



Genomics of “Wild-Type” GIST: Domestication In Progress

Jason Sicklick, MD

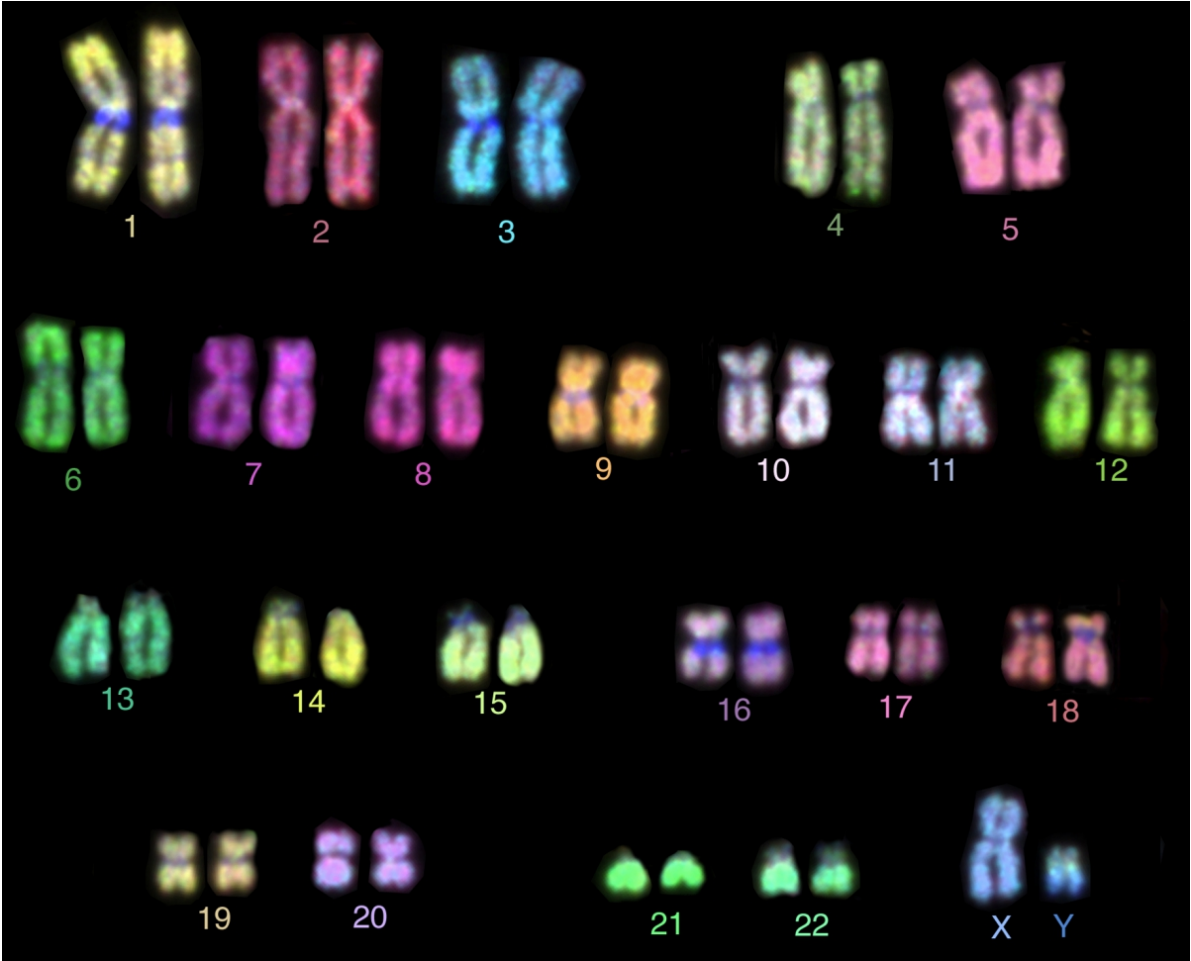
Associate Professor of Surgery



Where discoveries are delivered.SM

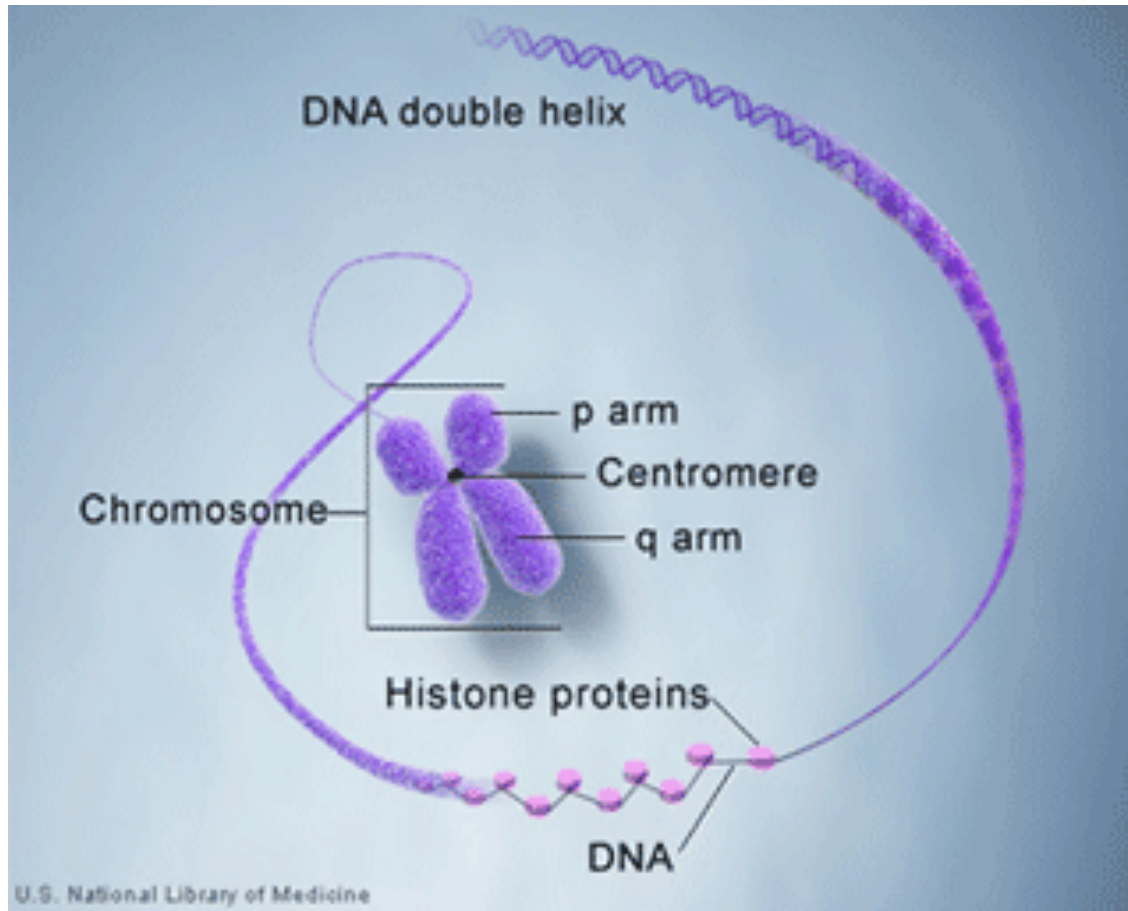
UC San Diego
HEALTH SYSTEM

Genomics 101



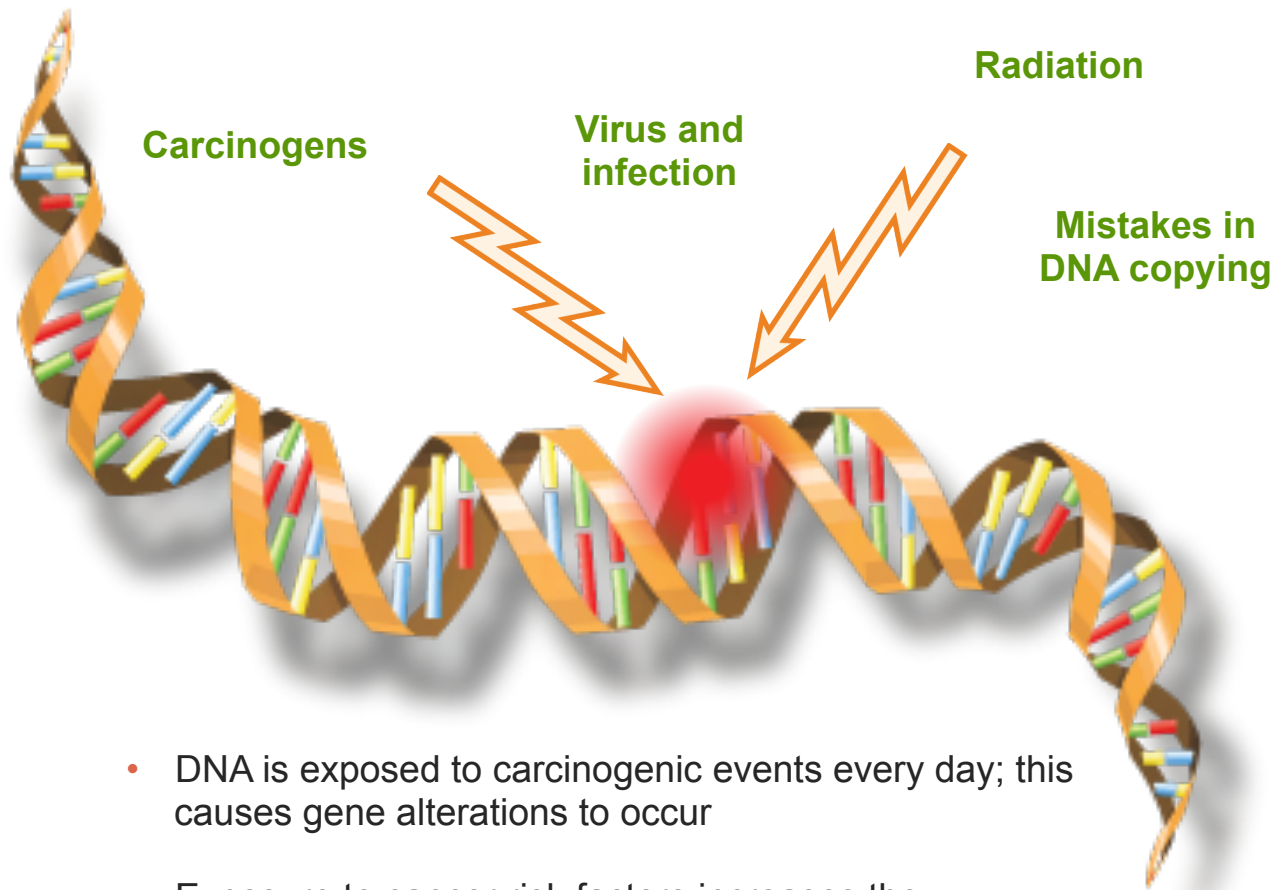
23 + 23 = 46 chromosomes

Genomics 101



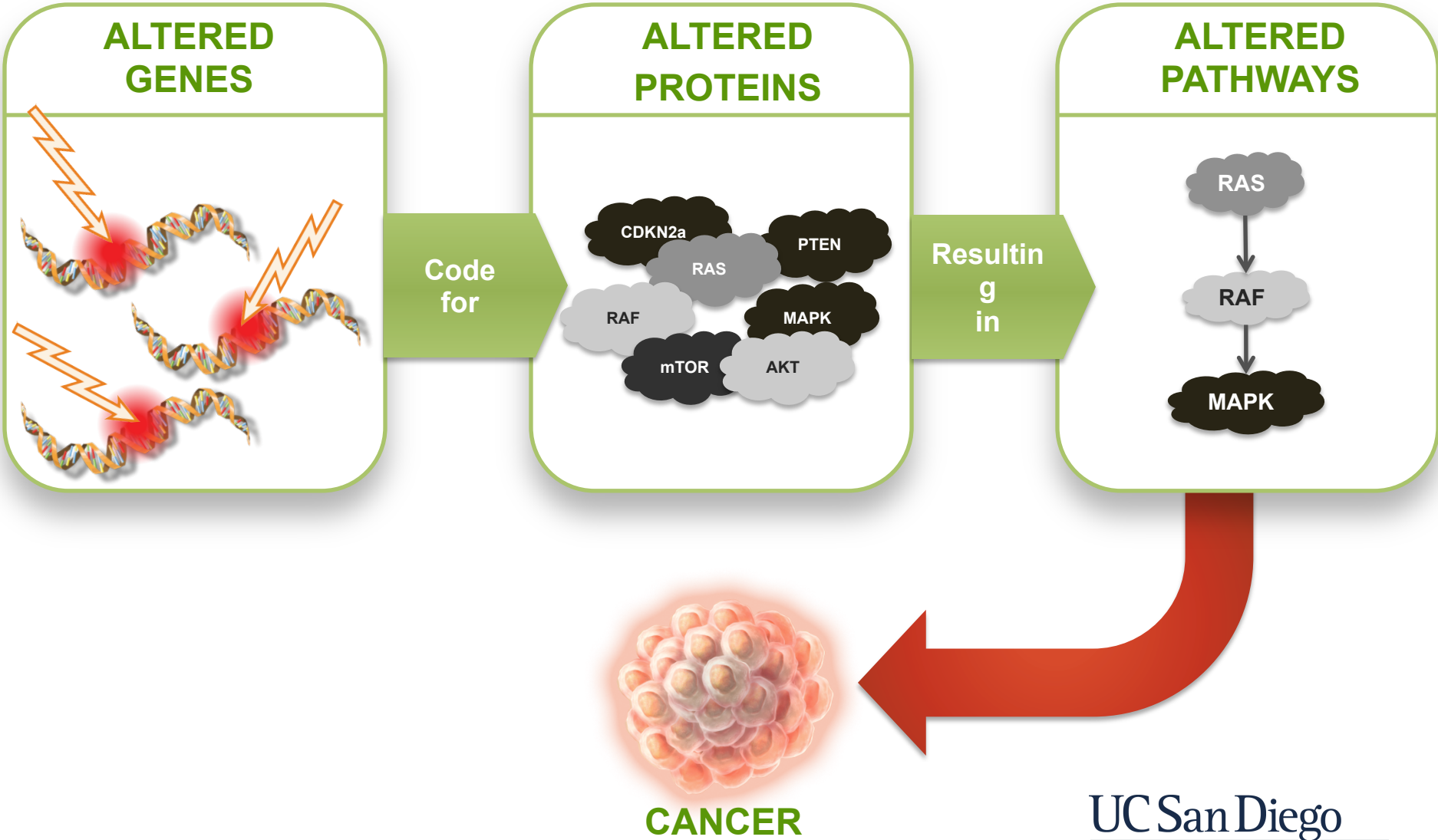
A = T
C ≡ G

Cancer Is A Disease Of The Genome

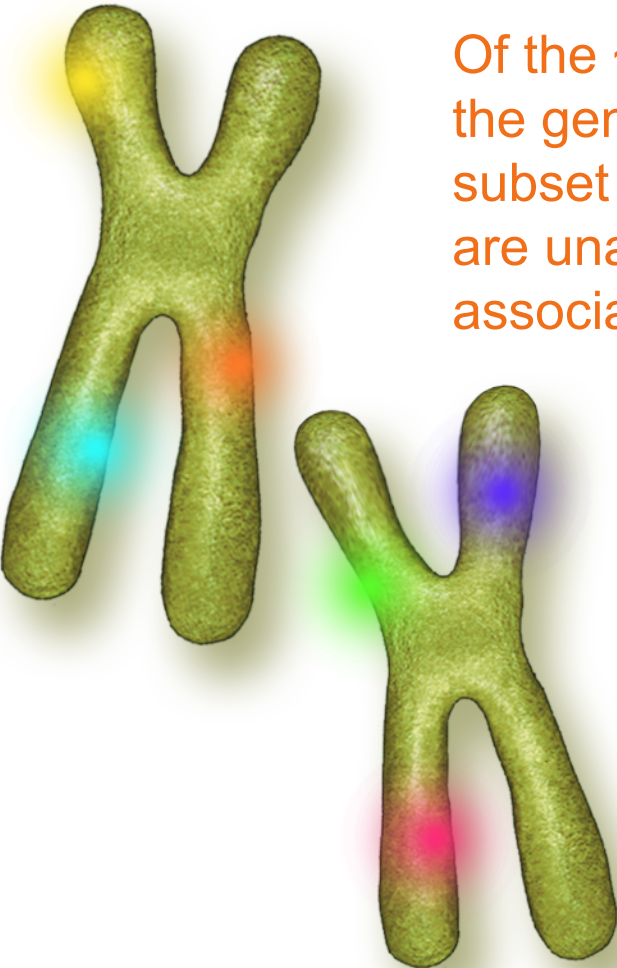


- DNA is exposed to carcinogenic events every day; this causes gene alterations to occur
- Exposure to cancer risk factors increases the chances of gene alterations

How Gene Alterations Can Cause Cancer



Cancer Related Genes



Of the ~20,000 genes in the genome, only a subset of a few hundred are unambiguously associated with cancer

Gene names
<i>KIT</i>
<i>PDGFRA</i>
<i>BRAF</i>
<i>KRAS</i>
<i>HRAS</i>
<i>NRAS</i>
<i>FGFR1</i>

Types Of Alterations In Cancer Genes



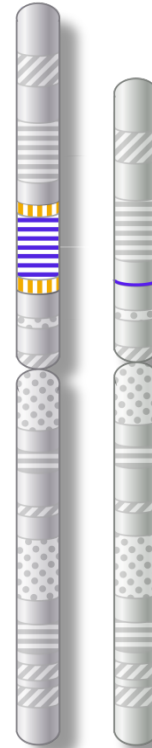
Normal



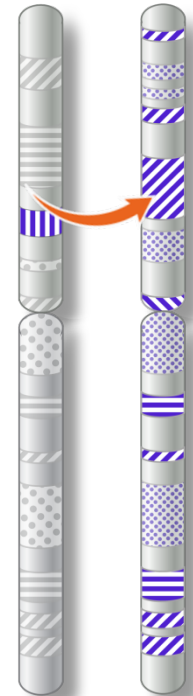
Copy number alterations



Substitutions (Missense)



Insertions and deletions



Rearrangements
Fusions

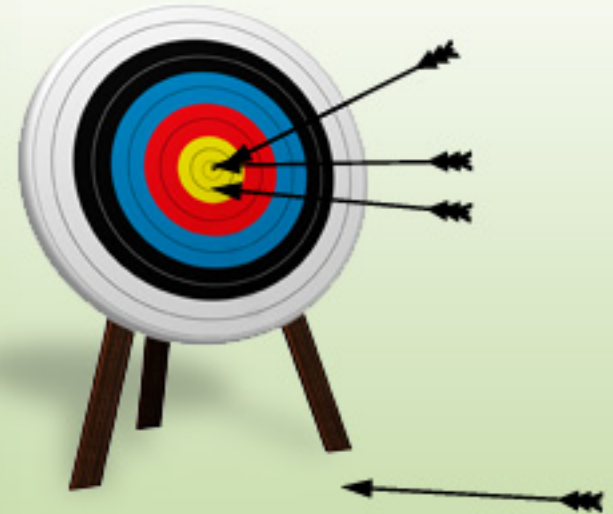
The Shift Toward Targeted Therapy

Chemotherapy



- Anticancer drugs may be highly effective in some, but less effective in others
- Patients encounter side effects which are often significant

Targeted Therapy

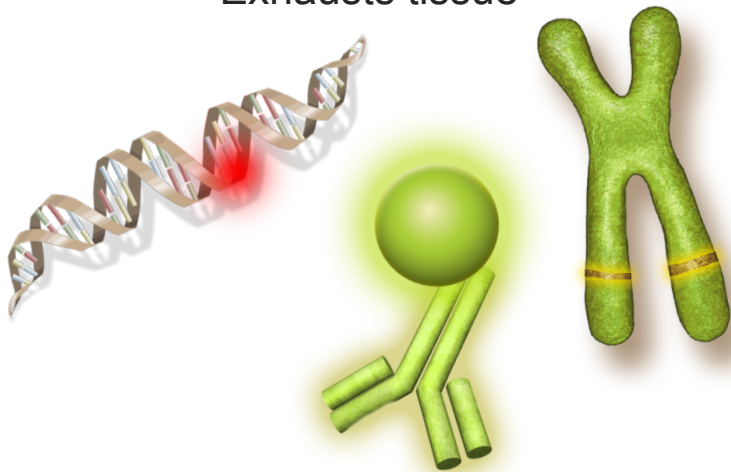


- In personalized medicine, clinicians use biomarkers to predict a patient's response to therapy
- Patients are more likely to get therapies with the greatest impact which often have fewer side effects

Advantages Of Comprehensive Genomic Profiling (CPG) vs. Traditional Hot Spot Testing

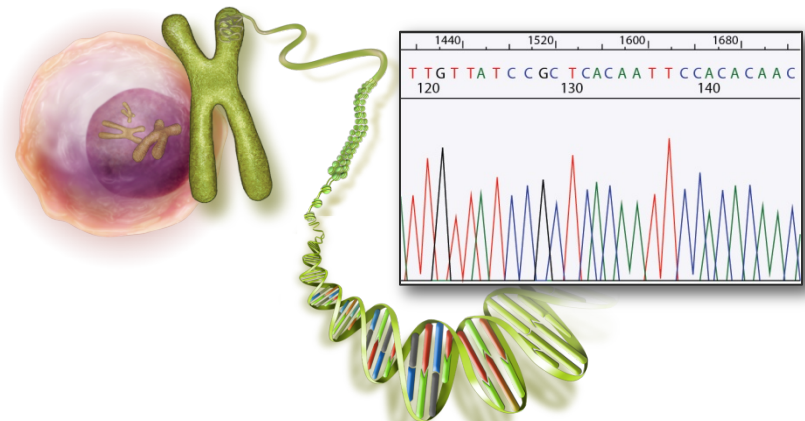
Hot Spot or Single-Marker Testing

- Misses some types of mutations (rearrangements/fusions, copy number alterations)
- Limited number of alterations screened at once
- Results are specific for the test used: need to know ahead of time what questions to ask
- Exhausts tissue



CGP

- Able to identify hundreds of clinically relevant mutations at once
- Allows the opportunity to identify all alterations
- Tissue sparing



CPG vs. Hot Spot

Alterations Detected

Normal



CGP

Hot Spot

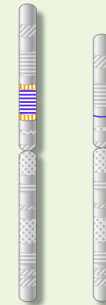
Substitutions
Missense



Copy number
alterations



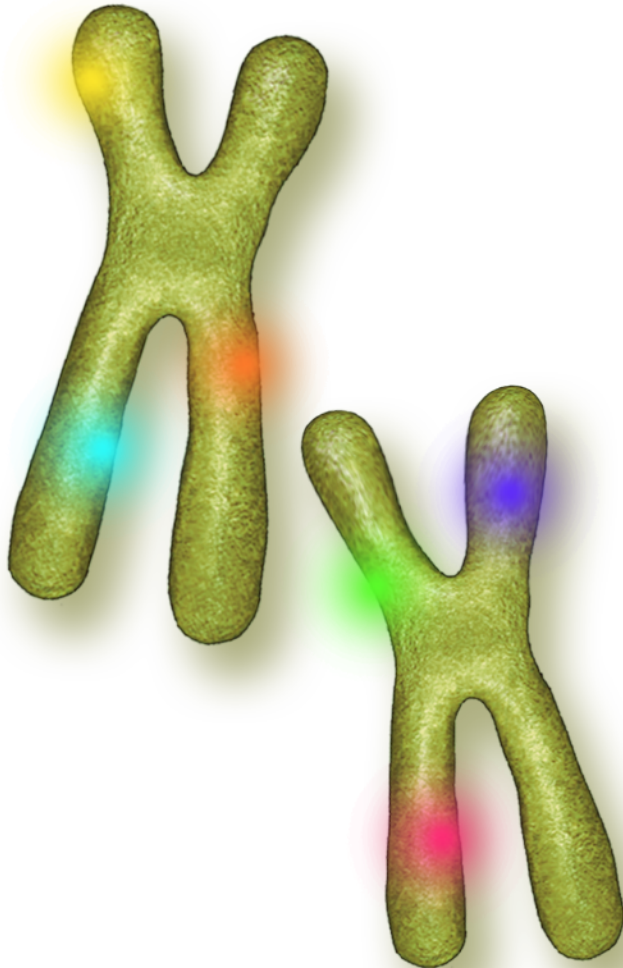
Insertions and
deletions



Rearrangements
Fusions

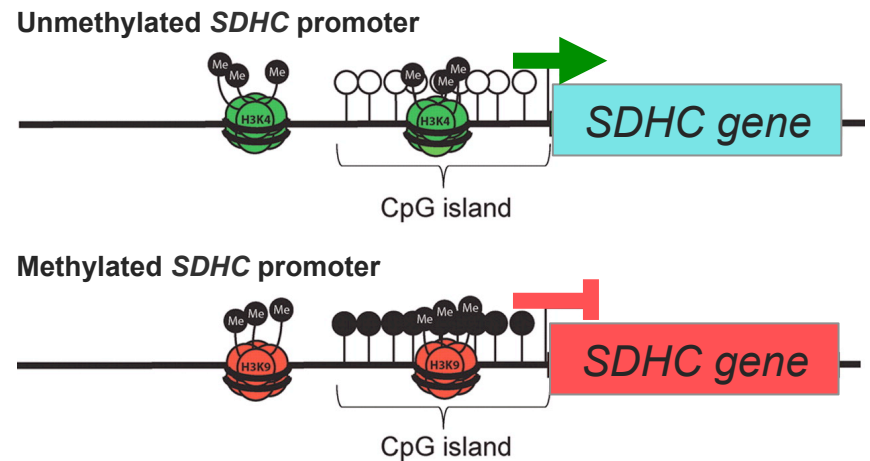
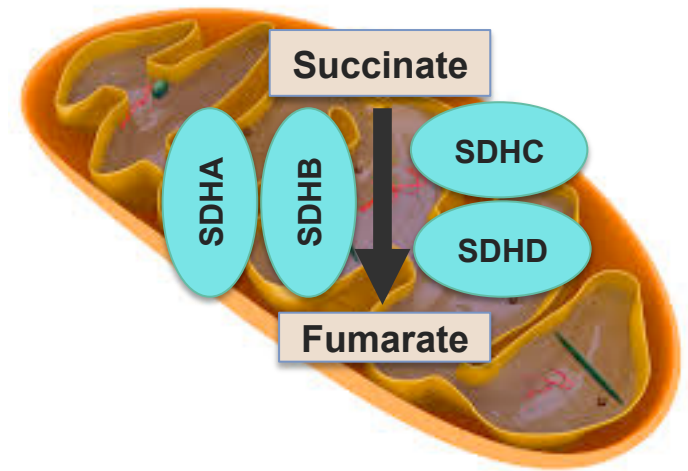
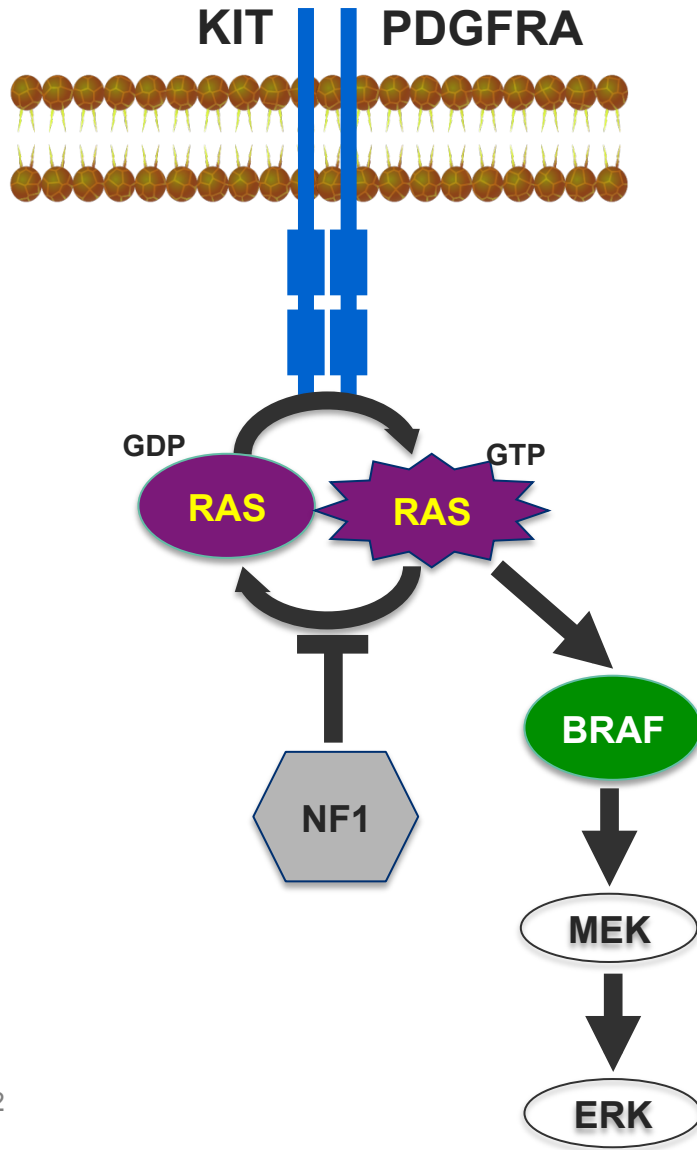


Cancer Related Genes in GIST



Gene names
<i>KIT</i>
<i>PDGFRA</i>
<i>BRAF</i>
<i>KRAS</i>
<i>HRAS</i>
<i>NRAS</i>
<i>FGFR1</i>

Known Driver Genes in 85-90% of GIST



Corless et al., *Nature Reviews Cancer*. 2011.
 Pantaleo et al., *Cancer Medicine*. 2015.
 Killian et al., *Sci Transl Medicine*. 2014.

Lack Mutations in *KIT*, *PDGFRA*, RAS Pathway (*NF1*, *RAS*, *BRAF*) and *SDH* Subunits

Quadruple Wild-type (qWT) GIST

SDHB+
IGF1R-

Any age?
Equal sex?
Site?
Multifocality?

- **Genomics?**
- **Epidemiology?**
- **Disease Biology?**

Hypothesis

Broad genomic profiling of “quadruple-WT (qWT)” GISTs would reveal insights into the genomic alterations and disease biology of this understudied patient population.

Methods

Patient Population and Data Collection

- Foundation Medicine, Inc. (FMI) database consisting of de-identified patients from across the U.S. (October 2012 – May 2015).
- Retrospectively analyzed this prospectively collected data.

Broad Genomic Profiling

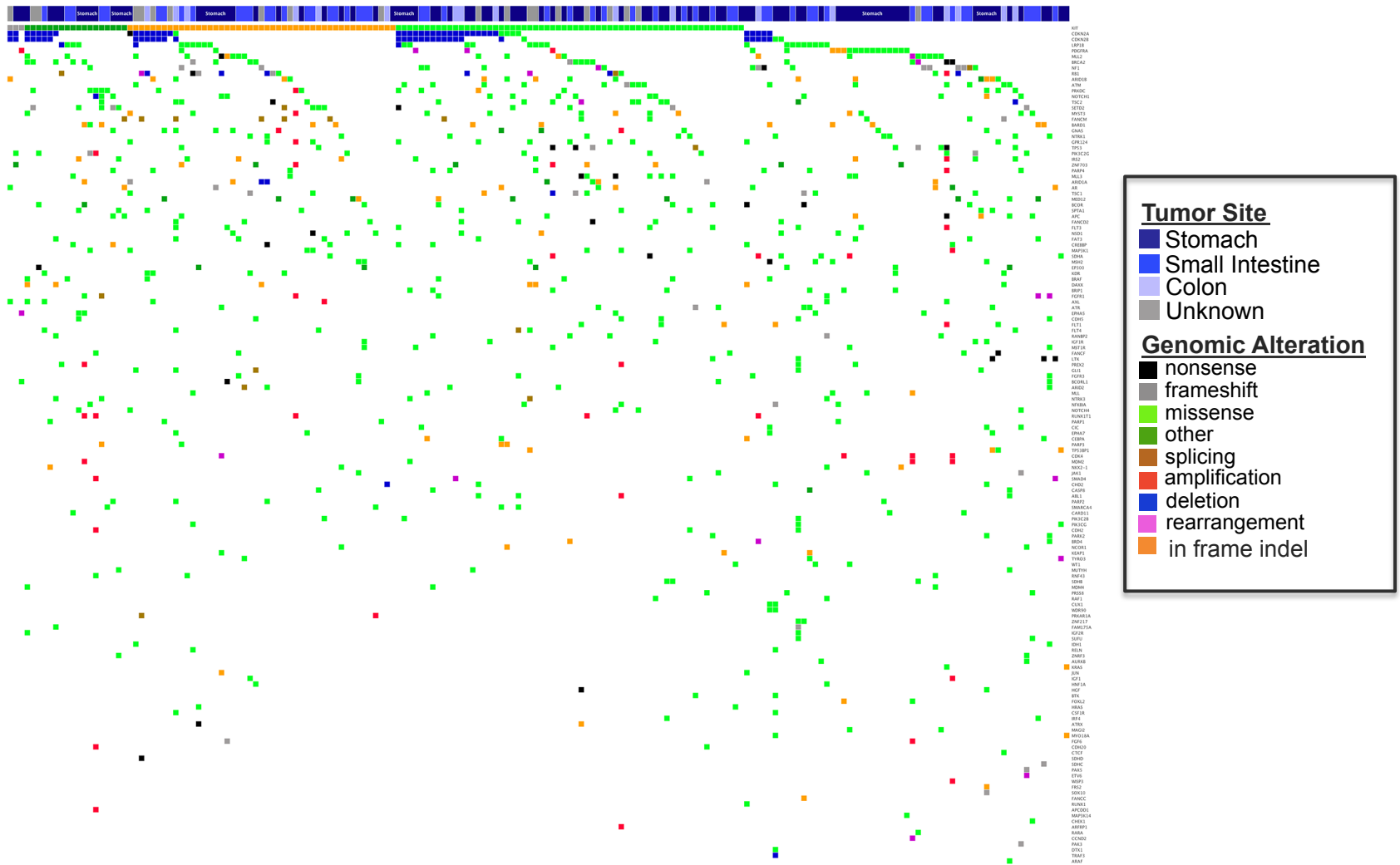
- DNA was extracted from FFPE tumor specimens.
- NGS assay utilizes the Illumina HiSeq 2500 instrument to sequence against hybridization-captured, adaptor ligation-based libraries for coding regions of 315 cancer-related genes plus introns from 28 genes frequently implicated in cancer transformation.

Methods (Continued)

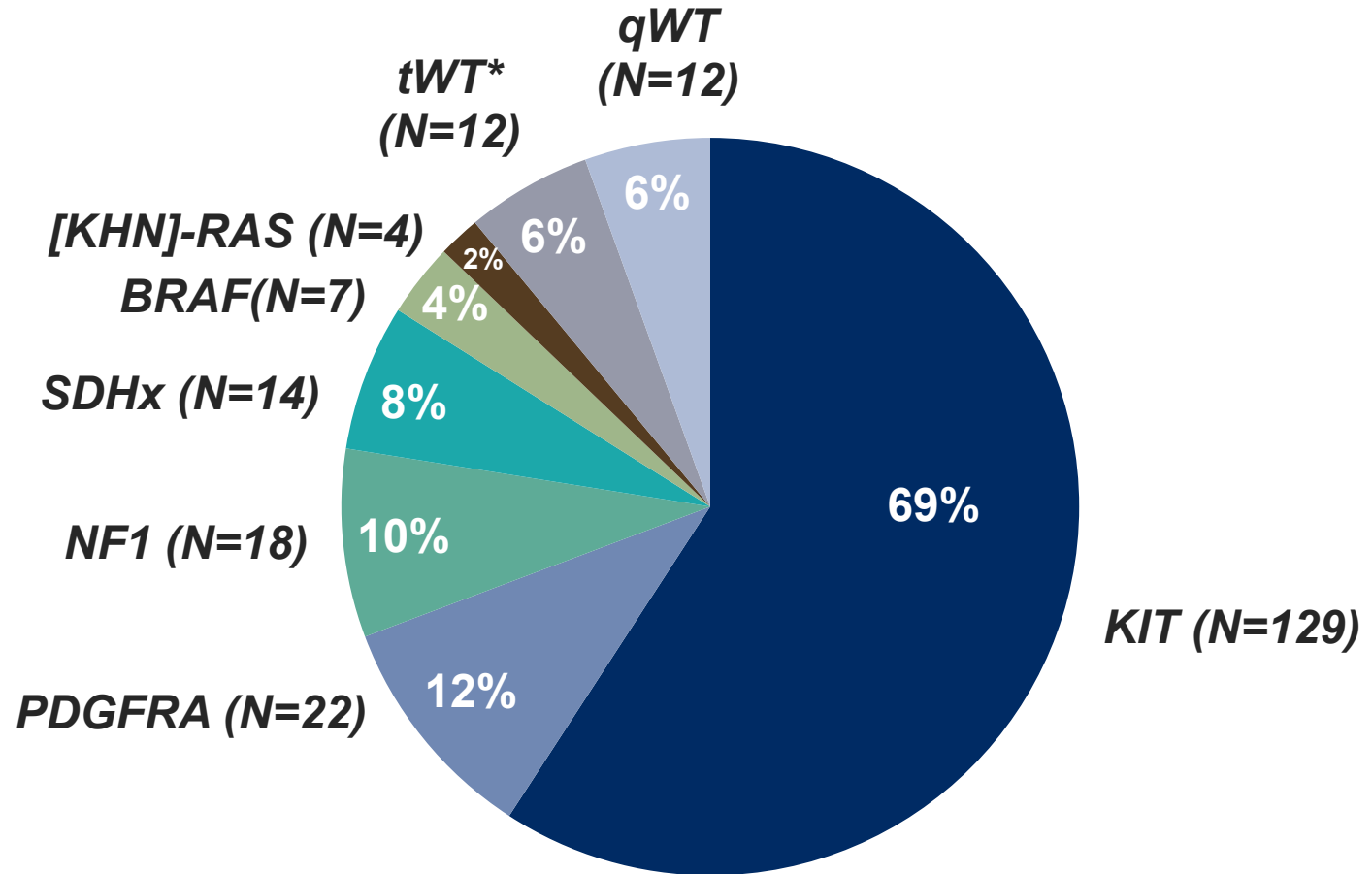
Data Analysis

- Genomic alterations were further categorized:
 - Known somatic
 - Likely somatic
 - Variant of unknown significance (VUS).
- To understand of the potential deleterious effects of all missense VUS's, we analyzed them with 4 prediction modeling programs (SIFT, PolypPhen, MutationTaster, and MutationAssessor).
- Considered *potentially deleterious* if they were predicted deleterious by $\geq 50\%$ tools. Of 1240 VUS's, we considered 325 (26.2%) potentially deleterious.
- Exome Aggregation Consortium (ExAC) Browser was used to exclude *missense variants* with a minor allele frequency $> 1\%$ (*NOTCH2*, *FANCD2*, *MAP3K1*, *MSH3*, and *ZNF217*).

Somatic Genomic Landscape in 186 GIST



Driver Mutations in 186 GIST



*tWT** = sequencing performed before FMI testing of SDHx genes

Demographics of GIST Patients

Variables		WT GIST	Non-WT GIST	P-value
		N (%)	N (%)	
Total Patients		24	162	
Age (years, mean \pm SD)		44.4 \pm 15.7	58.3 \pm 14.1	<0.01
Sex	Female	12 (50.0)	66 (40.7)	0.51
	Male	12 (50.0)	94 (58.0)	
	Not Reported	-	2 (1.2)	
Primary GIST Site	Colon	2 (8.3)	15 (9.3)	0.26
	Small intestine	9 (37.5)	44 (27.2)	
	Stomach	13 (54.2)	83 (51.2)	
	Other	0 (0.0)	20 (12.3)	

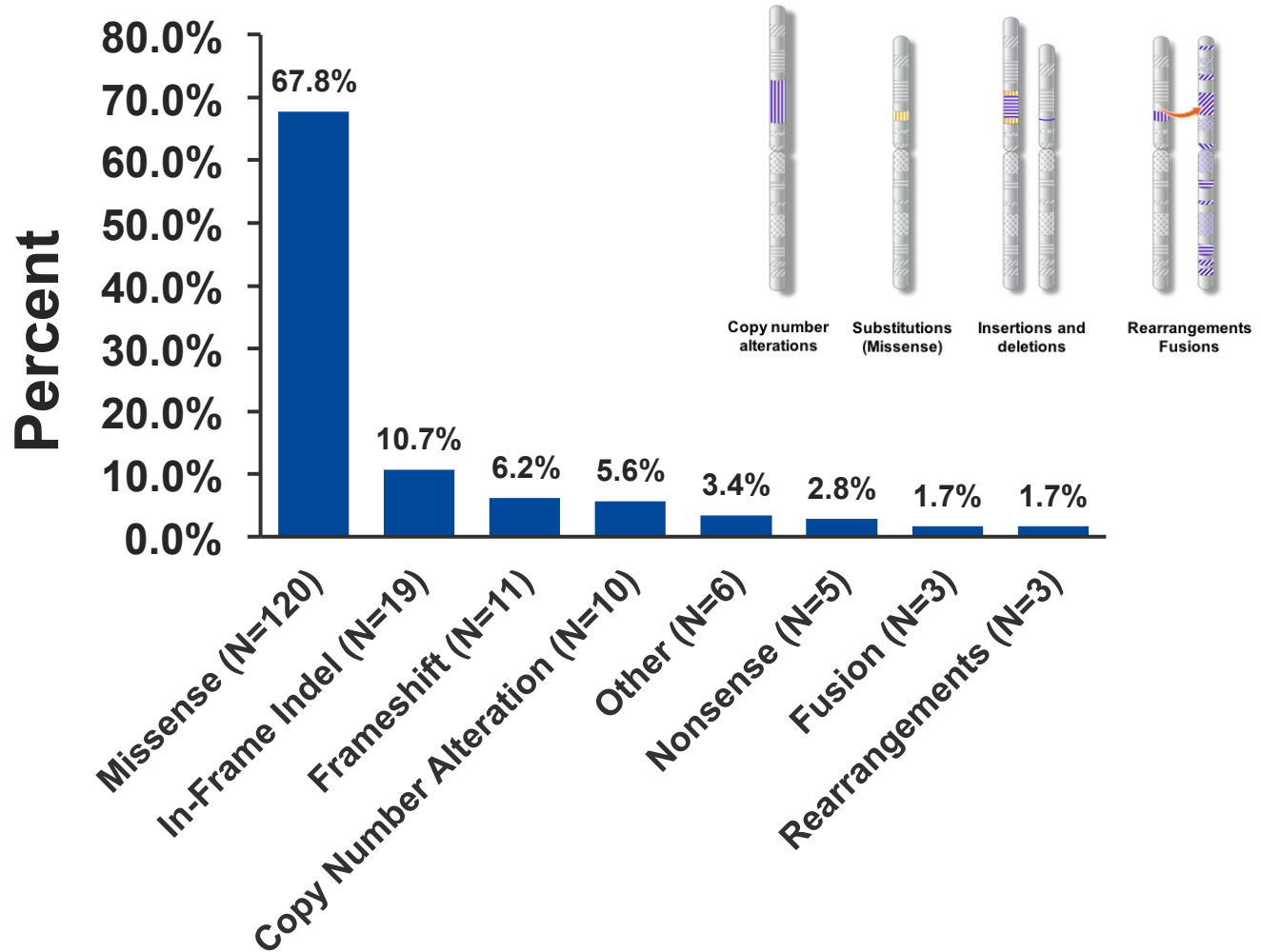
Demographics of GIST Patients

Variables		qWT GIST	tWT GIST	P-value
		N (%)	N (%)	
Total Patients		12	12	
Age (years, mean ± SD)		44.0 ± 14.9	44.8 ± 17.1	0.90
Sex	Female	5 (41.7)	7 (58.3)	0.68
	Male	7 (58.3)	5 (41.6)	
	Not Reported	-	-	
Primary GIST Site	Colon	0 (0.0)	2 (16.7)	0.36
	Small intestine	4 (33.3)	5 (41.6)	
	Stomach	8 (66.7)	5 (41.6)	

Demographics of GIST Patients

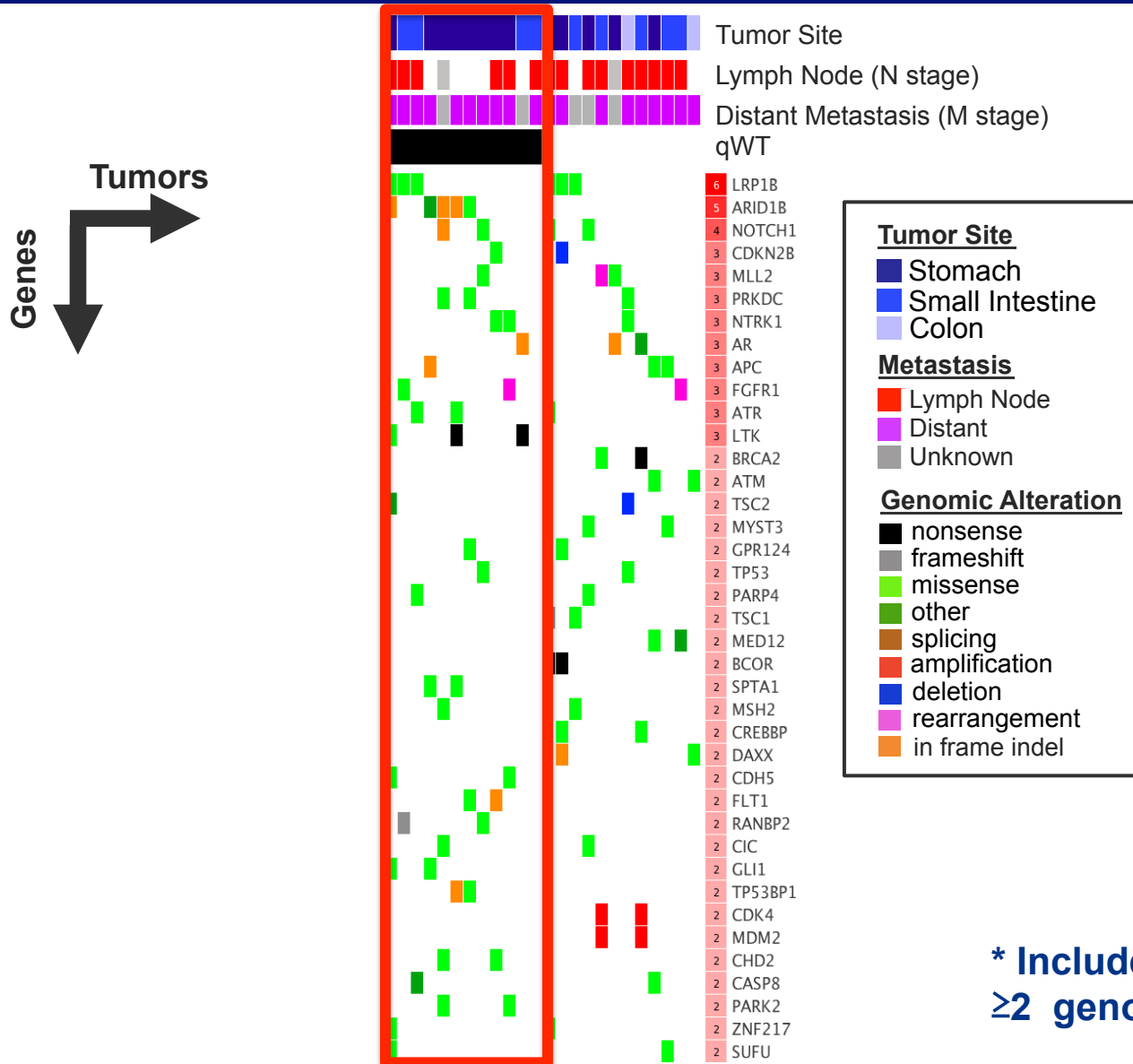
TNM Classification		qWT GIST	tWT GIST	P-value*
		N (%)	N (%)	
Tumor Size (T)	T1 (≤ 2 cm)	0 (0.0)	0 (0.0)	0.05
	T2 ($>2, \leq 5$ cm)	0 (0.0)	2 (16.7)	
	T3 ($>5, \leq 10$ cm)	11 (91.7)	5 (41.6)	
	T4 (>10 cm)	1 (8.3)	4 (33.3)	
	Tx	0 (0.0)	1 (8.3)	
Regional Lymph Nodes (N)	N0	6 (50.0)	2 (16.7)	0.14
	N1	3 (25.0)	8 (66.7)	
	Nx	3 (25.0)	2 (16.7)	
Distant Metastases (M)	M0	0 (0.0)	0 (0.0)	1.0
	M1	9 (75.0)	8 (66.7)	
	Mx	3 (25.0)	4 (33.3)	

Types of Genomic Alterations Detected



Heterogeneous Set of Genomic Alterations*

(Known/Likely + Potentially Deleterious VUS)

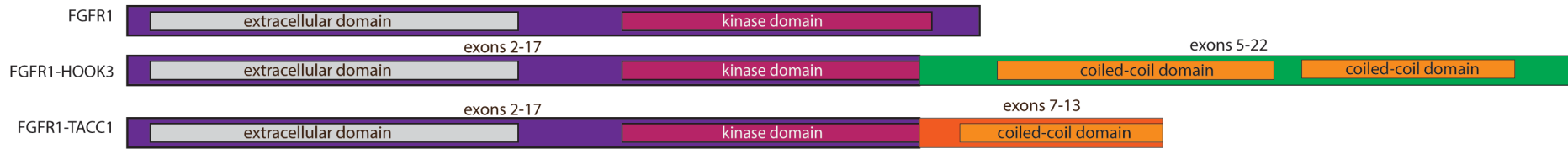


* Include only genes with ≥ 2 genomic alterations

7 Genes Significantly More Affected

Gene	Aliases	Alterations in non-WT (%)	Alterations in WT (%)	P-value
ARID1B	AT Rich Interactive Domain 1B	11 (6.79%)	5 (20.83%)	0.04
FGFR1	Fibroblast growth factor receptor 1	4 (2.47%)	3 (12.5%)	0.047
ATR	Ataxia telangiectasia and Rad3 related	4 (2.47%)	3 (12.5%)	0.047
LTK	Lymphocyte receptor tyrosine kinase	2 (1.23%)	3 (12.5%)	0.02
SUFU	Suppressor of Fused	0 (0%)	2 (8.33%)	0.02
ZNF217	Zinc Finger 217	0 (0%)	2 (8.33%)	0.02
PARK2	Parkin RBR E3 Ubiquitin Protein Ligase	1 (0.62%)	2 (8.33%)	0.044

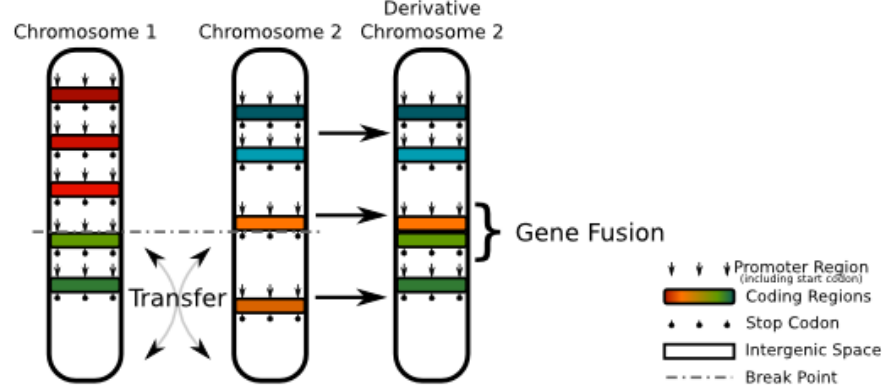
FGFR1 Gene Fusions Identified in 2/3rd GISTs



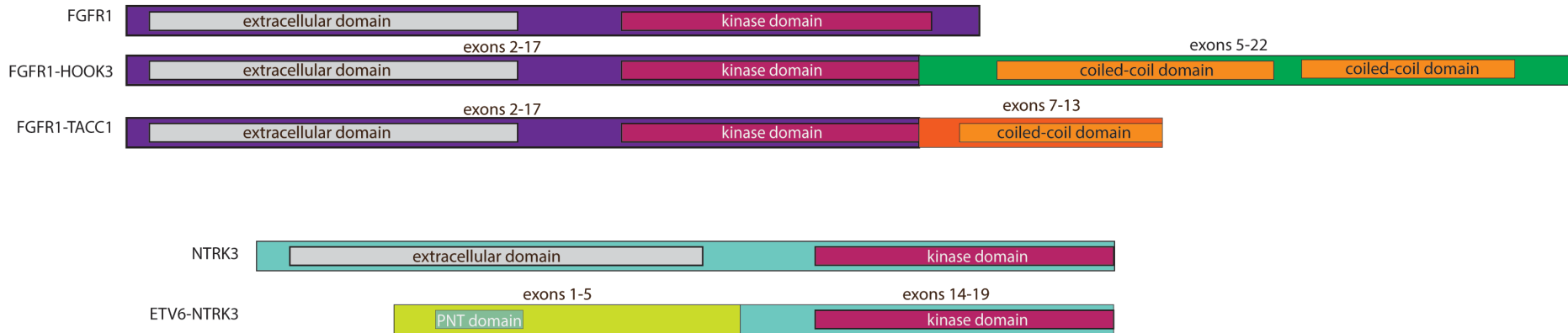
Gene Fusions

- Hybrid gene formed from 2 previously separate genes
- It can occur as a result of 3 mechanisms:

A. Chromosomal Translocation



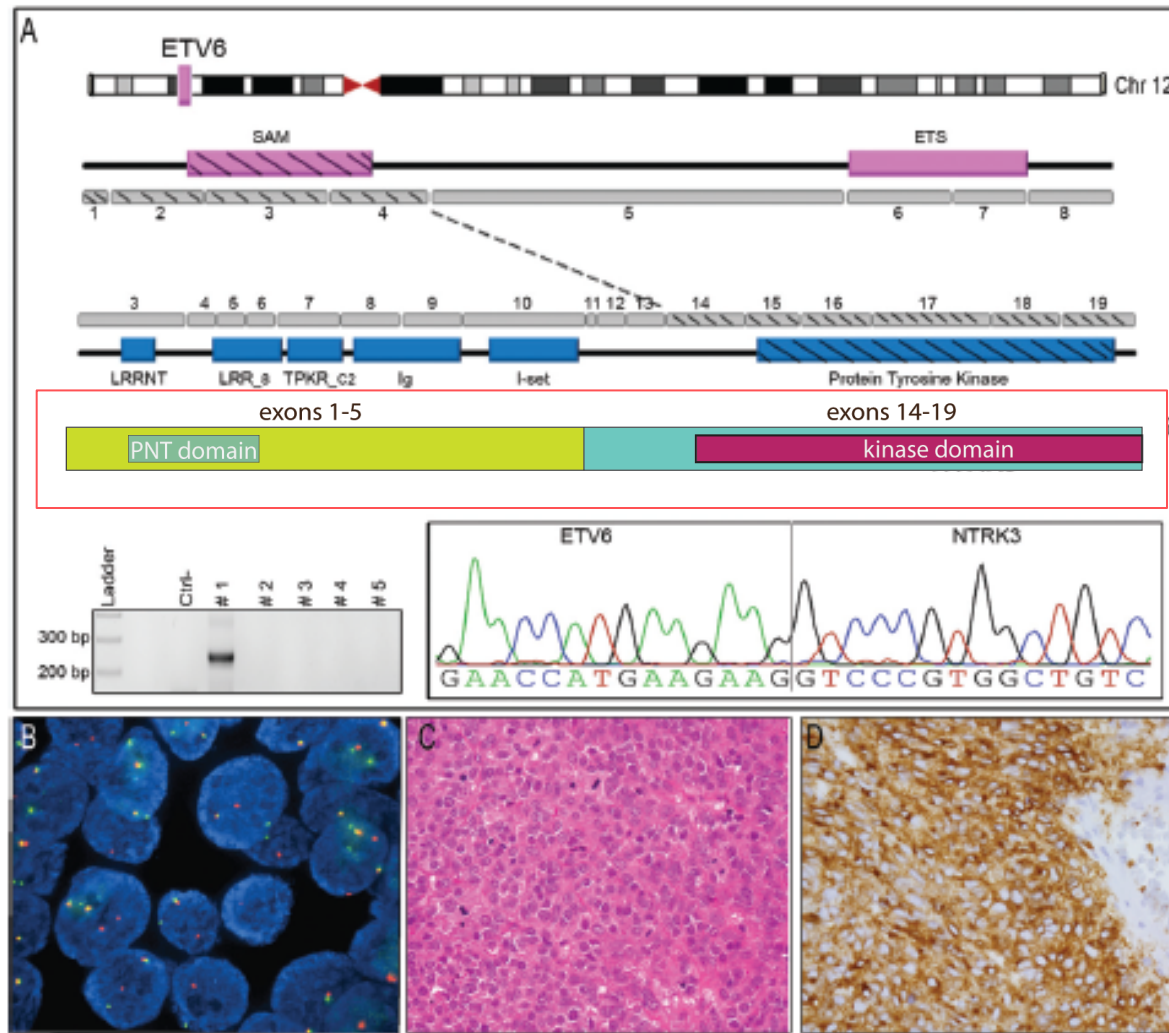
CTOS in November 2015



Gene	Fusion	Previously Reports
<i>FGFR1</i>	<i>FGFR1-TACC1</i>	Glioblastoma multiforme
	<i>FGFR1-HOOK3</i>	RET-HOOK3 fusion in papillary thyroid cancer
<i>ETV6</i>	<i>ETV6-NTRK3</i>	Infantile fibrosarcoma secretory breast carcinoma salivary gland tumors

Shaw *et al.*, Nature Reviews Cancer. 2013.

ETV6-NTRK3 in qWT GIST



Brenca *et al.*, *J Pathology*. March 2016.

OHSU Validation in 2nd Study Population

Target Kinase	Fusion Partners
<i>AKT3</i>	<i>MAGI3</i>
<i>ALK</i>	<i>ATIC, C2orf44, CARS, CLTC, EML4, FN1, KIF5B, KLC1, MSN, NPM1, PPFIBP1, PTPN3, SEC31A, SQSTM1, STRN, TFG, TPM3, TPM4, TRAF1, VCL</i>
<i>BRAF</i>	<i>AGK, AGTRAP, AKAP9, CLCN6, FAM131B, FCHSD1, GNAI1, KCTD7, KIAA1549, MAD1L1, MKRN1, NUDCD3, PLIN3, RNF130, SLC45A3, SOX6, TRIM24, ZKSCAN5</i>
<i>EGFR</i>	<i>EGFR variant III, CAND1, PSPH, SEPT14, SLC12A9</i>
<i>ERBB4</i>	<i>EZR</i>
<i>ERG</i>	<i>TMPRSS2</i>
<i>FGFR1</i>	<i>BAG4, CPSF6, ERLIN2, PLAG1, TACC1, ZNF703</i>
<i>FGFR2</i>	<i>AFF3, AHCYL1, BICC1, CASP7, CCDC6, CIT, KIAA1967, OFD1, SLC45A3</i>
<i>FGFR3</i>	<i>BAIAP2L1, TACC3</i>
<i>MET</i>	<i>MIR548F1, TPR</i>
<i>NTRK1</i>	<i>BCAN, CD74, MIR548F1, MPRIP, NFASC, TFG, TPM3, TPR</i>
<i>NTRK2</i>	<i>NACC2, QKI</i>
<i>NTRK3</i>	<i>ETV6</i>
<i>NRG1</i>	<i>CD74, SLC3A2</i>
<i>PDGFRA</i>	<i>KDR, SCAF11</i>
<i>PDGFRB</i>	<i>NIN</i>
<i>RAF1</i>	<i>DAZL, ESRP1, MSS51, SRGAP3</i>
<i>RET</i>	<i>AFAP1, CCDC6, ERC1, HOOK3, KIAA1468, KIF5B, NCOA4, PARG, PCM1, PRKAR1A, TRIM27, TRIM33</i>
<i>ROS1</i>	<i>CCDC6, CD74, CEP85L, EZR, GOPC, KDELR2, LRIG3, SDC4, SLC34A2, TFG, TPM3</i>

5 qWT GIST in OHSU Study Population

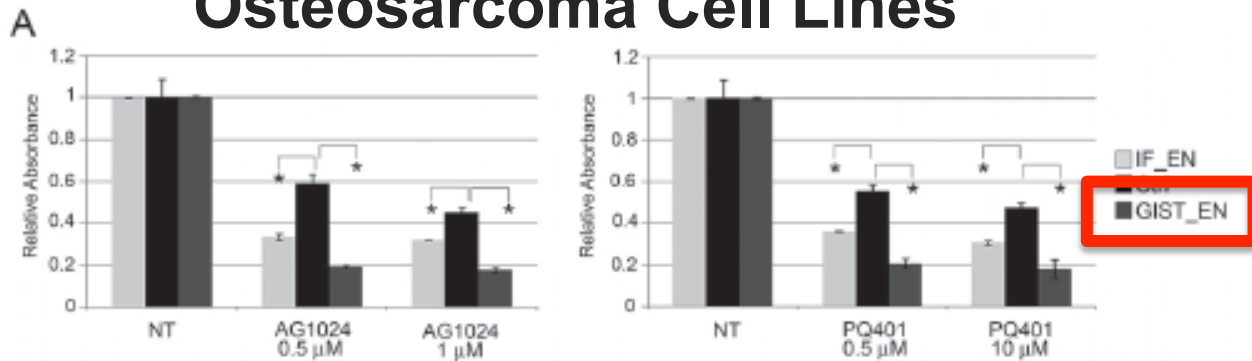
Age (Years)	Gender	Primary Tumor Location	Tumor Stage	SDHB Immunostaining	Fusion Panel Result
54	Male	Pelvic mass	Unknown	Unknown	<i>FGFR1-TACC1</i>
54	Male	Colon	Unknown	Positive	<i>ETV6-NTRK3</i>
49	Male	Small intestine	T3NxMx	Positive	None detected
51	Female	Unknown	TxN1Mx	Positive	None detected
53	Male	Stomach	Unknown	Unknown	None detected



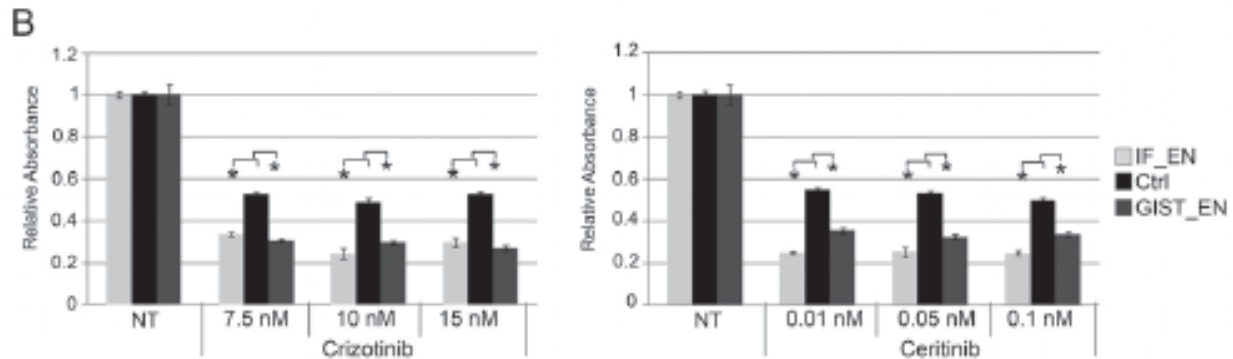
ETV6-NTRK3 Sensitizes Cells to IGF1R and ALK Inhibitors

Infantile Fibrosarcoma & Osteosarcoma Cell Lines

IGF-1R inhibitors

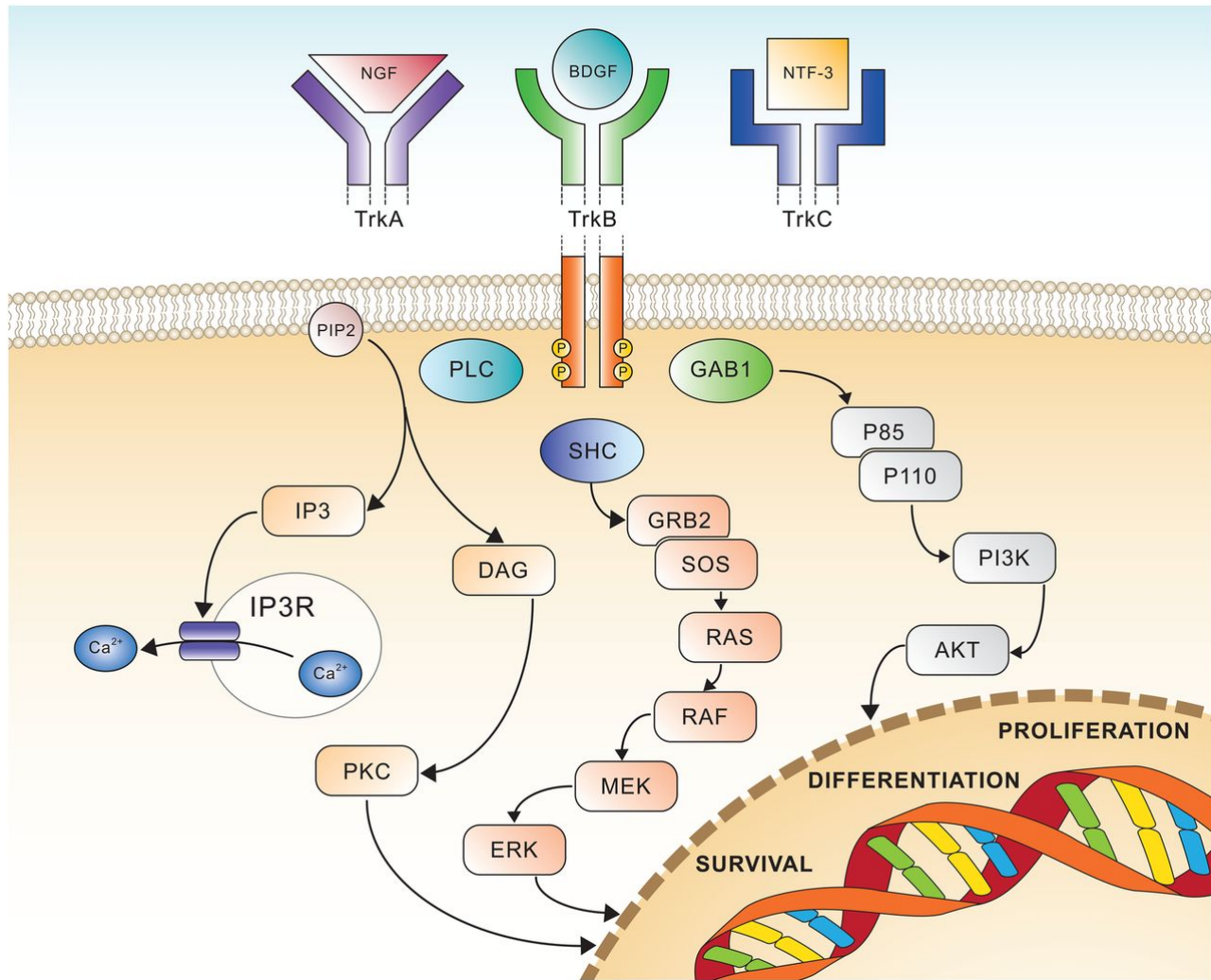


ALK inhibitors



Brenca et al., *J Pathology*. March 2016.

Neurotrophic tropomyosin receptor kinase (*NTRK*)



Amatu et al., *ESMO Open*. 2016.

NTRK Inhibitors

Table 2 Ongoing phase I/II trials involving drugs with known inhibitory activity of NTRK-related kinases

NCT/EudraCT number	Title	Drug	Targets	Phases	Patients	Start date
NCT02219711	Phase 1/1b study of MGCD516 in patients with advanced cancer	MGCD516	MET, AXL, c-kit, MER, DDR2, VEGFR, PDGFR, RET, Trk, Eph	1	120	August 2014
NCT02568267	Basket study of entrectinib (RXDX-101) for the treatment of patients with solid tumors harboring NTRK1/2/3, ROS1, or ALK gene rearrangements (fusions)	Entrectinib (RXDX-101)	TrkA, TrkB, TrkC, ROS1, ALK	2	300	October 2015
NCT02097810	Study of oral RXDX-101 in adult patients with locally advanced or metastatic cancer targeting NTRK1, NTRK2, NTRK3, ROS1, or ALK molecular alterations			1/2	175	June 2014
NCT02650401	Study of RXDX-101 in children with recurrent or refractory solid tumors and primary CNS tumors			1	80	December 2015
NCT02048488/2013-000686-37	A phase I/IIa open-label, dose escalation and cohort expansion trial of oral TSR-011 in patients with advanced solid tumors and lymphomas	TSR-011	TrkA, ALK	1/2	150	October 2012
NCT02637687	Oral TRK inhibitor LOXO-101 for treatment of advanced pediatric solid or primary central nervous system tumors	LOXO-101	TrkA, TrkB, TrkC	1	36	December 2015
NCT02122913	Oral TRK inhibitor LOXO-101 for treatment of advanced adult solid tumors			1	108	April 2014
NCT02576431	Study of LOXO-101 in subjects with NTRK fusion positive solid tumors			2	151	October 2015
NCT01804530	fusion-positive advanced non-small cell lung cancer and those with other genotypes: ROS1 or NTRK fusions or increased MET or AXL activity Phase 1 study of PLX7486 as single agent and with gemcitabine plus nab-paclitaxel in patients with advanced solid tumors	(XL184) PLX7486	ROS1, MET, AXL TrkA, TrkB, TrkC, FMS	1	160	August 2013
NCT02279433	A first-in-human study to evaluate the safety, tolerability and pharmacokinetics of DS-6051b	DS-6051b	TrkA, TrkB, TrkC, ROS1	1	70	September 2014
2013-003009-24	Phase I-II study of F17752 in patients with advanced solid tumours	F17752	ALK, ROS1, Trk	1/2	112	September 2015
NCT02228811	A study of DCC-2701 in participants with advanced solid tumors	Altiratinib (DCC-2701)	TrkA, TrkB, TrkC, MET, TIE2, VEGFR	1	48	June 2014

ALK, anaplastic lymphoma receptor tyrosine kinase; AXL, AXL receptor tyrosine kinase; c-kit, mast/stem cell growth factor receptor; CNS, central nervous system; DDR2, discoidin domain receptor 2; Eph, ephrin receptor tyrosine kinases; FMS, McDonough Feline Sarcoma Virus; MER, MER receptor tyrosine kinase; MET, hepatocyte growth factor receptor; PDGFR, platelet-derived growth factor receptor; RET, rearranged during transfection; ROS1, ROS proto-oncogene 1; TIE2, TEK receptor tyrosine kinase; TRK, topomycin-related kinases (also known as TrkA,B,C for kinase A, B and C); VEGFR, vascular endothelial growth factor receptor.

Amatu et al., ESMO Open. 2016.

The efficacy of larotrectinib (LOXO-101), a selective tropomyosin receptor kinase (TRK) inhibitor, in adult and pediatric TRK fusion cancers

Hyman DM,¹ Laetsch TW,² Kummar S,³ DuBois SG,⁴ Farago AF,⁵ Pappo AS,⁶ Demetri GD,⁷ El-Deiry WS,⁸ Lassen UN,⁹ Dowlati A,¹⁰ Brose MS,¹¹ Boni V,¹² Turpin B,¹³ Nagasubramanian R,¹⁴ Cruickshank S,¹⁵ Cox MC,¹⁵ Ku NC,¹⁵ Hawkins DS,¹⁶ Hong DS,¹⁷ Drilon AE¹

¹Memorial Sloan Kettering Cancer Center, New York, NY; ²University of Texas Southwestern, Dallas, TX; ³Stanford University School of Medicine, Palo Alto, CA; ⁴Dana-Farber Cancer Institute/Boston Children's Cancer and Blood Disorders Center, Boston, MA; ⁵Massachusetts General Hospital, Boston, MA; ⁶St. Jude Children's Research Hospital, Memphis, TN; ⁷Dana-Farber Cancer Institute/Harvard Medical School, Boston, MA; ⁸Fox Chase Cancer Center, Philadelphia, PA; ⁹Rigshospitalet, Copenhagen, Denmark; ¹⁰UH Cleveland Medical Center, Cleveland, OH; ¹¹Department of Otorhinolaryngology: Head and Neck Surgery, Abramson Cancer Center of the University of Pennsylvania, Philadelphia, PA; ¹²START Madrid CIOCC, Hospital HM Universitario Sanchinarro, Madrid, Spain; ¹³Cincinnati Children's Hospital Medical Center, Cincinnati, OH; ¹⁴Nemour's Children's Hospital, Orlando, FL; ¹⁵Loxo Oncology, Inc., San Francisco, CA; ¹⁶Seattle Children's Hospital, University of Washington, Fred Hutchinson Cancer Research Center, Seattle, WA; ¹⁷The University of Texas MD Anderson Cancer Center, Houston, TX

PRESENTED AT: ASCO ANNUAL MEETING '17

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#ASCO17

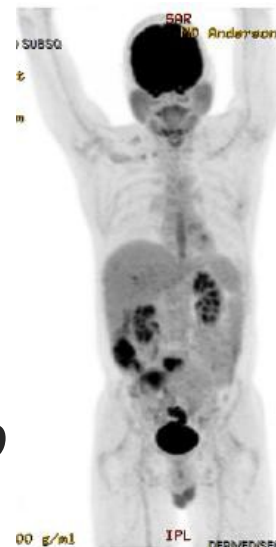
Hyman, LBA2501

Treatment Refractory *ETV6-NTRK3* GIST

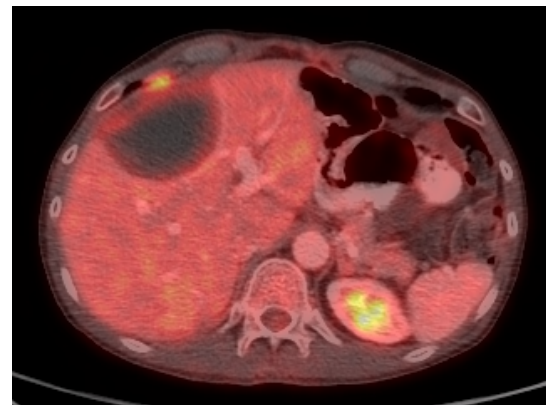
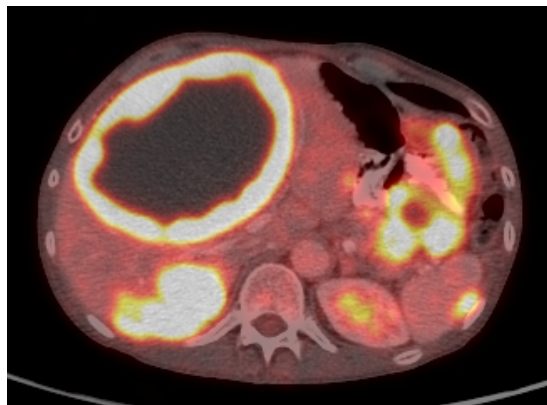
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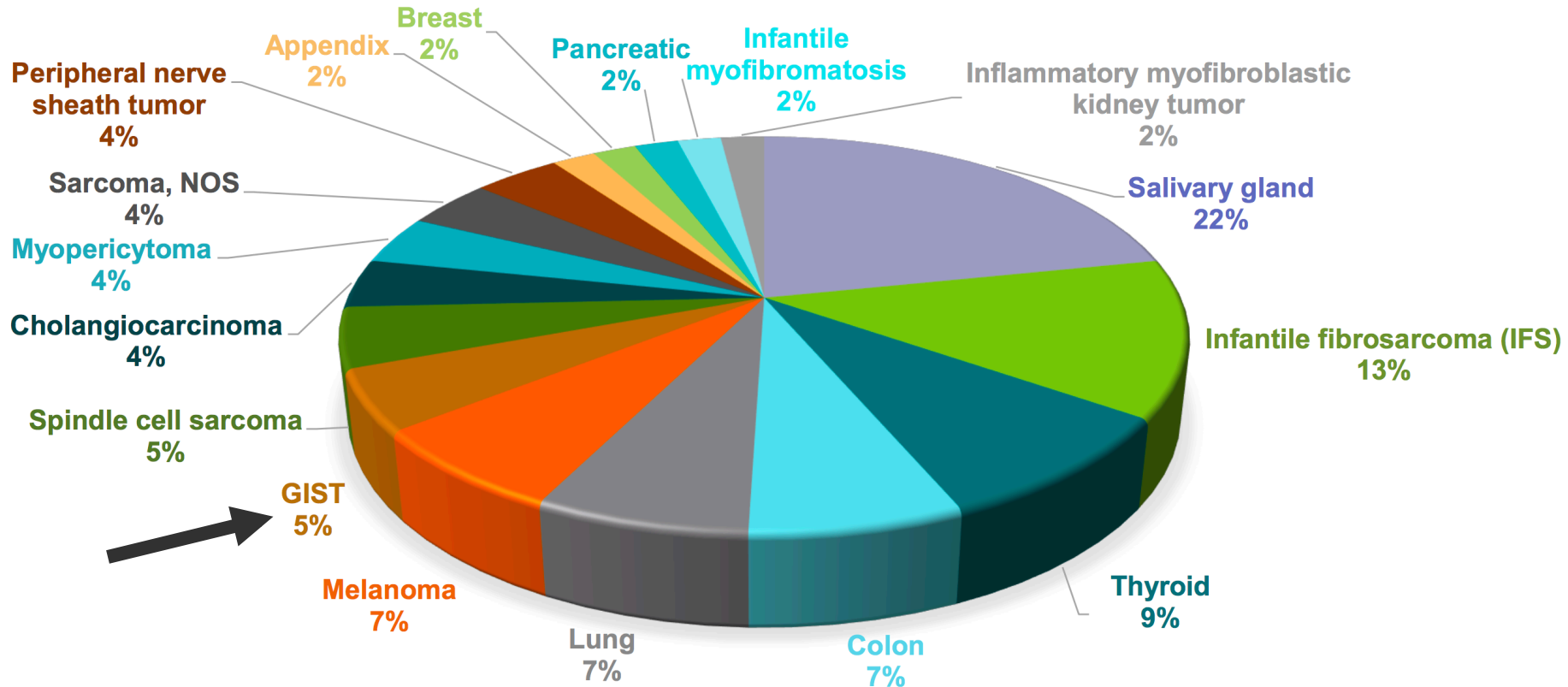
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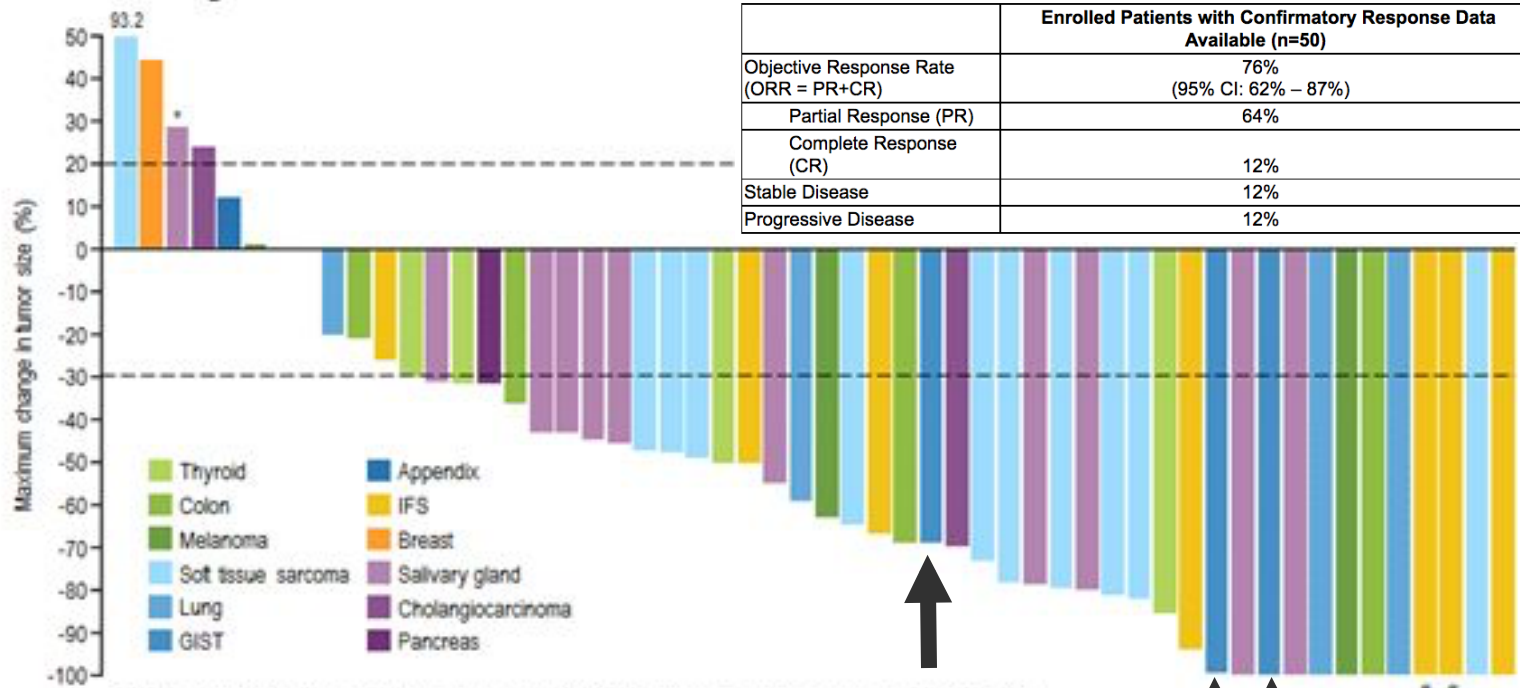
LOXO-101
→
Larotrectinib



Diversity of cancers treated - 17 unique types

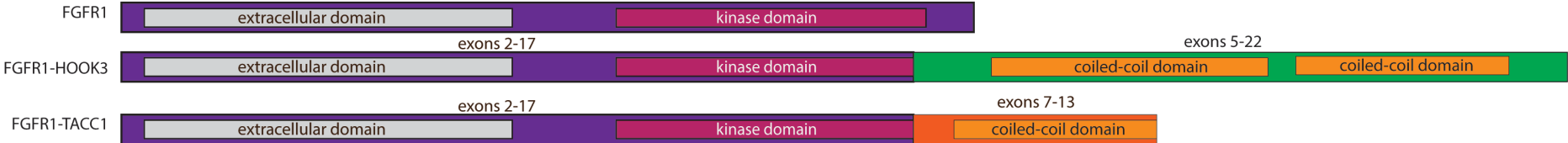


Efficacy of larotrectinib in TRK fusion cancers

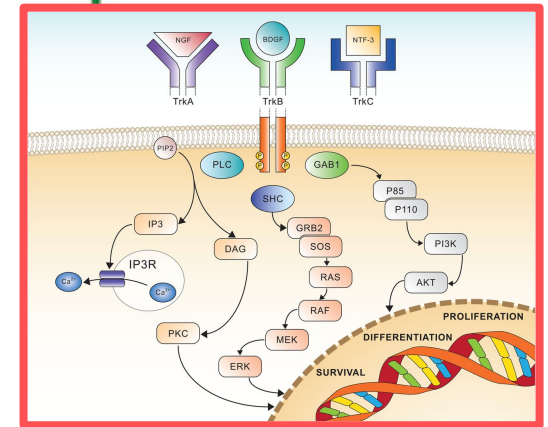
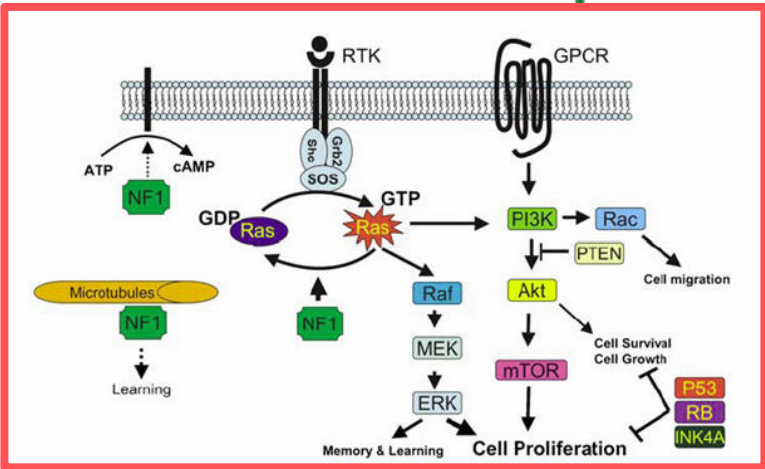
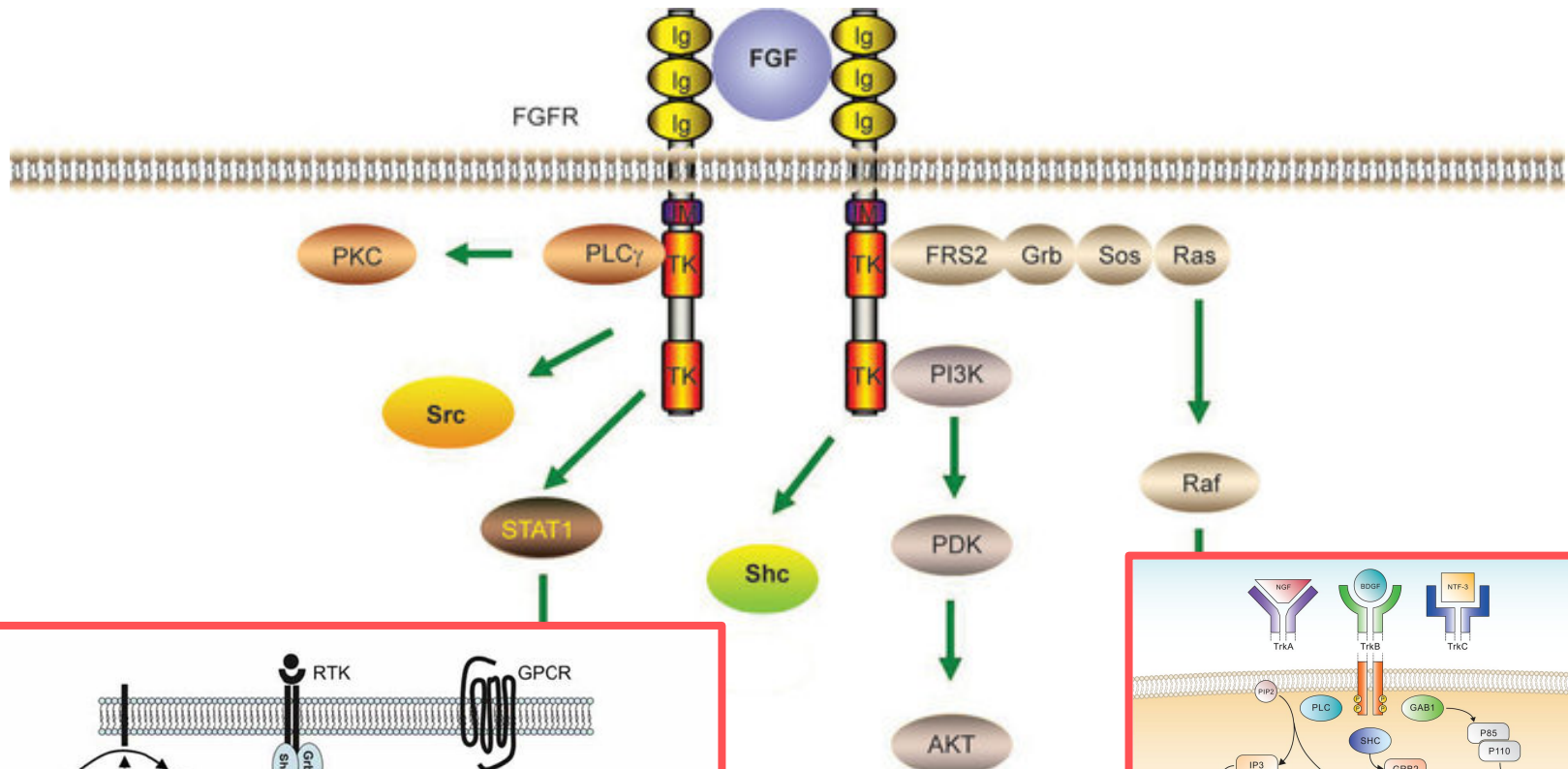


*Patient had TRK solvent front resistance mutation (NTRK3 G623R) at baseline due to prior therapy; *Pathologic CR
 Note: One patient not shown here. Patient experienced clinical progression and no post-baseline tumor measurements were recorded.

FGFR1 Gene Fusions Identified GIST



Fibroblast Growth Factor Receptor 1 (FGFR1)



Amatu et al., ESMO Open. 2016.
GSI Website

Lack Mutations in *KIT*, *PDGFRA*, RAS Pathway (*NF1*, *RAS*, *BRAF*) and *SDH* Subunits

Quadruple Wild-type (qWT) GIST

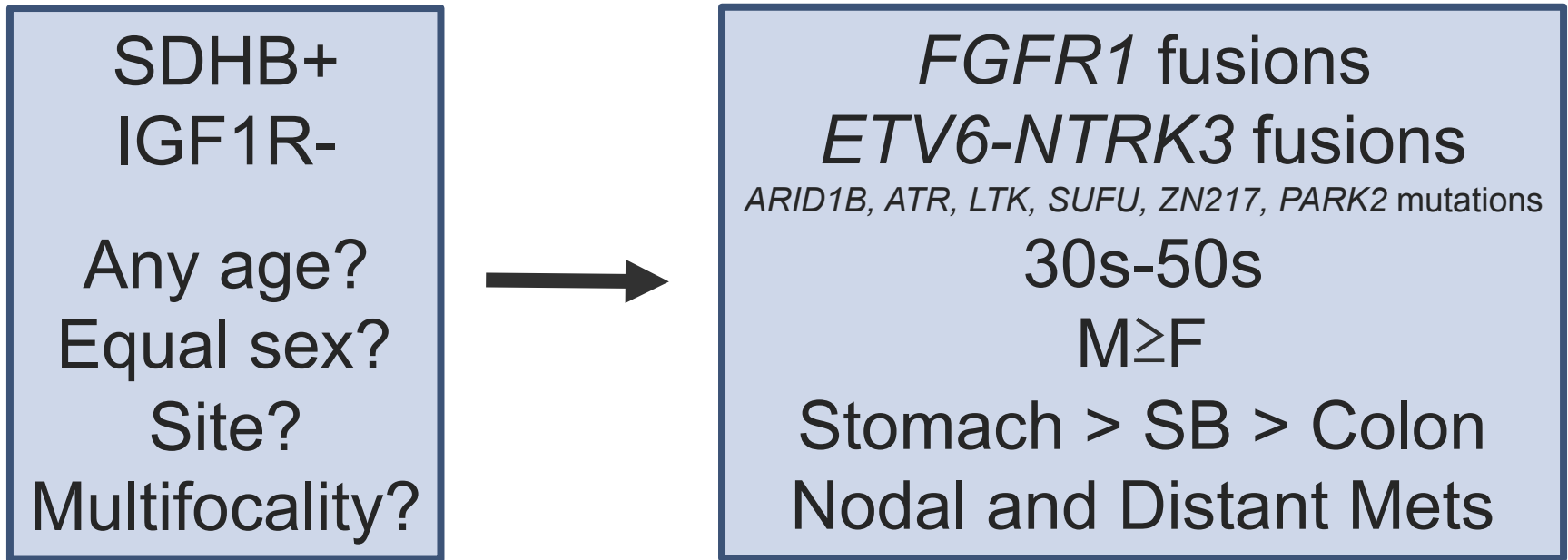
SDHB+
IGF1R-

Any age?
Equal sex?
Site?
Multifocality?

- **Genomics?**
- **Epidemiology?**
- **Disease Biology?**

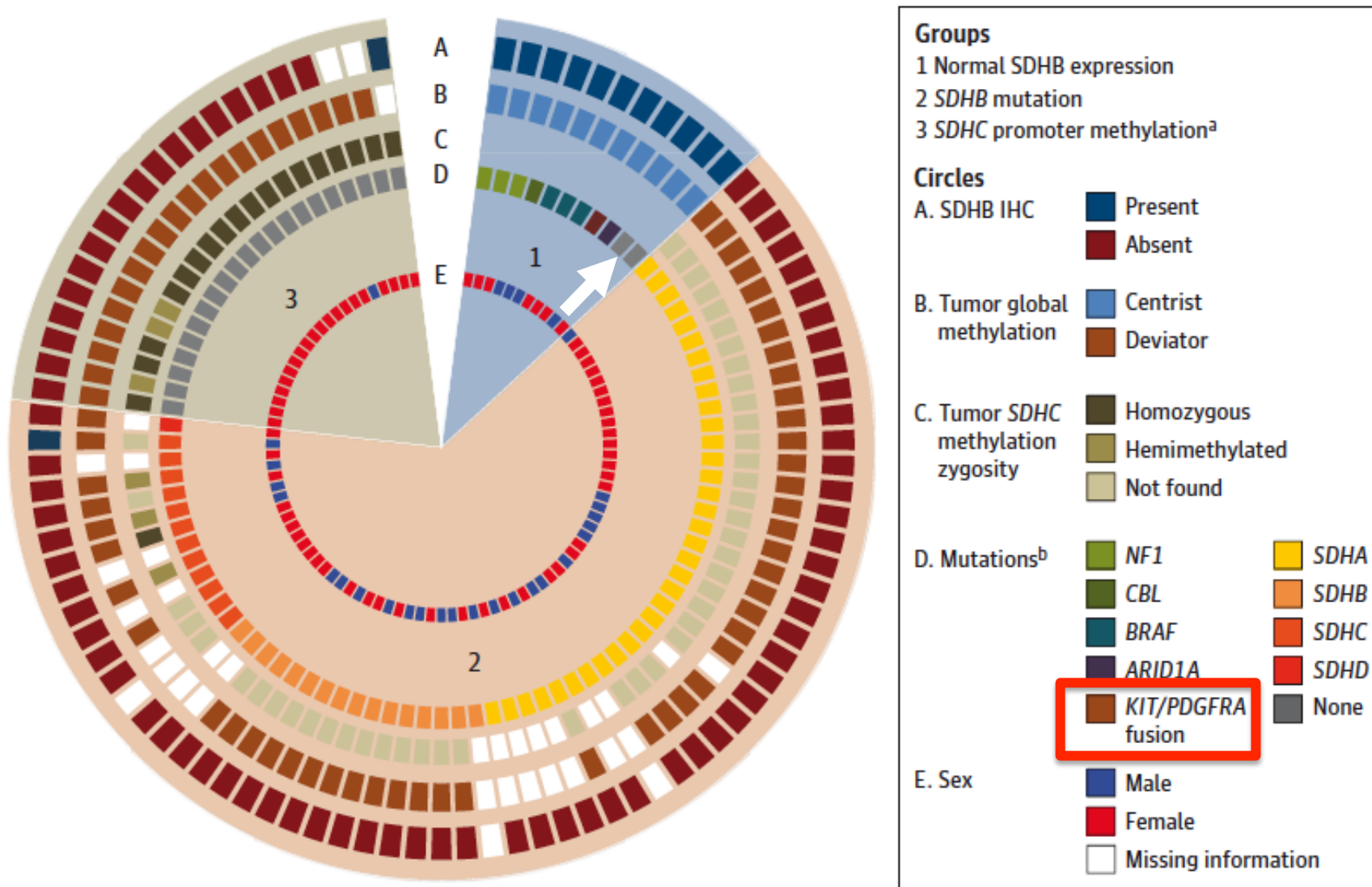
Lack Mutations in *KIT*, *PDGFRA*, RAS Pathway (*NF1*, *RAS*, *BRAF*) and *SDH* Subunits

Quadruple Wild-type (qWT) GIST



Shi *et al.*, *JTM*. 2016.

NIH Wild-Type GIST Clinic: *KIT-PDGFR*A fusion

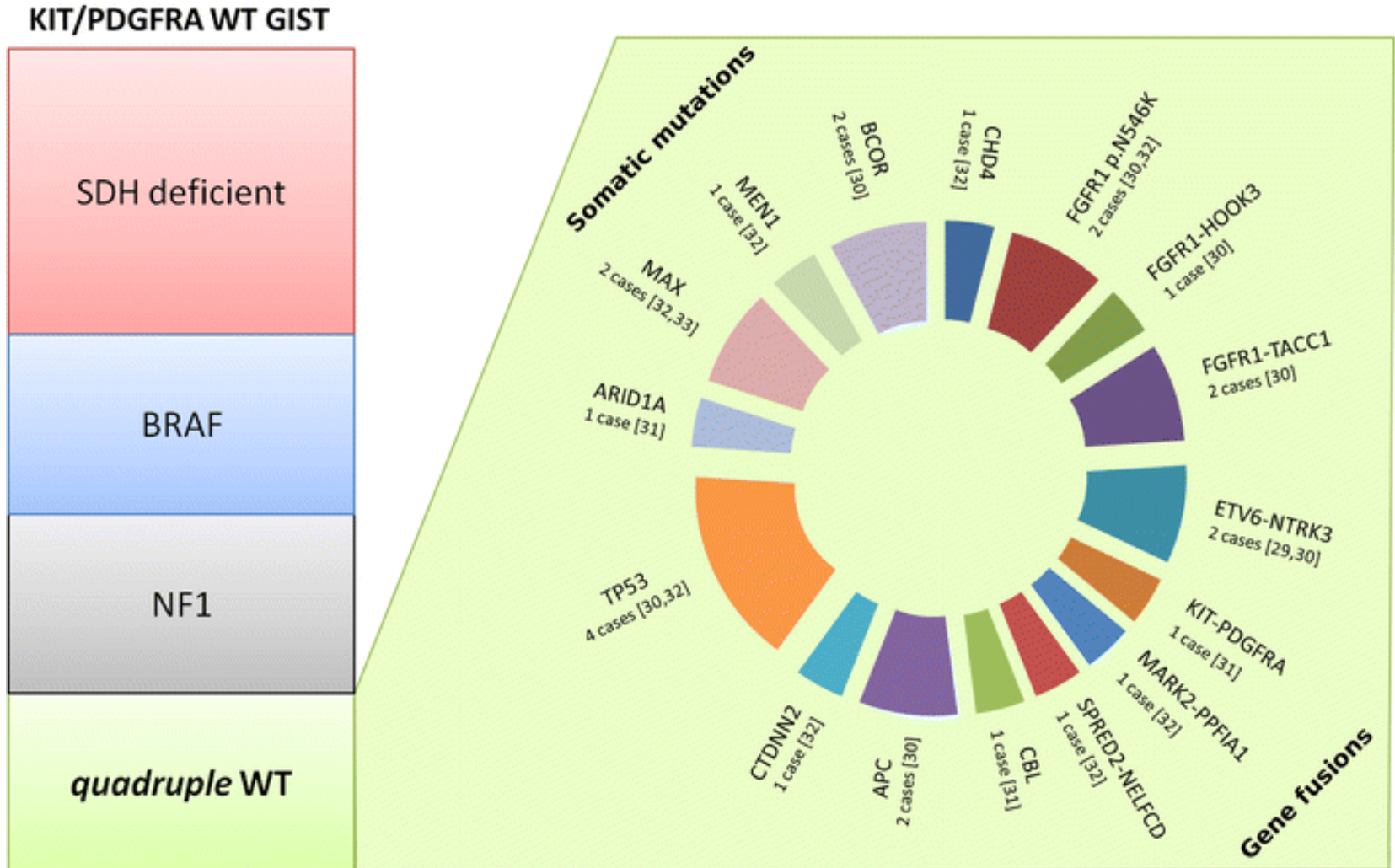


9 Known Gene Fusions in GIST

Patient	Age (Years)	Sex	Primary Tumor Location	Tumor Stage	Gene Fusion
1	55	Male	Small bowel	T3N0M1	<i>ETV6-NTRK3</i>
2	54	Male	Colon	Unknown	<i>ETV6-NTRK3</i>
3	44	Male	Rectum	T2NxM0	<i>ETV6-NTRK3</i>
4	54	Male	Pelvis mass	Unknown	<i>FGFR1-TACC1</i>
5	54	Male	Stomach	T3N1M1	<i>FGFR1-TACC1</i>
6	38	Female	Small bowel	T3N1M1	<i>FGFR1-HOOK3</i>
7	Unknown	Female	Unknown	Unknown	<i>KIT-PDGFR</i>
8	63	Female	Small bowel	T3N0M1	<i>MARK2-PPFIA1</i> <i>SPRED2-NELFCD</i>
9 *	30	Female	Small bowel	T4NxM0	<i>PRKAR1B-BRAF</i>
Summary	Average: 48 Median: 54	Male 56% Female 44%	44% small bowel, but spans stomach to rectum	22% nodal metastases 44% distant metastases	33% <i>ETV6-NTRK3</i> 33% <i>FGFR1</i> 33% <i>Others</i>

Shi *et al.* *J Translational Med.* December 2016.
 Brenca *et al.*, *J Pathology.* March 2016.
 Boikos *et al.*, *JAMA Onc.* July 2016.
 Pantaleo *et al.*, *Mol Cancer Res.* July 2017.
 * UCSD Patient (unreported to date)

Progressive Fragmentation of “WT” GIST



Abandoning WT GIST

Journal of the National Comprehensive Cancer Network

The Call of “The Wild”-Type GIST: It’s Time for Domestication

*Maha Alkhuziem, MBBS, MAS; Adam M. Burgoyne, MD, PhD;
Paul T. Fanta, MD; Chih-Min Tang, PhD; and Jason K. Sicklick, MD*

Alkhuziem et al., JNCCN. May 2017.

**Table 1. Matching Genomic Alterations With Targeted Therapies in GIST:
Theoretical Precision Actionabilities Meriting Investigations (cont.)**

Gene	Pathways/Signaling	Matching FDA-Approved, On-Label Agents With Targets in GIST	Matching FDA-Approved, Off-Label Agents With Targets in GIST	Clinical Trials Enrolling Patients With GIST
<i>KRAS</i>	MAPK		MEK inhibitors: cobimetinib, trametinib	
<i>LTK</i>	Transcriptional regulation Insulin receptor signaling		TKI: crizotinib	
<i>NF1</i>	MAPK		MEK inhibitors: cobimetinib, trametinib	
<i>NRAS</i>	MAPK		MEK inhibitors: cobimetinib, trametinib	
<i>PARK2</i>	E3 ubiquitin ligase Cyclin-CDK complexes		CDK4/6 inhibitor: palbociclib	Phase II (CDK4/6 inhibitor): palbociclib
<i>PDGFRA</i>	MAPK PI3K/AKT/mTOR JAK/STAT	Imatinib (first line) Sunitinib (second line) Regorafenib (third line)	TKI: ponatinib	Phase I (PDGFRA/TKI inhibitors): BLU-285, DCC-2618 Phase II (PDGFRA/TKI inhibitors): dovitinib, famitinib, olaratumab, onalespib, motesanib Phase III (PDGFRA inhibitor): crenolanib
<i>SDHA</i>	Epigenetic methylation HIF1-alpha expression		Hypomethylating agents: 5-azacytidine, decitabine	Phase I (glutaminase inhibitor): CB-839
<i>SDHB</i>	Epigenetic methylation HIF1-alpha expression		Hypomethylating agents: 5-azacytidine, decitabine	Phase I (glutaminase inhibitor): CB-839
<i>SDHC</i>	Epigenetic methylation HIF1-alpha expression		Hypomethylating agents: 5-azacytidine, decitabine	Phase I (glutaminase inhibitor): CB-839
<i>SDHD</i>	Epigenetic methylation HIF1-alpha expression		Hypomethylating agents: 5-azacytidine, decitabine	Phase I (glutaminase inhibitor): CB-839
<i>SUFU</i>	Hedgehog pathway		GLI inhibitor: arsenic trioxide	
<i>ZNF217</i>	Transcriptional regulation			

Table 1. Matching Genomic Alterations With Targeted Therapies in GIST: Theoretical Precision Actionabilities Meriting Investigations

Gene	Pathways/Signaling	Matching FDA-Approved, On-Label Agents With Targets in GIST	Matching FDA-Approved, Off-Label Agents With Targets in GIST	Clinical Trials Enrolling Patients With GIST
<i>ARID1A</i>	Chromatin remodeling PI3K/AKT/mTOR		mTOR inhibitors: everolimus, temsirolimus	Phase I (PI3K inhibitors): alpelisib, buparlisib, TGR-1202
<i>ARID1B</i>	Chromatin remodeling PI3K/AKT/mTOR		mTOR inhibitors: everolimus, temsirolimus	Phase I (PI3K inhibitors): alpelisib, buparlisib, TGR-1202
<i>ATR</i>	DNA repair		DNA damaging agents: cisplatin, gemcitabine, topotecan PARP inhibitors: olaparib, rucaparib Radiotherapy	
<i>BRAF</i>	MAPK	Regorafenib (third line)	BRAF V600E inhibitors: dabrafenib, vemurafenib MEK inhibitors: cobimetinib, trametinib	Phase II (BRAF V600E inhibitor): dabrafenib Phase II (MEK inhibitors): binimetinib, trametinib
<i>ETV6-NTRK3</i>	MAPK PI3K/AKT/mTOR JAK/STAT		TKI: crizotinib	Phase I (TRK inhibitor): larotrectinib Phase II (TRK inhibitor): entrectinib
<i>FGFR1</i>	FGF	Regorafenib (third line)	FGFR inhibitors: lenvatinib, pazopanib, ponatinib	Phase I (FGFR inhibitors): BGJ398, dovitinib Phase II (FGFR inhibitor): semaxanib
<i>HRAS</i>	MAPK		MEK inhibitors: cobimetinib, trametinib	
<i>KIT</i>	MAPK PI3K/AKT/mTOR JAK/STAT	Imatinib (first line) Sunitinib (second line) Regorafenib (third line)	TKIs: dasatinib, nilotinib, ponatinib	Phase I (TKIs): DCC-2618, OSI-930, PLX9486 Phase II (TKIs): BBI503, cabozantinib, dasatinib, famitinib, ganetespib, nilotinib, pexidartinib, sorafenib, sunitinib Phase III (TKI): masitinib

Summary #1

- “Quadruple Wild-Type: or “**Unclassified**” GIST occur in younger patients, occur in similar locations as non-qWT GIST, frequently metastasize to lymph nodes, and most are not truly “WT.”
- Potentially deleterious gene fusions occur in adults with GIST and these are potentially targetable with drugs.
 - KIT inhibitors (*KIT-PDGFR* fusion)
 - NTRK3 inhibitors (*ETV6-NTRK3* fusion)
 - FGFR1 inhibitors (*FGFR1-TACC1/HOOK3* fusions)
 - BRAF inhibitors (*BRAF-PRKAR1B* fusion)
- Other driver genes at play:
 - *ARID1A/D, ATR, LTK, MAX, PARK2, SUFU, ZNF217*

Shi *et al.* *J Translational Med.* December 2016.
Boikos *et al.*, *JAMA Onc.* July 2016.
Pantaleo *et al.*, *Mol Cancer Res.* July 2017.
Alkhuzeim *et al.*, *JNCCN.* May 2017.

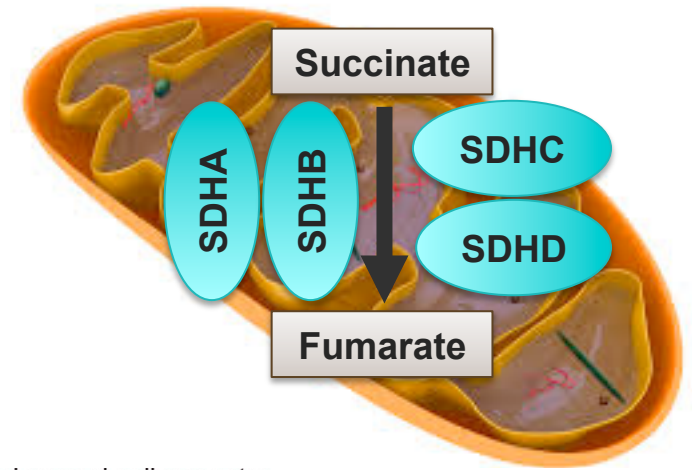
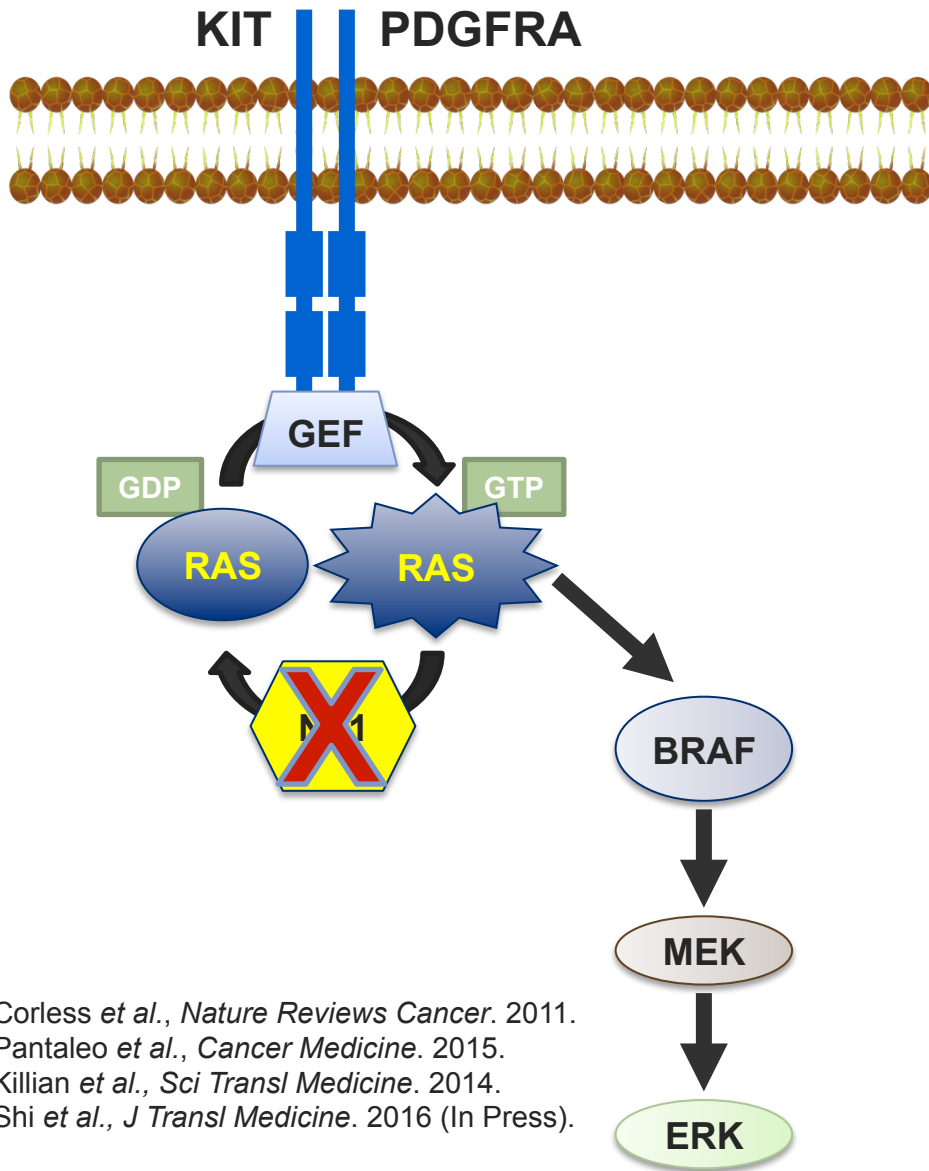
Is Location is a Biomarker for Gene Mutations?

**Location.
Location.
Location.**

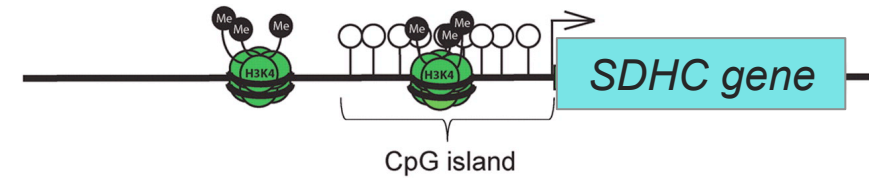


Why *WHERE* you buy is more important than *WHAT* you buy.

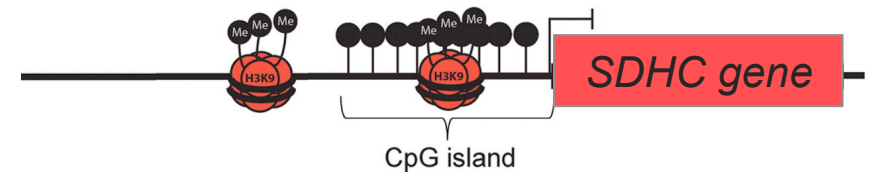
Known Driver Genes in GIST



Unmethylated normal cell promoter



Methylated cancer cell promoter



FGFR1-HOOK3 or -TACC1 fusions

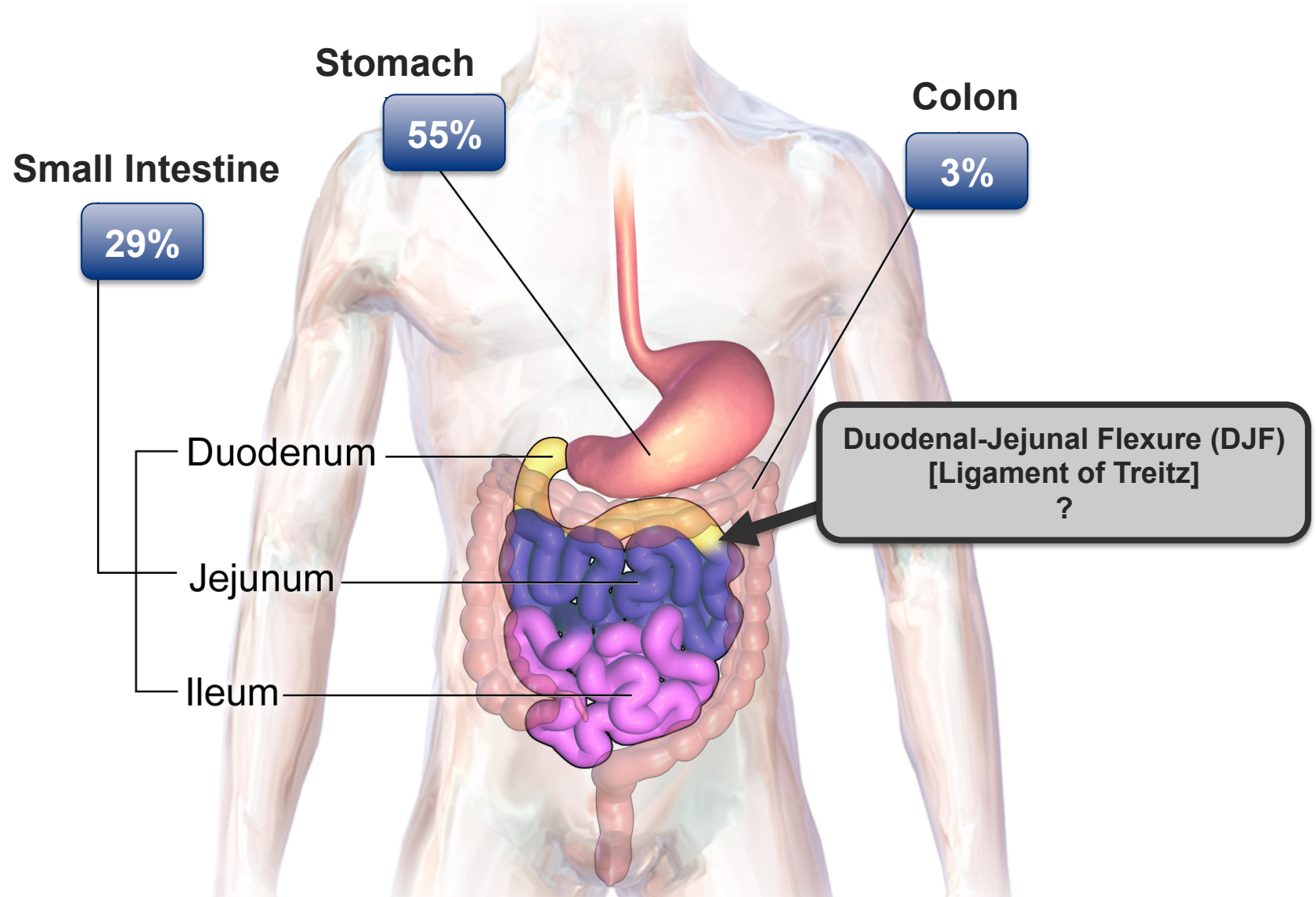


ETV6-NTRK3 fusion

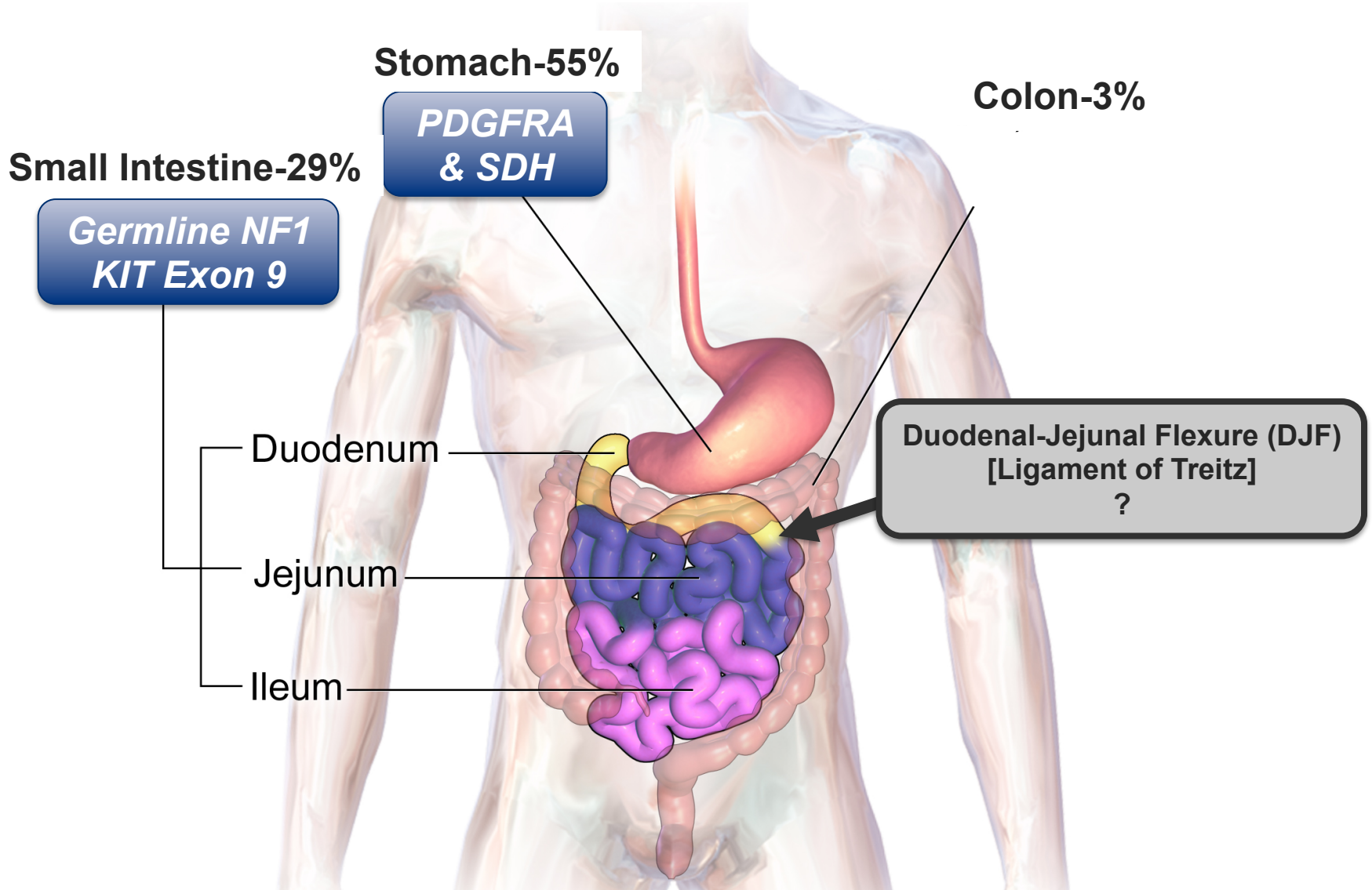


Corless *et al.*, *Nature Reviews Cancer*. 2011.
 Pantaleo *et al.*, *Cancer Medicine*. 2015.
 Killian *et al.*, *Sci Transl Medicine*. 2014.
 Shi *et al.*, *J Transl Medicine*. 2016 (In Press).

Anatomic Localization of GIST



Genes and Localization of GIST



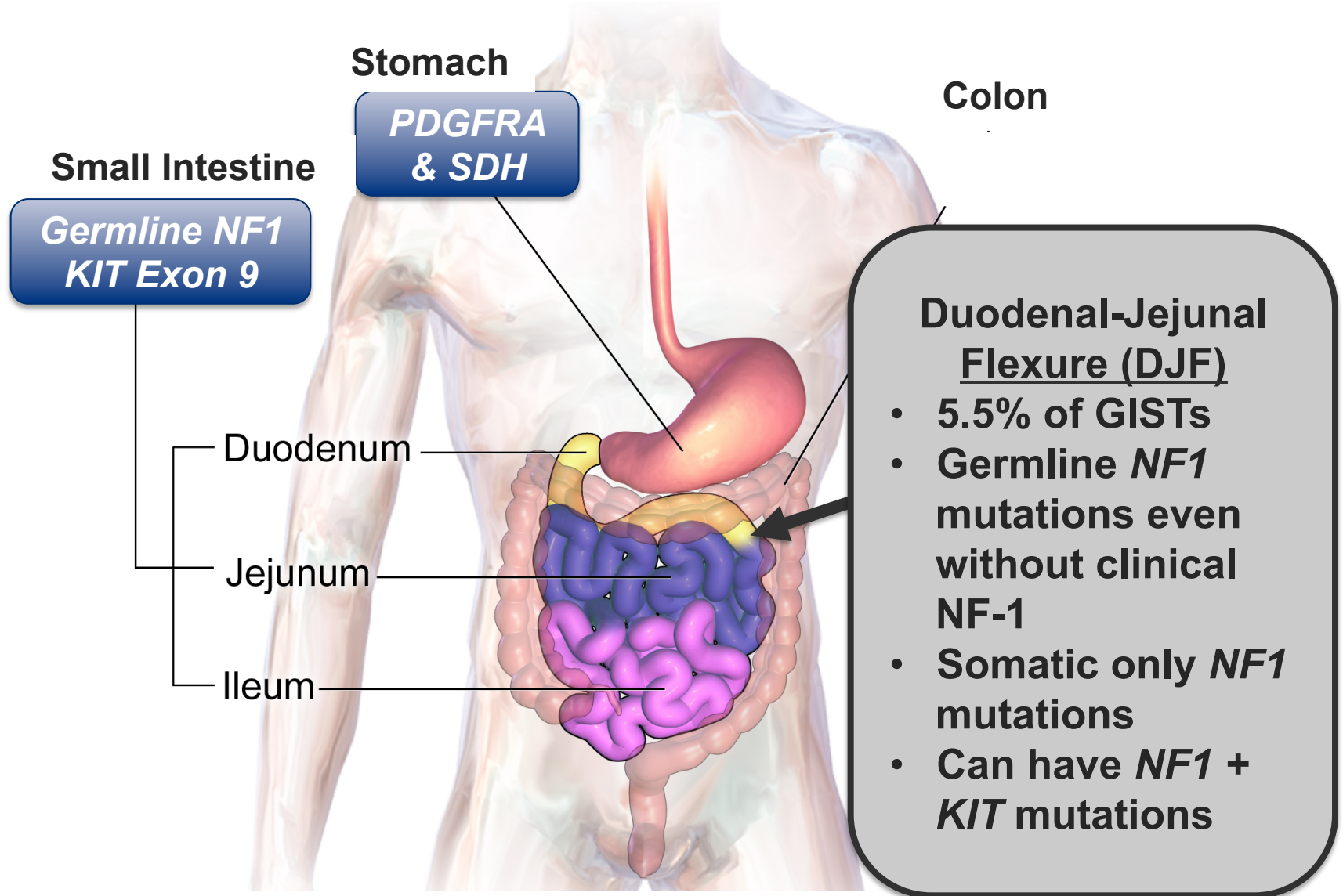
Background: *NF1* Mutant GIST

1. Often multifocal small intestine GISTs associated with Neurofibromatosis type 1 (NF-1)
2. NF-1 associated with 1.5% of GISTs
3. Somatic *NF1* mutant small bowel GIST was recently reported in the absence of a germline *NF1* mutation (Belinsky *et al.*, *BMC Cancer*, 2015).
4. *NF1* gene mutations associated with NF-1 were recently reported (Gasparotto *et al.*, *Clin Cancer Research*, 2016):
 - Frequent in GISTs lacking *KIT/PDGFR α /BRAF* mutations or *SDH* inactivation
 - Especially if multifocal or with a multinodular growth pattern and a non-gastric location.

New Key Findings

1. In three series, GISTs more frequently than 1.5% possess *NF1* genomic alterations
 - 6.1% (MSKCC, 7/115)
 - 9.7% (UCSD, 6/62)
 - 9.7% (FMI, 18/186)

New Key Findings



Methods

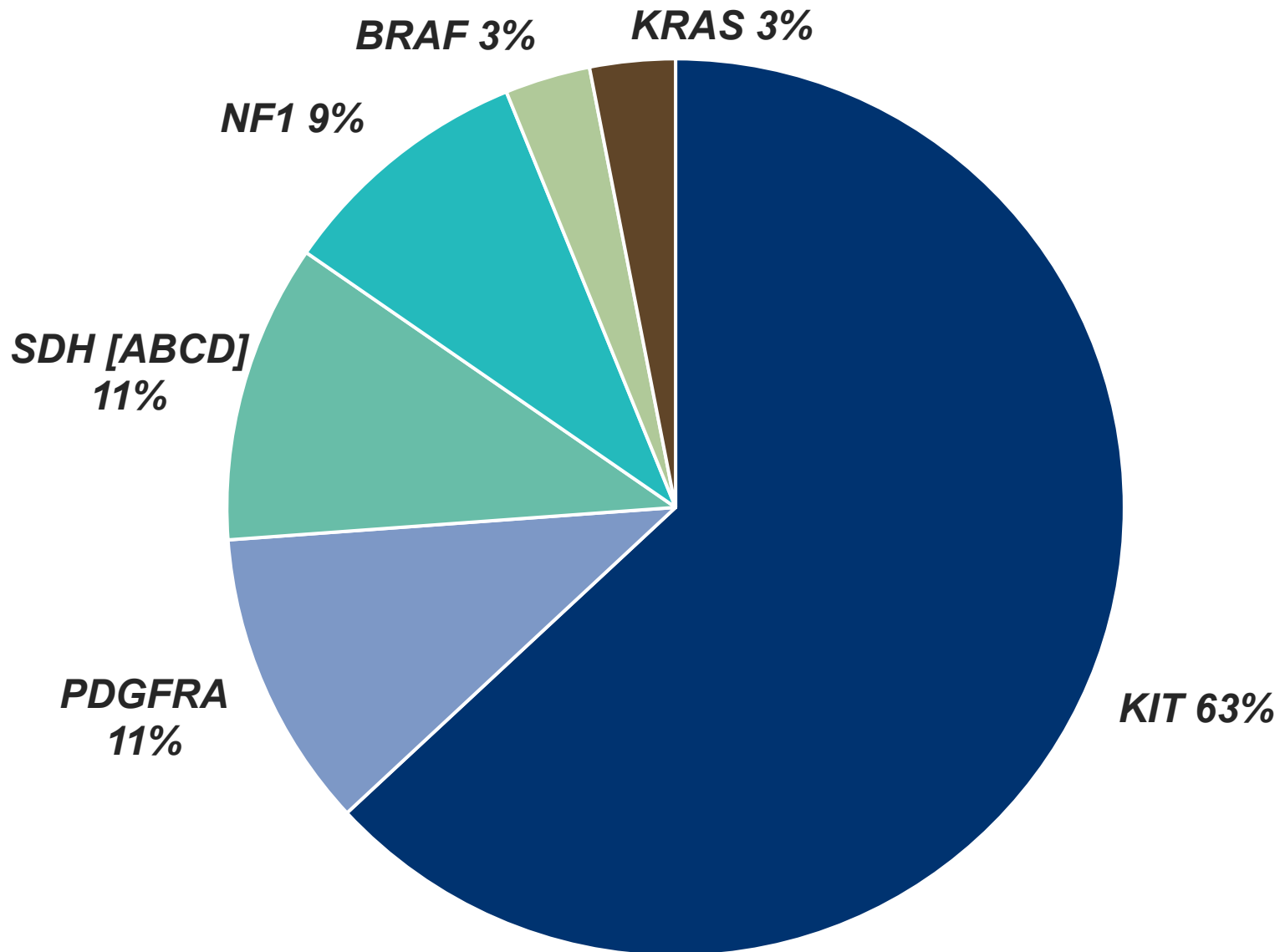
Primary Study Population

- Retrospective study of 165 GIST patients with from January 1, 2000 to April 30, 2017 at the UC San Diego Moores Cancer Center
- Data collected included age, sex, race, ethnicity, primary GIST site, tumor size, and mitotic index.

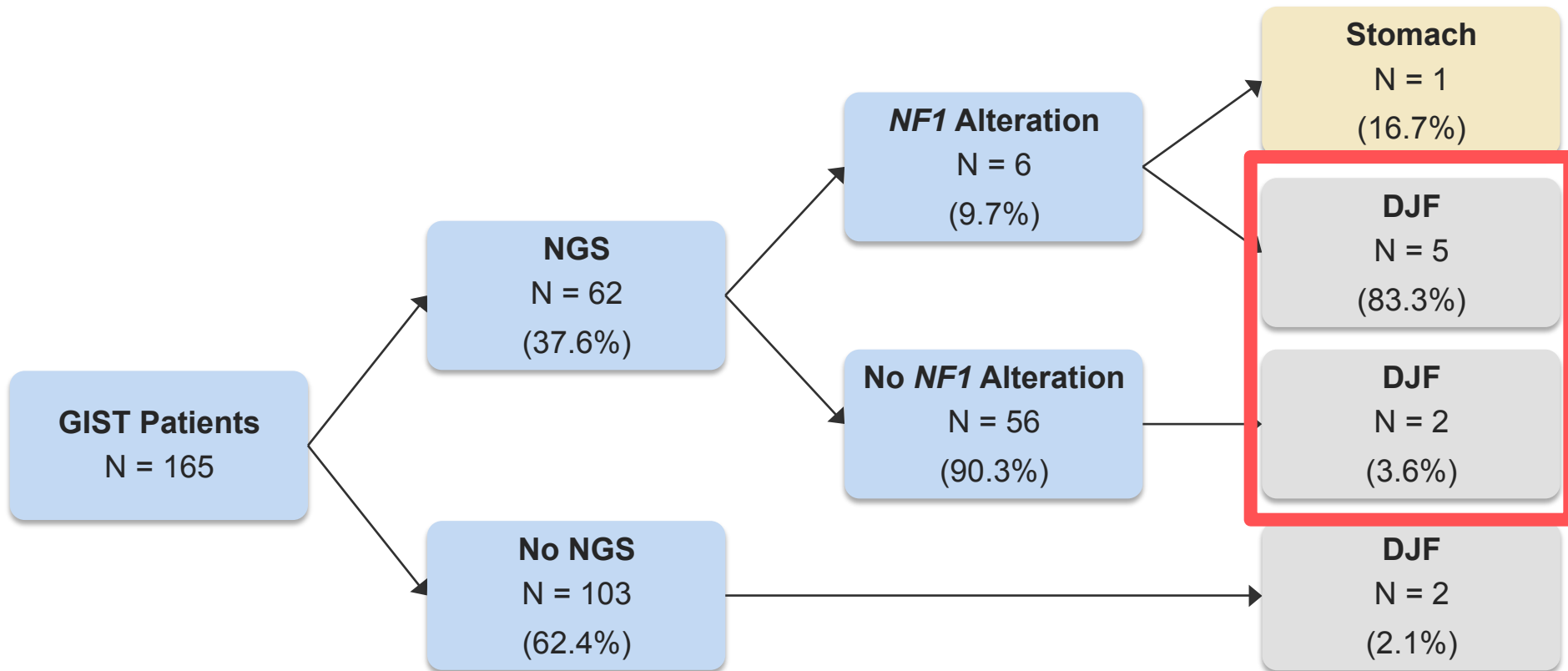
Next Generation Sequencing

- 62 patients underwent NGS of cancer-related genes beginning in 2014:
 - Foundation Medicine (315 genes)
 - UC San Diego Health System Clinical Genomics Laboratory (397 genes)

Driver Mutations in 62 UCSD GIST



NF1 Genomic Alterations are Frequent at DJF



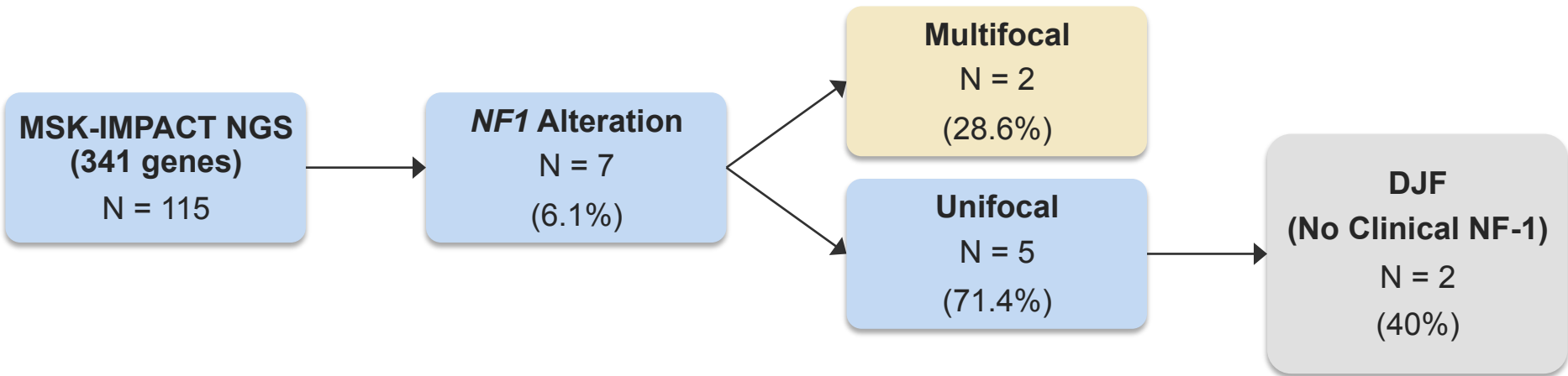
9 DJF GIST Patient Demographics

Characteristic	Number	%
Age, years		
Median (range)	55 (36-80)	
Average	55.9 ± 15	
Sex		
Male	4	44.4%
Female	5	55.6%
Race		
Caucasian	7	77.8%
African American	1	11.1%
Asian/Pacific Islander	1	11.1%
Ethnicity		
Non-Hispanic white	5	55.6%
Hispanic/Latino	4	44.4%

DJF GIST Clinicopathologic Features

Characteristic	Number	%
Stage		
Localized	6	66.7%
Regional	0	0.0%
Distant	1	11.1%
Unknown	2	22.2%
Tumor Size, cm		
Median (range)	9 (1.5 - 15)	
Average	8.0 ± 5.0	
Mitotic Index		
Low	4	44.4%
High	3	33.3%
Unknown	2	22.2%
Cell Morphology		
Spindle	5	55.6%
Epithelioid	0	0.0%
Mixed	3	33.3%
Unknown	1	11.1%

MSKCC Validation Cohort



3	11	2	1	4	5	10	7	6	CASE	
15	8	1.5	13	5.3	3	1	2.5	2.1	Size (cm)	Tumor
									MI (per 5 mm ²)	
									<i>NF1</i> (somatic)	Reported GIST Drivers
			SNP						<i>NF1</i> (germline)	
									<i>KIT</i> (somatic)	
									<i>BRAF</i> (somatic)	
									<i>ARID1A</i> (somatic)	
<i>CDC73</i>	<i>EP300</i>	<i>NOTCH2</i>		<i>MAML2</i>					Notch Pathway	Others
<i>ASXL1</i> <i>MEN1</i>	<i>ERBB4</i> <i>RB1</i> <i>TSC2</i>				<i>BCOR</i>				Others	

Mitotic Index

- High
- Low
- Unknown

Genomic Alteration

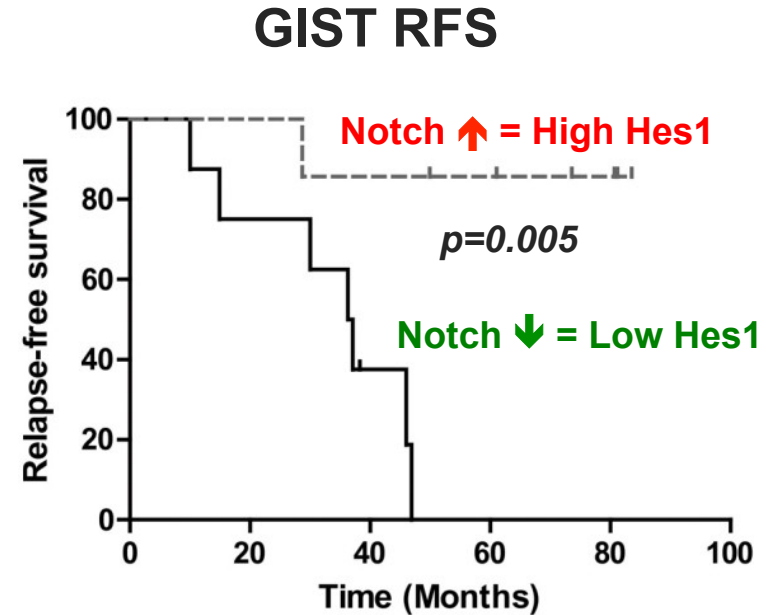
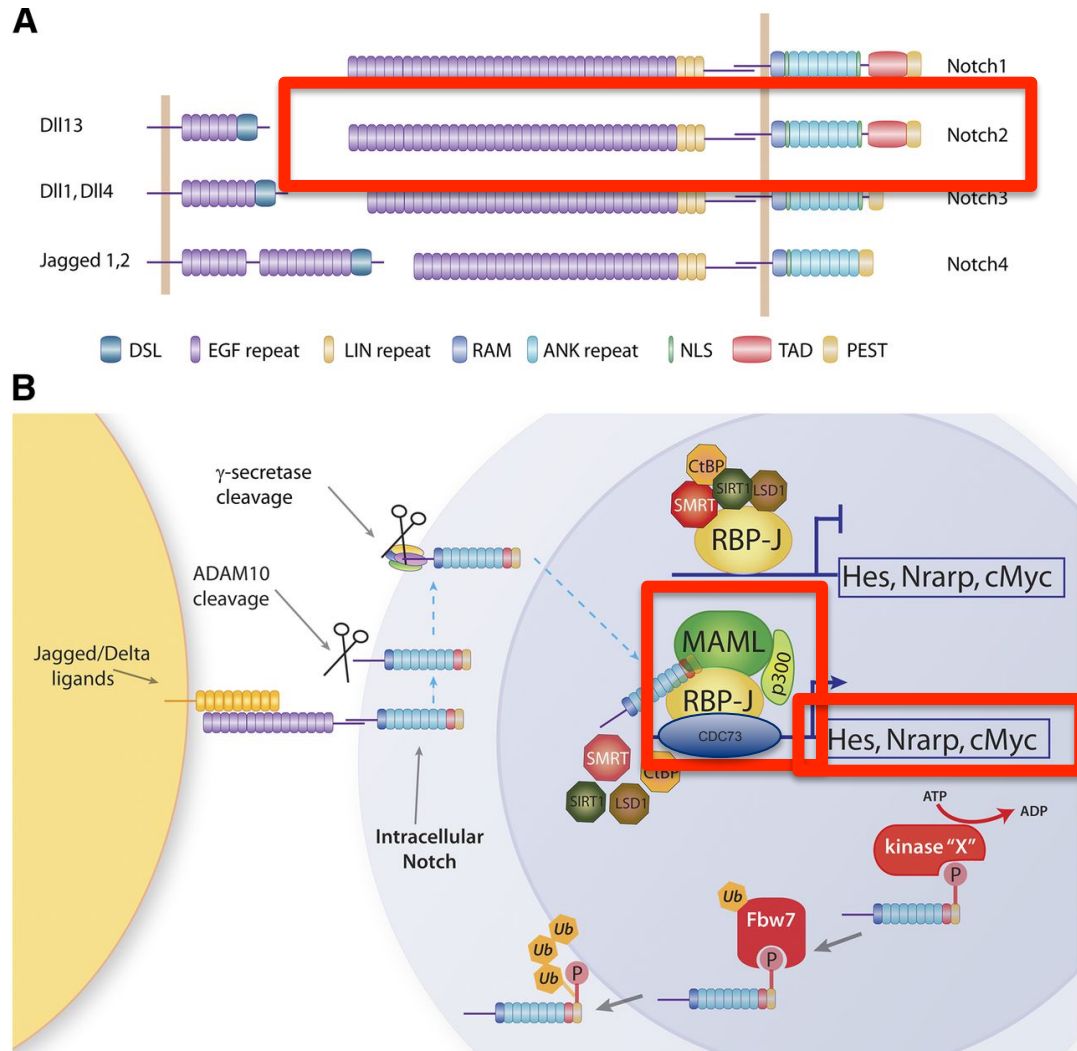
- Nonsense
- Frameshift
- Missense
- In frame indel
- Deletion
- Splicing

Summary #2

- Duodenal-jejunal Flexure (DJF) or Ligament of Treitz GISTs frequently possess *NF1* alterations (somatic and/or germline), which occur even in the absence of clinical NF-1
- This represents a previously unappreciated presentation of clinical NF-1.

Solitary GIST arising at the DJF may be a biomarker for clinically occult NF-1, even if single gene testing reveals a *KIT* mutation.

NF1 and Notch Genomic Alterations

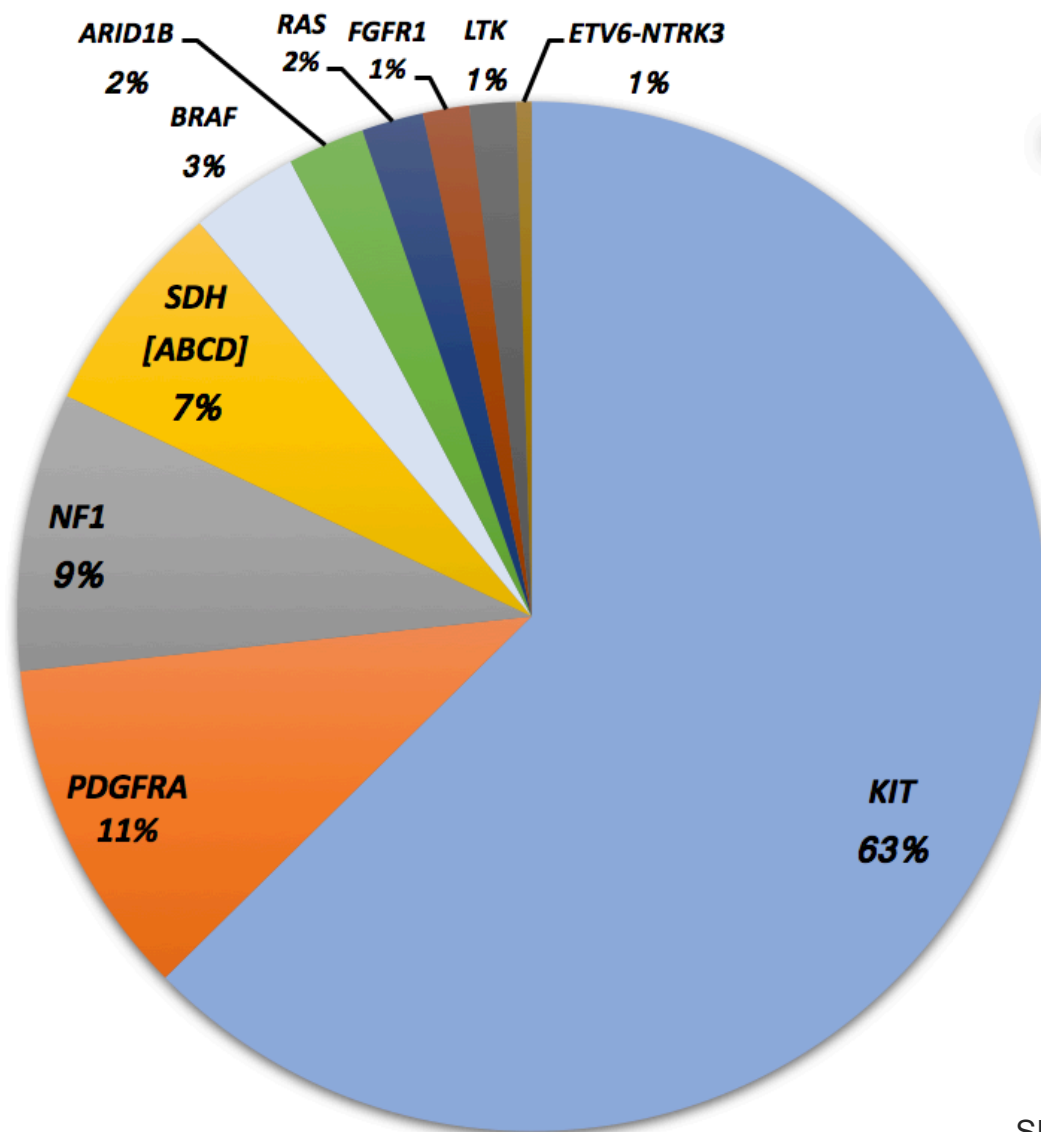


Clinical Implications

Any DJF GIST may be considered for *NF1* gene analysis, and any positive result has the following clinical implications:

1. Additional cancer screening according to expert guidelines.
2. Familial genetic counseling and screening.
3. Personalizing systemic therapy as *NF1* mutant GISTs tend to be imatinib-resistant.

Slicing the Pie...It's Time for Personalization

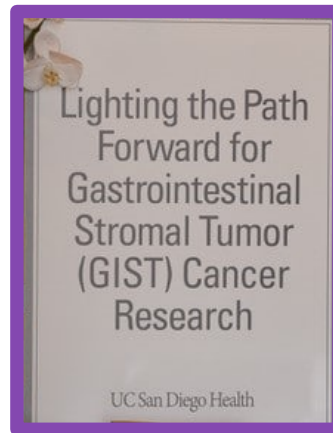




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MOORES CANCER CENTER



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Andrea Califano

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Where discoveries are delivered.SM

UC San Diego
HEALTH SYSTEM