UNIVERSITY OF LEICESTER

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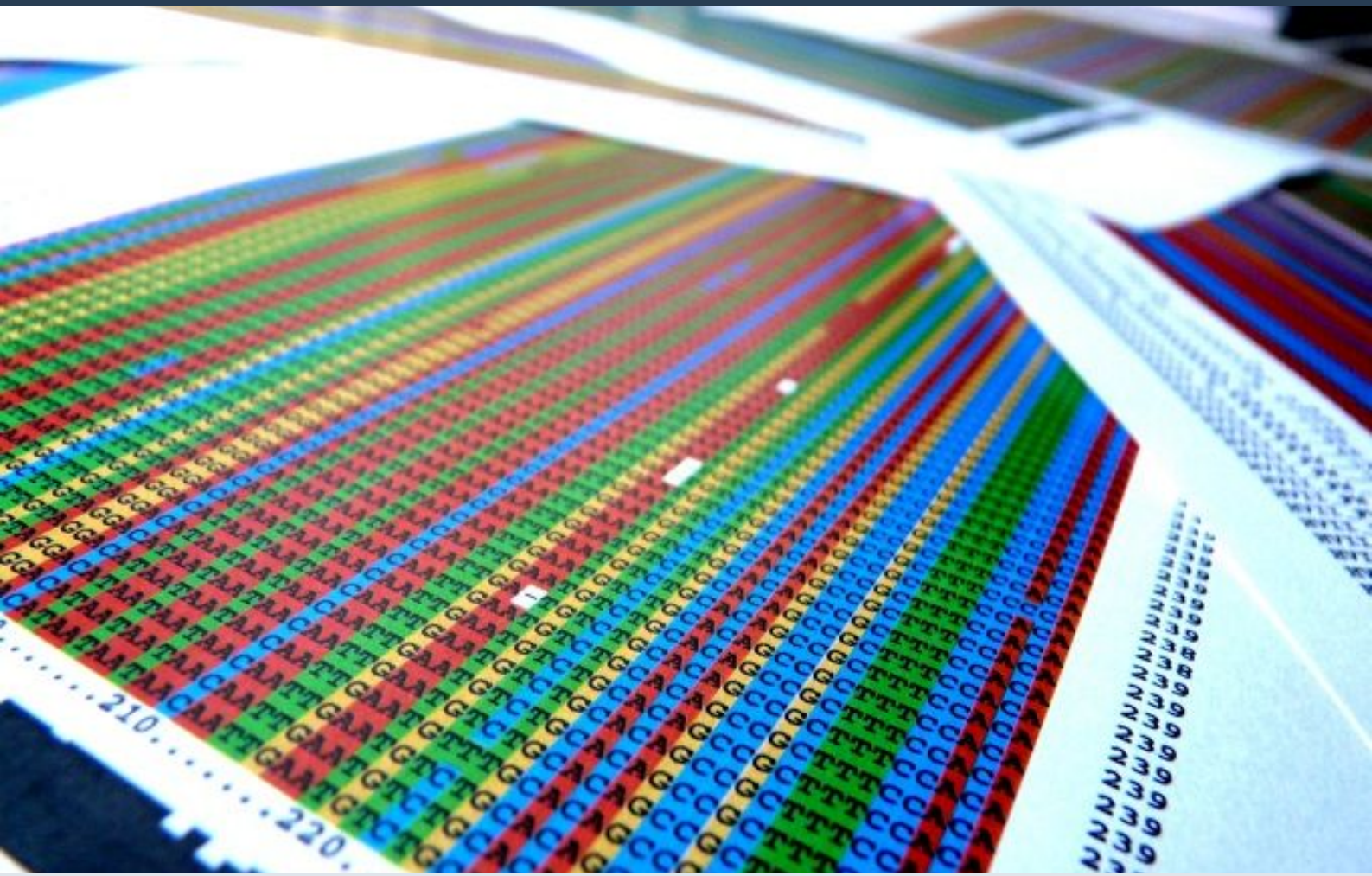
Increasing the Performance of Hybridisation-Based Target Enrichment For NGS

An enhanced method for enriching genomic DNA for sequencing studies.



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IP Status

Patent application submitted

Seeking

Licensing, Development partner

About **University of Leicester**

The University of Leicester works hand in hand with industry to generate business growth and find real applications for its leading innovation and research.

Background

Hybridisation Target Enrichment (HTE) is the most commonly used genomic DNA enrichment strategy in NGS studies, but the method has not significantly advanced in recent years. Researchers have now developed products and strategies that significantly improve the performance of HTE.

- Novel multifunctional blockers reduce non-specific sequence recovery almost 4x as effectively as commonly used DNA equivalents (Figure 1).
- Innovative approach to target recovery requires 10x fewer probes than other products e.g. >180kb of genomic bases evenly captured with ~2500 probes (Figure 2).
- High efficiency probe generation strategy dramatically lowers reagent costs.

Whole genome sequencing is not yet cost effective for most applications, so hybridisation targeted enrichment (HTE) remains popular. Existing HTE methods produce: Limited enrichment power, such that they are poorly useful unless targeting >1Mb Uneven recovery, such that many variants are missed or unreliably detected.

Tech Overview

Researchers have devised a new HTE procedure, incorporating several innovations, including:

- Unique RNA-based 'multi-functional' repetitive element blockers, that dramatically reduce non-specific sequence recovery
- A greatly improved method for cost effective preparation of biotinylated bait libraries
- Novel approaches to DNA fragment library preparation and bait design

Benefits

These combined enhancements dramatically improve HTE performance, enabling target regions to be recovered more specifically, more evenly, and at lower cost:

- Close to 4-FOLD better Enrichment Power compared to traditional DNA blockers
- Powerful enough to be applied to very short target regions (<<1Mb targets)
- Extremely even recovery of diverse targeted regions and sequences
- Novel 'bait' preparation method, sufficient for >100 fold more replicate experiments than typical procedures

Applications

- These approaches and products will enhance the performance of market leading HTE products

- The complete method could be adopted by companies in the NGS market that do not have an existing HTE product

Opportunity

Licensing, co-development and/or collaboration.

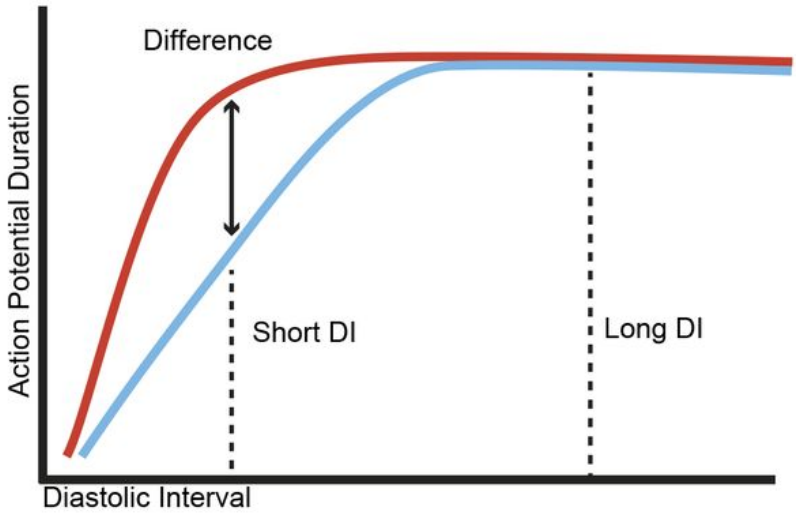
Patents

- This technology is protected by patent application. PCT/GB2016/051531

Appendix 1

Figure 1

Performance of unique RNA-based blockers compared to commonly used DNA based blockers. Blocker B1 alone achieves almost 2x reduction in non-specific sequence recovery than Cot-1 DNA alone. Combining Blockers B1 and B2 achieves almost 4x improvement relative to Cot-1 DNA alone.



Appendix 2

Figure 2

Even recovery of a 180kb of genomic bases using 2500 probes. 99.7% of bases covered 20x by aligned NGS reads when 10 enriched samples were sequenced in parallel on the MiSeq NGS platform (Illumina).