THE MOST COMPREHENSIVE VIEW OF THE **HUMAN GENOME**

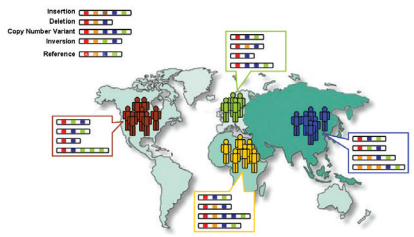
PACBIO®

HUMAN BIOMEDICAL RESEARCH

To understand the genetic factors underlying health and disease and to address hidden heritability, scientists require a more comprehensive view of all the variations in the human genome. Single Molecule, Real-Time (SMRT®) Sequencing delivers the read lengths, uniform coverage, and accuracy needed for accessing the complete size spectrum of sequence variant types – from single nucleotides to complex structural variants. PacBio's long single-molecule reads also provide direct variant phasing information across full-length genes and chromosome haplotype blocks. With SMRT Sequencing, scientists gain new insight into the genetic basis of health and disease.

CREATE GOLD-STANDARD POPULATION-BASED REFERENCES

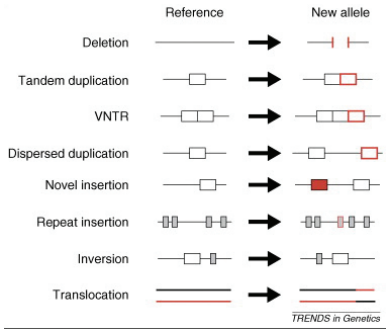
- Increase power by matching references to the genetic background of study populations[1]
- Access novel types of genetic variation and difficult-to-characterize regions[2]
- Improve variant calling with a more comprehensive reference genome[3]
- Cost-effectively validate novel variants with a highly accurate orthogonal platform



Genetic diversity varies both within and between populations[4].

RESOLVE STRUCTURAL VARIATION

- Uncover the hidden heritability linked to structural variation[5]
- Identify sequence-level breakpoints to unravel the genetic etiology of disease[6]
- See the unbiased range of structural variation of all sizes, types, and GC content in the genome[2]



"Non-SNP variants, ranging from small indels to large CNVs and inversions, accounted for 74% of the total number of variant bases."[7,8]

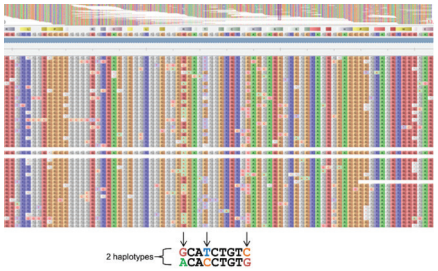
"TO GET A MEDICAL-GRADE GENOME … WE NEED TO HAVE THE MOST ACCURATE AND COMPLETE GENOME FOR EACH INDIVIDUAL. WE BELIEVE THE PACBIO SMRT MACHINES WILL HELP US REACH THIS GOAL."

—**J. CRAIG VENTER**, HLI CO-FOUNDER[9]

"WE NOW HAVE ACCESS TO A WHOLE NEW REALM OF GENETIC VARIATION THAT WAS OPAQUE TO US BEFORE."

—**PROFESSOR EVAN EICHLER**, UNIVERSITY OF WASHINGTON[5]

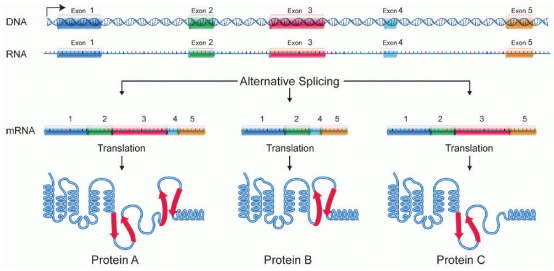
pacb.com/human



Resolution of two allelic copies of the MUC5AC gene[10]

CHARACTERIZE COMPLEX REGIONS UNDERLYING GENETIC DISEASE

- Sequence previously unsequenceable loci associated with genetic disease[11]
- Accurately and definitively phase polymorphisms across entire genes, such as HLA[12]
- Multiplex samples to cost-effectively scale research[12]



Alternative splicing can have important implications for protein structure and function[13].

PROFILE THE COMPLEXITY OF THE TRANSCRIPTOME WITH ISO-SEQ™ SEQUENCING

- Discover novel genes and gene isoforms[14]
- Directly sequence full-length transcripts to eliminate the need for transcript reconstruction[14]
- Differentiate isoform expression between cells, tissues, and disease states[15]

"WE BASICALLY CAN SEE THE ENTIRE PICTURE. WE'RE NOT LOOKING UNDER A LAMPPOST FOR THE KEYS. IT'S DAYLIGHT, AND WE CAN SEE THE WHOLE NEIGHBORHOOD. SO WE'RE GONNA FIND THE KEYS."

—**DAN GERAGHTY**,
FRED HUTCHINSON CANCER CENTER[16]

"THE POWER OF LONG-READ SEQUENCING IS REALLY TO BE ABLE TO CAPTURE ALL OF THE INFORMATION IN ITS INTACT FORM WITHOUT TRYING TO SOLVE A JIGSAW PUZZLE THAT YOU MAY HAVE PUT TOGETHER WRONG."

—**MIKE SNYDER**, STANFORD UNIVERSITY[17]

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