Slide 1: the leader will introduce us.

Good afternoon,

**Slide 2:**

Polycystic ovary syndrome (PCOS) is a common hormonal disorder that affects a significant number of women worldwide. It is characterized by hormonal imbalances, manifestating with various symptoms and lead to a chain of consequences, such as missed or irregular menstrual periods, excess hair growth, acne, weight gain, insulin resistance, infertility and so on.

The exact causes of PCOS remain unclear, but there are several factors believed to contribute to its development. Genetic factors play a significant role, as women with PCOS often have relatives with the condition. According to the DisGeNET database, 71 polymorphic loci and 153 genes (both protein-coding and regulatory genes) associated with PCOS are known.

However, the complete understanding of the participation of polymorphic loci in lncRNAs genes in the context of their distribution among common human populations has not been revealed.

**Slide 3:**

Reading from the slide about aim and objectives.

**Slide 4:**

This slide provides a graphical representation of our worflow. As a source of significant SNPs associated with PCOS, we used the GWS Catalog resource. 29 GWASs, including 111 polymorphic loci were selected for further studying.

Next, from the main list of SNPs, we mapped each SNP using the UCSC genomic browser, and filteredout two sets of SNPs: the first one, we filtered out just SNPs those were within or close to the lncRNA genes. In the second set, only SNPs that occurred in the GWASs two or more times were included. For these two sets, we applied several types of computational approaches: we studied the prevalence of effect alleles in common populations, examined the expression of mapped genes, and performed a Gene Ontology analysis for the second set of mapped genes.

**Slide 5:**

This slide exhibits the summary of the involded studies, involving 100 170 cases and 2 088 636 controls from four common populations: Europeans, Chinese and Koreans (which is EAS), Africans and Americans.

**Slide 6:**

Next, using UCSC Genome browser and hg19 genome assembly, we determined the list of SNP that are within the lncRNA genes (represented as green rows in the table).