JUNO GENETICS

PGT A Seq

INCREASED PROPORTION OF EMBRYOS CLASSIFIED EUPLOID WITH RESPECT TO SOME OTHER METHODS

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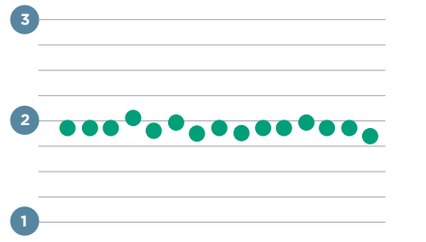
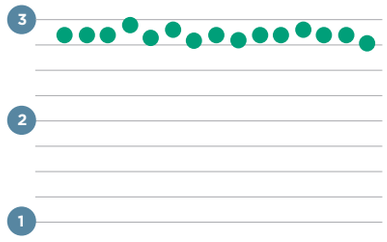
1 NGS

Juno uses next-generation sequencing to measure the amount of DNA at thousands of sites on each chromosome

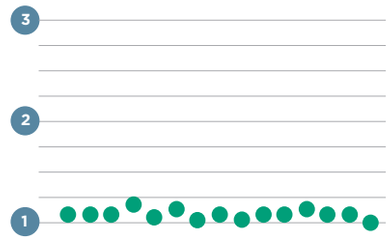
This allows the number of copies of the chromosome to be calculated with high accuracy



NORMAL EMBRYO



TRISOMY



MONOSOMY

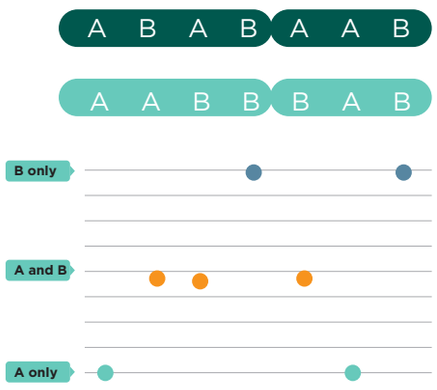
2 SNPs

Juno looks at thousands of places where the DNA sequence can differ between individual chromosomes

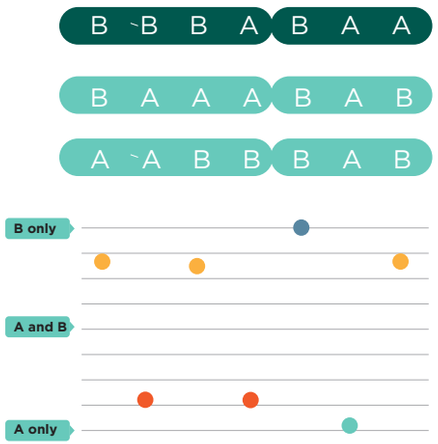
Each of these sites of variation can be type 'A' or type 'B'

Normal, Trisomy and monosomy each have characteristic patterns of As and Bs

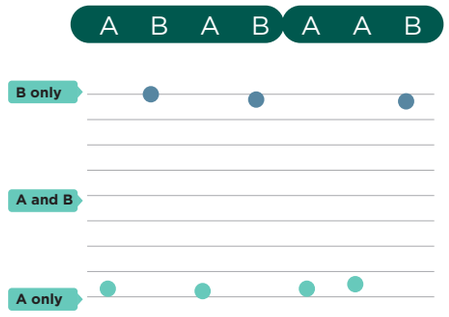
Together, the measurement of the amount of DNA and the analysis of the DNA sequence greatly increases the accuracy of PGT-A



Some sites have only A or B, but others have A and B equally



No sites have A and B equally, but some are AAB or BBA



All sites have either A or B, but never both types