A single nucleotide variation (SNV) is a type of genetic variation that involves the substitution of a single nucleotide (A, C, G, or T) at a specific position in a DNA molecule. SNVs are the most common type of genetic variation in the human genome and are estimated to occur at a rate of approximately 1 in every 300 nucleotides.

SNVs can have a wide range of effects on an individual's health and susceptibility to disease. Some SNVs are benign and have no significant impact on health, while others can cause genetic disorders or increase the risk of certain diseases. For example, some SNVs have been linked to an increased risk of cancer, cardiovascular disease, and other common health conditions.

SNVs can be identified through various genetic testing methods, including targeted sequencing, whole-exome sequencing, and whole-genome sequencing. Genetic testing can provide valuable information about an individual's genetic predisposition to certain health conditions, which can help inform medical decisions and treatment options.