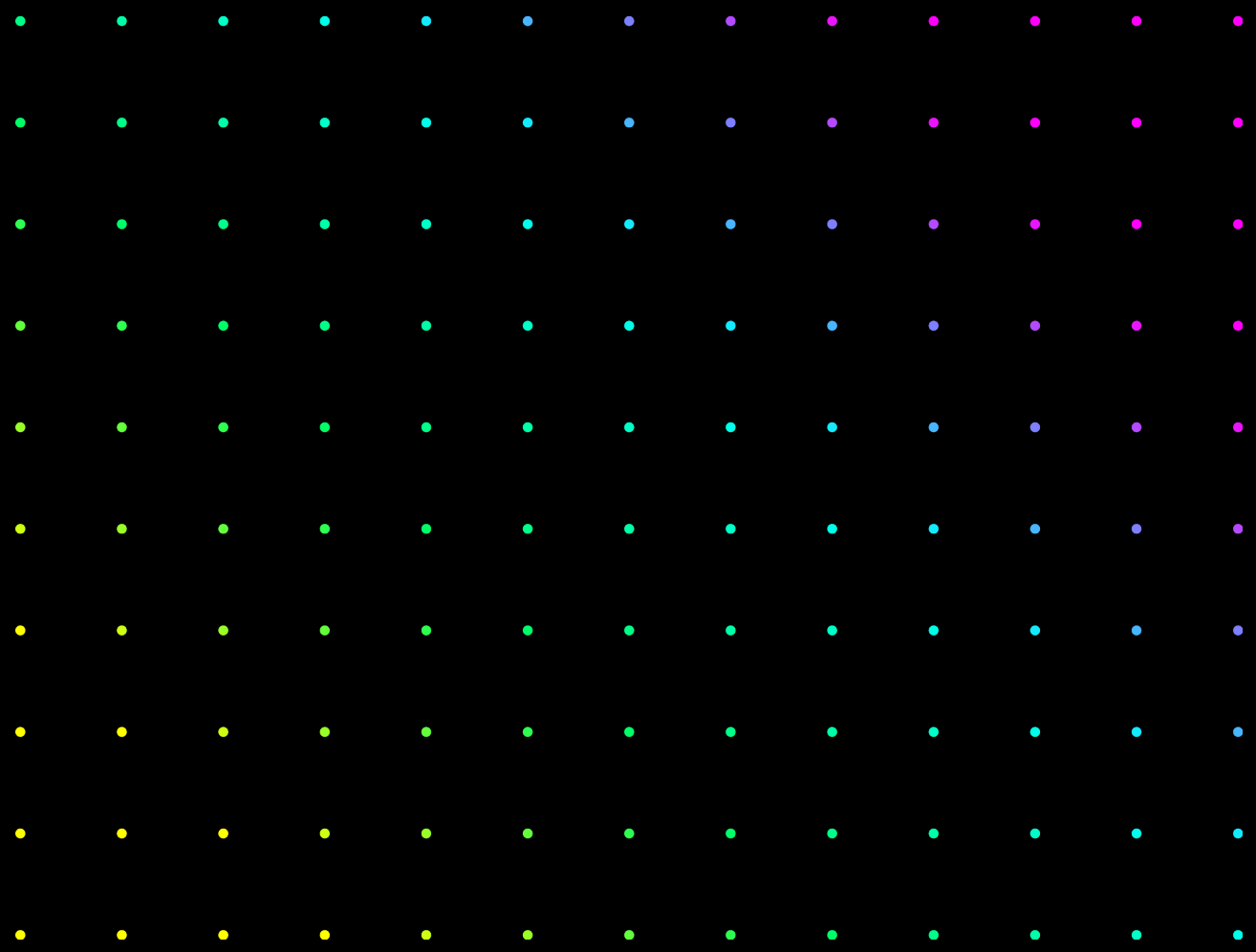
Human Sample ID & Integrity Panel

Panel 100_4



Aplex BIO

Human Sample ID & Integrity Panel for hpPCR

Panel description

The hpPCR Human ID panel delivers high-discrimination genotypes and quantitative mixture information across 44 indel loci, with analysis-ready results within one working day.

Benefits

Human identification workflows often force laboratories to choose between established STR analysis by capillary electrophoresis and broader marker analysis by next-generation sequencing. Both approaches are powerful, but each adds specialized instrumentation, consumables, and interpretation steps-especially when samples are degraded or contain more than one contributor. With Hyperplex PCR, laboratories can process up to 2 x 96-well plates per day with either manual workflow or with our fully automated workflow on Hamilton NGS STARlet. The result is high-resolution identity and mixture information in a format designed for routine, plate-scale use.

The hpPCR Human ID panel is for laboratories working with human DNA that need to verify identity, detect mixtures, or maintain sample integrity; because even a technically successful analysis can produce the wrong conclusion if a sample is misidentified, contaminated, mixed, or assigned to the wrong person.

The panel supports applications including:

- **Forensic analysis:** Generate high-discrimination identity profiles and investigate DNA mixtures, including samples containing a low-level contributor.
- **Sample quality control:** Confirm identity across accession, extraction, aliquoting, repeat analysis, and other workflow handoffs.
- **Biobanks and cohort studies:** Authenticate stored specimens and distributed aliquots before they enter valuable downstream studies.
- **Clinical and translational research:** Verify matched, paired, and longitudinal samples while detecting potential swaps or cross-contamination.
- **Cell-line and biospecimen authentication:** Confirm that human cell lines, cultures, and derived materials remain connected to the intended donor.
- **High-throughput identity testing:** Process large sample volumes where cost, turnaround time, and consistent interpretation are essential.

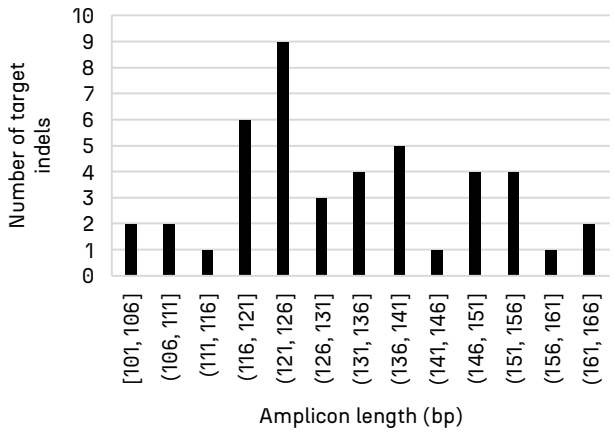
The hpPCR Human ID panel makes these identity checks practical at routine laboratory scale. Approximately 100 target sequences resolve 44 indel loci plus two sex markers, providing both discrete genotype profiles and quantitative mixture information. No capillary electrophoresis, sequencing run, or bioinformatics pipeline is required.

The panel's 100-168 bp amplicons are designed for challenging DNA. In the current technical dataset, all 40 tested Coriell samples produced complete, unique profiles. Population allele frequencies yield a theoretical global random-match probability of 1.99×10^{-19}, and a two-source dilution series demonstrated contributor-specific signals at 1–2%.

Product information

Component	Cat #
Panel	100_4
Primer mix	E0051-1
PLP mix	F0051-1
Panel control sample	H0051-1
Number of samples	96 samples (panel) 20 samples (control)
Detection kit compatibility	hpPCR Assay Kit 100-plex
Cycle setting	25 cycles (standard kit)
Validated cyclers	Bio-Rad T100 Applied Biosystems™ MiniAmp SensoQuest LabCycler Hamilton NGS Starlet ODTC
Validated plates	Sarstedt PCR plate half skirt, 96 well, transparent, High Profile, 200 µl, PCR Performance Tested, PP (72.1979.102) Thermo Scientific AB-0800/150 0.2 mL Skirted 96-well PCR plate (compatible with SensoQuest ONLY)
Validated sealing films	Sarstedt PCR film, free from DNase /RNase, material: PO, transparent (95.1994) Sarstedt PCR film, free from DNase /RNase, transparent (95.1992)

Amplicon distribution



Specifications

Feature	Specification
Sample type	Extracted DNA (e.g. buccal swabs, saliva, blood, cell cultures, tissue samples)
Input requirements	0.02-100 ng in 5 µL input sample volume
Total time	~6 h (excluding imaging)
Hands-on time	~55 min (manual) ~15 min (automated)
Targets	91-plex
Number of loci	44 indels + 2 sex markers
Amplicon length	100-168 bp
Identification sensitivity	<20 pg input (<3 cells), $<1x10^{-13}$ RMP
Quantification sensitivity	>1% for a two-source DNA mixture
Quantification precision	<10% CV for 50% mixtures

Panel control sample

The panel control sample comprises a pool of single stranded DNA sequences matching the sequences of each target amplicon corresponding to each target locus. The total concentration of the pool is adjusted to represent the expected readout of an average human DNA sample when used at 5 µL input per PCR reaction. While the representation of each ssDNA template in the panel control sample is approximately equimolar, there can be deviations of about ±20% copy numbers between targets, therefore, this readout should not be used for quantification purposes. The purpose of the control panel sample is to:

- Serve as a quick check that your setup is performing optimally
- Provide a reference point for monitoring consistency across runs
- Provide a reference for the location of each cluster in the C1-C2 Nanopixel code map

Performance data

Discrimination power performance

The 44 indel markers were selected to maximize individual discrimination, with allele frequencies close to 0.5 across population groups and genomic spacing designed to minimize linkage between loci. The resulting panel achieves very low theoretical random match probabilities across the populations evaluated, as shown below.

Population	Random match probability
Global	1.99 x 10-19
African / African-American	2.62 x 10-19
East Asian	2.99 x 10-19
Non-Finnish European	2.23 x 10-19
South Asian	2.61 x 10-19
Latino	2.41 x 10-19

Table 1. Theoretical random match probability for each Human population based on the minor allele frequencies listed in Table 4

All 40 human reference samples from the analyzed Coriell Human Variation Panel produced complete and unique genetic profiles, demonstrating reliable discrimination between individuals.

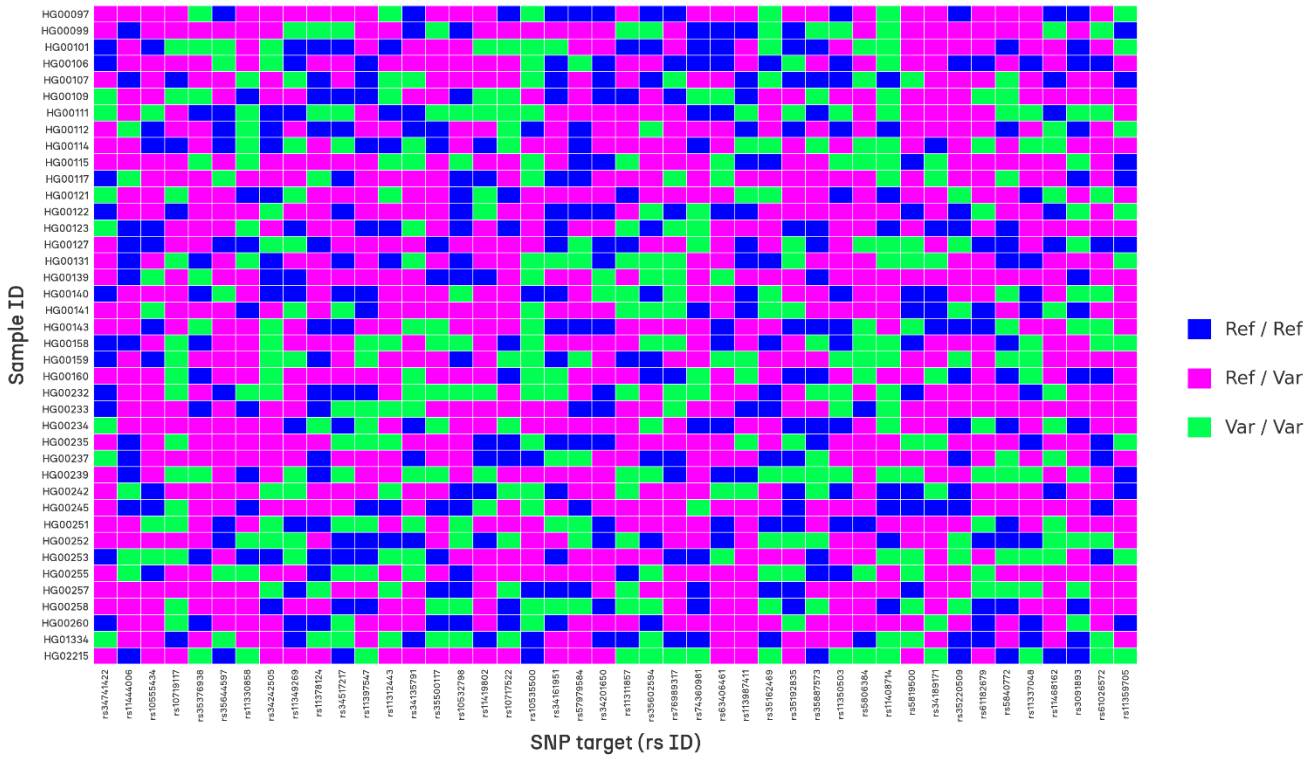


Figure 1. hpPCR Human ID panel genetic fingerprints for 40 individuals (MGP00003 Coriell Human variation panel, 20 males and 20 females). All samples produced complete, unique genotype profiles, demonstrating reliable human identification.

Performance data

Accurate genotype calling across 44 indel loci

The panel provides quantitative allele measurements that enable clear genotype calling across the 44 indel loci. Across the same 40 reference samples, homozygous and heterozygous genotypes formed distinct populations, supporting robust assignment of Ref/Ref, Ref/Var and Var/Var calls. Some targets show variable but reproducible proportions for the heterozygous readout due to existence of paralogous sequences in the human genome.

Figure 2. hpPCR Human ID genotype calls across 44 indel targets (n = 40 samples, (MGP00003 Coriell Human variation panel, 20 males and 20 females). For rs34517217 and rs10719117, the Var/Var population plateaus near 0.75 rather than 1.0, consistent with a low-level off-target signal from an identical sequence elsewhere in the genome.

Performance data

Technical repeatability across targets

Quantitative allele measurements were highly repeatable across the full panel, with a median CV of 5.0% for Var/Ref proportions. This performance was observed across all 44 indel targets using five Coriell DNA samples, with 6–27 technical replicates per target. This performance highlights the compatibility of the assay with the analysis of mixtures as demonstrated below.

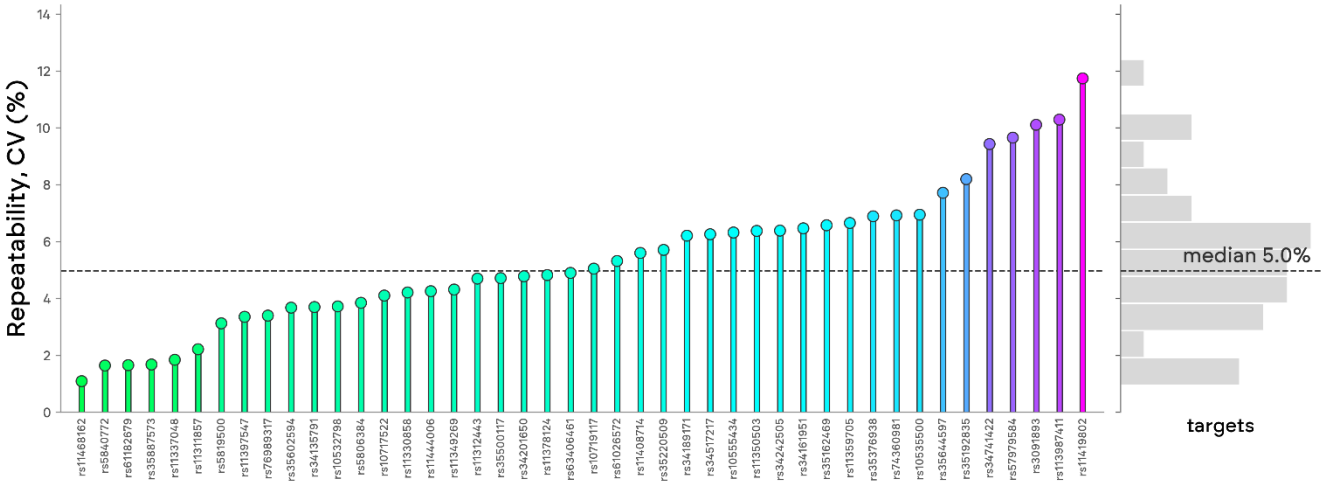


Figure 3. Repeatability of readout of var/ref proportions per target (n=6 to 27) for 5 different Coriell DNA samples covering all heterozygous cases for all 44 Indels.

Mixture discrimination down to 1-2% minor contributors

The hpPCR molecular counting architecture enables direct quantification of minor contributors in mixed samples. In a two-source dilution series, measured mixture fractions closely tracked the expected input down to 2%, with contributor-specific signals detectable at 1–2%.

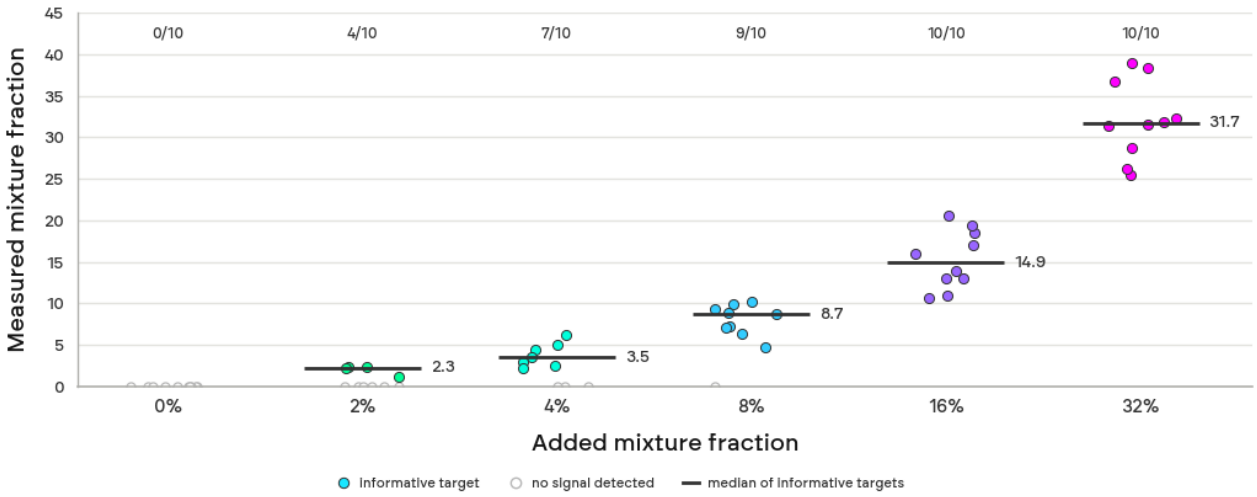


Figure 4. Dilution series of a mixture of 2800M in a background of NA24385 at different proportions. Shown targets are unique for 2800M and absent in NA24385. Inset values on the top show the total number of informative targets readable at each input fraction. Black horizontal lines indicate the median measured mixture fraction across informative targets, with the corresponding median value shown to the right.

High discrimination retained at low DNA input

High-discrimination profiles were retained as DNA input decreased. Across five single-source reference samples, 32–41 markers remained readable at 0.01 ng/µL, corresponding to theoretical random match probabilities between approximately 10^{-14} and 10^{-18}.

Sample	Readable indels (incl. SRY)	Approx. RMP (0.5 allele freq.)
2800M, 0,01 ng/uL	32	6.231E-14
2800M, 0,1 ng/uL	36	1.23E-15
2800M, 1 ng/uL	45	1.80E-19
NA24385, 0,01 ng/uL	36	1.23E-15
NA24385, 0,1 ng/uL	39	6.50E-17
NA24385, 1 ng/uL	45	1.80E-19
NIST 9947A, 0,01 ng/uL	35	3.28E-15
NIST 9947A, 0,1 ng/uL	37	4.62E-16
NIST 9947A, 1 ng/uL	45	1.80E-19
Component A, 0,01 ng/uL	38	1.73E-16
Component A, 0,1 ng/uL	45	1.80E-19
Component B, 0,01 ng/uL	41	9.14E-18
Component B, 0,1 ng/uL	45	1.80E-19

Table 2. Theoretical random match probability (RMP) for successfully genotyped targets at decreasing input DNA, across 5 commercial single-source samples (Components A/B are part of NIST SRM2391d).

Data output

Instant single-well multiplexing with up to 100 clean clusters

All 91 target sequences in this panel are multiplexed in a single well enabled by the Nanopixel technology (for more information about how our technology works read the technology note on our website), with clear and robust cluster separation. Below is an example of scatter plots obtained for the analysis of a single source DNA sample with up to 100 clusters distributed over C3-C5 channels.

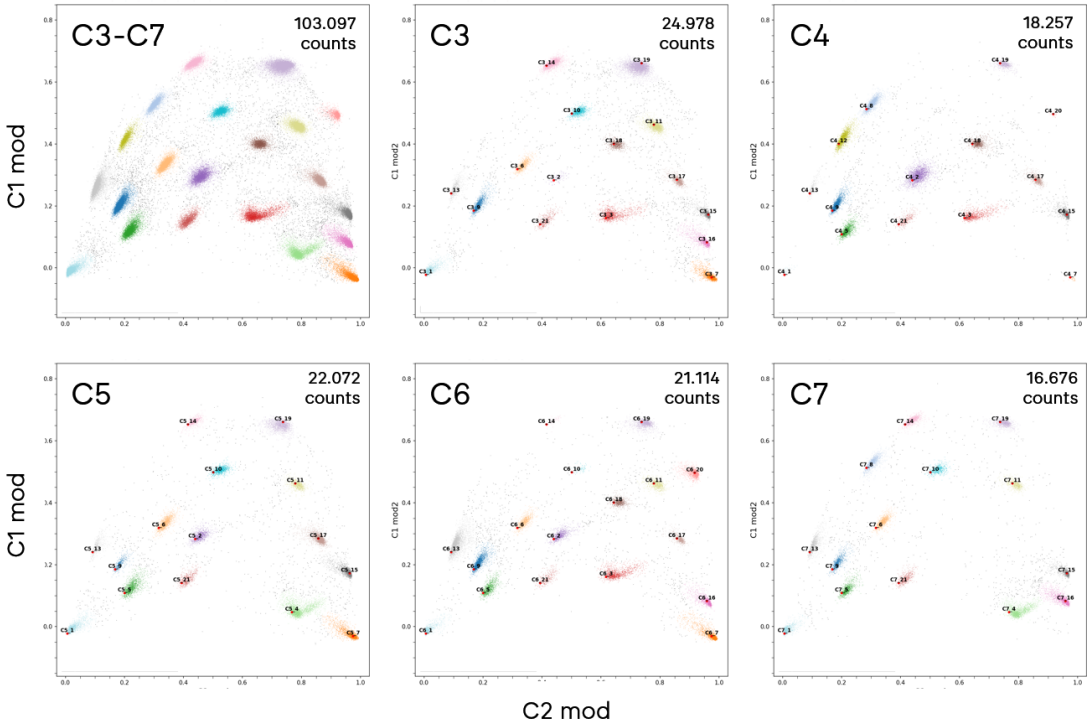


Figure 3. Example scatter plots for the readout of a representative Coriell sample. Count values as inset refer to total counts in each of the channels C3 to C7 mentioned on the plots.

Accurate quantification in each cluster enables low fraction counting

The Human ID panel is optimized to allow quantification of binary mixtures of samples as low as 1% fraction. The scatter plots below demonstrate a clean readout of a 1% mixture of 2800M in a background of NA24385, highlighting the target with code C6_10 as an example. Based on 44 total indels with average allele frequencies of 50%, typically 16.5 informative targets allowing accurate quantification are expected on average for non-related subjects following the condition "Major homozygous, minor carries opposite allele (minor may be AB or BB)" in unrelated individuals (11 for offspring and 9.6 for full siblings).

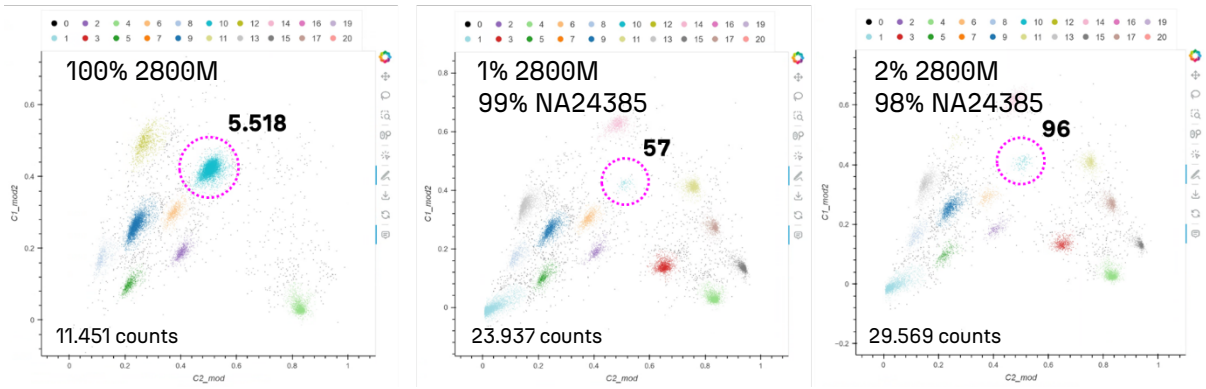


Figure 4. Example scatter plots obtained for the analysis of a single source DNA sample on the left, followed by 1% and 2% of that sample spiked in a different sample where the target sequence of code C6_10 is absent. Count values as inset refer to total counts in channel C6 mentioned on the plots. Outlier spots outside of expected cluster positions arising from RCP overlaps represent approximately 5-10% of total counts in the full cluster space, resulting in a readout precision of >99.9%, below the typical PLP specificity threshold.

Target list

Targets contain 44 Indels and 2 sex markers (AMELX/Y, SRY), selected for high minor allele frequency across populations, non-coding sequence, and ≥1 million bp spacing to avoid linkage disequilibrium.

Target ID	Chromosome	Position	Reference ID	REF	ALT	Code REF	Code Alt
1	chr1	15025165	rs34741422	TA	T	C3-2	C3-1
2	chr1	45540513	rs11444006	G	GA	C3-4	C3-3
3	chr1	95796644	rs10555434	CTTG	C	C3-6	C3-5
4	chr1	232613121	rs10719117	TG	T	C3-10	C3-9
5	chr2	95177335	rs35376938	TC	T	C3-12	C3-11
6	chr2	155547284	rs35644597	GTCT	G	C4-7	C4-8
7	chr3	169484790	rs11330858	AT	A	C3-8	C3-7
8	chr3	24467895	rs34242505	G	GA	C3-15	C5-10
9	chr3	126322245	rs11349269	CT	C	C3-18	C3-17
10	chr4	19724443	rs11378124	T	TG	C4-1	C4-2
11	chr4	36621938	rs34517217	TG	T	C4-4	C4-3
12	chr4	161017073	rs11397547	G	GT	C4-5	C4-6
13	chr4	153614716	rs11312443	CA	C	C4-9	C4-10
14	chr7	47762575	rs34135791	GC	G	C4-13	C4-14
15	chr7	133385738	rs35500117	TG	T	C4-15	C7-13
16	chr7	98727033	rs10532798	GGAC	G	C4-18	C4-17
17	chr7	155941424	rs11419802	T	TG	C4-19	C4-20
18	chr7	125082646	rs10717522	CA	C	C6-10	C6-9
19	chr8	40895155	rs10535500	AAG	A	C6-2	C6-1
20	chr8	124716287	rs34161951	A	AG	C6-3	C6-4
21	chr8	68525782	rs57979584	T	TTCA	C6-7	C6-8
22	chr9	87480014	rs34201650	AC	A	C6-6	C6-5
23	chr9	112557165	rs11311857	AC	A	C7-8	C7-7
24	chr10	28803435	rs35602594	AG	A	C6-12	C6-11
25	chr10	112384304	rs76989317	GTT	G	C6-14	C6-13
26	chr10	114466455	rs74360981	T	TAAC	C6-15	C7-14
27	chr12	32363609	rs63406461	TCA	T	C6-17	C6-18
28	chr12	29130141	rs113987411	T	TG	C6-19	C6-20
29	chr12	45687281	rs35162469	CA	C	C5-2	C5-1
30	chr12	8161501	rs35192835	C	CT	C7-9	C7-10
31	chr12	21463132	rs35887573	CAGG	C	C7-12	C7-11
32	chr13	87398147	rs11350503	AT	A	C5-4	C5-3
33	chr13	103730619	rs5806384	TA	T	C5-6	C5-5
34	chr15	79482236	rs11408714	A	AC	C5-7	C5-8
35	chr17	15014345	rs5819500	TG	T	C5-12	C5-11
36	chr18	23349797	rs34189171	AT	A	C7-16	C7-15
37	chr18	65448466	rs35220509	CAGG	C	C7-18	C7-17
38	chr19	20547969	rs61182679	AC	A	C5-16	C5-15
39	chr20	17490312	rs5840772	GA	G	C5-18	C5-17
40	chr20	39049255	rs11337048	TA	T	C5-20	C5-19
41	chr20	43383038	rs11468162	TAC	T	C7-2	C7-1
42	chr20	46578839	rs3091893	A	AGT	C7-3	C7-4
43	chr20	62224551	rs61026572	AT	A	C7-6	C7-5
44	chr22	24388788	rs11359705	TA	T	C7-20	C7-19
45	chr23	AMELX/Y	AMELX/Y	X	Y	C3-19	C3-20
46	chr23	SRY	SRY	-	-	C5-9	-

Table 3. Complete target list of the panel and Nanopixel code assignment.

Minor allele frequencies for different populations

Minor allele frequencies for each target and Human population (dbSNP build 157).

Ref. ID	Global	Afr/AA	Amish	Latino	Ashk. Jewish	East Asian	Finnish	Middle Eastern	Non-Fin. European	South Asian
rs34741422	0.49	0.51	0.42	0.53	0.46	0.42	0.48	0.48	0.49	0.43
rs11444006	0.50	0.59	0.49	0.51	0.50	0.60	0.48	0.46	0.44	0.50
rs10555434	0.47	0.44	0.45	0.47	0.52	0.56	0.53	0.46	0.48	0.49
rs10719117	0.54	0.60	0.44	0.53	0.50	0.43	0.44	0.46	0.53	0.56
rs35376938	0.47	0.41	0.58	0.44	0.48	0.47	0.52	0.46	0.50	0.52
rs35644597	0.47	0.43	0.46	0.56	0.50	0.51	0.47	0.50	0.47	0.46
rs11330858	0.48	0.43	0.41	0.49	0.47	0.46	0.45	0.47	0.51	0.60
rs34242505	0.51	0.54	0.41	0.53	0.53	0.45	0.50	0.49	0.50	0.56
rs11349269	0.49	0.46	0.47	0.41	0.52	0.42	0.55	0.48	0.53	0.56
rs11378124	0.47	0.51	0.49	0.45	0.54	0.45	0.44	0.54	0.46	0.40
rs34517217	0.49	0.45	0.43	0.42	0.49	0.44	0.59	0.48	0.53	0.42
rs11397547	0.47	0.45	0.60	0.48	0.45	0.45	0.44	0.45	0.47	0.53
rs11312443	0.55	0.57	0.40	0.50	0.53	0.48	0.56	0.45	0.57	0.49
rs34135791	0.49	0.40	0.45	0.50	0.43	0.41	0.59	0.51	0.53	0.48
rs35500117	0.48	0.42	0.50	0.59	0.46	0.59	0.60	0.43	0.47	0.49
rs10532798	0.54	0.52	0.54	0.56	0.47	0.59	0.58	0.46	0.54	0.52
rs11419802	0.51	0.44	0.56	0.53	0.54	0.54	0.46	0.57	0.55	0.50
rs10717522	0.44	0.42	0.54	0.45	0.45	0.42	0.50	0.43	0.45	0.41
rs10535500	0.54	0.49	0.45	0.58	0.54	0.53	0.45	0.43	0.58	0.56
rs34161951	0.47	0.54	0.43	0.50	0.49	0.40	0.43	0.43	0.44	0.53
rs57979584	0.50	0.51	0.54	0.48	0.52	0.40	0.51	0.51	0.52	0.42
rs34201650	0.43	0.43	0.42	0.47	0.52	0.49	0.50	0.53	0.41	0.48
rs11311857	0.54	0.57	0.56	0.53	0.47	0.48	0.49	0.45	0.55	0.57
rs35602594	0.52	0.43	0.54	0.50	0.58	0.59	0.51	0.49	0.58	0.52
rs76989317	0.49	0.44	0.56	0.50	0.43	0.52	0.46	0.50	0.51	0.58
rs74360981	0.49	0.50	0.41	0.51	0.50	0.55	0.47	0.50	0.47	0.48
rs63406461	0.49	0.52	0.46	0.40	0.51	0.44	0.48	0.55	0.49	0.46
rs113987411	0.48	0.48	0.45	0.41	0.45	0.56	0.49	0.44	0.48	0.50
rs35162469	0.49	0.49	0.43	0.47	0.54	0.49	0.42	0.51	0.51	0.49
rs35192835	0.47	0.49	0.49	0.53	0.49	0.52	0.48	0.44	0.43	0.60
rs35887573	0.49	0.50	0.54	0.51	0.46	0.53	0.45	0.58	0.49	0.42
rs11350503	0.44	0.43	0.52	0.40	0.54	0.43	0.46	0.53	0.44	0.46
rs5806384	0.52	0.50	0.46	0.51	0.56	0.42	0.48	0.52	0.54	0.57
rs11408714	0.48	0.43	0.58	0.45	0.51	0.45	0.43	0.54	0.52	0.45
rs5819500	0.49	0.48	0.53	0.45	0.49	0.40	0.53	0.52	0.50	0.44
rs34189171	0.52	0.58	0.46	0.49	0.54	0.43	0.48	0.57	0.50	0.59
rs35220509	0.46	0.51	0.58	0.40	0.54	0.60	0.40	0.47	0.44	0.46
rs61182679	0.46	0.44	0.58	0.53	0.53	0.56	0.46	0.51	0.45	0.52
rs5840772	0.49	0.43	0.48	0.52	0.53	0.46	0.47	0.51	0.52	0.57
rs11337048	0.47	0.49	0.46	0.51	0.54	0.57	0.42	0.60	0.44	0.52
rs11468162	0.50	0.41	0.45	0.58	0.59	0.46	0.46	0.58	0.55	0.50
rs3091893	0.51	0.52	0.44	0.51	0.50	0.59	0.57	0.54	0.48	0.54
rs61026572	0.50	0.48	0.42	0.52	0.47	0.53	0.46	0.55	0.52	0.59
rs11359705	0.52	0.55	0.41	0.53	0.47	0.55	0.50	0.44	0.51	0.44

Table 4. Minor allele frequency distribution in the population for targets in panel.