



*Groundbreaking and Innovative  
Embryo Screening Technology*



## What is PIMS?

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**Preimplantation Methylation Screening (PIMS)** is a groundbreaking and innovative embryo screening technology exclusively owned by **Guangzhou Nvwa Life Technology Co., Ltd.** PIMS can not only test chromosomal aneuploidy, but also DNA methylomes including whole-genome methylation level, DMRs (Differential Methylation Regions), imprinted genes and etc. It's the first and only technology in the world that can test molecular genetic and epigenetic information from embryo within single PIMS run.

## How PIMS was established ?

The founder of Nvwa Life and PIMS --- **Dr. LIU Jiang** spent more than 10 years in epigenetics-related scientific and clinical research to establish PIMS technology.



Early stage embryo of zebra fish inherits methylome mapping from sperm<sup>1</sup>

--- Jiang, L., et al. (2013). Cell



Active methylome reprogramming at paternal and maternal genes of mammals<sup>2</sup>

--- Wang, L., et al. (2014). Cell

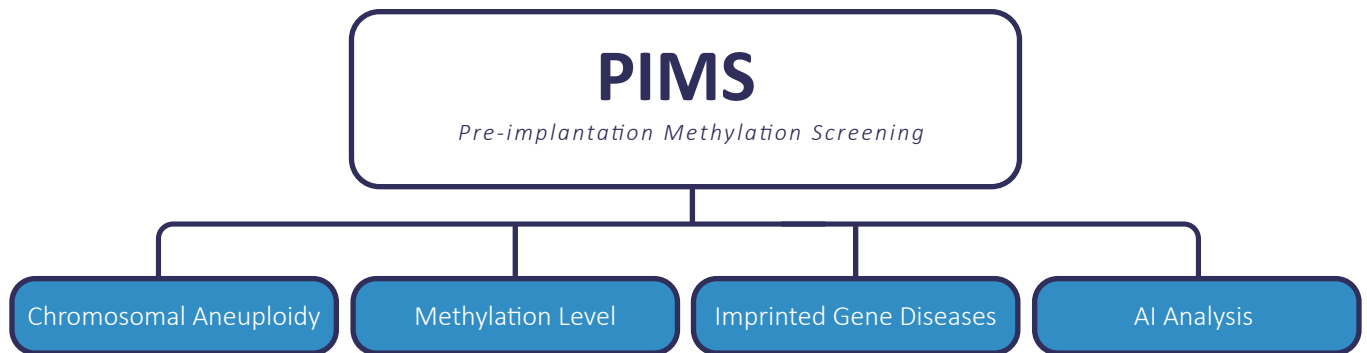


Methylome reprogramming related to assisted reproductive technology (ART)<sup>3</sup>

--- Li, G., et al. (2017). J Genet Genomics

## How *PIMS* works?

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## What *PIMS* achieve:

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### PIMS improve IVF outcomes:

PIMS (Pre-implantation Methylation Screening) is backed up by a prospective study<sup>4</sup>, which found that DNA methylation could affect IVF outcome and it could also be the new biomarker in current assisted reproductive technology (ART). When the methylation level (ML) is within **0.25-0.27** window\*:

- Increasing live birth rate from 50.4% (other ML windows) to **72.1% (PIMS)** (Table 1)
- Improving IVF outcomes for **all age groups**, including young and advanced maternal age (AMA) females (Table 2)
- Lowering birth defect risk by analyzing key imprinting control regions (**ICRs**) (Figure 1)
- Further improve IVF outcomes by applying **AI system** (Figure 2)

\*Optimal methylation level range for better IVF clinical outcome

Table 1. Pregnancy rate, live birth rate and pregnancy loss rate in different ML level range

	Other ML range <sup>1</sup>	ML=0.25-0.27 <sup>1</sup>
Pregnancy Rate	59.8% (70/117)	76.7% (33/43)
Live Birth Rate	50.4% (59/117)	72.1% (31/43)
Pregnancy Loss Rate	15.7% (11/70)	6.1% (2/33)

Table 2. Live birth rate (LBR) of different ML range in different age groups

LBR of different age	Other ML range <sup>1</sup>	ML=0.25-0.27 <sup>1</sup>
AMA group	50.0%	66.7%
Young age group	50.6%	74.2%

Imprinted genes on ICRs could affect embryo growth, placenta nutrient supply; and it might cause imprinting disorder, for example:

Unmethylated H19 is lacking of hypermethylated reads, which might cause **Silver-Russell Syndrome**.

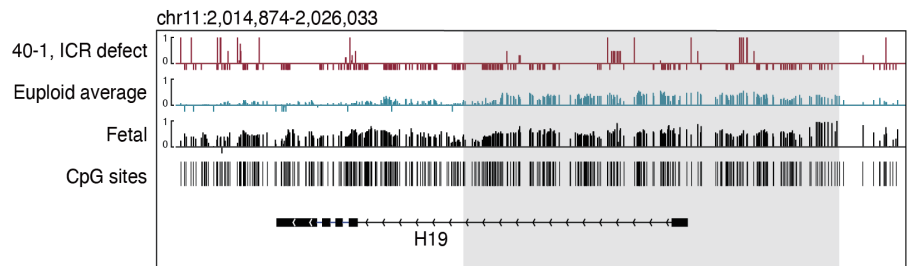


Figure 1. Visual track of un methylated H19 ICR compared with normal H19 ICR

Utilizing epigenetic multiple-modular AI algorithm to select better embryo and to further increase live birth rate

**Predict for 12 family**  
**100% Accuracy in 10 Family**

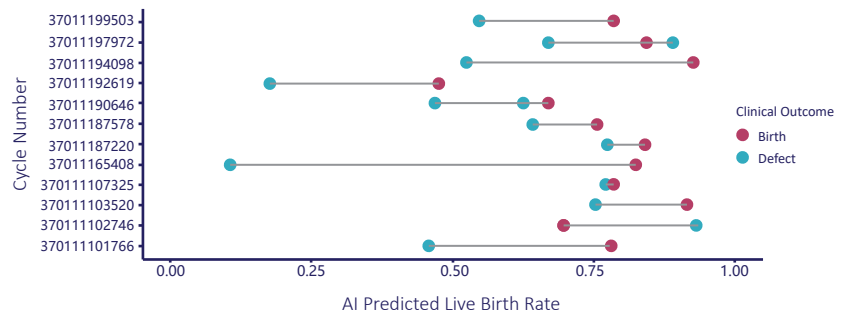
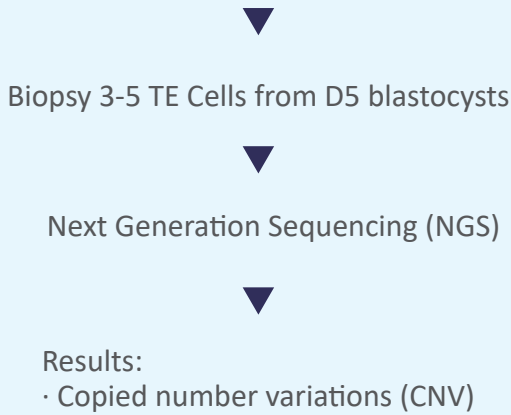


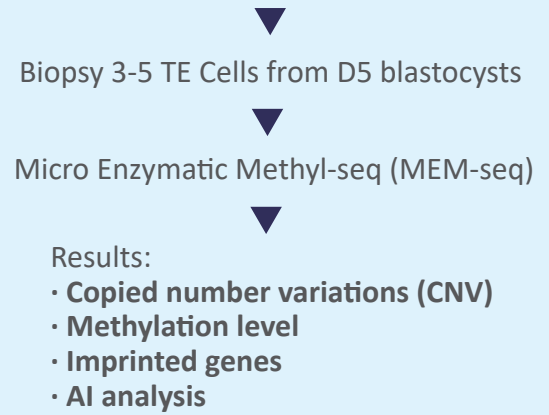
Figure 2. AI analysis to predict IVF clinical outcome

# How to distinguish **PIMS** ?

## PGT-A



## PIMS



No.	Project	Chromosomal Aneuploidy	Methylation Level	Imprinted Gene Diseases	AI Analysis
1	PIMS	●	●		
2	PIMS Premium	●	●	●	●

## Reference:

1. Jiang, Lan et al. "Sperm, but not oocyte, DNA methylome is inherited by zebrafish early embryos." Cell vol. 153,4 (2013): 773-84. doi:10.1016/j.cell.2013.04.041
2. Wang, Lu et al. "Programming and inheritance of parental DNA methylomes in mammals." Cell vol. 157,4 (2014): 979-991. doi:10.1016/j.cell.2014.04.017
3. Li, Guoqiang et al. "Genome wide abnormal DNA methylome of human blastocyst in assisted reproductive technology." Journal of genetics and genomics = Yi chuan xue bao vol. 44,10 (2017): 475-481. doi:10.1016/j.jgg.2017.09.001
4. Gao, Yuan et al. "A clinical study of preimplantation DNA methylation screening in assisted reproductive technology." Cell research vol. 33,6 (2023): 483-485. doi:10.1038/s41422-023-00809-z

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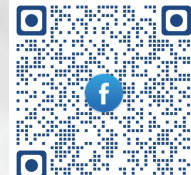
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