

Table S1. Sequencing data statistics table.

Sample	Raw Reads	Clean Reads	Clean Base(G)	Error Rate(%)	Q20 (%)	Q30 (%)	GC Content(%)
Ih-WT	48527378	47994832	7.2	0.01	98.9	96.57	47.44
Ih-MU	40223140	39724834	5.96	0.01	99.09	96.57	47.44

Table S2. Sample splicing results.

Type	Number	Mean Length	N50	N90	Total Bases
Transcript	59339	1251	1730	652	74238215
Unigene	33271	1459	1817	770	48540188

Table S3. Database annotation analysis of genes.

Database	Number of Genes	Percentage (%)
KEGG	23775	71.46
Nr	30908	92.9
SwissProt	23993	72.11
TrEMBL	30443	91.5
KOG	18301	55.01
GO	27189	81.72
Pfam	25287	76
Annotated in at least one Database	31111	93.51
Total Unigenes	33271	100

Figure S1. Unigene annotation statistics diagram.

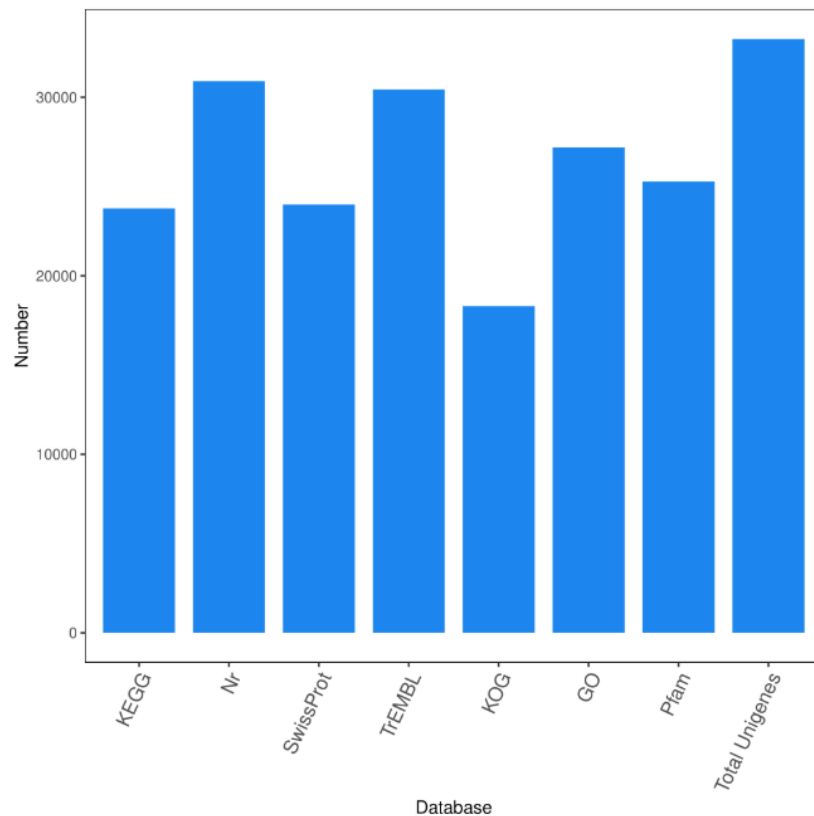


Figure S2.NR annotation diagram.

