# Introducing PGTai<sup>sm</sup> 2.0

Now including SNP analysis for increased data, deeper analysis, greater confidence, more transfers



#### What are SNPs?

A SNP (pronounced 'snip') is the change of a single nucleotide in a specific stretch of DNA. SNPs are a common form of genetic variation; each person has ~4 to 5 million SNPs throughout their genome. As specific variations occur in many individuals, SNPs act as biological markers. They help provide information about the inheritance of the stretch of DNA.

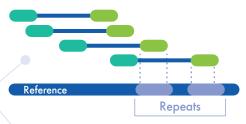
#### Why paired-end sequencing?

Paired-end sequencing allows for reading a DNA fragment from both ends, thus increasing the amount and quality of data generated from each sample. This not only improves sequence alignment, but also allows us to perform highly sensitive analyses.

#### **Paired-End Reads**



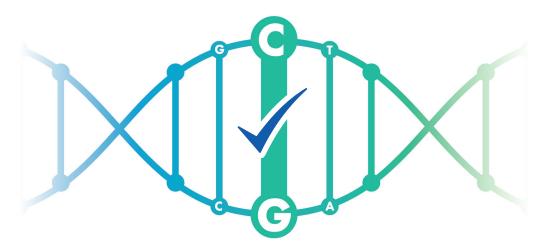
#### Alignment to the Reference Sequence



# Dedicated to advancing accuracy in PGT-A

## We are proud to announce that our already best-in-class PGTai technology platform is about to get even more accurate

By introducing single nucleotide polymorphism (SNP) analysis and paired-end sequencing, PGTai 2.0 provides even more robust PGT-A interpretation. This analysis interrogates DNA sequence variation (a SNP is one type) that originates from the parental gamete genomes. Most importantly for clinicians and patients, this means the platform will deliver added accuracy, thus allowing for prioritization with more confidence.



#### Why SNPs?

The PGTai technology platform already provides the most comprehensive and accurate detection of copy number variation (CNV). The addition of SNP analysis to PGTai 2.0 will provide a second layer of aneuploidy assessment by investigating allelic contributions. This double assessment provides added assurance in the PGT-A analysis and reporting.

### **Driving innovation**

## Introduction of PGTai

- Improved accuracy
- Removal of subjectivity
- Avoid human errors

#### Addition of SNP analysis

- Triploidy detection
- Secondary assessment of abnormality
- · Parent of origin option
- 2PN validation



#### **Clinical Impact**

- More euploid embryos available for transfer
- Increased confidence when prioritizing a euploid for transfer
- Decrease miscarriages from previously undetected forms of triploidy
- Aim to positively impact pregnancy rates





# A solution as unique as your business

## At CooperSurgical, we partner with you to drive clinical efficiency

When you partner with CooperSurgical you become part of a truly global network of clinical experts ready to support you with highly specialized solutions, both for individual clinics and across large organizations. By providing you with optimal products, services and training our aim is to offer you the best possible support to drive the efficiency of your clinic – and achieve the best results.

\*Day-to-day delivery may vary according to geographical location

