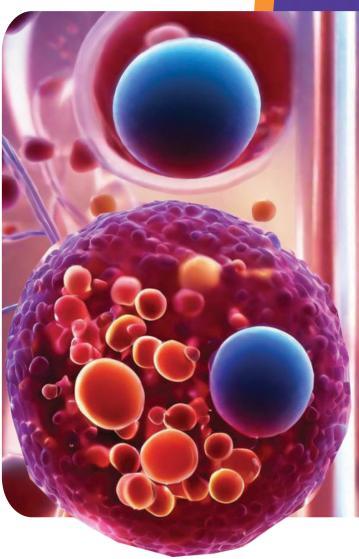


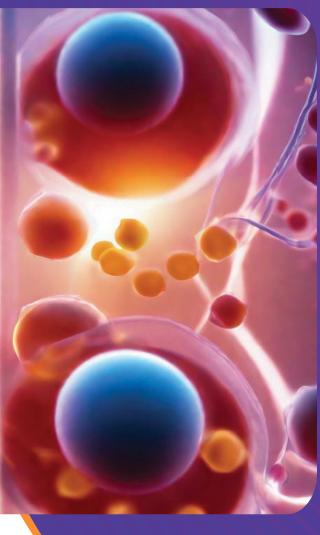
• India • UAE • South Africa • USA

INSIGHTS









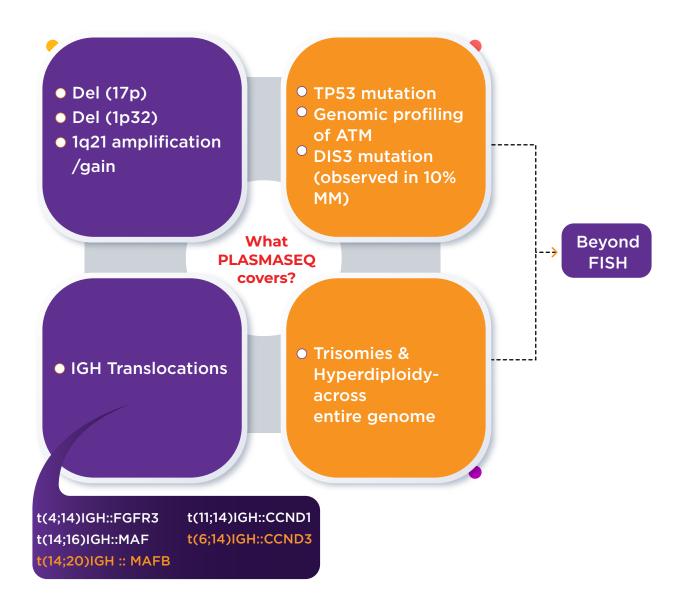
PLASMA**SE**

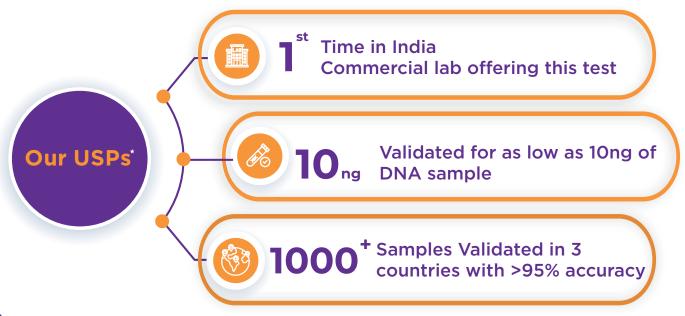
"Discover the Undiscovered with NGS Based Assay for Multiple Myeloma"





Stop Solution For Genetic Classification of Multiple Myeloma









FAB over Conventional Methods







Sample is not a limiting factor unlike in FISH where search for IGH partner can result into depletion of sample





Covers CNVs across the genome relevant to Myeloma; hence, trisomies in all relevant chromosomes can be detected which is not routinely checked by FISH.





| Test Code | Test Name | Biomarkers Used | Clinical Significance | Incidence | FISH | NGS |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------|---------------------------------------------|--------------------------|-----------|---------------------|--------------------------|
| MH020 | PLASMASEQ | TP53 mutation | High-Risk | 1-7% | 8 | Ø |
| | | ATM | Poor Prognosis | ~4% | 8 | Ø |
| | | DIS3 | Poor Prognosis | 10% | 8 | Ø |
| | | t(6;14)IGH::CCND3 | Standard-Risk | ~4% | ⊘ / ② | Ø |
| | | t(14;20) IGH :: MAFB | High-Risk | <2% | ⊘ / ② | Ø |
| | | Trisomies & Hyperdiploidy across the genome | Standard-Risk | >40% | ⊘ / ⊗ | Ø |
| | | Del (1p32) | Poor Prognosis | ~8% | | Ø |
| | | Del (17p) | High-Risk | 5-20% | Ø | Ø |
| | | 1q21 amplification/ gain | Standard-Risk | 40% | Ø | Ø |
| | | t(4;14) IGH::FGFR3 | High-Risk | 15% | Ø | Ø |
| | | t(14;16) IGH::MAF | High-Risk | 3.5% | Ø | Ø |
| A TO THE REAL PROPERTY. | | t(11;14) IGH::CCND1 | Standard-Risk | 15%-20% | Ø | Ø |
| ** Sample must reach the lab within reach this of sample 48 hrs of sample collection. 1st pull of collection. 1st pull of some marrow sample bone marrow sample is suggested. ** ** ** ** ** ** ** ** ** ** | | | | | | Not Routinely Covered |











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► CAP accredited Lab



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