**Chapter 4**

%% PRDM9 gene, meiotic recombination, hotspots

%% PRDM9 allele is determined through zinc finger repeat expansion and the mutations on the zinc finger repeat expansion

%% PRDM9 binding site per allele

%% PRDM9 genotype per sample

%% PRDM9 genotype per DNA molecule per sperm

%% relationship between PRDM9 allele and gene evolution rate

%% relationship between LD and meiotic recombniation hotspots

%% Trio-sequencing has been used to determine or the aftermath of meiotic recombniation per chromosome from a single meiotic event

%% long-range PCR has been used to genotype meiotic recombination from thousands of sperm samples in a target region

%% gene conversion tract length

%% meiotic mutagenesis: small snvs, indels and copy number variations or structural variations

%% linkage disequeiblirum

%% gene conversion as a violation of mendelian ratio

\section{Introduction}

\subsection{Meiotic recombination}

\subsection{Haplotype Map}

\subsection{Methods to study meiotic recombinant products}

\subsubsection{Trio-sequencing}

\section{Material \& Methods}

\section{Results}

\section{Discussion}