

# IntelliSpace Genomics

Challenges in Genomic Aberration Detection and Interpretation in Solid Tumors and Evidence-based Approaches for Targeted Therapy



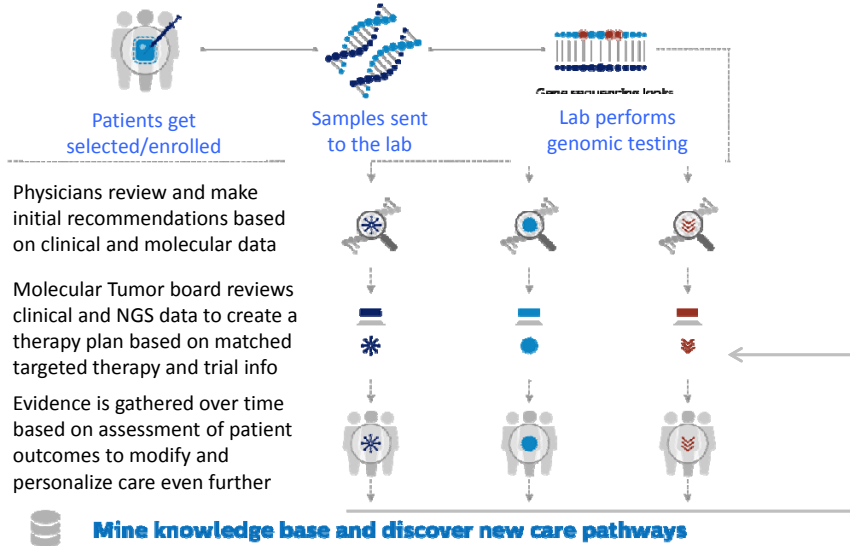
Nevenka Dimitrova, PhD, CTO Genomics, Healthcare Informatics, Philips  
Sheryl Elkin, PhD, N-of-One

Philips Healthcare Informatics – Genomics  
AMP Webinar March 14, 2017

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## Precision Medicine



- A Retrospective Analysis of Precision Medicine Outcomes in Patients With Advanced Cancer Reveals Improved Progression-Free Survival Without Increased Health Care Costs.

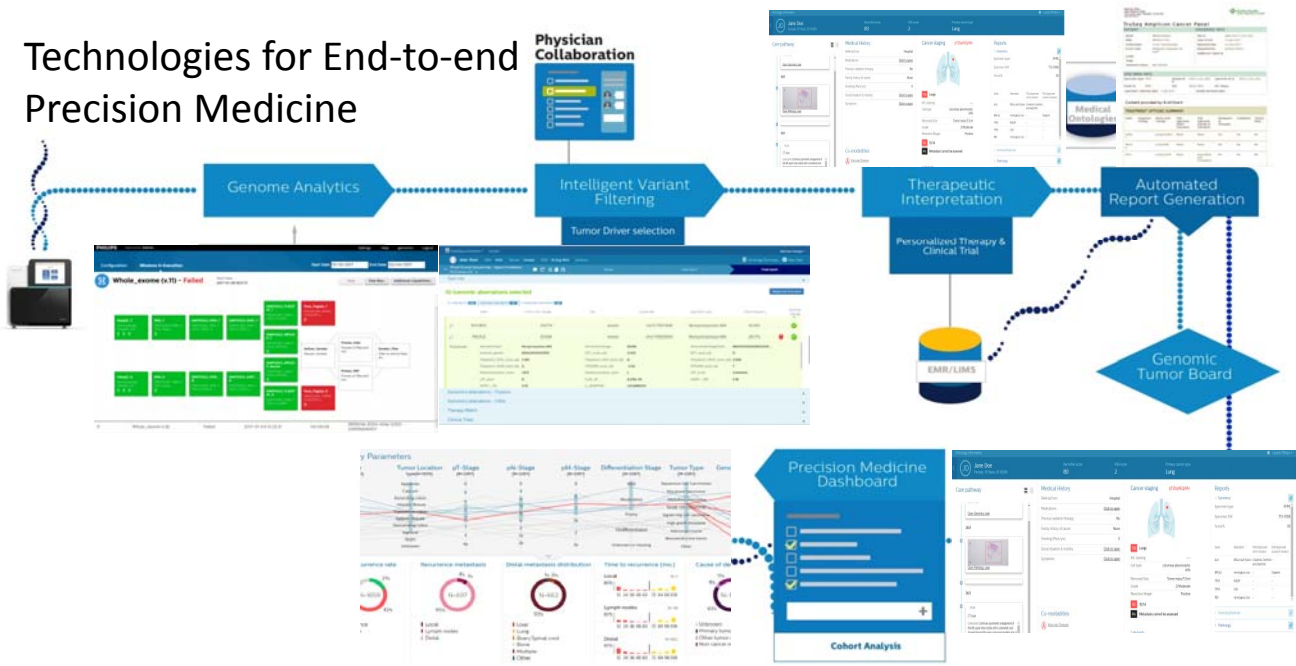
Haslem DS, Van Norman SB, Fulde G, Knighton AJ, Belnap T, Butler AM, Rhagunath S, Newman D, Gilbert H, Tudor BP, Lin K, Stone GR, Loughmiller DL, Mishra PJ, Srivastava R, Ford JM, Nadauld LD. *J Oncol Pract.* 2016 Sep 6. pii: JOPR011486

- Precision medicine in pediatric oncology: Lessons learned and next steps.

Mody RJ, Prensner JR, Everett J, Parsons DW, Chinnaiyan AM. *Pediatric Blood Cancer.* 2017 Mar;64(3). doi: 10.1002/pbc.26288. Review.

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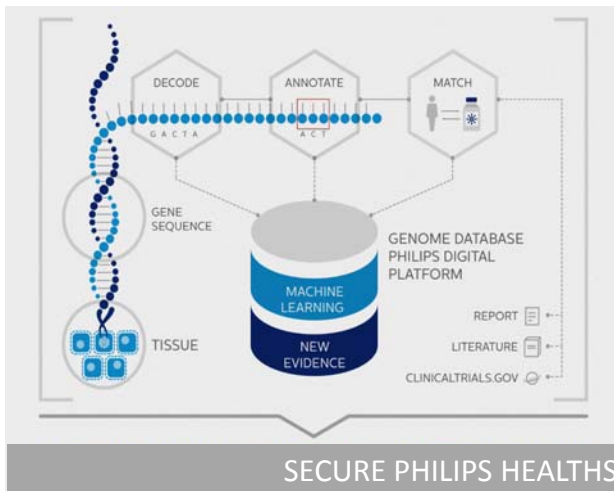
# Technologies for End-to-end Precision Medicine



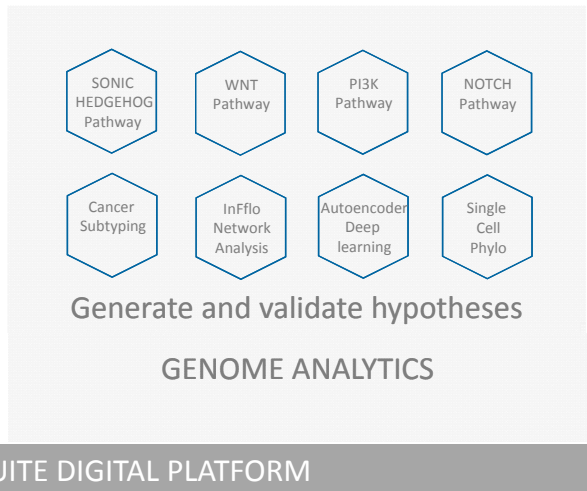
F. Andry, N. Dimitrova, A. Mankovich, V. Agrawal, A. Bder, A. David, *A Highly Scalable Cloud-based Framework for Genomic Processing*, 9th Int.Conf. Biomedical Engineering Systems and Technologies (BIOSTEC 2016) - BIOINFORMATICS, pp. 198-206, Rome,

# The End-to-end Platform

IntelliSpace Genomics **Clinical** Workflows



IntelliSpace Genomics **Research** Workflows



# The IntelliSpace Genomics Platform

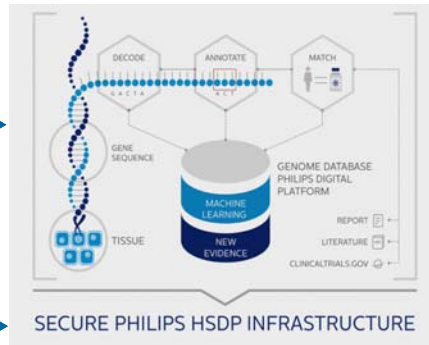
## Interoperability

- Synthesize clinical information
- Analyze genomics data



1 Clinical:  
HL7 – FHIR -  
patient  
specific  
information

2 Genomics:  
FASTA, FASTQ,  
BCL, VCF



3 Semantic conversion: ICD10, SNOMED, ICD-O3

4 Genomics  
reporting:  
XML, JSON

- Personalized Therapy plan
- Oncology therapy matching
- Personalized clinical trials

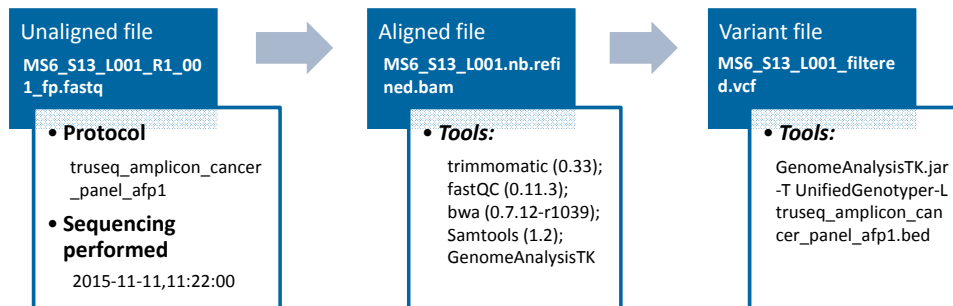


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## Audit and reproducibility

Controlled processing of raw next generation sequencing data using automated pipelines with quality checks, traceability

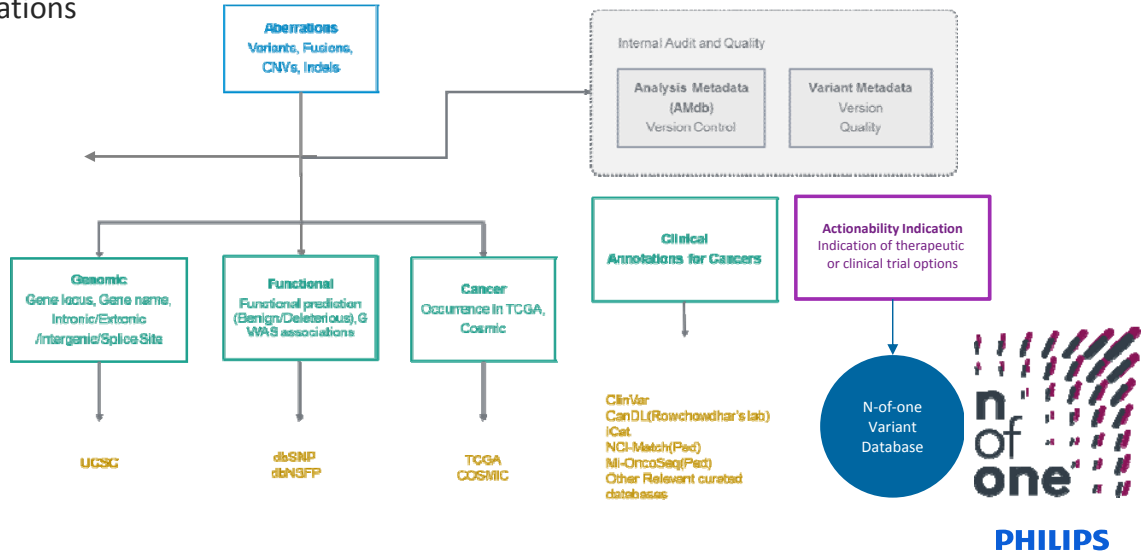
- Best in class algorithms
- Molecular test agnostic



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## Informed annotation

Variant annotation with therapy-indication - genomic, functional, and cancer-specific annotations



## N-of-One: Clinical Interpretation of Molecular Diagnostic Tests

- Acknowledged leader with 8-year track record of success
- High quality, patient-specific, data-driven therapeutic strategies with reproducible methodology
- Utilized by hospital and commercial labs worldwide: all size panels and on multiple test platforms
- Tens of thousands of patient cases interpreted across hundreds of cancer types
- Industry-leading proprietary tools, platform and database
- Experienced team of practicing oncologists and Ph.D. scientists



**PHILIPS**

IntelliSpace Genomics™ **worklist** Akerman Philip ▾

**Johnson Joanna** MRN MR4567785 Gender **Female** DOB **05 Apr 2016** Ethnicity **Not Hispanic or Latino** + New Test

... RNASeq deFuse Fusion v1 Review Initial report Final report

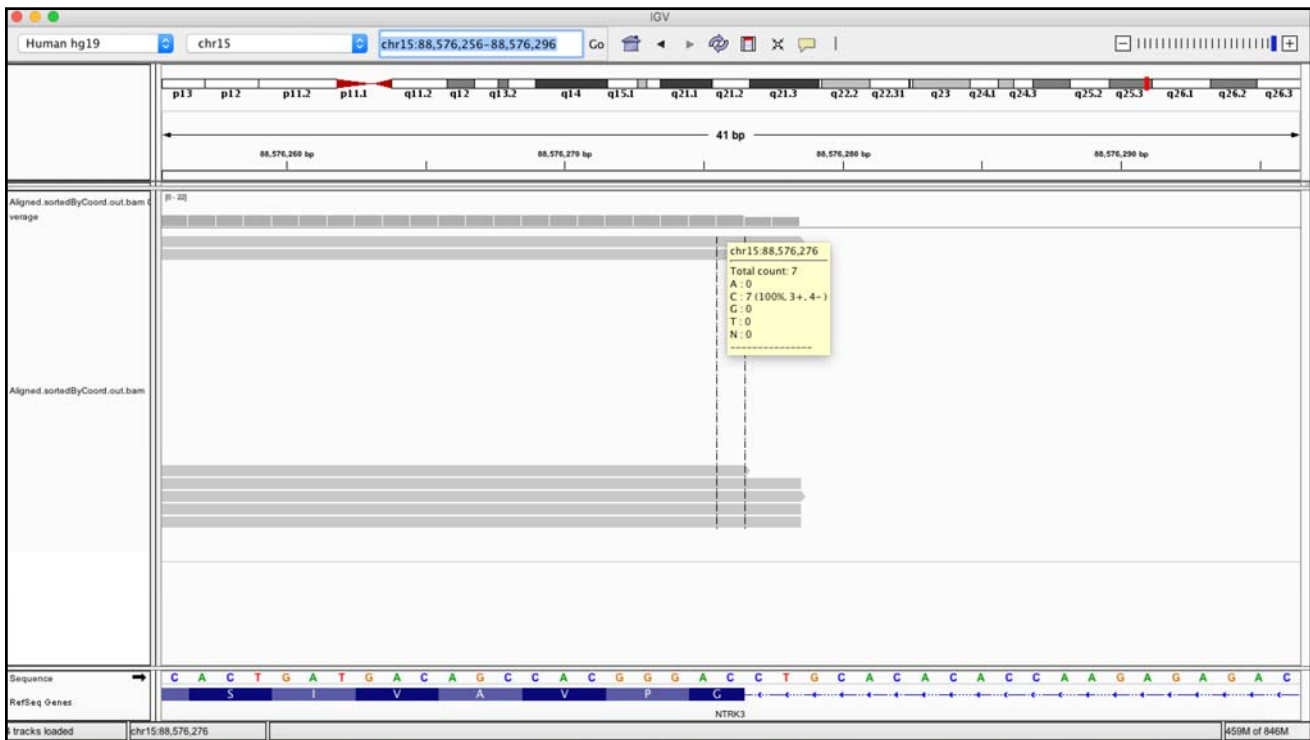
Test Info Genomic Aberrations Therapy Match Clinical Trials

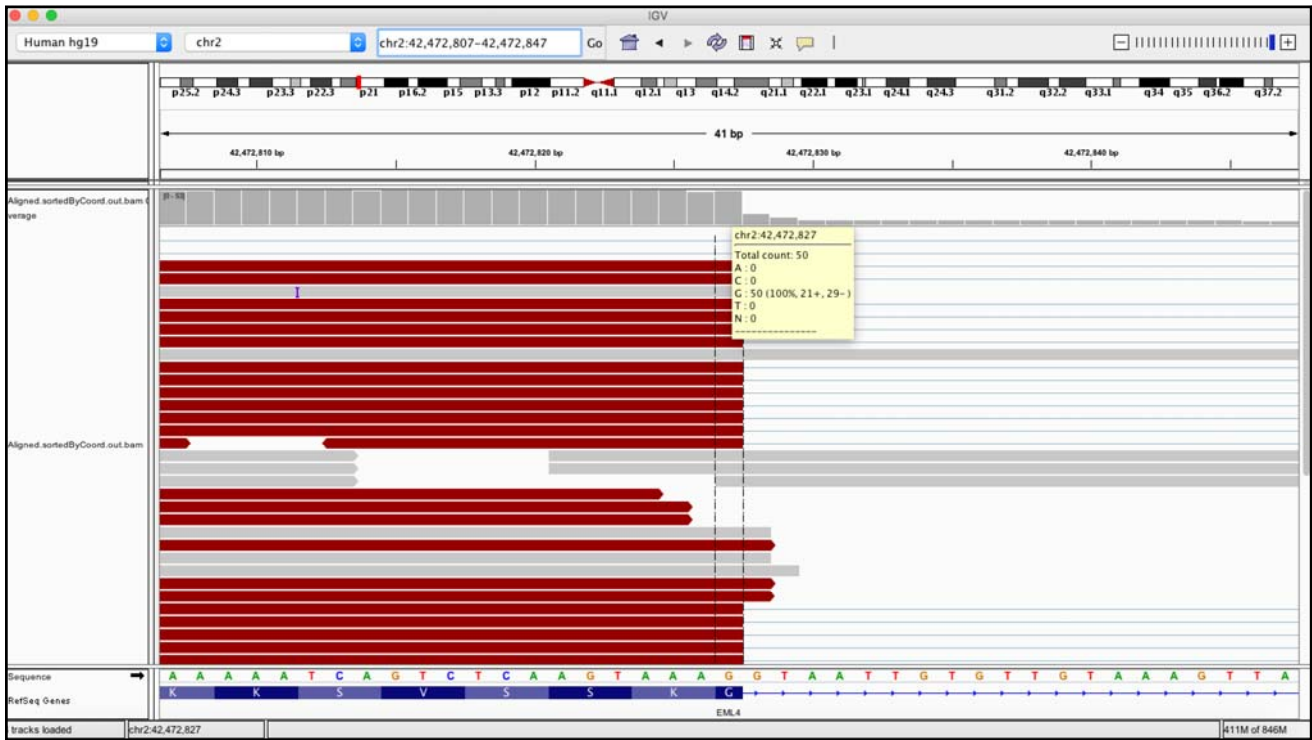
**Case Info**

Ordering physician	Jackson Elvira	Date of test	27 Feb 2017
Performing physician	Akerman Philip	Priority	urgent
Diagnosis	Malignant neoplasm of other connective and soft tissue	Reason	Late Stage
Histopathology	Fibrosarcoma, NOS	Site	Connective, Subcutaneous and other soft tissues of upper limb and shoulder
Treatment status		Tumor Stage	
Additional copies to	Wilson Jack	Recent imaging info	MRI imaging demonstrates a 3 × 5 × 4.2-cm soft tissue mass in the distal left forearm. PET-CT shows pulmonary metastasis.
Test Number	152		

**Tumor - Specimen Info** **Tumor - Sample Info**

Specimen ID	SU-127/16	Sample ID	CongenitalFibrosarcoma_Defuse_results
Specimen type	FFPE	Sample Received Date	07 Feb 2017
IHC Result	Vimentin positive; pancytokeratin negative, desmin negative, SMA negative, CD34 negative, S100 protein negative	Tumor percentage	50%
Collection method	Surgical Resection	Tumor grade	Grade 3
Specimen Collection Date	06 Feb 2017		





IntelliSpace Genomics™ worklist Akerman Philip ▾

**Johnson Joanna** MRN MR4567785 Gender Female DOB 05 Apr 2016 Ethnicity Not Hispanic or Latino + New Test

RNASeq deFuse Fusion v1 Review Initial report Final report

Test Info Genomic Aberrations Therapy Match Clinical Trials

68 Filtered results | 1 Genomic aberrations selected

Aberration type  Clear all filters

Gene 5'	Junction 5'	Strand 5	Gene 3'	Junction 3'	Strand 3	Spanning Reads	COSMIC	Akerman Philip
COL1A1	48261862	-	ZSCAN10	3142205	-	5	Matches mutation(s) wit...	⊖
CRKL	21265506	+	UNC45B	33478373	+	41		⊖
CRKL	21265521	+	DLG2	85195014	-	7		⊖
EML4	42472827	+	NTRK3	88576276	-	5	Matches mutation(s) wit...	⊕
Clinical	COSMIC ID	COSF1062	COSMIC ID	COSF1063	COSMIC ID	COSF1064		
	COSMIC ID	COSF1065	COSMIC ID	COSF1127	COSMIC ID	COSF1128		
	COSMIC ID	COSF1296	COSMIC ID	COSF1297	COSMIC ID	COSF1366		
	COSMIC ID	COSF1367	COSMIC ID	COSF1368	COSMIC ID	COSF1376		
	COSMIC ID	COSF1534	COSMIC ID	COSF1535	COSMIC ID	COSF1536		
	COSMIC ID	COSF1537	COSMIC ID	COSF1539	COSMIC ID	COSF1540		
	COSMIC ID	COSF1541	COSMIC ID	COSF1542	COSMIC ID	COSF1543		
	COSMIC ID	COSF1544	COSMIC ID	COSF1545	COSMIC ID	COSF408		
	COSMIC ID	COSF409	COSMIC ID	COSF410	COSMIC ID	COSF411		



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Johnson Joanna MRN MR4567785 Gender Female DOB 05 Apr 2016 Ethnicity Not Hispanic or Latino New Test

RNASeq deFuse Fusion v1 Review Initial report Final report

Test Info Genomic Aberrations **Therapy Match** Clinical Trials

### Therapy Match

Gene	Sequence Change	Aberration	Variant Qualifier	Treatment approach
NTRK3	NA	EML4-NTRK3 fusion		There are currently no approved therapies targeting NTRK3 alterations. However, several kinase inhibitors targeting the Trk family are currently under investigation in clinical trials. The pan-Trk inhibitors LOXO-101 and entrectinib have shown efficacy in multiple tumor types harboring both NTRK mutations and gene fusions (Hong et al., 2016; AACR 2016, Abstract CT008, Doebele et al., 2015; 26216294, De Braud et al., 2015; ASCO 2015, Abstract 2517, Drlon et al., 2016; AACR 2016, Abstract CT007, Ardini et al., 2016; 26939704, Iyer et al., 2016; 26797418). Other agents also reported to inhibit Trk activity, including the FDA-approved Alk inhibitor crizotinib, are also in clinical trials (Awad and Shaw, 2014; 25322323, Vaishnavi et al., 2015; 25527197, Reungwetwattana and Dy, 2013; 24574860, Ivanov et al., 2013; 23027130, Tatematsu et al., 2014; 25054037).

FDA approved therapies within indication  
**No available data**

FDA approved therapies outside this indication  
**Crizotinib**

Investigational therapies within indication  
**Crizotinib, LOXO-101, Entrectinib, DS-6051b, MGCD516, Altiratinib, PLX7486**

Resistance and Interactions  
**No available data**

Guidelines  
**No available data**

Detailed therapeutic relevance

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### Aberration effect

The EML4-NTRK3 rearrangement reported here is expected to result in a fusion of the N-terminal portion of the Eml4 protein with the C-terminal portion of TrkC, including the kinase domain (Integrative Genomics Viewer, v.2.3). An EML4-NTRK3 fusion retaining the TrkC kinase domain has been reported in a congenital fibrosarcoma case and was reported to result cellular transformation and tumorigenesis when expressed in fibroblasts (Tannenbaum-Dvir et al., 2015; 27148571). In addition, an EML4-NTRK3 fusion has been reported in a glioblastoma cell line that was more sensitive to crizotinib as compared with glioblastoma cell lines without EML4-NTRK3 fusions (Klijn et al., 2015; 25485619).

IntelliSpace Genomics™ worklist Akerman Philip

Johnson Joanna MRN MR4567785 Gender Female DOB 05 Apr 2016 Ethnicity Not Hispanic or Latino New Test

RNASeq deFuse Fusion v1 Review Initial report Final report

Test Info Genomic Aberrations Therapy Match **Clinical Trials**

### Clinical Trials

A Phase 1/2 Study of the Oral TRK Inhibitor LOXO101 in Pediatric Patients With Advanced Solid or Primary Central Nervous System Tumors				Recruiting
Target		Nearest Location		<a href="#">NCT02637687</a>
Age Group	30 Days to 21 Years	Contact	Penny Sinanian 1-855-NTRK-123 penny@loxooncology.com	

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**ClinicalTrials.gov**  
A service of the U.S. National Institutes of Health  
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### Oral TRK Inhibitor LOXO-101 (Larotrectinib) for Treatment of Advanced Pediatric Solid or Primary Central Nervous System Tumors (SCOUT)

**This study is currently recruiting participants.** (see [Contacts and Locations](#))

*Verified March 2017 by Loxo Oncology, Inc.*

**Sponsor:**  
Loxo Oncology, Inc.

**Information provided by (Responsible Party):**  
Loxo Oncology, Inc.

**ClinicalTrials.gov Identifier:**  
NCT02637687

First received: December 10, 2015  
Last updated: March 1, 2017  
Last verified: March 2017  
[History of Changes](#)

[Full Text View](#)   [Tabular View](#)   [No Study Results Posted](#)   [Disclaimer](#)   [How to Read a Study Record](#)

**Purpose**

This is a multicenter, open label, Phase 1/2 study in pediatric patients with advanced solid or primary CNS tumors. LOXO-101 (larotrectinib) will be administered orally (PO) twice daily (BID), with the dose adjusted by body surface area (BSA).

Condition	Intervention	Phase
Neoplasms Central Nervous System Neoplasms	Drug: LOXO-101 (larotrectinib)	Phase 1 Phase 2

[Access to an investigational treatment associated with this study is available outside the clinical trial. More info ...](#)

**Detailed Description:**

This is a multicenter, open label, Phase 1/2 study in pediatric patients with advanced solid or primary CNS tumors. LOXO-101 (larotrectinib) will be administered orally (PO) twice daily (BID), with the dose adjusted by body surface area (BSA).

Dose Escalation Phase will proceed through the planned 4 dose levels, or until the MTD is reached, or until the Sponsor determines that a suitable dose has been achieved based on PK exposure..

Expansion Cohorts may be enrolled to better characterize safety and efficacy in patients with specific abnormalities in the NTRK genes or proteins.

**Eligibility**

Ages Eligible for Study: 1 Month to 21 Years (Child, Adult)  
Sexes Eligible for Study: All  
Accepts Healthy Volunteers: No

**Criteria**

**Inclusion Criteria:**

- Pediatric patients ≥ 1 year old on Cycle 1 Day 1 (C1D1)
- Phase 1 only: Between 1 and 21 years of age at C1D1 with a locally advanced or metastatic solid tumor or primary CNS tumor that has relapsed, progressed or was nonresponsive to available therapies and for which no standard or available systemic curative therapy, or ≥1 month old with a diagnosis malignancy and with a documented NTRK fusion that has progressed or was nonresponsive to available therapies, and for which no standard or available curative therapy exists or patients with locally advanced infantile fibrosarcoma who would require, in the opinion of the Investigator, disfiguring surgery or limb amputation to achieve a complete surgical resection
- Phase 2 only: Ages >= 1 month of age at C1D1 with a locally advanced or metastatic infantile fibrosarcoma, Patients with locally advanced infantile fibrosarcoma who would require, in the opinion of the Investigator, disfiguring surgery or limb amputation to achieve a complete surgical resection enrollment or ages 1 month through 21 years of age at C1D1 with a locally advanced or metastatic solid tumor or primary CNS tumor that has relapsed, progressed or was nonresponsive to available therapies and for which no standard or available systemic curative therapy with a documented NTRK gene fusion (identified through molecular assays as routinely performed at CLIA or other similarly-certified laboratories) or (including Expansion Phase) potential patients older than 21 years of age with a tumor diagnosis with histology typical of a pediatric patient and an NTRK fusion may be considered for enrollment following discussion between the local site Investigator and the Sponsor's Medical Monitor.
- Karnofsky (those 16 years old or older) or Lansky (those younger than 16 years) performance score of at least 50
- Adequate hematologic function: Absolute neutrophil count (ANC) ≥ 1.0 10<sup>9</sup>/L, platelet count ≥ 100.0 10<sup>9</sup>/L and hemoglobin ≥ 8.0 g/dL (patients with bone marrow involvement will not be evaluable for hematologic DLT and can enroll with ANC ≥ 0.75 10<sup>9</sup>/L, platelet count ≥ 50.0 10<sup>9</sup>/L and hemoglobin ≥ 8.0 g/dL)
- Adequate hepatic function: Bilirubin (sum of conjugated + unconjugated) ≤ 1.5 upper limit of normal (ULN) for age (patients with documented Gilbert's Disease may be enrolled with Sponsor approval).



IntelliSpace Genomics™ **worklist** Akerman Philip ▾

**Chi Floren** MRN 1005 Gender Female DOB 08 Oct 1956 Ethnicity Not Hispanic or Latino + New Test

... Fusion analysis v1 Review Initial report Final report

Test Info Genomic Aberrations Therapy Match Clinical Trials

**Case Info**

Ordering physician	Jackson Elvira	Date of test	23 Feb 2017
Performing physician	Akerman Philip	Priority	routine
Diagnosis	Malignant neoplasm of thyroid gland	Reason	
Histopathology	Papillary adenocarcinoma, NOS	Site	Thyroid gland
Treatment status		Tumor Stage	Stage II
Additional copies to	none	Recent imaging info	
Test Number	199		

**Tumor - Specimen Info** **Tumor - Sample Info**

Specimen ID	236/34	Sample ID	A3BT_fusion
Specimen type	FFPE	Sample Received Date	06 Feb 2017
IHC Result	CK19 positive; CD 56 negative	Tumor percentage	50%
Collection method	Core Biopsy	Tumor grade	Grade 2
Specimen Collection Date	04 Feb 2017		

IntelliSpace Genomics™ **worklist** Akerman Philip ▾

**Chi Floren** MRN 1005 Gender Female DOB 08 Oct 1956 Ethnicity Not Hispanic or Latino + New Test

... Fusion analysis v1 Review Initial report Final report

Test Info Genomic Aberrations Therapy Match Clinical Trials

2 Filtered results | 2 Genomic aberrations selected

Fusion - Total reads  Aberration type  Clear all filters

Gene 5'	Junction 5'	Strand 5'	Gene 3'	Junction 3'	Strand 3'	Total Reads	COSMIC	Akerman Philip
ETV6	12006360	+	NTRK3	88576276	-	26	Matches mutation(s) wit...	✓
MKRN1	140159033	-	BRAF	140487384	-	30	Matches mutation(s) wit...	✓
<b>Clinical</b>	COSMIC ID	COSF1013	COSMIC ID	COSF1014	COSMIC ID	COSF1015		
	COSMIC ID	COSF1016	COSMIC ID	COSF1017	COSMIC ID	COSF1189		
	COSMIC ID	COSF1190	COSMIC ID	COSF1191	COSMIC ID	COSF1192		
	COSMIC ID	COSF1193	COSMIC ID	COSF1194	COSMIC ID	COSF1226		
	COSMIC ID	COSF1227	COSMIC ID	COSF1228	COSMIC ID	COSF1229		
	COSMIC ID	COSF1283	COSMIC ID	COSF1284	COSMIC ID	COSF1440		
	COSMIC ID	COSF1441	COSMIC ID	COSF1442	COSMIC ID	COSF1443		
	COSMIC ID	COSF1444	COSMIC ID	COSF1445	COSMIC ID	COSF1471		
	COSMIC ID	COSF1472	COSMIC ID	COSF1474	COSMIC ID	COSF1475		
	COSMIC ID	COSF1476	COSMIC ID	COSF1477	COSMIC ID	COSF1483		
	COSMIC ID	COSF1484	COSMIC ID	COSF1611	COSMIC ID	COSF1649		
	COSMIC ID	COSF1650	COSMIC ID	COSF1651	COSMIC ID	COSF1652		

IntelliSpace Genomics™ worklist Akerman Philip ▾

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... Fusion analysis v1 Review Initial report Final report

Test Info Genomic Aberrations **Therapy Match** Clinical Trials

### Therapy Match

Gene	Sequence Change	Aberration	Variant Qualifier	Treatment approach
BRAF	NA	MKRN1-BRAF fusion		<p>Braf signals upstream of the MAPK pathway, and BRAF amplification or activating alterations may confer sensitivity to inhibitors of Braf and/or components of the MAPK pathway, including MEK (Solit et al., 2006; 16273091). Sorafenib, an inhibitor of several tyrosine kinases, including Raf-1 and both wild-type and mutant Braf, has been approved in advanced renal cell carcinoma, advanced hepatocellular carcinoma, and some types of advanced thyroid carcinoma, and is in clinical trials in multiple tumor types (Hasskarl, 2014; 24756790). Braf and Raf-1 are among the targets of regorafenib, a multi-kinase inhibitor that is FDA-approved to treat metastatic colorectal cancer and advanced gastrointestinal stromal tumors (GIST) (Aprile et al., 2013; 23435872, Wilhelm et al., 2011; 21170960, Grothey et al., 2013; 23177514, Demetri et al., 2013; 23177515). Additional drug candidates targeting Braf and/or components of the downstream MAPK pathway, such as MEK, are under clinical investigation (Flaherty et al., 2012; 23020132). The MEK inhibitors trametinib and cobimetinib (in combination with vemurafenib) have been FDA-approved for BRAF V600E- and V600K-mutant melanoma and are currently being studied in clinical trials in solid tumors (Flaherty et al., 2012; 22663011, Larkin et al., 2014; 25265494). In addition, the combination of dabrafenib and trametinib has received accelerated FDA approval in BRAF-mutant melanoma (Menzies and Long, 2014; 24583796, Flaherty et al., 2012; 23020132). Inhibition of Hsp90 leads to the degradation of oncogenic proteins, such as Braf, which suggests that Hsp90 inhibitors may be particularly effective in malignancies with activating BRAF mutations, as well as malignancies where proteotoxic stress is involved (Banerji, 2009; 19118027, Neckers and Workman, 2012; 22215907).</p>

**Aberration effect**

The MKRN1-BRAF rearrangement reported here is expected to result in a fusion of the N-terminal portion of the Mkrn1 protein with the C-terminal portion of Braf, including the kinase domain (Kasaian et al., 2015; 26680454, Smallridge et al., 2014; 24297791, Jones et al., 2013; 23817572). Other BRAF rearrangements that result in the removal of the N-terminal inhibitory domain, but retention of the kinase domain, have been reported to result in constitutive Braf activation (Cin et al., 2011; 21424530, Forshew et al., 2009; 19373855, Jones et al., 2008; 18974108, Jones et al., 2013; 23817572). Therefore, although the BRAF rearrangement reported here has not been functionally characterized (PubMed, Nov 2016), it is predicted to be activating.

**FDA approved therapies within indication**  
**Sorafenib**

**FDA approved therapies outside this indication**  
**Sorafenib, Regorafenib, Trametinib, Cobimetinib**

**Investigational therapies within indication**  
**Regorafenib, Trametinib, Cobimetinib, Selumetinib, Ganetespib, Binimetinib, Defactinib, PDO325901, Refametinib, Pimasertib**

**Resistance and Interactions**  
**No available data**

**Guidelines**  
**No available data**

[Detailed therapeutic relevance](#)

IntelliSpace Genomics™ worklist Akerman Philip ▾

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... Fusion analysis v1 Review Initial report Final report

Test Info Genomic Aberrations Therapy Match **Clinical Trials**

### Clinical Trials

<b>A Phase I Trial of Single Agent Trametinib (GSK1120212) in Advanced Cancer Patients With Hepatic Dysfunction</b>			Recruiting
Target	Nearest Location	450 Brookline Ave, Boston, MA 02215, USA (267.44M)	<a href="#">NCT02070549</a>
Age Group	Contact	18 Years and older	
<b>A Phase 2 Study of Trametinib in Combination With Radioiodine (RAI) for RAS Mutant or RAS/RAF Wild-Type, RAI-Refractory Recurrent, and/or Metastatic Thyroid Cancers</b>			Recruiting
Target	Nearest Location	1275 York Ave, New York, NY 10065, USA (85.42M)	<a href="#">NCT02152995</a>
Age Group	Contact	18 Years and older	
<b>A Phase IB Study of the Combination of AZD6244 Hydrogen Sulfate (Selumetinib) and Cyclosporin A (CsA) in Patients With Advanced Solid Tumors With an Expansion Cohort in Metastatic Colorectal Cancer</b>			Recruiting
Target	Nearest Location	195 Little Albany St, New Brunswick, NJ 08903, United States (54.84M)	<a href="#">NCT02188264</a>
Age Group	Contact	18 Years and older	
<b>A Phase 1/Ib Study of MGCD516 in Patients With Advanced Solid Tumor Malignancies</b>			Recruiting
Target	Nearest Location	630 W 168th St, New York, NY 10032, USA (89.94M)	<a href="#">NCT02219711</a>
Age Group	Contact	Mirati Therapeutics Study Locator Services 1-844-356-0895 (toll-free) miratistudylocator@emergingmed.com	

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Test Info Genomic Aberrations Therapy Match Clinical Trials

Gene	Sequence Change	Aberration	Variant Qualifier	Treatment approach
NTRK3	NA	ETV6-NTRK3 fusion		<p>There are currently no approved therapies targeting NTRK3 alterations. However, several kinase inhibitors targeting the Trk family are currently under investigation in clinical trials. The pan-Trk inhibitors LOXO-101 and entrectinib have shown efficacy in multiple tumor types harboring both NTRK mutations and gene fusions (Hong et al., 2016; AACR 2016, Abstract CT008, Doebele et al., 2015; 26216294, De Braud et al., 2015; ASCO 2015, Abstract 2517, Drilon et al., 2016; AACR 2016, Abstract CT007, Ardini et al., 2016; 26939704, Iyer et al., 2016; 26797418). Other agents also reported to inhibit Trk activity, including the FDA-approved Aik inhibitor crizotinib, are also in clinical trials (Awad and Shaw, 2014; 25322323, Vaishnavi et al., 2015; 25527197, Reungwetwattana and Dy, 2013; 24574860, Ivanov et al., 2013; 23027130, Tatematsu et al., 2014; 25054037).</p>

FDA approved therapies within indication  
**No available data**

FDA approved therapies outside this indication  
**Crizotinib**

Investigational therapies within indication  
**Crizotinib , LOXO-101 , Entrectinib , PLX7486 , DS-6051b , MGCD516 , Alitratinib**

Resistance and Interactions  
**No available data**

Guidelines  
**No available data**

[Detailed therapeutic relevance](#)

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**Aberration effect**

The ETV6-NTRK3 (EN) fusion involves the N-terminal portion of the Etv6 protein, including its sterile- $\alpha$  motif domain, and the C-terminal region of the TrkC protein, including its protein kinase domain (Cetinbas et al., 2013; 23798677, Ricarte-Filho et al., 2013; 24135138). The EN fusion has been reported as a highly recurrent alteration in multiple cancer types (including mesoblastic nephroma, infantile fibrosarcoma, secretory breast carcinoma, mammary analog secretory carcinoma [MASC], and papillary thyroid carcinoma) and has been reported to transform normal cell lines and promote tumor cell growth (El et al., 2016; 27020209, Orbach et al., 2016; 26849118, Weigelt et al., 2010; 20452298, Luo et al., 2014; 25674280, Leeman-Neill et al., 2014; 24327398, Ricarte-Filho et al., 2013; 24135138, Tognon et al., 2002; 12450792). A case study of a patient with a MASC tumor that harbored an EN fusion and had recurred after initially responding to crizotinib reported that entrectinib treatment induced a best radiologic response of an 89% reduction in tumor burden; the disease recurred at seven months after acquisition of another NTRK3 mutation that was found to mediate entrectinib resistance in preclinical studies (Drilon et al., 2016; 26884591). In addition, preclinical studies have reported that the EN fusion is associated with crizotinib and dostaurin sensitivity in cell and animal models of cancer (Chi et al., 2012; 1561, Roberts et al., 2014; 25207766, Taipale et al., 2013; 23811600).

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Test Info Genomic Aberrations Therapy Match Clinical Trials

<p><b>A Phase 1, Multicenter, Open-Label Study of Oral Entrectinib (RXDX-101) in Adult Patients With Locally Advanced or Metastatic Cancer Confirmed to be Positive for NTRK1, NTRK2, NTRK3, ROS1, or ALK Molecular Alterations</b></p> <p>Target: NTRK3</p> <p>Age Group: 18 Years and older</p> <p>Nearest Location: 1275 York Ave, New York, NY 10065, USA (85.42M)</p> <p>Contact: Ignyta, Inc. 858-255-5959</p>	<p>Recruiting</p> <p><a href="#">NCT02097810</a></p>
<p><b>A Phase 1 Study of the Oral TRK Inhibitor LOXO-101 in Adult Patients With Solid Tumors</b></p> <p>Target: NTRK3</p> <p>Age Group: 18 Years and older</p> <p>Nearest Location: Philadelphia, PA 19104, USA (11.75M)</p> <p>Contact: Patient Advocacy 1-855-NTRK-123 clinicaltrials@loxooncology.com</p>	<p>Recruiting</p> <p><a href="#">NCT02122913</a></p>
<p><b>A Phase 1, Two-Part, Multi-Center, Non Randomized, Open-Label, Multiple Dose First-In-Human Study Of DS-6051b, An Oral ROS1 And NTRK Inhibitor, In Subjects With Advanced Solid Tumors</b></p> <p>Target: NTRK3</p> <p>Age Group: 18 Years and older</p> <p>Nearest Location: 450 Brookline Ave, Boston, MA 02215, USA (267.44M)</p> <p>Contact: Aaron Logue, MBA 513-579-9911 A.Logue@Medpace.com</p>	<p>Recruiting</p> <p><a href="#">NCT02279433</a></p>
<p><b>A Phase II Basket Study of the Oral TRK Inhibitor LOXO-101 in Subjects With NTRK Fusion-Positive Tumors</b></p> <p>Target: NTRK3</p> <p>Age Group: 18 Years and older</p> <p>Nearest Location: 130 S 9th St, Philadelphia, PA 19107, USA (9.82M)</p> <p>Contact: Maegan Deegan 1-855-NTRK-123 maegan@loxooncology.com</p>	<p>Recruiting</p> <p><a href="#">NCT02576431</a></p>

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### Study of LOXO-101 in Subjects With NTRK Fusion Positive Solid Tumors (NAVIGATE)

**This study is currently recruiting participants. (see Contacts and Locations)**  
 Verified November 2016 by Loxo Oncology, Inc.

**Sponsor:**  
 Loxo Oncology, Inc.

**Information provided by (Responsible Party):**  
 Loxo Oncology, Inc.

**ClinicalTrials.gov Identifier:**  
 NCT02576431

First received: October 12, 2015  
 Last updated: November 16, 2016  
 Last verified: November 2016  
[History of Changes](#)

[Full Text View](#) | [Tabular View](#) | [No Study Results Posted](#) | [Disclaimer](#) | [How to Read a Study Record](#)

**Purpose**

Phase II, multi-center, open-label study of patients with advanced solid tumors harboring a fusion of NTRK1, NTRK2 or NTRK3.

Condition	Intervention	Phase
Carcinoma, Non-Small-Cell Lung Thyroid Neoplasms Sarcoma Colorectal Neoplasms Salivary Gland Neoplasms	Drug: LOXO-101	Phase 2

Secure <https://clinicaltrials.gov/ct2/show/NCT02576431>

**Eligibility**

Ages Eligible for Study: 18 Years and older (Adult, Senior)  
 Sexes Eligible for Study: All  
 Accepts Healthy Volunteers: No

**Criteria**

**Key Inclusion Criteria:**

- Locally-advanced or metastatic malignancy with an NTRK1, NTRK2 or NTRK3 gene fusion, identified through molecular assays as routinely performed at CLIA or other similarly-certified laboratories.
- Subjects must have received prior standard therapy appropriate for their tumor type and stage of disease, or in the opinion of the Investigator, would be unlikely to tolerate or derive clinical benefit from appropriate standard of care therapy.
- Subjects must have at least one measurable lesion as defined by RECIST 1.1 (Eisenhauer 2009). Subjects without RECIST measurable disease (e.g., evaluable disease only) will be eligible for enrollment to Cohort 8, regardless of tumor type. Subjects in Cohort 7 (primary CNS tumors) should meet the following criteria:
  - Have received prior treatment including radiation and/or chemotherapy, with radiation completed > 12 weeks prior to C1D1 of therapy.
  - Have ≥ 1 site of bi-dimensionally measurable disease (confirmed by magnetic resonance imaging [MRI] and evaluable by RANO criteria), with the size of at least one of the measurable lesions ≥ 1 cm in each dimension and noted on more than one imaging slice.
  - Imaging study performed within 28 days before enrollment while on stable dose steroid medication for at least 5 days immediately before and during the imaging study.
- Adequate organ function as defined by the following criteria:
  - Serum aspartate transaminase (AST) and serum alanine transaminase (ALT) < 2.5 upper limit of normal (ULN), or AST and ALT < 5 ULN if liver function abnormalities are due to underlying malignancy.
  - Total bilirubin < 2.0 ULN. Subjects with a known history of Gilberts Disease and an isolated elevation of indirect bilirubin are eligible.
  - Serum creatinine < 2.0 ULN OR an estimated glomerular filtration rate ≥ 30 mL/minute using the Cockcroft-Gault formula.
- Ability to swallow capsules,

**Key Exclusion Criteria:**

- Symptomatic or unstable brain metastases. (Note: Subjects with asymptomatic brain metastases are eligible to participate in the study). Subjects with primary CNS tumors are eligible.
- Pregnancy or lactation.

**Contacts and Locations**

Choosing to participate in a study is an important personal decision. Talk with your doctor and family members or friends about deciding to join a study. To learn more about this study, you or your doctor may contact the study research staff using the Contacts provided below. For general information, see [Learn About Clinical Studies](#).



IntelliSpace Genomics™ worklist Akerman Philip ▾

**Kennedy John** MRN MR4567787 Gender Male DOB 03 Mar 1950 Ethnicity Not Hispanic or Latino + New Test

... SNV Annotation and Interpretation (VCF) Review Initial report Final report

Test Info **Genomic Aberrations** Therapy Match Clinical Trials

**Case Info**

Ordering physician	Jackson Elvira	Date of test	27 Feb 2017
Performing physician	Akerman Philip	Priority	routine
Diagnosis	Malignant neoplasm of bladder	Reason	
Histopathology	Transitional cell carcinoma, NOS	Site	Lateral wall of bladder
Treatment status	Not started	Tumor Stage	Stage III
Additional copies to	Adriana Angelica	Recent imaging info	
Test Number	233		

**Tumor - Specimen Info** **Tumor - Sample Info**

Specimen ID	AP-231	Sample ID	BladderCancer.snp.Somatic.hc
Specimen type	FFPE	Sample Received Date	06 Feb 2017
IHC Result	Ki-67 positive; Cytokeratin Positive	Tumor percentage	30%
Collection method	Core Biopsy	Tumor grade	Grade 2
Specimen Collection Date	04 Feb 2017		

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Test Info **Genomic Aberrations** Therapy Match Clinical Trials

Default SNV filters ▾ 18 Filtered results | 2 Genomic aberrations selected

**Quality**

Normal allele frequency  
from  % to  %

Tumor read depth

Tumor allele frequency

Fusion - Total reads

Clear filters values

Gene	Amino Acid Change	Location	Coordinate	Aberration Type	Tumor Read Depth	Tumor Allele Frequency	Akerman Philip
DNAH9	E1739Q	exonic	chr17:11607583	Nonsynonymous SNV	123	30.89%	⊖
EVC	A368T	exonic	chr4:5754566	Nonsynonymous SNV	104	37.5%	⊖
EVPL	G1147R;G1169R	exonic	chr17:74005847	Nonsynonymous SNV	84	34.52%	⊖
FGFR3	S249C;S69C	exonic	chr4:1803568	Nonsynonymous SNV	37	29.73%	✓
PCDH10	P322R	exonic	chr4:134072260	Nonsynonymous SNV	116	34.48%	⊖
PSMD11	H375Y	exonic	chr17:30807212	Nonsynonymous SNV	121	38.02%	⊖
SMCR8	Q778K	exonic	chr17:18221435	Nonsynonymous SNV	138	33.33%	⊖
TLR2	H398D	exonic	chr4:154625251	Nonsynonymous SNV	65	29.23%	⊖
TSC1	K630fs	exonic	chr9:135781073	Deletion	918	36.96%	✓
CLEC10A	Q66*	exonic	chr17:6980295	StopGain SNV	78	39.74%	⊖



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18 Filtered results | **2 Genomic aberrations selected**

Gene	Amino Acid Change	Location	Coordinate	Aberration Type	Tumor Read Depth	Tumor Allele Frequency	Akerman Philip
FGFR3	S249C;S69C	exonic	chr4:1803568	Nonsynonymous SNV	37	29.73%	✓
<b>N-of-One</b>	Aberration	S249C;FGFR3	Has approved therapies	yes	Has experimental therapies	yes	
	Infers resistance to therapies	no	Molecular effect	FGFR3 S249C is a ...			
<b>Genomic</b>	Gene	FGFR3	Strand	+	Location	exonic	
	Transcript ID	FGFR3:uc003gdq.3:+e ...	Chromosome	chr4	Position	1803568	
	Reference	C	Alternate	G	Variant type	SNV	
<b>Functional</b>	Aberration type	Nonsynonymous SNV	Amino acid change	S249C;S69C	Amino acid change detail	ENST00000481110:S249 ...	
	Ensembl gene ID	ENSG00000068078	SIFT score	0.0	SIFT prediction	D	
	Polyphen2 HDIV score	1.0	Polyphen2 HDIV prediction	D	Polyphen2 HVAR score	0.994	
	FATHMM score	-1.32	FATHMM prediction	T	Mutation assessor score	3.885	
	Mutation assessor prediction	H	LRT score	0.000000	LRT prediction	D	
			ExAC AF	8.325e-06	GERP++ NR	3.94	

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Test Info **Genomic Aberrations** **Therapy Match** Clinical Trials

### Therapy Match

Gene	Sequence Change	Aberration	Variant Qualifier
FGFR3	c.746C>G	p.Ser249Cys	

**Treatment approach**

FGFR3 amplification or mutations may lead to activation of Fgfr3 and may therefore confer sensitivity to Fgfr family inhibitors (Turner and Grose, 2010; 20094046, Socinski, 2011; 21641723). Several multi-kinase inhibitors that target Fgfrs, including pazopanib, ponatinib, and lenvatinib, have been FDA-approved for certain indications and continue to be studied in clinical trials (Schlumberger et al., 2015; 25671254, van der Graaf et al., 2012; 22595799, Sternberg et al., 2010; 20100962, Motzer et al., 2015; 26482279, Cortes et al., 2013; 24180494).

**Aberration effect**

FGFR3 S249C is a missense alteration located within the extracellular domain of the Fgfr3 protein (UniProt). FGFR3 S249C has been reported to be an activating alteration, leading to the induction of ligand-independent dimerization and activation of downstream signaling pathways (LogiÅ© et al., 2005; 15772091, Williams et al., 2013; 23175443, Tomlinson et al., 2007; 17384684, Adar et al., 2002; 12009017).

**FDA approved therapies within indication**  
No available data

**FDA approved therapies outside this indication**  
Pazopanib, Ponatinib, Nintedanib, Lenvatinib

**Investigational therapies within indication**  
Pazopanib, Ponatinib, Nintedanib, Lenvatinib, Dovitinib lactate, Lucitanib, JNJ-42756493, AZD4547, BGJ398, TAS-120, BAY1163877

**Resistance and Interactions**  
No available data

**Guidelines**  
No available data

[Detailed therapeutic relevance](#)

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**Molecular Analysis for Therapy Choice (MATCH)** Recruiting

Target	FGFR3	Nearest Location	1824 6th Ave S, Birmingham, AL 35233, USA (784.28M)	<a href="#">NCT02465060</a>
Age Group	18 Years and older	Contact		

**A Multicenter, Open-Label Phase 1b/2 Trial of Lenvatinib (E7080) Plus Pembrolizumab in Subjects With Selected Solid Tumors** Recruiting

Target	FGFR3	Nearest Location		<a href="#">NCT02501096</a>
Age Group	18 Years to 99 Years	Contact	Eisal Medical Services 1-888-422-4743	

**An Open-Label, Randomised, Multi-Drug, Biomarker-Directed, Multi-Centre, Multi-arm Phase 1b Study in Patients With Muscle Invasive Bladder Cancer (MIBC) Who Have Progressed on Prior Treatment (BISCAY).** Recruiting

Target	FGFR3	Nearest Location		<a href="#">NCT02546661</a>
Age Group	18 Years to 130 Years	Contact	AstraZeneca Clinical Study Information Center 1-877-240-9479 information.center@astrazeneca.com	

**A Phase 2a Study to Evaluate The Clinical Efficacy of JNJ-42756493, A Pan-Fibroblast Growth Factor Receptor (FGFR) Tyrosine Kinase Inhibitor, In Asian Patients With Advanced Non-Small-Cell Lung Cancer, Urothelial Cancer, Gastric Cancer, Esophageal Cancer Or Cholangiocarcinoma** Recruiting

Target	FGFR3	Nearest Location		<a href="#">NCT02699606</a>
Age Group	18 Years and older	Contact	Use link at the bottom of the page to see if you qualify for an enrolling site (see list). If you still have questions: JNJ.CT@sylogent.com	

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TSC1	K630fs	exonic	chr9:135781073	Deletion	918	36.96%	✔
<b>N-of-One</b>	Aberration	K630fs,TSC1	Has approved therapies	yes	Has experimental therapies	yes	
	Infers resistance to therapies	no	Molecular effect	TSC1 K630fs is ...			
<b>Genomic</b>	Gene	TSC1	Strand	-	Location	exonic	
	Transcript ID	TSC1.uc004cca.2--ex ...	Chromosome	chr9	Position	135781073	
	Reference	GCTTT	Alternate	G	Variant type	Deletion	
<b>Clinical</b>	COSMIC ID	COSM5010413	COSMIC match summary	SameNucleotideChange			

IntelliSpace Genomics™ worklist Akerman Philip ▾

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... SNV Annotation and Interpretation (VCF) Review Initial report Final report

Test Info	Genomic Aberrations	Therapy Match	Clinical Trials
Gene TSC1	Sequence Change c.1888_1891delAAAG	Aberration p.Lys630fs	Variant Qualifier
<p>FDA approved therapies within indication <b>No available data</b></p> <p>FDA approved therapies outside this indication <b>Everolimus, Temozolimus</b></p> <p>Investigational therapies within indication <b>Everolimus, Temozolimus, Ridaforolimus, CC-223, AZD2014, Sapanisertib, Apatolisib, LY3023414, PQR309, PF-05212384, SF112</b></p> <p>Resistance and Interactions <b>No available data</b></p> <p>Guidelines <b>No available data</b></p> <p><a href="#">Detailed therapeutic relevance</a></p> <p>Powered by N-of-One®</p>			<p>Treatment approach</p> <p>Currently no therapies directly targeting inactivation of Hamartin are approved or are under investigation in clinical trials. Loss or inactivation of TSC1 leads to activation of mTOR and therefore may predict sensitivity to mTOR inhibitors (Kuo et al., 2010; 20145209, Inoki et al., 2003; 12869586, Tee et al., 2003; 12906785). In a number of cancer types (including bladder, breast, thyroid, and PEComa), patients who have had exceptional responses to mTOR inhibitors have been found to harbor TSC1 or TSC2 inactivating alterations (Palma et al., 2014; SABCS 2014, Abstract P2-03-06, Iyer et al., 2012; 22923433, Wagle et al., 2014; 25295501, Wagner et al., 2010; 20048174, Dickson et al., 2013; 22927055, Lim et al., 2016; 26859683). The mTOR inhibitors everolimus and temsirolimus have been FDA approved for some indications. Everolimus has been approved in subependymal giant cell astrocytoma associated with tuberous sclerosis (due to TSC1 or TSC2 inactivation), as well as for other indications. These agents and other mTOR inhibitors are being studied in clinical trials in multiple tumor types (Lebwohl et al., 2013; 23659703, Bergmann et al., 2014; 24313573, Franz, 2013; 24143074).</p> <p><b>Aberration effect</b></p> <p>TSC1 K630fs is expected to effectively truncate the Hamartin protein at amino acid 630 of 1165, resulting in loss of the coiled coil domain (UniProt) (Hodges et al., 2001; 11741833). This truncation would not be expected to affect the Tuberin-binding region of Hamartin (Hodges et al., 2001; 11741833). However, a preclinical study reported that the N-terminal portion of Hamartin is required for stable Hamartin protein expression and Hamartin-Tuberin complex formation, as N-terminal truncations, including those at R509 and R692, resulted in reduced Hamartin stability and weak interaction with Tuberin (Hoogeveen-Westerveld et al., 2010; 10547222). Therefore, this alteration is predicted to be inactivating.</p>

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IntelliSpace Genomics™ worklist Akerman Philip ▾

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- Biomarker specific clinical trial matching

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