

## List of Tables

<b>Table 4.1</b>	Candidate gene primers and their associated exons
<b>Table 4.2</b>	Ensembl, HGNC, Entrez, Uniprot and OMIM ID's of the candidate genes from public database
<b>Table 4.3</b>	Candidate genes selected for the study and their functional role
<b>Table 5.1</b>	Univariate analysis of dietary and lifestyle factors
<b>Table 5.2</b>	Multivariate analysis of dietary and lifestyle factors
<b>Table 5.3</b>	Comparison of type 2 diabetes mellitus and control groups in relation to salivary protein (mg/dl) by ANOVA
<b>Table 5.4</b>	Comparison of type 2 diabetes mellitus and control groups in relation to serum protein (mg/dl) by ANOVA
<b>Table 5.5</b>	Comparison of type 2 diabetes mellitus and control groups in relation to microalbumin (mg/dl) by Paired t-test
<b>Table 5.6</b>	Allelic frequency distribution and risk associated with UCP3 variation in Mizo population
<b>Table 5.7</b>	Allelic frequency distribution and risk associated with MACF1 variation in Mizo population
<b>Table 5.8</b>	Plink data showing associated genes Red denotes associated; Yellow denotes less likely associated; Black denotes not associated
<b>Table 5.9</b>	Non synonymous variants observed in all the diabetic samples
<b>Table 5.10</b>	Missense variants previously reported in the databases
<b>Table 5.11</b>	Novel variants not reported in the databases

<b>Table 5.12</b>	Pathways and phenotype of the genes having variants which were not reported for diabetes
<b>Table 5.13</b>	Reported pathogenic variants based on GWAS panel
<b>Table 5.14</b>	Unreported pathogenic variants based on GWAS panel with HOPE prediction
<b>Table 5.15</b>	Pathways and phenotype of the genes having variants which were reported
<b>Table 5.16</b>	InDel's observed in the exonic region and not reported for any disease so far.
<b>Table 5.17</b>	InDel's observed in the intonic region and not reported for any disease so far.
<b>Table 5.18</b>	List of genes from our study previously reported as possible prognostic or diagnostic markers.
<b>Table 5.19</b>	Common variants of cases and controls with Mitomaster scores
<b>Table 5.20</b>	Sample specific variants with Mitomaster scores
<b>Table 5.21</b>	Potential impact of non-synonymous case specific as well as common variants as predicted by Pmut.
<b>Table 5.22</b>	Common variants of cases and control in D-loop
<b>Table 5.23</b>	Sample specific variants in D-Loop