Input: Paired-end sequencing data

Mapping
- BLAST of ME Reads
- Mapping of Flanking Reads

Filtering
- ME Reads filtering by BLAST bit-score
- Flanking Reads filtering by Mapping quality

Clustering Flanking Reads to putative MEIs

Remove reference ME primer binding sites

Putative MEIs loci

Identification

Human reference genome

Extract reference MEIs by RepeatMasker output and BLAST bit-score

Remove known ME deletion polymorphisms

Presumably Fixed MEIs

Calculating TPM/UR cutoffs and filtering putative MEIs

Remove MEI loci in parents and other samples from offspring

Output: pMEIs

Extract targeted MEIs

Known pMEIs

Remove known pMEIs

Output: Novel pMEIs

Output: de novo pMEIs

Published MEI papers, databases

Extract targeted MEIs

Known pMEIs

Remove known pMEIs

Output: Novel pMEIs