Comparison of AB Vector and main competitor kits in Preimplantation Genetic Testing for Aneuploidies (PGT-A)

Background

Analysis of embryos for chromosomal aberrations (PGT-A) is routinely used for making implantation decision in fertility clinics. PGT-A corresponds to about 20-30% of overall costs for fertility treatment[1] in the fast-growing fertility market[2].
Several fertility labs switched from the main competitor PGT-A kit to AB-PGT™ kit (AB Vector), http://www.abvector.com/AB-PGT.htm because of improved performance and lower cost per sample. Improved performance is due to advanced software and significantly better Whole Genome Amplification (WGA) technology (patent pending), which result in reduced noise, improved throughput and confidence in the data (slides 2 and 3).

PGT-A kit	Customer price per sample	Throughput samples/ MiSeq run	Number of steps	Total PCR cycles	Low stringency cycles	Software	Hazard	Illumina sequencer
Competitor (USA)	20-30% more	Up to 24	More	36	12	Visual annotation	Yes, requires fume hood	MiSeq only
AB-PGT™ (USA)	20-30% less	Up to 72	Less	28	2	Automatic annotation	No	MiSeq or NextSeq

1. https://www.fertilityiq.com/pgs-embryo-genetic-screening/costs-of-pgs
2. https://www.alliedmarketresearch.com/US-IVF-services-market

Comparison of AB Vector and competitor software

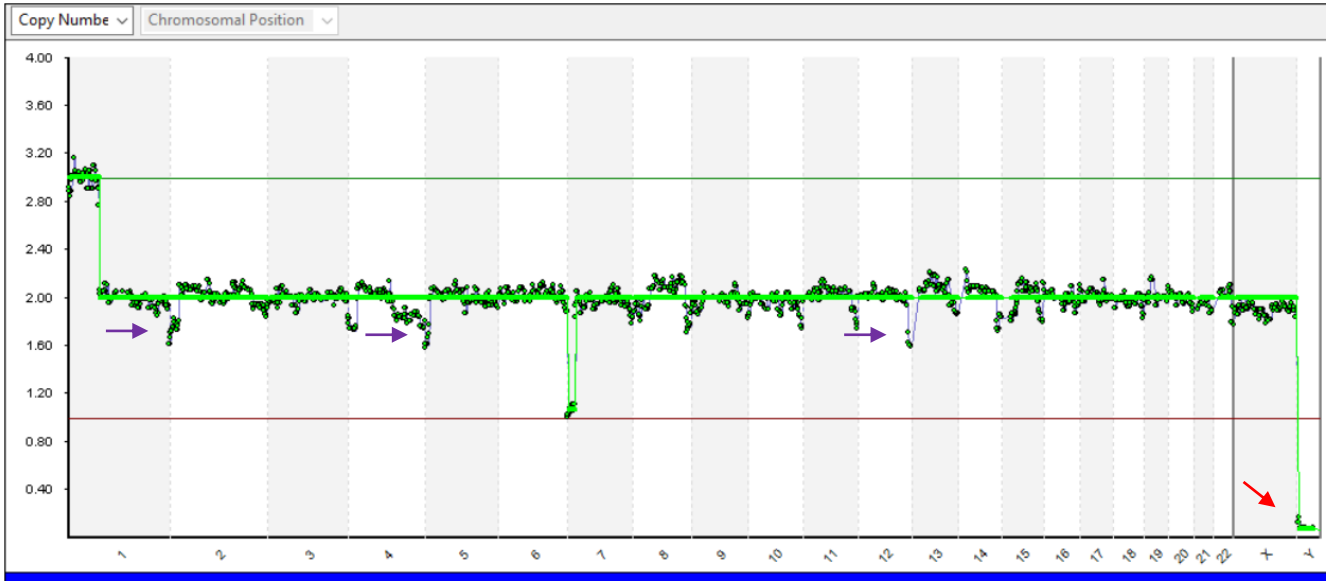
Biopsy sample was processed with the competitor kit and analyzed either using competitor or AB Vector software

Competitor software

Norm or aberration conclusions are based on visual examination of CNV profiles. The same color (**green**) is assigned for norm and for aberrations.

→ Artifact peaks at telomeres

→ Artifact at Y chromosome

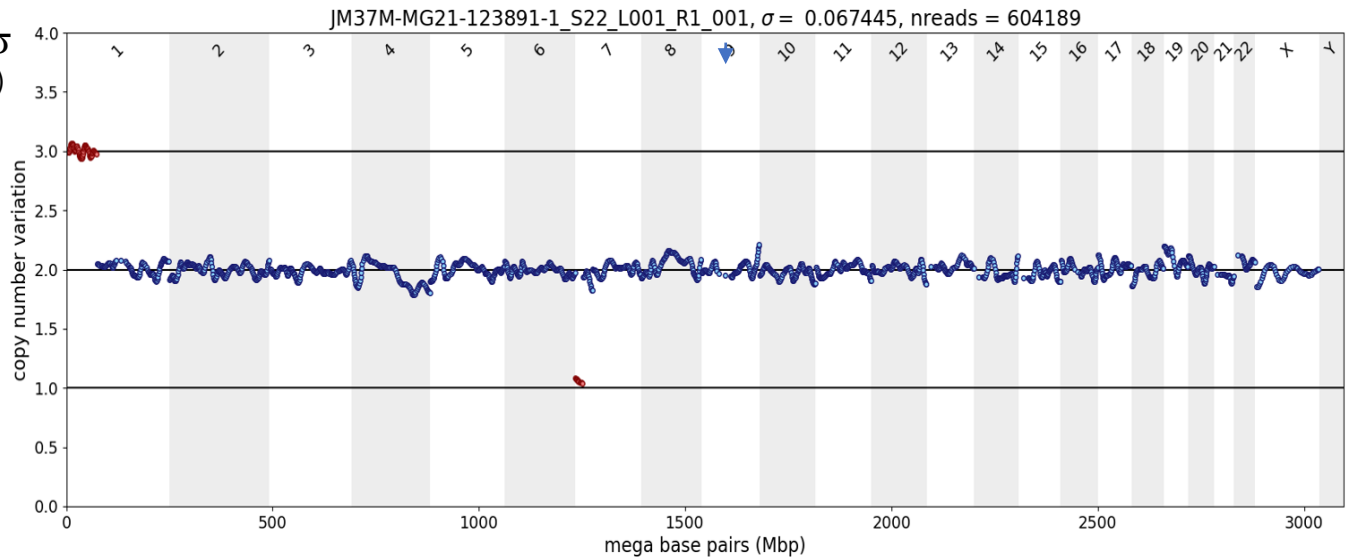


AB Vector software, the same sample

Statistical measure of noise: σ
(biopsy quality is the main component of noise)

Different colors assigned to aberrations (**red** in this case) based on standard deviation from the norm (**blue**). →

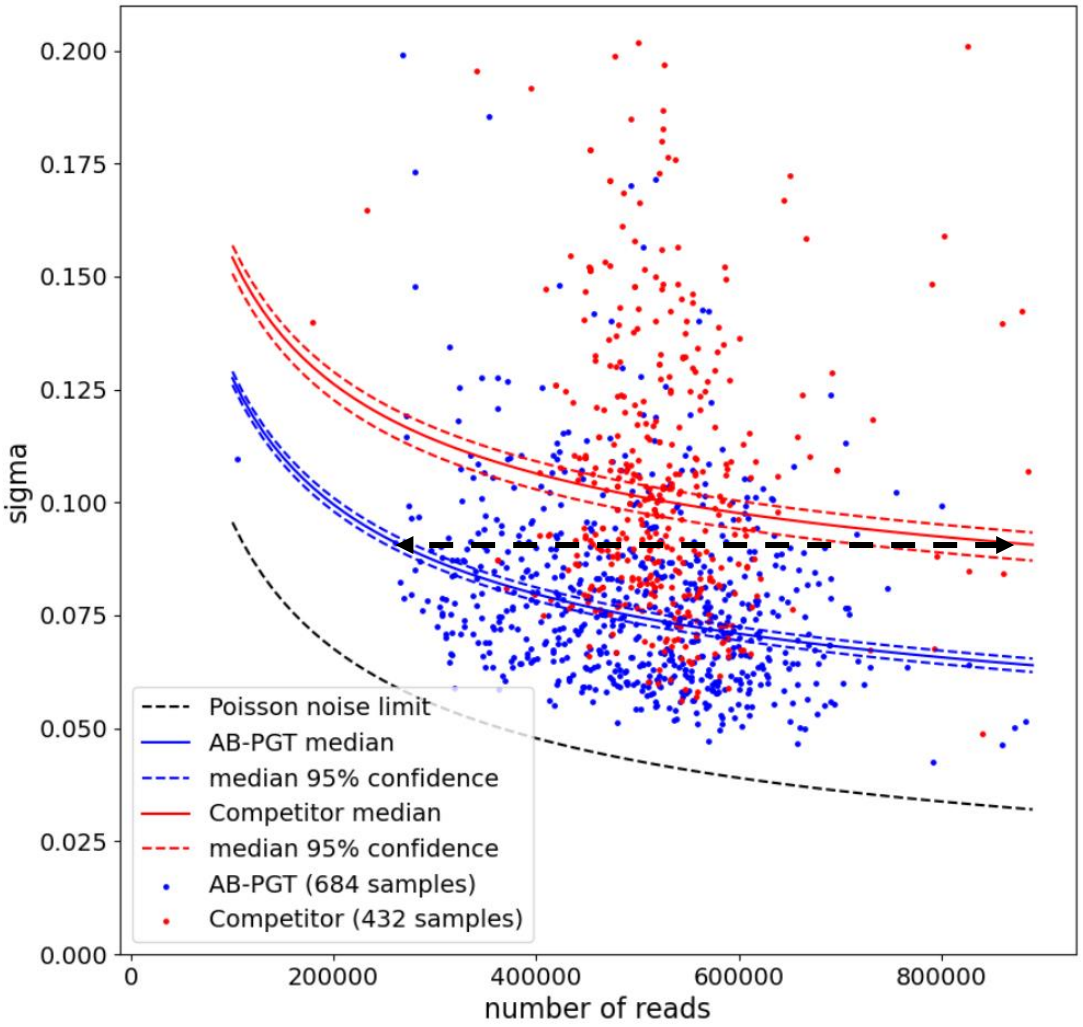
Statistical confidence of aberrations is automatically annotated (not shown).



Performance of AB-PGT™ and the competitor kits in a clinical setting

Sigma noise is dependent on:

a. biopsy quality
b. WGA method
c. number of reads per sample



Performance study done in a fertility laboratory that switched from the competitor to AB-PGT™ kit. Libraries, prepared using either method, were sequenced on MiSeq. FastQ files from both sets of libraries were processed using proprietary AB Vector software. The Poisson noise limit is a theoretical value wherein the WGA method and the biopsy quality are ideal and generate no noise. Thus, all the noise derives from the limited number of reads. Confidence intervals for the medians were determined using bootstrapping method (*Monte Carlo variation - Varian, H. (2005), "Bootstrap Tutorial", Mathematica Journal, 9, 768–775*). The horizontal black line indicates equivalent median noise observed with 260,000 reads using AB Vector kit versus 870,000 reads using competitor kit, meaning that the noise from **80** AB-PGT™ samples is no greater than **24** pooled competitor samples, a **>3-fold improvement** in throughput. This factor is a minimum given that higher noise (artifacts) is observed using competitor software (previous slide). Minimizing noise is pivotal for the detection of low-level mosaicisms (data not shown).