC POG DNA results
			Drive mindings Dediction of the second	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Second state of the second state of		IGW Sample IGHJ6 IGHM KLF9 NCOR1 NUP160 SLC29A1 SUZ12 ZBTB44 ZCCHC7 ETV6 CDKN2A CNR2 CNTNAP3B DMRTA1 MTAP PGBD4P5 PNRC2 RBM17P3 TJP2 FLT3 RAS PCNT PCNT NTRK3 KIT V48L ZNF521 IGF1R	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203FY203F	BC POG DNA resultsBC POG DNA results
			Divernmentge Concentre	CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Becentor Tyrosine Kinase (PTK)		Indew SampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGF1R	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203FY203F	BC POG DNA resultsBC POG DNA results
				CDKN2A homozygous loss loss RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Second		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGF1R	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossR3232LR3232RQ185KV48L – not characterizedV574IY203F	BC POG DNA resultsBC POG DNA results
			Drive informacion Concentration	CDKN2A homozygous loss loss RAS p.G12A RAS p.G12A RAS p.G13D	Image: Control of the second secon	Image: Second		Inew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGF1R	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY227MG12AG13DR3232LR3232RQ185KV48L – not characterizedV574IY203F	BC POG DNA resultsBC POG DNA results
TH06 0649 S01	Image:	Yes	Drive findings redicting Image: solid Image: solid Image: solid Image: solid Image: solid Image: solid	CDKN2A homozygous loss loss RAS p.G12A RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Second		Indew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGF1Rnew sample	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203FinterventionedY203F	BC POG DNA resultsBC POG DNA res
TH06_0649_S01	Image:	ICON ICON <t< td=""><td>Drive informacion Inducement Image: Solution information Image: Solution information Image: Solution information Image: Solid</td><td>Image: Control of the second state of the second state</td><td>RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK</td><td>Image: Second Second</td><td></td><td>Indew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGF1Rnew sample</td><td>translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203Findustion<td>BC POG DNA resultsBC POG DNA res</td></td></t<>	Drive informacion Inducement Image: Solution information Image: Solution information Image: Solution information Image: Solid	Image: Control of the second state	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Second		Indew sampleIGHJ6IGHMKLF9NCOR1NUP160SLC29A1SUZ12ZBTB44ZCCHC7ETV6CDKN2ACNR2CNTNAP3BDMRTA1MTAPPGBD4P5PNRC2RBM17P3TJP2FLT3RASPCNTPCNTNTRK3KIT V48LZNF521IGF1Rnew sample	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203Findustion <td>BC POG DNA resultsBC POG DNA res</td>	BC POG DNA resultsBC POG DNA res
	Image:	ICON ICON <t< td=""><td>Drive informacion Concentre Image: Solid Image: Solid Image: Solid Image: Solid Image: Solid Image: Solid</td><td>CDKN2A homozygous loss loss RAS p.G12A RAS p.G12A RAS p.G13D</td><td>RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK</td><td>Image: Second Second</td><td></td><td>IGW Sample IGHJ6 IGHM KLF9 NCOR1 NUP160 SLC29A1 SUZ12 ZBTB44 ZCCHC7 ETV6 CDKN2A CNR2 CNTNAP3B DMRTA1 MTAP PGBD4P5 PNRC2 RBM17P3 TJP2 FLT3 RAS PCNT PCNT PCNT NTRK3 KIT V48L ZNF521 IGF1R CST3</td><td>translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203Fduplicationduplication</td><td>BC POG DNA resultsBC POG DNA res</td></t<>	Drive informacion Concentre Image: Solid Image: Solid Image: Solid Image: Solid Image: Solid Image: Solid	CDKN2A homozygous loss loss RAS p.G12A RAS p.G12A RAS p.G13D	RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK RAS/RAF/MEK	Image: Second		IGW Sample IGHJ6 IGHM KLF9 NCOR1 NUP160 SLC29A1 SUZ12 ZBTB44 ZCCHC7 ETV6 CDKN2A CNR2 CNTNAP3B DMRTA1 MTAP PGBD4P5 PNRC2 RBM17P3 TJP2 FLT3 RAS PCNT PCNT PCNT NTRK3 KIT V48L ZNF521 IGF1R CST3	translocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationtranslocationdeletion/duplicationhomozygous losshomozygous lossY203Fduplicationduplication	BC POG DNA resultsBC POG DNA res

B. Comparative RNA-Seq analysis results for all 144 samples.

Sample ID	Activated gene set lead	Samples. Outlier support	Pathway support
TH01 0053 S01	New sample	acute myeloid leukemia	
TH01_0053_S01	B-cell receptor signaling	BTK (pc)	KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION (pc. up. 6/267)
TH01 0053 S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	REACTOME IMMUNE SYSTEM (pc up. 11/933)
TH01_0054_S01	New sample	acute lymphoblastic leukemia	
TH01_0054_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION (comm_up, 4/267 and pc_up, 7/267 and pd_up, 5/267)
TH01_0054_S01	Receptor Tyrosine Kinase (RTK)	FLT4 (pc)	HALLMARK_KRAS_SIGNALING_UP (pc_up, 5/200)
TH01_0054_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 8/88)
TH01_0055_S01	New sample	glioma	
TH01_0055_S01	N/A	No druggable outliers	N/A
TH01_0061_S01	New sample	germ cell tumor	
TH01_0061_S01	N/A	No druggable outliers	N/A
TH01_0062_S01	New sample	acute lymphoblastic leukemia	
TH01_0062_S01	B-cell receptor signaling		BIOCARTA_BCR_PATHWAY (pc_up, 7/37)
TH01_0062_S01			
TH01_0062_S01	JAK/STAT R coll recenter signaling		KEGG_JAK_STAT_SIGNALING_PATHWAY (pc_up, 10/155)
TH01_0062_301		PIK3CD (pc)	PID_PI3KCL_PATHWAY (nc, un, 7/49)
TH01_0062_S01	PI3K/AKT/mTOR	PIK3R5 (pc)	$PID_PI3KCI_PATHWAY (pc_up_7/49)$
TH01_0062_001	JAK/STAT	STAT5B (pc)	KEGG JAK STAT SIGNALING PATHWAY (pc. up. 10/155)
TH01 0063 S01	New sample	sarcoma	
TH01_0063_S01	JAK/STAT	STAT2 (pc, pd)	None
TH01_0064_S01	New sample	lymphoma	
TH01_0064_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (comm_up, 3/88 and pc_up, 11/88 and pd_up, 3/88)
TH01_0069_S01	New sample	sarcoma	
TH01_0069_S01	N/A	No druggable outliers	N/A
TH01_0120_S01	New sample	acute myeloid leukemia	
TH01_0120_S01	Cell Cycle	CDK6 (pc)	PID_CMYB_PATHWAY (pc_up, 6/84)
TH01_0120_S01	Receptor Tyrosine Kinase (RTK)	KIT (pc)	PID_CMYB_PATHWAY (pc_up, 6/84)
TH01_0121_S01	New sample	acute lymphoblastic leukemia	
TH01_0121_S01			KEGG_JAK_STAT_SIGNALING_PATHWAY (pc_up, 13/155)
TH01_0121_S01	JAK/STAT R coll recenter signaling		KEGG_JAK_STAT_SIGNALING_PATHWAY (pc_up, 13/155)
TH01_0121_S01			KEGG_PHOSPHATIDY INOSITOL_SIGNALING_SYSTEM (pc_up_9/76)
TH01_0121_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG PHOSPHATIDY INOSITOL SIGNALING SYSTEM (pc_up_9/76)
TH01_0121_001	PI3K/AKT/mTOR	PIK3R5 (pc)	KEGG PHOSPHATIDYLINOSITOL SIGNALING SYSTEM (pc. up. 9/76)
TH01 0121 S01	JAK/STAT	STAT5B (pc)	KEGG JAK STAT SIGNALING PATHWAY (pc up, 13/155)
TH01_0122_S01	New sample	acute lymphoblastic leukemia	
TH01_0122_S01	Cell Cycle	CDK6 (pc)	None
TH01_0122_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 6/88)
TH01_0122_S01	PI3K/AKT/mTOR	PIK3CD (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 6/75)
TH01_0122_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 6/75)
TH01_0123_S01	New sample	acute lymphoblastic leukemia	
TH01_0123_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 12/88)
TH01_0123_S01	Receptor Tyrosine Kinase (RTK)	FLT4 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 12/88)
TH01_0123_S01	JAK/STAT		KEGG_JAK_STAT_SIGNALING_PATHWAY (pc_up, 8/155)
TH01_0123_S01			REGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 12/88)
TH01_0123_501			$PID_PI3KCI_PATHWAY (pc_up, 7/49)$
TH01_0123_501	PI3K/AKT/mTOR	RPTOR (pc)	PID_PI3KCI_PATHWAY (pc_up_7/49)
TH01_0124_S01	New sample	acute lymphoblastic leukemia	
TH01 0124 S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG HEMATOPOIETIC CELL LINEAGE (pc up. 4/88)
TH01_0124_S01	PI3K/AKT/mTOR	PIK3CG (pc)	None
TH01_0125_S01	New sample	acute lymphoblastic leukemia	
TH01_0125_S01	B-cell receptor signaling	ВТК (рс)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 4/75)
TH01_0125_S01	Cell Cycle	CDK6 (pc)	PID_CMYB_PATHWAY (pc_up, 6/84)
TH01_0125_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 4/88)
TH01_0125_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 4/75)
TH01_0126_S01	New sample	acute lymphoblastic leukemia	
TH01_0126_S01	N/A	No druggable outliers	N/A
TH01_0127_S01	New sample	acute lymphoblastic leukemia	
TH01_0127_S01	B-cell receptor signaling		NEGG_B_GELL_REGETIOK_SIGNALING_PATHWAY (pc_up, ///5)
TH01_0127_S01	Receptor Tyrosine Kinase (RTK)		Nono
TH01_0127_001			KEGG B CELL RECEPTOR SIGNALING PATHWAY (no. up. 7/75)
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Sample ID	Activated gene set lead	Outlier support	Pathway support
TH01_0128_S01	New sample	acute lymphoblastic leukemia	
TH01_0128_S01	JAK/STAT	IL6R (pc)	KEGG_JAK_STAT_SIGNALING_PATHWAY (pc_up, 7/155)
TH01_0128_S01	PI3K/AKT/mTOR	PIK3CD (pc)	PID_PI3KCI_PATHWAY (pc_up, 4/49)
TH01_0128_S01	PI3K/AKT/mTOR	PIK3CG (pc)	PID_PI3KCI_PATHWAY (pc_up, 4/49)
TH01_0128_S01	PI3K/AKT/mTOR	PIK3R5 (pc)	PID_PI3KCI_PATHWAY (pc_up, 4/49)
TH01_0129_S01	New sample	acute lymphoblastic leukemia	
TH01_0129_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 6/88)
TH01_0129_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 6/75)
TH01_0130_S01	New sample	acute lymphoblastic leukemia	
TH01_0130_S01	Cell Cycle	CDK6 (pc)	None
TH01_0130_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 6/88)
TH01_0130_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 6/88)
TH01_0130_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 6/75)
TH01_0131_S01	New sample	acute lymphoblastic leukemia	
TH01_0131_S01	B-cell receptor signaling	BTK (pc)	ST_B_CELL_ANTIGEN_RECEPTOR (pc_up, 3/40)
TH01_0131_S01	Cell Cycle	CDK6 (pc)	PID_CMYB_PATHWAY (pc_up, 4/84)
TH01_0131_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 7/88)
TH01_0131_S01	Receptor Tyrosine Kinase (RTK)	FLT4 (pc)	BIOCARTA_VEGF_PATHWAY (pc_up, 3/29)
TH01_0131_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 9/75)
TH01_0132_S01	New sample	acute myeloid leukemia	
TH01_0132_S01	B-cell receptor signaling	BTK (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 4/75)
TH01_0132_S01	Cell Cycle	CDK6 (pc)	PID_CMYB_PATHWAY (pc_up, 6/84)
TH01_0132_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	None
TH01_0132_S01	PI3K/AKT/mTOR	PIK3CG (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 4/75)
TH01_0133_S01	New sample	acute lymphoblastic leukemia	
TH01_0133_S01	Receptor Tyrosine Kinase (RTK)		None
TH01_0134_S01	New sample	acute lymphoblastic leukemia	
TH01_0134_S01			PID_CMYB_PATHWAY (pc_up, 9/84)
TH01_0134_S01	Receptor Tyrosine Kinase (RTK)	ERBB2 (pd)	None
TH02_0074_S01		glioblastoma multiforme	
TH02_0074_S01	PI3K/AKT/MTOR		PID_PI3KCI_AKT_PATHWAY (comm_up, 3/35)
TH02_0074_S01	Cell Cycle	USD004.41 (no. nd)	Nepo
TH02_0074_501	Heat Shock Proteins	HSP00AR1 (pc, pd)	None
TH02_0074_501	Heat Shock Proteins	HSP00B1 (pd)	HALLMARK LINEOLDED PROTEIN RESPONSE (nd up. 13/113)
TH02_0074_501		IAK1 (pd)	KEGG JAK STAT SIGNALING PATHWAY (comm up 6/155 and no up 6/155)
TH02_0074_501		PIK3C3 (pd)	
TH02_0074_S01	PI3K/AKT/mTOR	PIK3B3 (pc, pd)	HALLMARK MTORC1 SIGNALING (pd up 21/200)
TH02_0075_S01	New sample	dioblastoma multiforme	
TH02_0075_S01	PI3K/AKT/mTOR	PIK3R3 (pc, pd)	None
TH02_0076_S01	New sample	dioblastoma multiforme	
TH02_0076_S01	Cell Cycle	CDK4 (pd)	REACTOME CELL CYCLE (comm up 8/421 and pd up 20/421)
TH02_0076_S01	Heat Shock Proteins	HSP90AA1 (pd)	None
TH02 0076 S01	Receptor Tyrosine Kinase (RTK)	MET (pd)	None
TH02 0077 S01	New sample	glioma	
TH02 0077 S01	PI3K/AKT/mTOR	AKT3 (pd)	REACTOME_PI3K_AKT_ACTIVATION (pc_up, 3/38)
TH02_0077_S01	Receptor Tyrosine Kinase (RTK)	PDGFRA (pc)	BIOCARTA_PDGF_PATHWAY (pc_up, 3/32)
 TH02_0077_S01	PI3K/AKT/mTOR	PIK3R1 (pc)	REACTOME_PI3K_AKT_ACTIVATION (pc_up, 3/38)
TH02_0077_S01	Sonic Hedgehog (SHH)	PTCH1 (pc)	None
TH02_0078_S01	New sample	glioma	
TH02_0078_S01	PI3K/AKT/mTOR	AKT3 (pd)	KEGG_GLIOMA (comm_up, 3/65 and pc_up, 5/65 and pd_up, 6/65)
TH02_0078_S01	RAS/RAF/MEK	BRAF (pd)	KEGG_GLIOMA (comm_up, 3/65 and pc_up, 5/65 and pd_up, 6/65)
TH02_0078_S01	Cell Cycle	CDK6 (pc, pd)	KEGG_GLIOMA (comm_up, 3/65 and pc_up, 5/65 and pd_up, 6/65)
TH02_0078_S01	Receptor Tyrosine Kinase (RTK)	PDGFRA (pc, pd)	KEGG_GLIOMA (comm_up, 3/65 and pc_up, 5/65 and pd_up, 6/65)
TH02_0078_S01	PI3K/AKT/mTOR	PIK3R1 (pc)	KEGG_GLIOMA (comm_up, 3/65 and pc_up, 5/65 and pd_up, 6/65)
TH02_0079_S01	New sample	glioma	
TH02_0079_S01	N/A	No druggable outliers	N/A
TH02_0080_S01	New sample	glioma	
TH02_0080_S01	N/A	No druggable outliers	N/A
TH02_0081_S01	New sample	glioblastoma multiforme	
TH02_0081_S01	PI3K/AKT/mTOR	AKT3 (pd)	REACTOME_PI_3K_CASCADE (pc_up, 5/56 and pd_up, 6/56)
TH02_0081_S01	BCL2/MDM2	BCL6 (pc)	None
TH02_0081_S01	Cell Cycle	CDK4 (pc, pd)	REACTOME_CELL_CYCLE (pd_up, 17/421)
TH02_0081_S01	PI3K/AKT/mTOR	PIK3C3 (pc, pd)	None
TH02_0081_S01	PI3K/AKT/mTOR	PIK3R1 (pc)	REACTOME_PI_3K_CASCADE (pc_up, 5/56 and pd_up, 6/56)
TH02_0082_S01	New sample	diffuse intrinsic pontine glioma	



Sample ID	Activated gene set lead	Outlier support	Pathway support
TH02 0082 S01	N/A	No druggable outliers	N/A
TH02_0082_001	New cample	diffuse intrinsic pontine glioma	
TH02_0083_501			
TH02_0083_501	Receptor Tyrosine Kinase (RTK)	PDGFRA (pc)	KEGG_MAPK_SIGNALING_PATHWAY (pc_up, 6/267)
TH02_0084_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0084_S01	N/A	No druggable outliers	N/A
TH02_0085_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0085_S01	Receptor Tyrosine Kinase (RTK)	PDGFRA (pc)	None
TH02_0086_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0086_S01	Sonic Hedgehog (SHH)	PTCH1 (pc)	None
TH02 0087 S01	New sample	diffuse intrinsic pontine glioma	
TH02_0087_S01	JAK/STAT	JAK1 (pd)	REACTOME INTEREERON SIGNALING (pd up 4/159)
TH02_0087_002	New sample	diffuse intrinsic pontine glioma	
TH02_0007_002		No druggoble outliere	Ν/Δ
TH02_0007_302	N/A		
THU2_0088_501	New sample	diffuse intrinsic pontine glioma	
TH02_0088_S01	N/A	No druggable outliers	N/A
TH02_0089_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0089_S01	N/A	No druggable outliers	N/A
TH02_0090_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0090_S01	Sonic Hedgehog (SHH)	PTCH1 (pc)	None
TH02_0091_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0091_S01	Receptor Tyrosine Kinase (RTK)	ALK (pc, pd)	None
	Receptor Tyrosine Kinase (RTK)	CSF1R (pc)	KEGG HEMATOPOIETIC CELL LINEAGE (pc up. 4/88 and pd up. 3/88)
TH02 0092 S01	New sample	diffuse intrinsic pontine glioma	
TH02_0092_S01	RAS/RAF/MEK	MAP2K1 (nc. nd)	KEGG MAPK SIGNALING PATHWAY (commun. 5/267 and nd up. 8/267)
TH02_0003_001	New sample	diffuse intrinsic pontine glioma	
TH02_0093_501		No druggoble outliere	
TH02_0093_501	N/A		N/A
TH02_0094_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0094_S01	Receptor Tyrosine Kinase (RTK)	MET (pd)	None
TH02_0095_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0095_S01	Sonic Hedgehog (SHH)	PTCH1 (pc)	None
TH02_0096_S01	New sample	diffuse intrinsic pontine glioma	
TH02_0096_S01	N/A	No druggable outliers	N/A
TH03_0003_S01	New sample	sarcoma	
TH03_0003_S01	N/A	No druggable outliers	N/A
TH03_0003_S03	New sample	sarcoma	
TH03_0003_S03	N/A	No druggable outliers	N/A
TH03 0003 S04	New sample	sarcoma	
TH03 0003 S04	N/A	No druggable outliers	N/A
TH03 0004 S02	New sample	hepatoblastoma	
TH03_0004_\$02	Ν/Δ	No druggable outliers	Ν/Δ
TH03_0004_S03	New sample	henatoblastoma	
TH02_0004_503		No druggoble outliere	
TH03_0004_303	N/A		
TH03_0004_504	New sample		
TH03_0004_S04	Heat Shock Proteins	HSP90B1 (pd)	HALLMARK_UNFOLDED_PROTEIN_RESPONSE (pd_up, 5/113)
TH03_0004_S04	JAK/STAT	IL6 (pc, pd)	HALLMARK_IL6_JAK_STAT3_SIGNALING (comm_up, 5/87 and pc_up, 5/87 and pd_up, 6/87)
TH03_0005_S01	New sample	nasopharyngeal carcinoma	
TH03_0005_S01	N/A	No druggable outliers	N/A
TH03_0006_S01	New sample	rhabdomyosarcoma	
TH03_0006_S01	Heat Shock Proteins	HSP90B1 (NA)	None
TH03_0006_S03	New sample	rhabdomyosarcoma	
TH03_0006_S03	N/A	No druggable outliers	N/A
TH03_0008_S01	New sample	neuroblastoma	
TH03_0008_S01	PI3K/AKT/mTOR	RPTOR (pc, pd)	HALLMARK_PI3K_AKT_MTOR_SIGNALING (comm_up, 5/105 and pc_up, 7/105 and pd_up, 9/105)
TH03 0008 S01	JAK/STAT	STAT5 (NA)	REACTOME IMMUNE SYSTEM (pc up, 22/933 and pd up, 31/933)
		acute leukemia of ambiguous lineage.	
TH03_0010_S01	New sample	CNS1	
TH03_0010_S01	B-cell receptor signaling	BTK (pc)	SIG_BCR_SIGNALING_PATHWAY (pc_up, 4/46)
TH03_0010_S01	Cell Cycle	CDK6 (pc)	PID_CMYB_PATHWAY (pc_up, 6/84)
TH03 0010 S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	None
TH03 0010 S01	JAK/STAT	STAT5A (pc)	PID IL4 2PATHWAY (pc up. 5/65)
		acute leukemia of ambiguous lineage.	
TH03_0010_S02	New sample	CNS1	
TH03 0010 S02	B-cell receptor signaling	BTK (pc)	REACTOME_SIGNALING_BY_THE B CELL RECEPTOR BCR (pd up, 6/126)
TH03 0010 S02	BCL2/MDM2	MDM2 (pd)	HALLMARK P53 PATHWAY (pd up. 5/200)
TH03 0010 S02	JAK/STAT	STAT5A (pc)	BIOCARTA IL3 PATHWAY (pc up 2/15)
TH03_0011_S01	New sample	acute lymphoblastic leukemia	

Sample ID	Activated gene set lead	Outlier support	Pathway support
TH03_0011_S01	B-cell receptor signaling	BTK (pc)	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR (pc_up, 10/126)
TH03_0011_S01	Cell Cycle	CCND3 (pc)	BIOCARTA_CELLCYCLE_PATHWAY (pc_up, 3/23)
TH03_0011_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 7/88)
TH03_0011_S01	JAK/STAT	IL6R (pc)	KEGG_JAK_STAT_SIGNALING_PATHWAY (pc_up, 6/155)
TH03_0012_S01	New sample	wilms tumor	
TH03_0012_S01	PI3K/AKT/mTOR	PIK3R1 (pd)	None
TH03_0012_S02	New sample	wilms tumor	
TH03_0012_S02	PI3K/AKT/mTOR	PIK3R1 (pd)	None
TH03_0012_S02	JAK/STAT	STAT3 (pd)	HALLMARK_IL6_JAK_STAT3_SIGNALING (pd_up, 7/87)
TH03_0013_S01	New sample	acute lymphoblastic leukemia	
TH03_0013_S01	B-cell receptor signaling	BTK (pc)	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR (pc_up, 9/126)
TH03 0013 S01	Cell Cycle	CCND3 (pc)	None
 TH03 0013 S01	Cell Cycle	CDK6 (pc)	PID CMYB PATHWAY (pc up, 8/84)
 TH03 0013 S01	PI3K/AKT/mTOR	PIK3CD (pc)	KEGG PHOSPHATIDYLINOSITOL SIGNALING SYSTEM (pc up. 4/76)
TH03 0013 S01	PI3K/AKT/mTOR	PIK3R5 (pc)	KEGG PHOSPHATIDYLINOSITOL SIGNALING SYSTEM (pc up. 4/76)
TH03 0013 S02	New sample	acute lymphoblastic leukemia	
TH03 0013 S02	Cell Cycle	CDK6 (pc)	PID CMYB PATHWAY (pc up. 9/84)
TH03 0013 S02	PI3K/AKT/mTOR	PIK3CD (pc)	KEGG PHOSPHATIDYLINOSITOL SIGNALING SYSTEM (pc up. 4/76)
TH03_0013_S02	PI3K/AKT/mTOR		KEGG PHOSPHATIDYLINOSITOL SIGNALING SYSTEM (pc_up, 4/76)
TH03_0014_S01	New sample	sarcoma	
TH03_0014_S01	JAK/STAT	JAK1 (pc. pd)	None
TH03_0015_S01	New sample	neuroblastoma	
TH03_0015_S01	Cell Cycle	CDK6 (pc)	REACTOME CELL CYCLE (nd up 7/421)
TH03_0016_S01	New sample	atypical teratoid/rhabdoid tumor	
TH03_0016_001	Receptor Tyrosine Kinase (RTK)	EBBB2 (pd)	REACTOME PI3K EVENTS IN ERBB2 SIGNALING (pd up 4/44)
TH03_0016_S01	Receptor Tyrosine Kinase (RTK)	EGER1 (pd)	PID EGE PATHWAX (pd up 4/55)
TH03_0016_S01			$PID_{II} \in \mathcal{T} PATHWAY (pc_{III}, 4/33)$
TH02_0017_S01		honotoblastema	
TH03_0017_501	RCI 2/MDM2	MDM2 (pc, pd)	KEGG P53 SIGNALING PATHWAY (pd up 4/69)
TH03_0018_S01			REGG_F35_5161REING_FATTWAT (pd_up, 4/09)
TH03_0018_S01	Peceptor Tyrosina Kinasa (PTK)	FLT4 (pc, pd)	HALLMARK KRAS SIGNALING LIP (commune 5/200 and poure 6/200 and poure 6/200)
TH02_0018_501	New comple		11200000000000000000000000000000000000
TH03_0018_502		Sarcoma	
TH03_0010_502	N/A		
TH03_0019_501		fibrolameliar nepatocellular carcinoma	
TH03_0019_501	Receptor Tyrosine Kinase (RTK)		PID_VEGF_VEGFR_PATHWAY (pd_up, 2/10)
TH03_0019_S01	Receptor Lyrosine Kinase (RTK)	KDR (pa)	PID_VEGF_VEGFR_PATHWAY (pa_up, 2/10)
TH03_0020_S01			
TH03_0020_S01	Sonic Hedgenog (SHH)		PID_HEDGEHOG_GLI_PATHWAY (pc_up, 3/48)
TH03_0022_S01		osteosarcoma	
TH03_0022_S01	Receptor Tyrosine Kinase (RTK)	FGFR1 (pc)	PID_FGF_PATHWAY (pc_up, 4/55)
TH03_0024_S01		adrenocortical carcinoma	
TH03_0024_S01	N/A	No druggable outliers	N/A
TH03_0025_S02		osteosarcoma	
TH03_0025_S02	N/A	No druggable outliers	N/A
TH03_0027_S01	New sample	osteosarcoma	
TH03_0027_S01	N/A	No druggable outliers	N/A
TH03_0029_S01		osteosarcoma	
TH03_0029_S01	N/A	No druggable outliers	N/A
TH03_0038_S01	New sample	osteosarcoma	
TH03_0038_S01	N/A	No druggable outliers	N/A
TH03_0103_S01	New sample	rhabdomyosarcoma	
TH03_0103_S01	RAS/RAF/MEK	MAP2K2 (pc, pd)	BIOCARTA_BARR_MAPK_PATHWAY (pd_up, 2/12)
TH03_0104_S01	New sample	hepatoblastoma	
TH03_0104_S01	N/A	No druggable outliers	N/A
TH03_0105_S01	New sample	rhabdomyosarcoma	
TH03_0105_S01	N/A	No druggable outliers	N/A
TH03_0106_S01	New sample	sarcoma	
TH03_0106_S01	JAK/STAT	JAK1 (pc)	None
TH03_0107_S01	New sample	hepatoblastoma	
TH03_0107_S01	N/A	No druggable outliers	N/A
TH03_0112_S01	New sample	sarcoma	
TH03_0112_S01	Receptor Tyrosine Kinase (RTK)	ERBB2 (pd)	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING (pd_up, 3/44)
TH03_0112_S01	PI3K/AKT/mTOR	MLST8 (pd)	REACTOME_PI3K_AKT_ACTIVATION (pd_up, 3/38)
TH03_0112_S02	New sample	sarcoma	
TH03_0112_S02	Receptor Tyrosine Kinase (RTK)	ERBB2 (pd)	None
TH03_0112_S02	Sonic Hedgehog (SHH)	GLI1 (pc)	PID_HEDGEHOG_GLI_PATHWAY (pc_up, 3/48)



Sample ID	Activated gene set lead	Outlier support	Pathway support
TH03 0112 S02	Sonic Hedgehog (SHH)	PTCH1 (pc)	PID HEDGEHOG GLI PATHWAY (pc up. 3/48)
TH03 0113 S01	New sample	myoepithelial carcinoma of the liver	
TH03 0113 S01	Receptor Tyrosine Kinase (RTK)	FGFR1 (pc. pd)	PID EGE PATHWAY (pd up. 3/55)
TH03_0113_S02	New sample	myoepithelial carcinoma of the liver	
TH03_0113_S02	Receptor Tyrosine Kinase (RTK)	EGER1 (nc. nd)	REACTOME EGER LIGAND BINDING AND ACTIVATION (comm up 2/22 and pc up 2/22)
TH03_0114_S01	New sample	fibrolamellar benatocellular carcinoma	
TH03_0114_001	N/A	No druggable outliers	Ν/Δ
TH02_0115_S01	Now comple	teratoma	
TH02_0115_S01	N/A	No druggoble outliers	
TH03_0115_501	N/A		
TH03_0116_501			
TH03_0116_501	N/A		N/A
TH03_0117_S01	New Sample		Nene
TH03_0117_S01	Heat Shock Proteins		
TH03_0117_S01	Receptor Tyrosine Kinase (RTK)		PID_PDGFRB_PATHWAY (pd_up, 9/129)
TH03_0118_S01	New sample		
TH03_0118_S01	B-cell receptor signaling		KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 4/75)
TH03_0118_S01	Receptor Tyrosine Kinase (RTK)	FLI3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 6/88)
TH03_0139_S01	New sample	osteosarcoma	
TH03_0139_S01		CCNE1 (pc, pd)	REACTOME_CELL_CYCLE (pd_up, 8/421)
TH03_0140_S01	New sample	osteosarcoma	
1H03_0140_S01	N/A	No druggable outliers	N/A
TH03_0141_S01	New sample	osteosarcoma	
TH03_0141_S01	Cell Cycle	CCND3 (pc, pd)	REACTOME_CELL_CYCLE (pc_up, 6/421 and pd_up, 5/421)
TH03_0141_S01	Cell Cycle	CDK4 (pc, pd)	REACTOME_CELL_CYCLE (pc_up, 6/421 and pd_up, 5/421)
TH03_0141_S01	BCL2/MDM2	MDM2 (pd)	BIOCARTA_P53_PATHWAY (pd_up, 2/16)
TH03_0141_S01	Sonic Hedgehog (SHH)	PTCH1 (pc)	None
TH03_0143_S01	New sample	osteosarcoma	
TH03_0143_S01	JAK/STAT	IL6 (pc, pd)	BIOCARTA_IL6_PATHWAY (pd_up, 2/22)
TH03_0143_S02	New sample	osteosarcoma	
TH03_0143_S02	N/A	No druggable outliers	N/A
TH03_0144_S01	New sample	wilms tumor	
TH03_0144_S01	PI3K/AKT/mTOR	MLST8 (pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 3/52)
TH03_0144_S01	JAK/STAT	STAT1 (pd)	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM (pd_up, 11/270)
TH03_0146_S01	New sample	sarcoma	
TH03_0146_S01	Cell Cycle	CCNE1 (pc)	None
TH03_0146_S01	Receptor Tyrosine Kinase (RTK)	FLT4 (pc, pd)	None
TH03_0148_S01	New sample	lymphoma	
TH03_0148_S01	B-cell receptor signaling	MS4A1 (pc, pd)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (comm_up, 8/88 and pc_up, 8/88 and pd_up, 8/88)
TH03_0149_S01	New sample	acute myeloid leukemia	
TH03_0149_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 8/88)
TH03_0156_S01	New sample	sarcoma	
TH03_0156_S01	N/A	No druggable outliers	N/A
TH03_0159_S01	New sample	osteosarcoma	
TH03_0159_S01	N/A	No druggable outliers	N/A
TH03_0159_S02	New sample	osteosarcoma	
TH03_0159_S02	N/A	No druggable outliers	N/A
TH03_0285_S01	New sample	juvenile myelomonocytic leukemia	
TH03_0285_S01	B-cell receptor signaling	BTK (pc)	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR (pc_up, 9/126)
TH03_0285_S01	Receptor Tyrosine Kinase (RTK)	CSF1R (pc)	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION (pc_up, 17/267 and pd_up, 6/267)
TH03_0285_S01	JAK/STAT	IL6 (pd)	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION (pc_up, 17/267 and pd_up, 6/267)
TH03_0285_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (comm_up, 3/88 and pc_up, 15/88 and pd_up, 4/88)
TH03_0286_S01	New sample	hepatocellular carcinoma	
TH03_0286_S01	Receptor Tyrosine Kinase (RTK)	PDGFRB (pd)	KEGG_MAPK_SIGNALING_PATHWAY (pd_up, 4/267)
TH03_0287_S01	New sample	neuroblastoma	
TH03_0287_S01	PI3K/AKT/mTOR	AKT3 (pd)	PID_PI3KCI_AKT_PATHWAY (pd_up, 3/35)
TH03_0288_S01	New sample	neuroblastoma	
TH03_0288_S01	Receptor Tyrosine Kinase (RTK)	ALK (pc)	None
TH03_0288_S01	Cell Cycle	CDK6 (pc)	BIOCARTA_CELLCYCLE_PATHWAY (pc_up, 3/23)
TH03_0288_S01	B-cell receptor signaling	MS4A1 (pc, pd)	None
TH03_0289_S01	New sample	acute lymphoblastic leukemia	
TH03_0289_S01	B-cell receptor signaling	BTK (pc)	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY (pc_up, 11/75)
TH03_0289_S01	Cell Cycle	CCND3 (pc)	REACTOME_CELL_CYCLE (pc_up, 10/421)
TH03_0289_S01	Receptor Tyrosine Kinase (RTK)	FLT3 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 11/88)
TH03_0289_S01	BCL2/MDM2	MDM2 (pc)	HALLMARK_P53_PATHWAY (pc_up, 6/200)
TH03_0289_S01	B-cell receptor signaling	MS4A1 (pc)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, 11/88)
TH03_0289_S01	PI3K/AKT/mTOR	PIK3C2B (pc)	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM (pc_up, 5/76)
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Sample ID	Activated gene set lead	Outlier support	Pathway support
TH03_0289_S01	PI3K/AKT/mTOR	PIK3CD (pc)	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM (pc_up, 5/76)
TH03_0290_S01	New sample	glioma	
TH03_0290_S01	JAK/STAT	IL6 (pd)	HALLMARK_INFLAMMATORY_RESPONSE (pd_up, 5/200)
TH03_0291_S01	New sample	ependymoma	
TH03_0291_S01	Receptor Tyrosine Kinase (RTK)	ERBB2 (pd)	None
TH03_0296_S01	New sample	osteosarcoma	
TH03_0296_S01	N/A	No druggable outliers	N/A
TH03_0296_S02	New sample	osteosarcoma	
TH03_0296_S02	Receptor Tyrosine Kinase (RTK)	TEK (pc, pd)	None
TH06_0284_S01	New sample	neuroblastoma	
TH06_0284_S01	Receptor Tyrosine Kinase (RTK)	ERBB3 (pd)	None
TH06_0610_S01	New sample	sarcoma	
TH06_0610_S01	Receptor Tyrosine Kinase (RTK)	ALK (pc, pd)	
TH06_0610_S01			PID_CMYB_PATHWAY (pd_up, 5/84)
TH06_0610_S01	Receptor Tyrosine Kinase (RTK)	FGFR1 (pd)	PID_FGF_PATHWAY (pd_up, 5/55)
TH06_0610_S01			BIOCARTA_IL10_PATHWAY (pd_up, 3/17)
TH06_0610_501		STATER (pd)	$\frac{\text{BIOCARTA_ILT0_PATHWAY (pd_up, 3/17)}}{\text{PIOCARTA_ILT0_PATHWAY (pd_up, 3/17)}}$
TH06_0611_S01	New sample	cranionbaryngioma	
TH06_0611_S01	Sonic Hedgebog (SHH)	PTCH1 (nc)	BIOCARTA SHH PATHWAY (pc up 3/16)
TH06_0612_S01	New sample	thyroid carcinoma	
TH06 0612 S01	N/A	No druggable outliers	N/A
TH06_0613_S01	New sample	atypical teratoid/rhabdoid tumor	
TH06_0613_S01	Cell Cycle	CCND3 (pd)	HALLMARK_P53_PATHWAY (pd_up, 6/200)
TH06_0613_S01	RAS/RAF/MEK	MAP2K1 (pc, pd)	BIOCARTA_ERK_PATHWAY (comm_up, 2/28 and pc_up, 2/28 and pd_up, 3/28)
TH06_0613_S01	RAS/RAF/MEK	MAP2K2 (pc, pd)	BIOCARTA_ERK_PATHWAY (comm_up, 2/28 and pc_up, 2/28 and pd_up, 3/28)
TH06_0613_S02	New sample	atypical teratoid/rhabdoid tumor	
TH06_0613_S02	Receptor Tyrosine Kinase (RTK)	PDGFRA (pd)	None
TH06_0615_S01	New sample	sarcoma	
TH06_0615_S01	Receptor Tyrosine Kinase (RTK)	KIT (pc)	None
TH06_0616_S01	New sample	glioblastoma multiforme	
TH06_0616_S01	PI3K/AKT/mTOR	AKT1 (pd)	HALLMARK_PI3K_AKT_MTOR_SIGNALING (pd_up, 4/105)
TH06_0616_S01	DNA repair	PARP1 (pd)	None
TH06_0616_S01	PI3K/AKT/mTOR	PIK3R2 (pc, pd)	REACTOME_PI3K_AKT_ACTIVATION (pd_up, 3/38)
TH06_0617_S01			
TH06_0617_S01	PI3K/AKT/MTOR	PIK3R1 (pc, pd)	None
THU6_0618_501		No I midline carcinoma	
TH06_0619_S01	New sample	angiosarcoma	
TH06_0619_S01	Receptor Tyrosine Kinase (RTK)	FGFR1 (pd)	REACTOME SIGNALING BY EGER IN DISEASE (pd up 5/127)
TH06_0619_S01	Receptor Tyrosine Kinase (RTK)		PID SHP2 PATHWAY (nc up $4/58$)
TH06 0620 S01	New sample	gliomatosis cerebri	
TH06_0620_S01	N/A	No druggable outliers	N/A
TH06_0621_S01	New sample	osteosarcoma	
TH06_0621_S01	PI3K/AKT/mTOR	MLST8 (pd)	REACTOME_MTORC1_MEDIATED_SIGNALLING (pd_up, 2/11)
TH06_0622_S01	New sample	neuroblastoma	
TH06_0622_S01	N/A	No druggable outliers	N/A
TH06_0623_S01	New sample	rhabdomyosarcoma	
TH06_0623_S01	Receptor Tyrosine Kinase (RTK)	ALK (pc)	None
TH06_0623_S01	Heat Shock Proteins	HSP90AA1 (pc, pd)	None
TH06_0624_S01	New sample	lung adenocarcinoma	
TH06_0624_S01	N/A	No druggable outliers	N/A
TH06_0625_S01	New sample	fibromatosis	
TH06_0625_S01	N/A	No druggable outliers	N/A
TH06_0626_S01		TIDFOMATOSIS	
THOS 0627 501		no uruggable outliers	
TH06_0627_501		AKT1 (nd)	PID PI3KCI AKT PATHWAY (nd up 3/35)
TH06_0627_501	BCL2/MDM2	BCL6 (pc)	None
TH06_0627_501	Receptor Tyrosine Kinase (RTK)	CSF1R (pc)	None
TH06 0627 S01	JAK/STAT	STAT1 (pd)	KEGG JAK STAT SIGNALING PATHWAY (pd up. 5/155)
TH06 0627 S01	JAK/STAT	STAT2 (pc, pd)	KEGG_JAK_STAT_SIGNALING PATHWAY (pd up. 5/155)
TH06_0628_S01	New sample	neuroblastoma	
TH06_0628_S01	Receptor Tyrosine Kinase (RTK)	CSF1R (pd)	PID_CMYB_PATHWAY (pd_up, 7/84)
TH06_0629_S01	New sample	neurofibromatosis type 1	
TH06_0629_S01	Receptor Tyrosine Kinase (RTK)	ERBB3 (pd)	REACTOME_SIGNALING_BY_ERBB2 (pd_up, 5/101)



Sample ID	Activated gene set lead	Outlier support	Pathway support
TH06_0630_S01	New sample	osteosarcoma	
TH06_0630_S01	PI3K/AKT/mTOR	MLST8 (pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 8/52)
TH06_0630_S01	PI3K/AKT/mTOR	PIK3R1 (pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 8/52)
TH06_0630_S01	JAK/STAT	STAT2 (pd)	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM (pd_up, 12/270)
TH06_0630_S01	PI3K/AKT/mTOR	TSC2 (pc, pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 8/52)
TH06_0631_S01	New sample	thyroid carcinoma	
TH06_0631_S01	Receptor Tyrosine Kinase (RTK)	CSF1R (pd)	KEGG_HEMATOPOIETIC_CELL_LINEAGE (pd_up, 5/88)
TH06_0631_S01	JAK/STAT	STAT2 (pd)	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM (pd_up, 13/270)
TH06_0631_S01	PI3K/AKT/mTOR	TSC2 (pd)	HALLMARK_PI3K_AKT_MTOR_SIGNALING (pd_up, 6/105)
TH06_0632_S01	New sample	wilms tumor	
TH06_0632_S01	BCL2/MDM2	BCL6 (pc, pd)	PID_P53_DOWNSTREAM_PATHWAY (pd_up, 10/137)
TH06_0632_S01	PI3K/AKT/mTOR	MLST8 (pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 6/52)
TH06_0632_S01	Receptor Tyrosine Kinase (RTK)	PDGFRB (pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 6/52)
TH06_0632_S01	PI3K/AKT/mTOR	PIK3R1 (pd)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 6/52)
TH06_0632_S01	JAK/STAT	STAT3 (pd)	HALLMARK_INTERFERON_GAMMA_RESPONSE (pd_up, 15/200)
TH06_0632_S01	PI3K/AKT/mTOR	TSC2 (pc)	KEGG_MTOR_SIGNALING_PATHWAY (pd_up, 6/52)
TH06_0633_S01	New sample	neurofibroma	
TH06_0633_S01	BCL2/MDM2	BCL6 (pd)	PID_P53_DOWNSTREAM_PATHWAY (pd_up, 14/137)
TH06_0633_S01	Receptor Tyrosine Kinase (RTK)	EGFR (pd)	KEGG_MAPK_SIGNALING_PATHWAY (comm_up, 11/267 and pc_up, 11/267 and pd_up, 23/267)
TH06_0633_S01	Receptor Tyrosine Kinase (RTK)	ERBB2 (pd)	REACTOME_SIGNALING_BY_ERBB2 (comm_up, 4/101 and pc_up, 4/101 and pd_up, 14/101)
TH06_0633_S01	Receptor Tyrosine Kinase (RTK)	FGFR1 (pd)	KEGG_MAPK_SIGNALING_PATHWAY (comm_up, 11/267 and pc_up, 11/267 and pd_up, 23/267)
TH06_0633_S01	Sonic Hedgehog (SHH)	GLI1 (pc, pd)	PID_HEDGEHOG_GLI_PATHWAY (comm_up, 3/48 and pc_up, 3/48 and pd_up, 7/48)
TH06_0633_S01	Receptor Tyrosine Kinase (RTK)	PDGFRB (pc, pd)	PID_PDGFRB_PATHWAY (comm_up, 6/129 and pc_up, 6/129 and pd_up, 14/129)
TH06_0633_S01	PI3K/AKT/mTOR	PIK3R1 (pd)	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING (pd_up, 7/44)
TH06_0633_S01	Sonic Hedgehog (SHH)	PTCH1 (pc, pd)	PID_HEDGEHOG_GLI_PATHWAY (comm_up, 3/48 and pc_up, 3/48 and pd_up, 7/48)
TH06_0633_S01	RAS/RAF/MEK	RAF1 (pd)	KEGG_MAPK_SIGNALING_PATHWAY (comm_up, 11/267 and pc_up, 11/267 and pd_up, 23/267)
TH06_0633_S01	JAK/STAT	STAT3 (pd)	REACTOME_IMMUNE_SYSTEM (pd_up, 40/933)
TH06_0633_S01	JAK/STAT	STAT5B (pd)	REACTOME_IMMUNE_SYSTEM (pd_up, 40/933)
TH06_0633_S01	PI3K/AKT/mTOR	TSC2 (pd)	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING (pd_up, 7/44)
TH06_0634_S01	New sample	osteosarcoma	
TH06_0634_S01	Cell Cycle	CDK4 (pd)	None
TH06_0645_S01	New sample	sarcoma	
TH06_0645_S01	Receptor Tyrosine Kinase (RTK)	EGFR (pd)	REACTOME_SIGNALING_BY_ERBB4 (pd_up, 4/90)
TH06_0645_S01	Receptor Tyrosine Kinase (RTK)	ERBB3 (pd)	REACTOME_SIGNALING_BY_ERBB4 (pd_up, 4/90)
TH06_0645_S01	Sonic Hedgehog (SHH)	PTCH1 (pc, pd)	KEGG_BASAL_CELL_CARCINOMA (comm_up, 3/55 and pc_up, 3/55 and pd_up, 3/55)
TH06_0646_S01	New sample	neurofibroma	
TH06_0646_S01	Receptor Tyrosine Kinase (RTK)	ERBB3 (pd)	None
TH06_0646_S01	Sonic Hedgehog (SHH)	PTCH1 (pc, pd)	None
TH06_0647_S01	New sample	diffuse intrinsic pontine glioma	
TH06_0647_S01	Receptor Tyrosine Kinase (RTK)	PDGFRA (pc)	None
TH06_0647_S01	Receptor Tyrosine Kinase (RTK)	PDGFRB (pd)	None
TH06_0648_S01	New sample	acute lymphoblastic leukemia	
I H06_0648_S01	B-cell receptor signaling		REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR (pc_up, 11/126)
THU6_0648_S01			REACTOME_G1_PHASE (pc_up, 3/38)
THU6_0648_S01			REACTOME_G1_PHASE (pc_up, 3/38)
THU6_0648_S01	Receptor Tyrosine Kinase (RTK)		KEGG_HEMATOPOIETIC_CELL_LINEAGE (pc_up, //88)
THU6_0649_S01			Nene
I ⊡00_0049_501	FISR/ART/IIITUK	ΓΕΙΟΚ (με, μα)	NOTE



b.

a.







Expression level log2(TPM+1)

eFigure 2. Treehouse analysis of sample TH03_0288_S01. A. Gene expression similarity analysis, visualized using TumorMap (eMethods), reveals that most correlated samples are neuroblastomas. B. Summary of outlier analysis and gene set overlap analysis of lists of outlier genes. ALK and CDK6 are pan-cancer over-expression outliers; CDK6 and BRAF are amplified in the tumor. The Hedgehog Signaling and Cell Cycle Pathway annotations are significantly enriched among outlier gene lists. C. Gene expression levels of ALK (top) and CDK6 (bottom) in the whole compendium (left) or all neuroblastoma samples (right). The outlier range is denoted in yellow, and the expression level in sample TH03_0288_S01 is indicated with a red bar.

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