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DNA Fingerprinting

Frequently Asked Questions

What is DNA fingerprinting?

DNA fingerprinting is the identification of a subject by comparing the typing of a sample to documented results. The Research Cell Bank (RCB) uses Short Tandem Repeat (STR) analysis, a method commonly used in forensic science. DNA can be submitted for analysis or RCB can extract DNA from cells or other sources before typing. Results can be used to confirm cell line identity if a reference typing is provided.

We employ a system for the identification of STR polymorphisms at 9 or more different loci, and the Amelogenin present on the sex chromosomes. The alleles are used to determine sex and distinguish between individuals. The combination of these polymorphisms across all loci in one person is known as their "DNA fingerprint."

How much DNA is required for testing?

We request 1 ug of DNA at 100 ng/ul. For an extra fee, we can extract DNA from a cell pellet for testing. We require a minimum of 1M cells but no more than 5M.

How Often Do You Run Tests?

Tests are performed on an as needed basis, but often no more than every two weeks. Once testing has started, it can take up to a week to receive results.

Can you test mouse/dog/non-human cells?

Unfortunately, no. You can find mouse cell STR typing services available at ATCC at https://www.atcc.org/en/Services/Testing_Services/Mouse_STR_Testing_Service.aspx.

Understanding Your Results

Controls in your test

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Positive control is the part of PCR kit. We use AmpFLSTR™ Identifiler™ PCR Amplification Kit (Catalog number: 4322288) to PCR amplify your sample. The positive controls come from the kit. The positive controls are there to test our master PCR mix, MgCl2 amounts, primer annealing temperature, and extension times. In other words, positive controls are needed to verify that PCR amplification worked.

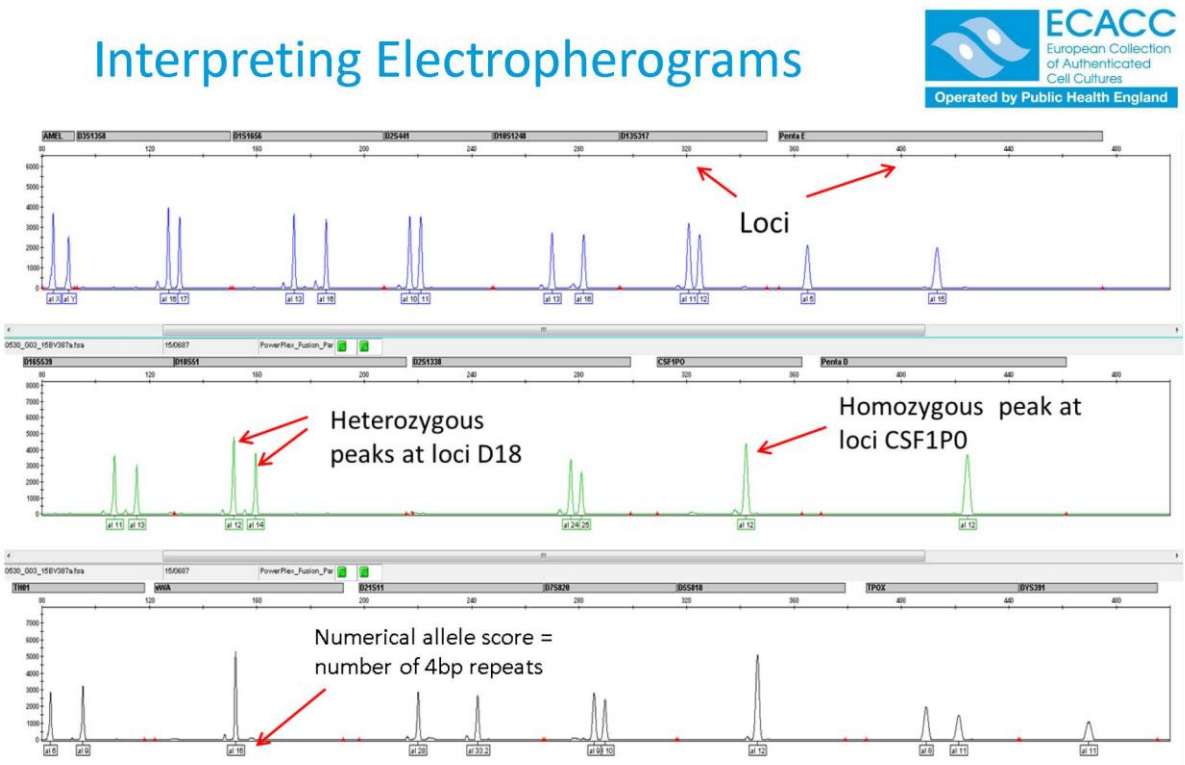
Negative control is ddH2O. Negative control should not have any peaks.

Electropherogram

Our PCR kit is designed to detect 16 loci and the American Type Culture Collection (ATCC) provides information for nine loci only. The Cellosaurus website that we use for search can match up to 32 loci.

Graphical representation of peaks saved in pdf format from GeneMapper software.

Primary cell lines have two peaks (alleles) max for each marker (one from mom one from dad). However, cancer cell lines due to number of passages can acquire additional alleles.



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What do I do with results/Where to look for reference cell line?

RCB runs results through the Cellosaurus website. This produces possible matches based on the results of typing. Another place typing information can be found is ATCC. They are a credible source to look for STR profiles.

Understanding the Matching Algorithm

Standards of profiling in STR typing look for an 80% match or higher in profiled loci. With 80% you can be reasonably confident that you're working with the cell line that you think you're working with. Per the ATCC website:

> *UNDERSTANDING THE MATCHING ALGORITHM*
>
> *The matching criterion is based on an algorithm that compares the number of shared alleles between two cell line samples, expressed as a percentage. Cell lines with ≥80% match are considered to be related; derived from a common ancestry. Cell lines with between a 55% to 80% match require further analysis for authentication of relatedness.*