

## SYGNIS TruePrime™ Single Cell WGA Kit



### SYGNIS TruePrime™ Single Cell WGA Kit

includes SYGNIS' revolutionary TruePrime™ multiple displacement amplification technology. This technology combines Phi29 DNA pol-based whole genome amplification with the unique properties of a new primase called TthPrimPol to eliminate the need of synthetic random primers and to provide sequences superior in quality to traditional approaches.

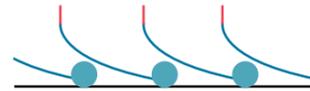
 TthPrimPol  
 Phi29 DNA pol

## How does TruePrime™ technology work?

1 TthPrimPol binds denatured DNA at different sites



4 Phi29 DNA pol performs strand displacement



2 TthPrimPol synthesizes short DNA primers



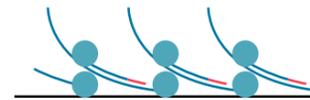
5 TthPrimPol binds to newly formed DNA and synthesizes new DNA primers



3 Phi29 DNA pol displaces TthPrimPol and begins polymerization



6 Phi29 DNA pol displaces TthPrimPol binds DNA primers and begins polymerization



# SYGNIS

 **Order now!**

[WWW.SYGNIS.COM/SHOP](http://WWW.SYGNIS.COM/SHOP)



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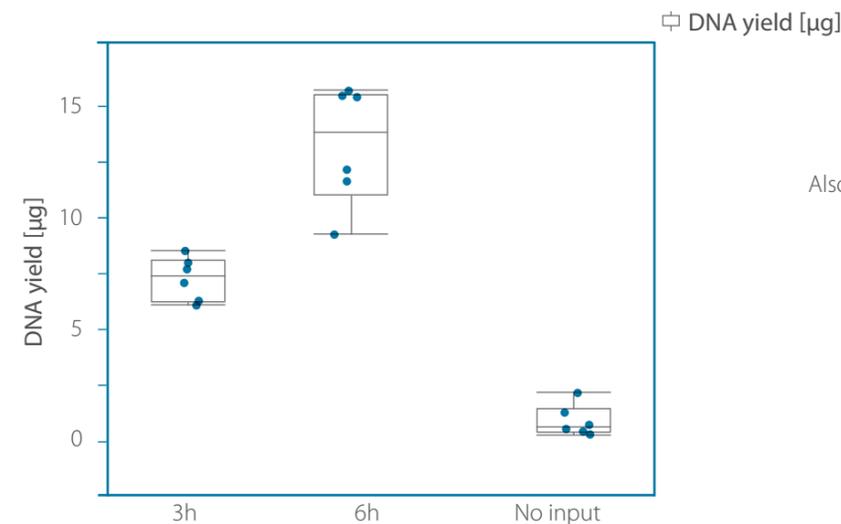
# SYGNIS

## TruePrime™ Single Cell WGA Kit

The revolution in DNA amplification: Primer-free MDA with superior performance

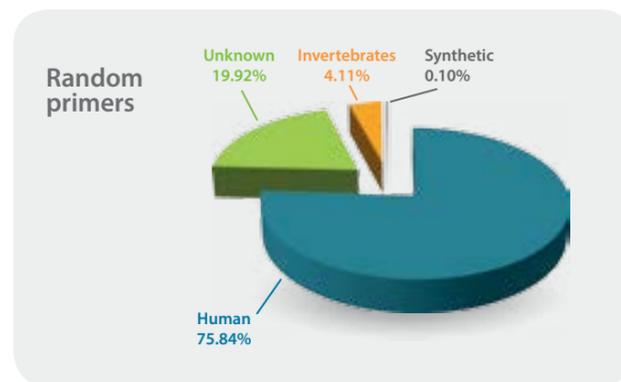
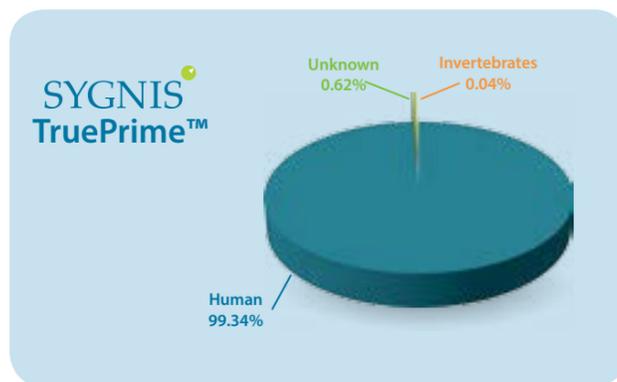


## TruePrime™ WGA with single human HEK293 cells



Also proved for COS cells and mouse primary neural stem cells.

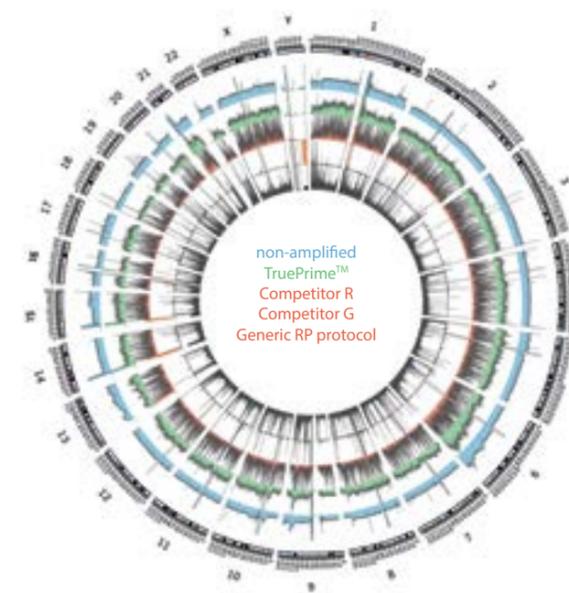
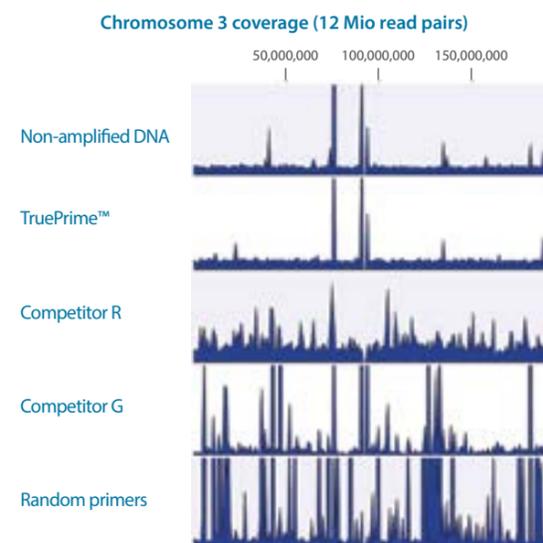
## TruePrime™ : Absence of primer artefacts



1 pg of human genomic DNA (~ 1/6 of the content of one human/mammalian cell) has been amplified using either TruePrime™ (TthPrimPol-based MDA) or random primed MDA reactions. Random primed reactions contain 20% of sequences that cannot be mapped to any organism in sequence databases.

## TruePrime™ shows superior coverage of the genome

Sample	Non-amplified DNA	TruePrime™ (1c)	Random primers	Competitor R	Competitor G
Mapped reads	99.53%	96.86%	97.42%	99.64%	98.62%
Reads in pair	92.03%	86.77%	59.07%	91.50%	37.94%
Fraction human genome covered	53%	49%	28%	38%	1%
Calculated ideal (Poisson) coverage	59%	57%	44%	59%	31%
Deviation observed from expected	10.2%	13.8%	35.76%	35.4%	96.7%



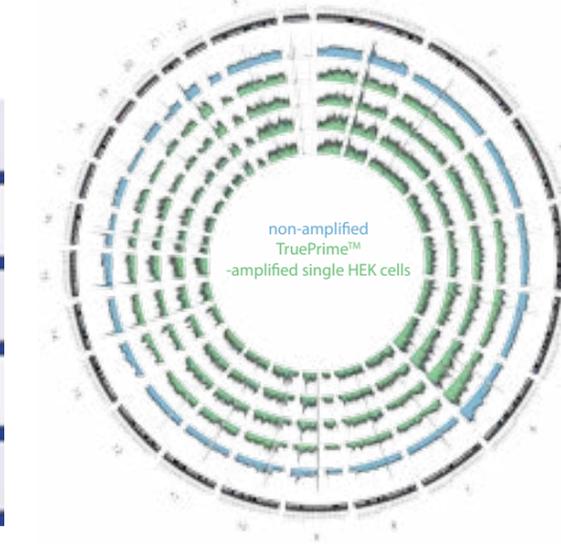
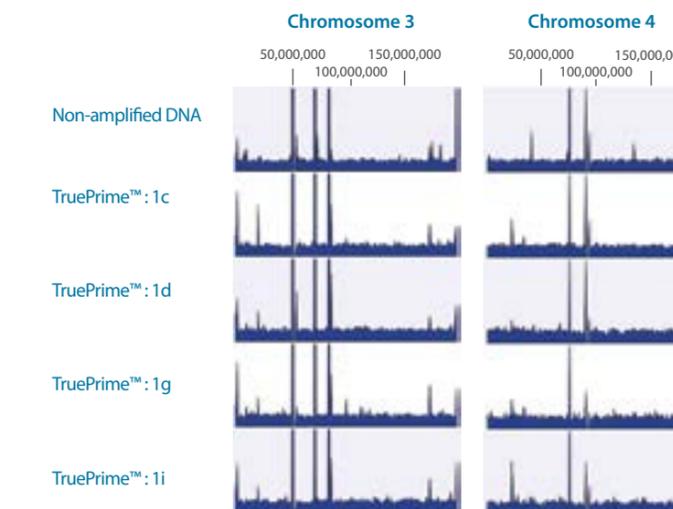
Excellent overall mapping data for TruePrime™ -amplified DNA, closest to non-amplified DNA coverage reached.

**Left:** Single Hek293 cells were amplified with different MDA-type single cell amplification methods and coverage compared to the theoretically possible coverage (Poisson) and the coverage in non-amplified DNA from the same Hek293 population. Exactly 12 mio read pairs were mapped to the human genome. Coverage graph for chromosome 3 depicting differences in evenness of coverage between the methods. Note the extreme similarity between nonamplified and TruePrime™.

**Right:** Circos plot showing the whole genome coverage for the different methods. Outward to inward: non-amplified, TruePrime™, competitor R, competitor G, generic random primed MDA.

## TruePrime™ has excellent reproducibility

DNA from 4 single human HEK293 cells was amplified following the TruePrime™ protocol for 3 or 6 h, subjected to library prep and sequencing (Illumina HiSeq), and 5 million read pairs were mapped onto the human genome. **Left:** Shown are comparisons of chromosome 3 and 4 coverage to non-amplified HEK293 cell DNA from the same cells. Note the evenness of coverage, and the high similarity between single cells. **Right:** Circos plot showing the whole genome coverage of the 4 replicates (blue=non-amplified; green=amplified).



## TruePrime™ Single Cell WGA Kit

- **Primer-free method:** TthPrimPol synthesizes the primers for Phi29 DNA pol.
- **No primer artefacts:** The absence of random synthetic primers prevents any amplification artefacts generated by random extension of primer dimers, etc.
- **Easy handling** in a convenient kit format.
- **Reliable results.**
- **Insensitive to external DNA contaminations.**
- **Exquisite reproducibility** when amplifying from **single mammalian cells**.
- **Reduced amplification bias in genome coverage** compared to methods based on random synthetic primers.
- **Ideally suited for next generation sequencing**, tested for Illumina and Ion Torrent workflows.

