



# Soft Tissue Sarcoma

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Soft Tissue  
Sarcoma  
2022  
ACS estimates

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Incidence

13,190

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Annual Deaths

5,130

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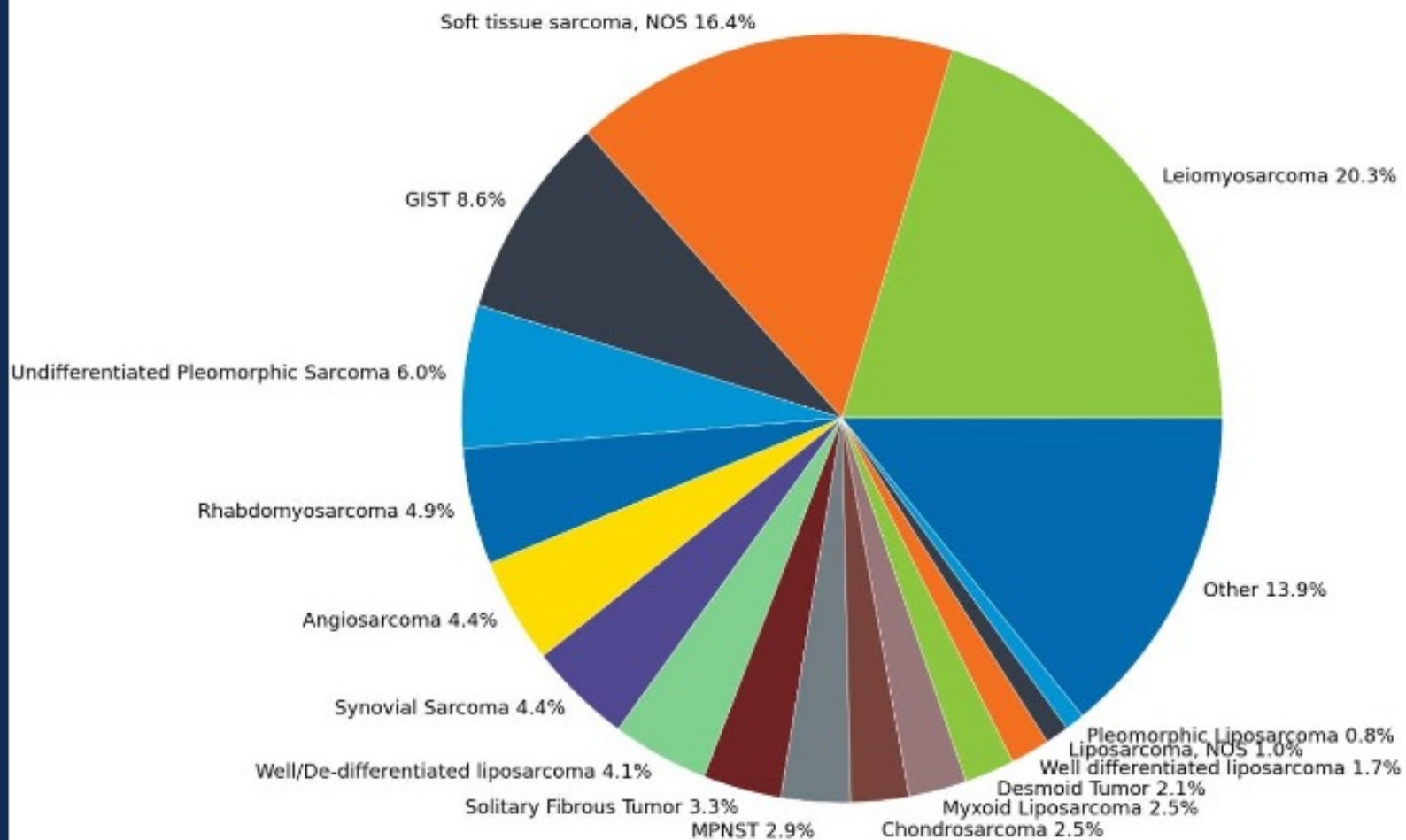
5 yr survival

65%

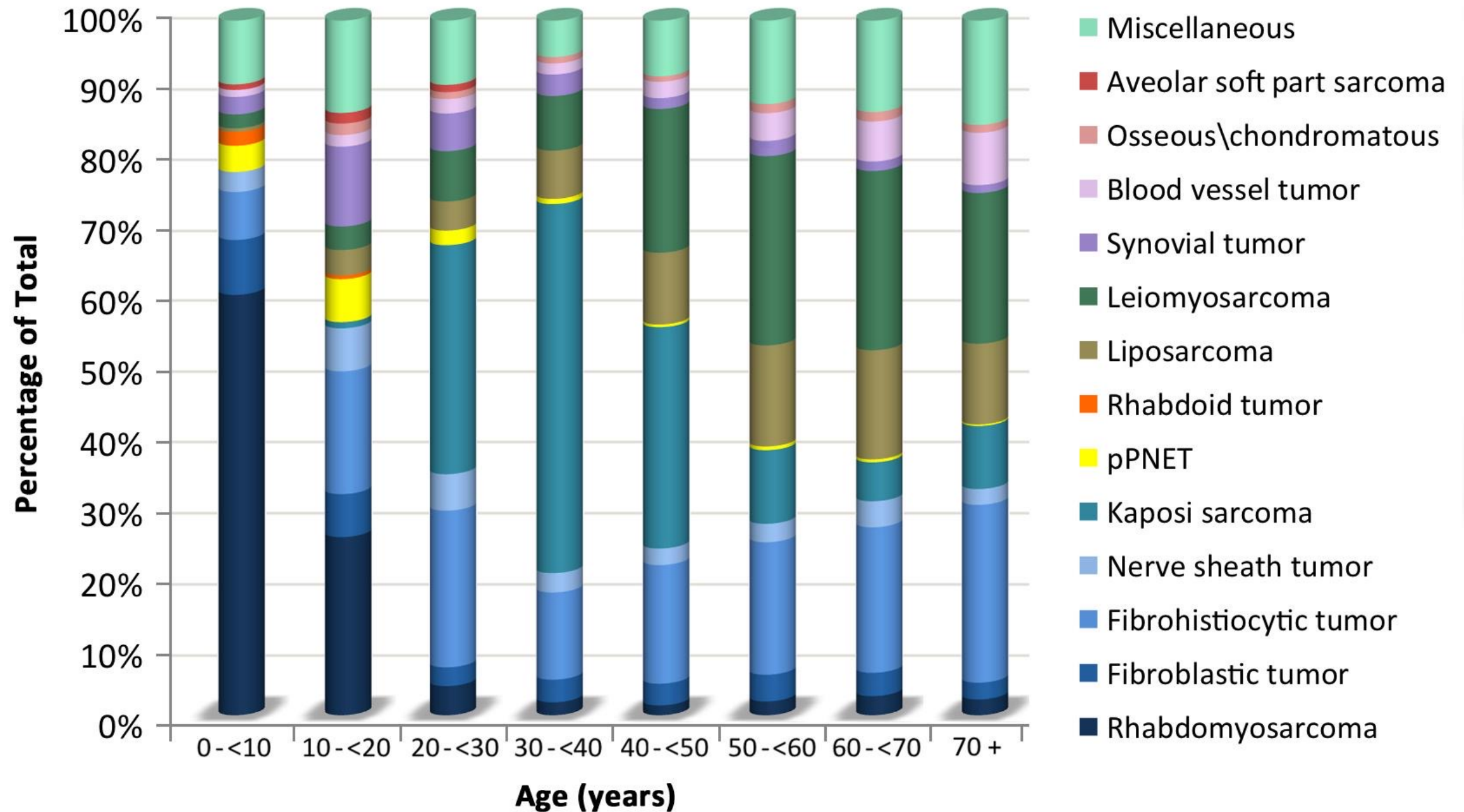
# Pitfalls in Sarcoma Treatment and Research

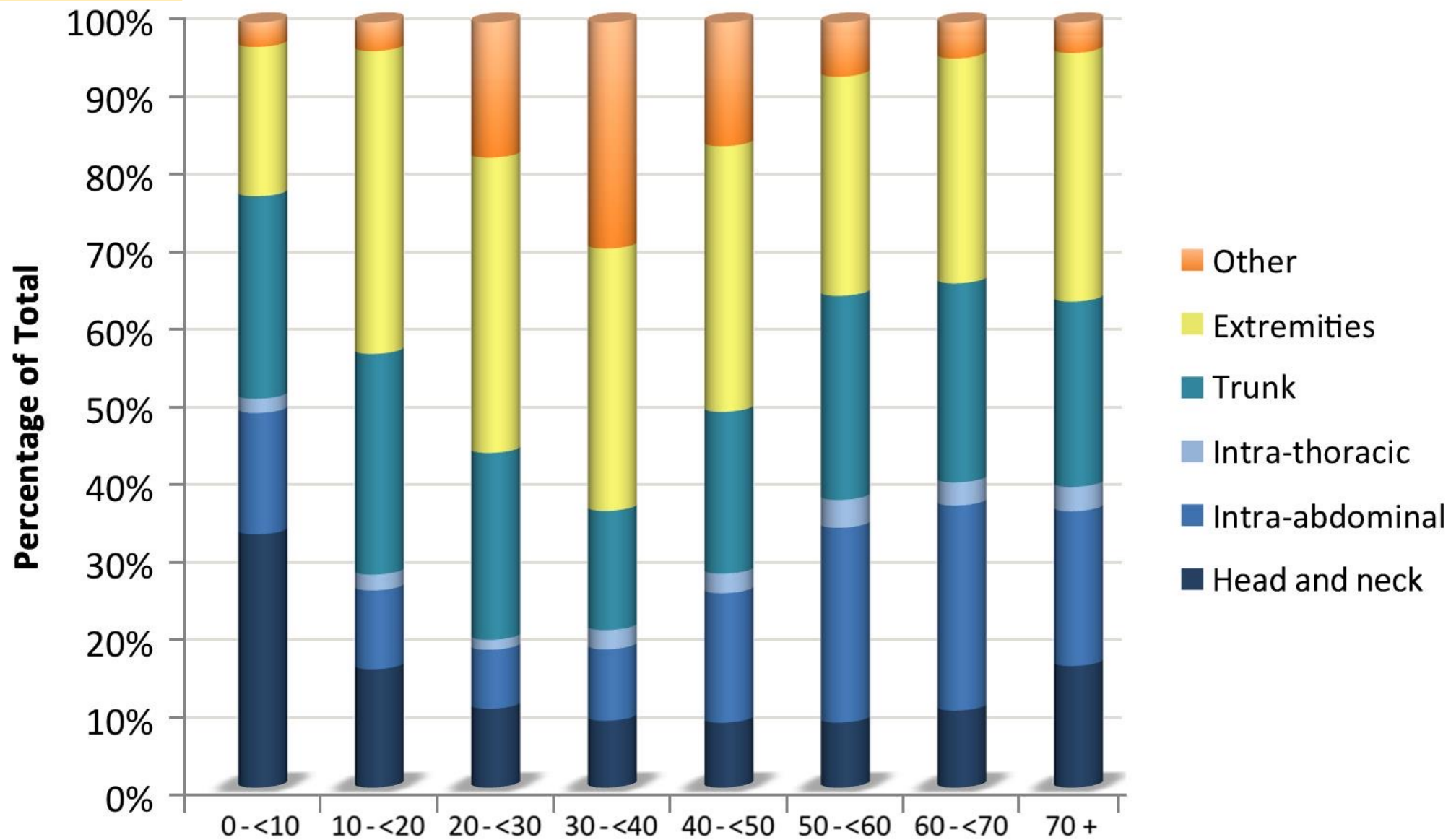
- Extensive variation in histologic subtypes
  - Descriptor “soft tissue sarcoma” is not a single entity
  - Specific molecular alterations may identify unique tumor types
  - Discordant diagnoses among pathologists at different centers problematic ( $\approx 30\%$ )
  - Similar molecular alterations may occur with different morphologic appearance (e.g., NTRK fusion)
- Incidence across the age spectrum from childhood to late adulthood
  - Distinct histologies occur in various age ranges
- Tumors of similar histology may occur in disparate locations complicating surgical access and local control

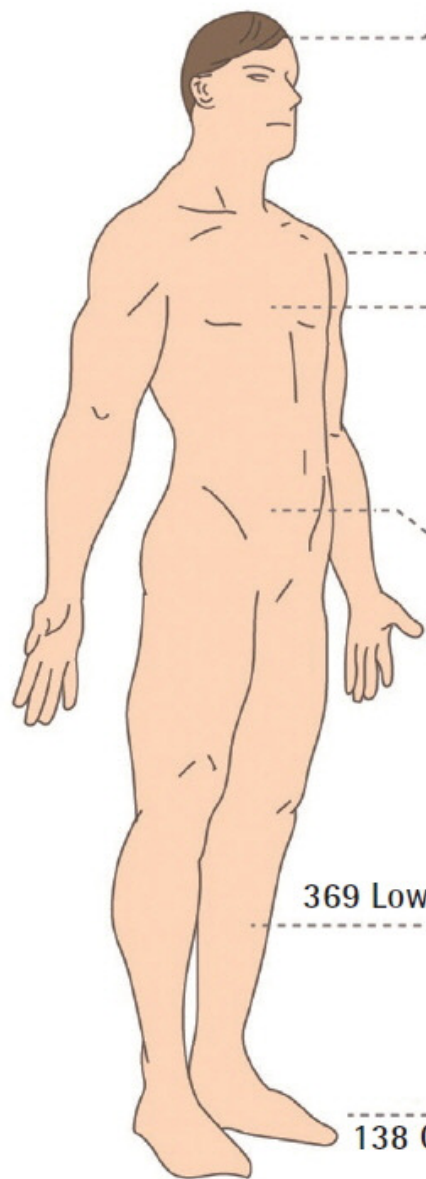
## 56 unique histology (n = 5749)



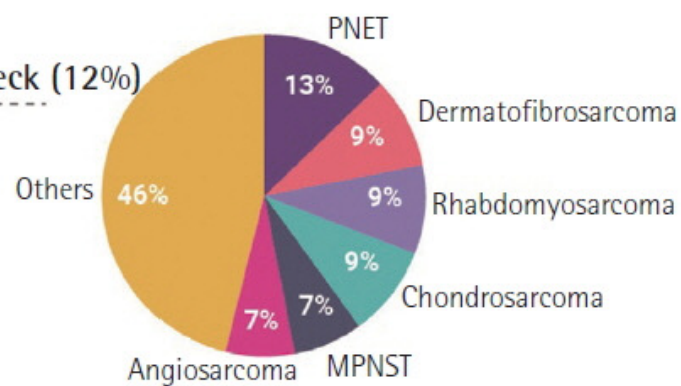
### Distribution of Soft Tissue Sarcoma by Histologic Subtype



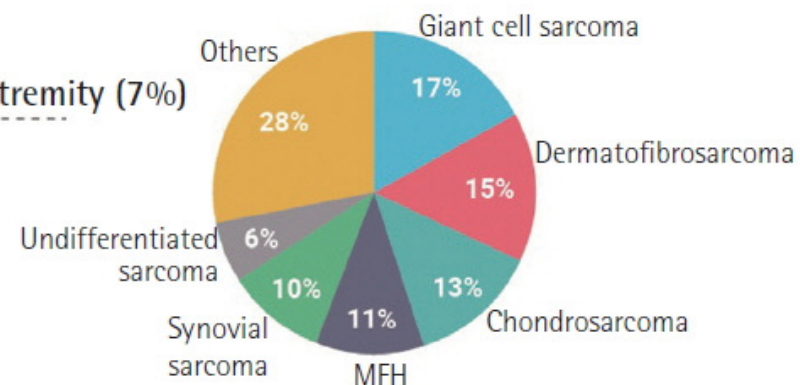




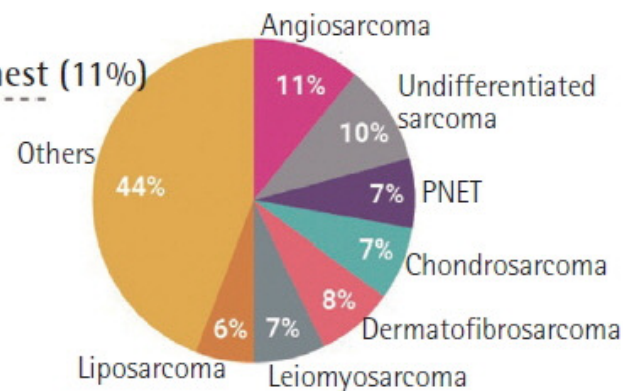
236 Head & neck (12%)



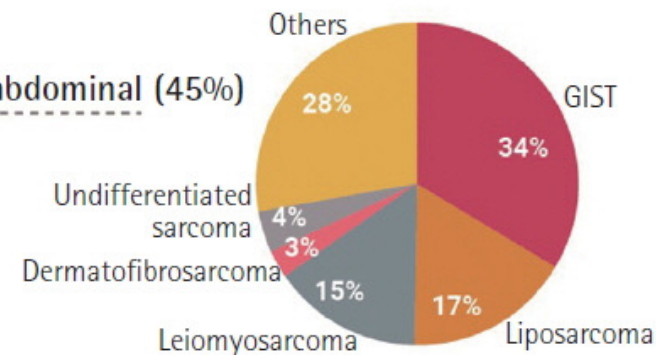
134 Upper extremity (7%)



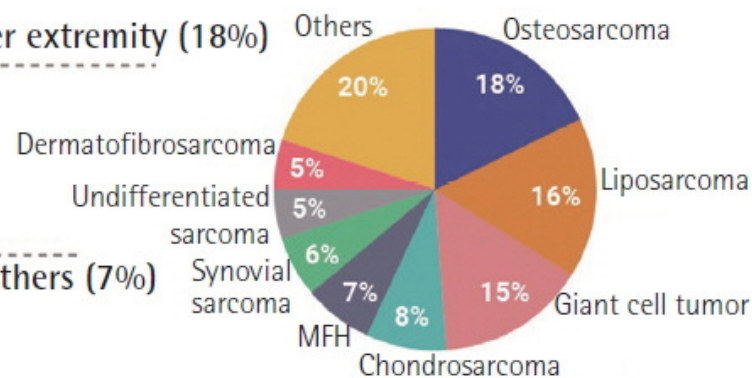
226 Chest (11%)



914 Retroperitoneum intra-abdominal (45%)



369 Lower extremity (18%)



138 Others (7%)



# Primary Therapy for STS

Requires the expertise of multiple disciplines

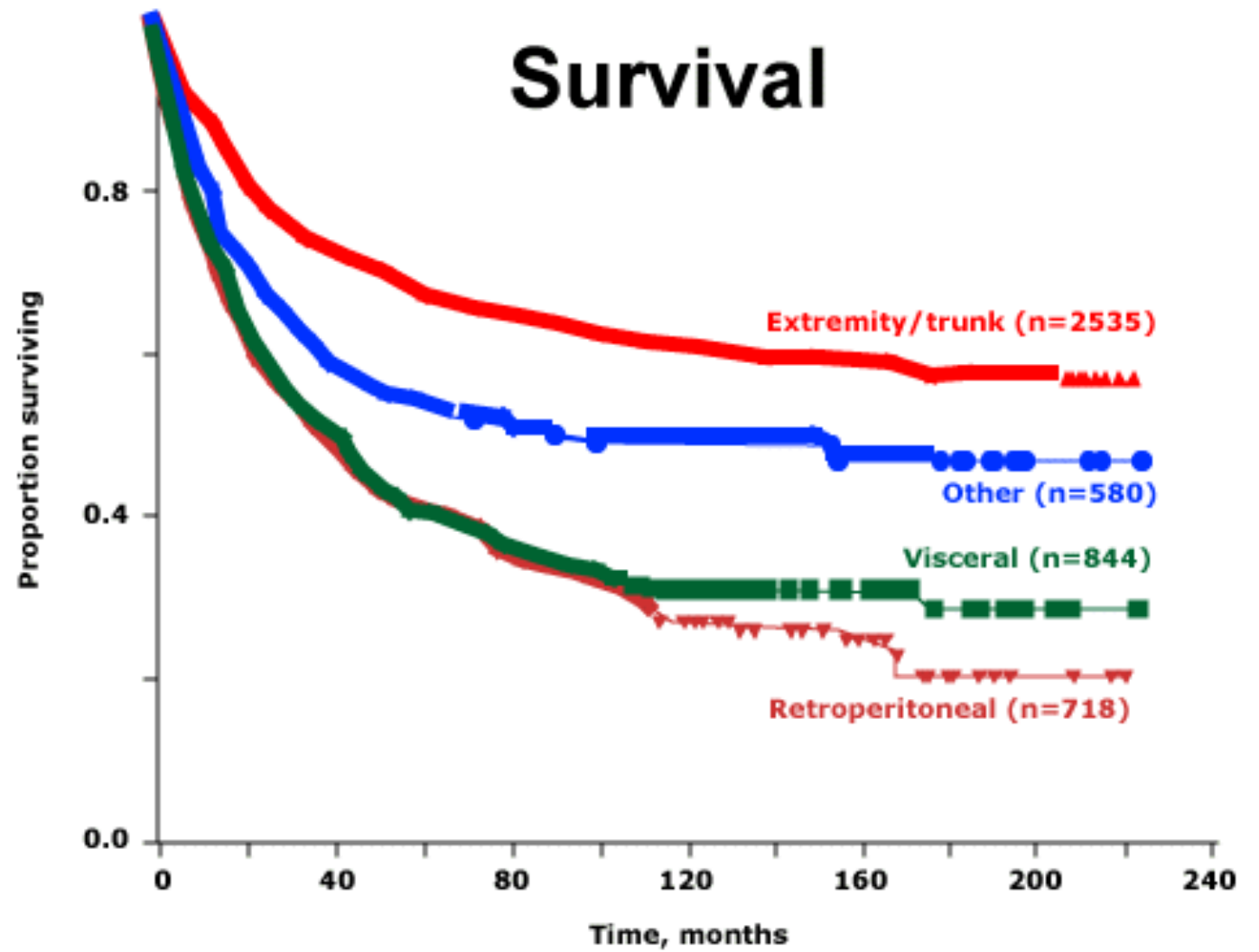
- Orthopedic Oncology/Surgical Oncology
- Radiation Oncology
- Adult Medical or Pediatric Oncology

Extensive reliance on expert pathology

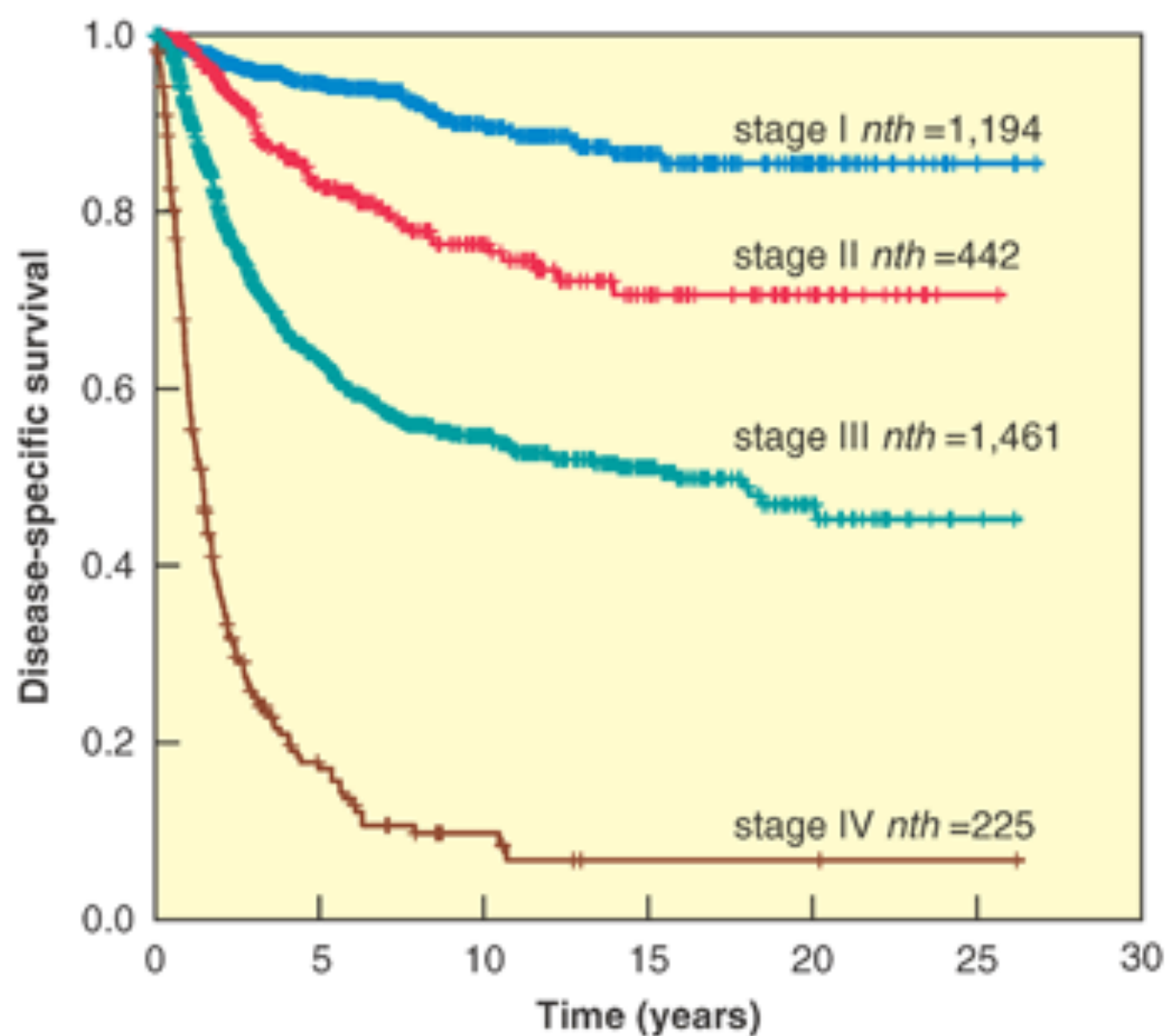
Availability of molecular/genomic testing



MSKCC  
1982-2001



Survival in primary soft tissue sarcoma according to primary site



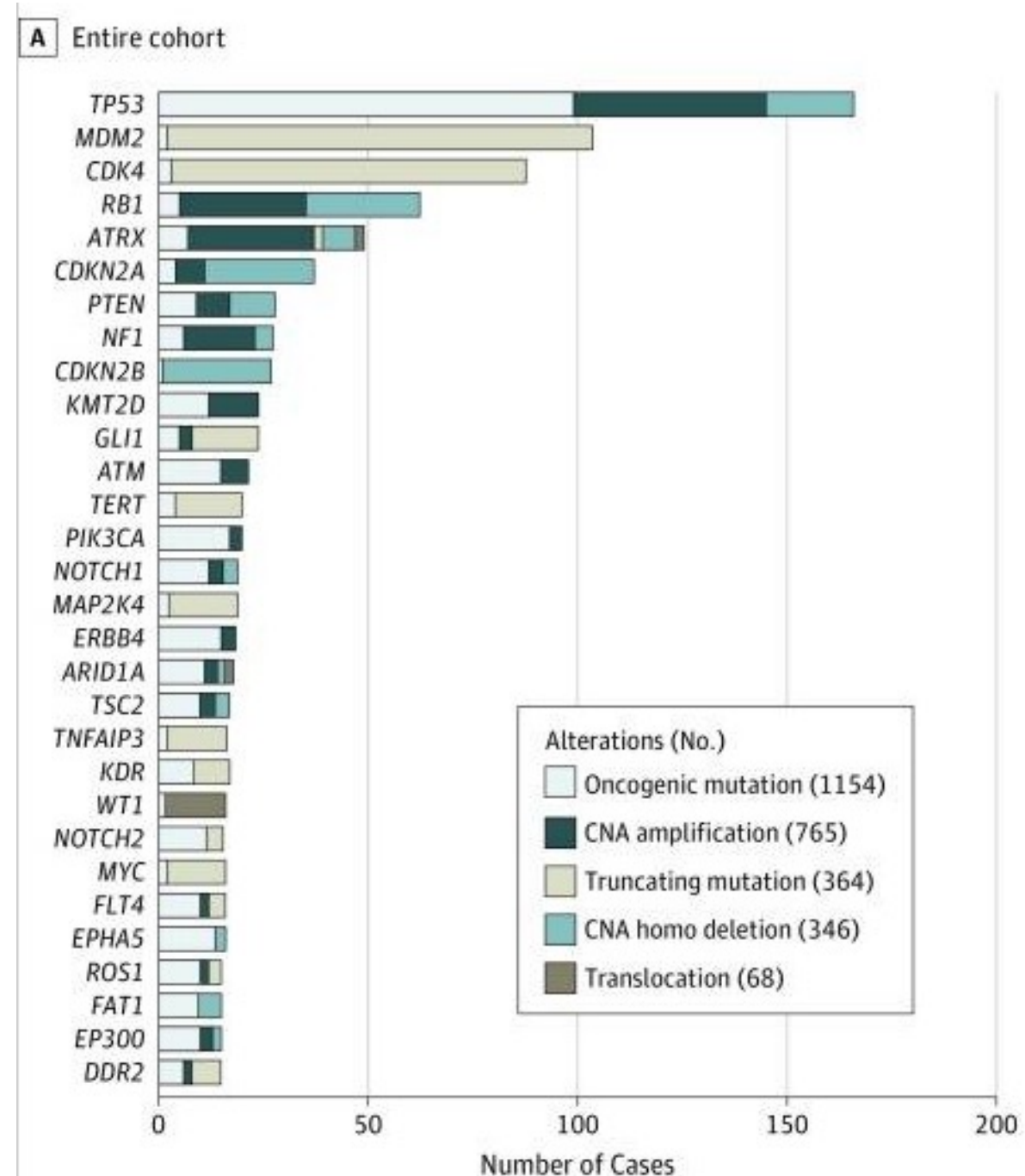
**Figure 90.3** Disease-specific survival for patients with extremity soft tissue sarcoma according to the 2010 American Joint Committee on Cancer staging system. The data are for 3,322 patients seen at Memorial Sloan Kettering Cancer Center from 1982 through 2013.

# Genomic alterations in STS

- Single reciprocal translocations
  - e.g., Ewing, synovial sarcoma, round cell liposarcoma
- Complex karyotypic abnormalities
  - e.g., Leiomyosarcoma, pleomorphic liposarcoma, undifferentiated pleomorphic sarcoma (UPS), angiosarcoma
- Specific oncogenic mutations or recurrent amplification
  - e.g., WD/DD Liposarcoma, epithelioid sarcoma

# Genetic alterations in STS

- 584 patients
  - Complex genomics 57%
  - Translocation 25%
  - Other 19%
- Genomic alterations in 84.6%
  - Most frequent genes
    - *TP53*, *MDM2*, *CDK4*, *RB1*, *ATRX*, *CDKN2A*, *PTEN*, *NF1*, *CDKN2B*, *KMT2D*, *GLI1*, *ATM*, *TERT*, *PIK3CA*, *NOTCH1*, *MAP2K4*, *ERBB4*, *ARID1A*, *TSC2*, and *TNFAIP3*.



# Actionable mutations

• 29.5%

Majority:

- MDM2 amplification
- CDK4 amplification

UPS Undifferentiated pleomorphic sarcoma  
A Angiosarcoma  
L Leiomyosarcoma  
S Sarcoma, NOS

M Myxofibrosarcoma  
SS Synovial sarcoma  
SFT Solitary fibrous tumor  
DST Desmoplastic small-round-cell tumor

DL Dedifferentiated liposarcoma  
WDL Well-differentiated liposarcoma

	Genomic					Transloc			Other			
Genomic Alteration	UPS	A	L	S	M	SS	SFT	DST	DL	WDL	Total	
MDM2 amplification	3			4	2	1			53	26	89	
CDK4 amplification	2			3					49	23	77	
CDKN2A deletions	10	3		3	2		1		1		20	
NF1 truncating mutations	4	1	3		2		1		1		12	
PIK3CA oncogenic mutations	4	4	1	1							10	
PTEN deletions	3		4	1		1		1			10	
KDR (VEGFR2) oncogenic mutations	2	1	3		1				1		8	
CDKN2A truncating mutations	3	3			1						7	
FGFR1 amplification	2			1			1		2		6	
KDR (VEGFR2) amplifications	2	4									6	
ATM truncating mutation		3	2								5	
PTEN truncating mutations	2		3								5	
MET amplification	2			1					1		4	
NF2 truncating mutations	1			1	1				1		4	
KIT mutation	3										3	
MET mutation	1	1	1								3	
ERBB2 oncogenic mutations	1		2								3	
NRAS oncogenic mutations		2	1								3	
TSC2 deletions	1	1	1								3	

# Sarcomas with reciprocal translocations

Fusion genes involving TET family		
Ewing's Sarcoma/PNET	EWS- FLI-1 (85%) -ERG (9-14%) -ETV1, ETV4, FEV (1-5%)	t(11;22) TET family RNA-binding protein (EWSR1) to ETS family transcription factor FLI-1 Overexpression : MYC, IGF-1
Desmoplastic Small Round Cell Tumor (DSRCT)	EWSR1-WT1 EWSR1-ERG	t(11;22)
Clear Cell Sarcoma	EWSR1-ATF1	t(12;22)
Extraskeletal Myxoid Chondrosarcoma	EWSR1-NR4A3	t(9;22) INI-1
Myxoid/Round Cell Liposarcoma	TLS-CHOP EWSR1-CHOP (DDIT3)	t(12;16) TET RNA binding protein to DDIT3  Overexpression: MDM2(TLS), CDK4, Met, PDGF $\alpha$ (EWSR1)

# Sarcomas with reciprocal translocations

	Fusion genes involving chromatin remodeling genes	
Synovial Sarcoma	SS18(SYT)-SSX1; SS18(SYT)-SSX2 (monophasic)	t(X;18)
	Fusion genes involving growth factors	
Dermatofibrosarcoma protuberans (DFSP)	COL1A1-PDGFB	t(17;22) upregulates expression of PDGFR
	Fusion genes involving RTK genes	
Inflammatory Myofibroblastic tumor	TPM3-ALK	Rearrangement of ALK gene
	Other fusion genes	
Alveolar Rhabdomyosarcoma	PAX3-FKHR (FOXO1A)	t(2;13)
Alveolar soft part sarcoma	ASPSL-TFE-3	t(X;17)
Solitary fibrous tumor (SFT)	NAB2-STAT6	Inv(12)
Tenosynovial Giant Cell tumor	COL6A3-CSF1	t (1;2)



# Sarcomas with specific oncogene mutations

GIST	Kit or PDGFR $\alpha$	Activating mutation
Fibromatosis	APC or CTNNB1 mutation	Beta catenin pathway alteration
Perivascular epithelioid cell tumor (PEComa)		LOH of TSC1
Epithelioid sarcoma	SMARCB-1 (INI-1)	del, mutation, inactivation of INI-1
Epithelioid Hemangioendothelioma	WWTR1-CAMTA1	Activation of MAP kinase pathway

# Actionable mutations

Disease	Actionable Genetic Alteration	Rx
ASPS	ASPSL-TFE-3	Cediranib, TKI
Alveolar Rhabdomyosarcoma	PAX3-FKHR (FOXO1A)	Temsirolimus + Cixutumumab
Dedifferentiated Liposarcoma	CDK4 amplification, MDM2	Palbociclib, (nutlins)
DFSP	COL1A1-PDGFB	Imatinib
Epithelioid sarcoma	INI-1 deficient	Tazemetostat
Fibromatosis	CTNNB1 or APC	Imatinib, sorafenib
GIST	C-kit PDGFRA D842V Mutation	Imatinib Avapritinib
IMF	TPM3-ALK	Crizotinib, Ceritinib
NTRK fusion sarcomas	NTRK	Larotrectinib
PEComa	LOH TSC1	mTOR inhibitor (sirolimus, everolimus)
Solitary fibrous tumor (SFT)	NAB2-STAT6	VEGF TKI, sunitinib
Tenosynovial Giant Cell tumor	COL6A3-CSF1	Pexidartinib

# *NTRK* gene fusions have a high incidence in sarcoma

- *NTRK* genes (*NTRK1*, *NTRK2* or *NTRK3*) encode the TRK receptors (TRKA, TRKB and TRKC, respectively)<sup>1,2</sup>
- There is a high incidence of *NTRK* gene fusions in both paediatric and adult sarcomas<sup>1,3</sup>
  - Around ¼ of adult *NTRK* gene fusions positive tumours are sarcomas<sup>2</sup>

## TUMOURS CLASSIFICATION BY *NTRK* GENE FUSIONS<sup>2</sup> INCIDENCE OF *NTRK* GENE FUSIONS IN SARCOMA<sup>3</sup>

### Cancers enriched for TRK fusions

#### ● Frequency >90%

- MASC
- Cellular and mixed congenital mesoblastic nephroma
- Secretory breast carcinoma
- Infantile fibrosarcoma

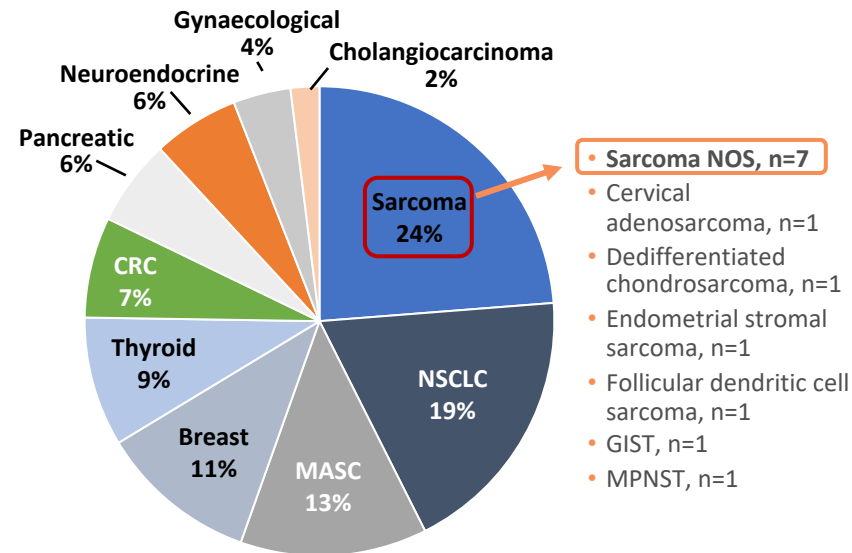
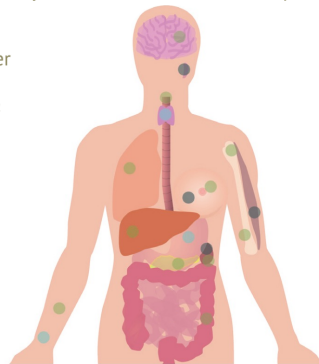
### Cancers harbouring TRK fusions at lower frequencies

#### ● Frequency 5% to 25%

- Gastrointestinal stromal tumour (pan-negative)
- Spitzoid tumours
- Thyroid cancer

#### ● Frequency <5%

- Acute lymphoblastic leukaemia, acute myeloid leukaemia, histiocytosis, multiple myeloma and dendritic cell neoplasms
- Breast cancer
- Cholangiocarcinoma
- Head and neck cancer
- Pancreatic cancer
- Renal cell carcinoma
- Sarcoma
- Colorectal cancer
- High-grade glioma
- Lung cancer
- Melanoma
- Sarcoma

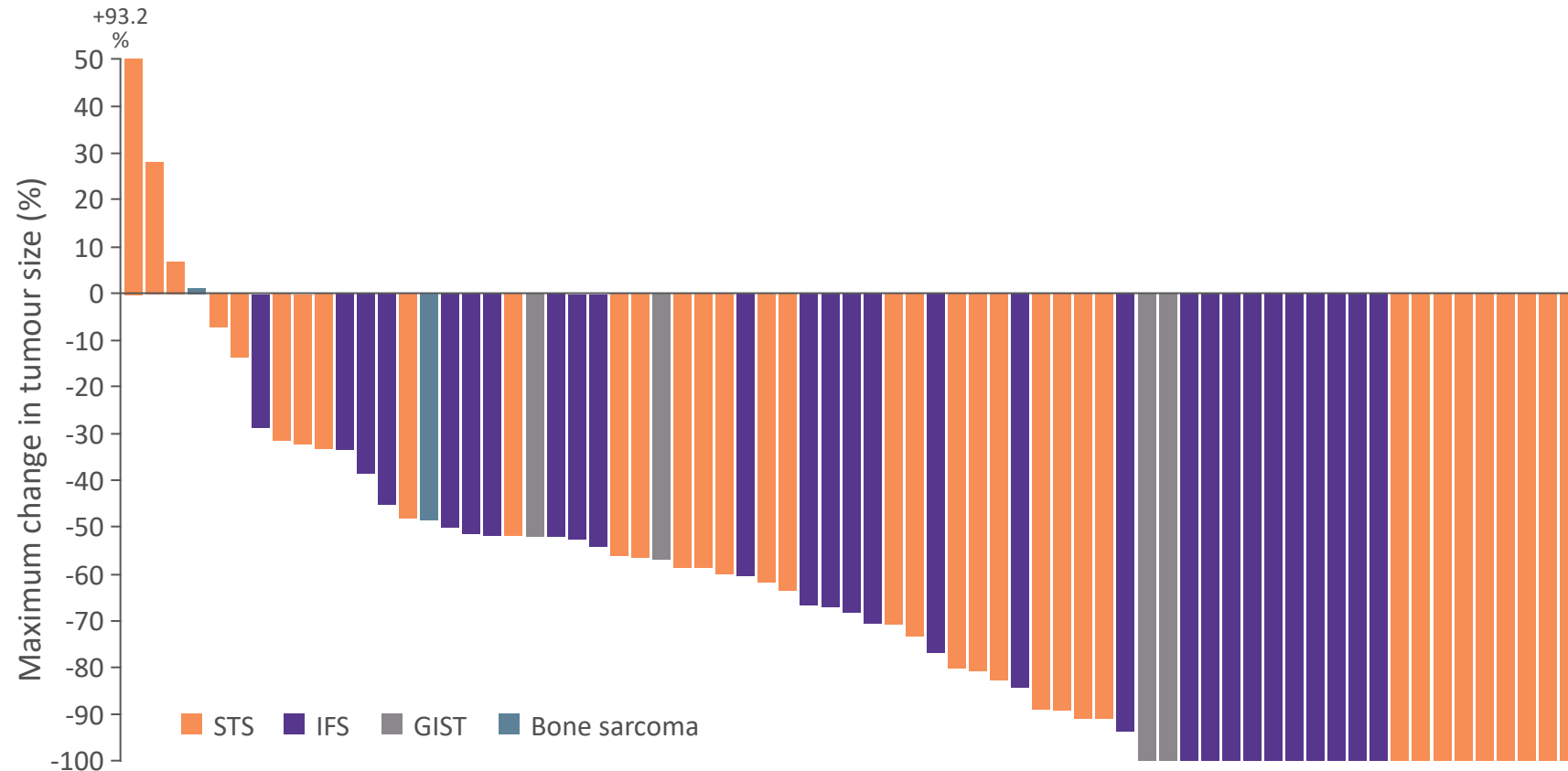


CRC, colorectal cancer; GIST, gastrointestinal stromal tumour; NOS, not otherwise specified; MASC, mammary analogue secretory carcinoma; MPNST, malignant peripheral nerve sheath tumour; NSCLC, non-small cell lung cancer; *NTRK*, neurotrophic tropomyosin-related kinase; TRK, tropomyosin receptor kinase

1. Cocco, et al. Nat Rev Clin Oncol 2018;15:731–47; 2. NTRK CONNECT Blueprint. Available from: <https://ntrkconnect.info/ntrk-gene-fusions-trk-inhibitors-and-testing-approaches-blueprint/>. Accessed March 2020; 3. Doebele, et al. Lancet Oncology 21:271–282; 21:271–82

# TRK-INHIBITION PROVIDES ROBUST RESPONSES IN PATIENTS WITH *NTRK* GENE FUSION-POSITIVE SARCOMA

## EFFICACY OF LAROTRECTINIB IN SARCOMAS HARBOURING TRK FUSIONS: BEST CHANGE IN TARGET LESIONS

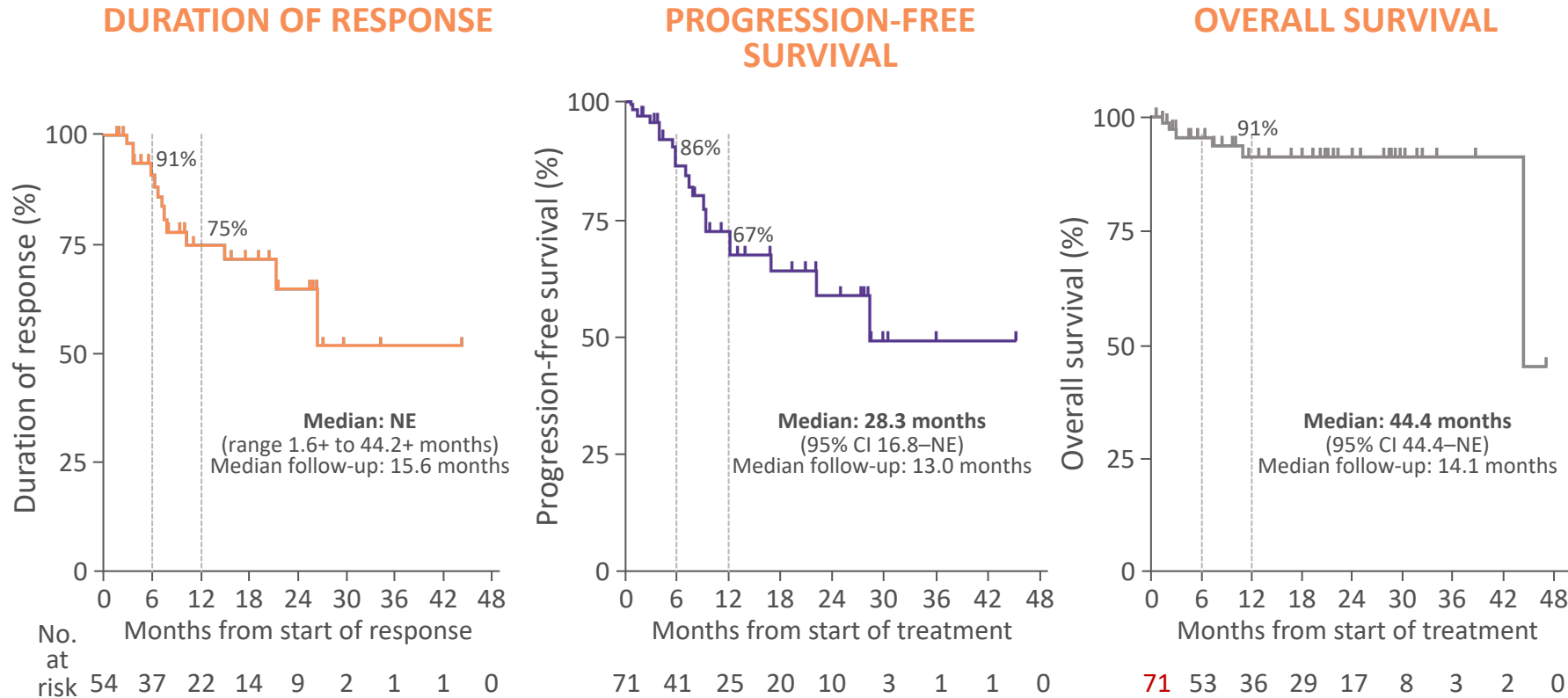


Data cut-off: Feb 19, 2019

IFS, infantile fibrosarcoma; *NTRK*, neurotrophic tropomyosin receptor kinase; STS, soft tissue sarcoma; TRK, tropomyosin receptor kinase; GIST, gastrointestinal stromal tumour

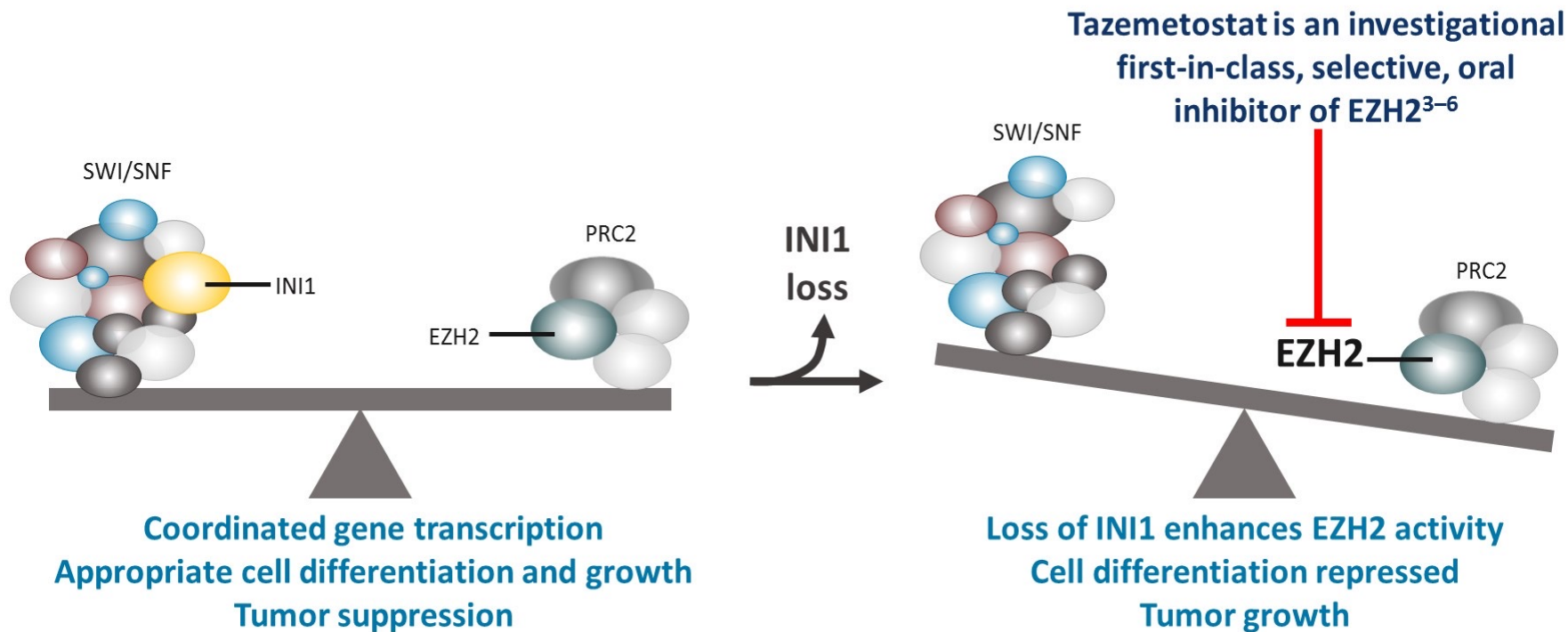
Demetri GD, et al. CTOS 2019. Abstract #3254588

# TRK-INHIBITION PROVIDES DURABLE RESPONSES IN PATIENTS WITH *NTRK* GENE FUSION-POSITIVE SARCOMA



Data cut-off: Feb 19, 2019

## ▶ LOSS OF INI1 CREATES AN ONCOGENIC DEPENDENCY ON ENHANCER OF ZESTE HOMOLOG 2 (EZH2)



### LOSS OF INI1 CREATES AN ONCOGENIC DEPENDENCY ON ENHANCER OF ZESTE HOMOLOG 2 (EZH2)

	Histology	#pts	PR	SD	CBR	
Tazemetostat 800 mg po BID	Epithelioid sarcoma > 90% INI-1(-)	62	9 (15%); No prior Rx 6 (24%)	35	71%	selective inhibitor of EZH2 Phase II: 51% pts with tumor regression, mPFS 23.7 wk: no prior Rx 42.1 wk; (c/w doxo 12wk) DOR NR (34.1wks –NE)

# GIST

	# Pts	PFS at 12	CR/PR	SD	CBR	Comments
Avapritinib 300/400 QD	PDGFRA ex 18	43 38 D842V 5 non- D842V	3/33	5	95 %	mDOR NE  AEs: Nausea/vomiting, Fatigue, Anemia, Cognitive Effects, Periorbital Edema. Diarrhea Gr 3 anemia 33%, fatigue 13%



# New Agents

	Histology	# Pts	CR/PR	SD	Comments
Nab-sirolimus IV qw 2/3	PEComa	31	1/11 (39 ) 5 > 1 y	52%	25: mutations TSC2 (9) Responses 8/9 mPFS 10.6 m; mOS 40.8 m
Abemaciclib 200 mg po BID	DDLPS	30  50% = 1L	1 PR 3 (>10% ↓)		PFS @ 12 wks: 76% (c/w 40%) mPFS 30.4w AE gr ¾: cytopenias, diarrhea

# APROMISS Trial

- Phase III trial of AL3818 (anlotinib/catequentinib) v DTIC
- Multi-targeted TKI: VEGFR, C-kit, PDGF  $\beta$ , FGFR1/2/3
- Second line therapy
- Randomized 2:1
- 79 pts
- PFS: 2.89 v 1.64 mos p. 0.0015
- % progression free at 4, 6, 12 mos
  - TKI: 48.1%, 42.3%, 26.9%
  - DTIC 14.8%, 11.1%, 3.7%

# Epithelioid Hemangioendothelioma (EHE)

- Translocation of WWTR1 (TAZ) and CAMTA1 results in fusion protein → activation of MAP kinase pathway
- Tremetinib (MEK inhibitor) 2 mg po daily
- No. Patients: 42 F>M
- TAZ-CAMTA1
  - Positive 27; Negative 7
- AE (#pts): rash (35) fatigue (22), alopecia (12), edema (11) GI, anemia (14), hypoalbuminemia (11)
- 0 CR, 3 PR (TAZ-CAMTA1 negative), SD 40% > 6 months
- mPFS 8.2 m, OS 15 m
- QOL: decreased pain at 4 weeks

# Immunotherapy and STS

Agent	ORR (%)	mPFS (m)	RR by subtype	
Ipilimumab	0	1.9	SS	Maki, 2013
Pembrolizumab	<b>18</b>	4.5	<b>UPS 23%</b> (2 CR), LPS 10%	Burgess, 2019
Atezolizumab	<b>42</b>	NR	<b>ASPS</b>	Coyne, 2018
Nivolumab	0	1.8	Uterine LMS	Ben-Ami, 2017
Nivolumab	5	1.7	ASPS, LMS	D'Angelo, 2018
Nivolumab +Ipilimumab	<b>16</b>	4.1	UPS 28.6, LPS 14.3	
Durvalumab/Tremelimumab	<b>14.3</b>	2.8	<b>ASPS 50%</b> , chordoma 20%, AS/UPS 20%	Somaiah, 2020

# ST Sarcoma histology specific response to immunotherapy






Histology	Drugs	Response Rate
UPS	Pembrolizumab	23%
	Nivolumab + Ipilimumab	29%
ASPS	Atezolizumab	42%
	Pembrolizumab + axitinib	55%
Angiosarcoma	Anti-CTLA4, Pembrolizumab, Axitinib + Pembrolizumab	71%
DDLPS	Pembrolizumab	10%
	Nivolumab + ipilimumab	14%
Uterine LMS	Nivolumab	0%

Tawbi et al. Lancet Oncology 2018, Chen et al. ASCO 2020, Coyne et al. CTOS 2018, Florou et al. JTC 2019, Wilky et al. Lancet Oncology 2019, Ben-Ami Cancer 2017

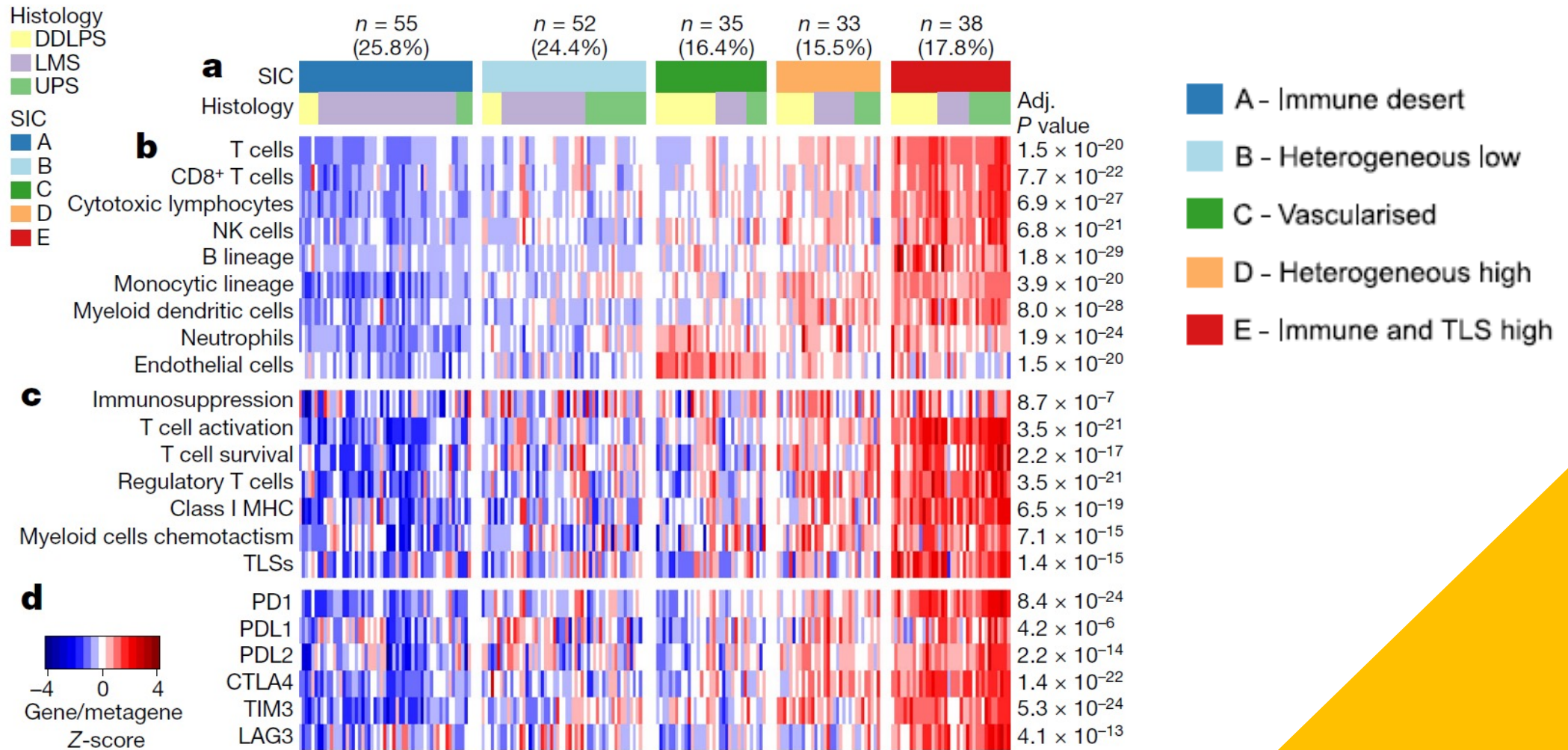
# Sarcoma Immune Classification (SIC)

Petitprez, Nature, January 2020

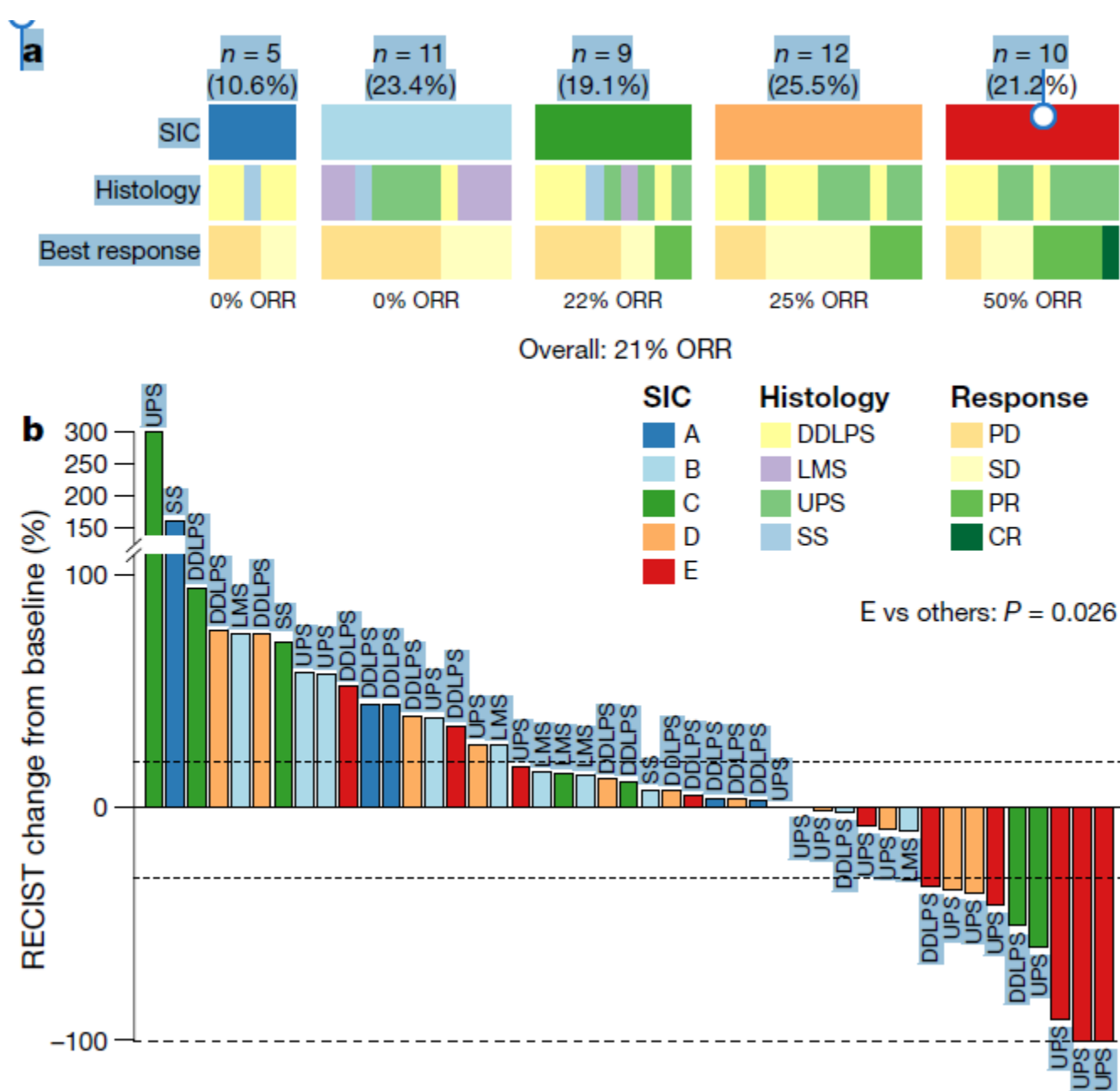
- Gene expression profiling of 4 independent cohorts
  - Composition of tumor microenvironment (TME) by MCP counter
    - e.g., T cells, NK cells, dendritic cells, endothelial cells, B cells
  - Functional orientation of immune TME incl tertiary lymphoid structures (TLS)
  - Expression of genes related to immune checkpoints
  - Association of SIC profile with histology

-  A - Immune desert
-  B - Heterogeneous low
-  C - Vascularised
-  D - Heterogeneous high
-  E - Immune and TLS high

## Sarcoma Immune Classification (SIC)/Sarc028







**Fig. 4 | SICs are strongly associated with STS response to PD1 blockade**

# IO/chemo combinations

Agent	ORR (%)	mPFS (m)	RR by subtype	
Pembrolizumab	18	4.5	UPS 23% (2 CR), LPS 10%	Burgess, 2019
Pembrolizumab + Doxorubicin	22	7.8	UPS 66%, LPS 40%, LMS 30%	Pollack, 2019
Pembrolizumab + Cyclophosphamide	2	1.4	SFT	Toulmonde, 2018
Pembrolizumab + Eribulin	5.3	2.8	LMS	Nathenson, 2020
Pembrolizumab + Axitinib	25	4.7	ASPS 54.5; non-ASPS 9.5	Wilky, 2019
Nivolumab	5	1.7	ASPS, LMS	D'Angelo, 2018
Nivolumab + Sunitinib	9.3	5.9	AS, ESMC, SS, ASPS	Martin-Broto, 2019
Nivolumab + Ipilimumab + Trabectedin	22	NR	Multiple	Chawla, 2019

# SPEARHEAD 1 Trial

- Sarcomas expressing MAGE-A4 in patients with HLA-A\*02
- Leukapheresis collection of autologous T cells for processing: SPEAR (specific peptide enhanced affinity receptor) cells
- Afamitresgene autoleucel (Afami-cel)
- At least one prior Rx with doxo or IFOS
- 37 pts (screened > 300)
  - 32 Synovial Sarcoma
  - 5 MRC LPS
- Pretreatment with leucodepleting drug
- Response (n =25)
  - ORR 39%
    - CR 2 (SS)
  - Disease control rate (DCR) 85%
  - MDR NR, durable
- Adverse effects (> 30% pts)
  - Cytokine release syndrome 22/37
    - 95% ≤ Grade 2
  - Neutropenia
  - Lymphopenia
  - Nausea
  - Fatigue
  - Pyrexia
  - Anemia
  - Cytopenia
    - ≥ G3 at 4 weeks in 6 pts

# New Immunotherapy Agents

- APX005M + Doxorubicin
  - CD40 agonist antibody, CD40 acts as a master regulator of immunity by mobilizing multiple arms of the immune system to initiate highly effective CD8 + T-cell-mediated responses against foreign pathogens and tumors.
- Lurbinectedin
  - selective inhibitor of oncogenic transcription that binds preferentially to guanines located in the GC-rich regulatory areas of DNA gene promoters. Prevents binding of transcription factors to their recognition sequences, inhibiting oncogenic transcription and leading to tumor cell apoptosis.
  - Inhibits activated transcription in tumor-associated macrophages, thereby affecting the tumor microenvironment landscape.

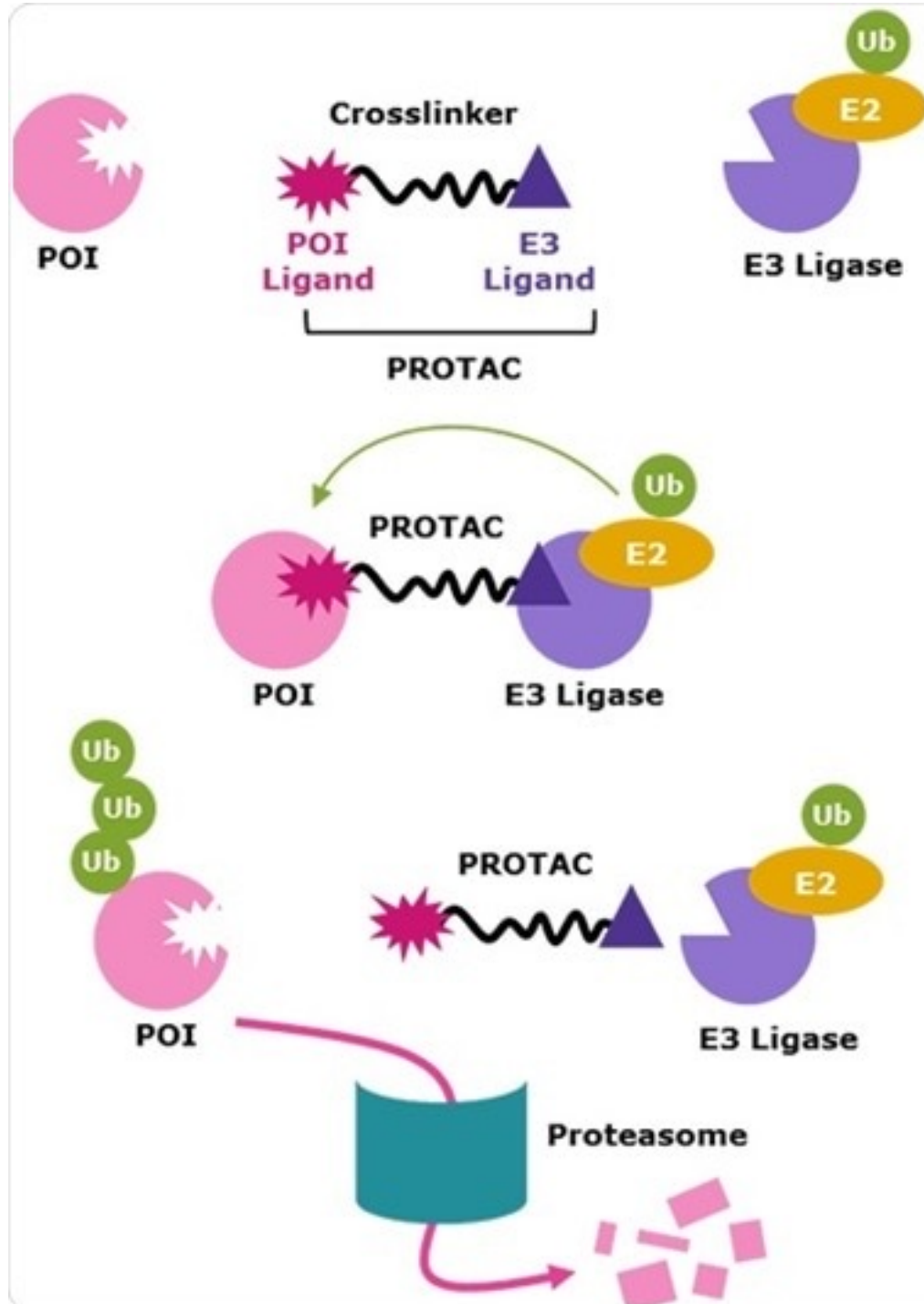
# Phase I Trials

NCIttrials.gov

- Sintilimab
  - anti PD-1
- AGEN1884 (Zalifrelimab)
  - anti-CTLA-4 human monoclonal antibody
- L19TNF
  - fusion protein consisting of human tumor necrosis factor (TNF)- $\alpha$  fused to the L19 antibody specific to the extra-domain B of fibronectin

# Targeted Protein Degradation (TPD)

- Strategy to target proteins with
  - active sites which are broad,
  - shallow pockets that are difficult to bridge with small molecules
  - ‘smooth’ surfaces that offer few sites for a small molecule to bind.
- Class of agents defined as proteolysis-targeting chimera (PROTAC) protein degraders
  - Heterobifunctional small molecules consisting of two ligands joined by a linker: one ligand recruits and binds a protein of interest (POI) while the other recruits and binds an E3 ubiquitin ligase, examples c-myc, kras
  - Molecular glues, promote ubiquitylation of a POI by enhancing a protein–protein interaction (PPI) between a ligase and a potential substrate



1

### PROTAC design

Constructed to bind both protein of interest (POI) and E3 ligase through a crosslinker

2

### Ternary complex

PROTAC recruits POI to E3 ligase

3

### Polyubiquitination

Ubiquitin (Ub) added to POI Lys residues

4

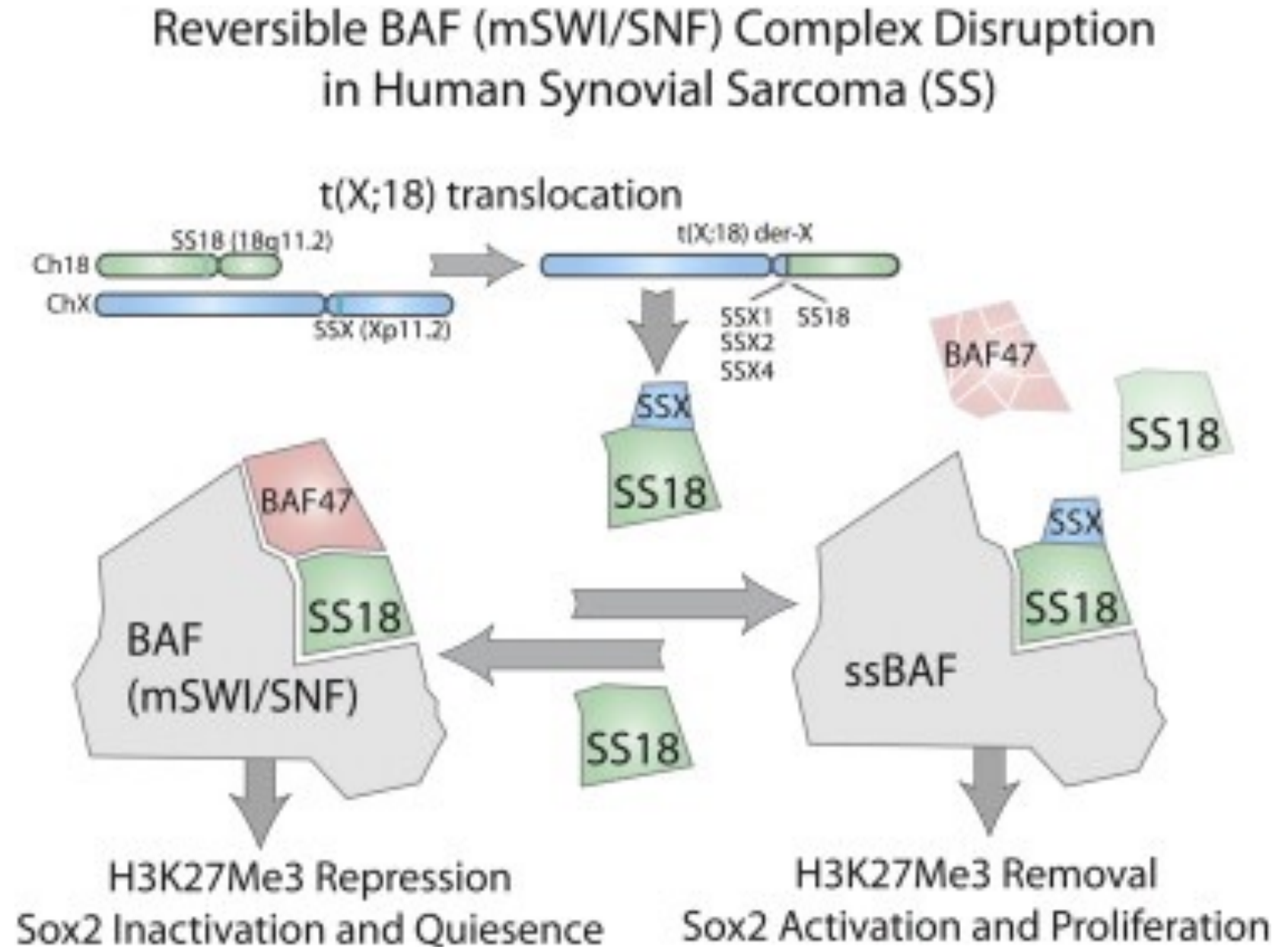
### Target degradation

Ub-marked POI is degraded by the proteasome



## Phase I FHD-609

- Protein degrader
- Target: BRD9 component SWI-SNF complex



# Summary

- “Soft tissue sarcomas” represent a heterogenous population of diseases with varying genetic alterations
- Genomic profiling is critical to identify targets for effective therapy
- Only a modest percentage of sarcoma types are responsive to immunotherapy. SPEAR cell technology is intriguing but at present applies to a minority population
- At present most effective therapies involve inhibition of tyrosine kinases with small molecules
- Emerging protein degradation technology offers possibility to target sarcomas with defined genetic alterations which at present are considered undruggable