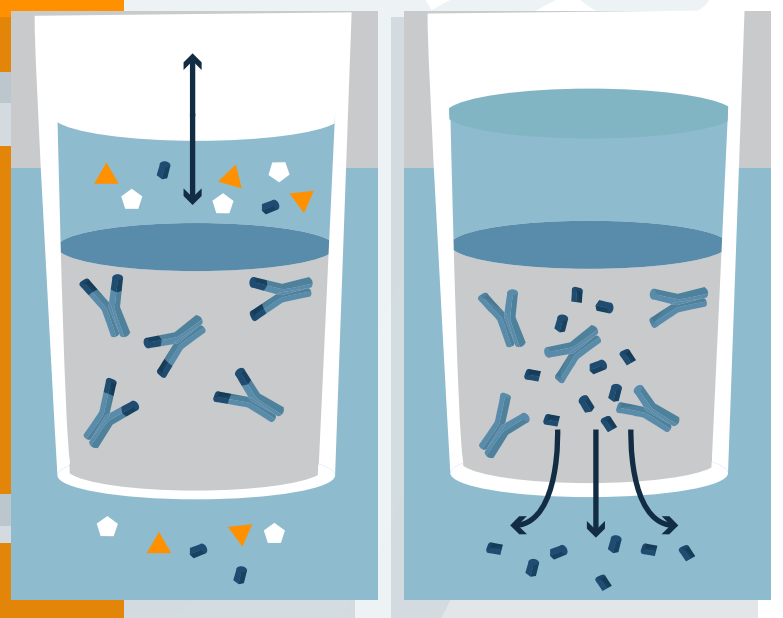


# Considerations for developing a smart biomarker assay

## Compound class

- ?** Is it amenable to LC-MS/MS without modification?  
(e.g., eicosanoids or small peptides)
- ?** Will the compound need to be derivatized?  
(e.g., sugars, steroids) Will the resulting compound be ionizable via GC-MS/MS or via LC-MS/MS?
- ?** Will the compound need to be digested?  
(e.g., larger peptides or proteins)



## Endogenous compound concentration

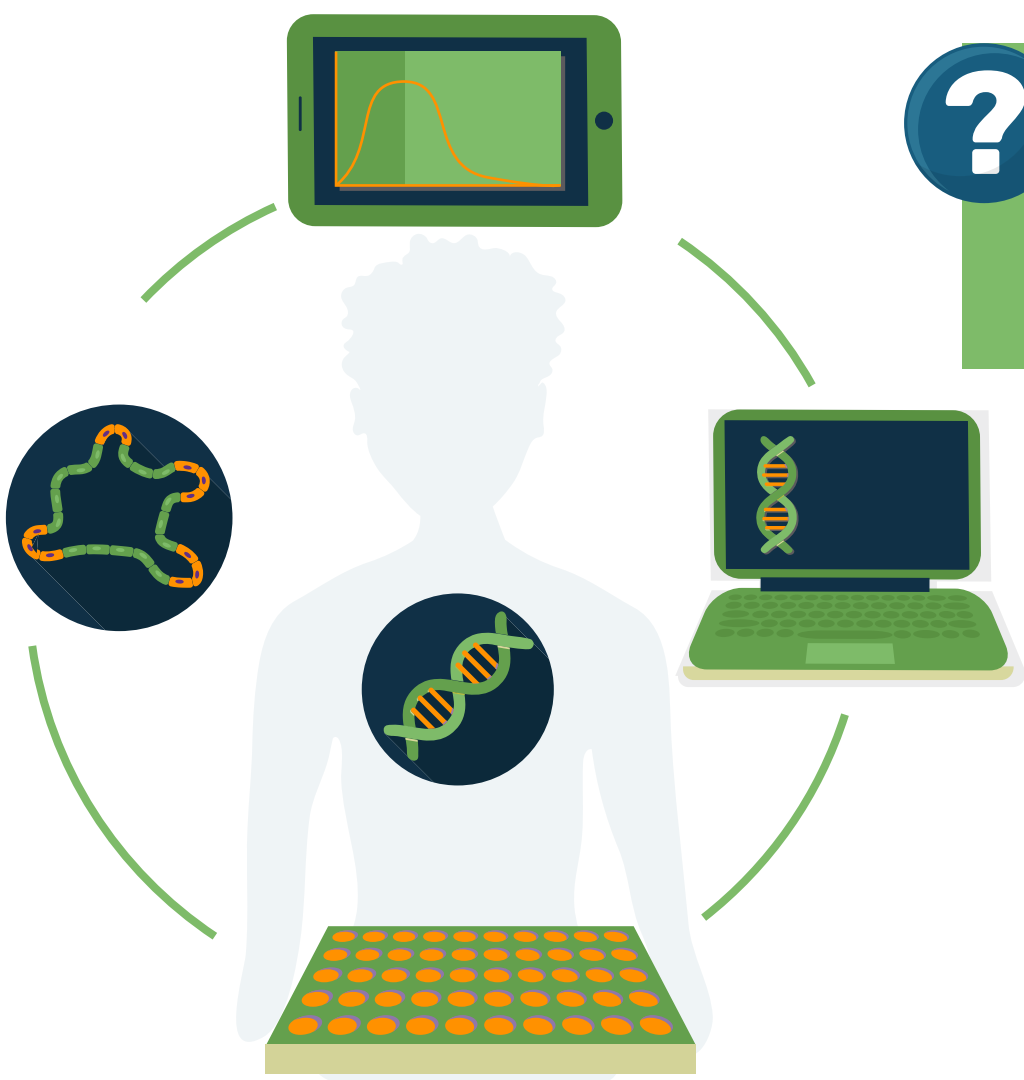
- ?** What is the LLOQ required to be able to measure a significant change in the biomarker?
- ?** What is the endogenous concentration of the biomarker and is it consistent between individuals or between disease state and normal?

**?** If the LLOQ is significantly higher than the levels in control matrix, no heroic measures are needed

**?** If screening matrices to find sufficiently blank authentic matrix is possible, this will minimize matrix effects

**?** If unable to use authentic matrix, surrogate matrix is a suitable alternative, but must be shown to accurately measure the compound in authentic matrix through parallelism experiments

**?** A surrogate analyte is also a suitable alternative, but for MS based assays, this requires two differently labeled versions of the authentic compound and also a demonstration of parallelism between the measurement of the authentic compound and the labeled compound



## Study Objective/Endpoint

- ?** Is the data intended to support a safety endpoint?
- ?** Is the data intended to support dose adjustment?
- ?** Is the data intended to measure patient responses to a therapy via a PK/PD endpoint?



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CAP CLIA

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