

DNA strand designations

Back

03/15/18

Customer Strand: Same as the Source strand. For custom content, it is the strand submitted by the customer for probe design.

ILMN Strand, a.k.a. Design Strand: The strand used by Illumina to design probes based on thermodynamic stability and locus specificity according to [NCBI BLAST](#). For this reason, it can differ from the Customer/ Source strand.

Forward/Reverse (Fwd/Rev) Strand: Used by [dbSNP](#), Fwd/Rev designations can change with NCBI Genome Build updates, so Genome Build must be specified when reporting Fwd/Rev strands. **1.** For SNPs in standard array products, Fwd strand = Source strand, and originates from dbSNP. **2.** For custom array product SNPs without rsid’s, the customer can identify the Source strand as Fwd or Rev, based on their own criteria. Illumina custom product files use the customer’s Fwd/Rev designations. **Note:** The Fwd strand, as identified in Illumina standard product files, should not be confused with Plus (+) strand, which HapMap interchangeably calls the “forward strand.”

Plus/Minus (+/-) Strand: The standard designation for all eukaryotic organisms used by [HapMap](#) and [1000 Genomes Project](#). The 5’ end of the (+) strand is at the tip of the short arm (p arm) of the chromosome and the 5’ end of the (-) strand is at the tip of the long arm (q arm). (+/-) designations can change with NCBI Genome Build updates, so Genome Build must be specified when reporting (+/-) strands.

Source Strand: Same as the Customer strand. The strand submitted to the Illumina designer for probe design. **1.** For standard SNPs, it is the Fwd strand as reported in the source database (i.e., dbSNP). **2.** Custom content can be reported as rsid’s or as the DNA sequences or chromosomal regions, depending on the format submitted by the customer.

Top/Bottom (Top/Bot) Strand:Top/Bot nomenclature was developed by Illumina using sequence-based context to assign strand designations that does not change regardless of database or genome assembly used. (e.g., depending on the NCBI Genome Build referenced, strand and allele designations can change). Top/Bot is not directly related to Fwd/Rev or (+/-).Top/Bot strand is determined by examining the SNP and the surrounding DNA sequence and it only applies to SNPs with two possible alleles. See the Top/Bot A/B Allele bulletin for more details.

Contact Us



Other Support



Innovative technologies

At Illumina, our goal is to apply innovative technologies to the analysis of genetic variation and function, making studies possible that were not even imaginable just a few years ago. It is mission critical for us to deliver innovative, flexible, and scalable solutions to meet the needs of our customers. As a global company that places high value on collaborative interactions, rapid delivery of solutions, and providing the highest level of quality, we strive to meet this challenge. Illumina innovative sequencing and array technologies are fueling groundbreaking advancements in life science research, translational and consumer genomics, and molecular diagnostics.



For Research Use Only. Not for use in diagnostic procedures (except as specifically noted).

© 2019 Illumina, Inc. All rights reserved.

All trademarks are the property of Illumina, Inc. or their respective owners.
For specific trademark information, see www.illumina.com/company/legal.html.