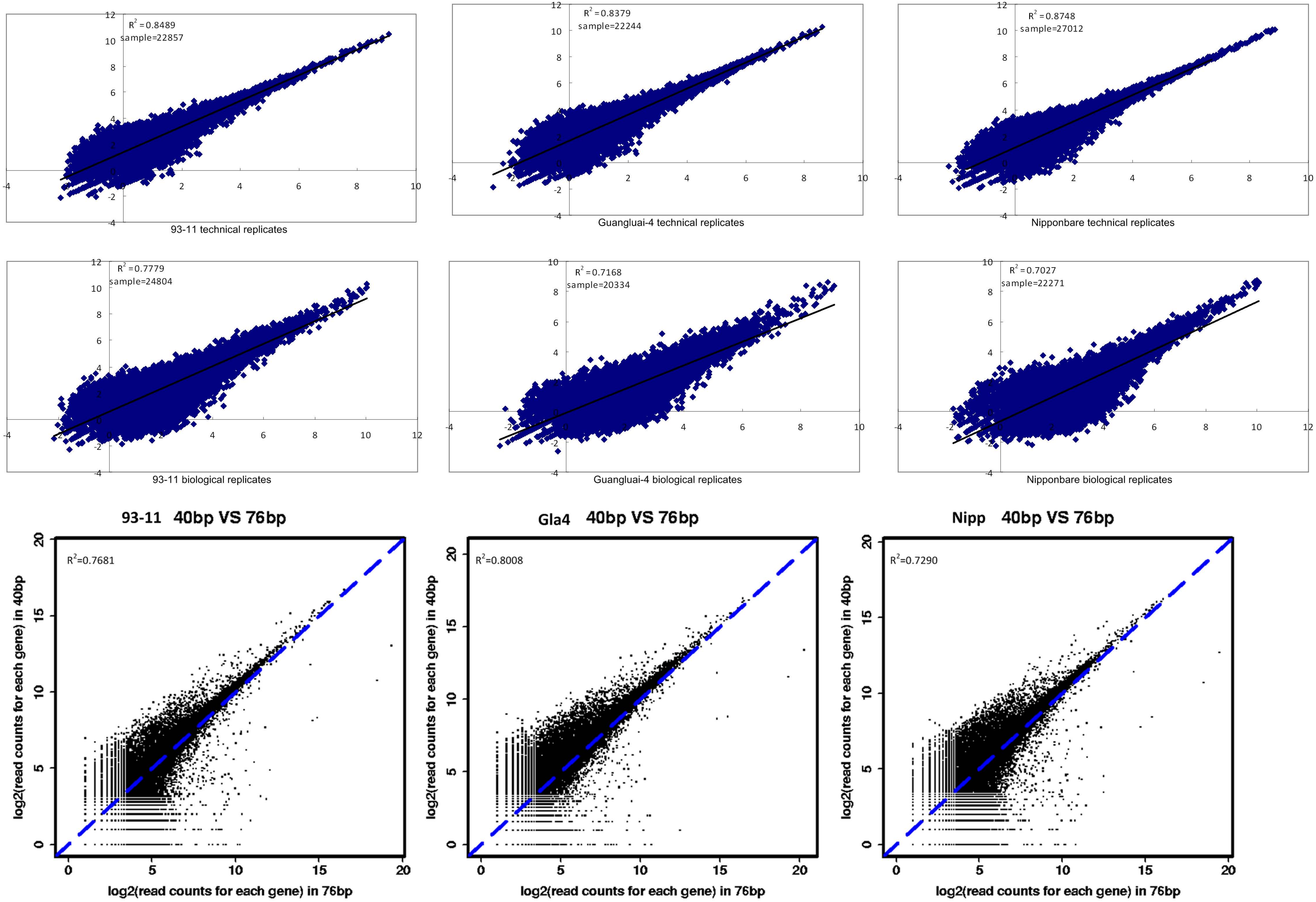
Figure S1



R^2 = 0.8489
sample=22857
-4
-2
0
2
4
6
8
10
12
93-11 technical replicates
R^2 = 0.8379
sample=22244
Guangluai-4 technical replicates
R^2 = 0.8748
sample=27012
Nipponbare technical replicates
R^2 = 0.7779
sample=24804
93-11 biological replicates
R^2 = 0.7168
sample=20334
Guangluai-4 biological replicates
R^2 = 0.7027
sample=22271
Nipponbare biological replicates
93-11 40bp VS 76bp
R^2=0.7681
Gla4 40bp VS 76bp
R^2=0.8008
Nipp 40bp VS 76bp
R^2=0.7290
0
5
10
15
20
log2(read counts for each gene) in 40bp
log2(read counts for each gene) in 76bp

Figure S2

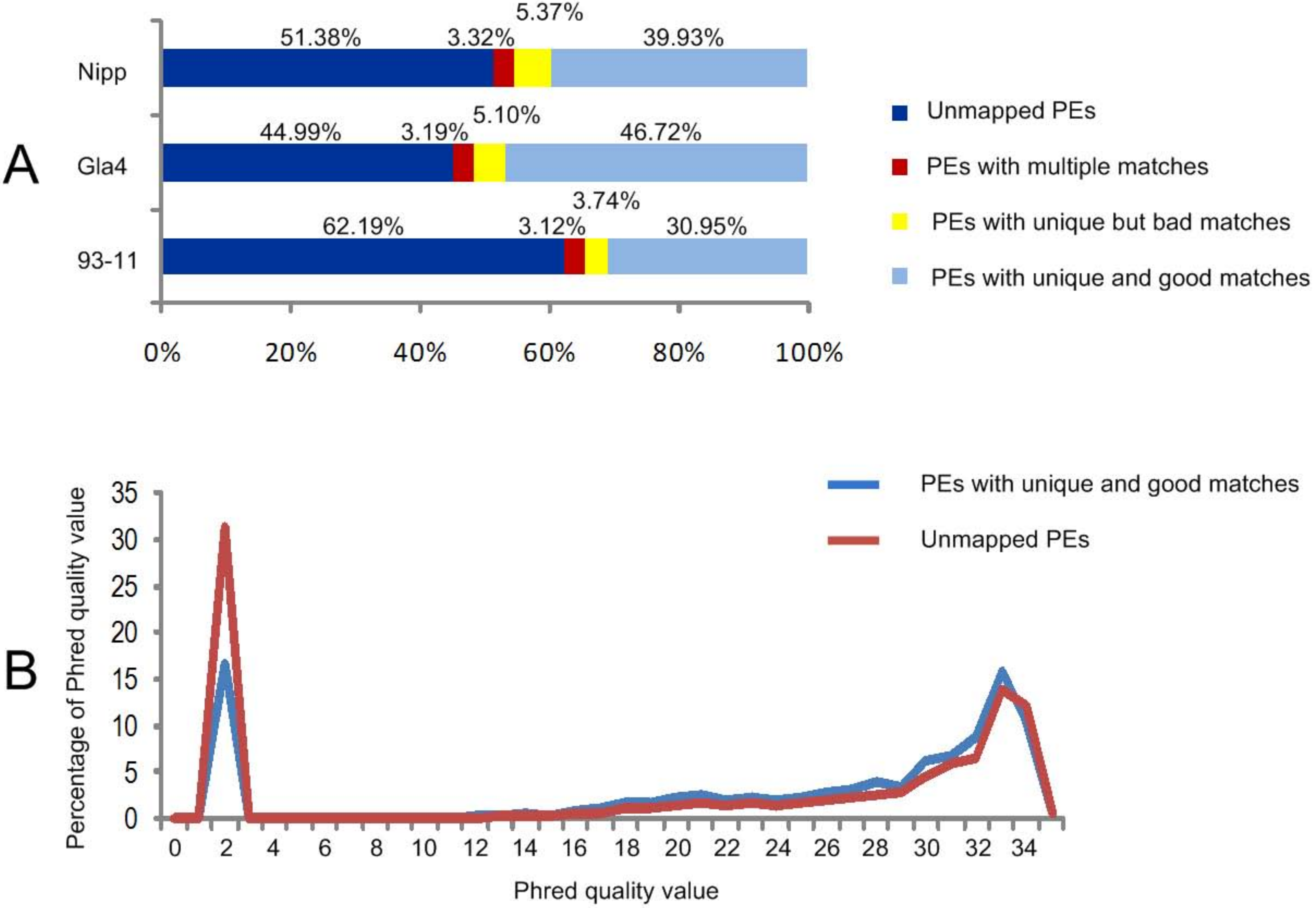

A
Nipp
Gla4
93-11
51.38%
3.32%
5.37%
39.93%
44.99%
3.19%
5.10%
46.72%
62.19%
3.12%
3.74%
30.95%
0%
20%
40%
60%
80%
100%
Unmapped PEs
PEs with multiple matches
PEs with unique but bad matches
PEs with unique and good matches
B
Percentage of Phred quality value
35
30
25
20
15
10
5
0
0
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
32
34
Phred quality value
PEs with unique and good matches
Unmapped PEs

Figure S3

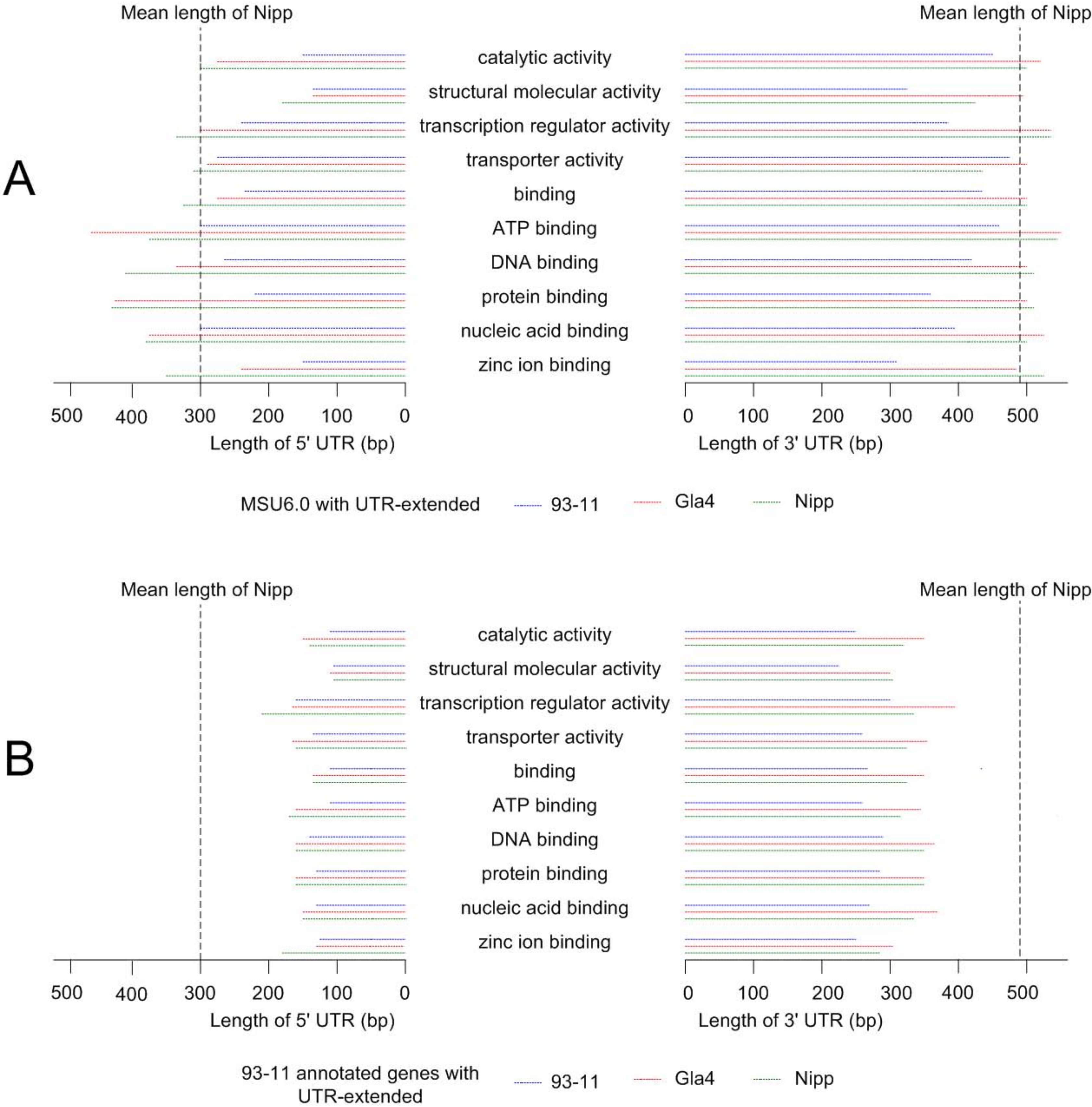
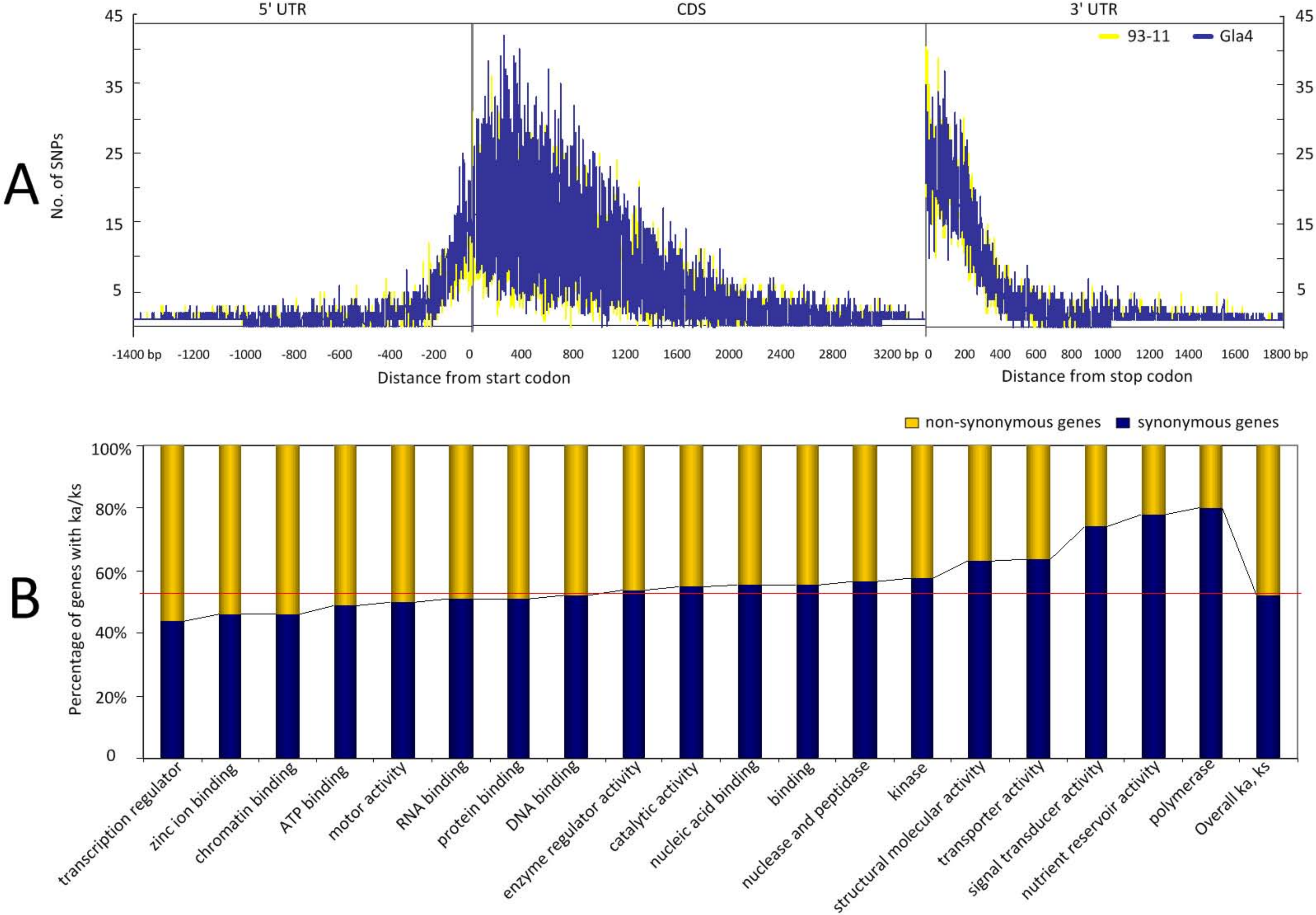

A
Mean length of Nipp
Mean length of Nipp
catalytic activity
structural molecular activity
transcription regulator activity
transporter activity
binding
ATP binding
DNA binding
protein binding
nucleic acid binding
zinc ion binding
500
400
300
200
100
0
Length of 5' UTR (bp)
0
100
200
300
400
500
Length of 3' UTR (bp)
MSU6.0 with UTR-extended
93-11
Gla4
Nipp
B
Mean length of Nipp
Mean length of Nipp
catalytic activity
structural molecular activity
transcription regulator activity
transporter activity
binding
ATP binding
DNA binding
protein binding
nucleic acid binding
zinc ion binding
500
400
300
200
100
0
Length of 5' UTR (bp)
0
100
200
300
400
500
Length of 3' UTR (bp)
93-11 annotated genes with UTR-extended
93-11
Gla4
Nipp

Figure S4


A
5' UTR
CDS
3' UTR
93-11
Gla4
No. of SNPs
45
35
25
15
5
-1400 bp
-1200
-1000
-800
-600
-400
-200
0
400
800
1200
1600
2000
2400
2800
3200 bp
Distance from start codon
0
200
400
600
800
1000
1200
1400
1600
1800 bp
Distance from stop codon
B
non-synonymous genes
synonymous genes
Percentage of genes with ka/ks
100%
80%
60%
40%
20%
0
transcription regulator
zinc ion binding
chromatin binding
ATP binding
motor activity
RNA binding
protein binding
DNA binding
enzyme regulator activity
catalytic activity
nucleic acid binding
binding
nuclease and peptidase
kinase
structural molecular activity
transporter activity
signal transducer activity
nutrient reservoir activity
polymerase
Overall ka, ks

Supplementary Figure 1. Scatterplots comparing gene expression scores based on technical replicates, biological replicates and 40bp versus 76bp of 93-11, Guangluai 4 and Nipponbare, respectively.

Supplementary Figure 2. (A) Overall mapping results of paired-end reads (PE) referring to the *indica* 93-11 genome sequence. (B) Statistical analysis of each Phred quality value of PEs with uniquely mapped reference and unmapped PEs.

Supplementary Figure 3. (A) MSU v6.0 transcripts with significantly larger or smaller UTRs for GO categories based on RNA-seq data of 93-11, Guangluai 4 and Nipponbare are shown. (B) 93-11 annotated gene models with significantly larger or smaller UTRs for GO categories based on the RNA-seq data of 93-11, Guangluai 4 and Nipponbare are shown.

Supplementary Figure 4. Summary of identified SNPs. (A) SNP density across UTR regions and coding sequence. (B) Synonymous and non-synonymous SNP distribution in 19 major protein molecular functions.