**Human Cell Line Verification STR Result Interpretation**

Documents in results download folder:

Excel table listing genotypes for each sample

PDF file with chromatographs for each STR marker

Potential outcomes: Unique (not in any database), authenticated, mis-identified, or cross-contaminated

**Verification of commercially available (or common) cell lines**

1. Look up STR genotypes in publically accessible databases; search by cell line name

Easy to use databases (some you need to register as a user):

<https://web.expasy.org/cellosaurus/>

<https://www.atcc.org/> (after finding cell line click on specifications for genotypes)

<http://www.jhsf.or.jp/bank/Category-Index.html>

<https://www.dsmz.de/services/services-human-and-animal-cell-lines/online-str-analysis.html>

1. If your cell line matches all of the listed STR profiles, you have authenicated your line.
2. For any STR markers that don’t match the expected genotype, check the chromatogram traces for the markers of interest to confirm genotypes listed in the excel file. Peak imbalances can sometimes cause issues with genotype calling; these are frequent in cancer cell lines. Extra peaks can be frequent in cells that have mutations causing genomic instability.
3. Some cell lines (especially tumor cells or those that are mismatch repair deficient) show genetic drift over time. Cell lines that match 8 or 9 of the 10 markers are often still correct.
4. If your cell line matches all of the listed STR profiles, but has additional genotypes for multiple markers it is likely that you have a mixed culture.
5. If your cell line matches 7 or fewer of the markers then it is likely that there has been a cell line mix-up. You can search to identify what cell line you may have using by creating an account in the ATCC database and entering your STR genotypes.

https://www.atcc.org/STR\_Database.aspx

Or see if your cell line is one that has been identified as problematic.

https://web.expasy.org/cgi-bin/cellosaurus/search?input=%27problematic%20cell%20line%27

**Verification of newly generated/unique/private cell lines or PDX models**

1. Ideally perform STR genotyping on newly developed cell lines and DNA from the tumor/tissue/host used to create the cell line. If obtained from another source/lab ask for the genotypes for STR profiling completed by the source lab.
2. If source DNA is not available consider mRNA expression profiling for genes/pathways uniquely expressed or enriched in the suspected cell, and/or mutational analyses for mutations that are known to be present in the original tissue sample. Also run your STR markers through ATCC to rule out contamination by another cell line.
3. Consider submission of genotypes for your cell line to Cellosaurus to serve as an official reference for future researchers using your line.

**Best practices**

Upon receipt of a cell line, collect DNA from an early passage that you can use as a comparison to later passages/aliquots.

Perform STR genotyping for new lines to confirm identify and to use as a comparison for later validation.

Consider using the Cellosaurus unique cell line identifier in your methods as there are in some cases names that are not unique to one cell line.

Remember to also check your cell lines for mycoplasma contamination on a frequent basis as these can impact phenotypic studies.

Genotype after starting a frozen aliquot, before starting new sets of experiments, and after 4-6 months in culture.