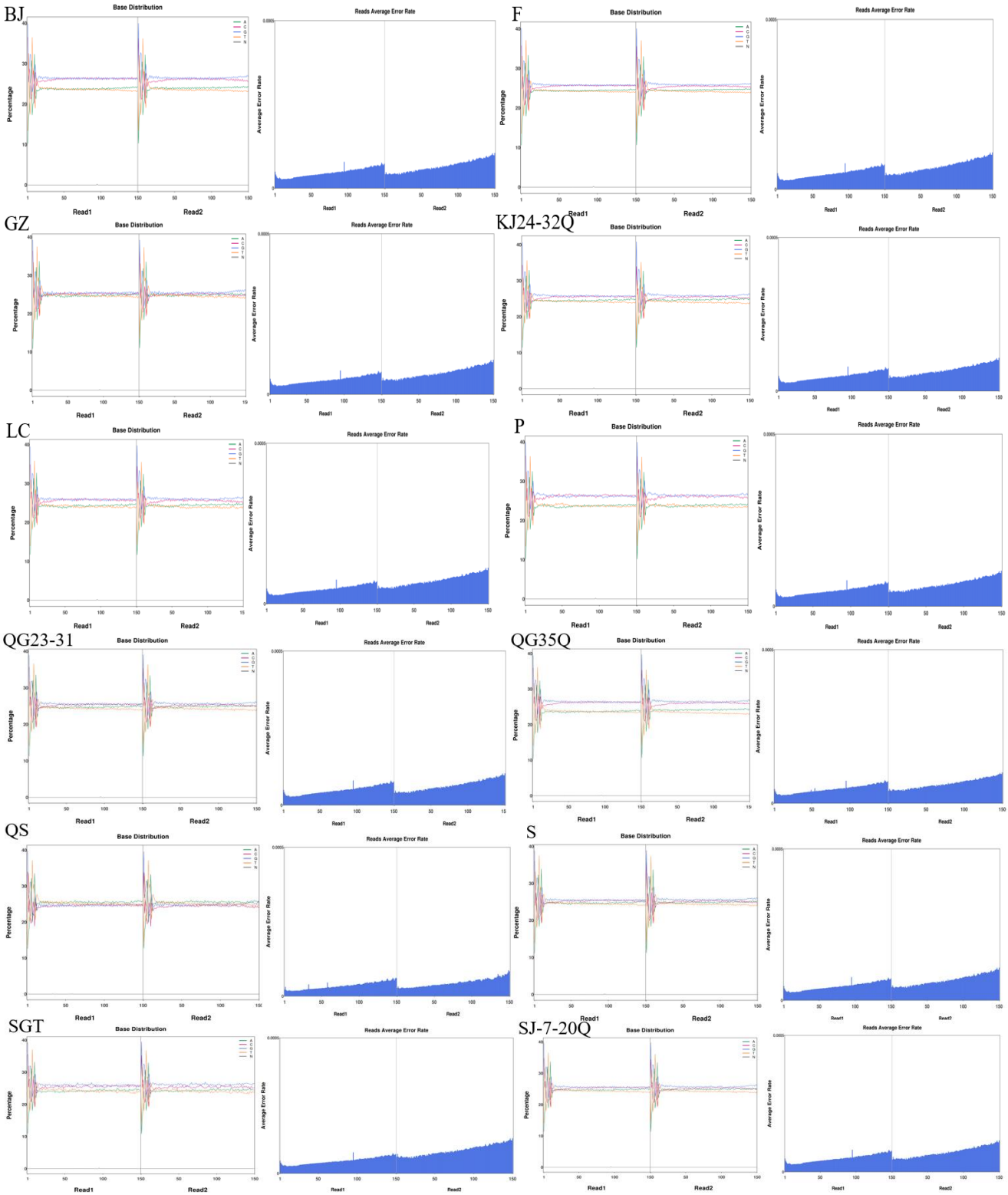
Supplementary material



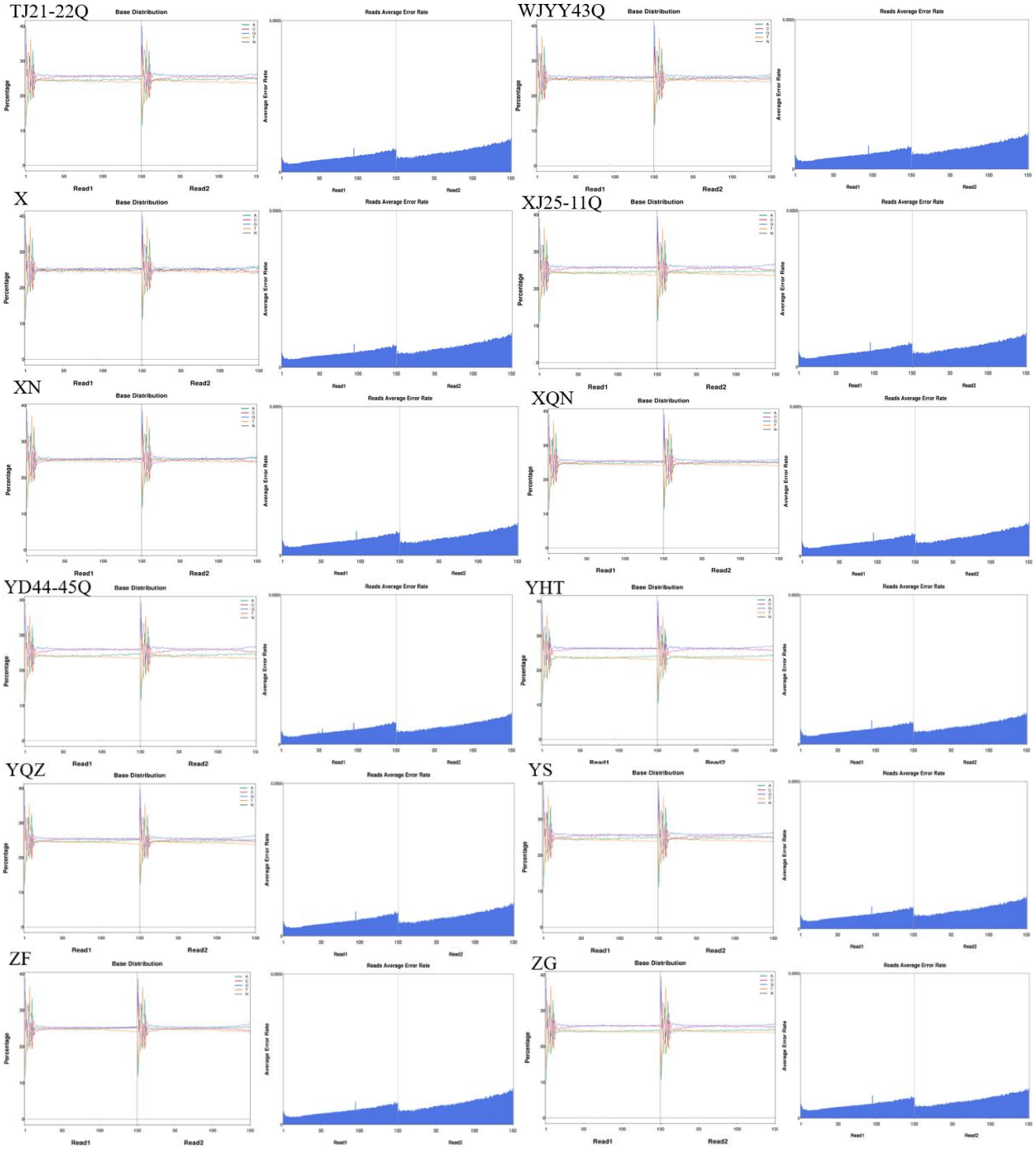


Figure S1. The data quality of the samples with ATCG content distribution and base error rates.

[Note: abscissa is the base position of a read, the ordinate is the proportion of base and average error rate for the single base].

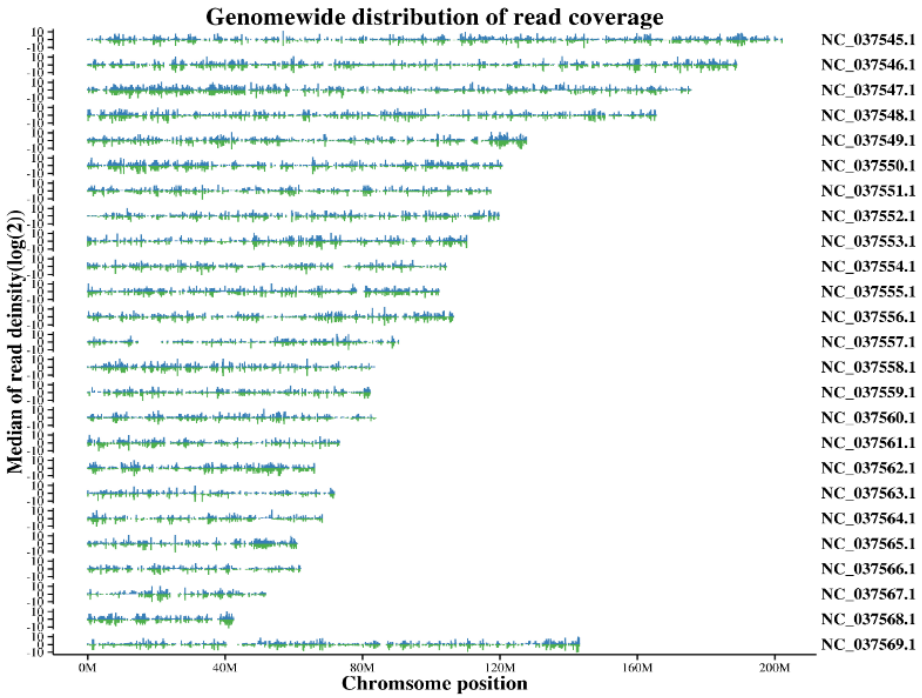
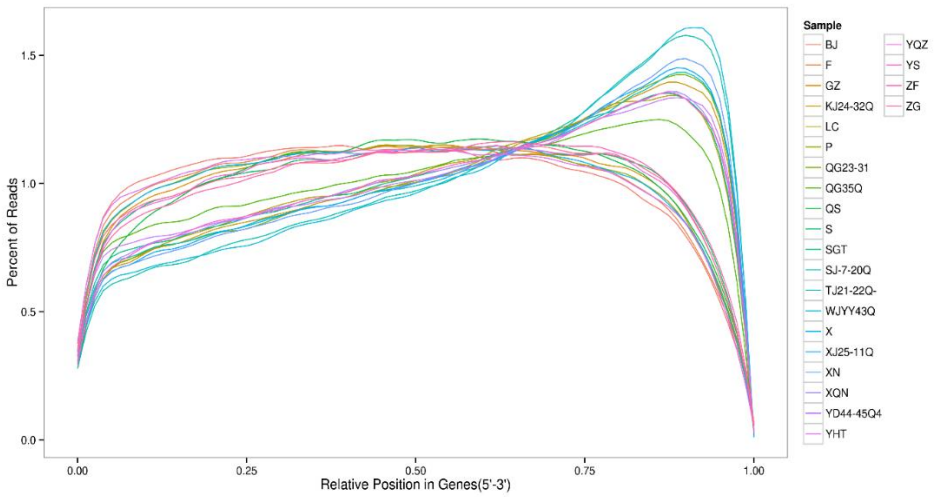


Figure S2. Position of mapped reads on the reference genome and coverage depth distribution.

(A)



(B)

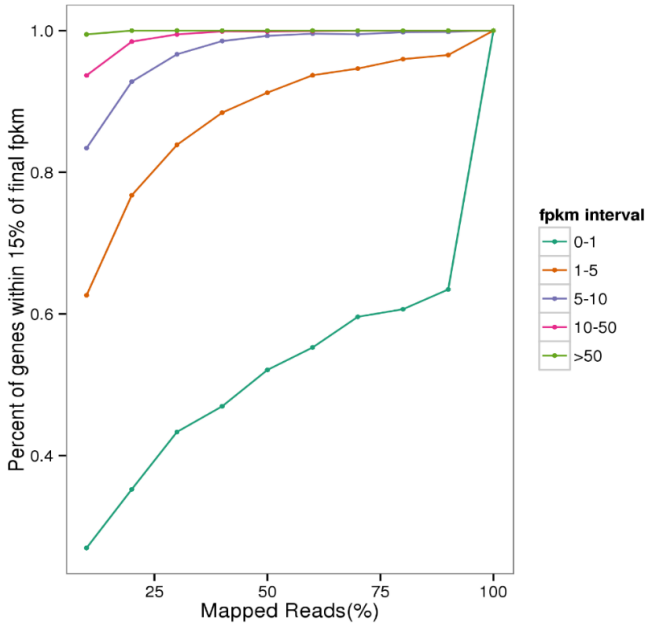


Figure S3. (A) The depth distributions of mapped reads on transcripts **(B)** the RNA-seq data saturation simulation.

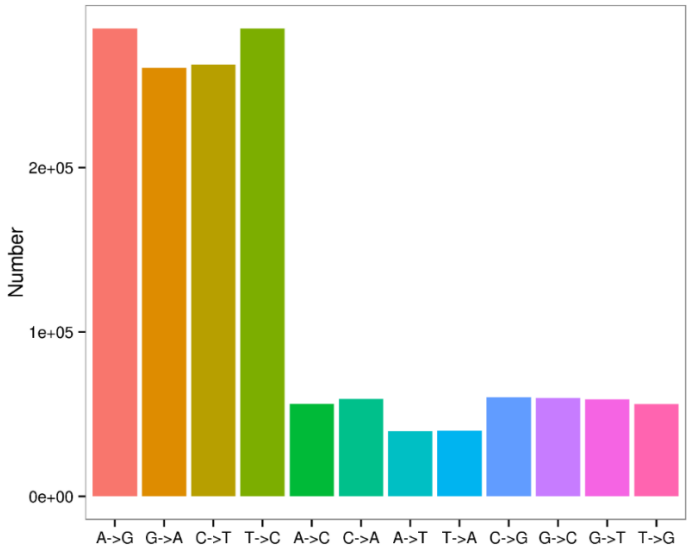


Figure S4. The types of SNP mutations in sequenced data (transition and transversion).

[Note: The horizontal axis represents the SNP mutation types, the vertical axis represents the number of the corresponding SNPs].

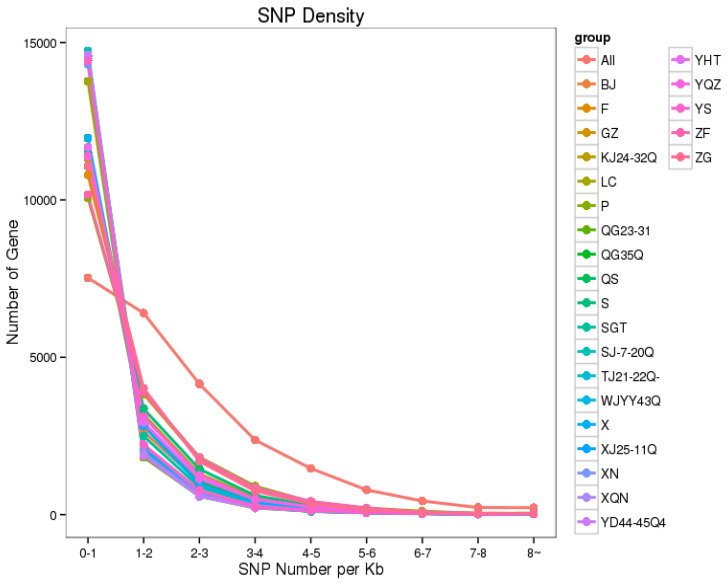
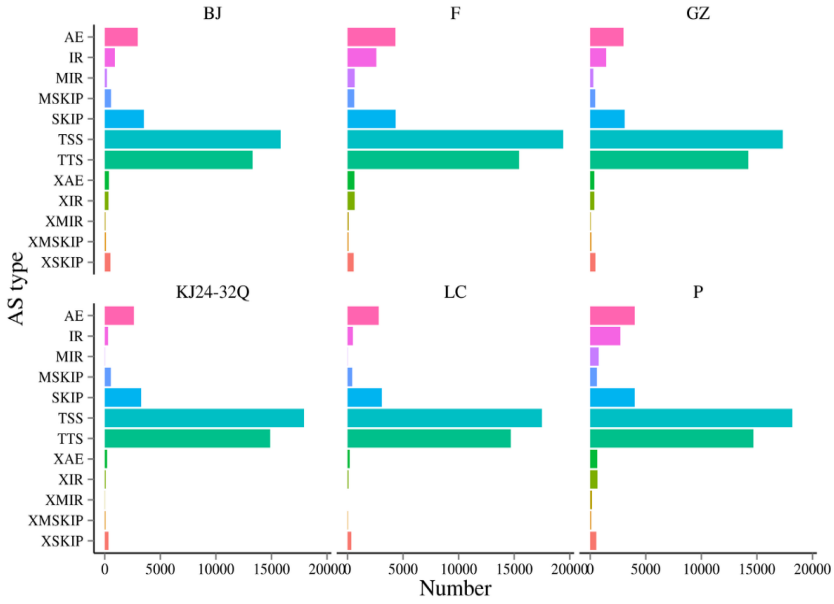
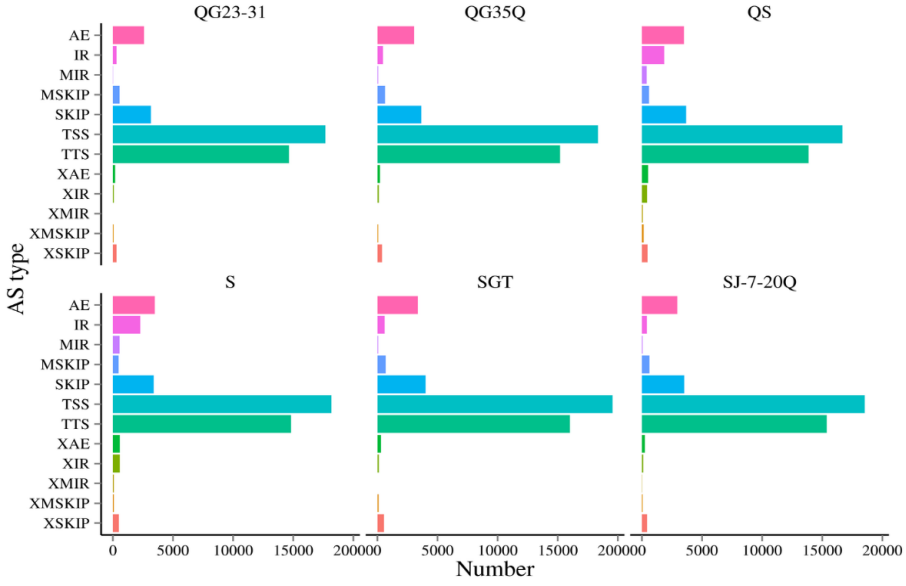
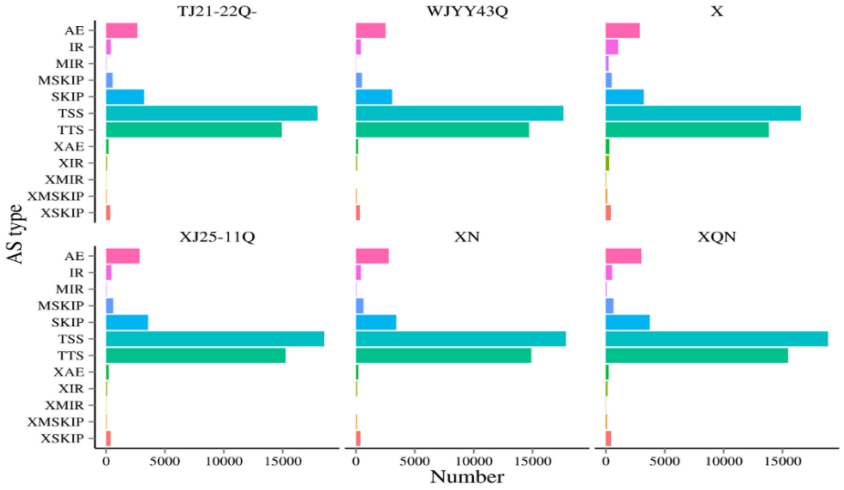


Figure S5. The genes SNP density distribution.

[Note: The abscissa represents the average number of SNPs distribution per 1000bp gene sequence, the ordinate represents the number of genes.]




QG23-31
QG35Q
QS
S
SGT
SJ-7-20Q
AE
IR
MIR
MSKIP
SKIP
TSS
TTS
XAE
XIR
XMIR
XMSKIP
XSKIP
AS type
0
5000
10000
15000
200000
20000
Number


TJ21-22Q-
WJYY43Q
X
XJ25-11Q
XN
XQN
AE
IR
MIR
MSKIP
SKIP
TSS
TTS
XAE
XIR
XMIR
XMSKIP
XSKIP
AS type
0
5000
10000
15000
Number

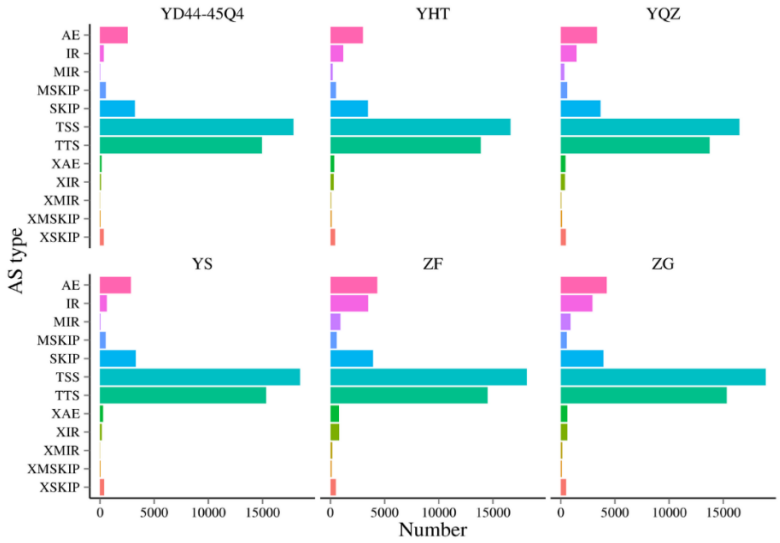


Figure S6. Statistics of alternative splicing events.

[Note: The horizontal axis represents a number to one of the alternative transcripts, the vertical axis represents types of alternative splicing events.1-TSS: Alternative 5' first exon (transcription start site) the first exon splicing; 2-TTS: Alternative 3' last exon (transcription terminal site) the last exon splicing; 3-SKIP: Skipped exon (SKIP_ON, SKIP_OFF pair) single exon skipping; 4-XSKIP: Approximate SKIP (XSKIP_ON, XSKIP_OFF pair) single exon skipping (fuzzy boundary); 5-MSKIP: Multi-exon SKIP (MSKIP_ON, MSKIP_OFF pair) multi-exon skipping; 6-XMSKIP: Approximate MSKIP (XMSKIP_ON, XMSKIP_OFF pair) multi-exon skipping (fuzzy boundary); 7-IR: Intron retention (IR_ON, IR_OFF pair) single intron retention; 8-XIR: Approximate IR (XIR_ON, XIR_OFF pair) single intron retention (fuzzy boundary); 9-MIR: Multi-IR (MIR_ON, MIR_OFF pair) multi-intron retention; 10-XMIR: Approximate MIR (XMIR_ON, XMIR_OFF pair) multi-intron retention (fuzzy boundary); 11-AE: Alternative exon ends (5', 3', or both); 12-XAE: Approximate AE variable 5' or 3' end (fuzzy boundary)].

Table S1. The statistics of the sequenced data.

Samples	Clean reads	Clean bases	GC Count	%≥Q30
BJ	21,868,067	6,560,420,100	52.67%	92.42%
F	25,386,599	7,615,979,700	51.46%	92.29%
GZ	26,166,123	7,849,836,900	50.63%	92.34%
KJ24-32Q	23,320,858	6,996,257,400	51.44%	92.17%
LC	27,749,317	8,324,795,100	51.79%	92.07%
P	26,472,161	7,941,648,300	52.63%	92.52%
QG23-31	23,323,713	6,997,113,900	51.05%	92.33%
QG35Q	21,971,799	6,591,539,700	52.68%	92.62%
QS	28,337,044	8,501,113,200	49.47%	94.61%
S	22,618,701	6,785,610,300	50.87%	92.29%
SGT	27,371,168	8,211,350,400	51.66%	91.27%
SJ-7-20Q	28,331,213	8,499,363,900	51.07%	91.84%
TJ21-22Q-	24,040,796	7,212,238,800	51.37%	91.98%
WJYY43Q	24,677,989	7,403,396,700	50.76%	91.77%
X	25,449,910	7,634,973,000	50.46%	92.25%
XJ25-11Q	24,869,758	7,460,927,400	51.57%	92.19%
XN	26,251,060	7,875,318,000	50.39%	92.06%
XQN	24,571,518	7,371,455,400	50.82%	92.11%
YD44-45Q4	22,511,689	6,753,506,700	52.05%	92.59%
YHT	23,406,717	7,022,015,100	52.77%	92.28%
YQZ	25,582,045	7,674,613,500	50.92%	92.20%
YS	23,182,550	6,954,765,000	51.21%	92.26%
ZF	25,817,126	7,745,137,800	50.48%	92.10%
ZG	21,970,637	6,591,191,100	51.56%	92.46%

[Note: Samples: sample name; Clean reads: Paired-end numbers of Clean Data; Clean bases: total base number of Clean Data; GC content: GC content percentage of Clean Data, namely the percentage of Clean Database G and C; ≥Q30%: the base which quality value is greater than or equal to 30 percentage of Clean Data].

Table S2. The sequenced data mapping statistics.

Sample	Total Reads	Mapped Reads	Unique Mapped Reads	Multiple Map Reads	Reads Map to (+)	Reads Map to (-)
BJ	43,736,134	41,462,810 (94.80%)	40,299,471 (92.14%)	1,163,339 (2.66%)	20,637,894 (47.19%)	20,661,919 (47.24%)
F	50,773,198	47,925,692 (94.39%)	46,594,374 (91.77%)	1,331,318 (2.62%)	23,842,833 (46.96%)	23,889,168 (47.05%)
GZ	52,332,246	49,731,001 (95.03%)	47,888,782 (91.51%)	1,842,219 (3.52%)	24,736,589 (47.27%)	24,804,154 (47.40%)
KJ24-32Q	46,641,716	44,355,163 (95.10%)	43,052,932 (92.31%)	1,302,231 (2.79%)	21,990,611 (47.15%)	22,066,742 (47.31%)
LC	55,498,634	52,015,315 (93.72%)	49,334,684 (88.89%)	2,680,631 (4.83%)	25,859,450 (46.59%)	25,785,017 (46.46%)
P	52,944,322	47,443,076 (89.61%)	44,938,700 (84.88%)	2,504,376 (4.73%)	23,671,040 (44.71%)	23,184,563 (43.79%)
QG23-31	46,647,426	44,247,268 (94.85%)	43,033,828 (92.25%)	1,213,440 (2.60%)	21,923,341 (47.00%)	21,997,123 (47.16%)
QG35Q	43,943,598	41,748,439 (95.00%)	40,461,427 (92.08%)	1,287,012 (2.93%)	20,689,864 (47.08%)	20,773,280 (47.27%)
QS	56,674,088	50,738,692 (89.53%)	49,403,052 (87.17%)	1,335,640 (2.36%)	25,265,088 (44.58%)	25,208,609 (44.48%)
S	45,237,402	42,974,783 (95.00%)	41,801,772 (92.41%)	1,173,011 (2.59%)	21,382,931 (47.27%)	21,422,436 (47.36%)
SGT	54,742,336	51,760,825 (94.55%)	49,866,550 (91.09%)	1,894,275 (3.46%)	25,642,929 (46.84%)	25,735,273 (47.01%)
SJ-7-20Q	56,662,426	53,600,479 (94.60%)	52,158,660 (92.05%)	1,441,819 (2.54%)	26,593,449 (46.93%)	26,655,872 (47.04%)
TJ21-22Q-	48,081,592	45,672,174 (94.99%)	44,346,935 (92.23%)	1,325,239 (2.76%)	22,636,452 (47.08%)	22,708,367 (47.23%)
WJYY43Q	49,355,978	46,817,969 (94.86%)	45,645,423 (92.48%)	1,172,546 (2.38%)	23,275,082 (47.16%)	23,287,090 (47.18%)
X	50,899,820	48,428,087 (95.14%)	47,343,162 (93.01%)	1,084,925 (2.13%)	24,176,677 (47.50%)	24,162,981 (47.47%)
XJ25-11Q	49,739,516	46,820,454 (94.13%)	45,374,560 (91.22%)	1,445,894 (2.91%)	23,212,367 (46.67%)	23,274,660 (46.79%)
XN	52,502,120	49,968,072 (95.17%)	48,583,120 (92.54%)	1,384,952 (2.64%)	24,817,682 (47.27%)	24,847,822 (47.33%)
XQN	49,143,036	46,862,566 (95.36%)	45,559,665 (92.71%)	1,302,901 (2.65%)	23,238,763 (47.29%)	23,307,461 (47.43%)
YD44-45Q4	45,023,378	42,562,217 (94.53%)	41,196,162 (91.50%)	1,366,055 (3.03%)	21,090,218 (46.84%)	21,156,215 (46.99%)

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YHT	46,813,434	44,161,365 (94.33%)	42,794,150 (91.41%)	1,367,215 (2.92%)	21,972,723 (46.94%)	21,998,425 (46.99%)
YQZ	51,164,090	47,976,420 (93.77%)	46,582,386 (91.05%)	1,394,034 (2.72%)	23,837,781 (46.59%)	23,882,301 (46.68%)
YS	46,365,100	43,731,874 (94.32%)	42,463,219 (91.58%)	1,268,655 (2.74%)	21,711,132 (46.83%)	21,764,078 (46.94%)
ZF	51,634,252	48,206,664 (93.36%)	46,979,834 (90.99%)	1,226,830 (2.38%)	23,894,475 (46.28%)	23,999,694 (46.48%)
ZG	43,941,274	41,592,901 (94.66%)	40,530,999 (92.24%)	1,061,902 (2.42%)	20,616,304 (46.92%)	20,673,396 (47.05%)

[Note: Samples: sample name; Total Reads: Reads number of Clean Data, not paired-end reads; Mapped Reads: Reads Number Mapped to the reference genome and the percentage in Clean Reads; Unique Mapped Reads: Reads Number Mapped uniquely mapped to the reference genome and the percentage in Clean Reads; Multiple Mapped Reads: Reads number multiply mapped to reference genome and the percentage in Clean Reads; Reads Map to (+): Reads number mapped to the sense chain and the percentage in Clean Reads. Reads Map to (-): Reads number mapped to the antisense chain and the percentage in Clean Reads].

Table S3. Percentage of exonic, intergenic, and intronic regions of mapped reads on the reference genome.

Sample	**Exon**	**Intergenic**	**Intron**
BJ	83.47%	6.43%	10.10%
F	78.75%	6.86%	14.57%
GZ	82.38%	6.04%	11.58%
KJ24-32Q	87.63%	7.26%	5.11%
LC	88.49%	6.46%	5.05%
P	76.56%	7.32%	16.12%
QG23-31	87.39%	7.38%	5.23%
QG35Q	87.08%	7.36%	5.56%
QS	80.10%	7.72%	12.18%
S	78.45%	7.36%	14.19%
SGT	85.92%	7.86%	6.22%
SJ-7-20Q	87.20%	7.45%	5.35%

TJ21-22Q-	87.32%	7.18%	5.50%
WJYY43Q	87.24%	7.49%	5.27%
X	82.70%	7.06%	10.24%
XJ25-11Q	86.90%	7.46%	5.64%
XN	87.29%	7.33%	5.38%
XQN	86.40%	7.66%	5.94%
YD44-45Q4	87.97%	6.79%	5.24%
YHT	83.68%	6.40%	9.92%
YQZ	81.62%	6.87%	11.51%
YS	86.48%	7.23%	6.29%
ZF	75.81%	7.45%	16.74%
ZG	77.09%	7.89%	15.02%

Table S4. SNP statistics detected in all samples.

Sample	SNP Number	Genic SNP	Intergenic SNP	Transition	Transversion	Heterozygosity
BJ	305,396	264,414	40,982	72.57%	27.43%	20.62%
F	494,560	433,053	61,507	72.18%	27.82%	21.65%
GZ	360,607	321,024	39,583	72.55%	27.45%	21.19%
KJ24-32Q	189,058	155,893	33,165	73.01%	26.99%	25.04%
LC	193,900	164,494	29,406	73.08%	26.92%	24.78%
P	495,289	440,056	55,233	72.12%	27.88%	21.50%
QG23-31	189,382	154,890	34,492	72.79%	27.21%	24.71%
QG35Q	209,565	174,205	35,360	73.22%	26.78%	23.95%
QS	339,545	295,807	43,738	72.11%	27.89%	20.31%
S	413,458	362,909	50,549	72.42%	27.58%	20.63%
SGT	258,726	209,218	49,508	72.48%	27.52%	23.95%
SJ-7-20Q	215,004	174,830	40,174	72.83%	27.17%	24.59%
TJ21-22Q-	191,806	158,908	32,898	72.92%	27.08%	24.44%
WJYY43Q	188,314	154,813	33,501	73.03%	26.97%	24.57%

X	304,751	266,582	38,169	72.54%	27.46%	21.09%
XJ25-11Q	213,327	176,274	37,053	72.98%	27.02%	24.22%
XN	205,645	166,926	38,719	72.75%	27.25%	24.66%
XQN	226,332	186,483	39,849	72.78%	27.22%	23.85%
YD44-45Q4	183,666	153,151	30,515	73.03%	26.97%	24.67%
YHT	316,166	276,746	39,420	72.70%	27.30%	20.82%
YQZ	360,544	315,887	44,657	72.28%	27.72%	20.71%
YS	223,159	187,640	35,519	72.86%	27.14%	23.50%
ZF	525,235	456,941	68,294	71.94%	28.06%	21.44%
ZG	479,652	418,661	60,991	72.17%	27.83%	21.69%

[Note: Samples: sample name; SNP Number: total numbers of SNPs; Genic SNP: total numbers of SNPs in the genic region; Intergenic SNP: total numbers of SNPs between genes; Transition: the percentage that the transition-type SNP accounts for all SNP loci's; Transversion: the percentage that the transversion-type SNP loci account for all SNP sites; Heterozygosity: the percentage that the heterozygous SNPs account for all SNPs].