Supplementary Table 1

	segments (10 runs)	avg. length (cM)	avg. length (SNPs)
Trio-phasing	4	3.60	1184.5
Singleton-phasing	5	3.69	1238.4

Supplementary Table 2

	AJ	CEU	CHB
CEU	0.02		
CHB	0.12	0.11	
YRI	0.15	0.16	0.18

Supplementary Table 3

	No. shared segments (per pair)			*Segment length (cM per segment)*			*Genomewide sharing (cM per pair)*		
	HUG-AJ	**IDB-AJ**	**IDB-EU**	**HUG-AJ**	**IDB-AJ**	**IDB-EU**	**HUG-AJ**	**IDB-AJ**	**IDB-EU**
HUG-AJ	11.961			5.51			65.90		
IDB-AJ	10.203	9.835		5.51	5.52		56.19	54.25	
IDB-EU	0.369	0.381	0.440	4.46	4.42	4.11	1.64	1.68	1.81

Supplementary Table 4

Population		avg[1]	Std.dev[2]
HUG	AJ	0.671	0.055
IDB	AJ	0.669	0.069
	EU	0.415	0.135
HM3	ASW	0.833	0.704
	CEU	0.364	0.233
	CHB	0.247	0.071
	CHD	0.268	0.049
	GIH	0.456	0.065
	JPT	0.257	0.084
	LWK	0.502	0.111
	MEX	0.411	0.179
	MKK	0.650	0.104
	TSI	0.478	0.153
	YRI	0.492	0.238

[1] Geometric average of decay factors per centiMorgan over the range between 3cM and the genetic length at which sharing is more rare than 1 in a thousand pairs of individuals (varies by population)

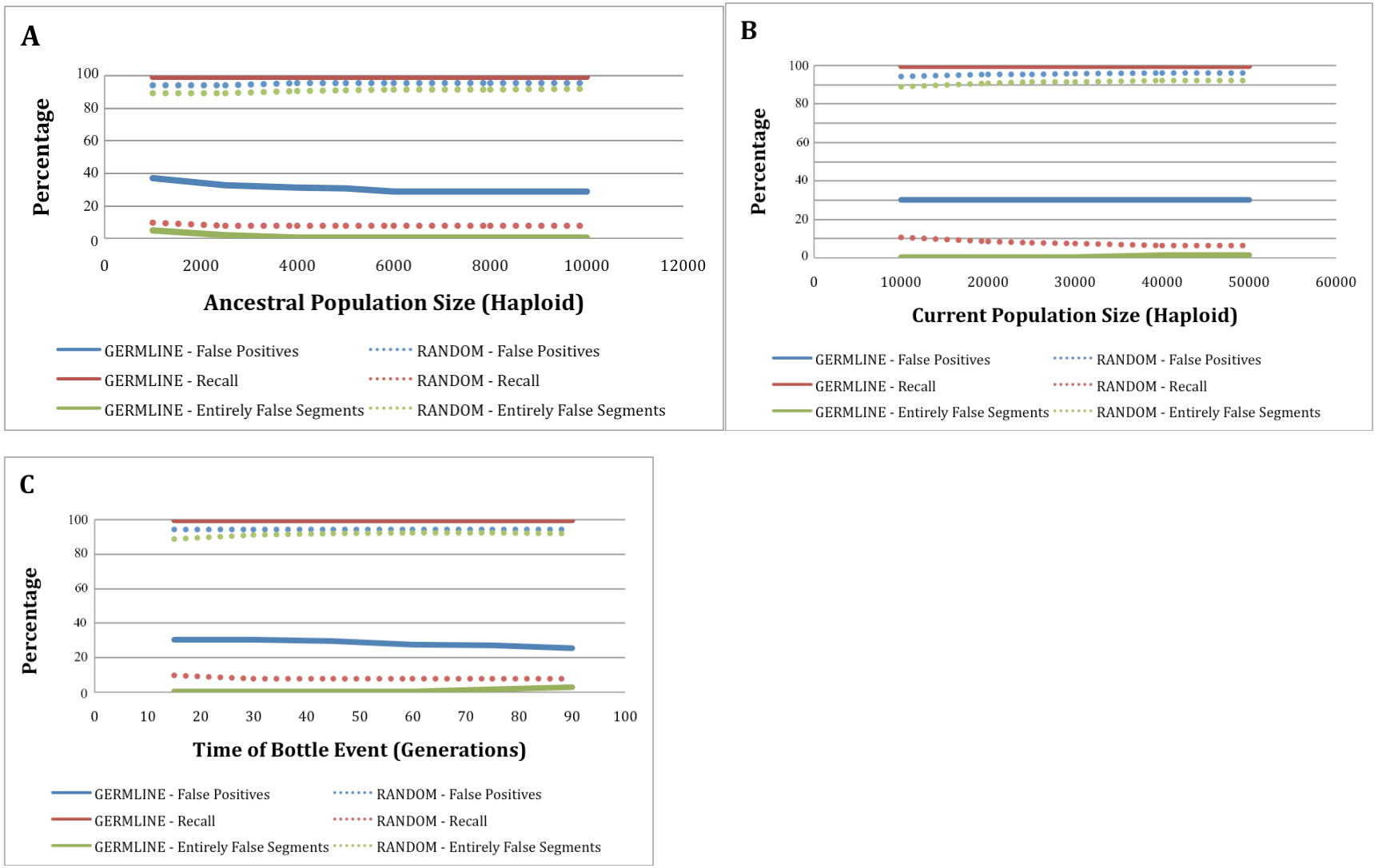
[2] Exponentiation of the log of the decay factors

Supplementary Table 5

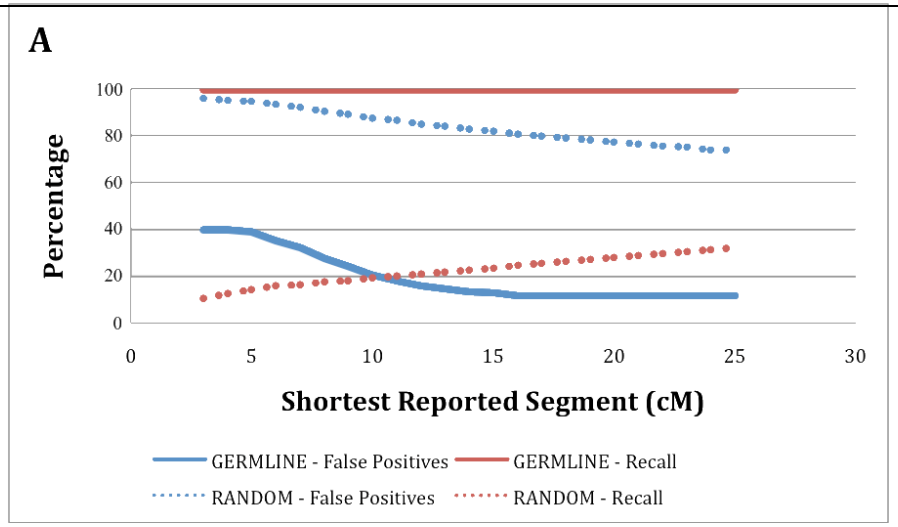
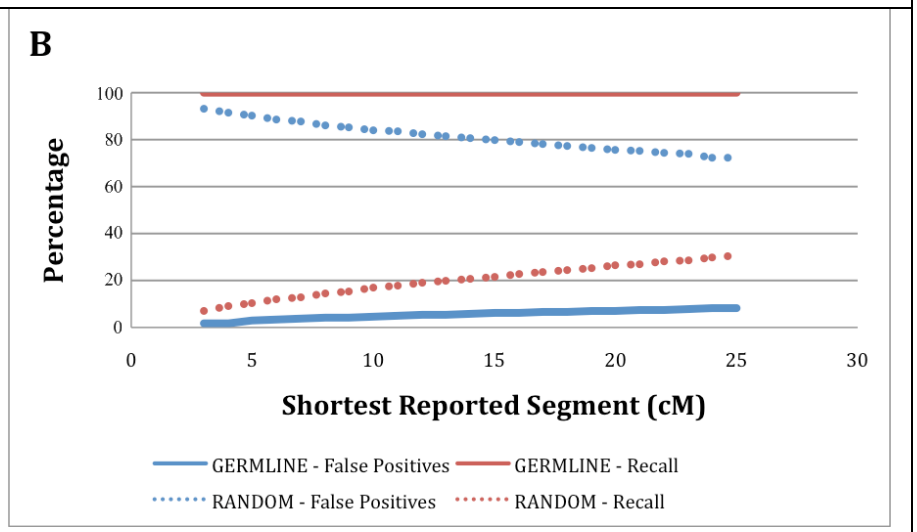
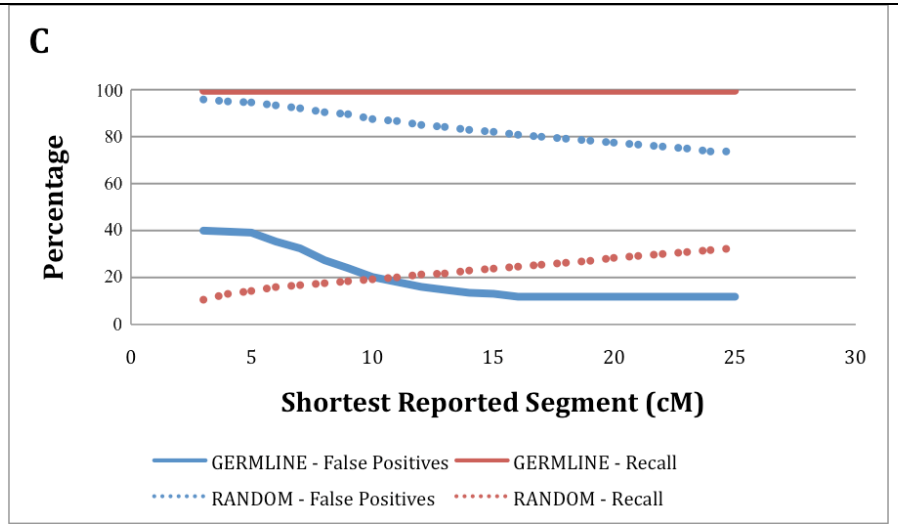
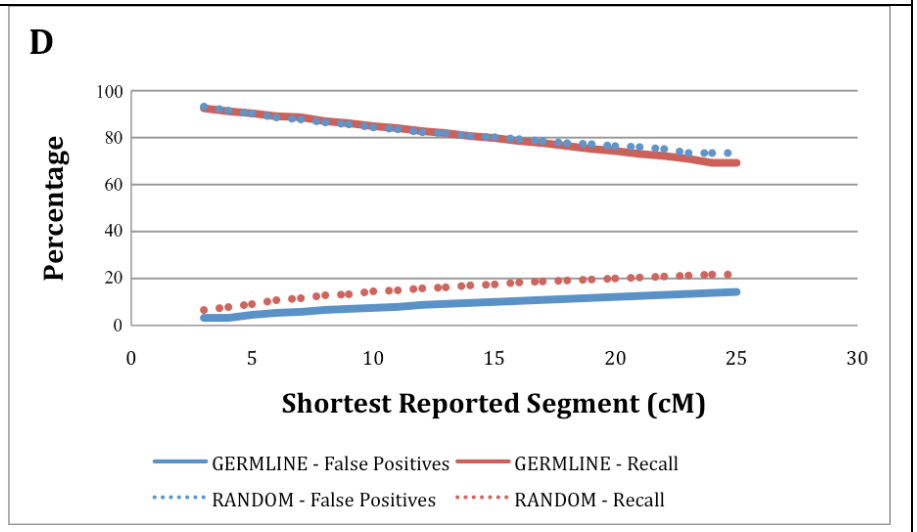
chr	region	Peak	region		pairs[1]	Structural Variation	
1	q42.3-q43	235,000,000	234,000,000	235,000,000	472	35528	CNV
2	q32.3-q33.1	196,000,000	193,000,000	199,000,000	805	221355	CNV
4	p15.1-p14	33,000,000	31,000,000	36,000,000	2,817	319772	CNV
8	p23.1-p22	12,000,000	11,000,000	13,000,000	1,296	5081341	INV
16	p13.11-p12.3	16,000,000	16,000,000	17,000,000	525	1863800	CNV
17	q22-q23.2	55,000,000	53,000,000	57,000,000	586	703400	CNV

[1] Population mean = 111.2; stdev = 170.7

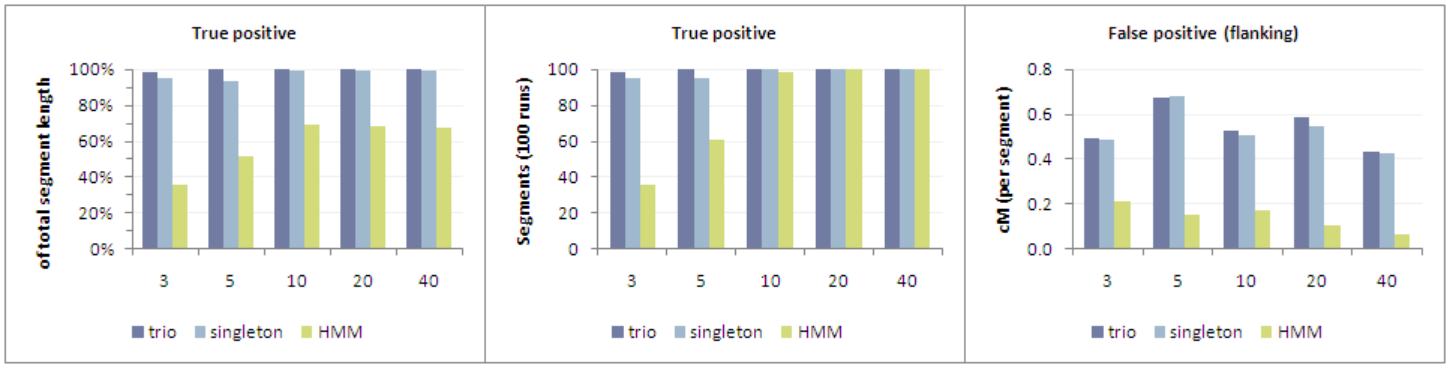
Supplementary Figure 1



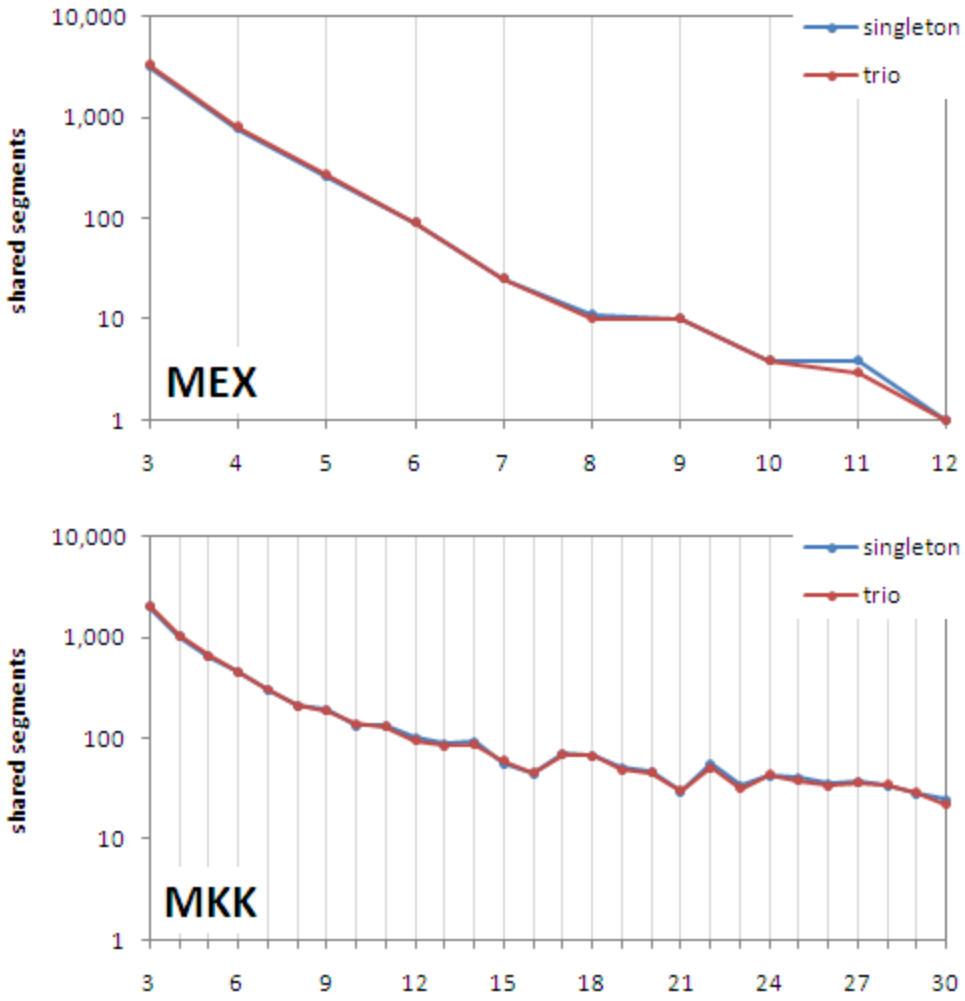
Supplementary Figure 2

	Genotype Extension	Haplotype extension
Perfect Phase		
Computational Phase		

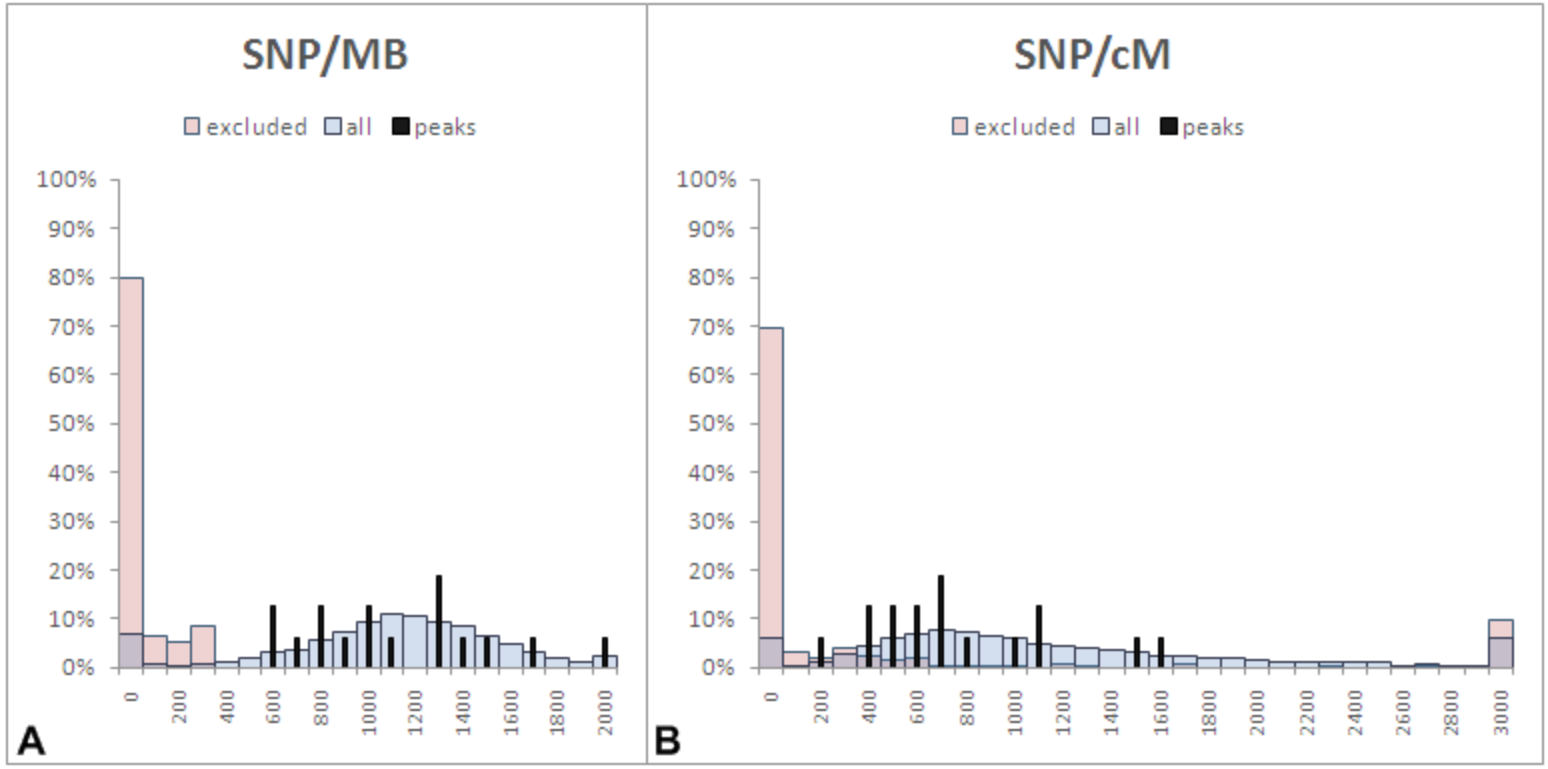
Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5



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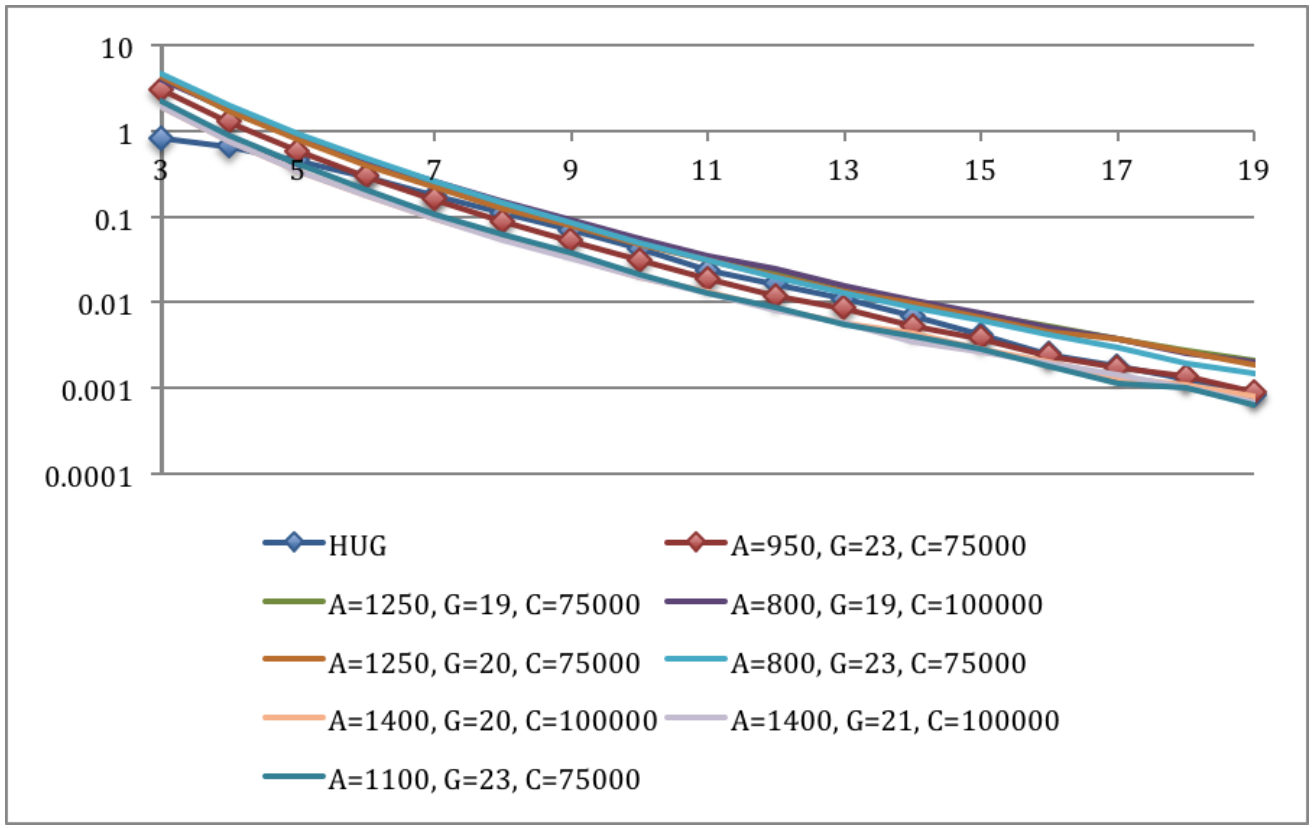

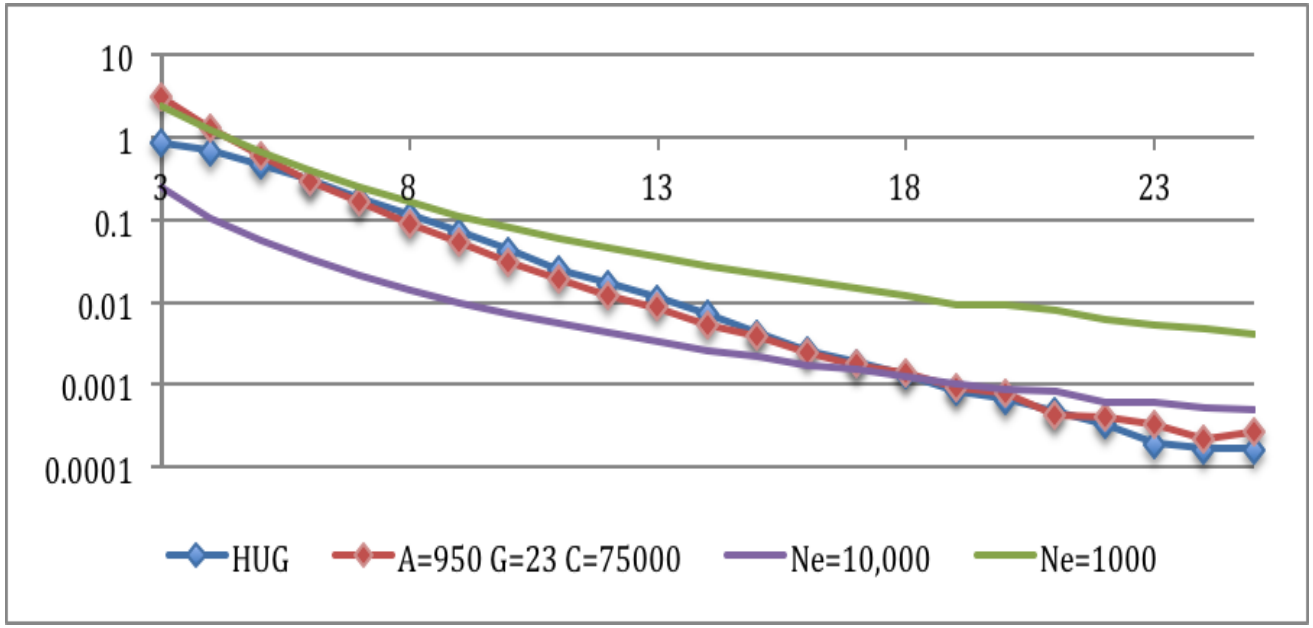
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HUG
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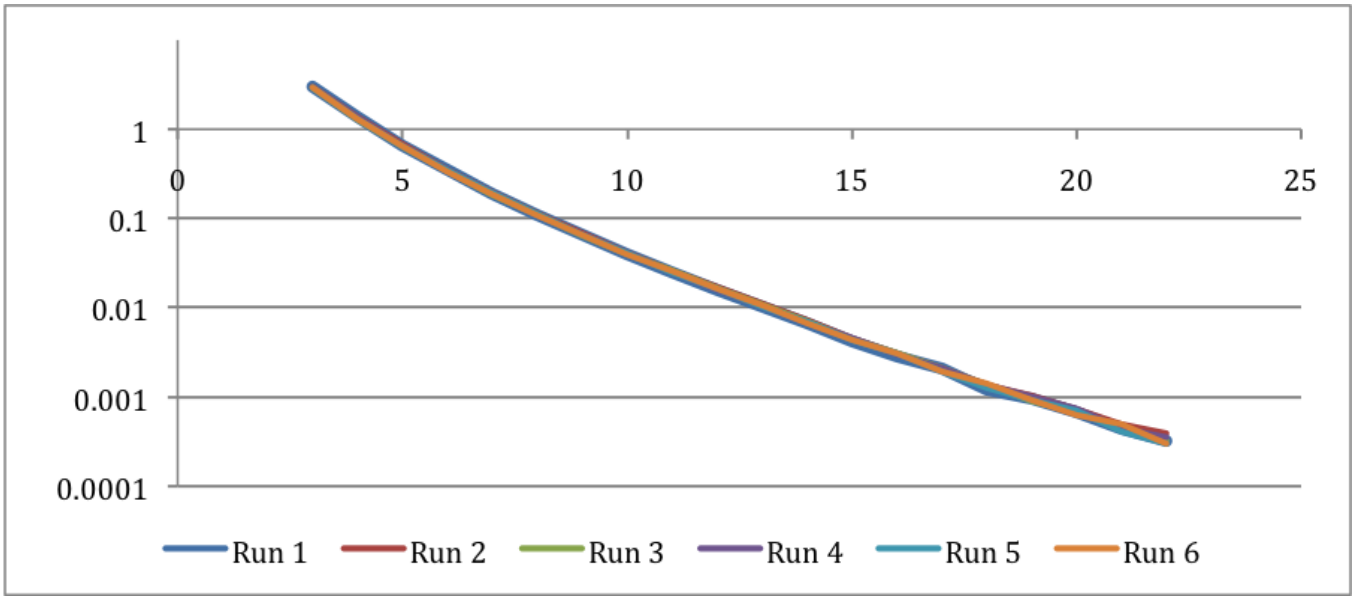
Supplementary Figure 7



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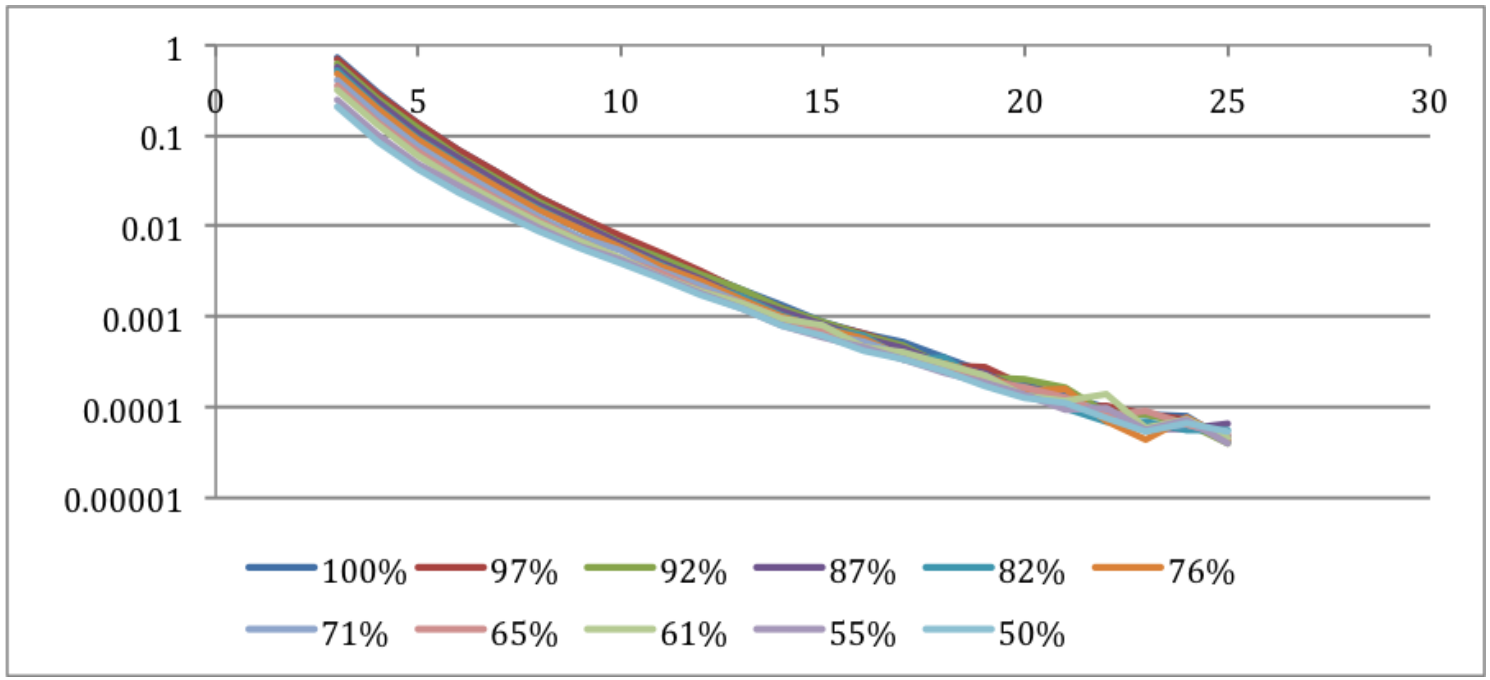

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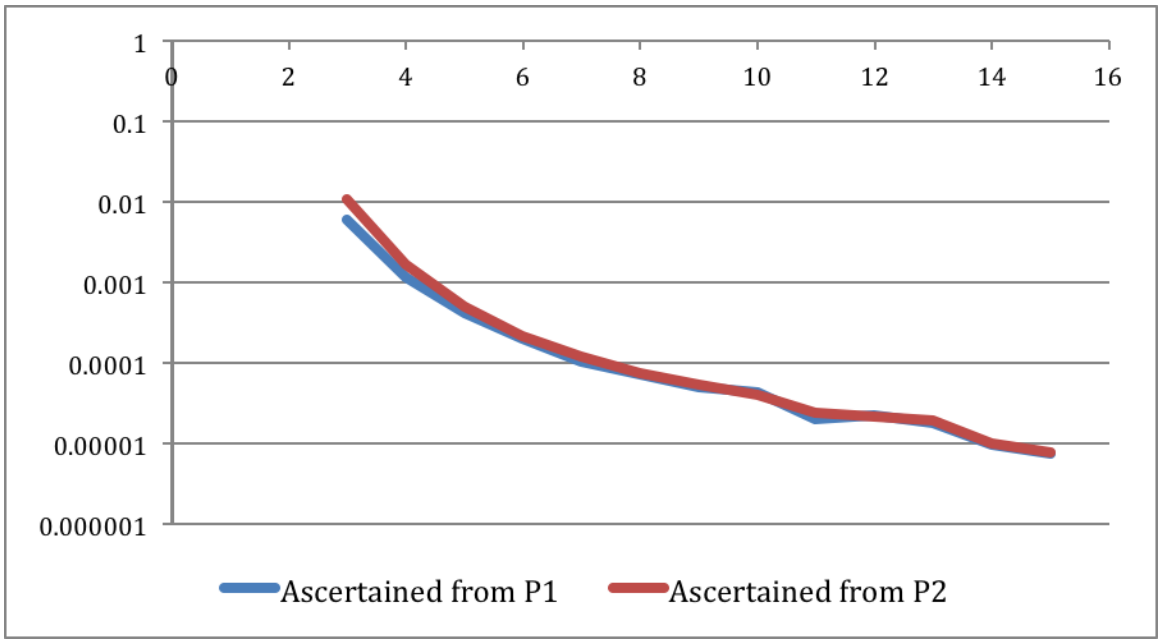

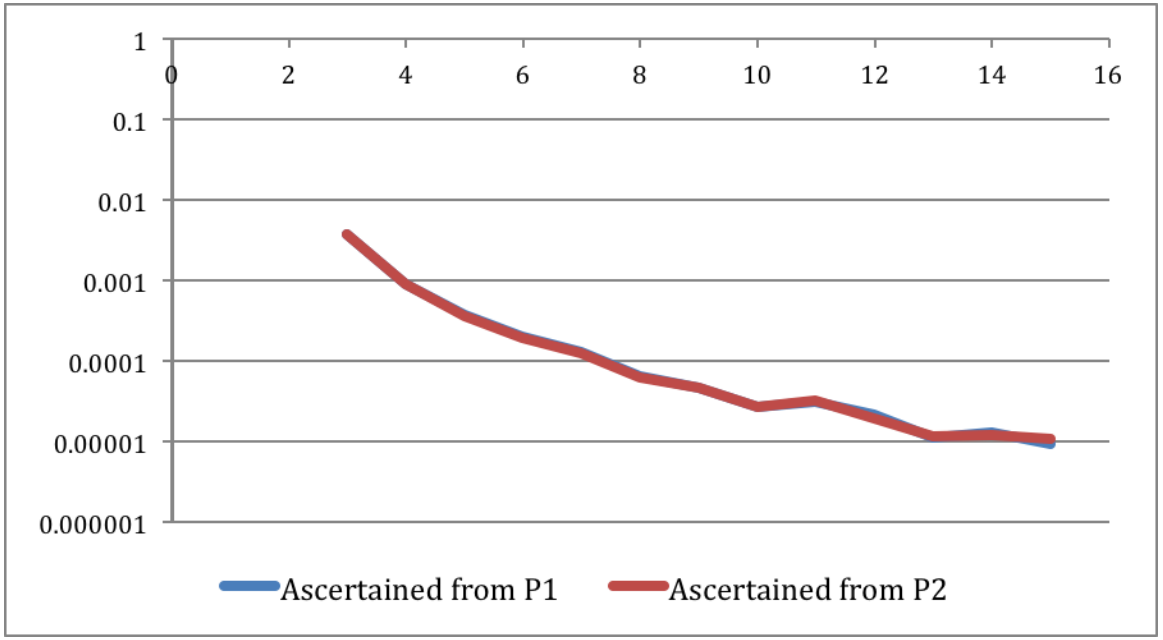

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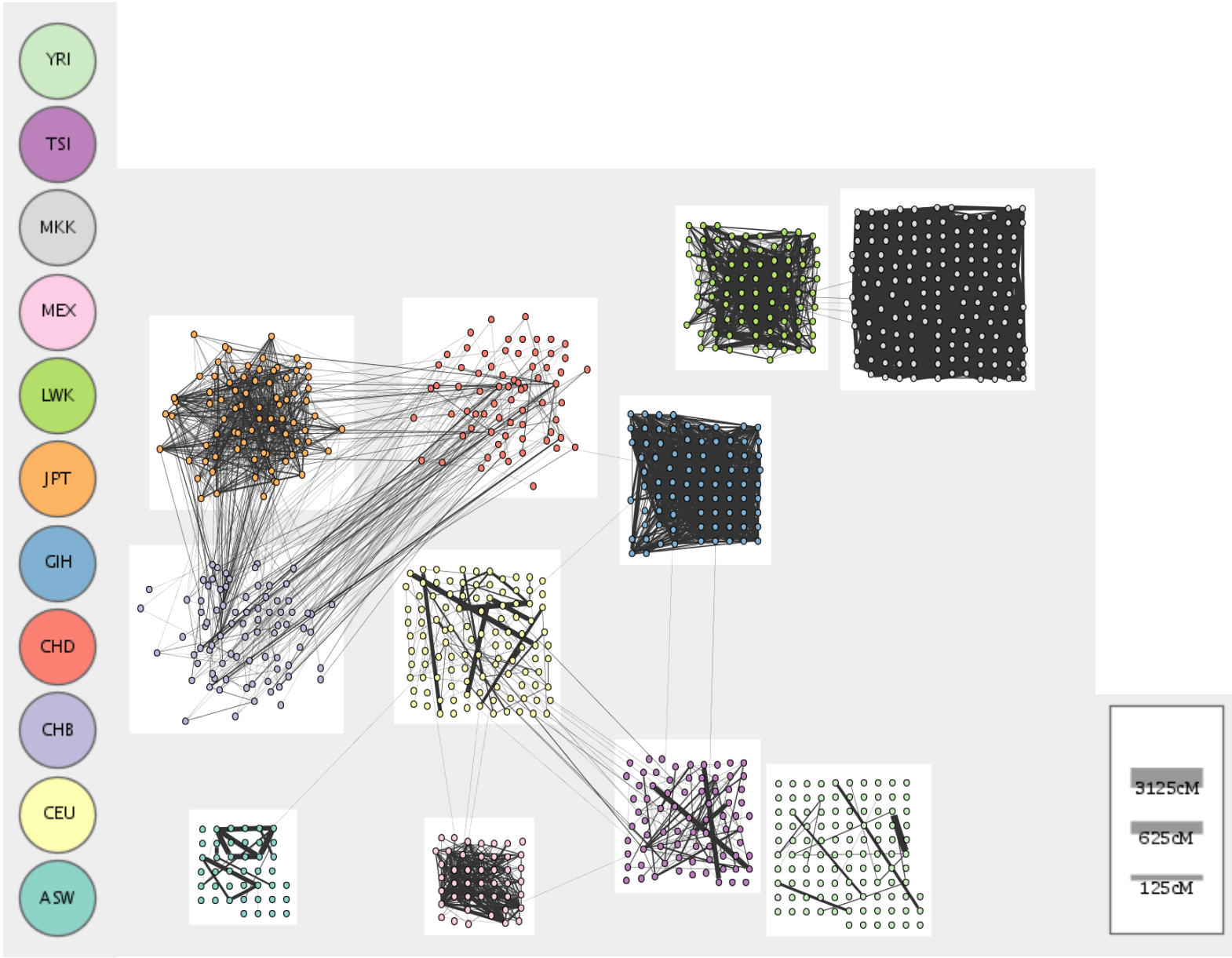

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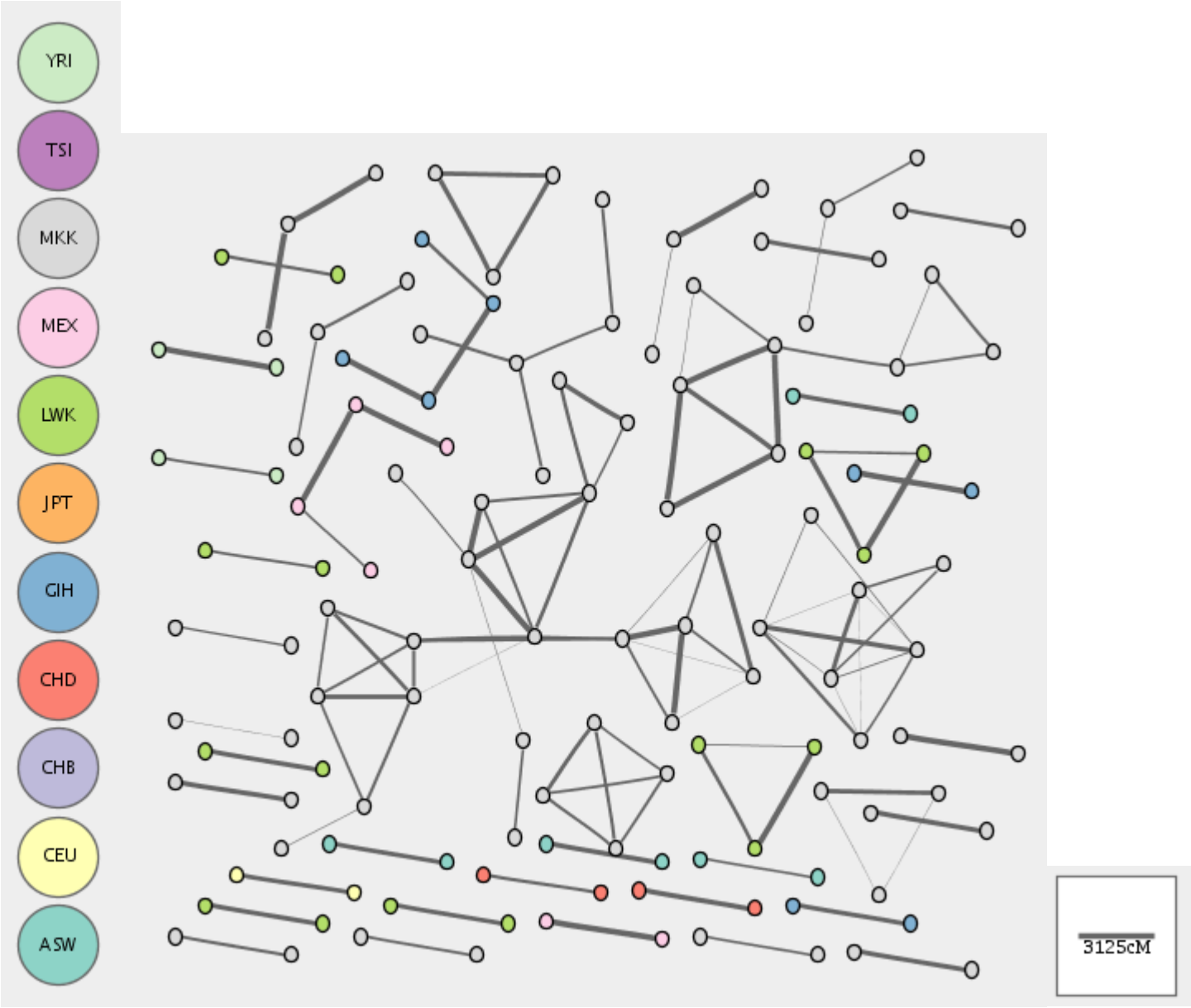

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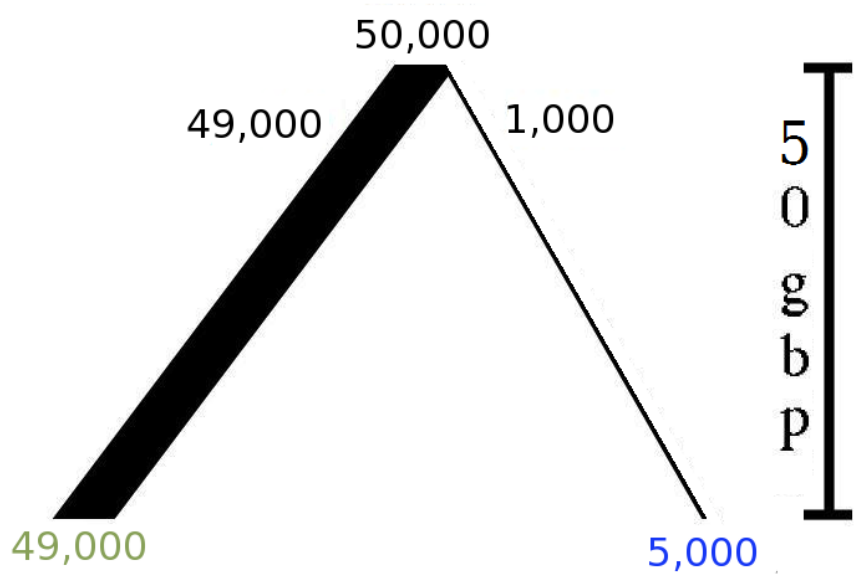
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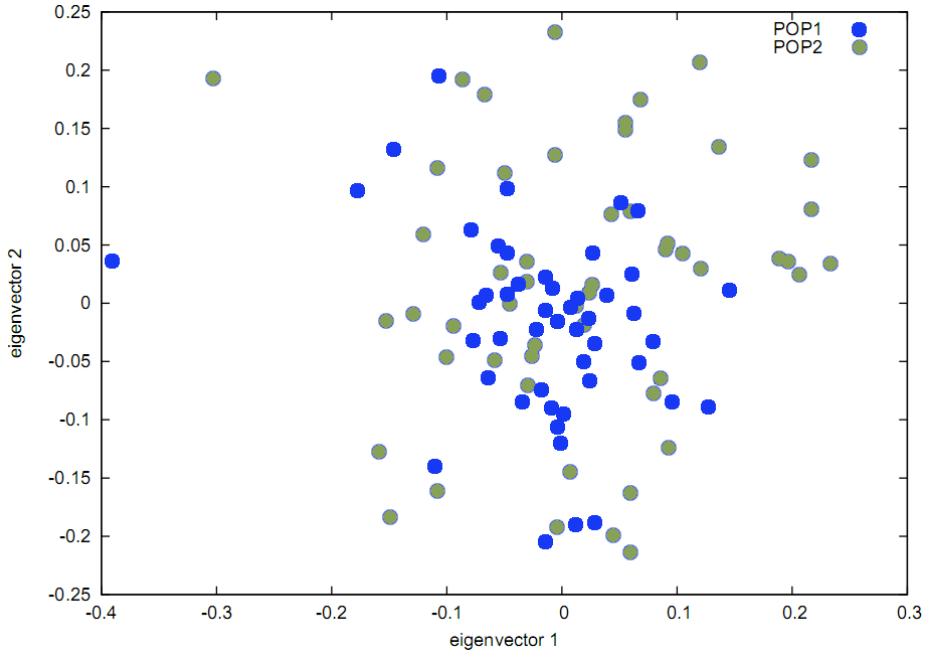
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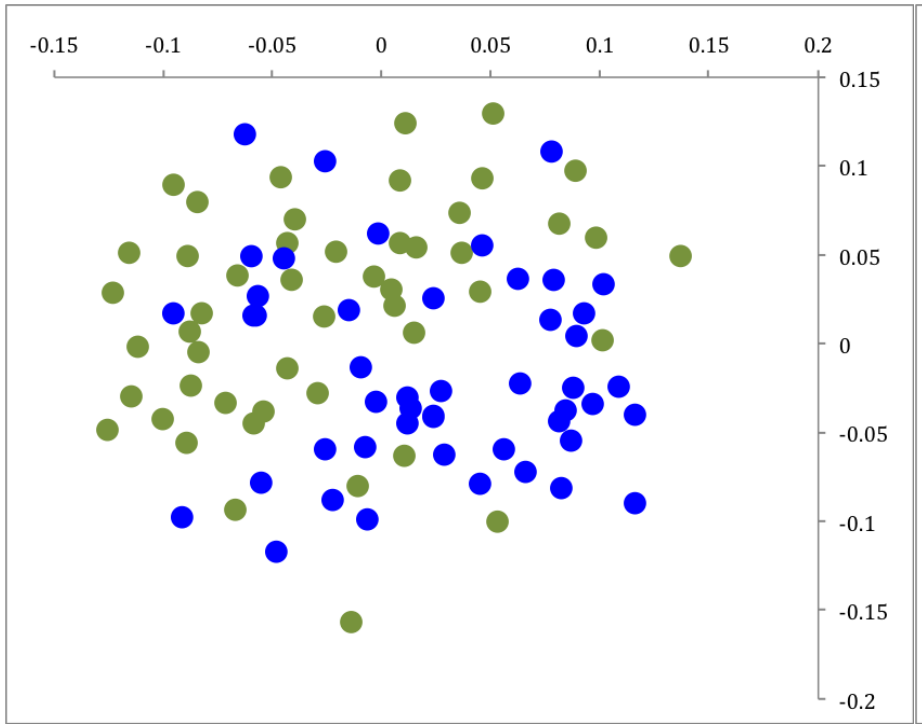
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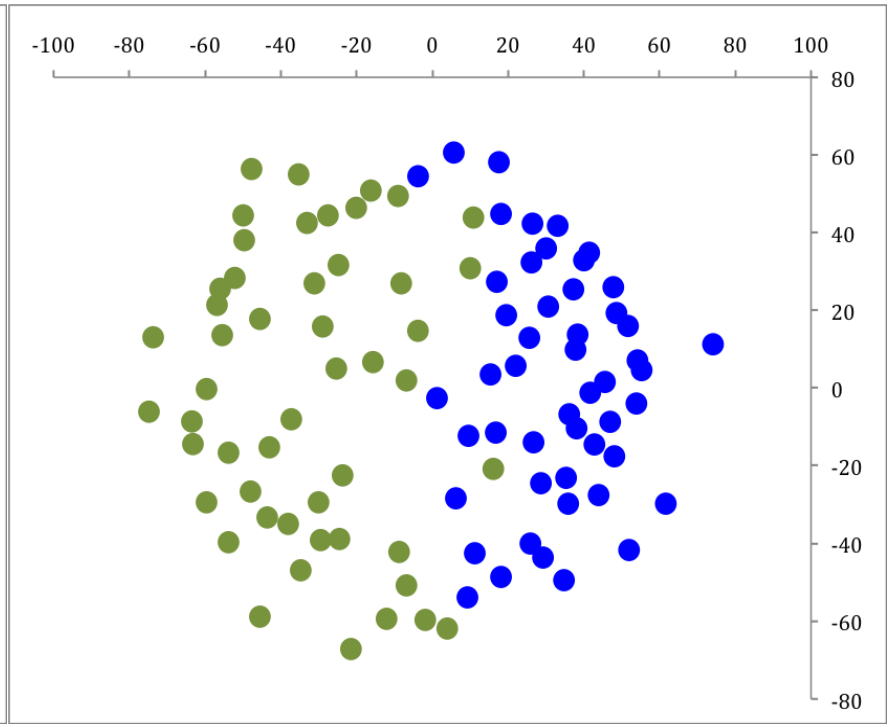
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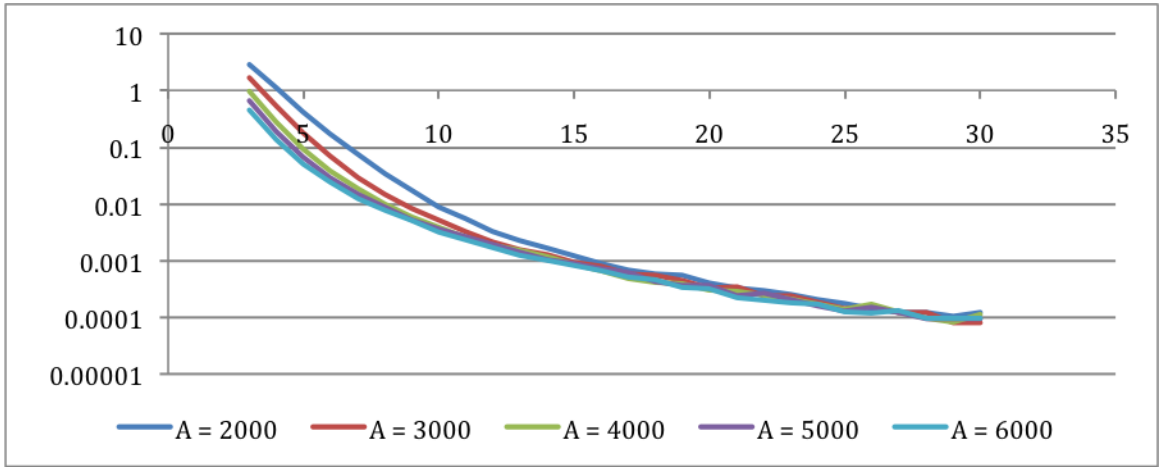
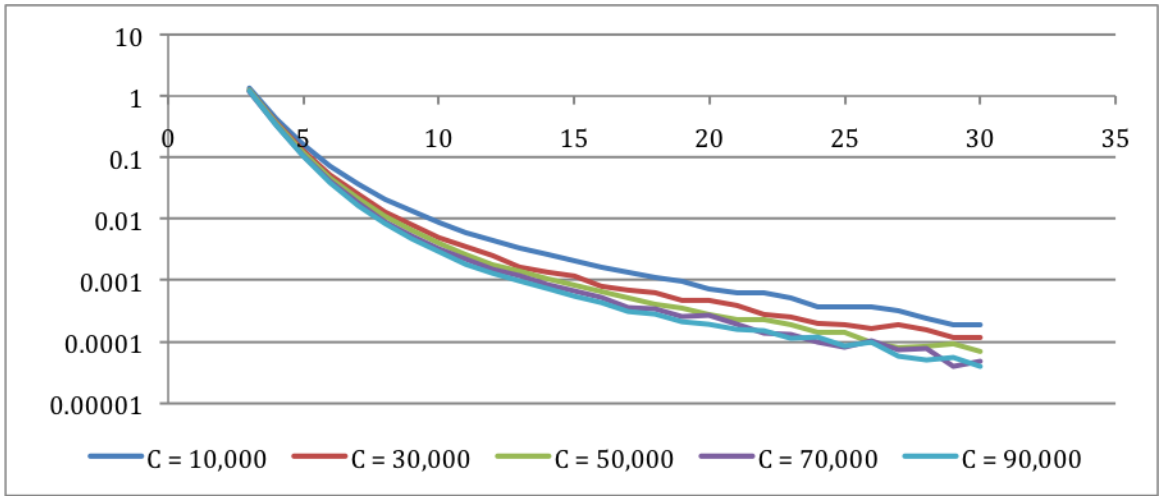
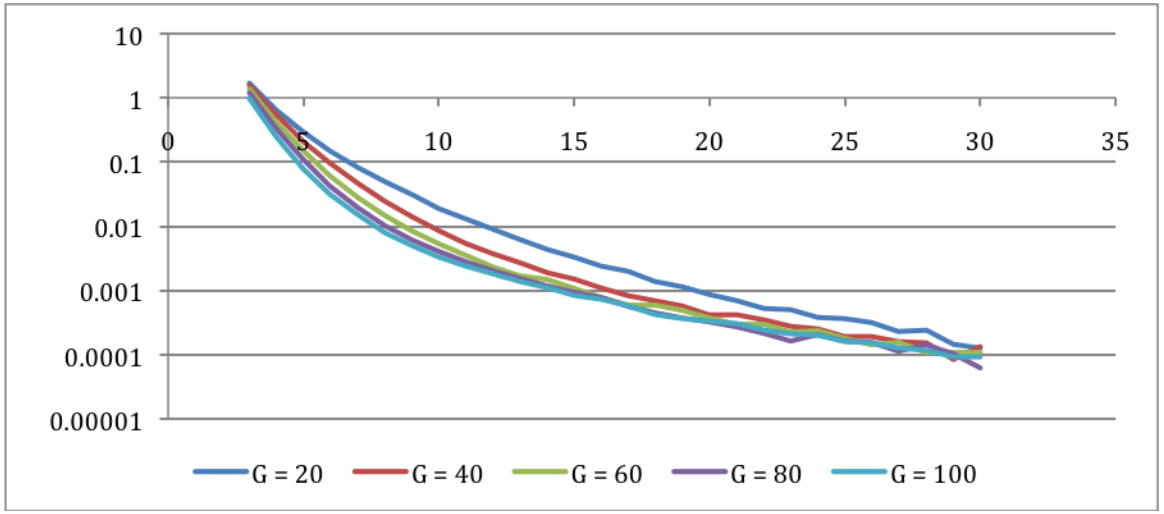
Supplementary Figure 13



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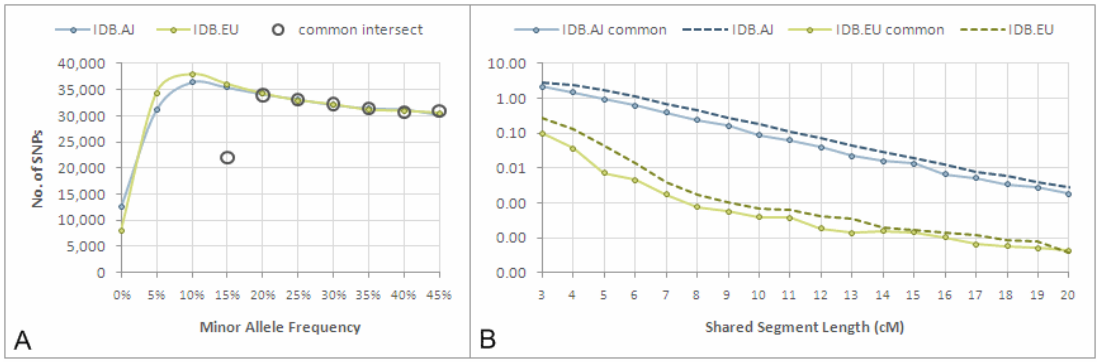
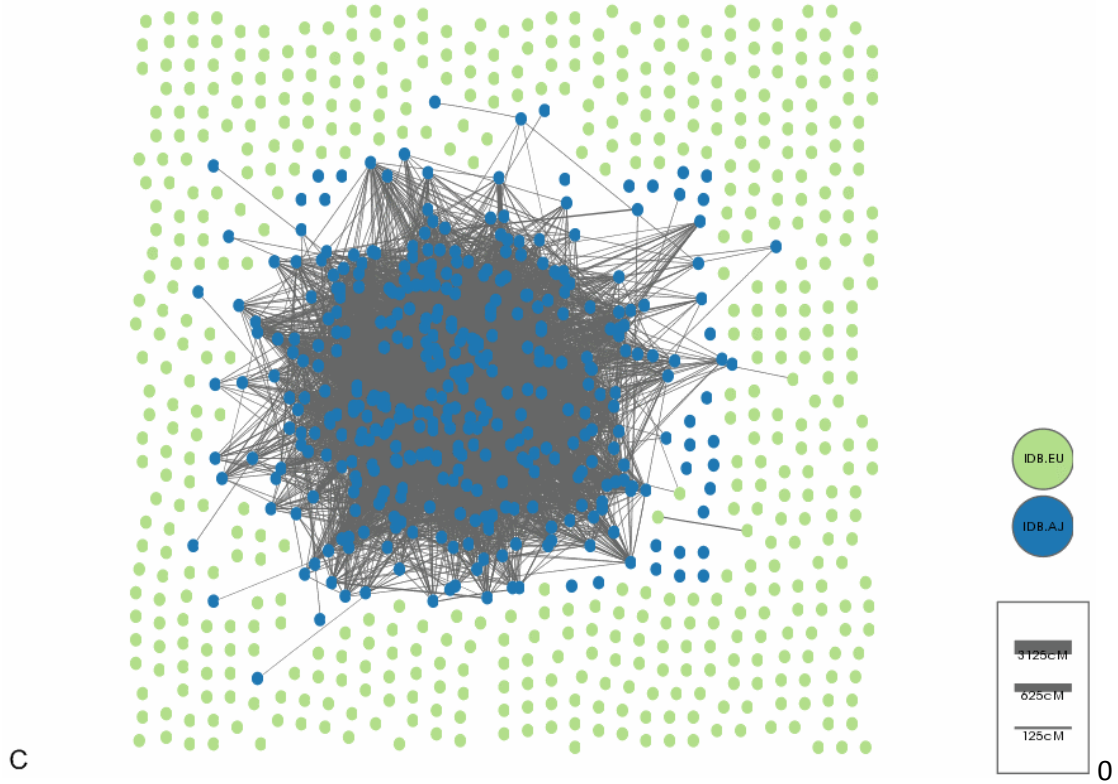
Supplementary Figure 14





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