



Non Invasive Prenatal Testing (NIPT)

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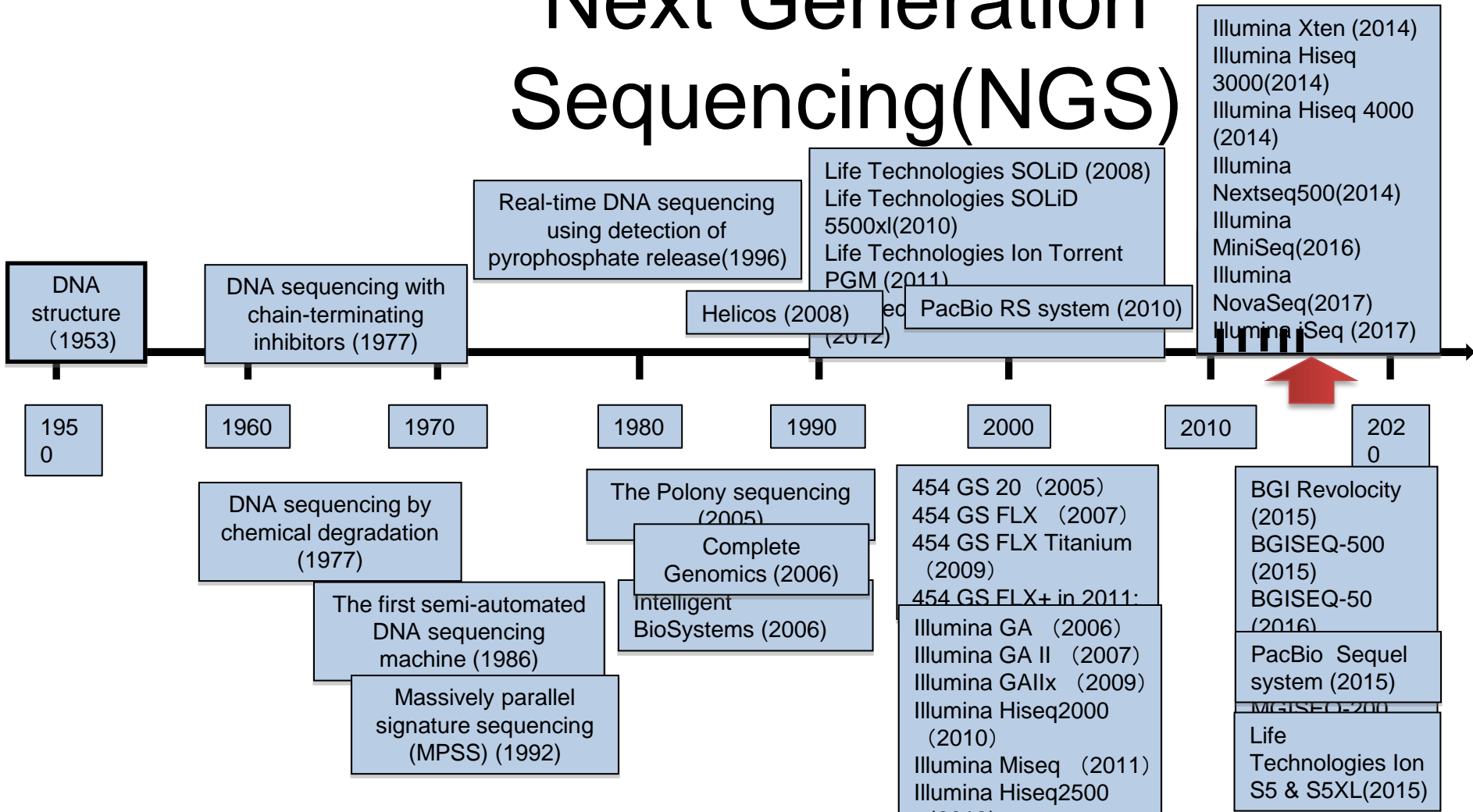
Genetics Dept., DeNA Lab, Tehran, Iran

Shiraz, Iran

April, 2019



Next Generation Sequencing(NGS)

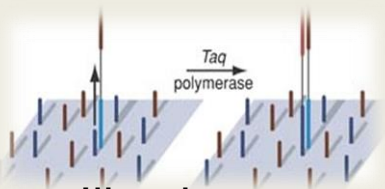


The past decade (2007-2017) has witnessed the quick development of sequencing technology as well as the fast transfer of this new technology from basic science research to practical clinical application *(from dream to reality)*

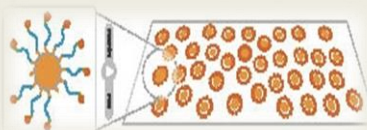
Cost for one human genome dropped from \$3,000,000,000 (Human genome project) to \$1,000



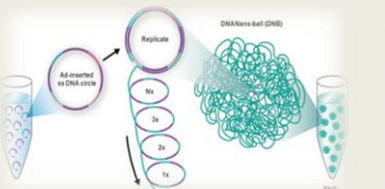
Sequencing technologies



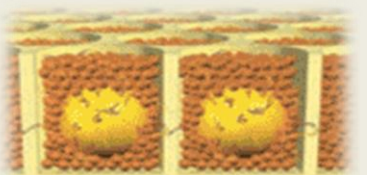
Illumina



SOLiD (ABI)

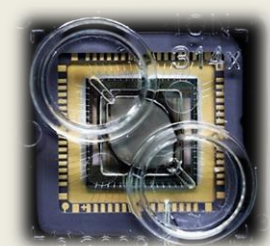


Complete Genomics



454 (Roche)

Optical Sequencing



PGM/Proton

Semi-conductor Sequencing

Key characteristics:

- Massively parallel analysis
- High throughput
- Reduced cost
- Short read length
- Higher error rate than 1st generation

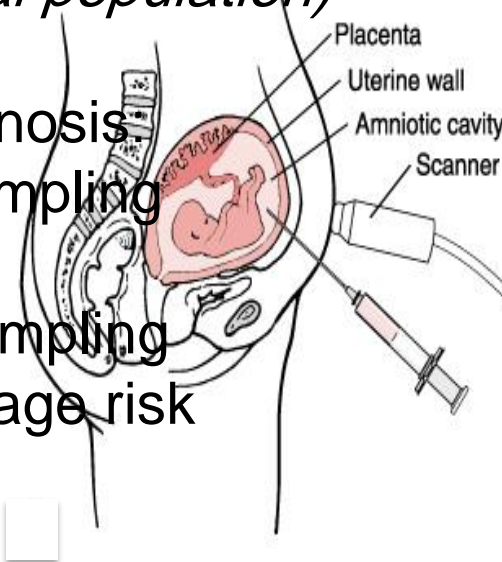




NIPT and NGS

- NIPT: noninvasive prenatal testing (*screen the high-risk subgroup from general population*)

- Invasive prenatal diagnosis
 - chorionic villus sampling
 - Amniocentesis
 - umbilical blood sampling
 - 0.5%-1% miscarriage risk



- NIPT refers to a wide scope of all prenatal cares in a noninvasive or minimal invasive way. Yet currently, **NIPT is mostly related to the cell free DNA-based testing of genetic diseases, especially**

chromosomal aneuploidies.



Cell-free fetal DNA and NIPT



- Short DNA fragments ~145-200bp, circulating in maternal peripheral blood and originating from placental trophoblasts.
- Can be observed since the 5th gestation week (GA)
- Content is proportional to GA and inversely proportional to maternal BMI
- Averagely 10%, diverse among individuals





Sequencing strategies for NIPT

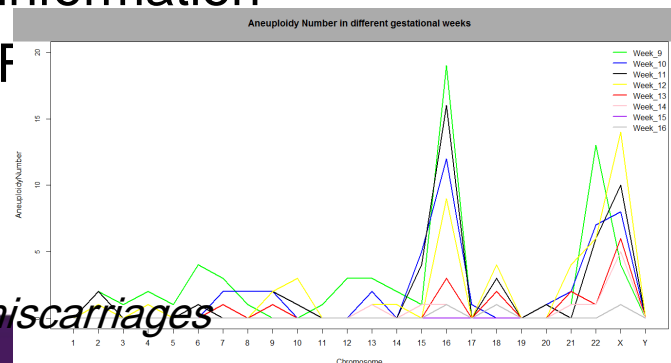
- **Whole genome sequencing**

- Non-polymorphism unique region in the human genome(>95%)
- Detect aneuploidies in 24 chromosomes and smaller deletion/duplication parallel
- Discriminate standard T21, partial T21 and mosaic T21
- Fetal fraction estimated by chromosomal Y specific or chromosomal specific sequence

- **Target region sequencing**

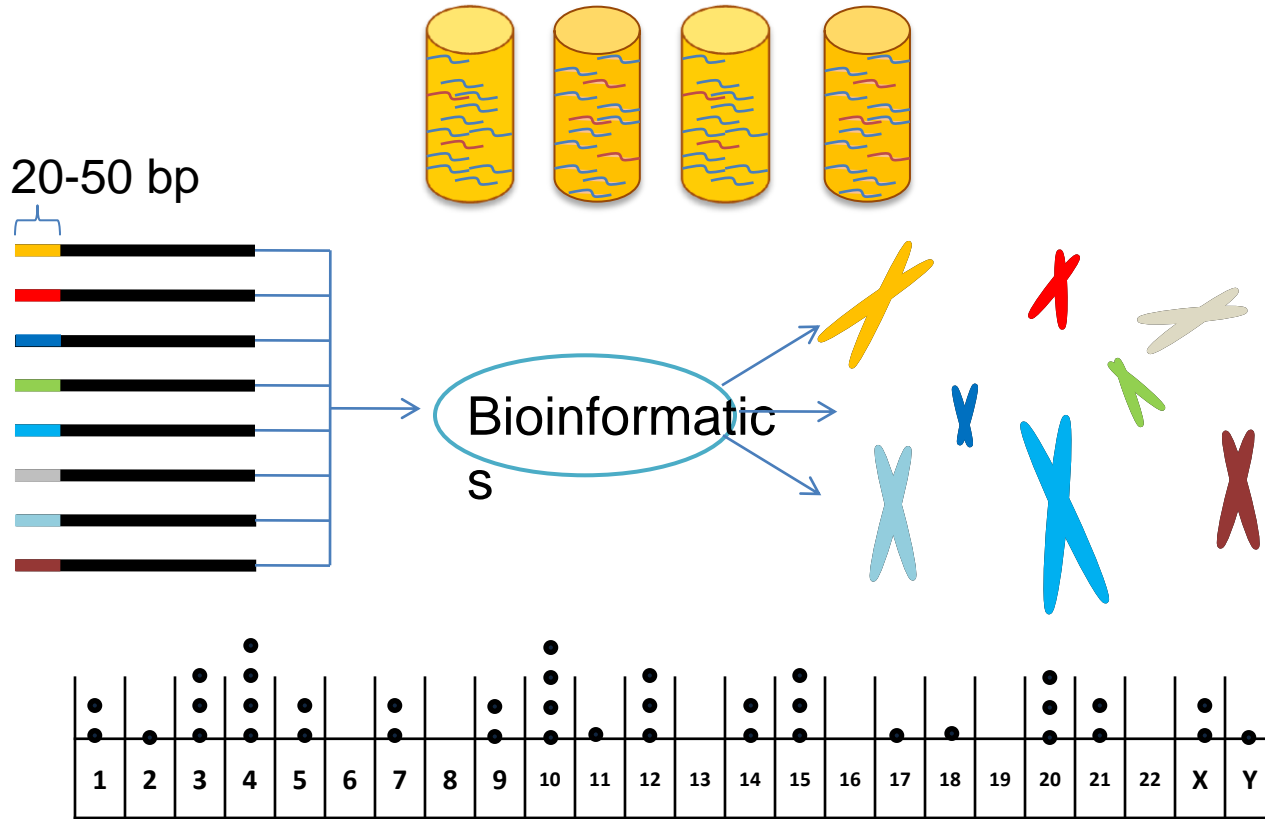
- Polymorphism region in the human genome(2000-10,000 SNPs)
- Can detect aneuploidies at selected chromosomes and regions (21,18,13,X,Y)
- Fetal fraction estimated by chromosomal Y specific or father-inherited SNP ratio information

– F





Principals of Sequencing-Based NIPT



$$\%chrN = \frac{\text{Unique fragments for chrN}}{\text{Total unique fragments}}$$

Plasma DNA extraction



Sequencing & alignment



Chromosome counting

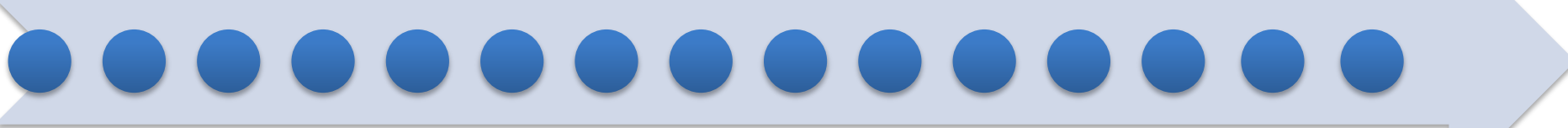


Coverage computation



Professional Guideline

2012.01 ISPD	2012.11 NSGC	2013.2 ACMG	2013.3 JSO	2014.7 ISUOG	2015.3 ESHG and ASHG	2015.9 ACOG update	2016.7 ACMG update
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2012.11 Chinese Prenatal Diagn	2012.12 ACOG	2013.2 SOGC	2013.5 Italian college of Fetal Mater	2014.8 Israeli Society of Medical	2015.4 ISPD update	2015.10 Austrian-German-Swiss
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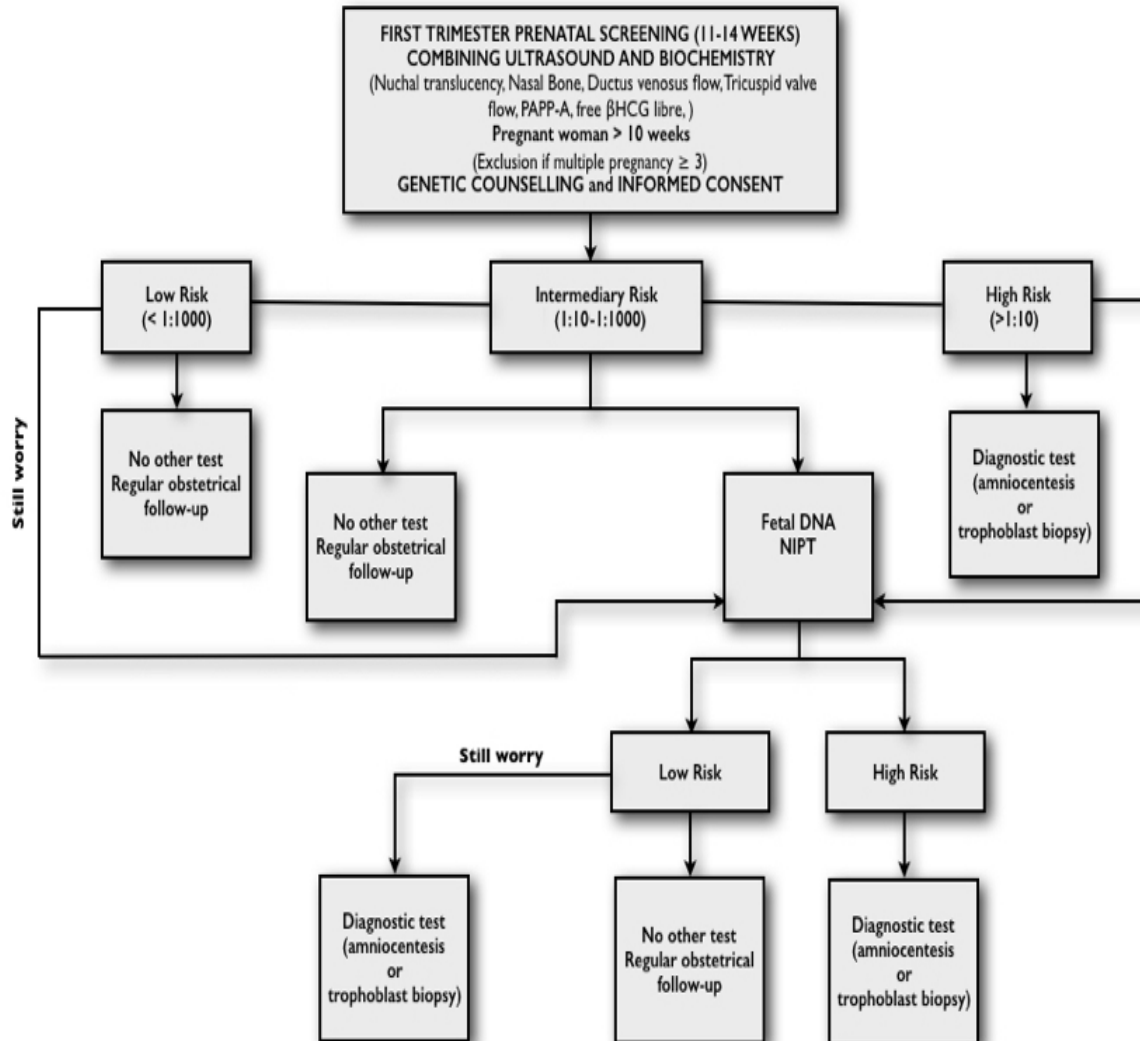
ACOG (American College of Obstetricians and Gynecologists)	ISPD (International Society for Prenatal Diagnosis)	ESHG-ASHG (European Society of Human Genetics- American Society of Human Genetics)	ACMG (American College of Medical Genetics and Genomics)
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2015.6.26 online published	2015.6.4 online published	2015.3.18 online published	2016.7 online published
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|---|---|---|--|
| <p>Recommended:</p> <ul style="list-style-type: none"> • Not applied in micro-deletion/duplication syndrome • Need more | <p>Recommended:</p> <ul style="list-style-type: none"> • Only include disease with clinical significance • Equip with trained | <p>Recommended:</p> <ul style="list-style-type: none"> • Not to expand NIPT to other syndrome: not deny the potential value • Target region based methods has limitations | <p>Recommended:</p> <ul style="list-style-type: none"> • NIPS is the most sensitive screening option for traditionally screened aneuploidies • Restrict only in disease with severe clinical significance • Not to expand NIPS to other chromosome aneuploidy, need more validation |
|---|---|---|--|

Non invasive prenatal screening using the detection of fetal DNA circulating in maternal blood

Proposed algorithm



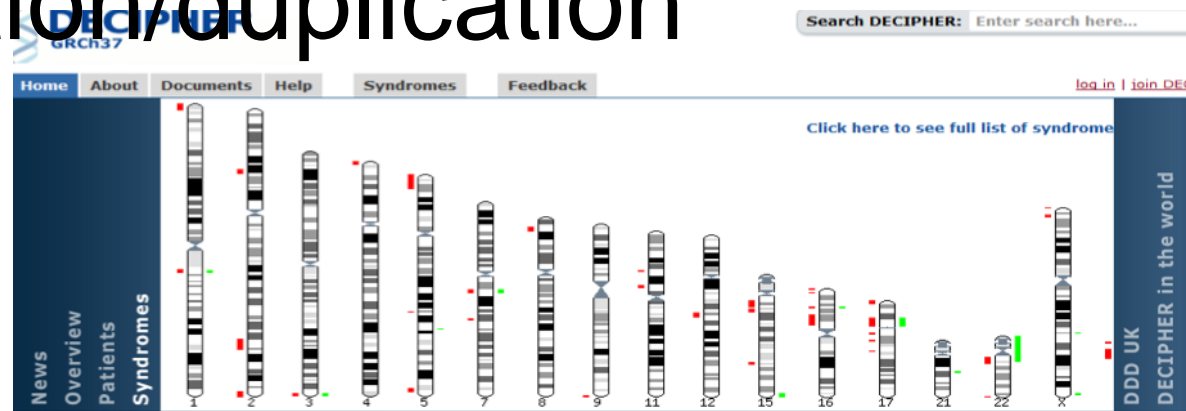
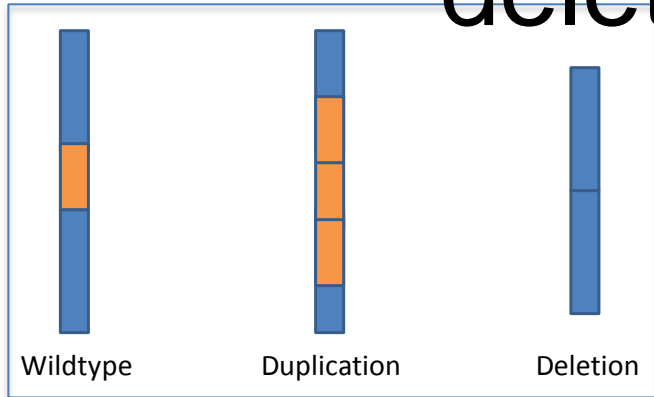


Challenges in current NIPT service

- **Simpler processing** (Automation-software-figure)
- **Easier explanation** (Z score/risk assessment-figure)
- **Faster turnaround time** (1-3-5-7-10 days)
- **Cheaper** (1000-500-300-100 USD)
- **Flexible throughput** (3456-768-196-16-1 samples per run)
- **Regulation** (CE/FDA/CAP/CLIA)
- **Easy training** (nurses/doctors/bioinformatics guys)
- **Social education** (Pregnant women/Family member)



NIPT detecting fetal micro-deletion/duplication



Author	Accuracy
Chen et al.2013	1311 clinical cases : Correctly identifies 3 cases of micro-deletion/duplication with 100% sensitivity. One false positive was found resulting in 99.92% specificity. No false negative results (>10M deletion/duplication)
Li et al.2016	117 clinical cases : 18 CNV (>1M) were identified through microarray, 10 of 11 cases with CNV >5M were identified with NIPT; Among 7 cases with CNV >1M but <5M, NIPT identified 1 case (2.82M). Therefore, NIPT sensitivity for detecting CNV >1M was 61.1% with 5% false negative rate.
Zhao et al.2015	For 3-40M micro-deletion/duplication , 17 case were identified in 18 cases. Sensitivity and specificity were 94.4% and 99.4%, respectively.
Helgeson et al.2015	In 175393 clinical cases , 55 sub-chromosomal abnormality were identified with false positive rate of 0.0017%. The most common abnormality was 22q11.2, with 70.5% detection rate
Pescia et al.2016	6388 clinical cases, identifies 3 T22, 6 T7 with false positive rate of 0.71%. In other sub-chromosomal abnormality(CNV) aspect, 8 CNV were identified, including 3 false positive and 1 false negative.

Evolving NIFTY

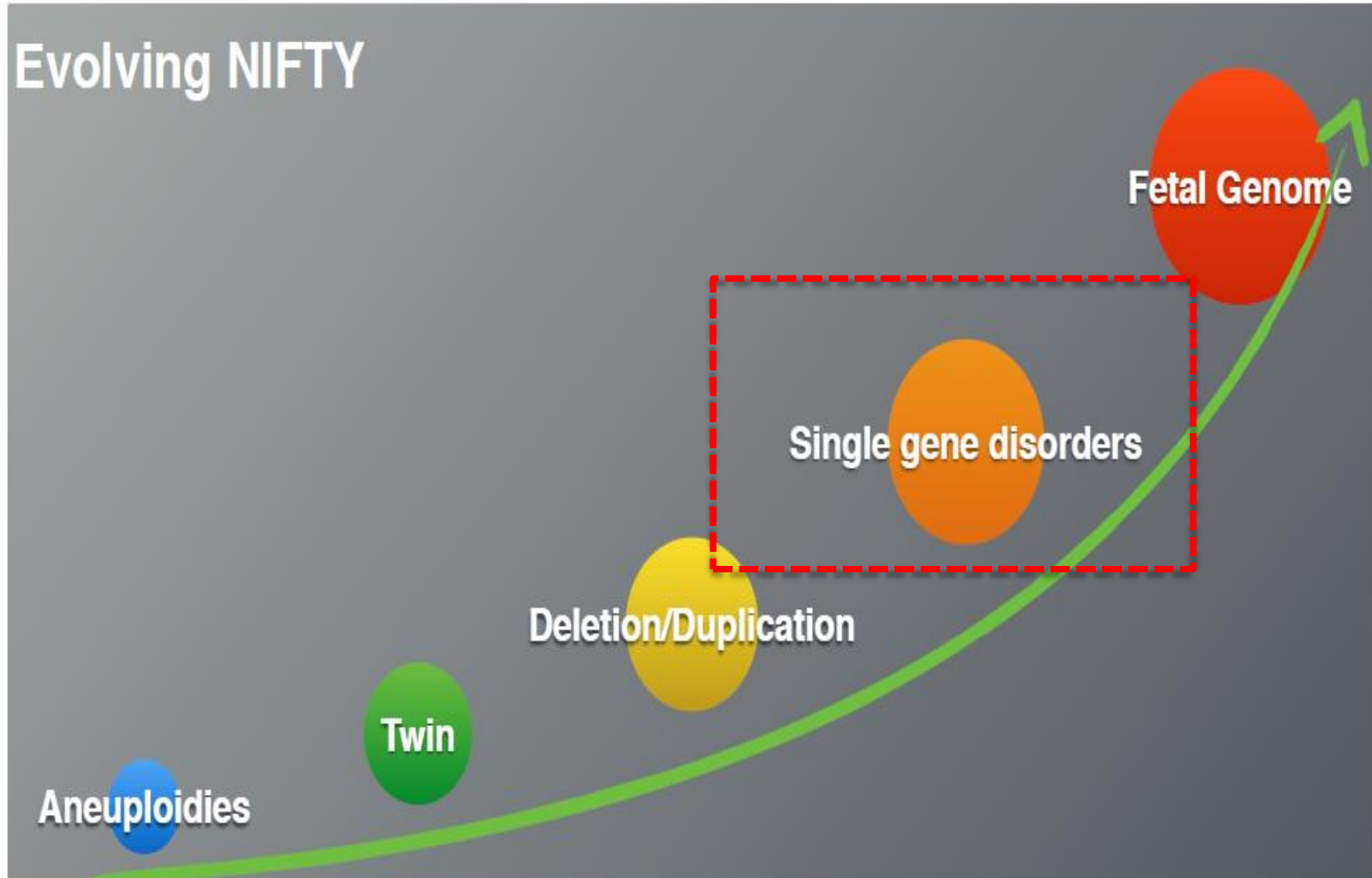
Aneuploidies

Twin

Deletion/Duplication

Single gene disorders

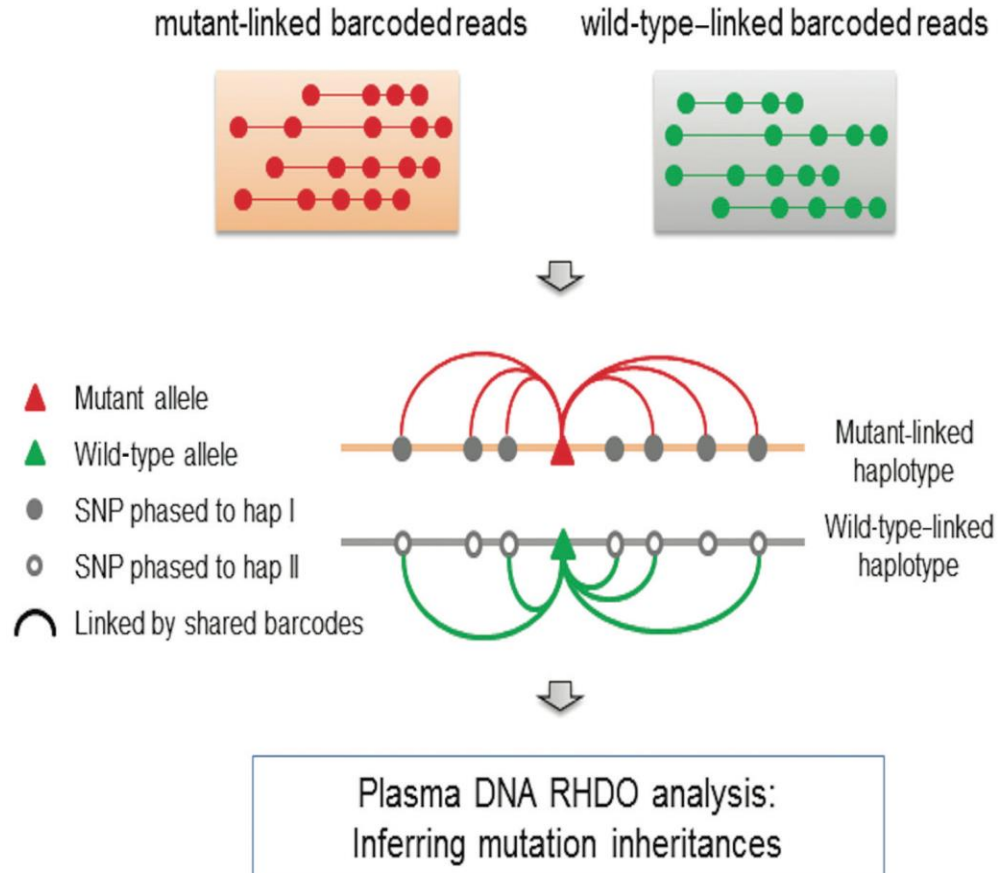
Fetal Genome





Haplotype-assisted method for NIPD

Direct haplotyping from parental DNA





NIPT and Maternal cancer

Amant F, et al. JAMA Oncol. 2015 Sep;1(6):814-9.

Brief Report

Presymptomatic Identification of Cancers in Pregnant Women During Noninvasive Prenatal Testing

Frédéric Amant, MD, PhD; Magali Verheecke, MD; Iwona Wlodek, MD, PhD; Nathalie Brison, PhD; Kris Van Den Bogaert, PhD; Daan Dierckx, MD, PhD; Thomas Tousseyn, MD, PhD; Philippe Moerman, MD, PhD; Adriaan Van den Berghe, MD, PhD; Patrick Neven, MD, PhD; Patrick Berteloot, MD; Katrien Putseers, MD, PhD; Peter Vandenberghe, MD, PhD; Eric Legius, MD, PhD; Joris Ruysschaert, MD, PhD

- 4000 case for NIPT, 3 cases showed multiple abnormalities
- MRI image, tissue slice and genetic testing confirmation ;
- tumor tissue CNV concordant with NIPT

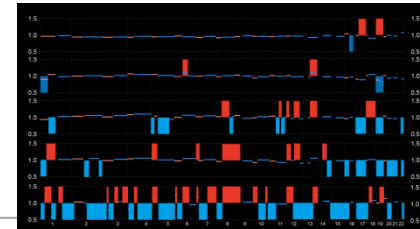
Bianchi, DW, et al. JAMA. 2015 Jul 14;314(2):152-8.

Preliminary Communication

Noninvasive Prenatal Testing and Incidental Detection of Occult Maternal Malignancies

Diana W. Bianchi, MD; Darya Chudova, PhD; Amy J. Sehnert, MD; Tracy L. Prosen, MD; Judy E. Garber, MD; Louise Wilkins-Hau, MD; Stephen Warsof, MD; James Goldberg, MD; Tina Ziainia, MD;

- 125,426 case for NIPT, 10 cases with confirmed cancer
- NIPT give discordant results with karyotyping





Article | Published: 12 April 2019

Identifying occult maternal malignancies from 1.93 million pregnant women undergoing noninvasive prenatal screening tests

Xing Ji, MD^{1,2}, Jia Li, PhD³, Yonghua Huang, MD⁴, Pi-Lin Sung, MD^{5,6}, Yuying Yuan, BS³, Qiang Liu, BS³, Yan Chen, PhD³, Jia Ju, MS³, Yafeng Zhou, PhD³, Shujia Huang, PhD³, Fang Chen, PhD³, Yuan Han, BS⁷, Wen Yuan, MS⁷, Cheng Fan, BS³, Qiang Zhao, PhD⁴, Haitao Wu, PhD⁸, Suihua Feng, MS⁴, Weiqiang Liu, MD⁹, Zhihua Li, MD¹⁰, Jingsi Chen, MD¹⁰, Min Chen, MD¹⁰, Hong Yao, MD¹¹, Li Zeng, MD¹², Tao Ma, MD¹³, Shushu Fan, MD¹⁴, Jinman Zhang, MD^{15,16}, Ka Yiu Yuen, BS¹⁷, So Hin Cheng, BS¹⁷, Irene Wing Shan Chik, BS¹⁷, Nien-Tzu Liu, MS¹⁷, Jianyu Zhu, BS³, Siyuan Lin, BS¹⁷, Jeremy Cao, BS¹⁷, Steve Tong, BS¹⁷, Zhiyuan Shan, BS¹⁸, Wenyan Li, MS³, **Mohammad Reza Hekmat**, MS¹⁹, **Masoud Garshasbi**, PhD^{19,20}, Javier Suela, PhD²¹, Yaima Torres, MSc²¹, Juan C. Cigudosa, PhD²¹, F. J. Pérez Ruiz, MD²², Laura Rodríguez, PhD²³, Mónica García, PhD²³, Janez Bernik, MS²⁴, Eva Traven, MS²⁴, Uršula Reš, MD²⁵, Nataša Tul, MD²⁶, Ching-Fong Tseng, MS²⁷, Depeng Zhao, MD²⁸, Luming Sun, MD²⁸, Qiong Pan, MS²⁹, Li Shen, MD³⁰, Mengyao Dai, MD^{1,2}, Yuying Wang, PhD³, Jian Wang, MS^{3,31}, Huanming Yang, PhD^{3,31}, Ye Yin, PhD^{3,32}, Tao Duan, MD^{b 28}, Baosheng Zhu, MD^{15,16}, Mahesh Choolani, PhD³³, Xin Jin, PhD^{3,34,35}, Yingwei Chen, MD¹ and Mao Mao, MD, PhD^{b 3}



Thank you for your attention

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