

Table S1 Sample sequencing data statistics

Varieties	Clean_Reads	Clean_Base	Q30(%)	GC(%)
Zhongmai 175	1 013 423 192	303 651 869 238	93.61	46.46
Yili 053	1 098 471 243	329 150 128 306	93.72	47.66

Table S2 Statistical results of comparison between samples and reference genomes

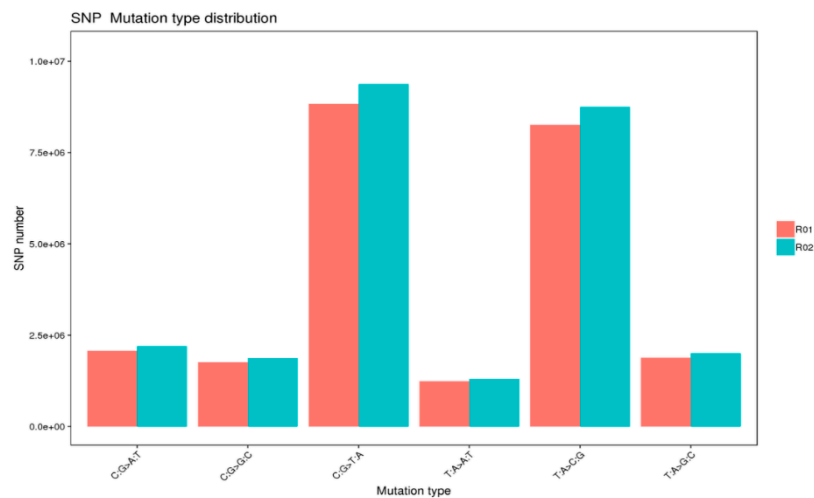
Varieties	Total_reads	Mapped(%)	Properly_mapped(%)
Zhongmai 175	2 026 846 384	99.37	96.18
Yili 053	2 196 942 486	99.67	96.33

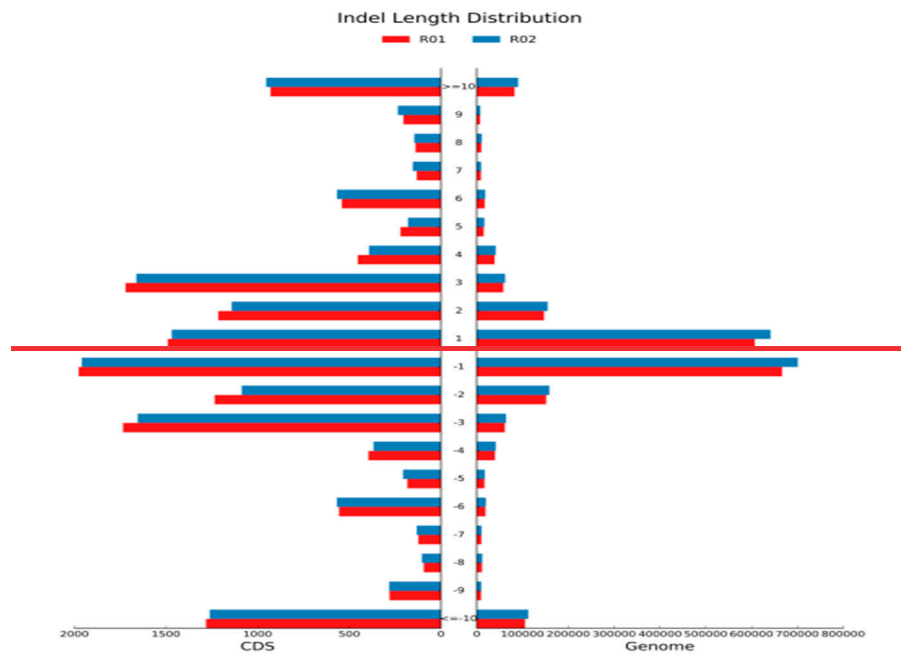
Table S3 Statistical results of detected SNPs

Varieties	SNPnumber	Transition	Transversion	Ti/Tv	Heterozygosity	Homozygosity	Het-ratio
Zhongmai 175	24085517	17103510	6982007	2.44	3927004	20158513	16.3%
Yili 053	25534555	18137285	7397270	2.45	4042195	21492360	15.83%

Table S4 The distribution of the InDel

Varieties	CDS-Insertion	CDS-Deletion	CDS-Homo	CDS-Het	CDS-Total	Ratio of Insertion	Ratio of Deletion
Zhongmai 175	7154	7925	7313	7766	15079	47.44%	52.56%
Yili 053	7012	7680	7389	7303	14692	47.73%	52.27%
Total	11050	12200	--	--	23250	-	-
Varieties	Genome-Insertion	Genome-Deletion	Genome-Homo	Genome-Het	Genome-Total	Ratio of Insertion	Ratio of Deletion
Zhongmai 175	1059702	1144272	1710302	493672	2203974	48.08%	51.92%
Yili 053	1119222	1199252	1811166	507308	2318474	48.27%	51.73%
Total	1566939	1707589	--	--	3274528	-	-

**Figure S1 Distribution of the SNP mutation type**



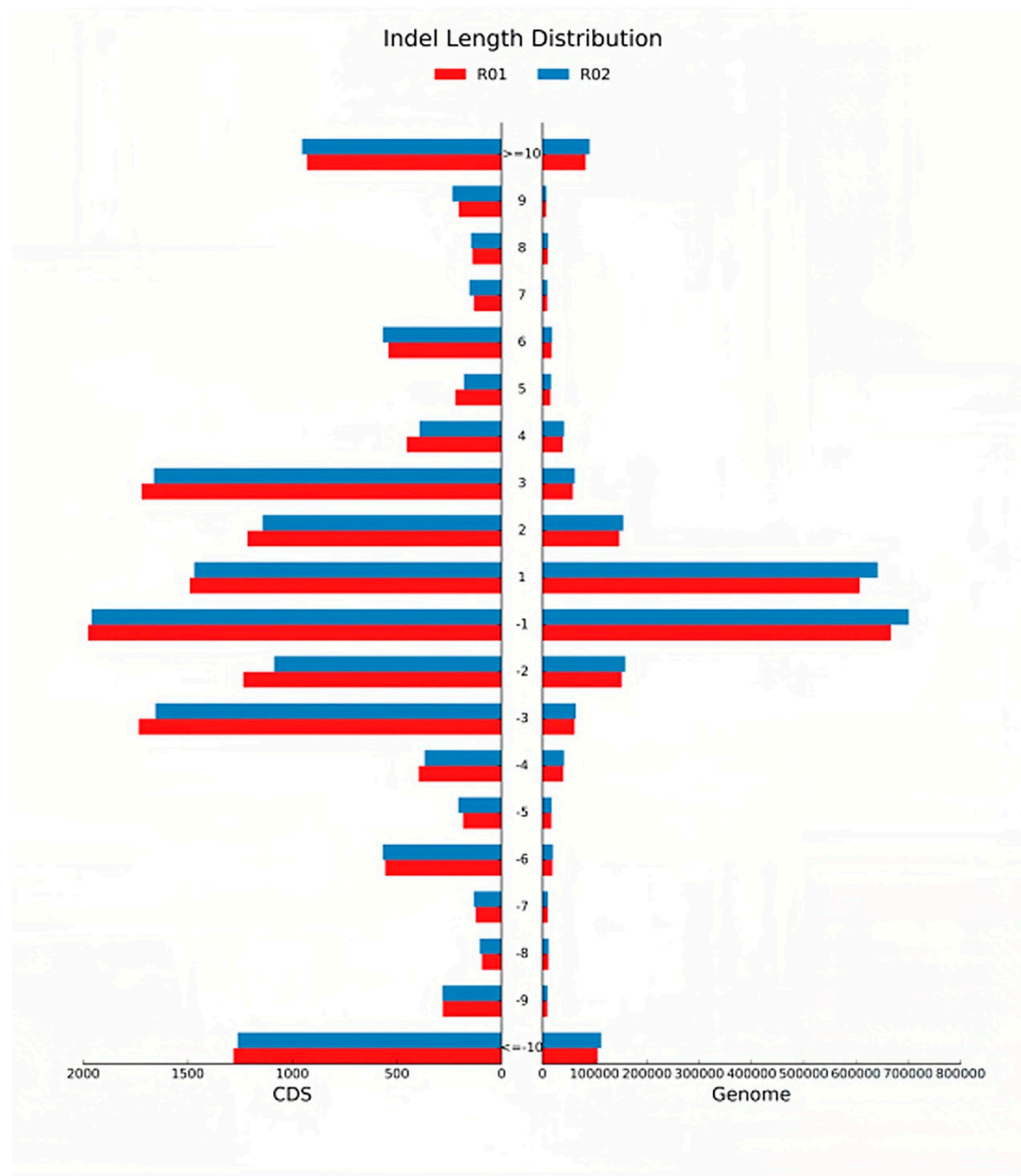
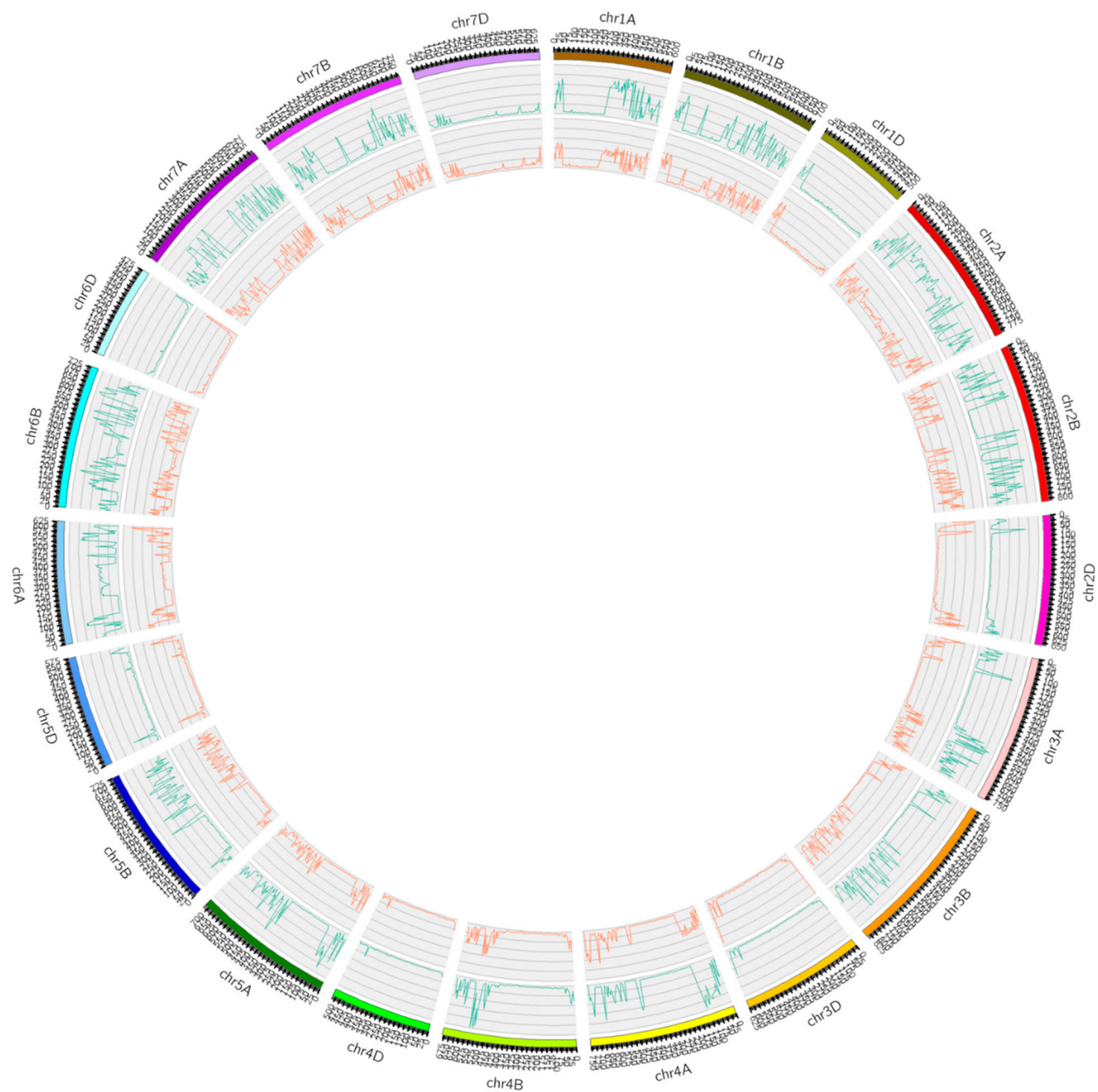
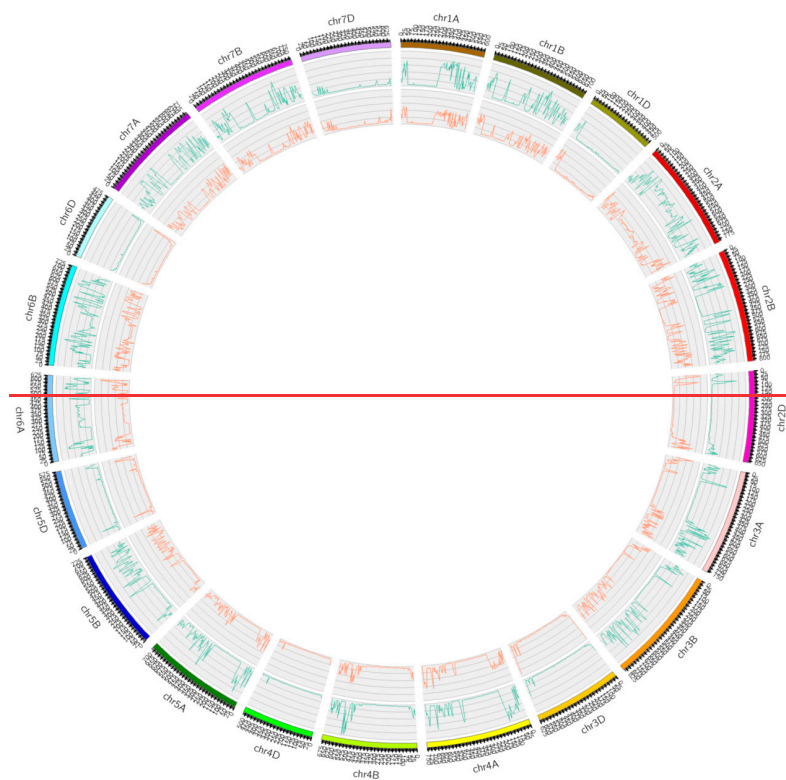


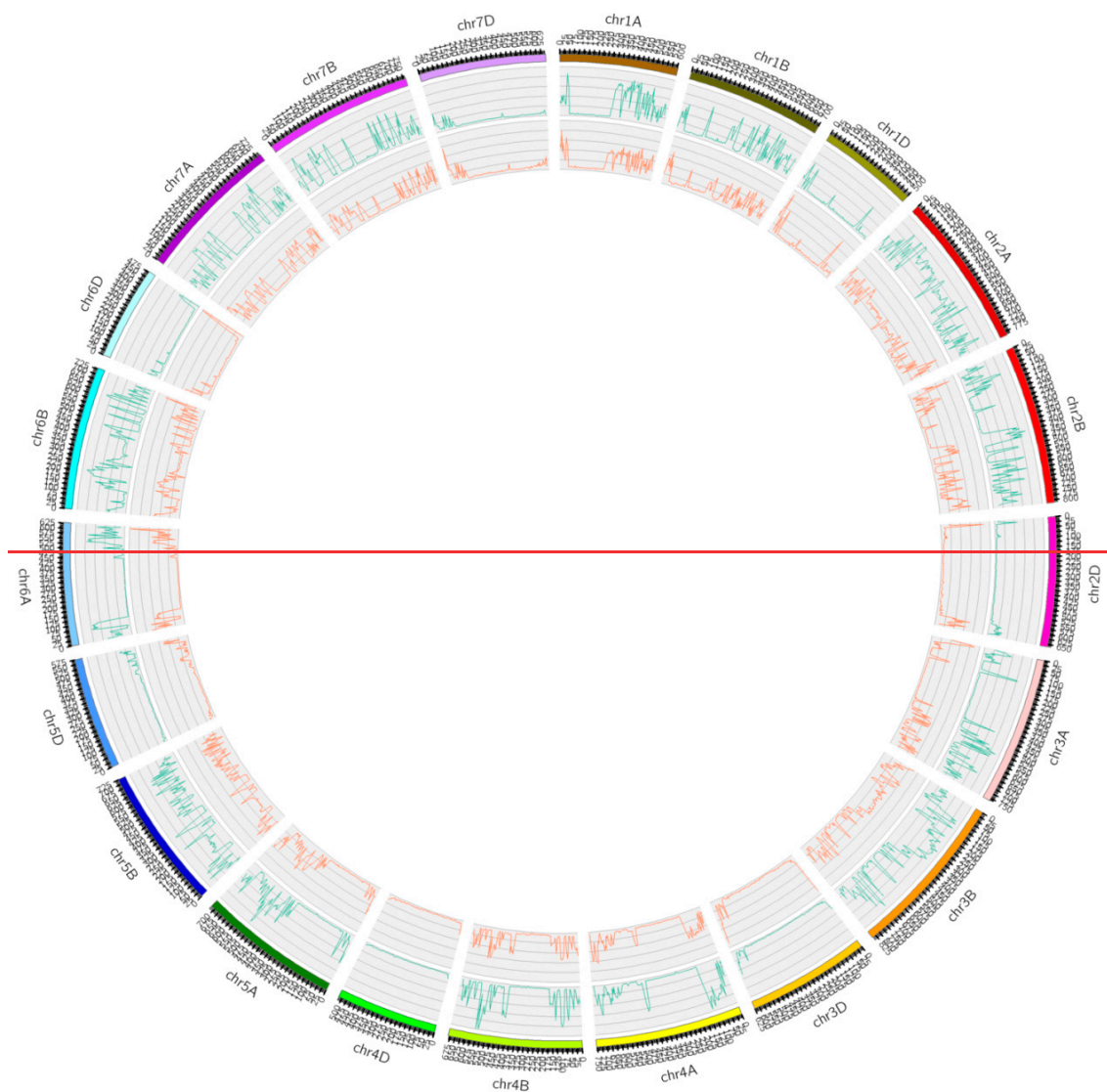
Figure S2 Distribution of the InDels type

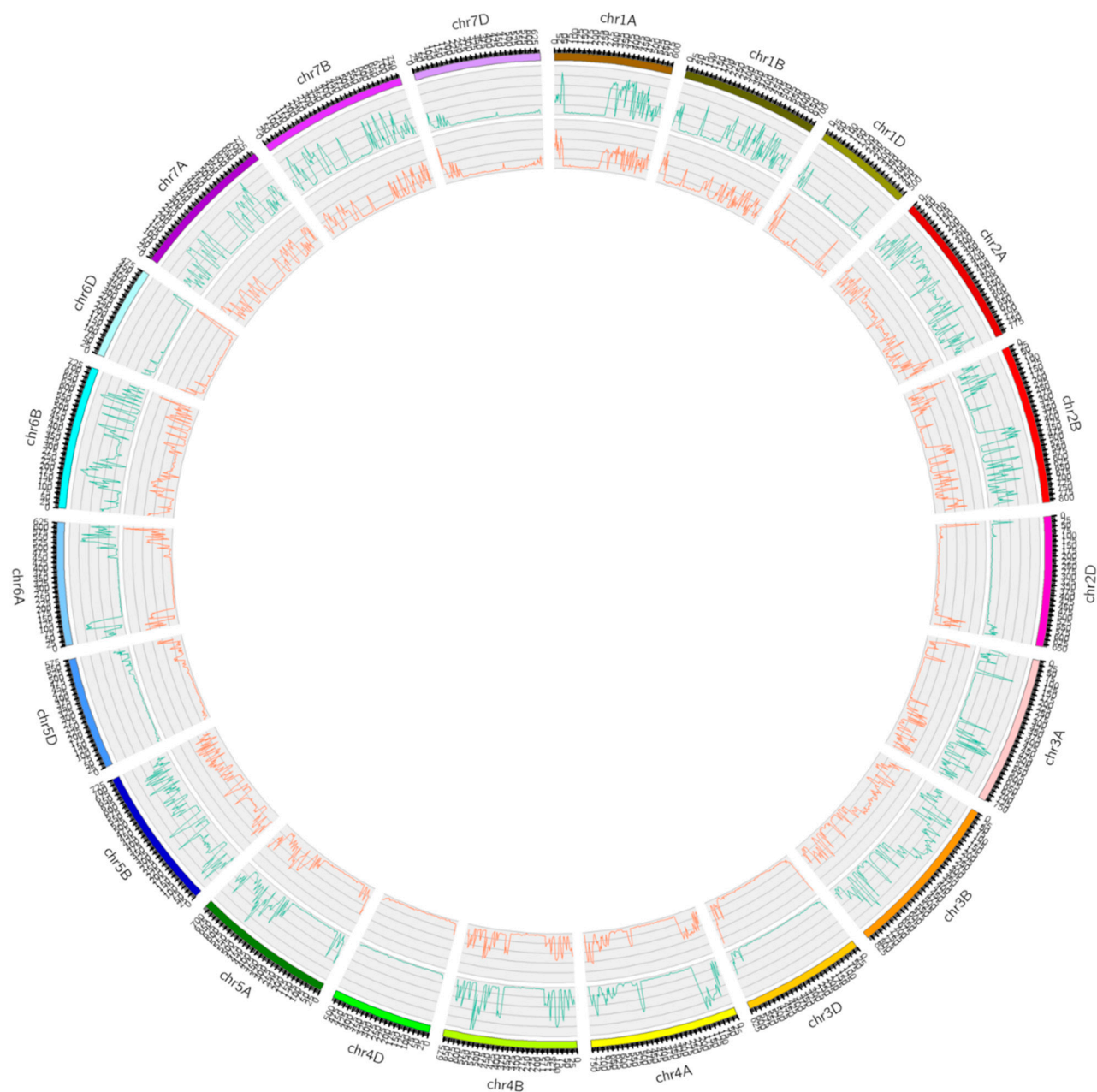
Note: The ordinate is the InDel length (within 10bp), greater than 0 is Insertion, less than 0 is Deletion, and the abscissa is the corresponding quantity.





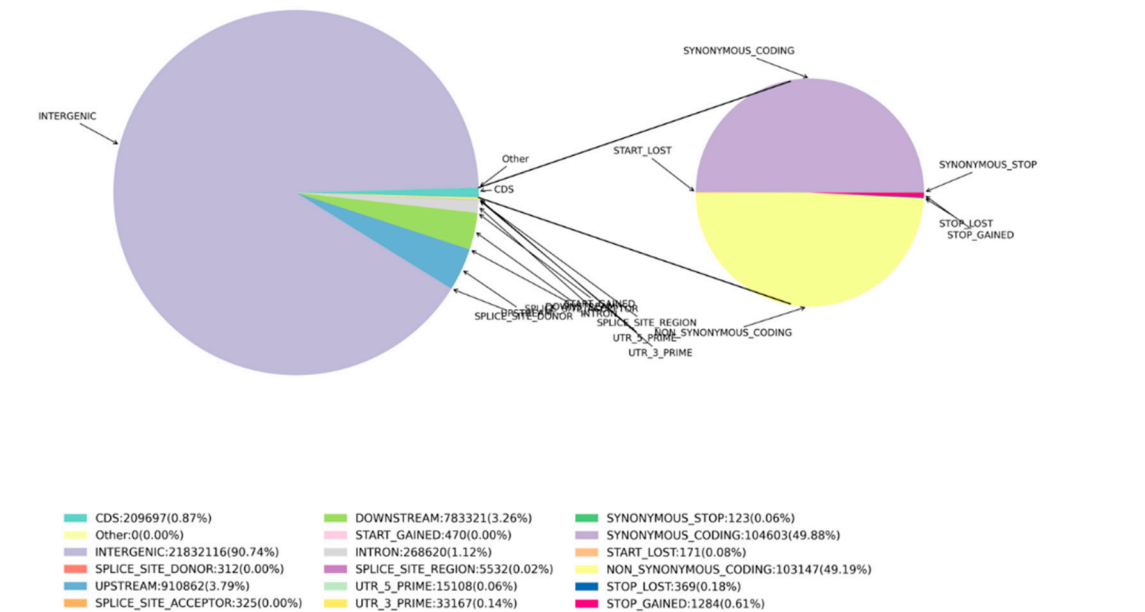
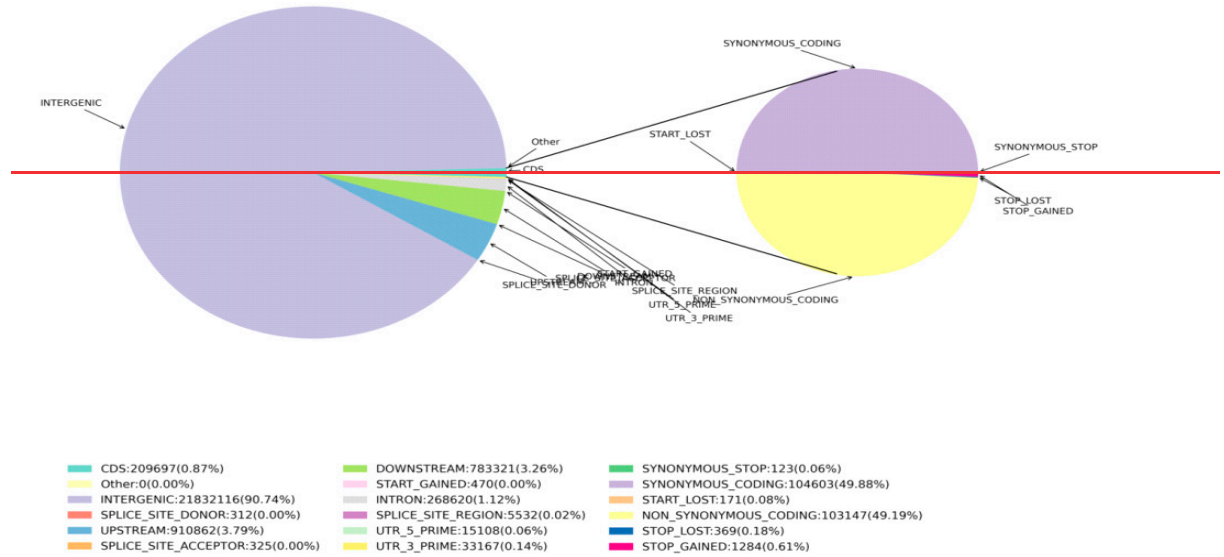
(a) SNP



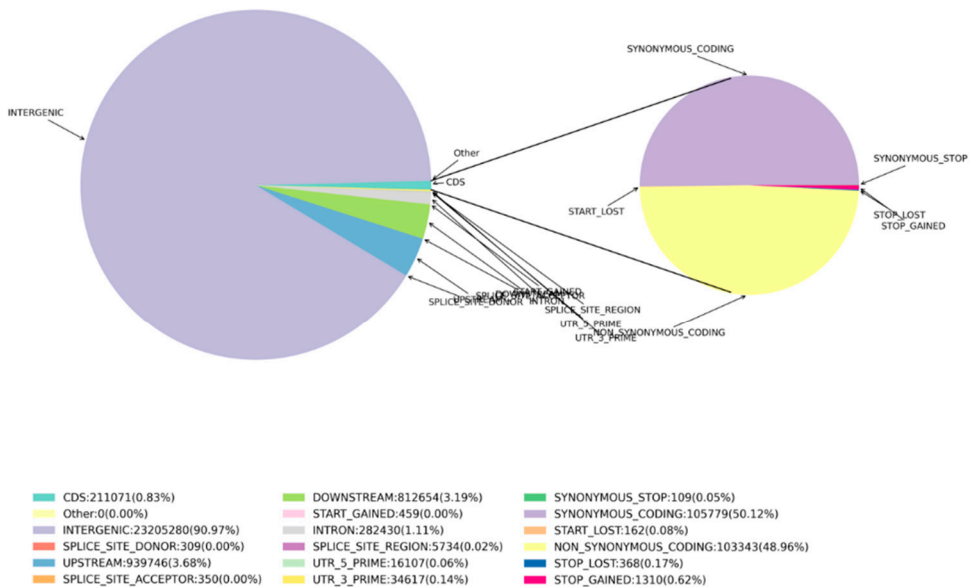
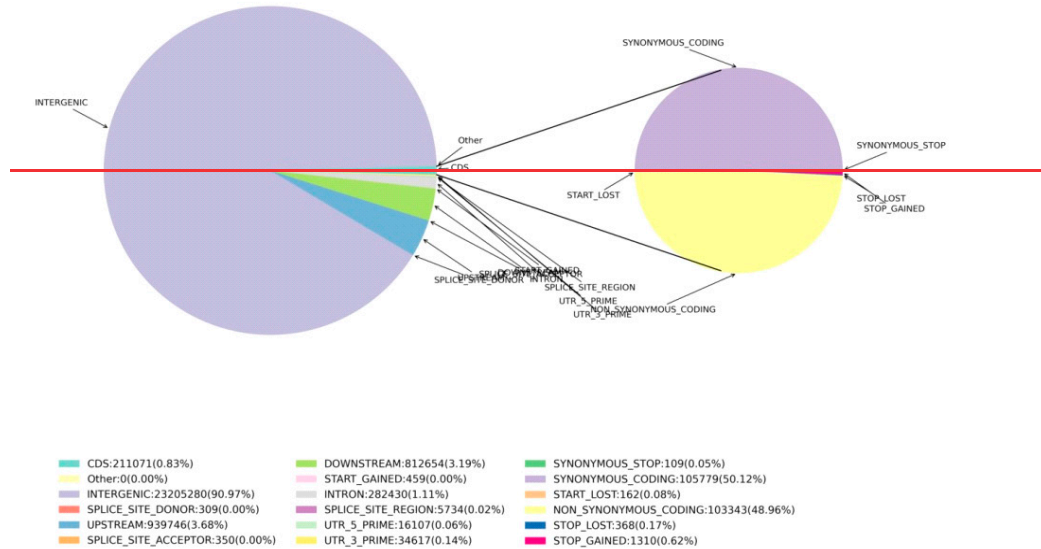


(b) InDel

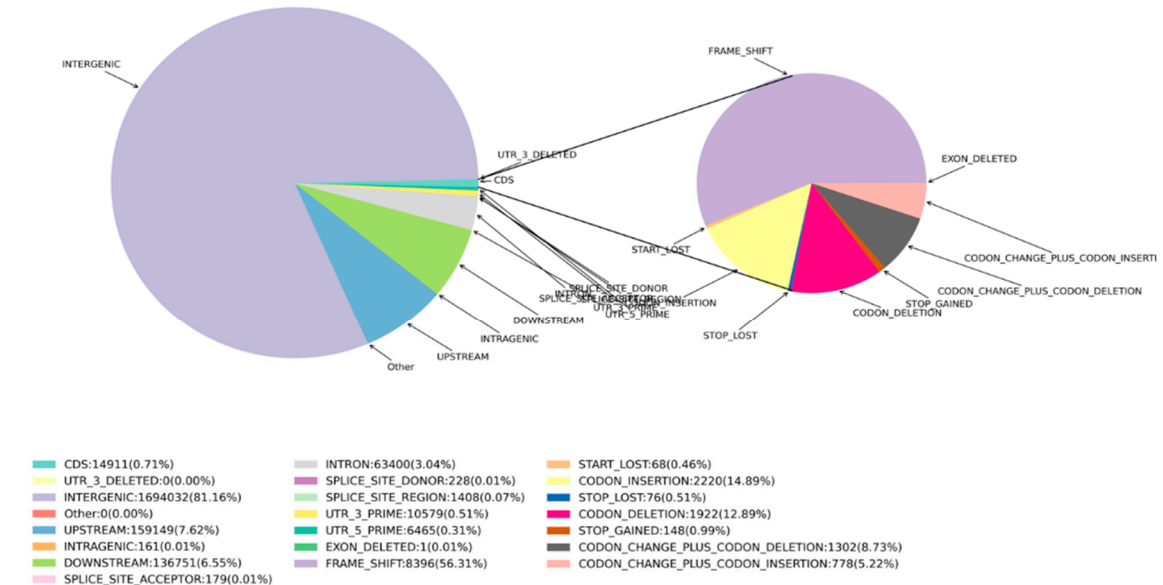
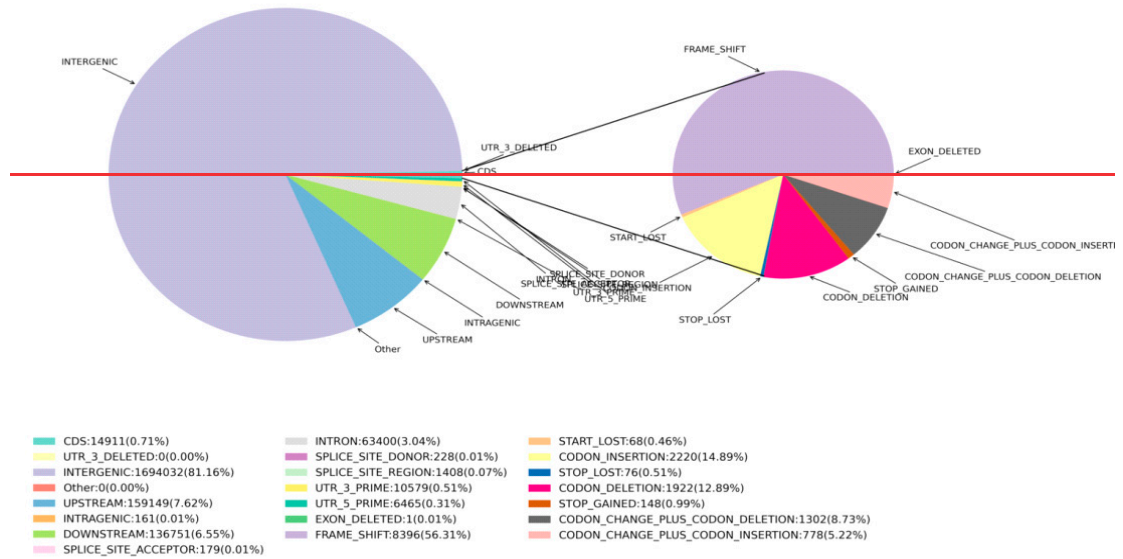
Figure S3 From outside to inside, the distribution of chromosome coordinates, SNP density distribution and InDel density distribution on the genome (unit: M).



(a) Zhongmai175-SNPs



(b) Yili35-SNPs



(c) Zhongmai175- InDels



(d) Yili35-InDels

Figure S4 The distribution of detected SNPs and InDels

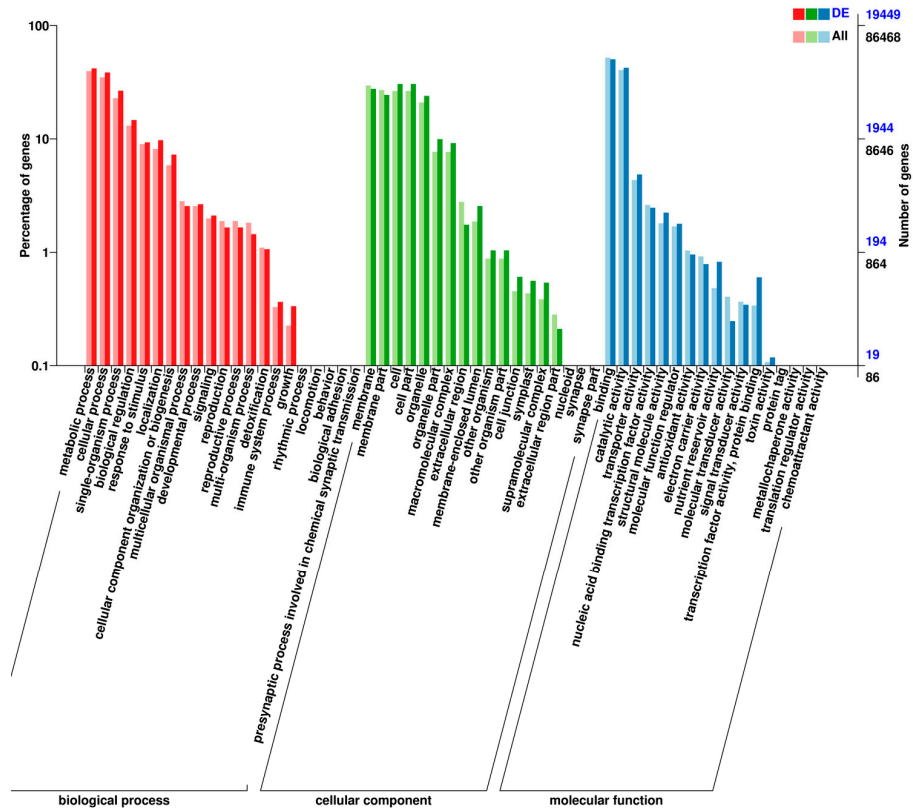
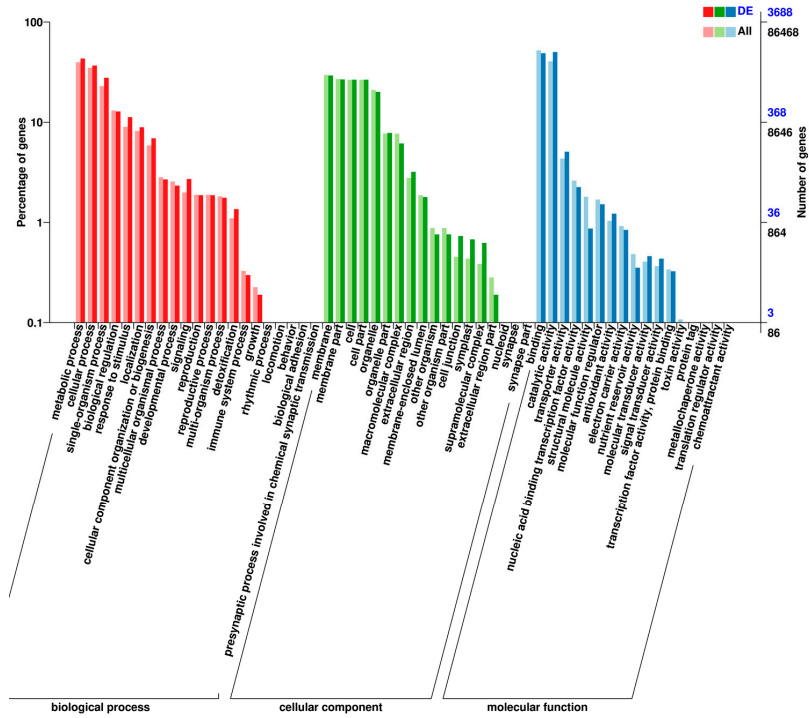
Table S5 Statistical of RNA sequencing data

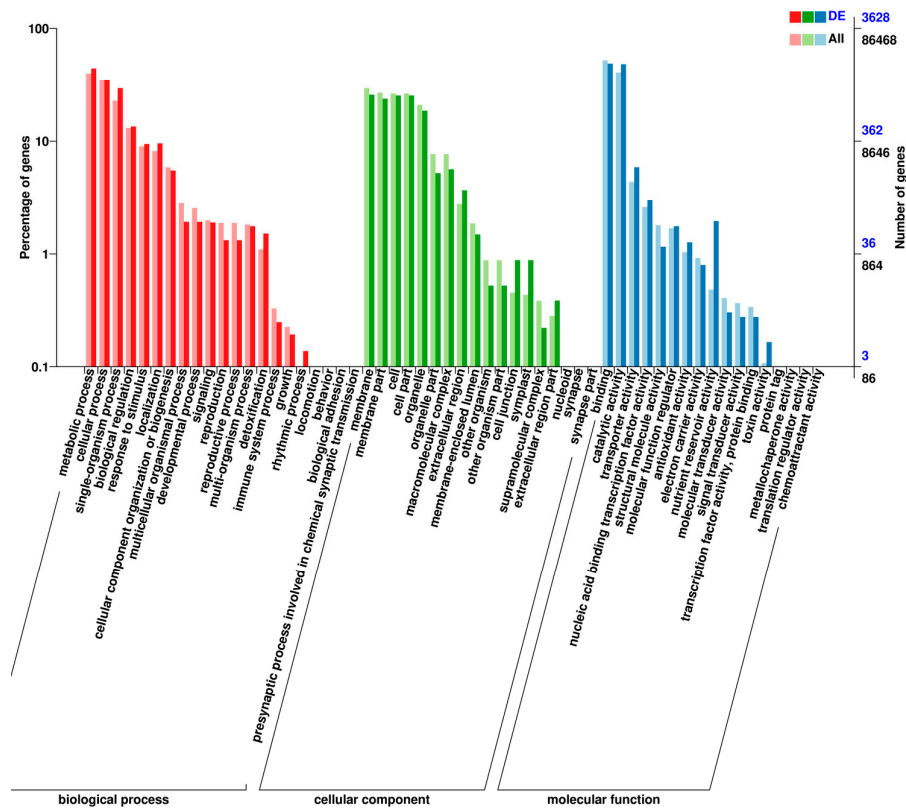
Name	Clean reads	Clean bases	GC Content (%)	%≥Q30 (%)
I-YLC1	33 846 470	10 118 821 246	55.69	95.46

I-YLC2	38 588 627	11 517 825 572	54.84	95.00
I-YLC3	37 958 897	11 343 101 536	54.37	95.01
I-YLI1	37 731 986	11 276 627 552	57.82	93.91
I-YLI2	35 408 404	10 561 674 364	58.70	93.97
I-YLI3	43 665 455	13 042 812 834	58.55	93.90
I-ZMC1	46 351 695	13 859 971 274	53.30	93.61
I-ZMC2	33 043 832	9 877 042 464	53.23	93.59
I-ZMC3	39 213 222	11 719 342 324	53.53	93.86
I-ZMI1	39 334 112	11 736 793 442	57.90	94.08
I-ZMI2	34 939 631	10 434 142 052	58.39	94.07
I-ZMI3	42 808 935	12 810 248 222	58.27	93.61
II-YLC1	37 424 109	11 172 643 120	51.80	91.54
II-YLC2	39 668 019	11 817 094 732	52.53	91.17
II-YLC3	43 770 044	13 052 803 514	51.85	91.92
II-YLI1	41 044 118	12 272 430 466	56.42	93.91
II-YLI2	41 626 954	12 447 001 058	56.32	93.99
II-YLI3	43 680 494	13 053 542 618	56.40	93.96
II-ZMC1	43 848 261	13 091 674 164	52.32	90.85
II-ZMC2	46 930 995	14 010 256 938	52.47	91.39
II-ZMC3	35 503 431	10 596 875 466	52.88	91.04
II-ZMI1	32 780 524	9 760 655 060	52.15	90.77
II-ZMI2	40 222 234	11 979 004 022	52.35	90.79
II-ZMI3	44 797 780	13 334 563 452	52.26	90.97
III-YLC1	41 024 047	12 249 838 096	57.04	93.24
III-YLC2	42 236 376	12 634 731 488	56.04	94.14
III-YLC3	36 526 906	10 892 077 864	56.40	93.28
III-YLI1	43 832 299	13 101 853 390	58.51	93.54
III-YLI2	43 363 058	12 976 495 304	58.83	93.85
III-YLI3	45 101 790	13 488 891 936	58.73	93.80
III-ZMC1	37 741 594	11 253 577 368	55.98	93.36
III-ZMC2	36 194 533	10 817 335 954	56.65	93.34
III-ZMC3	37 219 406	11 087 564 962	55.67	93.42
III-ZMI1	32 791 493	9 791 366 044	58.57	93.87
III-ZMI2	36 361 003	10 873 095 430	58.61	94.10
III-ZMI3	33 880 154	10 127 859 878	58.35	93.70

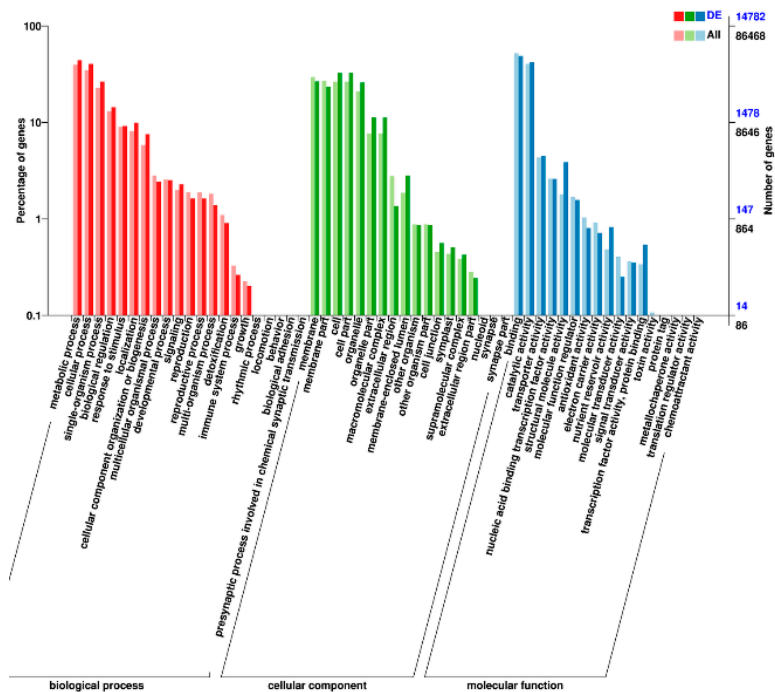
Table S6 Statistical of DEG in two varieties at different growth period

DEG Set	DEG Number	up-regulated	down-regulated
I-YLC1_I-YLC2_I-YLC3_vs_I-YLI1_I-YLI2_I-YLI3	3,930	1,148	2,782

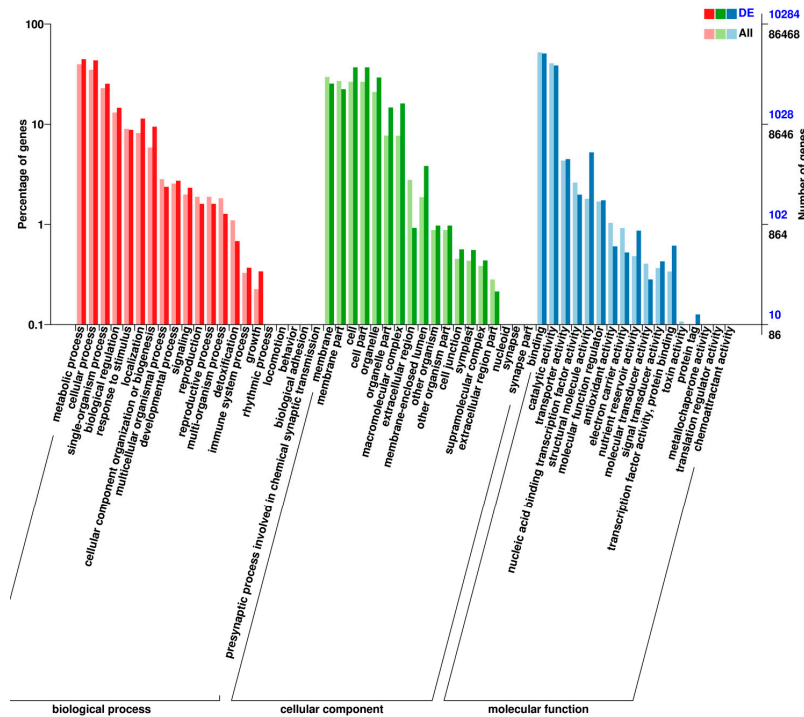




group4: ZMC vs II-ZMI;



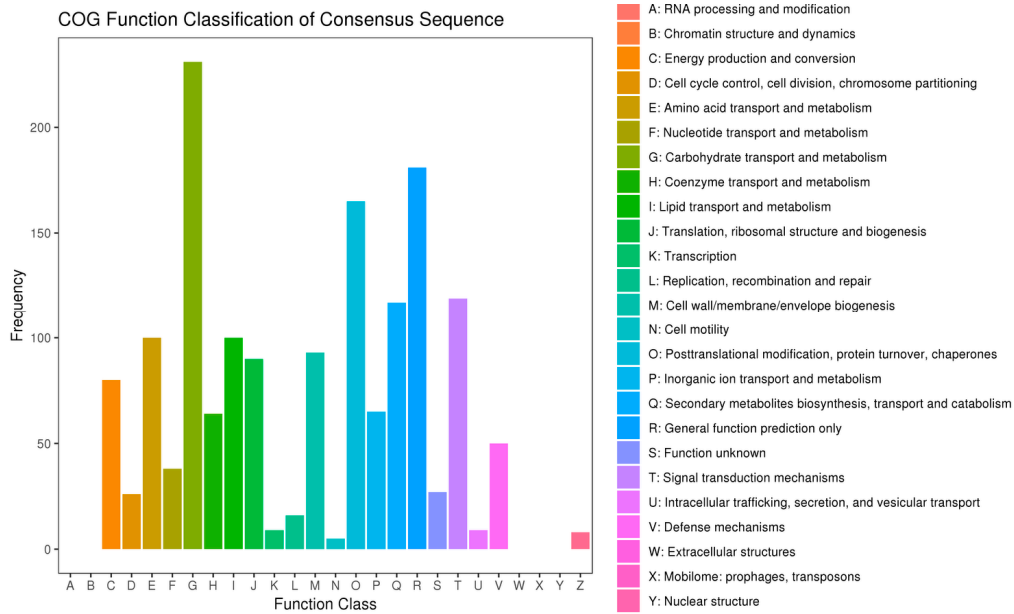
group5: III-YLC vs III-YLI;



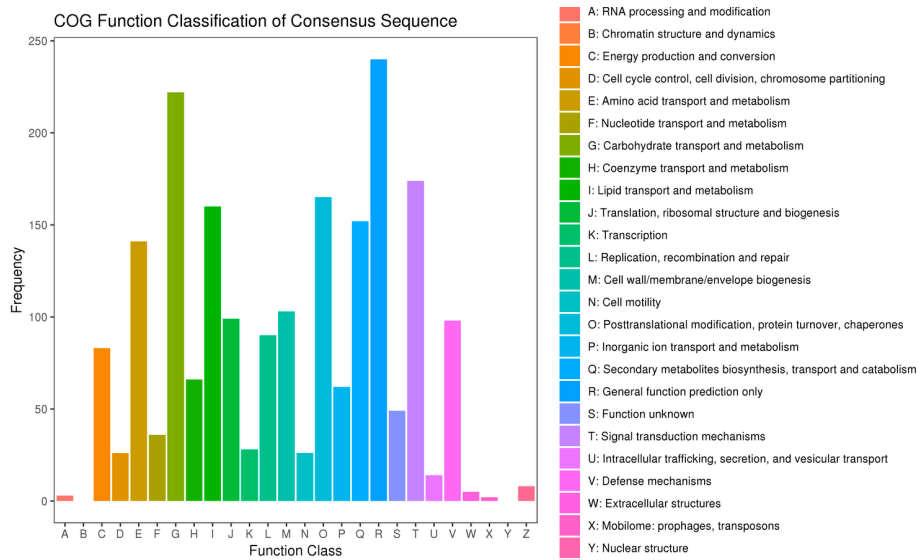
group6: III-ZMC vs III-ZMI

Figure S5 GO annotation of Zhongmai 175 and Yili 053

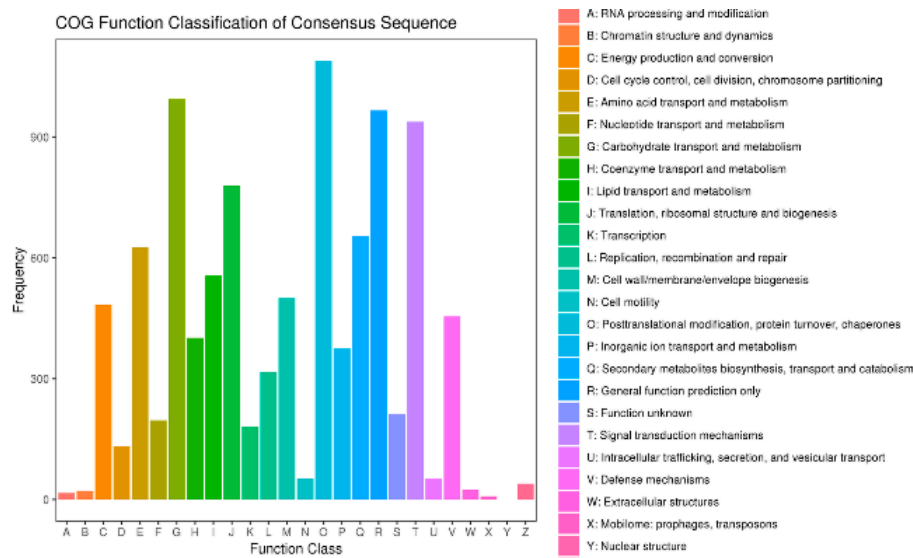
Note: The abscissa is the classification content of GO, the left side of the ordinate is the percentage of the number of genes, and the right side is the number of genes. group 1: I-YLC vs I-YLI; group2: I-ZMC vs I-ZMI; group3: II-YLC vs II-YLI; group4: ZMC vs II-ZMI; group5: III-YLC vs III-YLI; group6: III-ZMC vs III-ZMI



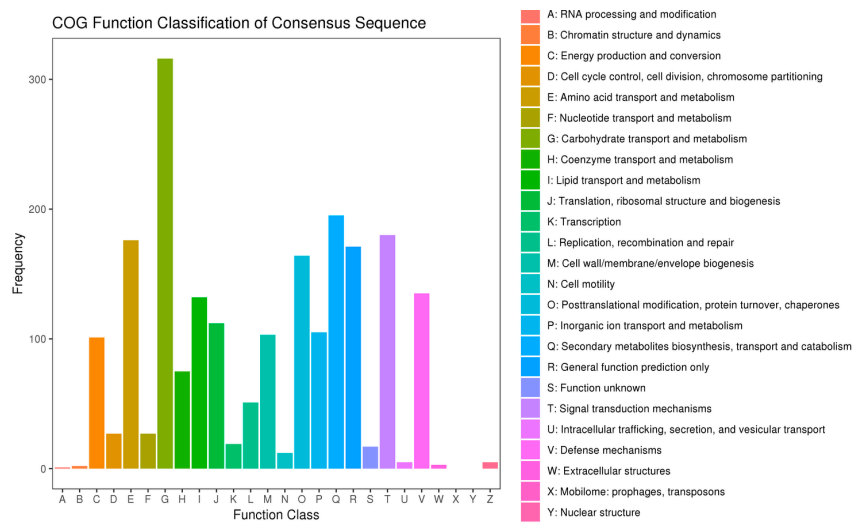
group 1: I-YLC vs I-YLI;

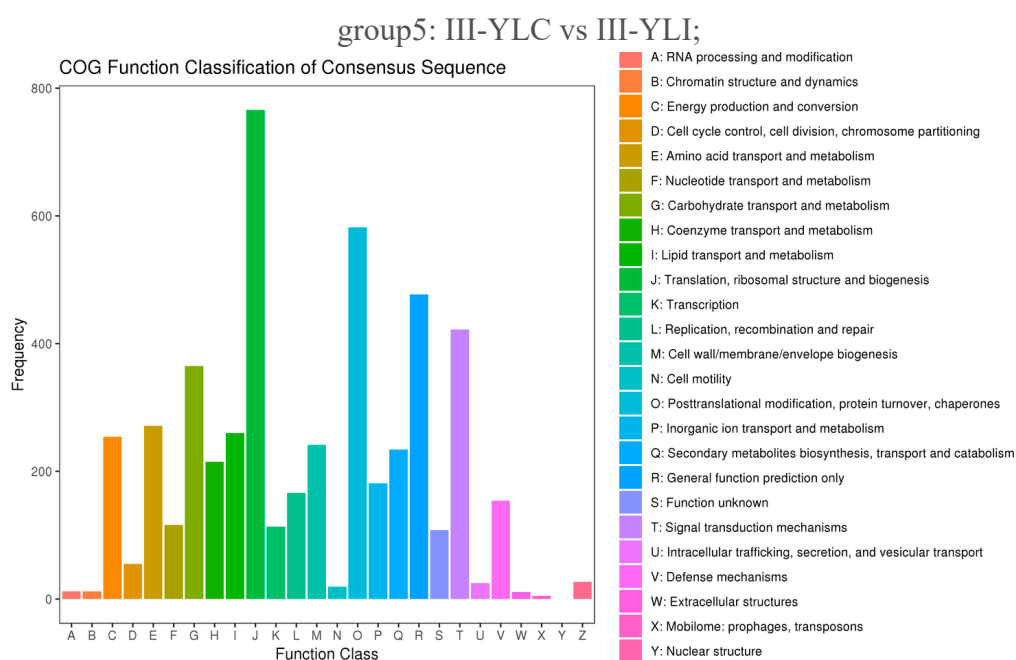
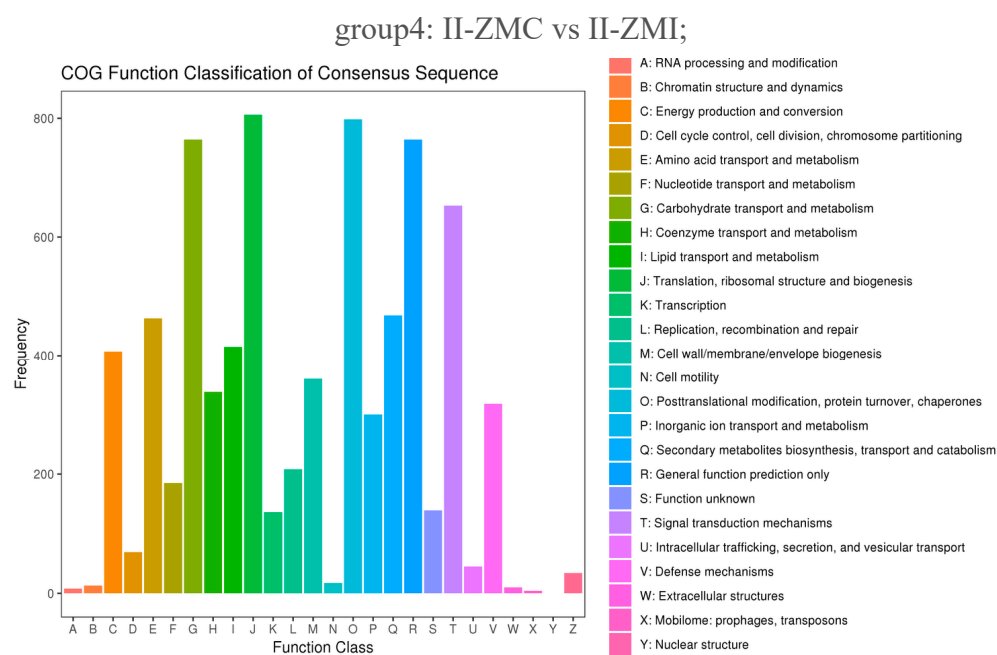


group2: I-ZMC vs I-ZMI;



group3: II-YLC vs II-YLI;





group6: III-ZMC vs III-ZMI

Figure S6 COG annotation of Zhongmai 175 and Yili 053

Note: The abscissa is the classification content of COG, and the ordinate is the number of genes. group 1: I-YLC vs I-YLI; group2: I-ZMC vs I-ZMI; group3: II-YLC vs II-YLI; group4: ZMC vs II-ZMI; group5: III-YLC vs III-YLI; group6: III-ZMC vs III-ZMI