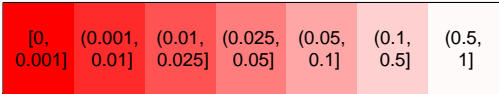


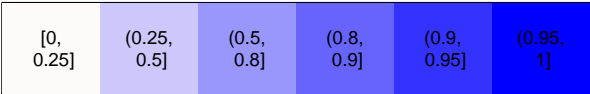
Linkage Disequilibrium

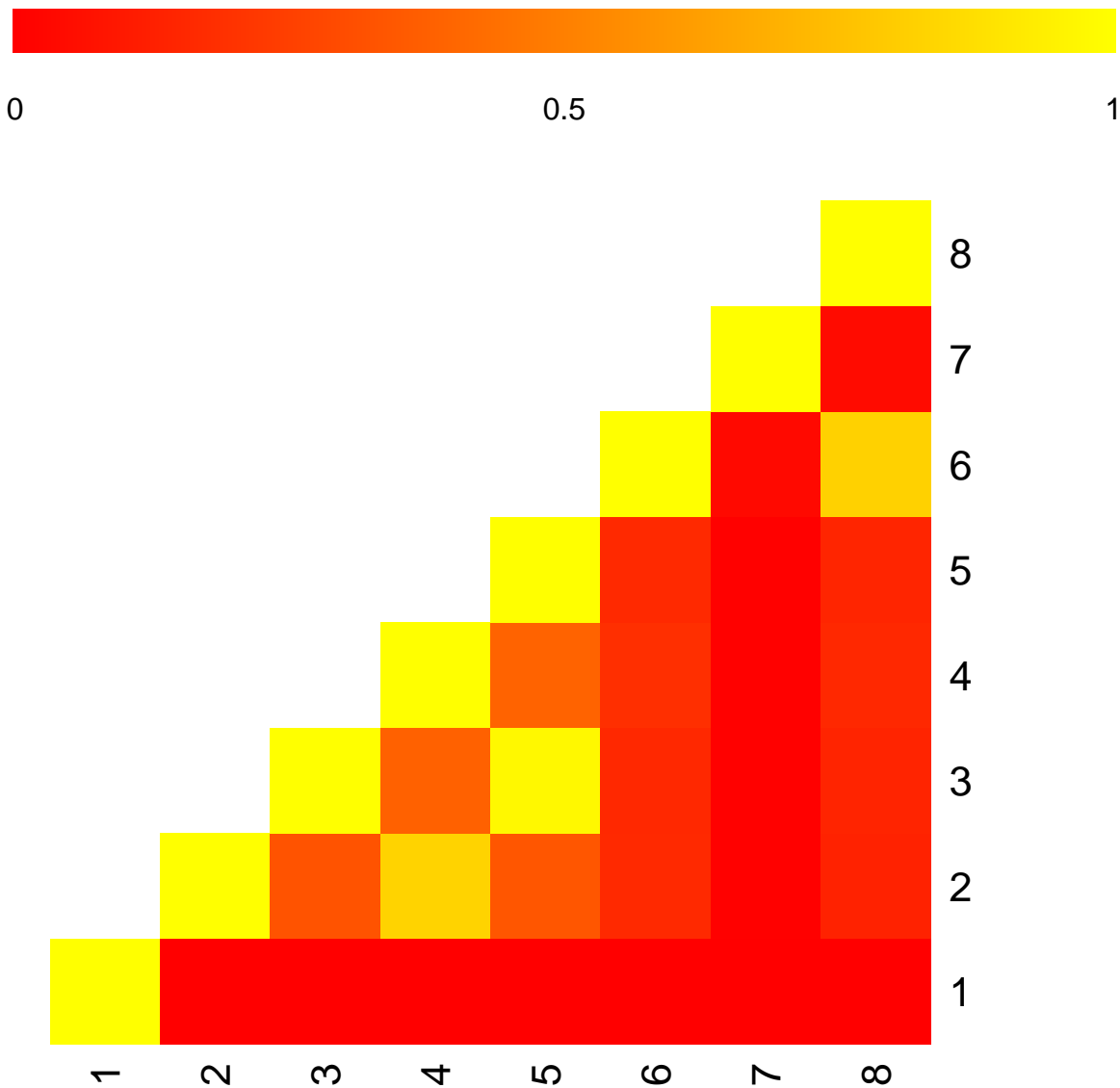
	m709	m654	m47	p46	p79	p252	p491	p523
m709	m709	0.004	0.001	0.003	0.001	0.001	0.000	0.000
m654	0.002153	m654	0.328	0.826	0.339	0.164	0.006	0.137
m47	0.073119	< 2e-16	m47	0.380	0.972	0.157	0.007	0.142
p46	0.005412	< 2e-16	< 2e-16	p46	0.390	0.186	0.007	0.156
p79	0.069645	< 2e-16	< 2e-16	< 2e-16	p79	0.161	0.007	0.146
p252	0.257283	< 2e-16	< 2e-16	< 2e-16	< 2e-16	p252	0.038	0.820
p491	0.677682	4.82e-06	0.000514	1.07e-06	0.000168	< 2e-16	p491	0.044
p523	0.388425	< 2e-16	< 2e-16	< 2e-16	< 2e-16	< 2e-16	< 2e-16	p523

P-value



R^2

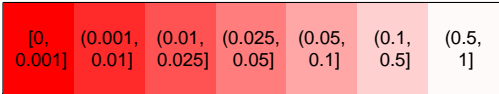




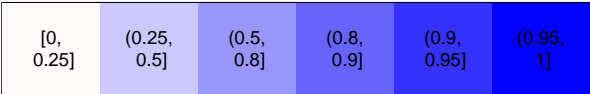
Linkage Disequilibrium

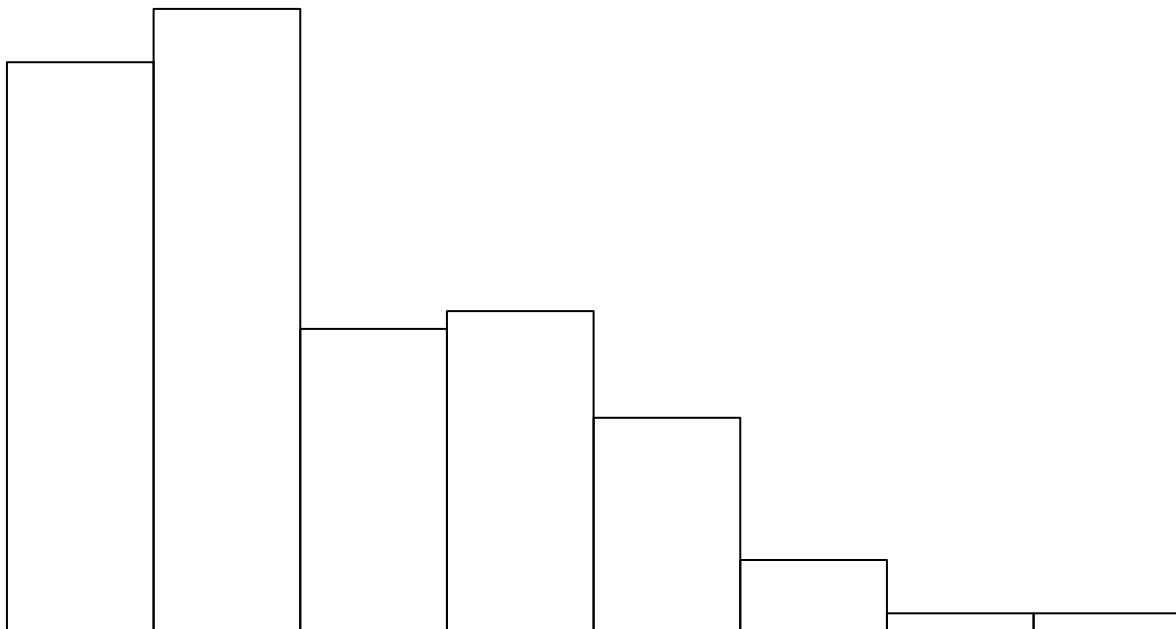
	m709	m654	m47	p46	p79	p252	p491	p523
m709	m709	0.004	0.001	0.003	0.001	0.001	0.000	0.000
m654	0.002153	m654	0.328	0.826	0.339	0.164	0.006	0.137
m47	0.073119	< 2e-16	m47	0.380	0.972	0.157	0.007	0.142
p46	0.005412	< 2e-16	< 2e-16	p46	0.390	0.186	0.007	0.156
p79	0.069645	< 2e-16	< 2e-16	< 2e-16	p79	0.161	0.007	0.146
p252	0.257283	< 2e-16	< 2e-16	< 2e-16	< 2e-16	p252	0.038	0.820
p491	0.677682	4.82e-06	0.000514	1.07e-06	0.000168	< 2e-16	p491	0.044
p523	0.388425	< 2e-16	< 2e-16	< 2e-16	< 2e-16	< 2e-16	< 2e-16	p523

P-value



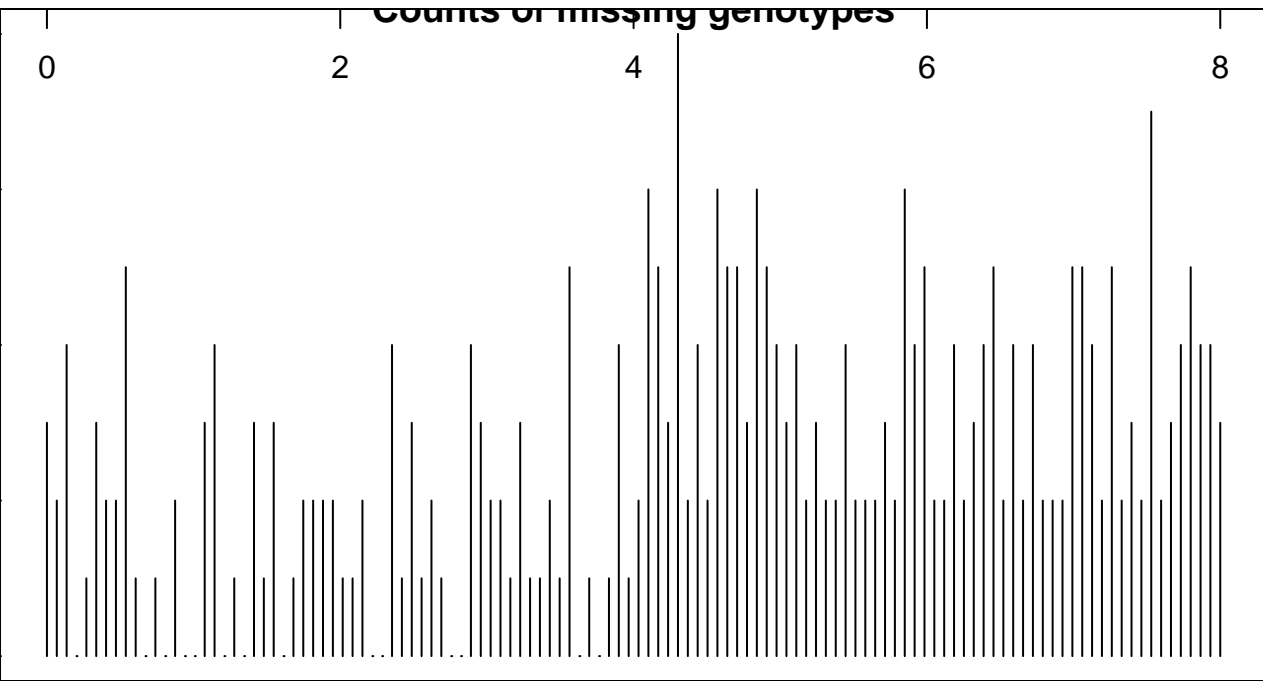
R^2

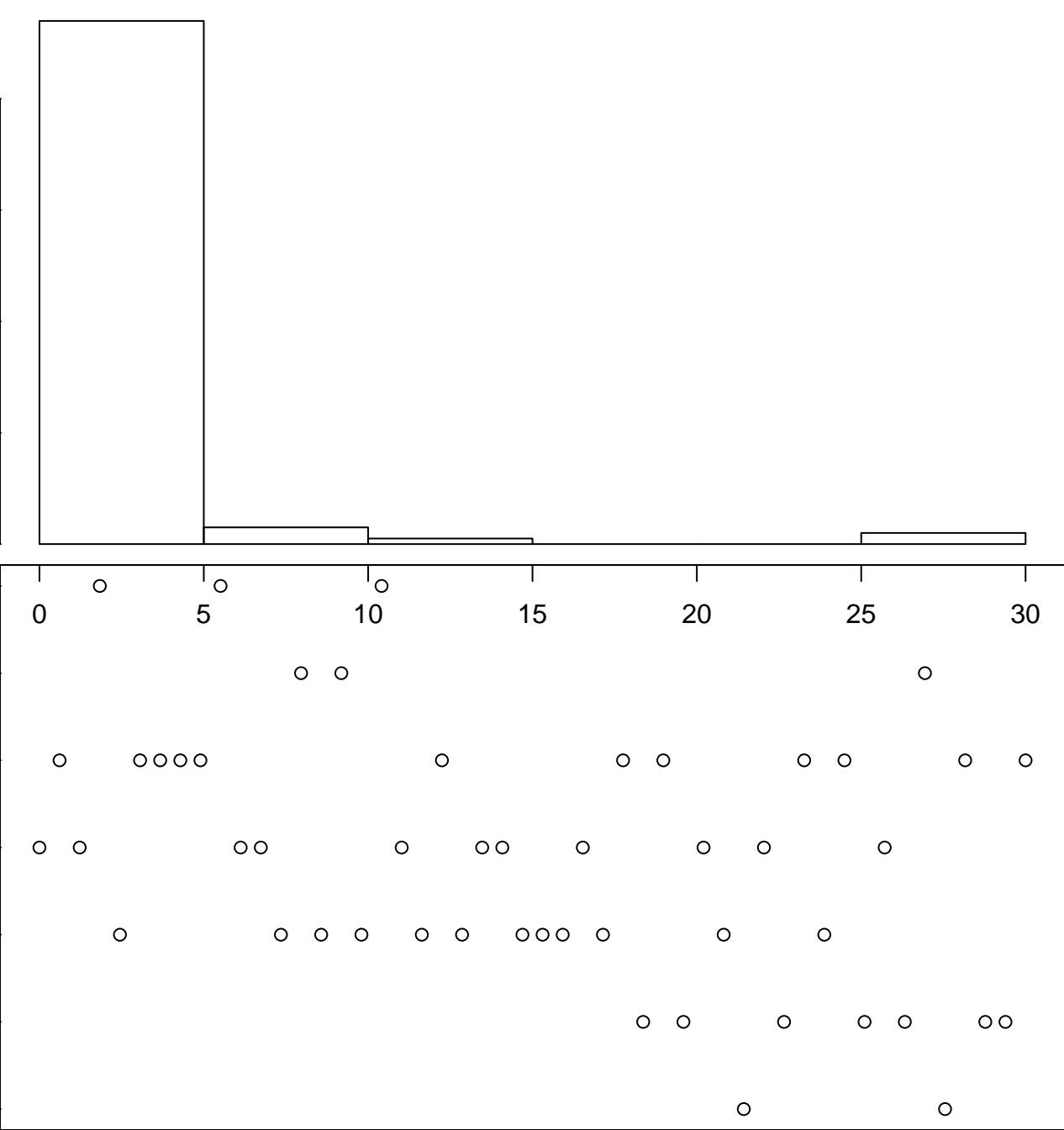




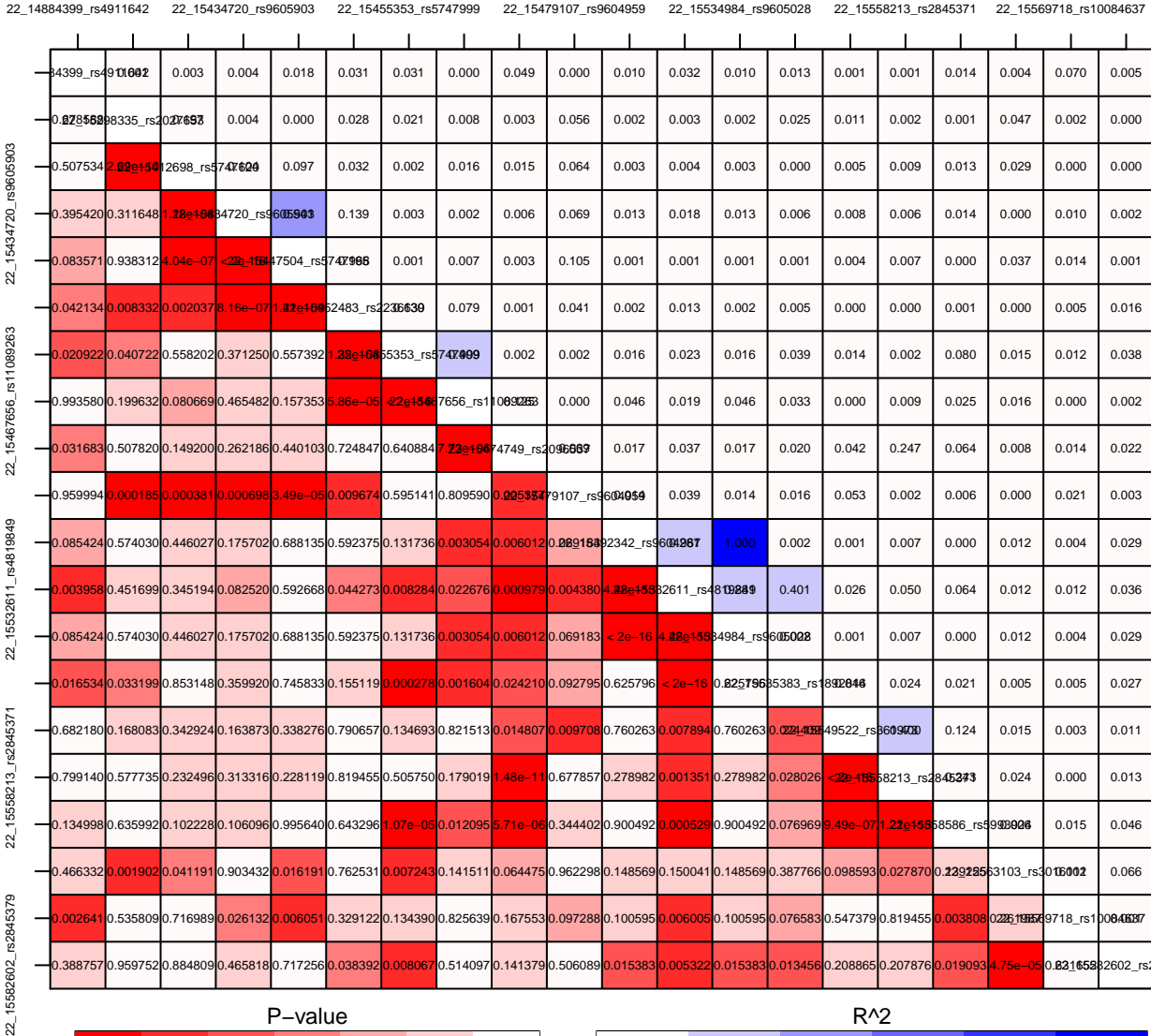
Counts of missing genotypes

0 2 4 6 8





Linkage Disequilibrium

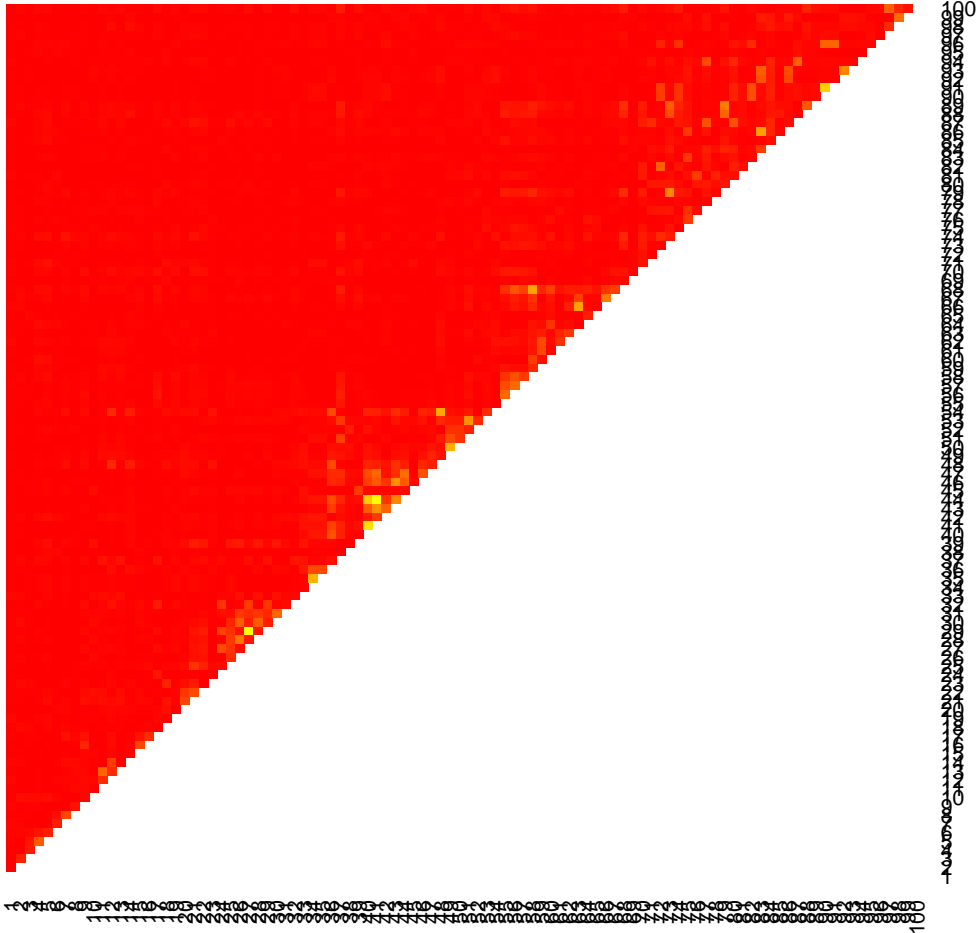




0

0.5

1



Per-marker statistical significance

