

TaqMan® OpenArray® Genotyping Barcode Panel

High-throughput sample identification on the OpenArray® platform

The OpenArray® technology is a nanofluidics platform for low volume, solution-phase reactions that streamlines real-time PCR studies using large numbers of samples and assays. A single TaqMan® OpenArray® Genotyping Barcode Panel plate holds 3,072 real-time PCR reactions and contains a defined selection of human SNP markers. These panels combine the efficiency of high-throughput platforms with the robust genotyping performance of TaqMan® Assays.



Tracks sample identity

As the number of biological research samples expands by orders of magnitude, the proper tracking and confirmation of sample identity has become increasingly critical. The TaqMan® OpenArray® Genotyping Barcode Panels are reliable DNA fingerprinting panels that provide quality control for sample storage and experimental processing. The barcode panels determine gender and sample identity within the context of genomewide studies, biobanks, and genomic centers.

A variety of panel formats

The TaqMan® OpenArray® Barcode Panels are available as two 32 SNP panels and an extended 64 SNP panel (Table 1). The 32A SNP panel consists of three Y markers for gender confirmation and 29 autosomal SNPs, which allow for unique identification of individual samples for biorepository applications.

The set of markers in the 32A panel are sufficient for the unique identification of most samples. If additional specificity is required, results from the 32B panel may be used to supplement results from the 32A panel or the extended panel may be run together using the 64 panel. The extended panel consists of three Y-chromosome markers and 61 autosomal SNPs to allow for increased stringency. A total of 96 samples can be run with the 32 SNP panel and 48 samples can be run with the 64 SNP panel (Figure 1). The QuantStudio™ 12K Flex Real-Time PCR System can run four plates at once, generating over 12,000 data points.

Table 1. Genotyping barcode panels (32A and 32B SNP). An extended 64 SNP panel is available that includes all SNPs from both the 32A and 32B panel.

SNP ID (rs)	TaqMan® Assay ID	Chr	Mb	Allele 1	Allele 2	HapMap*		N
						Average Freq 1	Average Freq 2	
32A SNP panel								
rs3010325	C_2728408_10	1	59.34	C	T	0.51	0.49	2404
rs2136241	C_1563023_10	1	161.56	C	T	0.47	0.53	2404
rs2259397	C_15935210_10	1	206.14	T	C	0.52	0.48	2402
rs7564899	C_33211212_10	2	11.12	G	A	0.48	0.52	2406
rs4971536	C_3227711_10	2	20.95	C	T	0.49	0.51	2406
rs10194978	C_30044763_10	2	50.38	G	A	0.50	0.50	2402
rs4855056	C_11821218_10	3	183.12	A	G	0.50	0.50	2404
rs6554653	C_1670459_10	5	11.92	C	T	0.51	0.49	2404
rs9396715	C_29619553_10	6	10.02	T	C	0.51	0.49	2406
rs441460	C_1007630_10	6	25.66	G	A	0.52	0.48	2402
rs7773994	C_26546714_10	6	37.68	T	G	0.53	0.47	2398
rs1415762	C_7421900_10	6	125.08	C	T	0.54	0.46	2392
rs6927758	C_27402849_10	6	163.64	C	T	0.49	0.51	2400
rs7796391	C_2953330_10	7	125.90	A	G	0.51	0.49	2402
rs2336695	C_16205730_10	8	1.02	A	G	0.49	0.51	2404
rs1157213	C_8850710_10	8	104.28	T	C	0.50	0.50	2406
rs10869955	C_1801627_10	9	79.48	C	A	0.48	0.52	2402
rs1533486	C_7431888_10	10	1.50	T	G	0.48	0.52	2404
rs4751955	C_1250735_20	10	117.91	A	G	0.47	0.53	2406
rs10771010	C_1902433_10	12	23.66	T	C	0.52	0.48	2392
rs12318959	C_31386842_10	12	28.67	C	T	0.53	0.47	2394
rs3742257	C_26524789_10	13	42.07	T	C	0.47	0.53	2404
rs1377935	C_8924366_10	14	24.91	T	C	0.50	0.50	2406
rs946065	C_43852_10	14	55.00	C	A	0.48	0.52	2404
rs6598531	C_11522992_10	15	96.95	T	G	0.53	0.47	2402
rs4783229	C_10076371_10	16	81.18	T	C	0.49	0.51	2406
rs1567612	C_7457509_10	18	34.09	G	A	0.51	0.49	2362
rs11660213	C_1122315_10	18	40.74	A	G	0.51	0.49	2406
rs11083515	C_11710129_10	19	44.39	A	G	0.47	0.53	2400
rs768983**	C_1027548_20	Y	6.88					
rs3913290**	C_8938211_20	Y	8.66					
rs2032598**	C_1083232_10	Y	13.36					
32B SNP panel								
rs6427699	C_29222350_10	1	161.16	G	A	0.50	0.50	2400
rs891700	C_7539584_10	1	239.88	A	G	0.49	0.51	2404
rs7588807	C_2915497_10	2	220.44	G	T	0.52	0.48	1152
rs1983085	C_3036007_20	3	15.50	C	T	0.48	0.52	2406
rs6791084	C_1525594_10	3	30.10	G	A	0.46	0.54	2406
rs10938367	C_233438_10	4	44.53	G	A	0.51	0.49	2402
rs2561183	C_2934686_10	5	68.77	C	A	0.52	0.48	2406
rs2560588	C_26138080_10	5	116.74	A	G	0.59	0.41	1146
rs245057	C_3221475_10	5	149.32	C	A	0.49	0.51	2392
rs9395021	C_30289524_10	6	44.55	C	T	0.53	0.47	2406
rs1337823	C_8768119_10	6	49.92	A	G	0.51	0.49	1156
rs974110	C_8307036_10	6	66.17	A	G	0.50	0.50	2400
rs2268666	C_15875060_10	6	146.79	C	T	0.45	0.55	2406
rs2189730	C_26760518_10	7	8.84	G	A	0.45	0.55	2404
rs7802855	C_43039996_10	7	18.97	T	C	0.49	0.51	2402
rs4716945	C_29867302_10	7	155.43	A	G	0.49	0.51	2406
rs4521710	C_126001_10	7	157.74	G	A	0.47	0.53	2404
rs11787149	C_1204228_10	8	18.20	C	T	0.50	0.50	2406
rs2970636	C_15964363_10	8	37.00	C	T	0.52	0.48	2404
rs10955074	C_1677881_20	8	87.93	C	T	0.51	0.49	2404
rs7925270	C_8466143_10	11	120.07	C	T	0.51	0.49	2400
rs12049869	C_31697299_10	11	127.22	A	G	0.48	0.52	2400
rs2239177	C_2608181_20	12	11.93	T	C	0.54	0.46	2404
rs7979054	C_29016807_10	12	93.24	A	G	0.49	0.51	2400
rs4148542	C_29558839_10	13	94.48	T	C	0.51	0.49	2406
rs2153532	C_11476140_10	14	86.01	T	C	0.52	0.48	2402
rs2251110	C_8793799_20	15	31.39	G	T	0.53	0.47	2394
rs4984473	C_29415394_10	15	94.33	G	A	0.52	0.48	2406
rs312729	C_2333563_10	17	65.82	G	A	0.53	0.47	2404
rs2247021	C_9217468_10	18	42.83	G	T	0.53	0.47	2404
rs607127	C_7910532_10	18	58.74	C	T	0.57	0.43	238
rs1942719	C_11200035_10	18	69.39	C	T	0.51	0.49	2382

*HapMap Data Rel 28 Phases II+III, August 10, on NCBI B36 assembly, dbSNP b126 (alleles, average allele frequencies based on N individuals genotyped within the 11 populations)

11 HapMap populations used: ASW

- (A) African ancestry in Southwest USA; CEU
- (C) Utah residents with Northern and Western European ancestry from the CEPH collection; CHB
- (H) Han Chinese in Beijing, China; CHD
- (D) Chinese in metropolitan Denver, Colorado; GIH
- (G) Gujarati Indians in Houston, Texas; JPT
- (J) Japanese in Tokyo, Japan; LWK
- (L) Luhya in Webuye, Kenya; MEX
- (M) Mexican ancestry in Los Angeles, California; MKK
- (K) Maasai in Kinyawa, Kenya; TSI
- (T) Toscani in Italy; YRI
- (Y) Yoruba in Ibadan, Nigeria

Y markers included for gender discrimination based on presence or absence of genotype call period

Notes:

1. The lowest average MAF = 0.43 for any SNP. The lowest MAF = 0.35 for any SNP in any individual population.
2. Assays were selected by a collaboration of individuals at Life Technologies and the John P. Hussman Institute for Human Genomics, Miller School of Medicine, University of Miami, Miami FL. Contributors include Patrice L. Whitehead, Gary W. Beecham, Susan Slifer, Ioanna Konidari, William F. Hulme, Kathleen Hayashibara, Margaret A. Pericak-Vance, Jeffery M. Vance, John R. Gilbert, Dale J. Hedges, Jacob L. McCauley. Abstract is available at: www.ashg.org/2010meeting/abstracts/fulltext/f21684.htm

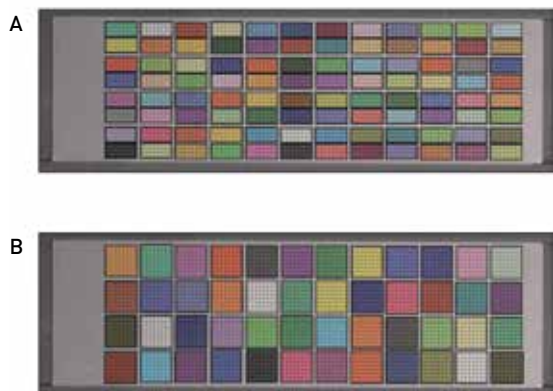


Figure 1. OpenArray® plate formats. (A) 32 assays and 96 samples. (B) 64 assays and 48 samples.

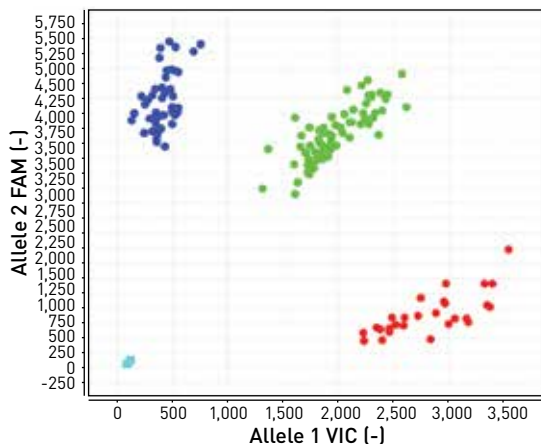


Figure 2. SNP genotyping data for rs4751955 obtained using the QuantStudio™ 12K Flex system with OpenArray™ Block.

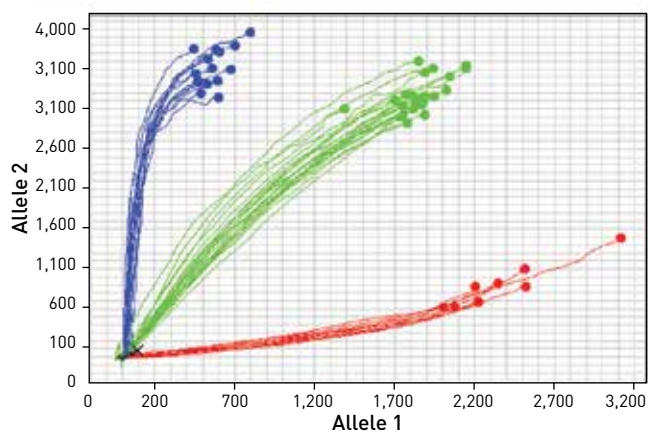


Figure 3. Trace plot of SNP genotyping data for rs4751955 obtained using the QuantStudio™ 12K Flex system with OpenArray® Block.

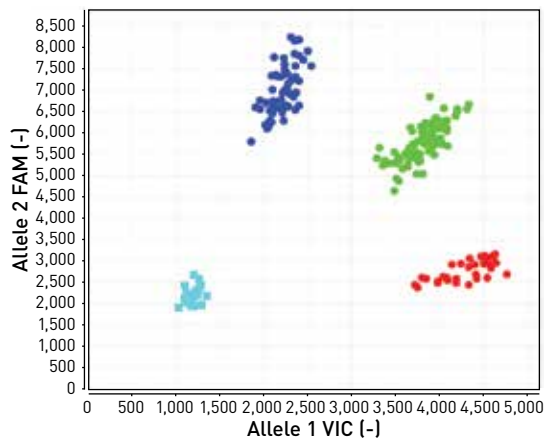


Figure 4. SNP genotyping data for rs4751955 obtained using the OpenArray® Real-Time PCR System.

The TaqMan® OpenArray® Barcode Panels are available for both the QuantStudio™ 12K Flex Real-Time PCR System and the OpenArray® Real-Time PCR System. Users can be confident of high quality results on any OpenArray® platform. Figures 2–3 depict the breadth of data that can be generated using the TaqMan® OpenArray® panel with the QuantStudio™ 12K Flex system. OpenArray® Real-Time PCR System data can be seen in Figure 4.

Determination of panel size

To determine the number of SNPs to use in the panel, SNPs with MAF of 0.4 were simulated against unrelated samples to examine the probability of a random match between unrelated individuals (Table 2). The number of SNPs represents the available common genotyping plate formats available using OpenArray® technology. The number of samples represents those that may be present within a given genome-wide genotyping set, a particular study or collection, or the entire collection of a large biobank. These simulations indicate that, in a set of

Table 2. Probability of a random match between two unrelated individuals, assuming MAF = 0.41.

No. unrelated samples	No. SNPs	Probability of a random match
5,000	16	94.9545%
5,000	32	<0.0001%
5,000	64	<0.0001%
10,000	16	100%
10,000	32	0.0003%
10,000	64	<0.0001%
100,000	16	100%
100,000	32	0.0285%
100,000	64	<0.0001%
200,000	16	100%
200,000	32	0.1141%
200,000	64	<0.0001%
500,000	16	100%
500,000	32	0.7108%
500,000	64	<0.0001%

5,000 samples, the probability of a random match of all genotypes between any two individuals is <0.0001% for either the 32 or 64 SNP panel. In a case of 200,000 samples, the probability is 0.1141% with the 32 SNP panel and <0.0001% with the 64 SNP panel.

Fully optimized selection of SNP assays

Markers for the panels have been selected based on a number of criteria. These include high minor allele frequency (MAF) in multi-ethnic populations, representation on high-throughput genotyping platforms, and robust genotyping performance. Marker selection started from the identification of SNPs

common to multiple Genome-Wide Association Study (GWAS) datasets. This set was then refined to several hundred SNPs by examining HapMap genotype data (>0.35 MAF in all 11 Phase III HapMap populations). The marker set was narrowed further by choosing SNPs with the highest average MAF across populations and a high genotyping efficiency (>98%) within our internal GWAS datasets. The resulting panels of 32 and 64 SNPs were determined based on highest ranking genotyping efficiency, concordance between OpenArray® and original GWAS genotyping calls, and low probability of linkage disequilibrium between selected markers.

Ordering information

Product	Contents	Cat. No.
TaqMan® OpenArray® Genotyping Barcode Panel 32A QuantStudio™ 12K Flex	1 plate	4475386
TaqMan® OpenArray® Genotyping Barcode Panel 32B QuantStudio™ 12K Flex	1 plate	4475387
TaqMan® OpenArray® Genotyping Barcode Panel 64 QuantStudio™ 12K Flex	1 plate	4475394
TaqMan® OpenArray® Genotyping Barcode Panel 32A (for OpenArray® Real-Time PCR System)	1 plate	4475366
TaqMan® OpenArray® Genotyping Barcode Panel 32B (for OpenArray® Real-Time PCR System)	1 plate	4475367
TaqMan® OpenArray® Genotyping Barcode Panel 64 (for OpenArray® Real-Time PCR System)	1 plate	4475374
Related products required for use with panels		
TaqMan® OpenArray® Genotyping Accessories Kit (for use with the OpenArray® Real-Time PCR System)	Enough for 10 plates	4404572
QuantStudio™ 12K Flex OpenArray® Accessories Kit	Enough for 10 plates	4469576

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