**Supplementary Figure 1.** a) Percent of intact and partial gene duplication and deletions.

b) Distribution of duplication and deletion CNVs across populations in all chromosomes.

**Supplementary Figure 2a-c.Categorization of genes under CNVs based on functional properties**. Representation of genes under CNVs that are involved in (a) biological processes (b) molecular function and (c) cellular components.

**Supplementary Figure 3. Phenotypic abnormalities pathway.** Pathway represents the genes under CNVs involved in causing phenotypic abnormalities found in the study and their significance. Genes contributing to abnormalities of the thyroid gland, decreased fetal movement, hirsutism and hypopigmented skin patches were found in the different populations studied.

**Supplementary Figure 4.** Represents the molecular pathway involving the genes underlying CNVs in the different populations studied.

**Supplementary Figure 5.**Represents the cellular pathway involving the genes underlying CNVs in the different populations studied.

**Supplementary Figure 6.**Represents the biological pathway involving the genes underlying CNVs in the different populations studied.

**Supplementary Figure 7. Map of gene clusters in different chromosomes across populations.** Green line represents the genomic positions of gene clusters in CNVs found in more than 50% of individuals across all populations.

**Supplementary Figure 8. CNV-genes map of identified genes shared across populations** CNV map of 126190 shared CNVs across all chromosomes and populations**.** The outermost to innermost tracks are: pair-wise clustering of shared CNV-genes in percent across all chromosomes in this Circos image.