

Table 1 Statistics of apple genome resequencing for each accession

Sample name	Clean reads	Clean bases	Q20 ratio (%)	GC ratio (%)	Coverage
C18-01B	82 285 164	12 275 896 018	96.81	38.40	17.05
C18-02A	89 077 308	13 313 277 436	97.01	38.59	18.49
C18-03A	83 072 050	12 394 531 092	97.09	39.12	17.21
C18-04A	97 305 218	14 527 586 044	96.95	38.58	20.18
C18-05A	86 562 736	12 940 574 192	97.20	38.27	17.97
C18-06A	80 125 972	11 965 621 824	96.95	38.08	16.62
C18-07A	74 530 532	11 122 786 992	97.06	38.96	15.45
C18-08A	75 995 538	11 356 852 292	97.21	38.62	15.77
C18-09A	90 068 930	13 407 382 642	96.73	39.20	18.62
C18-10A	101 224 890	15 134 111 712	97.17	38.73	21.02
C18-11B	69 321 342	10 326 757 324	96.82	38.29	14.34
C18-12A	100 502 502	15 007 629 504	97.05	38.33	20.84
C18-13-1A	71 054 910	10 597 863 906	96.82	38.84	14.72
C18-13-2B	81 541 908	12 157 333 396	96.49	38.36	16.89
C18-14B	68 947 114	10 293 832 588	96.67	38.84	14.30
C18-15A	76 776 466	11 445 569 550	97.06	38.26	15.90
C18-16A	78 836 884	11 769 458 430	96.76	38.36	15.95
C18-17A	63 602 864	9 494 133 904	97.12	38.35	13.19
C18-18A	77 680 304	11 605 708 802	96.72	38.31	16.12
C18-19B	54 867 846	8 184 033 800	97.30	38.48	11.37
C18-20A	85 924 614	12 849 242 938	97.07	38.37	17.85
C18-21A	81 690 936	12 211 575 458	97.07	39.10	16.96
C18-22A	92 507 878	13 784 235 218	96.65	38.42	19.14
C18-23B	76 286 322	11 396 088 188	97.32	38.46	15.83
C18-24B	82 677 084	12 345 285 852	96.41	38.34	17.15
C18-25B	85 568 414	12 765 677 658	97.03	38.26	17.73
C18-26B	74 209 450	11 075 213 404	96.99	38.54	15.38
C18-27B	78 213 462	11 677 414 082	96.92	38.56	16.22
C18-28B	62 762 662	9 363 987 448	96.90	38.49	13.01
C18-29B	61 273 994	9 125 369 346	96.72	38.49	12.67
C18-30B	51 288 314	7 650 121 178	96.49	39.08	10.63