**Illumina Primer 1.1**

**Illumina Primer 1.2**

**DNA sequencing using Illumina Gene Analyzer 2.0**
DNA sequence data file
(Illumina format; 4 lines/read)

Extract reads, convert to fasta format

Query
Fasta file

- gDNA: 15 million reads / lane
- cDNA: 10 million reads / lane

BLAST matches

Pick only matches with highest identity

Sort according to sequences in the library

Index 1
Gene 1-forward

Index 1
Gene 1-reverse

Index 52
Gene 74-reverse

7696 files

Align sequences at mSNPs

Use upstream and downstream 20 bp sequences for quality control

Combine results from forward- and reverse-strands

Calculate the ratio of two alleles
Figure S3

(a) Graph showing reads of indicated length and cumulative reads over different read lengths. The percentage of reads decreases as the read length increases.

(b) Bar graph showing the percentage of reads discarded and saved across different read lengths. The graph indicates that as the read length increases, both the percentage of reads discarded and saved decreases.
a

Genomic DNA

Number of genes (total = 70)

b

cDNA

Number of genes (total = 70)
Number of genes (total = 70)

Average gDNA AEI ratio

\[ y = 6E-07x + 0.0077 \]

\[ R^2 = 0.0003 \]

Log\(_2\) (gDNA AEI ratio)

DNA sequencing reads

\[ y = 6E-07x + 0.0077 \]

\[ R^2 = 0.0003 \]
Illumina Assay-1 Log₂ AEl ratio

Illumina Assay-2 Log₂ AEl ratio

**SORCS1** ($R^2=0.9454$)

**TBX1** ($R^2=0.9360$)

**ARVCF** ($R^2=0.8748$)

**CYFIP1** ($R^2=0.8288$)

**AGER** ($R^2=0.9287$)

**CH25H** ($R^2=0.8337$)

**DBH** ($R^2=0.9435$)

**GR1A2** ($R^2=0.8890$)

**TNFRSF21** ($R^2=0.7951$)

**PSEN2** ($R^2=0.7989$)

**COMT** ($R^2=0.6924$)

**ADAM17** ($R^2=0.6467$)

**GABRB3** ($R^2=0.5902$)

**DGCR8** ($R^2=0.4547$)

(P Value < 0.000)

(P Value < 0.005)

(P-Value<0.01)

(P-Value<0.05)