About 85% of the maize genome consists of highly repetitive sequences that are interspersed by low-copy, gene-coding sequences. The maize community has dealt with this genomic complexity by the construction of an integrated genetic and physical map (iMap), but this resource alone was not sufficient for ensuring the quality of the current sequence build. For this purpose, we constructed a genome-wide, high-resolution optical map of the maize inbred line B73 genome containing >91,000 restriction sites (averaging 1 site/?23 kb) accrued from mapping genomic DNA molecules. Our optical map comprises 66 contigs, averaging 31.88 Mb in size and spanning 91.5% (2,103.93 Mb/?2,300 Mb) of the maize genome. A new algorithm was created that considered both optical map and unfinished BAC sequence data for placing 60/66 (2,032.42 Mb) optical map contigs onto the maize iMap. The alignment of optical maps against numerous data sources yielded comprehensive results that proved revealing and productive. For example, gaps were uncovered and characterized within the iMap, the FPC (fingerprinted contigs) map, and the chromosome-wide pseudomolecules. Such alignments also suggested amended placements of FPC contigs on the maize genetic map and proactively guided the assembly of chromosome-wide pseudomolecules, especially within complex genomic regions. Lastly, we think that the full integration of B73 optical maps with the maize iMap would greatly facilitate maize sequence finishing efforts that would make it a valuable reference for comparative studies among cereals, or other maize inbred lines and cultivars.