The diagram illustrates the expected fraction of coverage for traditional haploid sequencing and diploid medical sequencing, as a function of haploid redundancy. The BAC calibration range is also shown, indicating the range of haploid redundancy values for consistent coverage.

- Traditional haploid sequencing is represented by a dashed line.
- Diploid medical sequencing is represented by a solid line.

The curves are labeled with the number of reads (1 read, 2 reads, 3 reads, 4 reads, 5 reads) to indicate the number of sequencing reads required to achieve the expected coverage.