Supplement：

Table S1. The number of different variation types among the chromosomes

CHR	Summary	Copy number allele									INS	INV
		0	0/2	0/2/3	0/2/3/4	2345	2	23	234	*		
1	4671	2433	148	5	1	0	344	18	1	4	372	1345
2	4894	2728	203	11	0	0	399	2	0	0	1488	63
3	4180	2322	153	9	0	0	383	1	1	1	1252	58
4	4068	2173	162	8	1	0	392	7	0	0	1271	54
5	3811	2029	167	3	2	3	414	3	1	1	1137	51
6	3622	1955	159	2	0	0	336	4	4	1	1108	53
7	3658	2031	190	5	1	0	396	4	3	0	967	61
8	3151	1758	155	1	3	0	309	7	0	1	864	53
9	2623	1478	168	9	1	0	228	7	0	0	690	42
10	2755	1473	129	7	1	0	297	8	5	0	794	41
11	2912	1614	129	3	2	2	297	4	0	1	825	35
12	2898	1548	114	5	2	0	334	10	0	0	843	42
13	2138	1081	96	2	0	1	232	1	0	0	695	30
14	1829	1001	64	2	0	0	186	4	1	2	546	23
15	1612	862	78	1	0	7	161	1	0	7	483	16
16	1806	1103	121	5	8	6	211	4	3	4	325	16
17	1680	995	85	1	0	0	181	6	1	0	389	22
18	1720	980	101	0	3	0	155	0	0	0	465	16
19	1437	973	102	2	0	0	136	3	0	0	212	9
20	1290	732	55	1	0	0	151	0	0	0	334	17
21	761	415	22	0	2	0	67	3	0	0	241	11
22	732	466	41	4	7	1	76	4	1	0	127	5
X	1803	974	326	5	0	3	28	0	0	2	465	
Sum	60051	33124	2968	91	34	23	5713	101	21	24	17956	

* represents the value of the copy number allele is larger than 4

Table S2. The performance of different copy number allele on the same framework

	Random Forest					
	Accuracy	Precision	Recall	F-Measure	ROC Area	PRC Area
CN0	0.833	0.852	0.833	0.808	**0.975**	0.920
CN012	0.8841	0.892	0.884	0.885	0.965	0.889
CN02	**0.9003**	**0.900**	**0.900**	**0.947**	0.914	**0.924**
CN023	0.5897	0.590	0.590	0.742	0.675	0.680
CN0234	0.7273	0.710	0.727	0.830	0.575	0.621
CN4+	0.5455	0.624	0.545	0.484	0.742	0.650
	Multilayer Perceptron					
	Accuracy	Precision	Recall	F-Measure	ROC Area	PRC Area
CN0	**0.841**	**0.842**	**0.841**	**0.840**	**0.928**	**0.826**
CN012	0.6667	0.667	0.667	0.800	0.298	0.452
CN02	0.7563	0.688	0.756	0.797	0.840	0.762
CN023	0.7395	0.671	0.739	0.774	0.848	0.768
CN0234	0.7576	0.733	0.758	0.545	0.522	0.583
CN4+	0.2121	0.398	0.212	0.150	0.526	0.561
	SVM					
	Accuracy	Precision	Recall	F-Measure	ROC Area	PRC Area
CN0	**0.855**	**0.850**	**0.855**	**0.851**	**0.908**	**0.790**
CN012	0.820	0.743	0.819	0.577	0.840	0.760
CN02	0.748	0.671	0.748	0.786	0.790	0.650
CN023	0.641	0.622	0.641	0.286	0.563	0.507
CN0234	0.758	0.733	0.758	0.846	0.636	0.625
CN4+	0.515	0.550	0.515	0.498	0.617	0.433
	Naive Bayes					
	Accuracy	Precision	Recall	F-Measure	ROC Area	PRC Area
CN0	**0.870**	**0.878**	**0.870**	**0.872**	**0.955**	**0.869**
CN012	0.752	0.740	0.750	0.577	0.806	0.828
CN02	0.530	0.757	0.529	0.474	0.843	0.752
CN023	0.308	0.570	0.308	0.322	0.699	0.607
CN0234	0.212	0.398	0.212	0.150	0.526	0.561
CN4+	0.364	0.413	0.364	0.325	0.641	0.506
	Decision Tree					
	Accuracy	Precision	Recall	F-Measure	ROC Area	PRC Area
CN0	**0.790**	0.597	**0.790**	0.748	**0.905**	**0.740**
CN012	0.789	0.570	**0.790**	**0.752**	0.864	0.581
CN02	0.622	0.567	0.622	0.594	0.647	0.518
CN023	0.744	0.611	0.783	0.733	0.639	0.584
CN0234	0.697	**0.716**	0.697	0.607	0.401	0.503
CN4+	0.394	0.302	0.394	0.330	0.486	0.345

Table S3. The performance of different copy number allele on the same framework

Feature Importance	AC	AF	NS	AN	EAS_AF	EUR_AF	AFR_AF	AMR_AF	SAS_AF
Data 1	0.15	0.15	0.00	0.00	0.11	0.16	0.15	0.15	0.00
Data 2	0.18	0.00	0.00	0.16	0.15	0.10	0.18	0.00	0.07
Data 3	0.18	0.00	0.05	0.16	0.15	0.10	0.18	0.00	0.00
Data 4	0.16	0.16	0.00	0.00	0.10	0.24	0.16	0.16	0.00
Data 5	0.18	0.00	0.00	0.16	0.15	0.10	0.18	0.00	0.10

Precision：Precision=TP/(TP+FP)
Recall：Recall=TP/(TP+FN)
F-measure：F−measure=2×Precision×Recall/(Precision+Recall)
Accuracy：Accuracy=(TP+TN)/(TP+TN+FP+FN)

$$AUC = \frac{\sum_{ie\ positiveClass} rank_i - \frac{M(1+M)}{2}}{M \times N}$$