* 1. ***In silico* analysis of the PTCome distribution on PTP (Kernel plots)**
     1. Potential PTCome

1. To obtain the potential PTCome, extract from Gene database (NCBI, https://www.ncbi.nlm.nih.gov/gene/) the cDNA sequence of the desired gene. Copy it in a text document.
2. Import the text document in the PTCMAKER program or run the online code (*see* **Note 9**).
3. Run the code in () to obtain unique potential PTC residues.
   * 1. Germline-associated PTCome
4. To obtain the germline-associated PTCome, browse for the desired PTP in the HGMD database (https://www.hgmd.cf.ac.uk). HGMD displays a data frame with missense and nonsense mutations together (*see* **Note 10**).
5. Import the downloaded file in RStudio by File > Import Dataset > From Excel, or using the *read\_excel()* function.
6. Run the code in () to obtain unique PTC mutated residues.
   * 1. Kernel plot representation
7. Insert the amino acid length and the name of your protein of interest.
8. Run the code in () to obtain a kernel plot representation. The three vectors (potential PTCome, cancer-associated PTCome and germline-associated PTCome) are rescaled to 100 to facilitate comparisons between proteins. Mirror vectors are generated to avoid bias at boundaries and a density is calculated of sum of the parental vector and the mirror vectors. The final plot contains black, red and blue curves, which represent the potential PTCome, the cancer-associated PTCome and the germline-associated PTCome, respectively.