myBaits® Compass 1.2M SNP Kit

Simultaneously genotype millions of human genome-wide SNPs informative for forensic genetic genealogy (FGG) and other research applications

Overview

By focusing the power of massively parallel sequencing (MPS) / next-generation sequencing (NGS) on large numbers of informative genome SNP variants, the myBaits Compass workflow is significantly more effective and more efficient than alternative sequencing- or array-based genotyping methods, allowing cost-effective achievement of the highest-resolution FGG analysis (fifth degree or higher relationships). Sufficient numbers of SNPs for FGG analysis can even be called from highly degraded and/or contaminated DNA sources that are incompatible with other FGG genotyping methods.

Description

Panel design

The kit targets ~1.2 million human autosomal and X/Y-linked SNPs, as well as the full mitogenome, which have been selected to maximize compatibility with multiple databases and workflows commonly used for FGG analysis. The large number of targeted markers allows for robust kinship analysis, and for many samples, enables variant calling based on direct read coverage observation without the need for genomic imputation. The panel was curated to remove known ClinVar-associated SNPs (as of time of design).

Kit configuration

The myBaits Compass 1.2M SNP kit is available in 5 kit sizes, with scaled per reaction pricing to suit any throughput requirement.

SKU	Description
3601008.V5	myBaits Compass 1.2M SNP Kit, 8 Reactions
3601048.V5	myBaits Compass 1.2M SNP Kit, 48 Reactions
3601096.V5	myBaits Compass 1.2M SNP Kit, 96 Reactions
3601384.V5	myBaits Compass 1.2M SNP Kit, 384 Reactions
3601768.V5	myBaits Compass 1.2M SNP Kit, 768 Reactions

Features and benefits

✓ **Efficient marker recovery**

Achieve cost-effective variant calling of large numbers of FGG-compatible SNPs, from any sample type that is compatible with MPS/NGS.

✓ **Easy workflow integration**

Platform-agnostic myBaits reagents are compatible with any upstream library prep and downstream sequencing platform (e.g. Illumina NovaSeq® or Element AVITI®).

✓ **Flexible analysis**

Analyze data from your preferred platform, using your preferred pipeline of choice. Data are compatible with existing whole-genome sequencing workflows (adjusted for expected post-enriched X/Y ratios).

✓ **Robust marker coverage**

Datasets are compatible with a broad range of user-defined analysis parameters (e.g. minimum unique read coverage thresholds; +/- genomic imputation; sex inference; mitogenome haplogroup; Y haplogroup).

✓ **Expert support**

Daicel Arbor's experienced team has combined decades of experience working with academic and industry forensics and other degraded DNA researchers.

Performance

Figure 1. Compass capture retrieves sites that whole-genome sequencing (WGS) cannot access

We compared site retrieval rates of Compass capture and direct WGS for samples of different starting levels of endogenous human DNA. At 20 Gbp of PE150 sequencing, Compass-enriched libraries retrieved dramatically more sites at informative coverage levels than direct WGS, whether the starting library was built from 100% human DNA ("WGS-100%" / "Cap-100%") or 10% human ("WGS-10%" / "Cap –10%"). For heavily contaminated samples, Compass enables sequencing of orders of magnitude in more sites than is possible with 20 Gbp direct sequencing. The six genomic DNA samples were commercially purchased and were associated with the following identified ethnicity/ancestry labels: (1) American Indian or Alaskan Native, (2) Arab, (3) Finnish / Italian, (4) Black / African American, (5) Hispanic/Latino, (6) Ashkenazi Jewish. Samples with 10% human DNA comprised 90% microbial DNA built from a commercial standard.

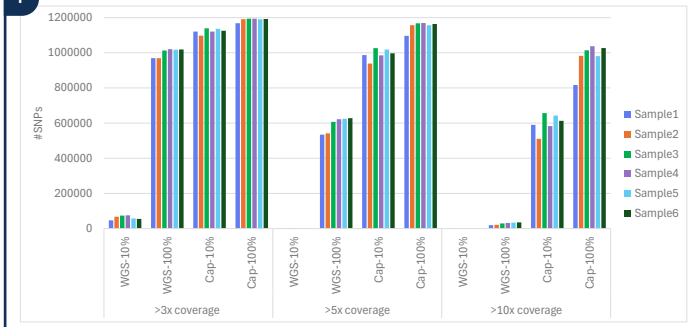
Figure 2. Compass capture accurately retrieves the true genotype of geographically diverse samples

Using a diverse collection of individuals from six regional populations, we show that Compass enrichment coupled with 20 Gbp PE150 sequencing ("Cap") achieves >99.5% concordance with calls from the same samples using deep (>15X) WGS ("Ref"). The genomic DNA samples were commercially purchased and had the following identified ethnicity/ancestry labels: (1) American Indian or Alaskan Native, (2) Arab, (3) Finnish / Italian, (4) Black / African American, (5) Hispanic/Latino, (6) Ashkenazi Jewish.

Figure 3. Achieve high coverage of informative SNPs, even from samples with low human DNA

Sequencing reads from a library built from a control low-human DNA sample (10% human genomic DNA + 90% bacterial background DNA) and enriched with the myBaits Compass 1.2M SNP kit, mapped to the human genome. The Blue bar indicates the region that is targeted by overlapping bait probes, which covers two target SNPs separated by 166bp. Read coverage is concentrated in the baited region.

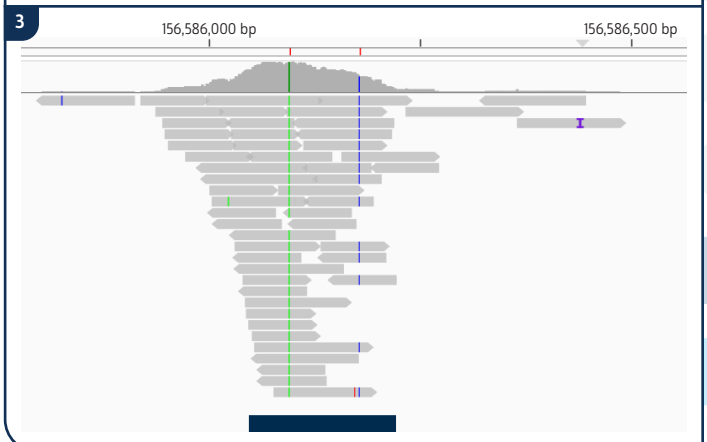
1



2

Samples	1 Ref	2 Ref	3 Ref	4 Ref	5 Ref	6 Ref
1 Cap	99.6%	61.4%	62.8%	58.2%	61.6%	62.4%
2 Cap	61.4%	99.7%	61.3%	58.8%	60.7%	61.8%
3 Cap	62.6%	61.3%	99.7%	58.1%	61.1%	62.2%
4 Cap	58.0%	58.7%	58.0%	99.7%	58.2%	58.3%
5 Cap	61.5%	60.5%	61.2%	58.2%	99.7%	61.3%
6 Cap	61.1%	60.7%	61.2%	57.2%	60.2%	99.7%

3



Questions? Contact us via the methods listed below. Our team is happy to assist you!

Web: www.arborbiosci.com
Email: info@arbor.daicel.com
Phone: 1-734-998-0751
X: @ArborBio
Bluesky: @arborbio.bsky.social