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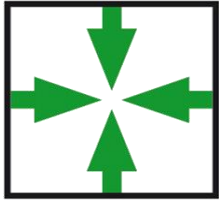
L'importanza della ricerca in Oncologia

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**10-11 OTTOBRE 2019 - ROMA**

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VOI Donna Camilla Savelli Hotel - Via Garibaldi, 27



# MOLECULAR CHARACTERIZATION AND ITS CORRELATION TO CLINICAL OUTCOME IN ADVANCED GASTRIC CANCER: FROM BED TO BENCHSIDE

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SALVATORE CORALLO

ISTITUTO NAZIONALE DEI TUMORI  
MILANO

# THE UNMET NEED

**BENCH**



**BEDSIDE**

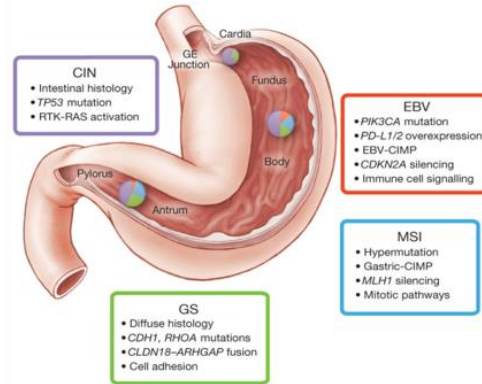


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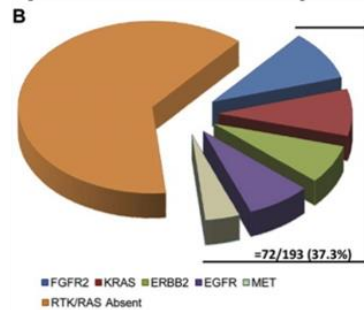
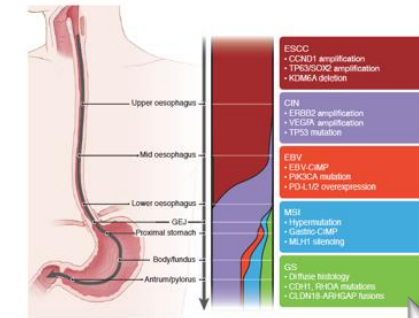


# Recent evolution of understanding the biology of gastroesophageal cancer

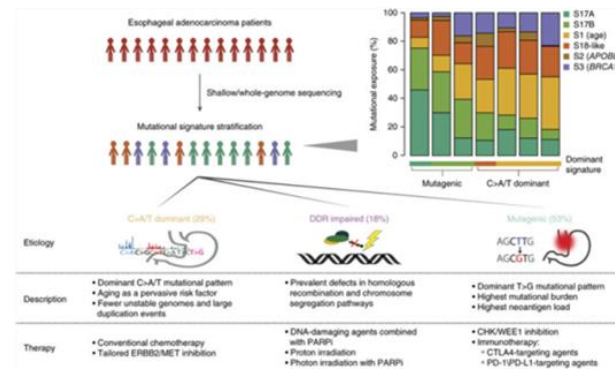
2011  
Identification of RTK amplification



2016  
Subclassification of oesophageal adenocarcinoma



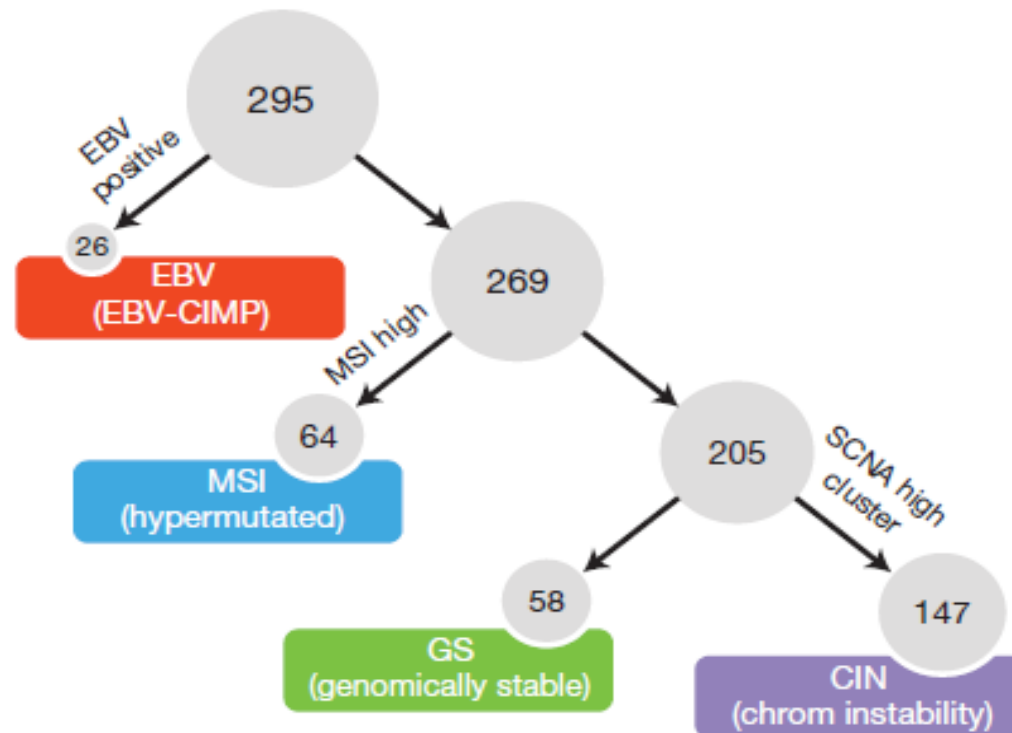
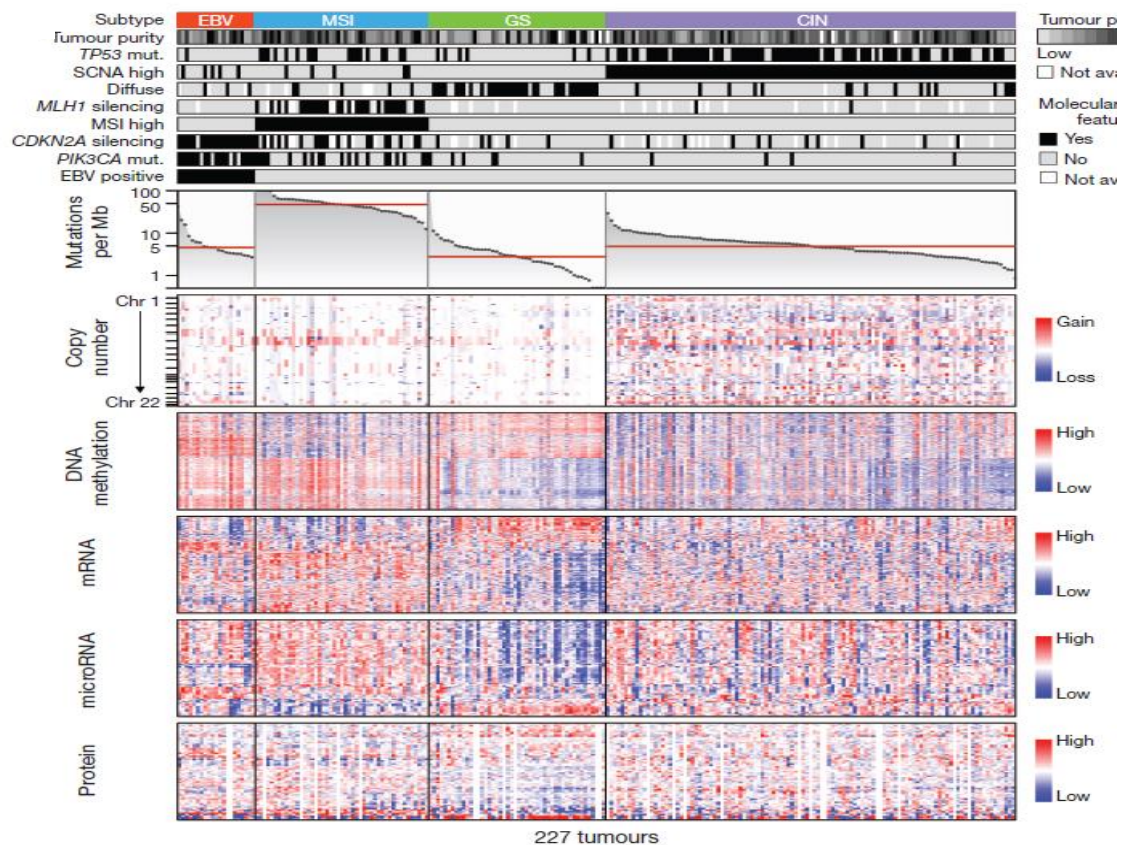
2014  
Gastric cancer  
TCGA



2017  
Oesophageal cancer  
TCGA

Deng et al, Gut 2011  
Gastric Cancer TCGA, Nature 2014  
Secrier et al, Nature Genetics 2016  
Oesophageal Cancer TCGA, Nature 2017

# The TCGA classification: a Copernican Revolution?



The Cancer Genome Atlas Research Network, *Nature* 2014.

# Limits of the TGCA classification

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- Lack of prognostic/predictive impact (only few follow-up data from patient in the TGCA cohort are available)
- Uncertain applicability in the metastatic setting
- Low reproducibility in clinical practice (need of multiple genomic and proteomic data sets).



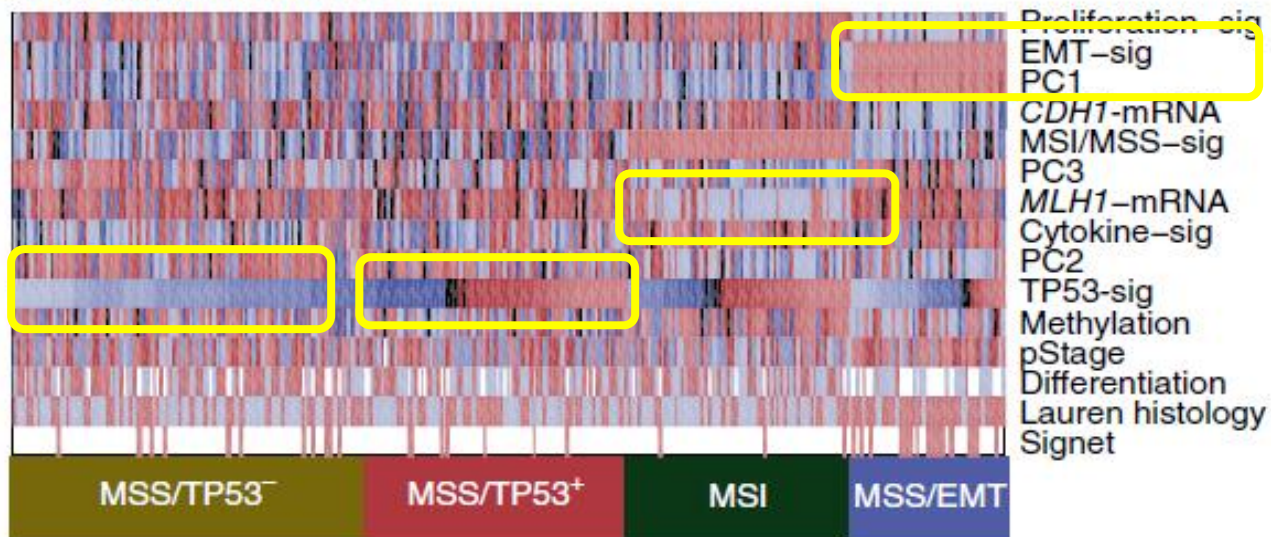


# Overcoming the limits of the TGCA classification: the ACRG proposal

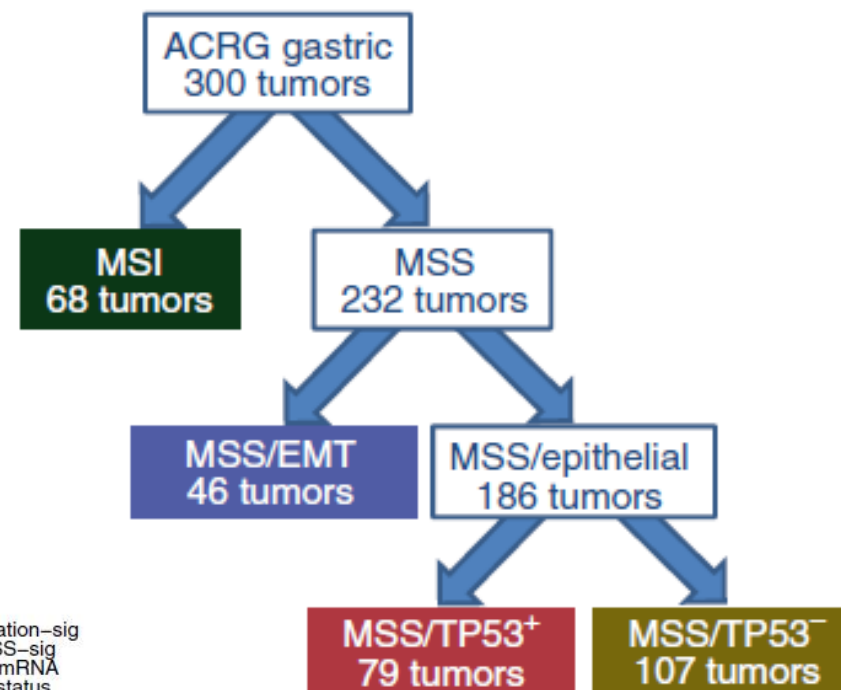


# The ACRG classification

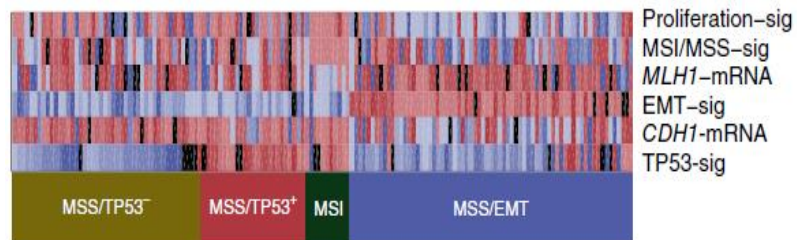
ACRG gastric tumors



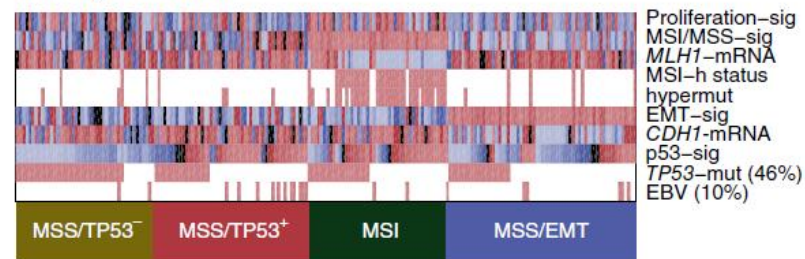
ACRG gastric tumors



Singapore gastric tumors



TCGA gastric tumors



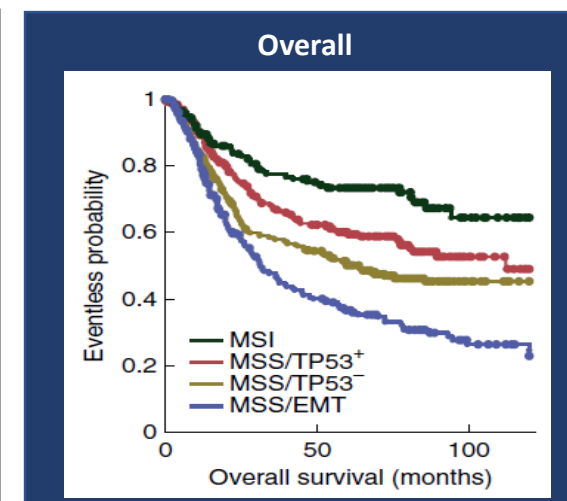
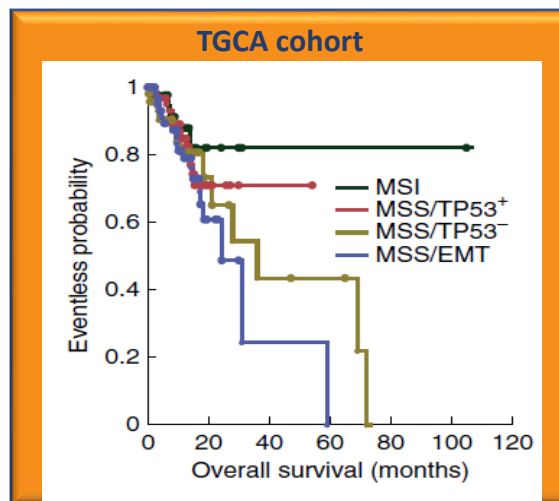
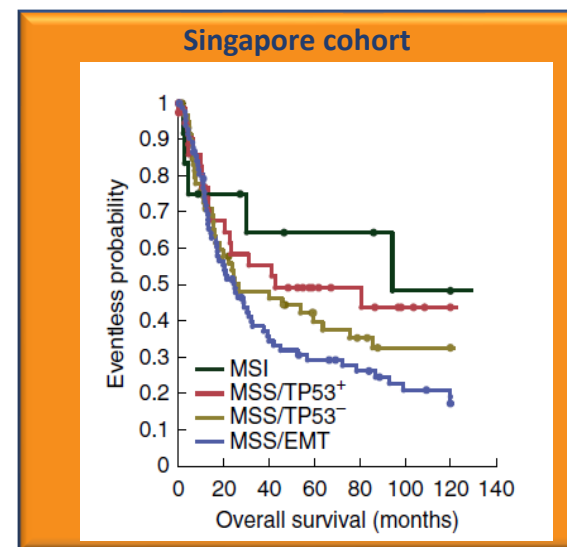
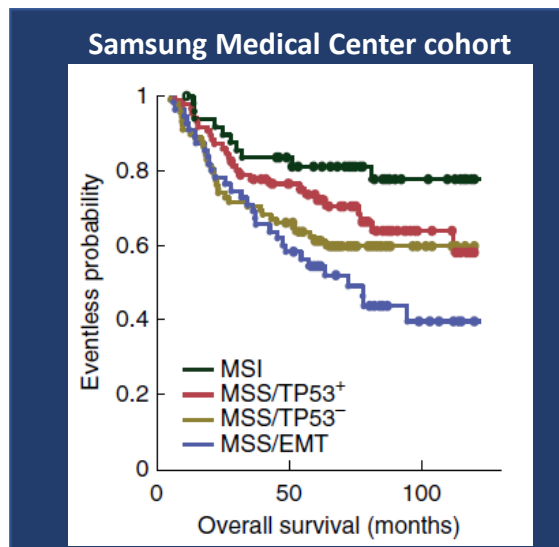
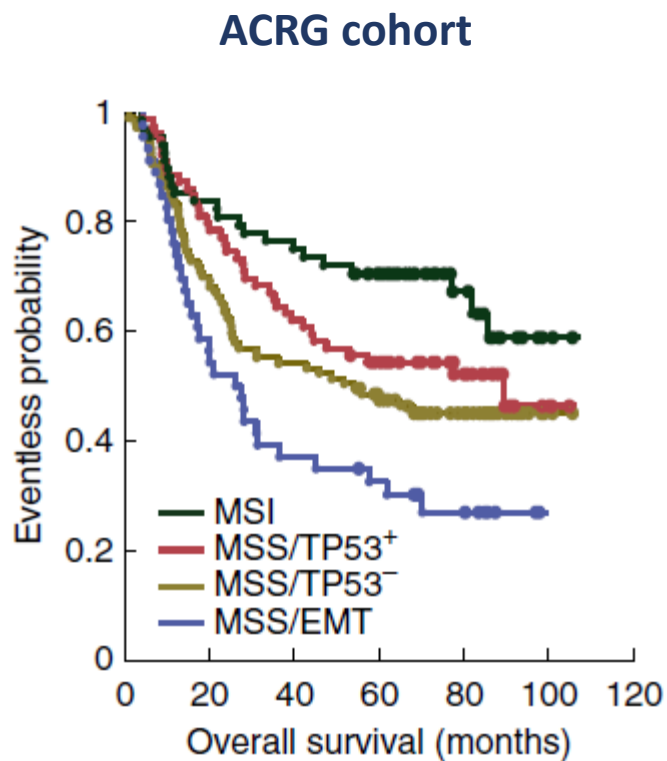
Cristescu R, *Nature Medicine* 2015.



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# ACRG classification and its prognostic significance



Cristescu R, *Nature Medicine* 2015.

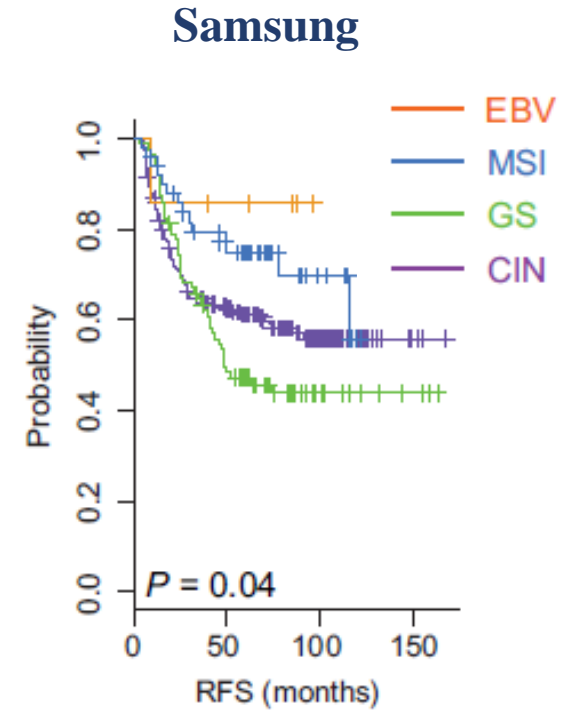
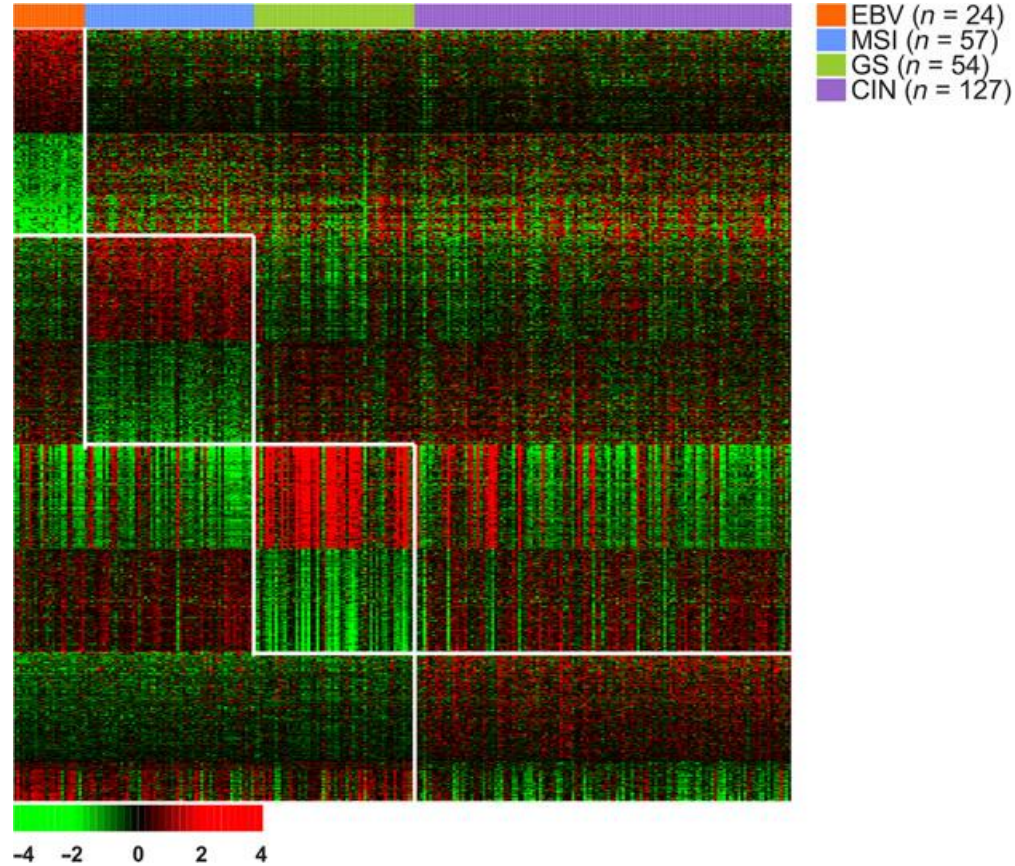
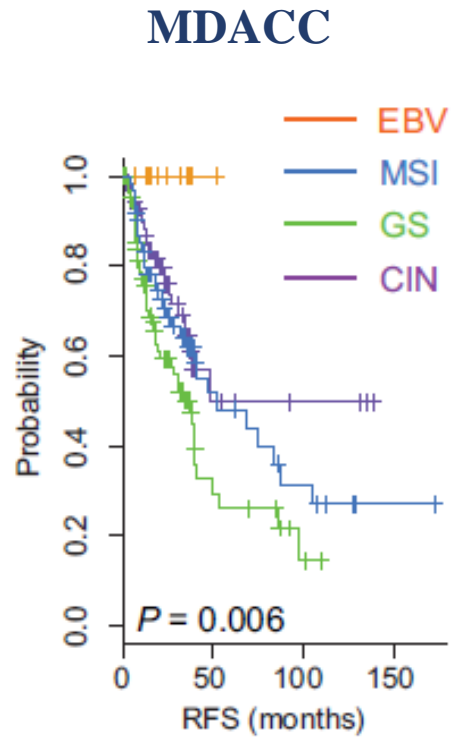


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# TGCA vs ACRG



# TGCA classification and its prognostic significance



Sohn et al, Clin Cancer Res, 2017; 23:4441



# Limits of the TCGA classification:

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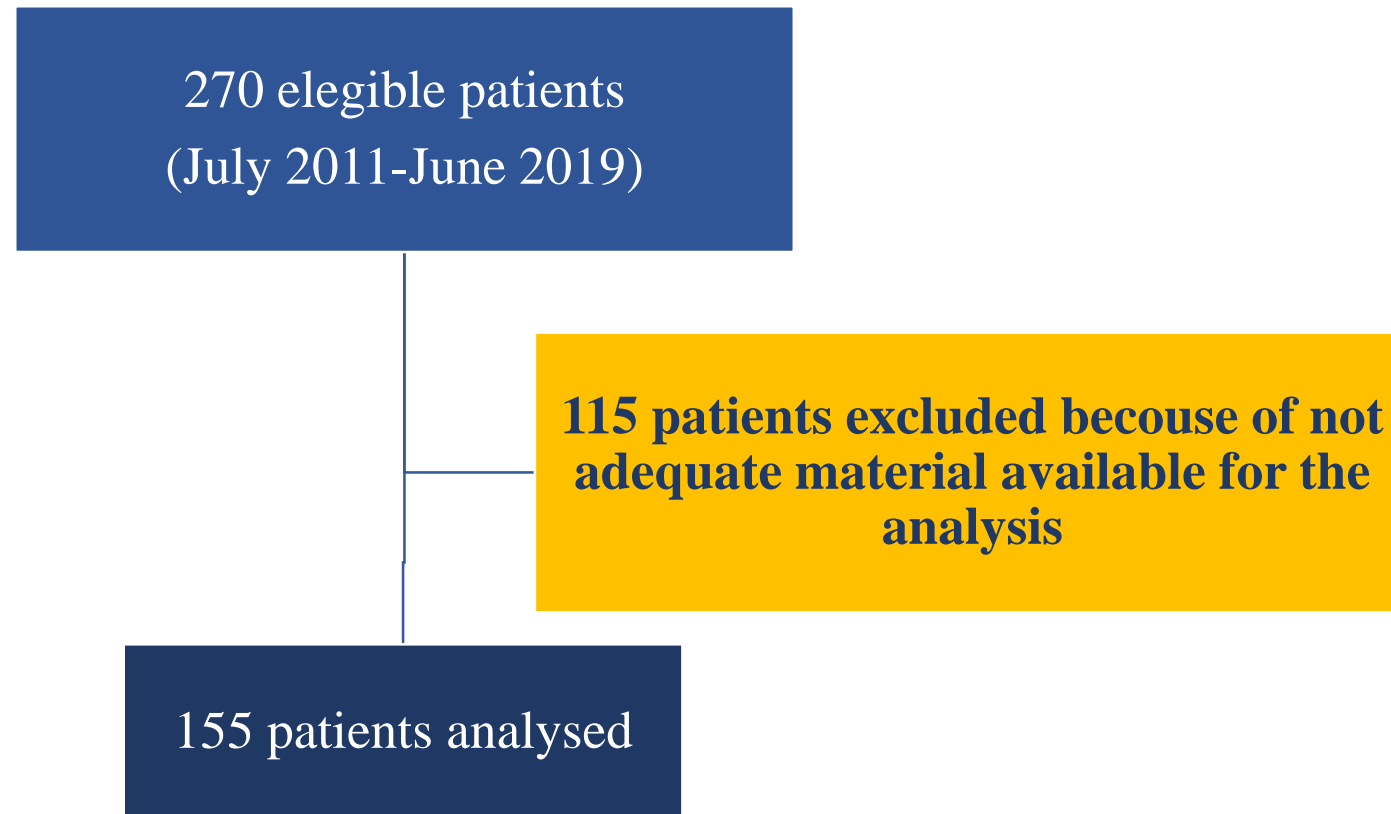
- Lack of prognostic/predictive impact (only few follow-up data from patient in the TCGA cohort are available)
- Uncertain applicability in the metastatic setting
- Low reproducibility in clinical practice (need of multiple genomic and proteomic data sets).





# Study Design

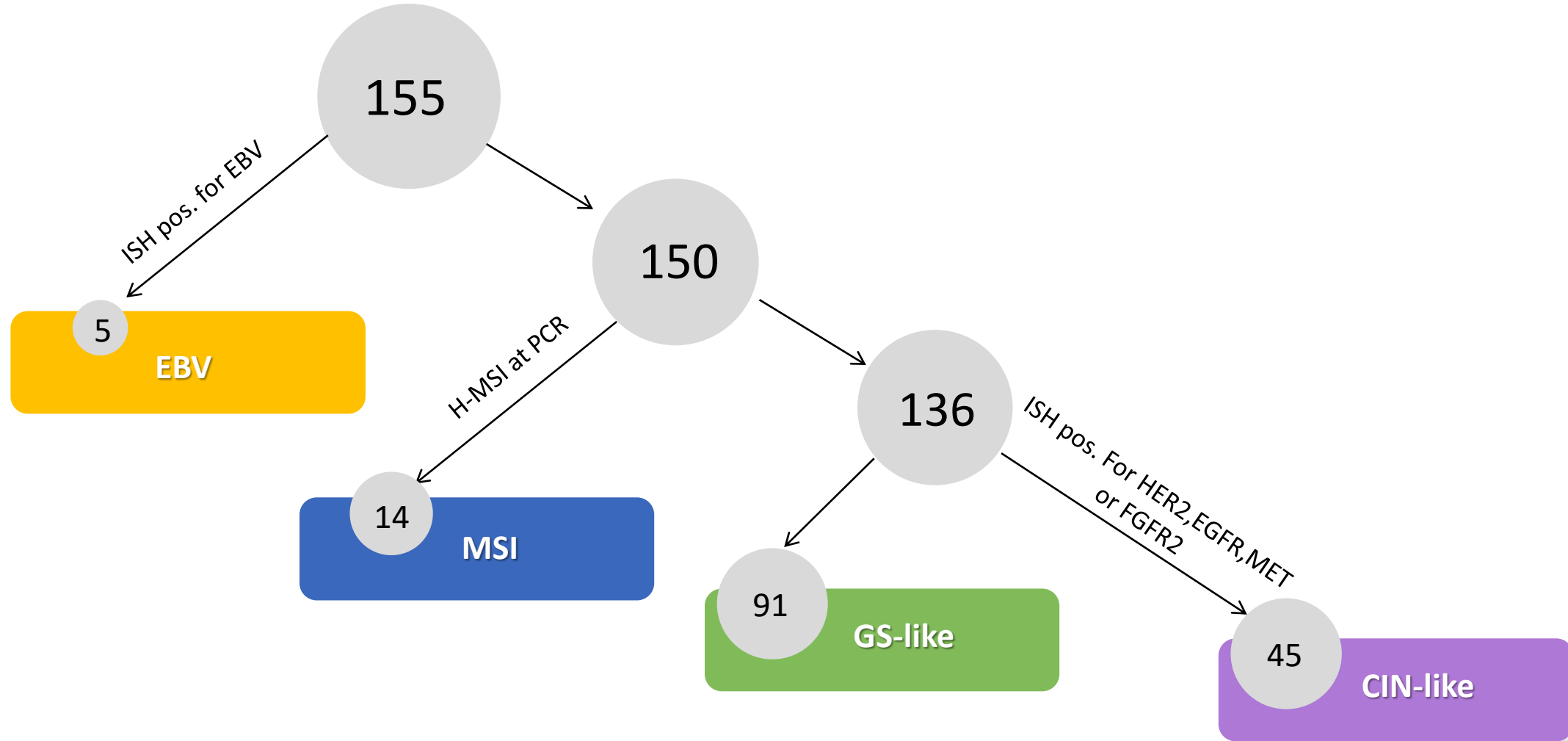
Samples from metastatic GC patients were analysed via bright-field ISH for HER2/EGFR/FGFR2/MET amplifications and EBV infection and PCR for MSI.



INT database, unpublished data



# Study Design: Methods



INT database, unpublished data

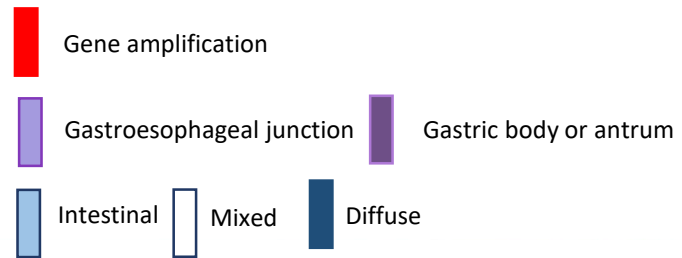
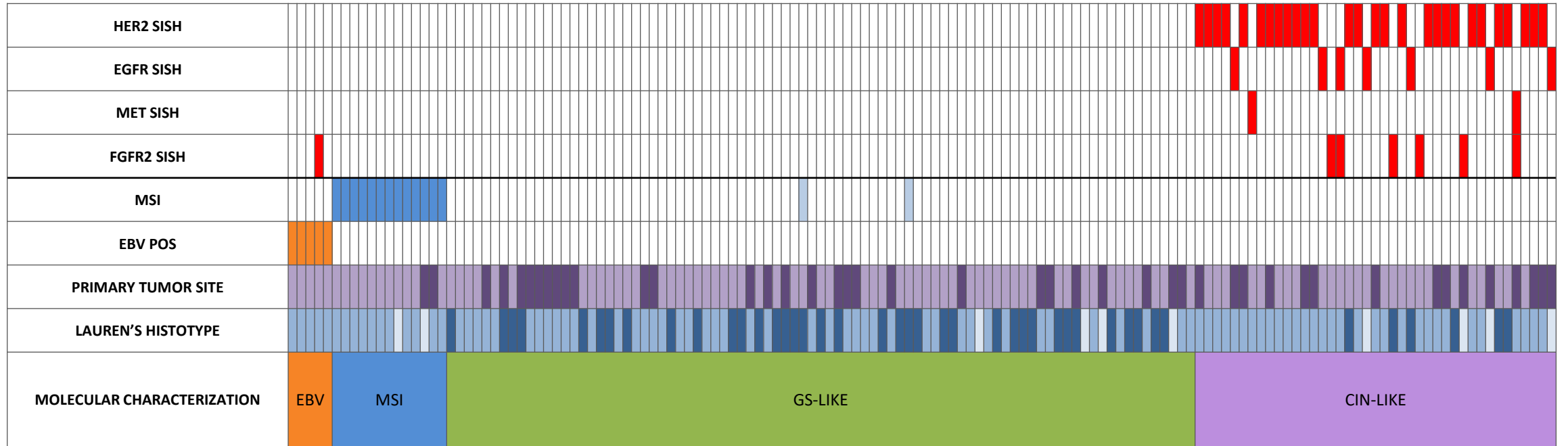




# Patient Characteristics

Patient Characteristics	CIN-LIKE n=45 (29%)	GS-LIKE n=91 (58.7%)	MSI n=14 (9%)	EBV positive n=5 (3.2%)	Overall n=155(%)
<b>Age, median (IQR)</b>	<b>60 (48-71)</b>	<b>62 (50-69)</b>	<b>66 (58-72)</b>	<b>68 (61-78)</b>	<b>62 (51-70)</b>
< 65	28 (62.2)	36 (39.6)	6 (42.9)	1 (20)	90 (58)
≥ 65	17 (37.8)	55 (60.4)	8 (57.1)	4 (80)	65 (42)
<b>Sex</b>					
Male	30 (66.7)	55 (60.4)	7 (50)	4 (80)	96 (62)
Female	15 (33.3)	36 (39.6)	7 (50)	1 (20)	59 (38)
<b>Site</b>					
Gastro-oesophageal junction	16 (35.6)	29 (31.9)	2 (14.3)	0	47 (30)
Gastric body or antrum	29 (64.4)	62 (68.1)	12 (85.7)	5 (100)	108 (70)
<b>Histotype</b>					
Intestinal	35 (77.8)	47 (51.6)	12 (85.7)	4 (80)	98 (63.2)
Diffuse	7 (15.6)	40 (44.0)	0	0	47 (30.3)
Mixed	3 (0.6)	4 (4.4)	2 (14.3)	1 (20)	10 (6.5)
<b>Metastatic disease at diagnosis</b>					
Yes	34 (75.6)	75 (82.4)	10 (71.4)	4 (80)	123 (79.4)
Not	11 (24.4)	16 (17.6)	4 (28.6)	1 (20)	32 (20.6)
<b>Site of metastases</b>					
Liver metastases	20 (44.4)	21 (23.1)	1 (7.1)	0	42 (27.1)
Peritoneal metastases	16 (35.6)	47 (51.6)	8 (57.1)	3(60)	74 (47.7)

INT database, unpublished data-4449

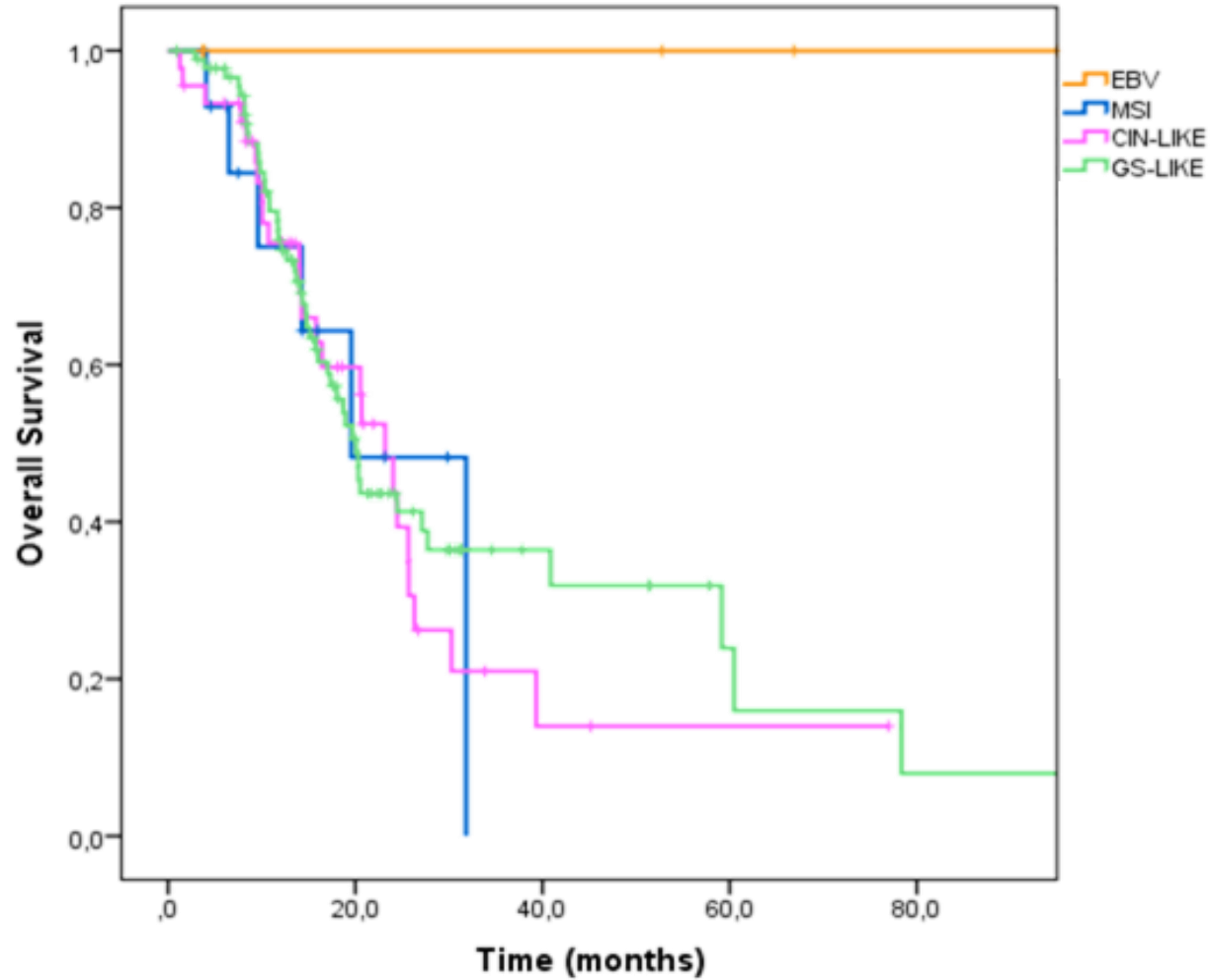


INT database, unpublished data





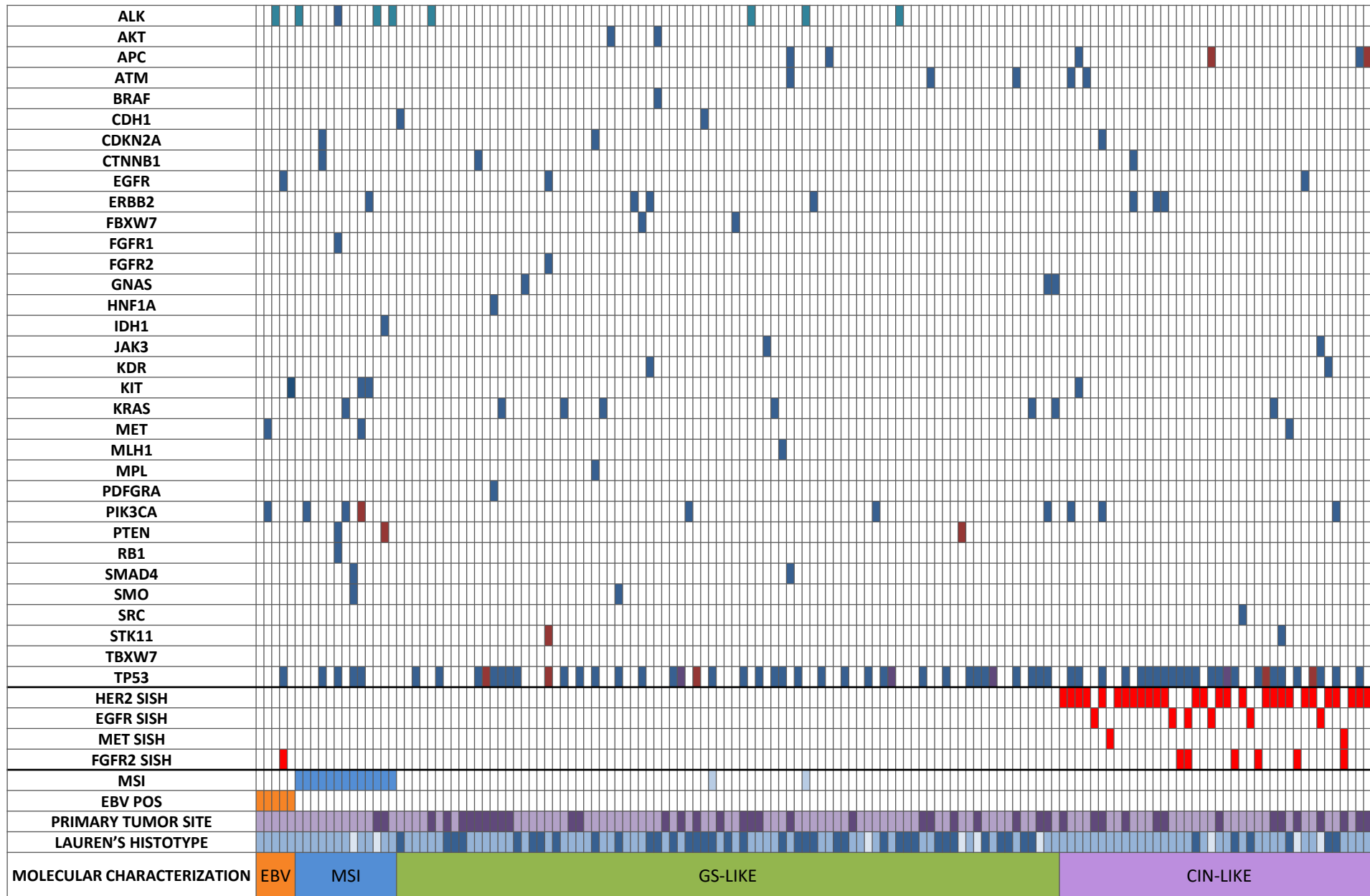
# Survival Analysis



MOLECULAR SUBGROUPS	MEDIAN OS (MONTHS)
EBV	NR
MSI	31.8
CIN-LIKE	23.2
GS-LIKE	19.7
OVERALL	20.3
p value (Chi Square test): 0.2	

INT database, unpublished data





- Single gene mutation
- Single gene deletion
- Double gene deletion

- Gene amplification
- Junction vs Body-antrum
- Lauren's classification: Intestinal vs mixed vs diffuse

INT database, unpublished data



# CONCLUSIONS

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- Selected molecular alterations might be used to characterize in clinical practice GC patients identifying potentially targetable molecular alterations, subgroups of patients sensible to check-point inhibitors and EBV positive patients with good prognosis.
- Given their extraordinary sensibility to immuno-checkpoint inhibitors, the greater effort should be done to characterize MSI e EBV+ GC patients.



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