recomb	**0.25**	<-- change this value to change the recombination freq.
sa	**0.99**	<-- change this value to change selection against the a allele
sb	**0.99**	<-- change this value to change selection against the b allele
z	**0**	<-- change this value to 1 to get independent effects of selection on a and b
		for values > 1, the ab genotype is less fit than expected
		for values < 1, the same type is more fit than expected

There are two haploid loci, each with two alleles
There are four genotypes: AB, Ab, aB, ab

genotype-->	**A-------B**	**A-------b**	**a-------B**	**a-------b**		Freq of A	Freq of B
N. individuals before selection	**25**	**25**	**25**	**25**	**100**		
pij = Freq before selection	0.25	0.25	0.25	0.25	**1**	0.50	0.50
Wij = fitness of genotype	**1**	**0.01**	**0.01**	**1.00**			
Calculation of Wij	1	(1 - sb)	(1 - sa)	[(1-sa)(1-sb)]^z			
Freq after selection: Wij*pij	0.250	0.003	0.003	0.250	0.51	0.50	0.50
Normalized freq= Wij/Wbar	0.495	0.005	0.005	0.495	1.0	0.50	0.50
Freq, after free recombination							
equal to **(1-r)*pij + r*pi*pj**	0.434	0.066	0.066	0.434	1.0	0.50	0.50

Linkage disequilibrium
D
p(ab)*p(AB) - p(aB)*p(Ab)
or
p(ab) - p(a)*p(b)

0.000

0.2450

0.1838

Epistasis
E
ln([Wab*WAB]/[WaB*WaB])
or
ln(Wab) - ln(WaWb)

9.2103

0.2450 0.2450495

Note, the effect of free recombination was to reduce linkage disequilbrium.
In, general, D' = D(1-r), where r is the rate of recombination between loci.

D' calculated as D*(1-r) **0.1838** <-- this value was incorrect in the previous sheet. Thanks to Pauline for catching this error
(I had D*r instead of D*(1-r))

Note: freq. after free recombination calculated from normalized freqs.

Things to note:
1. The p(ij) frequencies before selection (line 13) assume linkage equilibrium (no covariance between alleles). See cell L13 (pink cell)
2. For z = 1, there is no epistasis for fitness, and no linkage disequilibrium is generated. Change z to equal 1. D should be zero.
3. For z < 1, there is positive epistasis for fitness (gray cell). Meaning, the ab genotype is more fit than expected based on selection against the a and b alleles.
4. For z > 1, there is negative epistasis for fitness. Meaning, the ab genotype is less fit than expected based on selection against the a and b alleles.
5. Positive epistasis for fitness gives rise to positive D (green cell)
6. Negative epistasis for fitness gives rise to negative D
7. Recombination reduces D. D after recombination D' = D(1 - r) (see blue cells)