Access Array Target-Specific Primers

(PNs: ASY-AA, ASY-AAX)

1. How many 48.48 Access Array integrated fluidic circuits (IFCs) can I run with the provided assays?

Primers are provided in volumes sufficient for a minimum of 100 Access Array™ IFCs.

2. What is provided with my order of Access Array target-specific primers?

- Mixed forward and reverse primer pairs in 96-well plate(s). Access Array target specific primers are provided in a final concentration of 50 µM for each uniplex primer and 60 µM for each multiplex primer. Each primer is provided in nuclease-free water for a final volume of 100 µL.
- Customer informatics packet

3. What information is provided in the customer informatics packet?

- Microsoft® Excel® file that contains the primer sequences, genomic coordinates of primers, amplicon GC%, primer pair well location in the primer plate(s), and amplicon sequence and length
- Microsoft® PowerPoint® presentation that displays an amplicon gel image (for uniplex orders only)

4. What is the design turnaround time?

Designs are available for review within 72 hours of submission. Fluidigm® will deliver non-wet tested primers within four weeks and wet-tested primers within six weeks.

5. Are the Access Array target-specific primers validated?

Uniplex primers are wet-tested by gel-electrophoresis. Multiplex primers are not wet-tested.

6. Which genomic DNAs are used for wet-lab testing of uniplex primers (PN ASY-AA)?

Three Coriell genomic DNA samples (PNs GM17317, GM17316 and GM0620) are pooled and used for wet-lab testing.

7. What factors does Fluidigm® bioinformatics consider when designing primers?

Access Array target-specific primers are designed with proprietary primer design software. This software provides optimal target-specific primer pairs that avoid nonspecific amplification. We require customers to review the primer designs before placing an order. Primer design considerations by Fluidigm bioinformatics include, but are not limited to:

- Primer and amplicon specificity
- Avoiding placing primers over SNPs where they could impact specificity
- Avoiding placing primers on highly structured GC-rich regions or repeats
- Primer melting temperatures within an order are typically +/–2 °C where possible.

8. What defines difficult genomic regions, and can primers be designed to cover these regions?

Regions with high GC content (≥65%), polypurine (GA) runs, and repeats are considered difficult. Any SNP(s) present within eight bases of the 3’ end of the primer sequence will also decrease design and amplification success rate. We can design to these difficult regions; however, they will be considered nonstandard assays. Calculation of the overall success rate will not include nonstandard assays, and our specifications also do not apply to nonstandard assays.

9. Do you design for repeat regions?

Fluidigm does not specifically design primers for repeat regions. However, if a combination of forward and reverse primers can be designed to create a unique hit in the genome, we will design to that region.

10. Can Fluidigm design intron-targeting primers?

Yes. Please provide genomic coordinates in D3™ assay design.

For further information, please refer to the Access Array System for the 454 Sequencing Platform User Guide (PN 68000158) and the Access Array™ System for Illumina Sequencing Platform User Guide (PN 100-3770).

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