

# Importance of accurate *EPCAM* deletion characterization to prevent misdiagnosis of Lynch syndrome



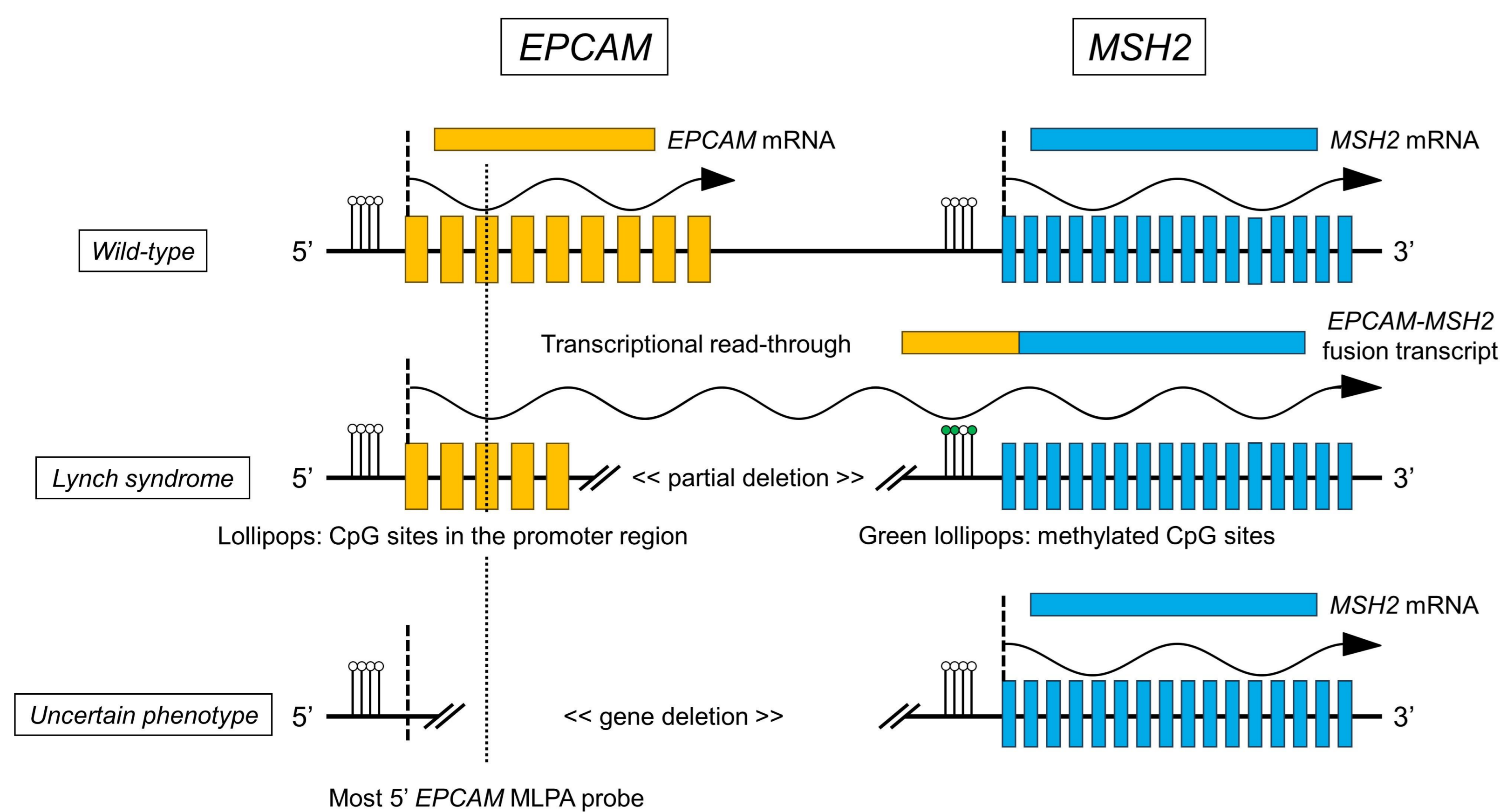
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## BACKGROUND

Prior to the introduction of NGS, *EPCAM* deletion screening was typically performed by one MLPA kit throughout the country. The only MLPA kit available does not have probe coverage 5' of exon 3, making it difficult to determine if a deletion spans the entire gene. Phenotypes of individuals with isolated whole *EPCAM* deletions are not well described and may have different clinical implications than individuals with partial deletions.

FIGURE 1. *EPCAM* and *MSH2* disease mechanism



## METHODS

All cases with a gross deletion including *EPCAM* identified at a single laboratory from 2011-2021 were evaluated to determine how many had a known or possible full *EPCAM* deletion detected via MLPA or microarray. Amsterdam criteria II (AC) and revised Bethesda criteria (BC) were assessed in families with full and partial deletions.

FIGURE 2. Cohort Selection

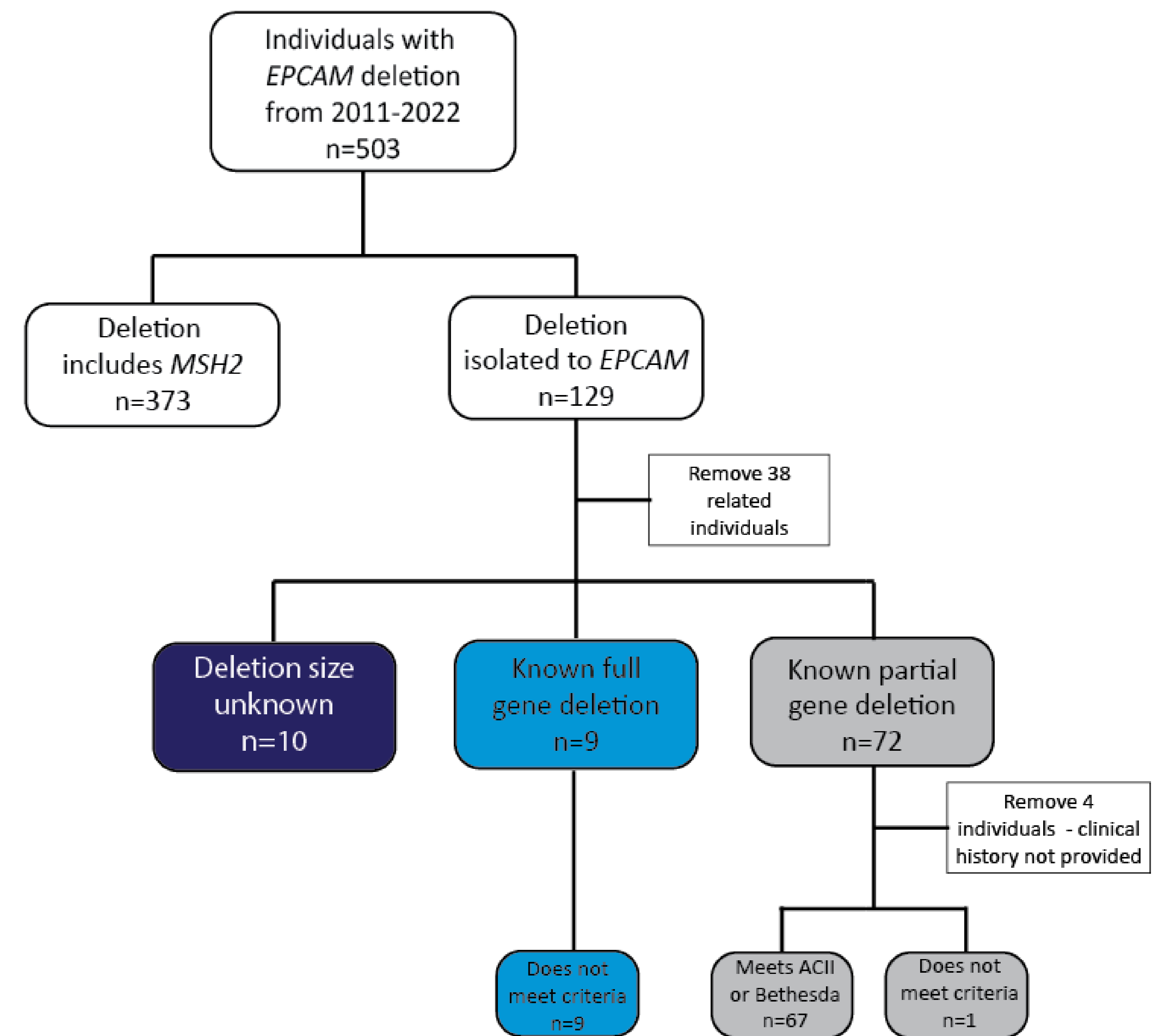


FIGURE 3. Sample MLPA Result

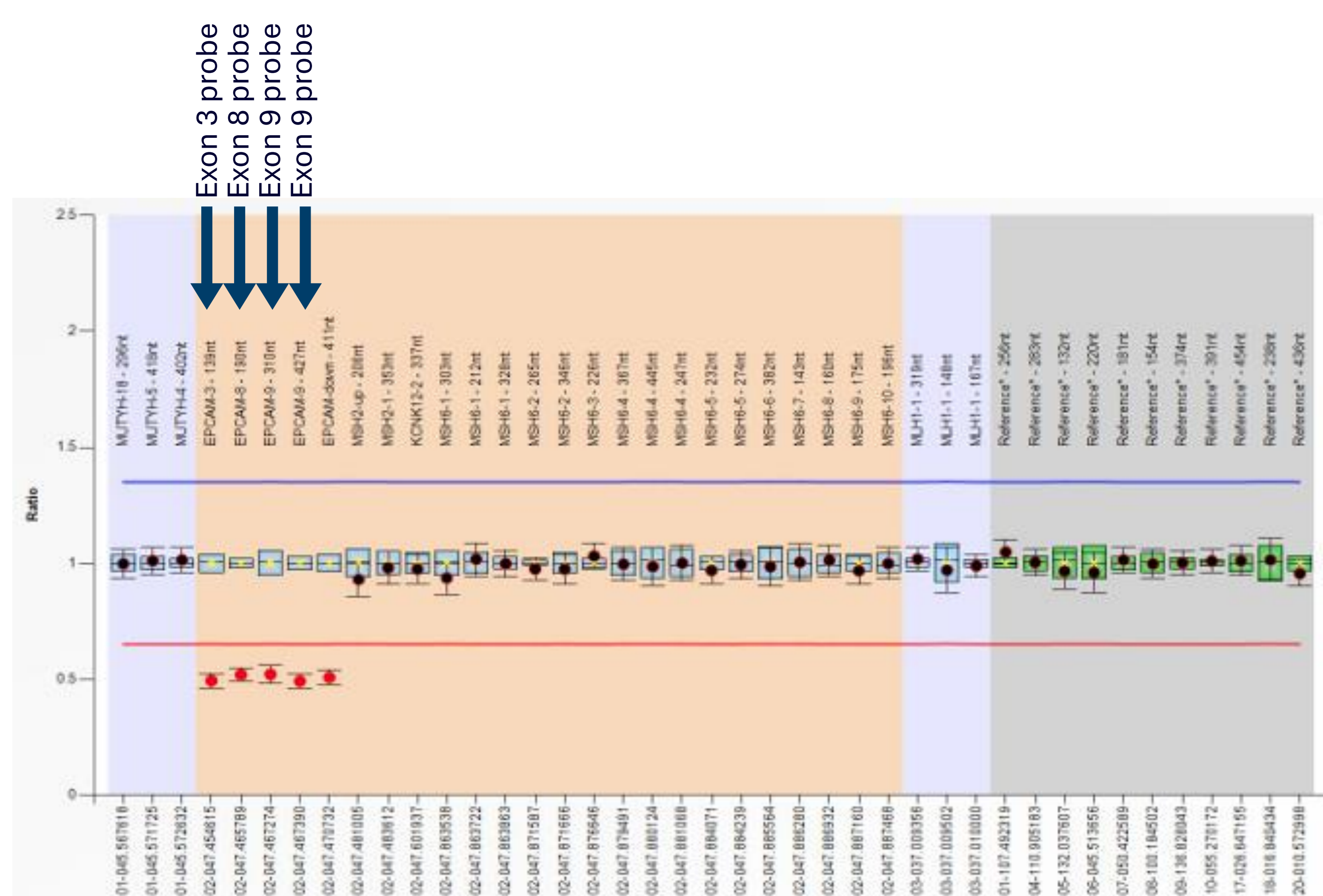
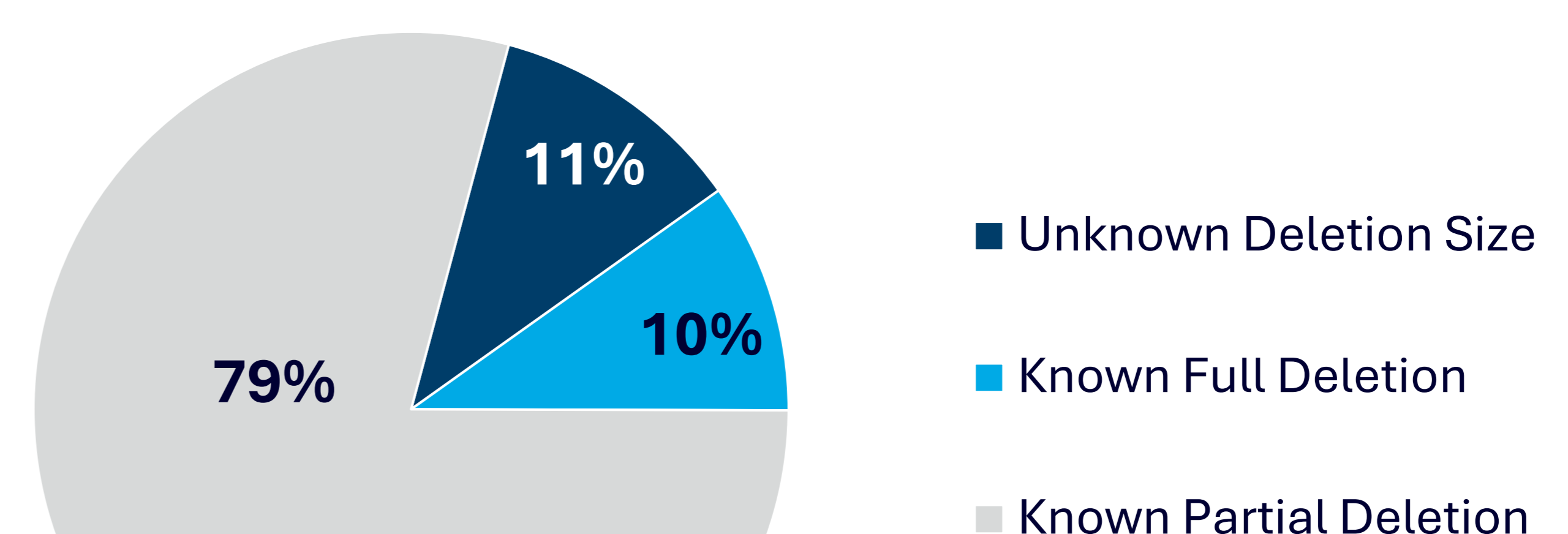


FIGURE 4. Isolated *EPCAM* Deletion Size



21% of individuals with isolated *EPCAM* deletions may have a full deletion.

Re-evaluation in individuals not meeting criteria should be considered.

## TAKE HOME POINTS

1. Isolated whole-gene *EPCAM* deletions do not appear to cause Lynch syndrome.
2. Some patients with *EPCAM*-associated Lynch syndrome may be misdiagnosed and eligible for re-evaluation.