enables the production of multiprotein complexes that can be readily modified with fluorescent tags, protein cross-linkers or specific post-translational modifications such as glycans (to name just a few possible applications) through the introduction of noncanonical amino acids containing bio-orthogonal, chemically reactive handles for labeling. The authors used the approach to cross-link a transcription factor complex in order to study its conformational dynamics, demonstrating the power of the technology.

**Brief Communication p997**

**CRISPR-based genetic screens**

An emerging generation of CRISPR–Cas9 tools goes beyond inducing gene deletions or regulating gene expression to instead modify particular nucleotides in the target region. Two complementary approaches—TAM (targeted AID-mediated mutagenesis), by Chang and colleagues, and CRISPR-X, by Bassik and colleagues—direct a cytidine deaminase (AID) to a region of interest where it triggers the conversion of cytidine to any other base. TAM recruits AID by fusing it to dead Cas9, whereas CRISPR-X associates AID with the single guide RNA. Both approaches result in a large diversity of mutations at the target loci and allow the identification of gain-of-function variants at high resolution. TAM identifies mutations at the BCR–ABL locus that confer resistance to a leukemia drug; CRISPR-X mutates a gene encoding a proteasome subunit to identify mutations resulting in resistance to a proteasome inhibitor.

**Articles p1029, p1036; News & Views p983**

**From one genome, two assemblies**

The genomes of species that are highly outbred or arise from hybridization events are notoriously challenging to assemble from raw sequence data, and the distinctions between parental chromosomes are typically lost. Schatz, Chin and colleagues have developed open-source software tools for fully phased diploid genome assembly. FALCON uses read-error correction and string graphs to assemble long-read sequencing data into contiguous sequences, and FALCON-Unzip resolves assemblies into haplotypes. With these tools, the authors generated a de novo–assembled genome of an Arabidopsis thaliana hybrid from two distant accessions that is highly accurate, contiguous and correctly phased. They also assembled the outcrossed grape cultivar Vitis vinifera cv. Cabernet Sauvignon and a highly heterozygous fungus, Clavicorona pyxidata, which has evaded assembly with short-read sequencing data.

**Articles p1029, p1036; News & Views p983**

**New FPs for multicolor imaging**

Red and far-red fluorescent proteins (FPs) are important for multicolor applications and for biological imaging at less damaging wavelengths. Papers from Lin and colleagues and from Lin, Yasuda and colleagues describe new far-red and red FPs, respectively. The new far-red FP is mMaroon1, which enables four-color imaging with cyan, green and orange FPs without the need for spectral unmixing. This advance enabled the development of Fucci4, a cell-cycle reporter that uniquely identifies all four phases of the cell cycle. The new red FP is CyRFP1, which has a long Stokes shift and is uniquely suited for two-color two-photon imaging along with GFP and GFP-based sensors. CyRFP1 was used in FRET sensors with mMaroon1 to enable two-color functional imaging in neurons.

**Brief Communications p993, p989**