

Analysis of MET Amplification (*METamp*) with FISH and NGS Methods in SACHI Trial

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BACKGROUND

- METamp* is widely recognized as one of the key mechanisms of acquired resistance to EGFR-TKI therapy in EGFR-mutated non-small cell lung cancer (NSCLC) patients (pts) [1,2]. Therapeutic strategies targeting MET have therefore emerged as important avenues for overcoming this resistance mechanism.
- Savolitinib is a highly selective oral MET tyrosine kinase inhibitor [3].
- In the Phase 3 SACHI trial (NCT05015608), savolitinib (savo) plus osimertinib (osi) significantly improved mPFS versus standard chemotherapy (pemetrexed plus carboplatin/cisplatin) in pts with *METamp* NSCLC who had progressed on prior EGFR-TKI treatment. Based on these compelling clinical outcomes, this combination therapy (savo+osi) was approved by NMPA in June 2025.
- Here, using SACHI baseline tumor tissue and ctDNA samples, we evaluated the concordance between Fluorescence in Situ Hybridization (FISH) and Next Generation Sequencing (NGS) in detecting *METamp*. Furthermore, we analyzed clinical efficacy in NGS-profiled pts enrolled in the SACHI study, with tumor responses evaluated by investigators according to RECIST 1.1 criteria.

METHODS

Study design and tumor/ctDNA collection for *METamp* analysis

Key eligibility criteria

- Unresectable or metastatic NSCLC
- EGFRm, PD on first-line EGFR-TKI
 - For pts progress on 1st/2nd generation (G) EGFR-TKI, EGFR-T790M negative is required;
- METamp* by FISH in central lab
- ECOG PS 0-1

Savolitinib 600 mg (BW≥50kg) or 400 mg (BW<50 kg) QD, + **Osimertinib** 80 mg QD
N = 106

Platinum + Pemetrexed 4-6 cycle, then Pemetrexed maintenance
N = 105

Primary endpoint:

PFS assessed by investigator review (RECIST v1.1)

Until PD or intolerable toxicity

- Baseline tumor samples underwent *METamp* screening via FISH as eligibility assessment.
- A portion of baseline tumor samples underwent NGS testing with subsequent *METamp* analysis in comparison with FISH.
- 10 mL peripheral blood was collected at baseline for randomized pts.

METamp criteria by FISH

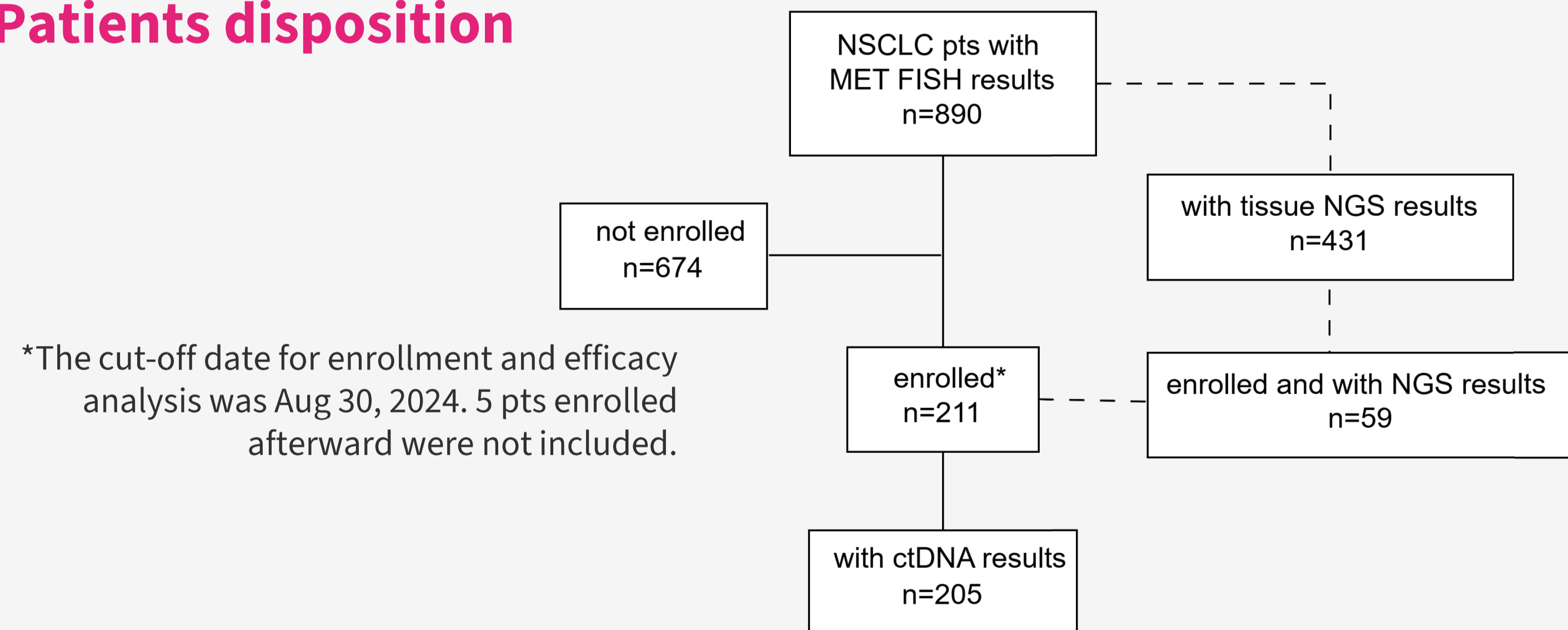
- METamp* in tumor tissue by FISH was defined as MET gene copy number (GCN)≥5 or MET/CEP7≥2 for pts treated with prior 1st/2nd generation (G) EGFR-TKIs, and MET GCN≥10 for those with prior 3rd generation EGFR-TKIs, using AmoyDx c-Met Gene Amplification Kit. MET GCN was categorized as <5, 5-10, or ≥10 by FISH for concordance comparison with NGS.

NGS sequencing and analysis

- DNA extraction and sequencing: DNA was isolated from tumor tissue using MagPure FFPE LQ Kit (Magen), and NGS was performed using panel OncoCompass 68-gene panel (Burning Rock).
- ctDNA extraction and sequencing: ctDNA was isolated from the plasma using QIAamp circulating nucleic acid Kit (QIAGEN), and NGS was performed using panel OncoCompass Target ctDNA 168-gene panel (Burning Rock).
- METamp* analysis in NGS: The process begins with standardization of sequencing, followed by correction of biases introduced by GC content and probe design. A genomic region is identified as exhibiting copy number variation (CNV) if its coverage data significantly deviates both quantitatively and statistically from a baseline established using a set of CNV-negative samples. The cutoff of gene amplification for CN is set at ≥2.25.

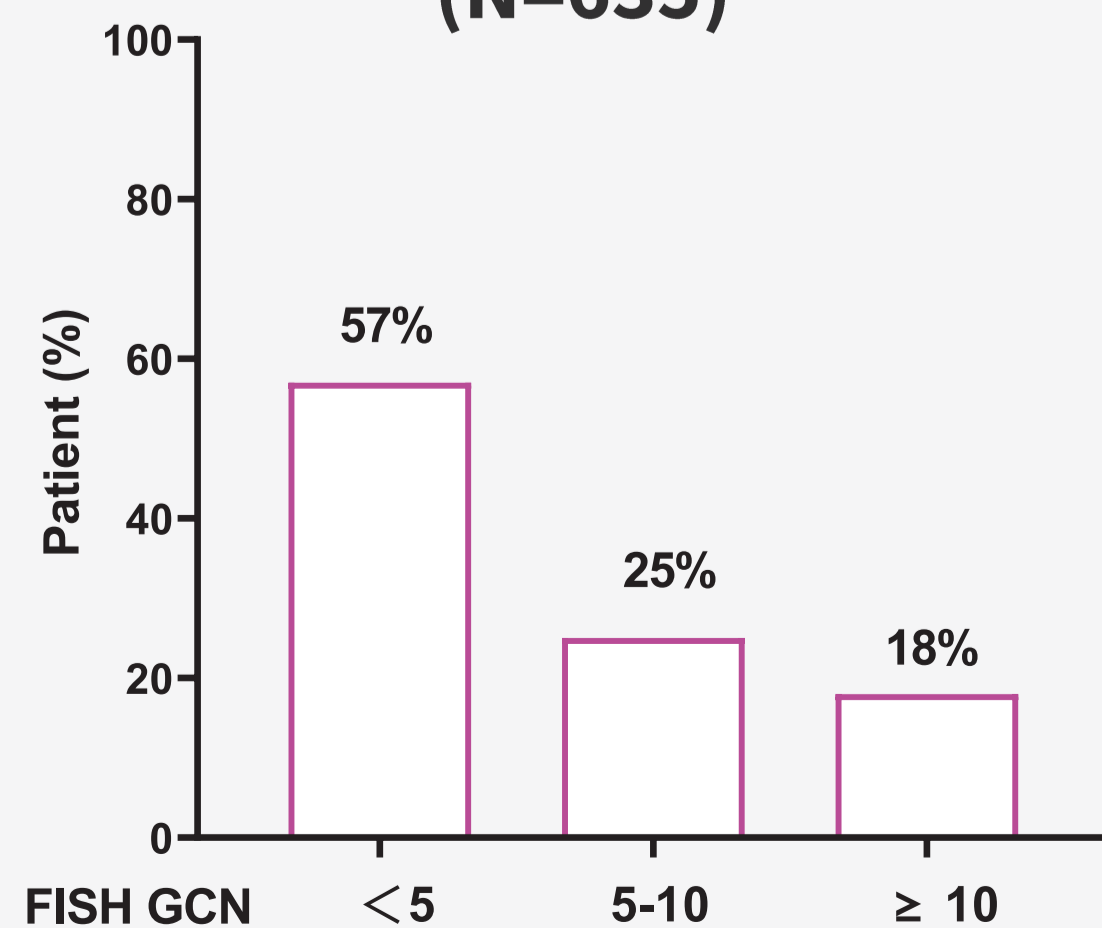
RESULTS

Patients disposition

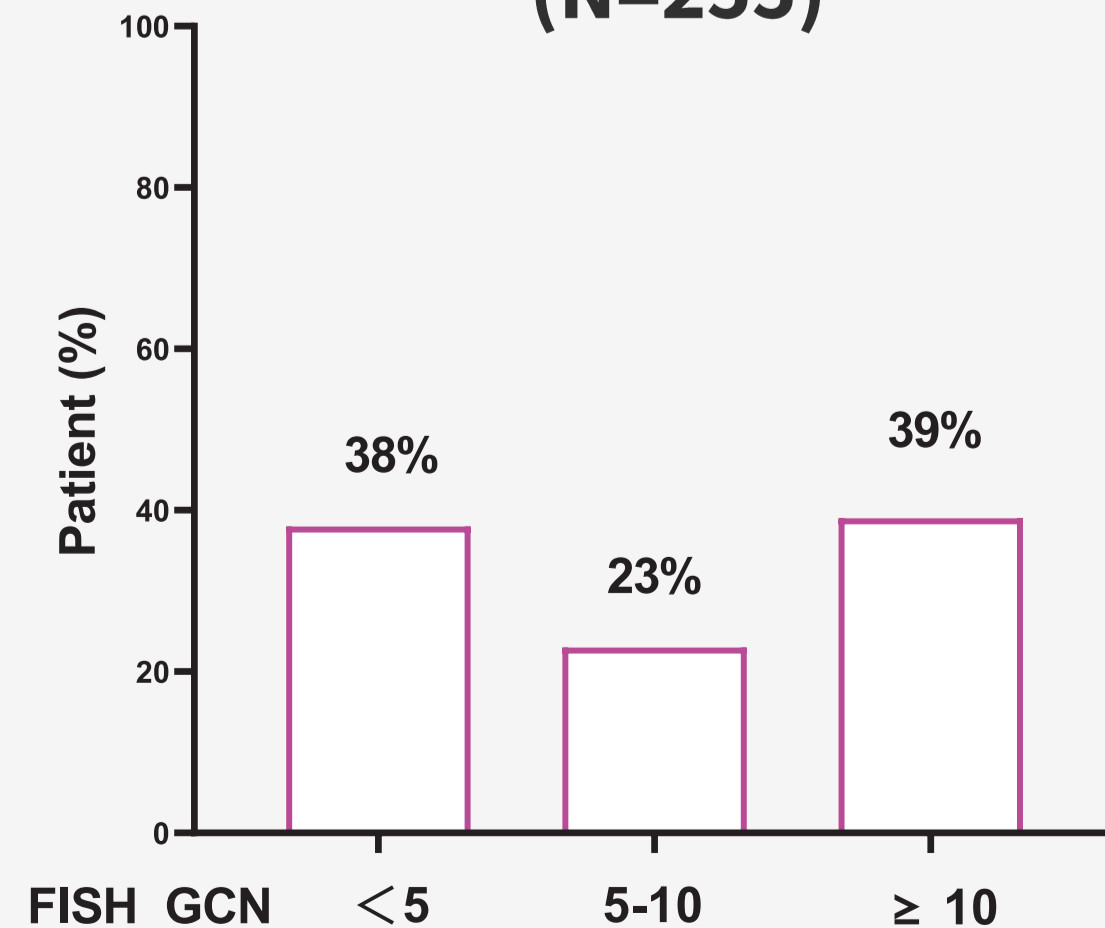


METamp prevalence by FISH in EGFR-TKI resistant NSCLC patients

MET GCN distribution in post 1st/2nd EGFR TKI (N=635)

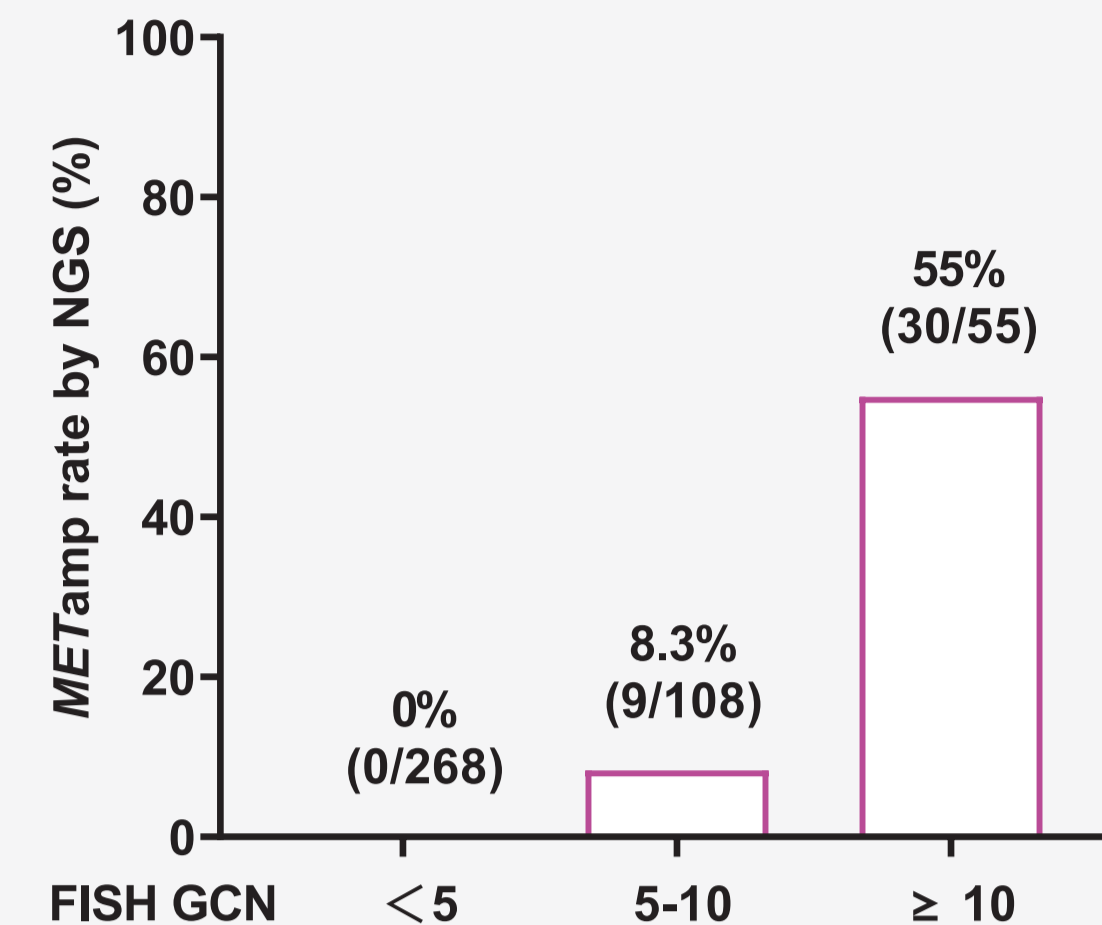
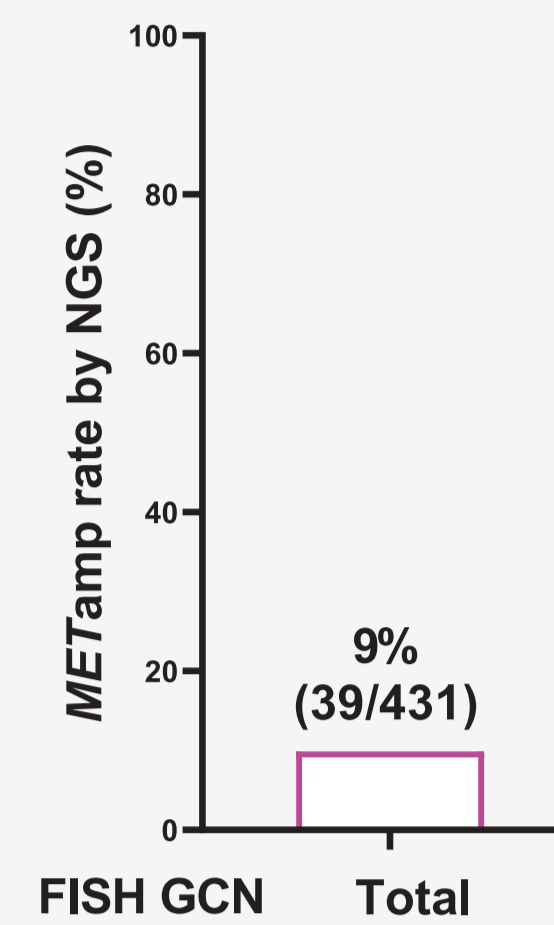


MET GCN distribution in post 3rd EGFR TKI (N=255)



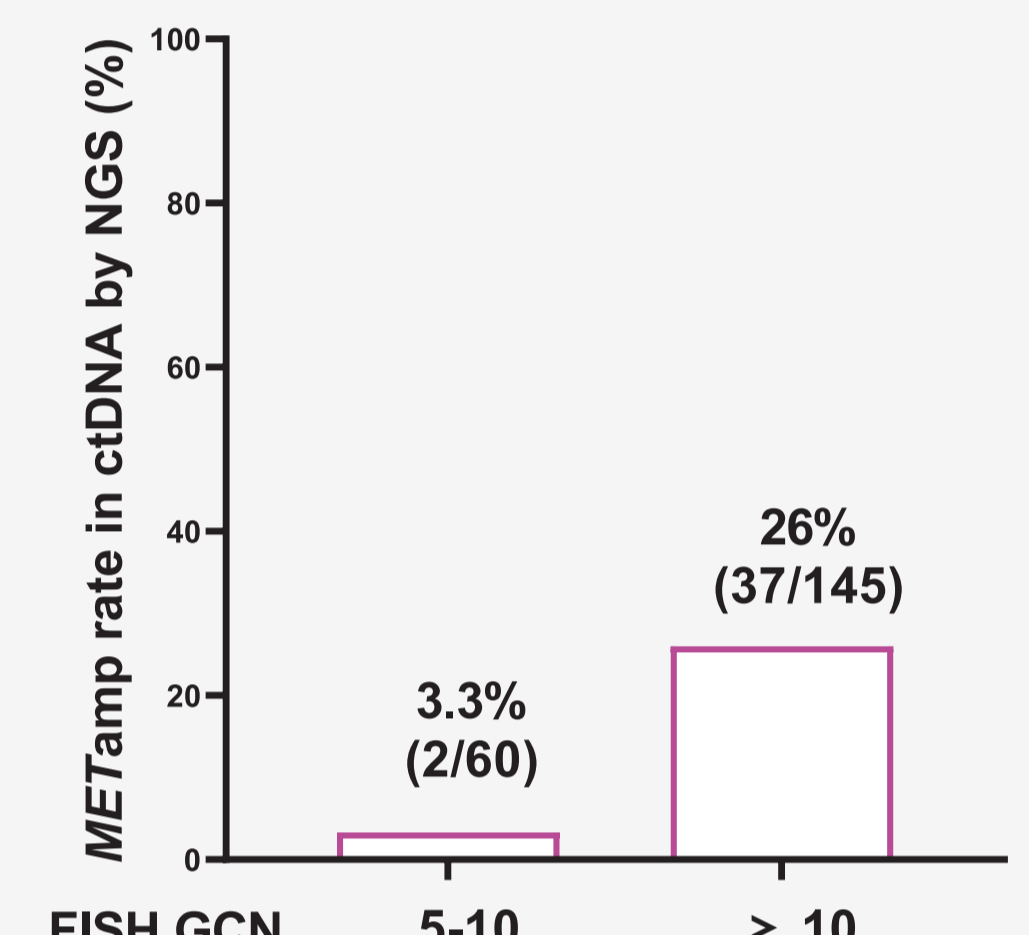
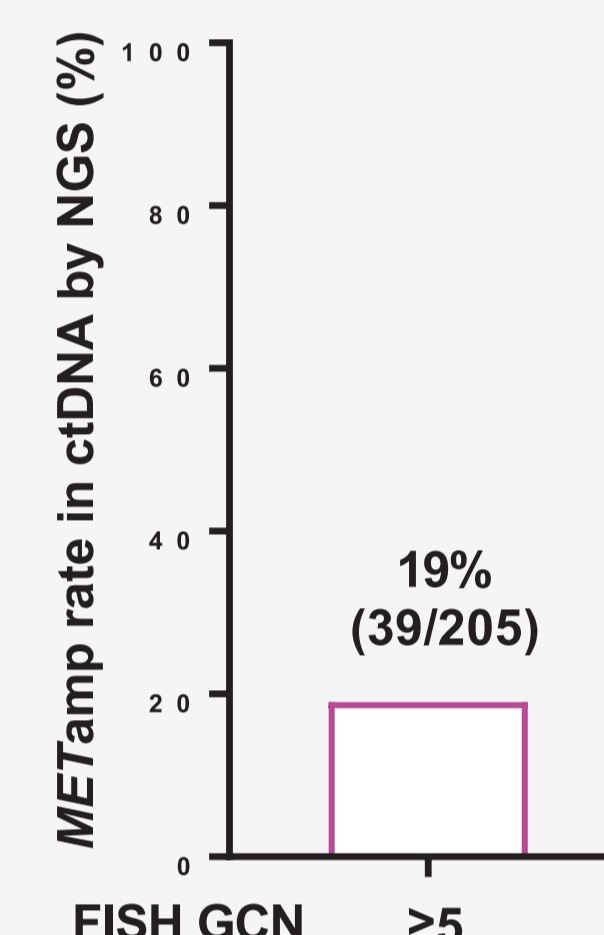
- METamp* was detected by FISH in 43% (272/635) of pts with 1st/2nd G EGFR-TKI-resistance and in 39% (99/255) of pts with 3rd G EGFR TKI-resistance.
- High-level *METamp* (GCN≥10) were enriched in 3rd G EGFR TKI-resistant pts. The proportions of MET GCN≥10 is 39% in 3rd G EGFR TKI-resistant pts while 18% in 1st/2nd G EGFR TKI-resistant pts.

METamp prevalence by tissue NGS in EGFR-TKI resistant NSCLC (N=431)



- In 431 pts with NGS results, the **overall *METamp* rate by NGS was 9% (39/431)**. (Left Figure)
- NGS detection rates of *METamp* demonstrated a tiered correlation with FISH-quantified GCN: **0% (GCN≤5), 8.3% (5<GCN<10), and 55% (GCN≥10)**. (Right Figure)

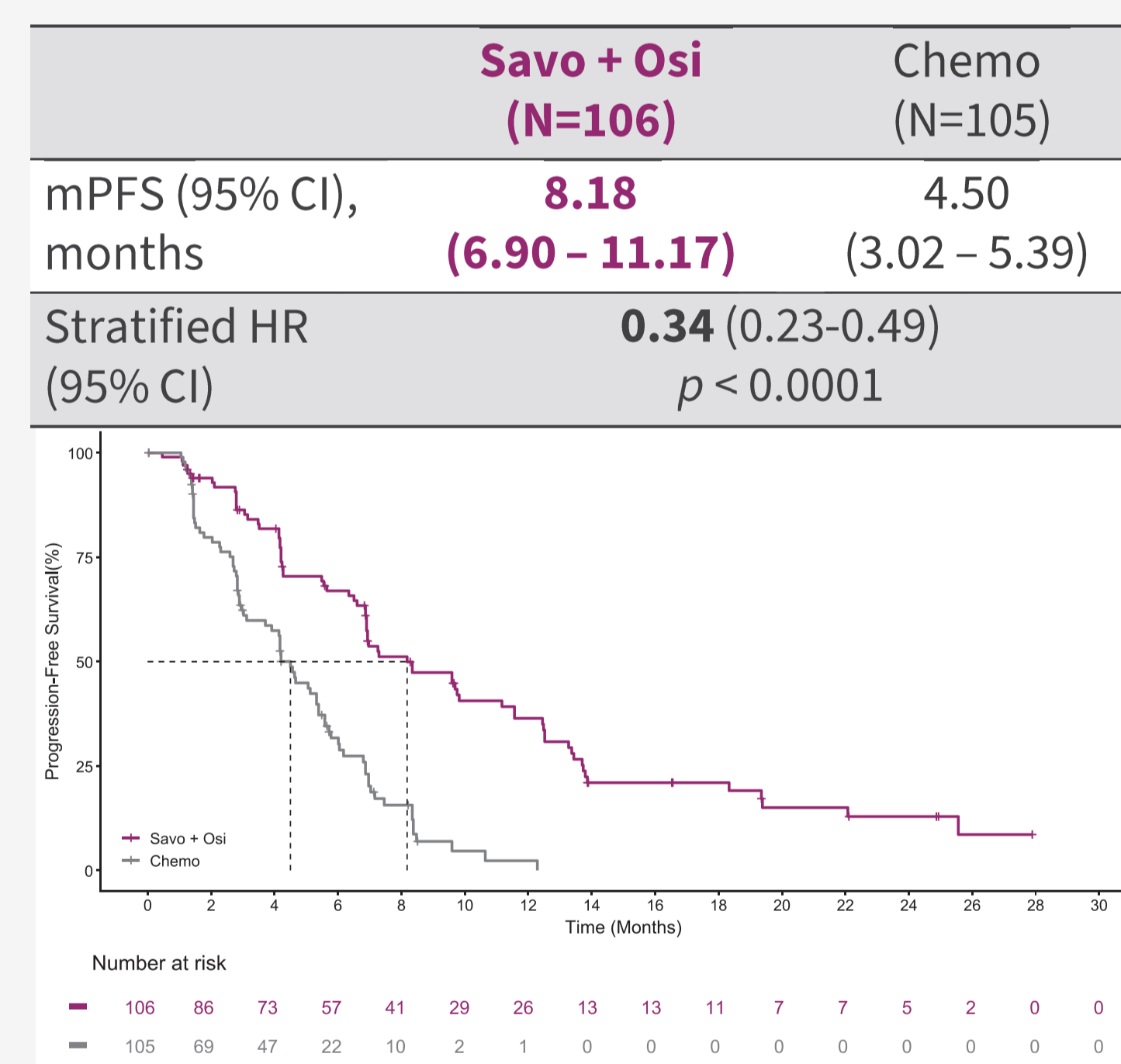
METamp prevalence in ctDNA among enrolled patients (N=205)



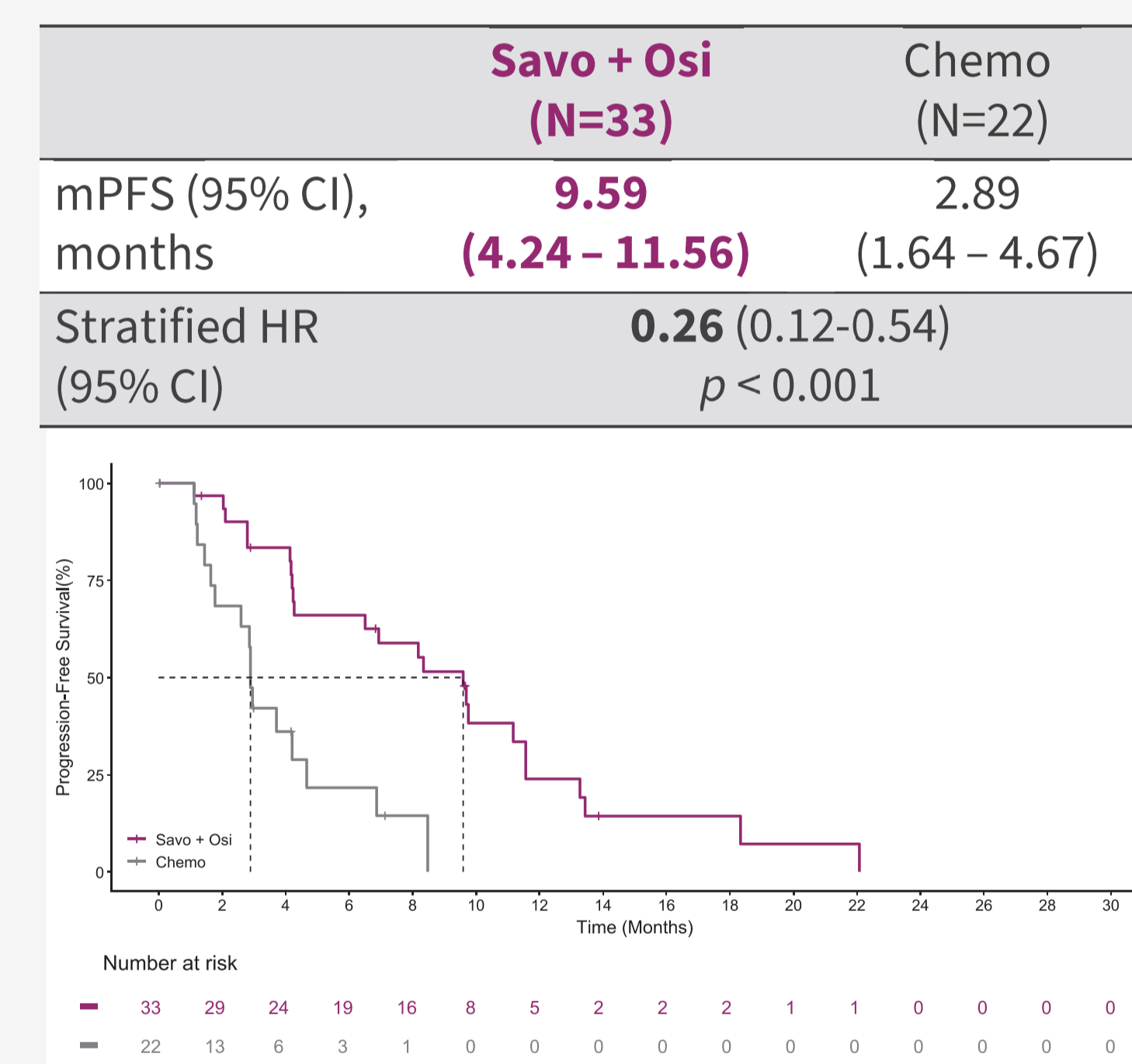
- In enrolled 205 pts with ctDNA NGS data, the **overall *METamp* rate in ctDNA by NGS was 19%**. (Left Figure)
- METamp* detection rate in ctDNA elevated with FISH quantified GCN: **3.3% (5≤GCN<10) and 26% (GCN≥10)**. (Right Figure)

Therapeutic outcomes by NGS (ITT vs *METamp*)

ITT population (N=211)



NGS *METamp* population (N=55)



- In SACHI ITT population, savo+osi combination demonstrated a clinically significant **3.68-month of ΔmPFS versus chemotherapy** (hazard ratio [HR]=0.34, *p*<0.0001). (Left Figure)
- In the enrolled pts with NGS data available, 55 pts were *METamp* positive in either tumor tissue or ctDNA samples.
- Among the 55 pts with *METamp* in NGS and FISH, pts treated with savo+osi demonstrated **6.70-month of ΔmPFS versus chemotherapy**. (Right Figure)

CONCLUSIONS

- FISH-based *METamp* detection demonstrated superior sensitivity compared to NGS in EGFR TKI-resistant NSCLC patients.**
- Both tissue and plasma (ctDNA) based NGS demonstrated detectable *METamp* rates exclusively in high-copy populations (GCN≥10), with positivity rates reaching 55% in tumor biopsies versus 26% in plasma.**
- Savolitinib combined with osimertinib achieved superior median PFS compared to chemotherapy in patients with *METamp* confirmed by both FISH and NGS.**

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CONFLICT OF INTEREST
Longhua Sun has nothing to declare.

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