**RESULTS**

- Median maternal age was 31 years and median gestational age was 12 weeks.
- Fetal fraction (FF), the proportion of cfDNA originating from the placenta, can impact the accuracy of NIPS, and many laboratories fail samples with low FF, commonly defined as FF <4%.

**INTRODUCTION**

- For millions of pregnant patients, noninvasive prenatal screening (NIPS) based on cell-free DNA (cfDNA) detects whether their pregnancies are at elevated risk for fetal chromosomal abnormalities.
- Fetal fraction (FF), the proportion of cfDNA originating from the placenta, can impact the accuracy of NIPS, and many laboratories fail samples with low FF, commonly defined as FF <4%.
- FF has been shown to negatively correlate with body mass index (BMI), pregnancies with trisomy 18 or 13, and early gestational age, resulting in higher test failure rates in these populations.
- A whole-genome sequencing (WGS)-based NIPS that employs FF amplification (FFA) technology for all samples has been shown to increase FF by 3.9-fold for samples with low FF.\(^1\)

**METHODS**

- We retrospectively analyzed results from 19,464 patients who underwent NIPS with FFA during a two-month period.
- The FFA technology increased FF by preferentially sequencing short cfDNA fragments, known to be enriched for fetal-derived cfDNA. FF was assessed for patients who received a screening result (N= 19,433).
- BMI data were available for 12,579 patients.

**CONCLUSION**

- A commercial NIPS using FFA for all samples provides confident results regardless of a patient’s risk factors for low FF. FFA provides ample FF, preventing unnecessary test failures in NIPS.