MNM DIAGNOSTICS

Dear Researcher,

As cancer genomics professionals our goal is to provide best quality data on clinical utility of WGS in breast cancer diagnostics.

If You sequence and analyze BC genomes, please run our algorithm and provide us with the information about Your results. It may help us to refine our classifier and recognize WGS as a robust and evidence-based diagnostic method.

Thank You for Your time and effort,

MNM Diagnostics Team

HER2 WGS classifier result questionnaire

1. **What feature/features were determined as relevant?**
   ……

2. **If Ploidy-corrected ERBB2 CN was the only meaningful feature, what threshold was determined for Your results?**

   ……

3. **What copy number variant caller do You use?**

   ……

4. **How do You determine ploidy?**

   ……

[verte]

5. **What was your mean depth of coverage?**

- [ ] <20x
- [ ] 20-30x
- [ ] 30-60x
- [ ] above 60x

6. **What chemistry do You use?**

- [ ] Library prep with PCR amplification
- [ ] PCR-free transposon-bead based
- [ ] PCR-free, other
