

Table 1 .The similarity values of ancestral genomes in the first simulated data

		50 genes	60 genes	70 genes	80 genes	90 genes	100 genes	110 genes	120 genes	130 genes	140 genes	150 genes	mean
3 leaves	RAGPM	0.827	0.697	0.735	0.678	0.764	0.723	0.722	0.685	0.701	0.861	0.712	73.68%
	PMAG+	0.580	0.661	0.792	0.71	0.683	0.719	0.704	0.661	0.764	0.710	0.688	69.75%
	ProCars	0.715	0.72	0.765	0.74	0.743	0.714	0.804	0.714	0.563	0.785	0.720	72.57%
	inferCars	0.651	0.683	0.727	0.746	0.804	0.774	0.748	0.702	0.732	0.733	0.697	72.70%
4 leaves	RAGPM	0.729	0.731	0.661	0.697	0.721	0.742	0.695	0.746	0.808	0.728	0.755	72.85%
	PMAG+	0.665	0.609	0.653	0.761	0.691	0.715	0.677	0.742	0.696	0.701	0.736	69.51%
	ProCars	0.806	0.779	0.704	0.631	0.68	0.678	0.645	0.608	0.714	0.638	0.745	69.35%
	inferCars	0.714	0.715	0.638	0.701	0.71	0.774	0.734	0.741	0.732	0.736	0.728	72.03%
5 leaves	RAGPM	0.711	0.667	0.665	0.618	0.681	0.770	0.707	0.733	0.747	0.853	0.758	71.91%
	PMAG+	0.619	0.632	0.634	0.692	0.686	0.675	0.695	0.751	0.764	0.769	0.831	70.44%
	ProCars	0.834	0.658	0.641	0.684	0.647	0.736	0.639	0.635	0.748	0.755	0.769	70.42%
	inferCars	0.709	0.659	0.598	0.76	0.745	0.627	0.731	0.651	0.724	0.769	0.778	70.46%
6 leaves	RAGPM	0.623	0.678	0.694	0.748	0.641	0.704	0.646	0.719	0.752	0.762	0.781	70.44%
	PMAG+	0.592	0.618	0.611	0.639	0.665	0.733	0.673	0.745	0.680	0.688	0.781	67.50%
	ProCars	0.766	0.579	0.68	0.61	0.641	0.784	0.646	0.782	0.653	0.662	0.785	68.98%
	inferCars	0.679	0.716	0.647	0.639	0.669	0.782	0.757	0.547	0.679	0.688	0.797	69.09%
7 leaves	RAGPM	0.675	0.676	0.595	0.727	0.687	0.682	0.773	0.723	0.762	0.712	0.680	69.93%
	PMAG+	0.62	0.694	0.714	0.71	0.659	0.647	0.693	0.738	0.588	0.788	0.659	68.27%
	ProCars	0.646	0.672	0.693	0.687	0.672	0.708	0.669	0.721	0.613	0.732	0.701	68.31%
	inferCars	0.721	0.696	0.637	0.676	0.698	0.644	0.709	0.685	0.452	0.761	0.685	66.95%
8 leaves	RAGPM	0.684	0.642	0.575	0.599	0.583	0.670	0.629	0.686	0.651	0.623	0.639	63.46%
	PMAG+	0.552	0.582	0.563	0.635	0.624	0.618	0.646	0.640	0.674	0.641	0.700	62.50%
	ProCars	0.564	0.54	0.536	0.622	0.682	0.660	0.623	0.577	0.632	0.709	0.663	61.89%
	inferCars	0.588	0.695	0.693	0.647	0.556	0.596	0.617	0.608	0.580	0.666	0.589	62.14%
9 leaves	RAGPM	0.619	0.657	0.667	0.572	0.618	0.644	0.668	0.633	0.645	0.645	0.543	62.83%
	PMAG+	0.615	0.618	0.696	0.628	0.646	0.600	0.587	0.555	0.568	0.572	0.574	60.54%

	ProCars	0.669	0.682	0.507	0.66	0.643	0.575	0.549	0.660	0.576	0.651	0.586	61.44%
	inferCars	0.683	0.631	0.628	0.68	0.543	0.539	0.613	0.662	0.570	0.563	0.593	60.95%
10 leaves	RAGPM	0.682	0.515	0.675	0.603	0.642	0.621	0.652	0.578	0.675	0.627	0.617	62.61%
	PMAG+	0.619	0.559	0.592	0.647	0.554	0.630	0.639	0.596	0.604	0.526	0.540	59.15%
	ProCars	0.648	0.612	0.642	0.626	0.613	0.612	0.608	0.515	0.501	0.627	0.567	59.74%
	inferCars	0.743	0.567	0.486	0.456	0.623	0.623	0.529	0.563	0.647	0.707	0.726	60.64%

Table 2. Table 2 The similarity values of ancestral genomes in the second simulated data

Num of leaf	Method	2-chromosomes	3-chromosomes	4-chromosomes	5-chromosomes	6-chromosomes	mean
3 leaves	RAGPM	0.677	0.606	0.489	0.460	0.451	53.66%
	PMAG+	0.673	0.547	0.462	0.532	0.403	52.34%
	ProCars	0.586	0.526	0.479	0.512	0.495	51.96%
	inferCars	0.600	0.550	0.509	0.531	0.476	53.32%
4 leaves	RAGPM	0.624	0.532	0.581	0.494	0.432	53.26%
	PMAG+	0.622	0.539	0.588	0.405	0.432	51.72%
	ProCars	0.591	0.447	0.492	0.507	0.547	51.68%
	inferCars	0.652	0.533	0.536	0.485	0.395	52.02%
5 leaves	RAGPM	0.646	0.559	0.557	0.470	0.415	52.94%
	PMAG+	0.311	0.451	0.549	0.559	0.611	49.62%
	ProCars	0.316	0.455	0.546	0.561	0.607	49.70%
	inferCars	0.603	0.569	0.436	0.420	0.454	49.64%
6 leaves	RAGPM	0.591	0.534	0.594	0.413	0.391	50.46%
	PMAG+	0.568	0.523	0.496	0.410	0.388	47.70%
	ProCars	0.571	0.424	0.488	0.405	0.496	47.68%
	inferCars	0.458	0.573	0.436	0.461	0.467	47.90%
7 leaves	RAGPM	0.572	0.559	0.482	0.492	0.420	50.50%
	PMAG+	0.561	0.442	0.478	0.503	0.424	48.16%

	ProCars	0.472	0.451	0.578	0.516	0.432	48.98%
	inferCars	0.517	0.502	0.476	0.498	0.408	48.02%
8 leaves	RAGPM	0.475	0.533	0.534	0.471	0.483	49.92%
	PMAG+	0.477	0.501	0.419	0.462	0.486	46.90%
	ProCars	0.542	0.494	0.487	0.431	0.486	48.80%
	inferCars	0.525	0.474	0.490	0.516	0.432	48.74%
9 leaves	RAGPM	0.251	0.548	0.593	0.562	0.524	49.56%
	PMAG+	0.176	0.536	0.487	0.617	0.536	47.04%
	ProCars	0.167	0.536	0.591	0.504	0.614	48.24%
	inferCars	0.418	0.484	0.504	0.427	0.430	45.26%
10 leaves	RAGPM	0.564	0.482	0.444	0.429	0.406	46.50%
	PMAG+	0.422	0.490	0.440	0.440	0.391	43.66%
	ProCars	0.421	0.491	0.445	0.447	0.501	46.10%
	inferCars	0.449	0.424	0.518	0.433	0.442	45.32%

Table 3. The loss rates of ancestral genomes in the second simulate data

	3 leaves	4 leaves	5 leaves	6 leaves	7 leaves	8 leaves	9 leaves	10 leaves	mean
RAGPM	1.10%	1.31%	1.55%	1.56%	1.83%	1.85%	2.07%	2.42%	1.71%
PMAG+	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
ProCars	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
inferCars	1.63%	1.65%	1.86%	1.51%	1.78%	1.96%	2.30%	2.51%	1.90%

Table 4. Table 4 The average of the rate of interaction for five ancestors

HC				MR				HCR				HCRMR				HCRMRD			
r	InferCars	PMAG+	Procars	r	InferCars	PMAG+	Procars	r	InferCars	PMAG+	Procars	r	InferCars	PMAG+	Procars	r	InferCars	PMAG+	Procars
RAGPM	90.70%	80.90%	91%	RAGPM	53.70%	84.40%	83%	RAGPM	66.70%	76.70%	77%	RAGPM	69.02%	59.63%	59%	RAGPM	41.32%	56.40%	39%
InfertCars		87.10%	98.30%	InfertCars		53.90%	54.60%	InfertCars		79.80%	81.50%	InfertCars		80.54%	79.98%	InfertCars		45.53%	33.83%
PMAG+			87.90%	PMAG+			92.60%	PMAG+			96.20%	PMAG+			91.94%	PMAG+			67.05%

