Gemcitabine is an anti-cancer drug effective to several solid tumors, including pancreatic and lung cancers. Gemcitabine is rapidly metabolized to its inactive metabolite, 2',2'-difluorodeoxyuridine (dFdU), by cytidine deaminase (CDA). In order to identify single nucleotide polymorphisms (SNPs) of CDA in a Japanese population, we sequenced the 5'-flanking region (approximately 800 base pairs from the translation initiation codon), all of the 4 exons, and the surrounding intronic regions using genomic DNA from 205 Japanese individuals, who were administered gemcitabine. Twenty-four SNPs and insertion/deletion polymorphisms, including twelve novel ones were detected: -182G>A, -116G>A, -81G>A, 210T>C (A70A), IVS2+72_+87(TCAT)>(TCAT)5, IVS3-194_-193insAlu (ca. 320 bp), IVS3-56G>A, IVS3-36G>A, IVS3-23C>T, 633_637C>C, and 676A>G (A of the translational start codon of NCBI Accession # NT_004610.16 is numbered 1). Allele frequencies of two known non-synonymous SNPs, 79A>C (K27Q) and 208G>A (A70T), were 0.224 and 0.039, respectively. Five polymorphisms, IVS3-194_-193insAlu, IVS3-56G>A, IVS3-36G>A, IVS3-23C>T, and 633_637C>C, were always associated with the known synonymous SNP 435C>T (T145T) and their frequencies were 0.312. Our data, including these 5'-flanking and intronic polymorphisms, can be utilized for comprehensive CDA haplotyping and their associations with PK/PD of gemcitabine.