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We developed an automated system for discovering GPCR sequences in the whole human genome using algorithms of gene finding, sequence search, motif and domain assignment, transmembrane helix prediction and the gene quality refinement. This system is intended to detect sequences of multiple exon or remote homologues that can not be detected by using conventional sequence search alone. With careful assessment of the analyzing components, we obtained candidate gene datasets of various confidence levels, among which we found at least 888 and at most 2,298 candidate GPCR genes from human genome.