iPLEX® Pro Sample ID Panel

Rapid and Accurate Sample Management

The iPLEX® Pro Sample ID Panel provides a highly accurate and rapid method for identification and quantification of samples. Designed with over 50 markers in a single-well assay, the panel presents a cost-effective solution for sample authentication.

- Ideal SNP coverage for accurate and comprehensive sample comparisons.
- Built-in controls to easily quantify amplifiable copies of DNA.
- Automated software for rapid sample matching and DNA quantification.
- Robust algorithm for matching tumor and normal sample pairs.
- Suitable for analysis with cell line, tissue, and blood samples.

The panel contains 44 SNPs, 3 assays for gender identification, and 5 controls to quantify from as little as 500 to 18,000 amplifiable copies (~1ng to 60ng) of DNA.

SNPS AND GENES IN THE iPLEX PRO SAMPLE ID PANEL			
albumin_1	rs11781516	rs1994997	rs3819854
albumin_10	rs13050660	rs2010253	rs717302
albumin_5	rs1335873	rs2040411	rs727811
albumin_8	rs1357617	rs2046361	rs729172
albumin_9	rs1360288	rs2056277	rs740910
AMEL_XY	rs136337	rs2076848	rs8037429
ARSD_XY	rs1382387	rs214054	rs826472
TGIF2L_XY	rs1413212	rs2247221	rs876724
rs1005533	rs1454361	rs2518968	rs891700
rs1024116	rs1463729	rs251934	rs901398
rs1028528	rs1468118	rs2714854	rs914165
rs10495407	rs1493232	rs2831700	rs9583190
rs10771010	rs1982986	rs354439	rs964681

vA

The panel includes 44 SNPs (designated by reference sequence [rs]), 5 DNA copy number control assays (albumin), and 3 gender identifiers (AMEL, ARSD, and TGIF2L). SNP assays were selected with 45-55% heterozygosity across six major populations in the HapMart tool.

Disclaimer: The iPLEX Pro Sample ID Panel is not intended for forensic, parentage, or ethnicity identification. The panel is also not intended for differentiating certain individuals (monozygotic twins).

Agena BIOSCIENCE

Key Features of the iPLEX Pro Sample ID Report Software

The Sample ID Panel uses MassARRAY® Typer 4.0 software for standard plate setup, data acquisition, signal processing, and for generating a database from which you can quickly manage sample data and interpret relationships. The HTML-based Sample ID report tool offers Summary, Plate, Match, and Sample Reports.

- Automated reports provide the SNP profile, gender, and number of amplifiable DNA copies for every sample.
- Build an in-house database of all samples processed in the lab.
- Data can be quickly queried to identify sample matches and mismatches across the entire database or within a run.
- Matching algorithm accounts for loss of heterozygosity (LOH) when matching tumor to normal samples.

Historical Comparison

The historical comparison performs a global search across the entire database to identify sample relationships. It is ideal for comparing different tissues sourced from the same individual, performing longitudinal studies and establishing chain of custody. The database accommodates a growing number of samples for medium to large-scale biobanks.

Local Comparison

The local comparison allows for quick analysis of samples within a run.

Summary Report

The Summary Report provides a quick overview, highlighting any unexpected sample matches or mismatches. It also lists samples that may have failed quality control due to poor or low quality DNA.

Figure 1. Sample ID Report Summary

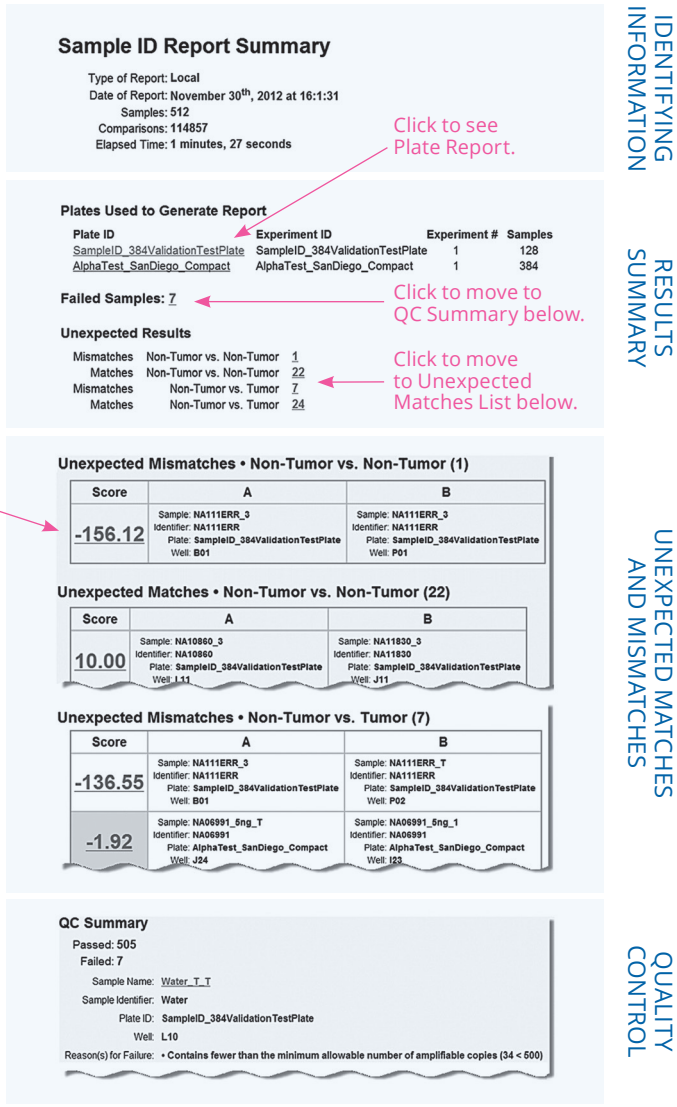


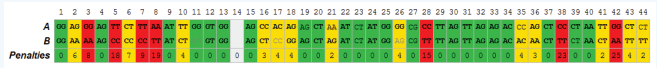
Plate Report

The Plate Report lists results for every well in the plate, including the number of successful SNP calls, number of amplifiable copies, gender, whether it passed quality control, and the number of matches and mismatches found.

Match Report

The Match Report lists identifying information for the two samples involved in a comparison, details of the SNP calls for each sample, and the matching score. Figure 2 shows an excerpt from an unexpected mismatch report.

Figure 2. Sample ID Match Report



Legend	
	Match
	Heterozygous Mismatch
	Homozygous Mismatch
	Missing/Ignored SNP
AT	Conservative Call
AT	Moderate Call
AT	Aggressive Call

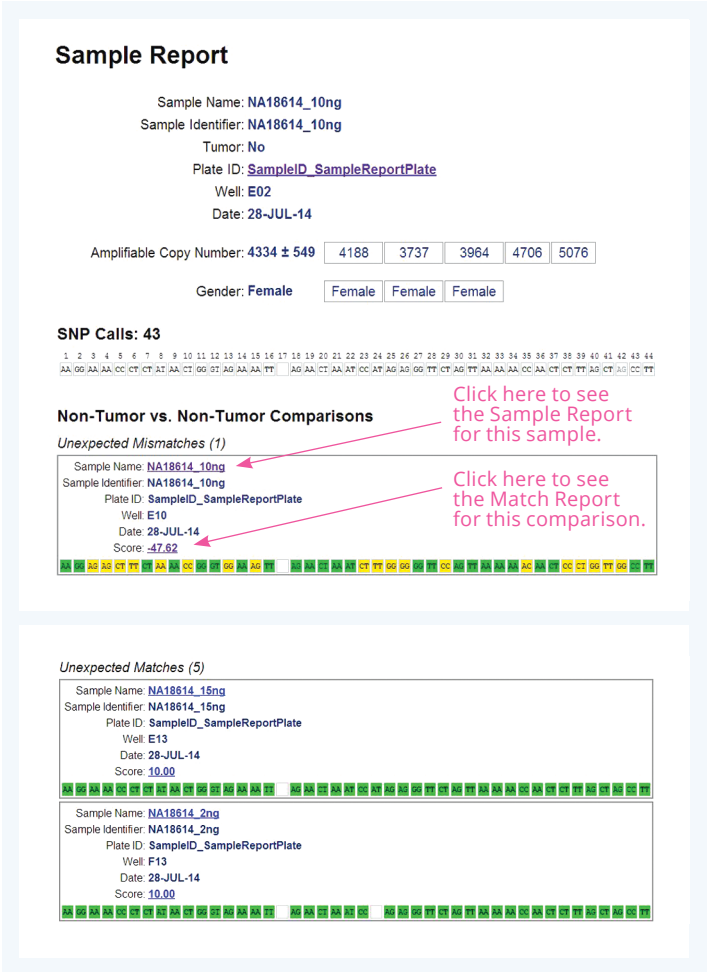
Total Score: -156.12

Heterozygous SNP Matches: 16
Homozygous SNP Matches: 7
Heterozygous SNP Mismatches: 13
Homozygous SNP Mismatches: 7
Missing/Ignored SNPs: 1

Sample Report

Each Sample Report (Figure 3) contains results for the five copy number control assays, the three gender assays, and the 44 SNP assays. It also provides the details of each match or mismatch with other samples.

Figure 3. Sample ID Sample Report



iPLEX Pro Sample ID Panel Components

AMPLIFY		PCR Enzyme PCR Accessory Set Sample ID PCR Primers Sample ID Q-Mix
EXTEND		iPLEX Pro Reagent Set Sample ID Extend Primers
DETECT		SpectroCHIP® Array and Clean Resin (8 x 24, 10 x 96, 2 x 384)
ANALYZE		Sample ID HTML Report Tool (Typer)

Ordering Information

CATALOG NO	FORMAT	SAMPLES/KIT
25094	2 x 384	768
25093	10 x 96	960
10311	8 x 24	192

References

1. Sanchez J, et al. A multiplex assay with 52 single nucleotide polymorphisms for human identification. *Electrophoresis* 2006;27:1713–1724.
2. Demichelis F, et al. SNP panel identification assay (SPIA): A genetic-based assay for the identification of cell lines. *Nucleic Acids Research* 2008;1-11.

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