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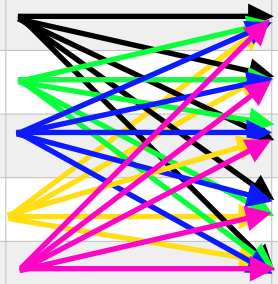
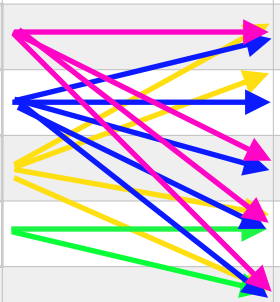
Report on simulation

These are three cases of simulation:
1. When the one gene affects to one Hallmark.
2. When the one gene affects to many Hallmarks.
3. More realistic case (colorectal cancer data)

1. When the one gene affects to one Hallmark.		
G1	→	Ha
G2	→	Hb
G3	→	Hi
G4	→	Him
G5	→	Hd

2. When the one gene affects to many Hallmarks.		
G1		Ha
G2		Hb
G3		Hi
G4		Him
G5		Hd

3. The case of colorectal cancer			
			List Hallmarks
APC		Ha	Ha, Hi, Him, Hd
KRAS		Hb	Ha, Hb, Hi, Him, Hd
TP53		Hi	Ha, Hb, Him, Hd
PIK3CA		Him	Him, Hd
		Hd	

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Coefficients for ALL simulations are same:	
E0 <- 2E-5	# coefficient for cell division process
F0 <- 1E1	# coefficient for cell division process
m <- 4E-10	# mutation probability
uo <- 0.5	# oncogene mutation probability
us <- 0.5	# suppressor mutation probability
s <- 10	# coefficient for sigma function
k <- 0.19	# Environmental death probability
censore_n <- 30 000	# Max cell number where the program forcibly stops

The ALL simulations started from 1 clone with <u>normal</u> 10 000 cells.

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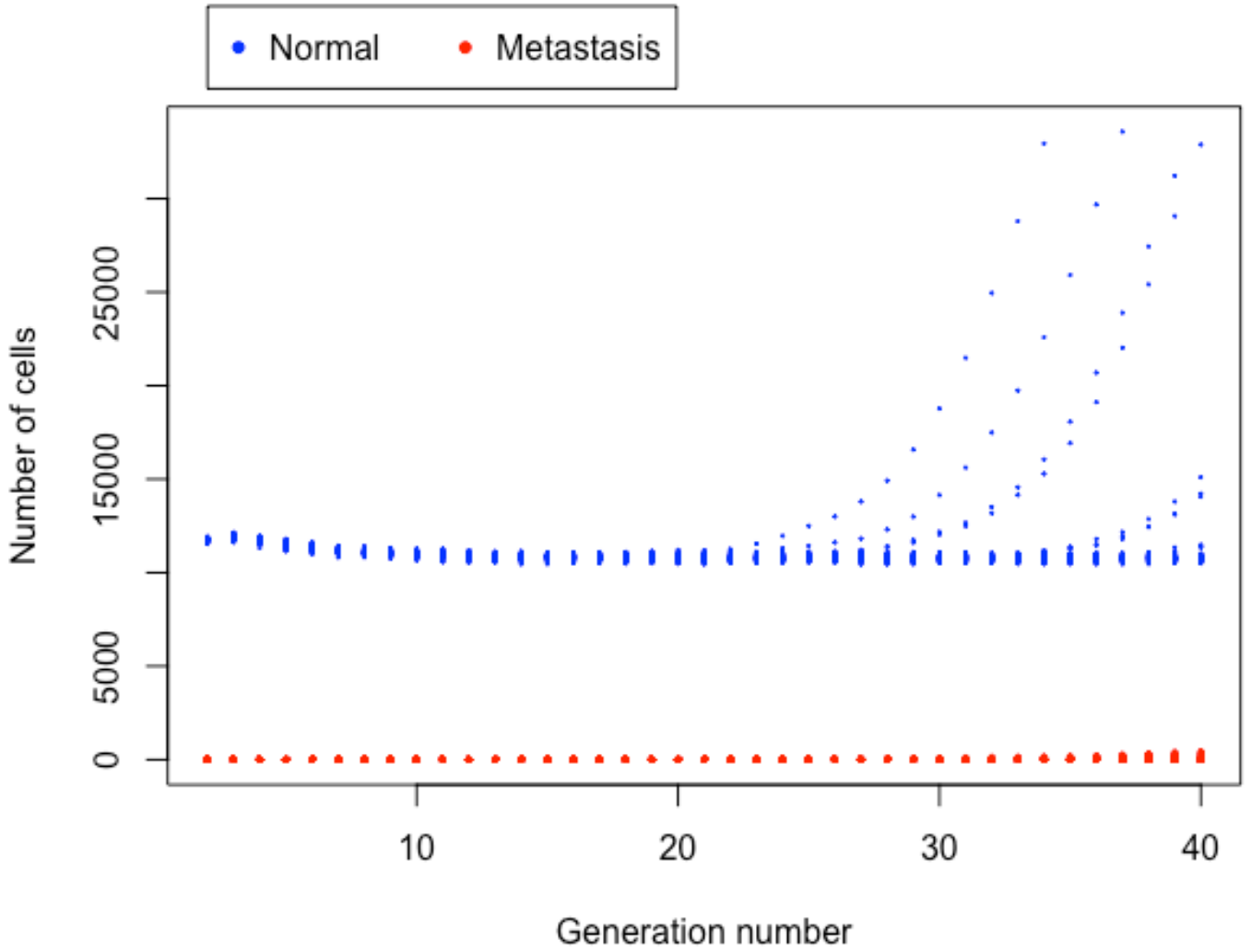
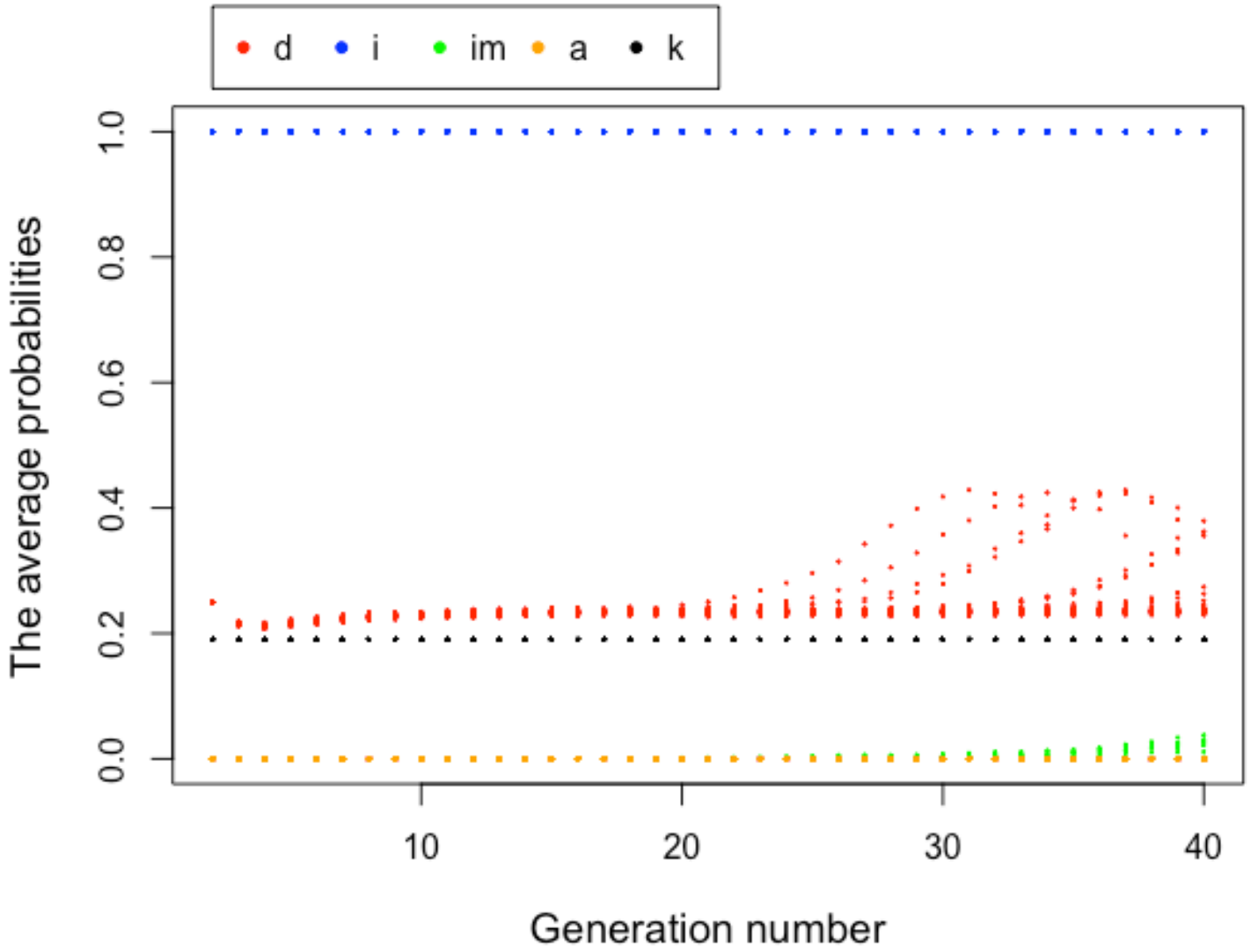
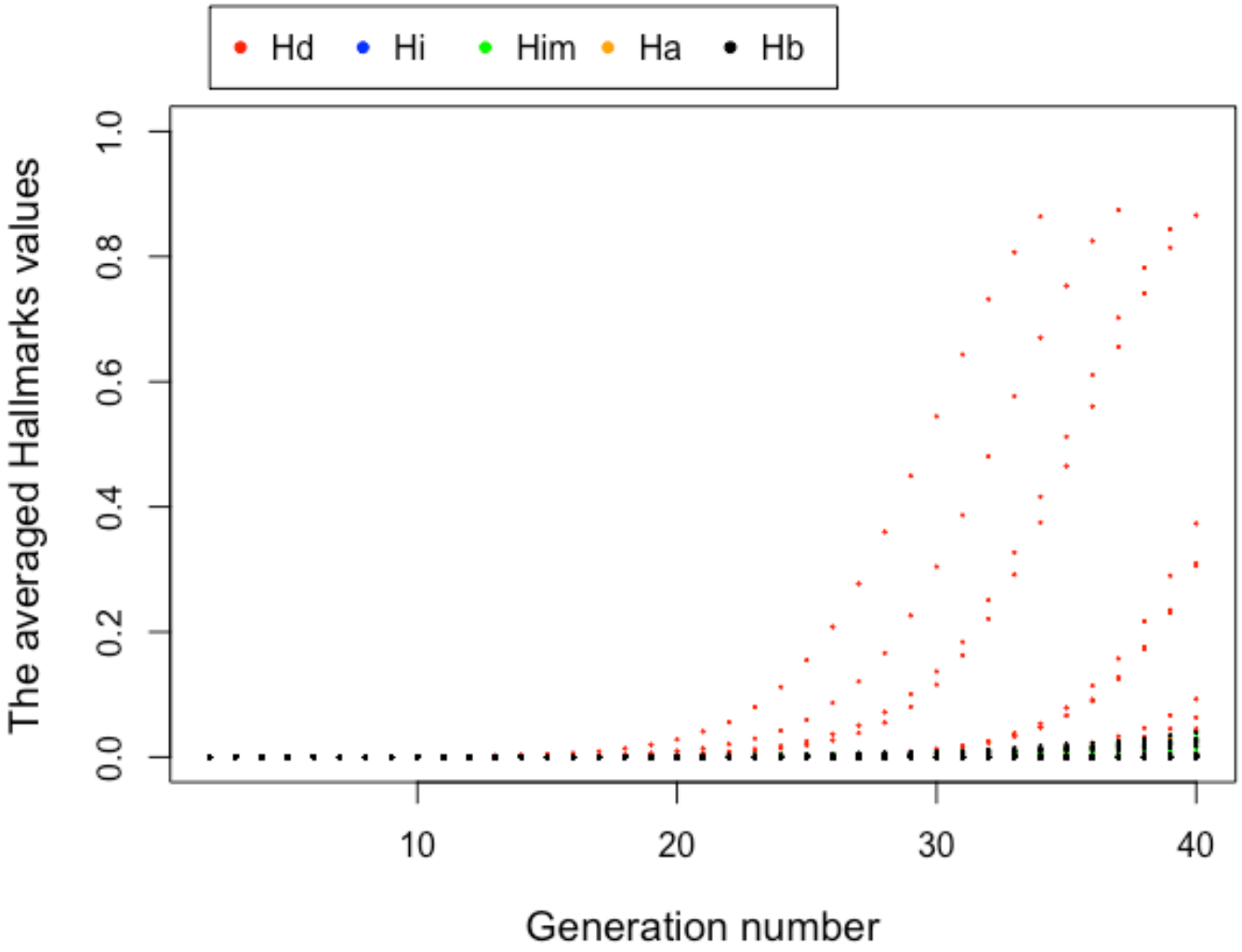
I. The results for SINGLE case (one gene affects to one Hallmark):




d
i
im
a
k
The average probabilities
0.0
0.2
0.4
0.6
0.8
1.0
10
20
30
40
Generation number


Hd
Hi
Him
Ha
Hb
The averaged Hallmarks values
0.0
0.2
0.4
0.6
0.8
1.0
10
20
30
40
Generation number

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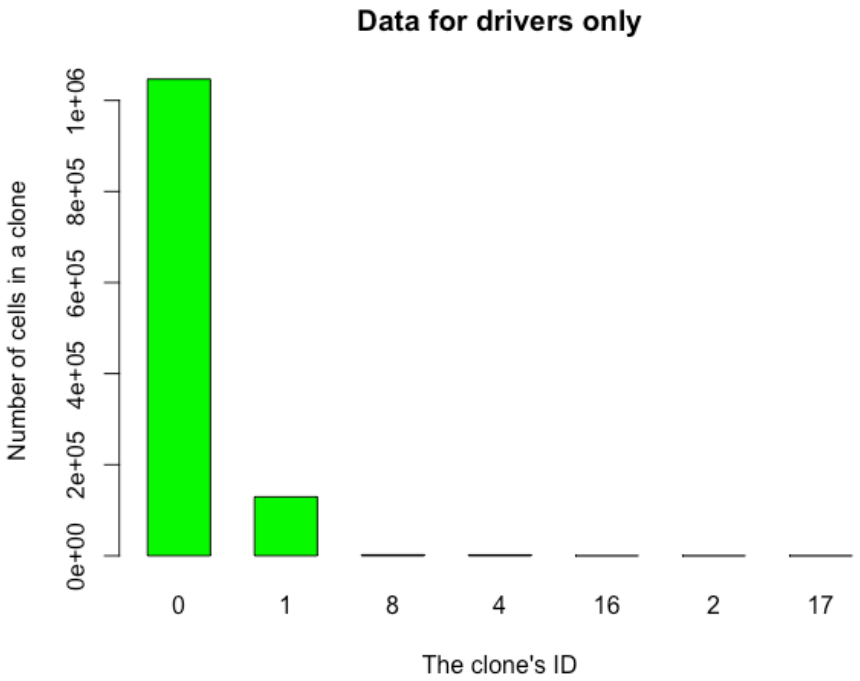
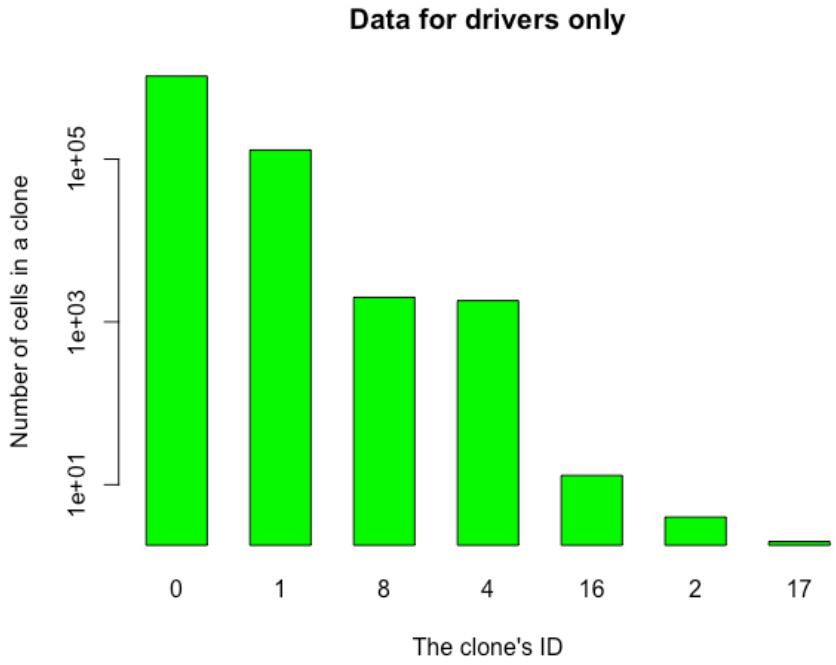

Data for drivers only
Number of cells in a clone
0e+00
2e+05
4e+05
6e+05
8e+05
1e+06
0
1
8
4
16
2
17
The clone's ID


Data for drivers only
Number of cells in a clone
1e+01
1e+03
1e+05
0
1
8
4
16
2
17
The clone's ID

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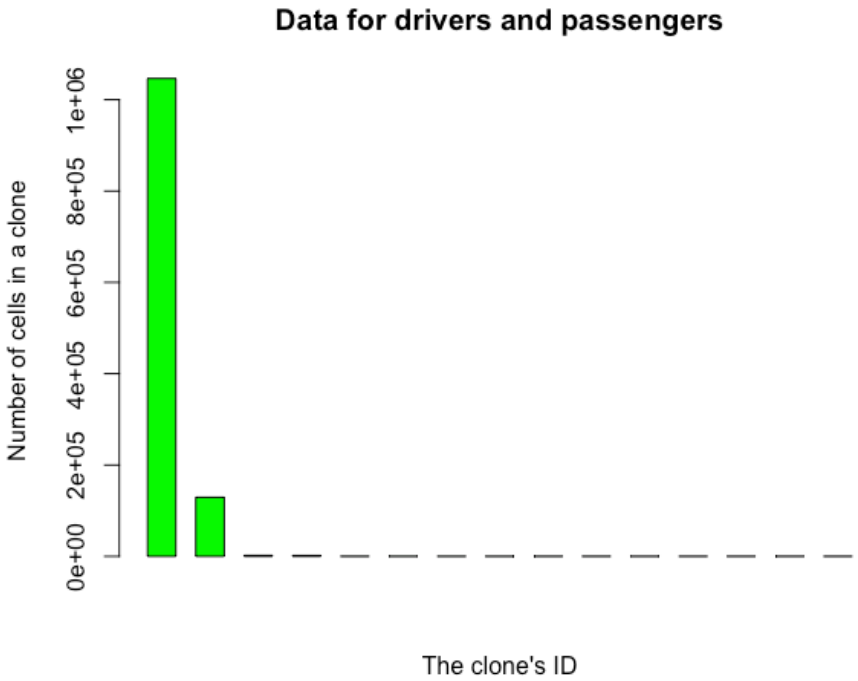
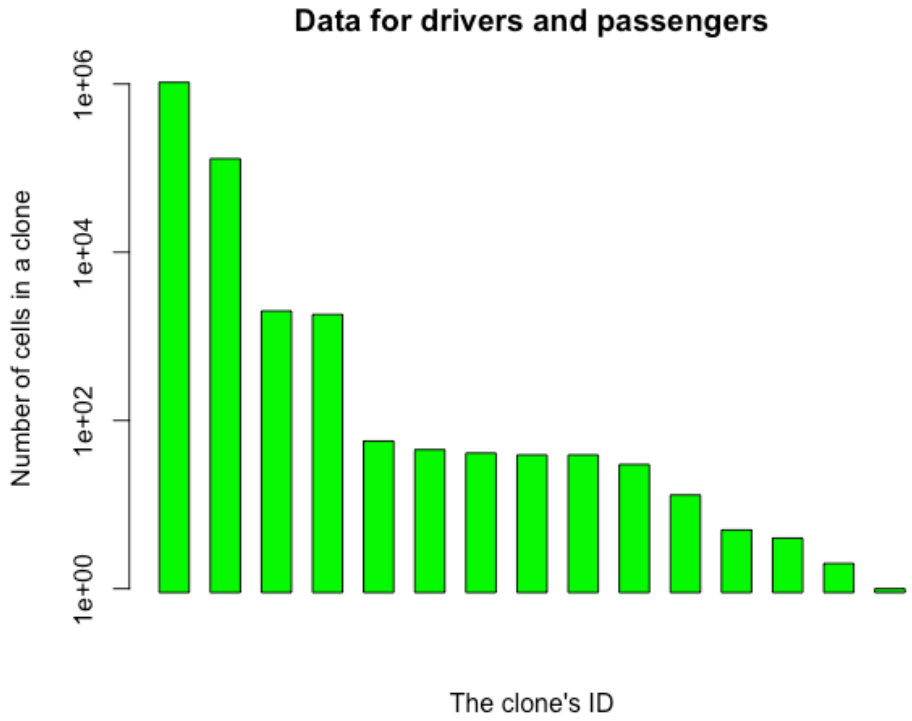

Data for drivers and passengers
Number of cells in a clone
0e+00
2e+05
4e+05
6e+05
8e+05
1e+06
The clone's ID


Data for drivers and passengers
Number of cells in a clone
1e+00
1e+02
1e+04
1e+06
The clone's ID

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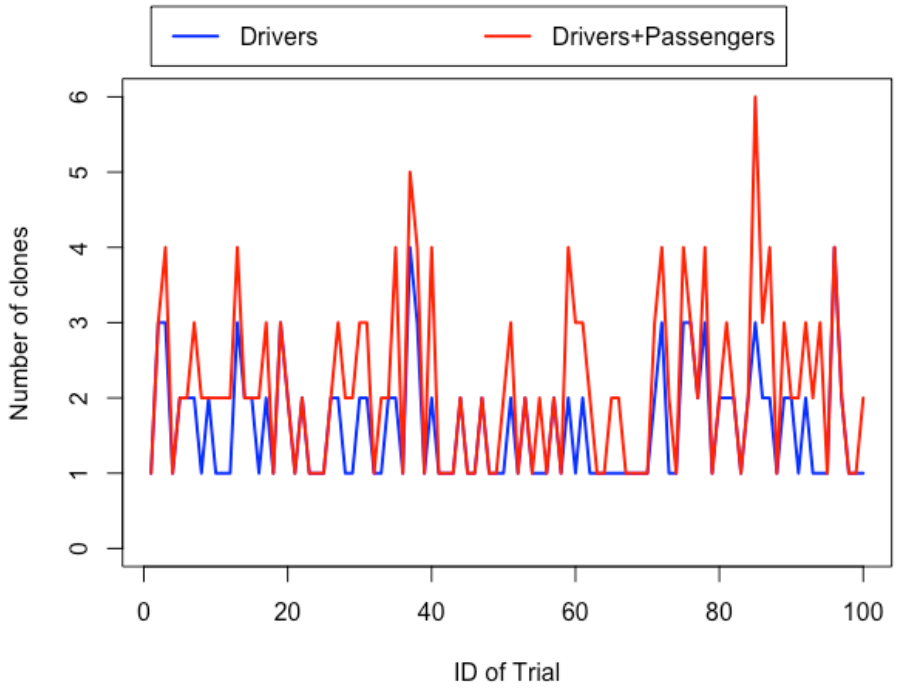
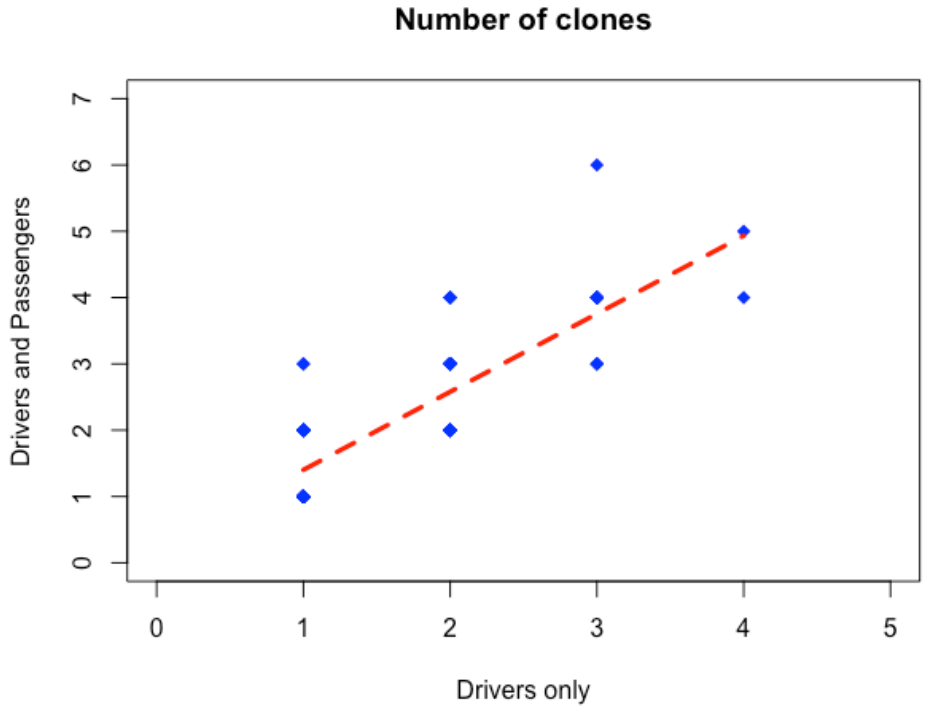

Drivers
Drivers+Passengers
Number of clones
0
1
2
3
4
5
6
0
20
40
60
80
100
ID of Trial


Number of clones
Drivers and Passengers
0
1
2
3
4
5
6
7
0
1
2
3
4
5
Drivers only

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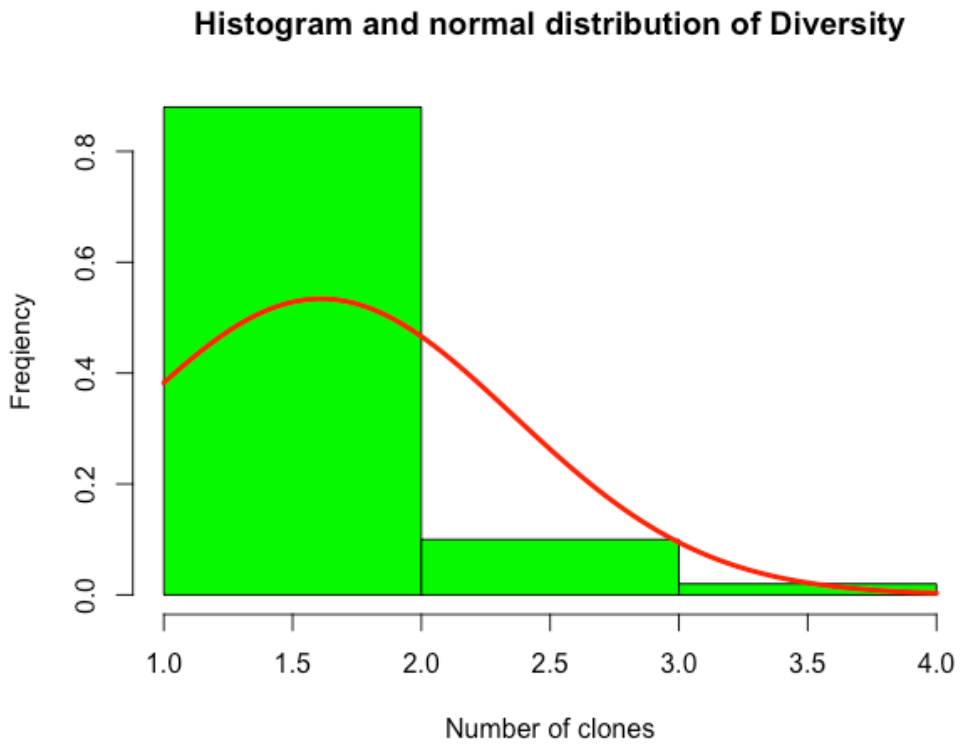
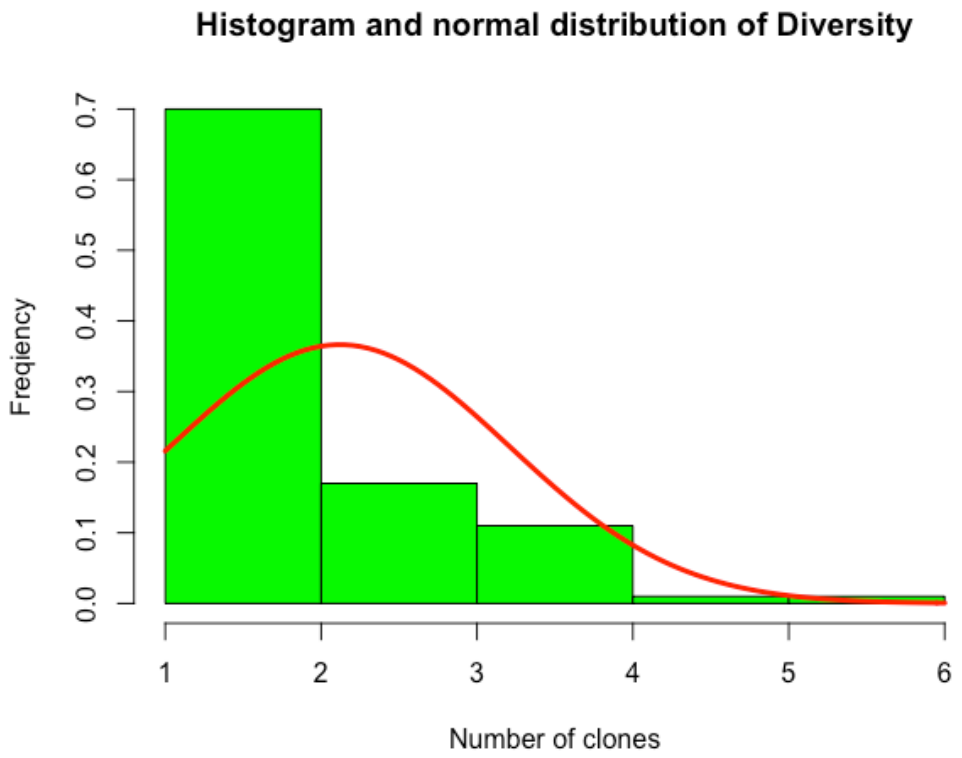
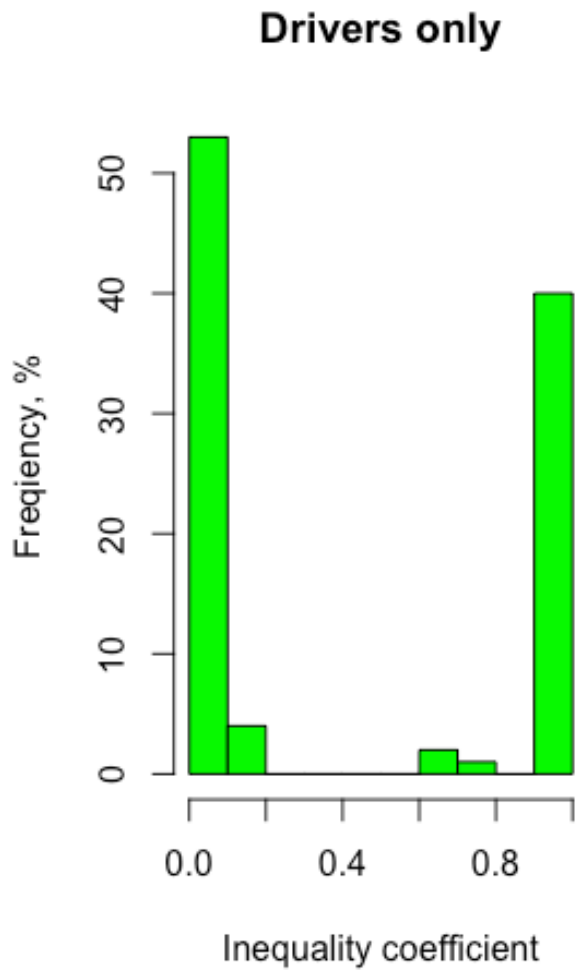
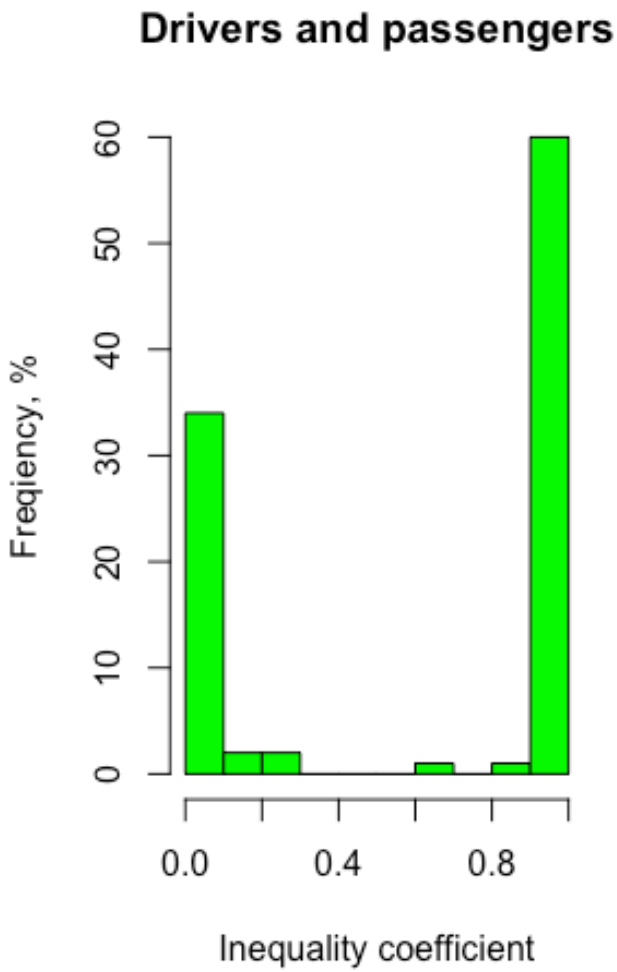
DRIVERS ONLY



Drivers and Passengers




Drivers only
Freqiency, %
0
10
20
30
40
50
0.0
0.4
0.8
Inequality coefficient


Drivers and passengers
Freqiency, %
0
10
20
30
40
50
60
0.0
0.4
0.8
Inequality coefficient

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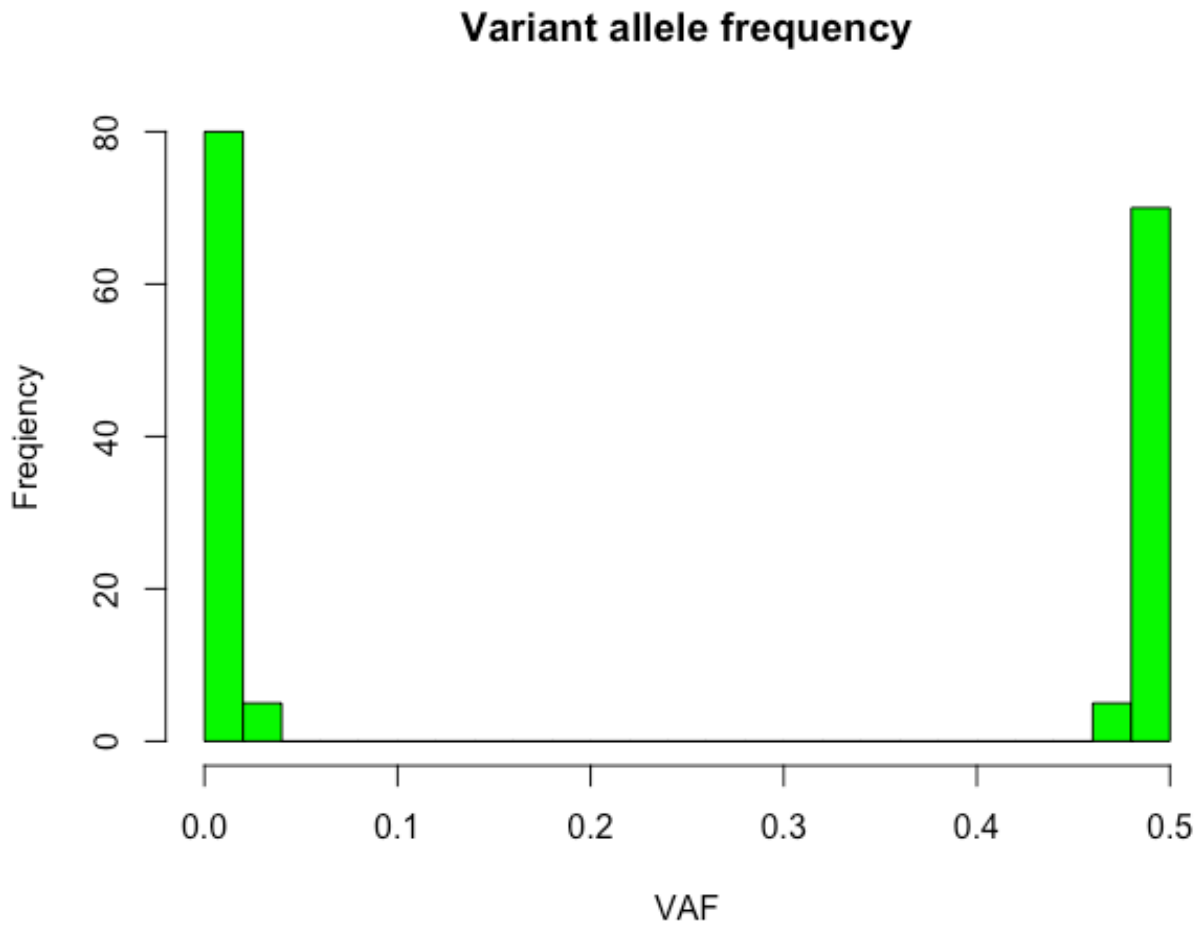
Variant allele frequency
Freqiency
0
20
40
60
80
0.0
0.1
0.2
0.3
0.4
0.5
VAF

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ORDER of GENE DYSFUNCTIONS		
[1] "GD - 129461"		
[1] "GB - 2005"		
[1] "GIM - 1822"		
[1] "GA - 13"		
[1] "GI - 4"		
[1] "GD->GA - 2"		

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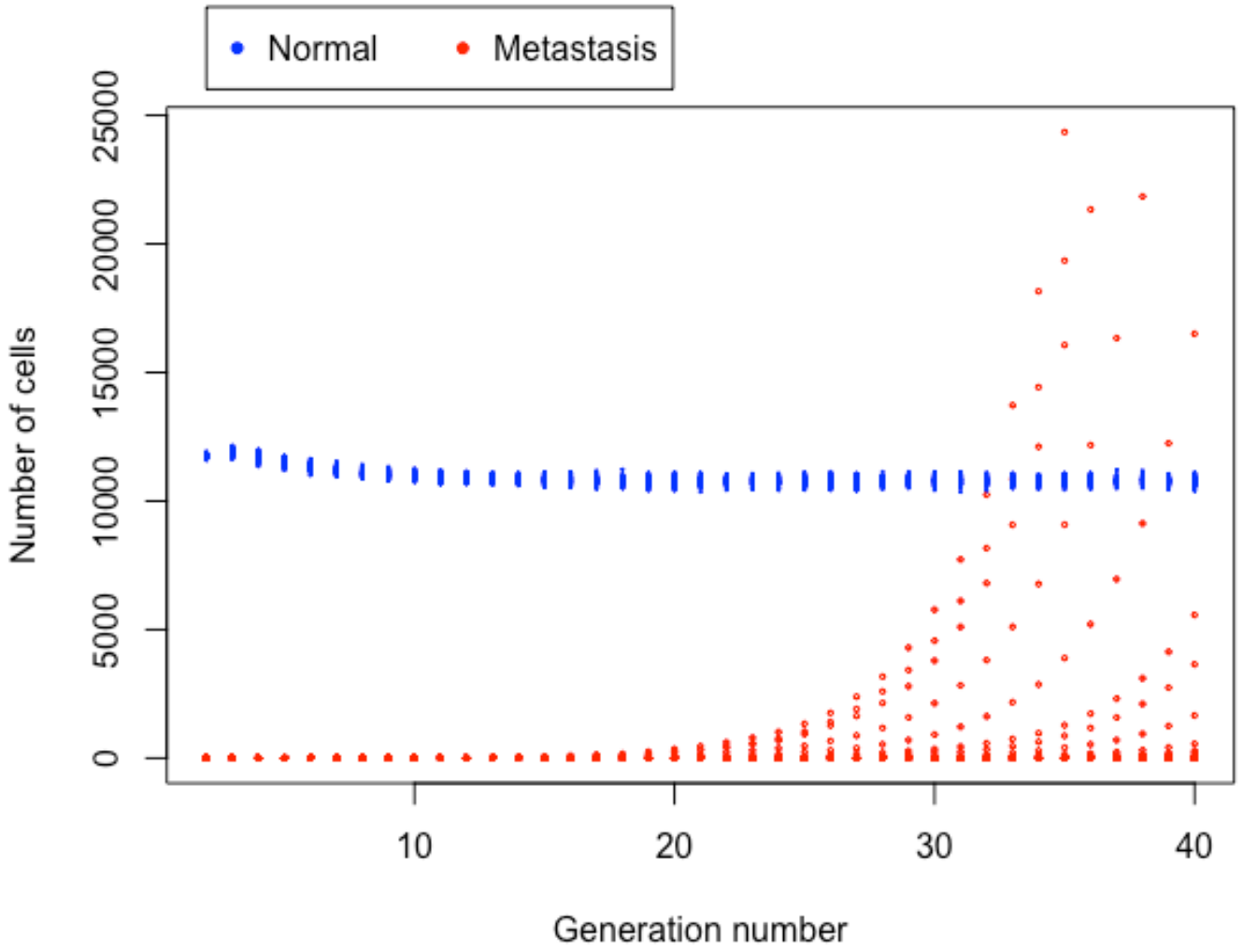
II. The results for many Hallmarks (one gene affects to all Hallmarks):



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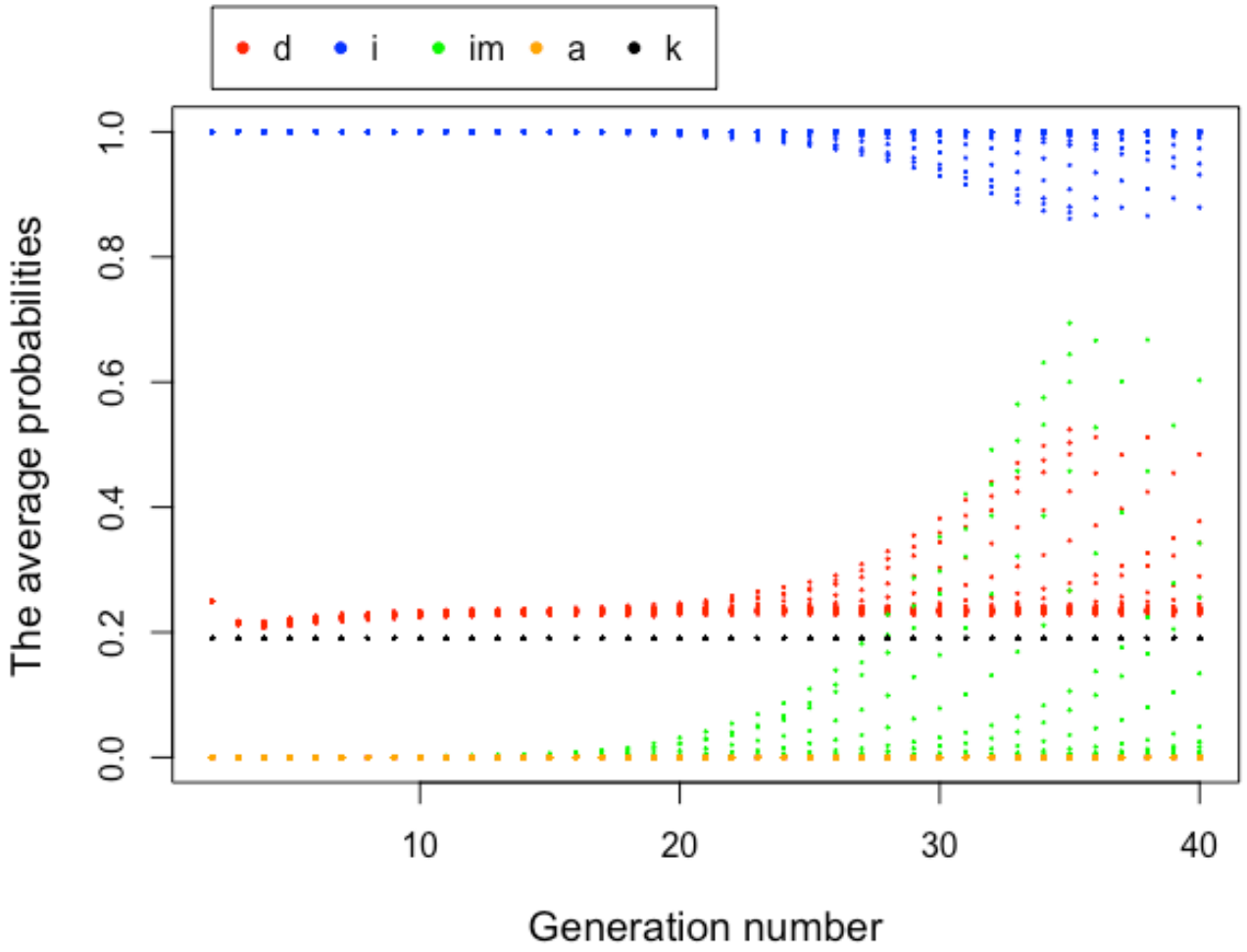
d
i
im
a
k
The average probabilities
0.0
0.2
0.4
0.6
0.8
1.0
10
20
30
40
Generation number

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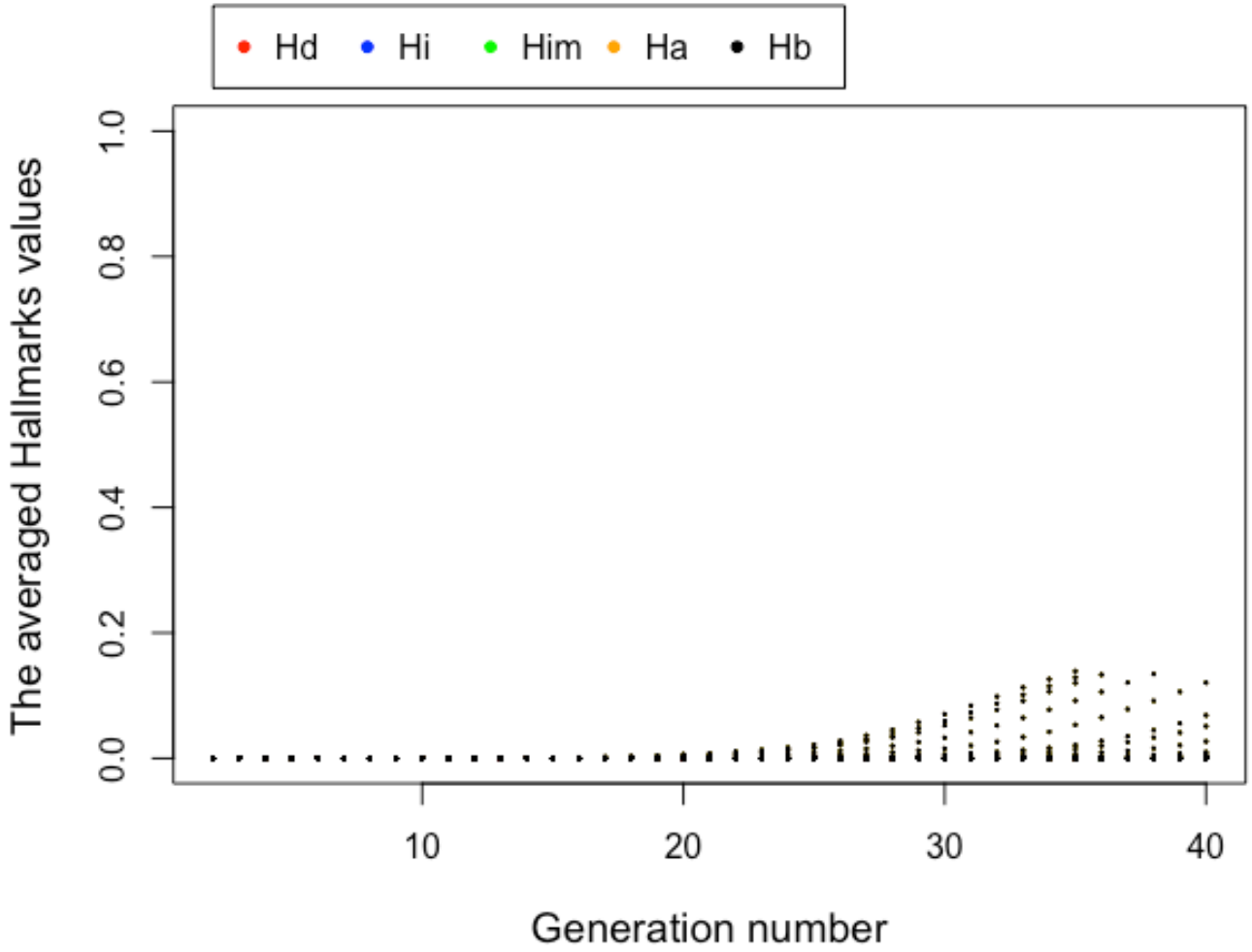
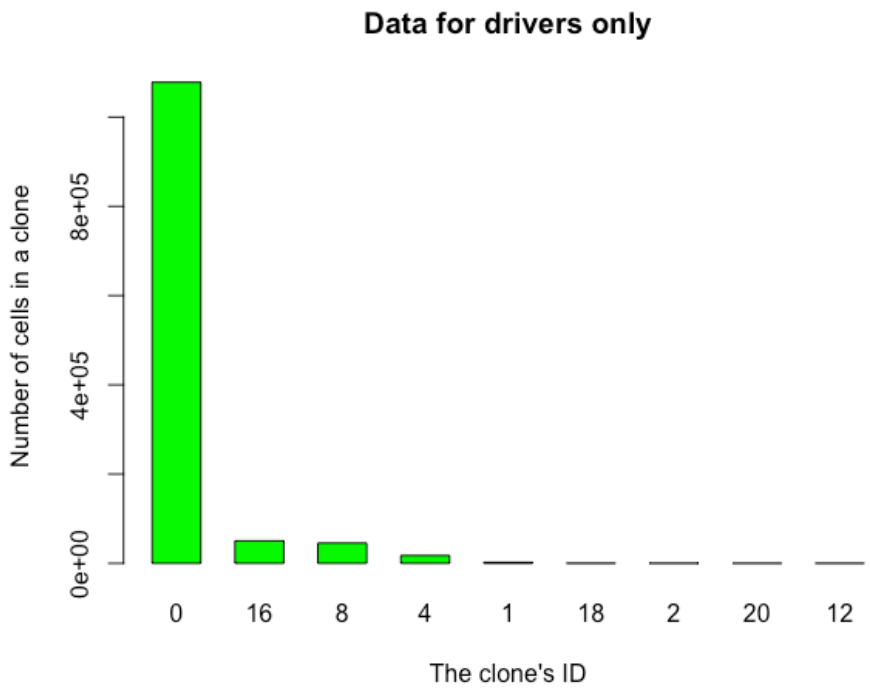
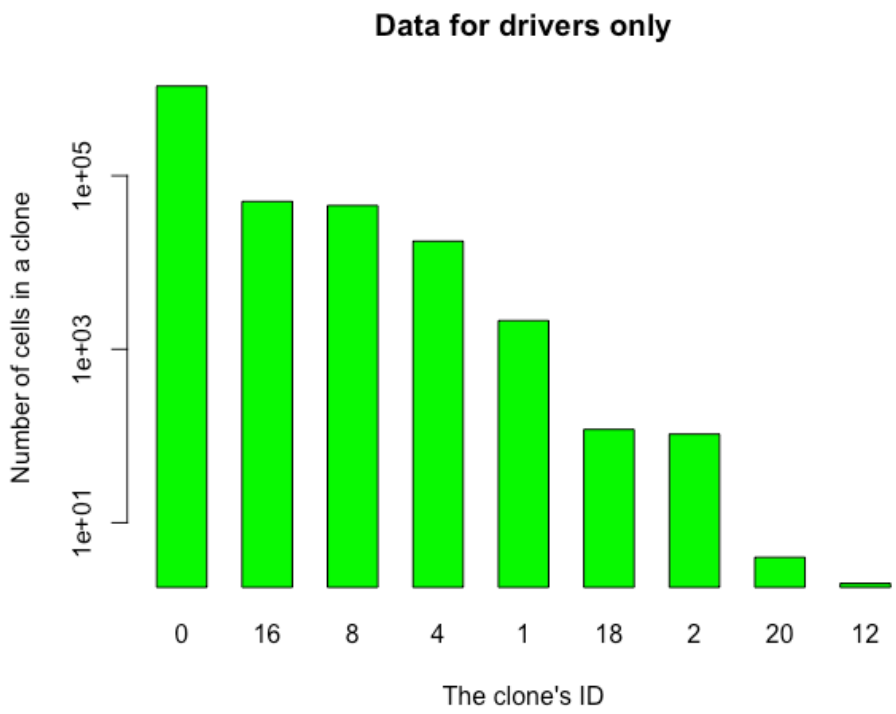

Hd
Hi
Him
Ha
Hb
The averaged Hallmarks values
0.0
0.2
0.4
0.6
0.8
1.0
10
20
30
40
Generation number

25.02.19


Data for drivers only
Number of cells in a clone
0e+00
4e+05
8e+05
0
16
8
4
1
18
2
20
12
The clone's ID


Data for drivers only
Number of cells in a clone
1e+01
1e+03
1e+05
0
16
8
4
1
18
2
20
12
The clone's ID

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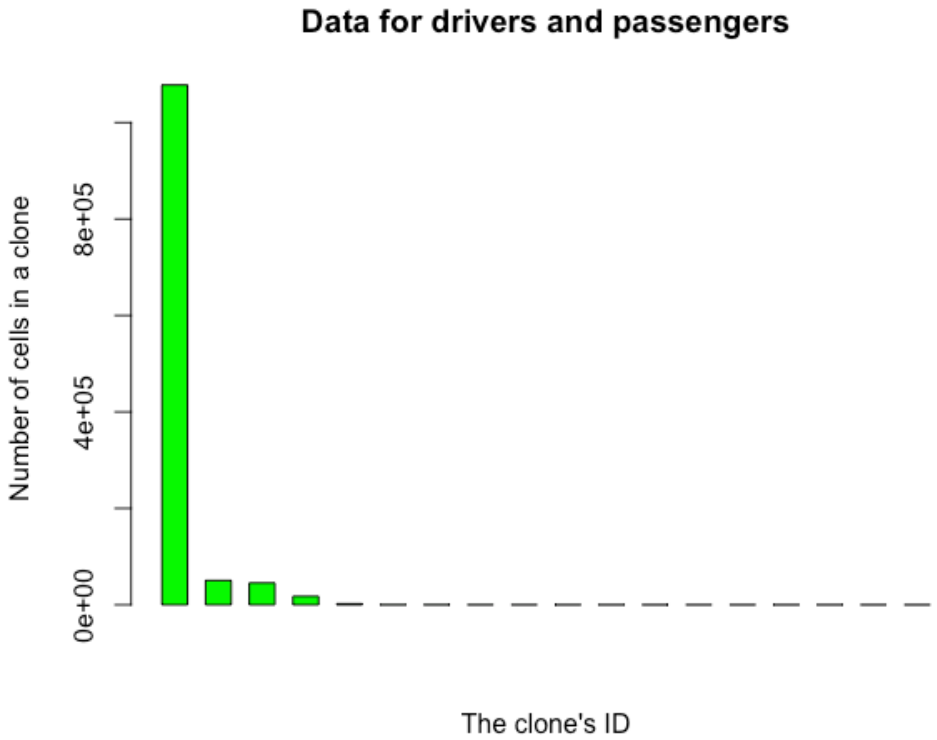
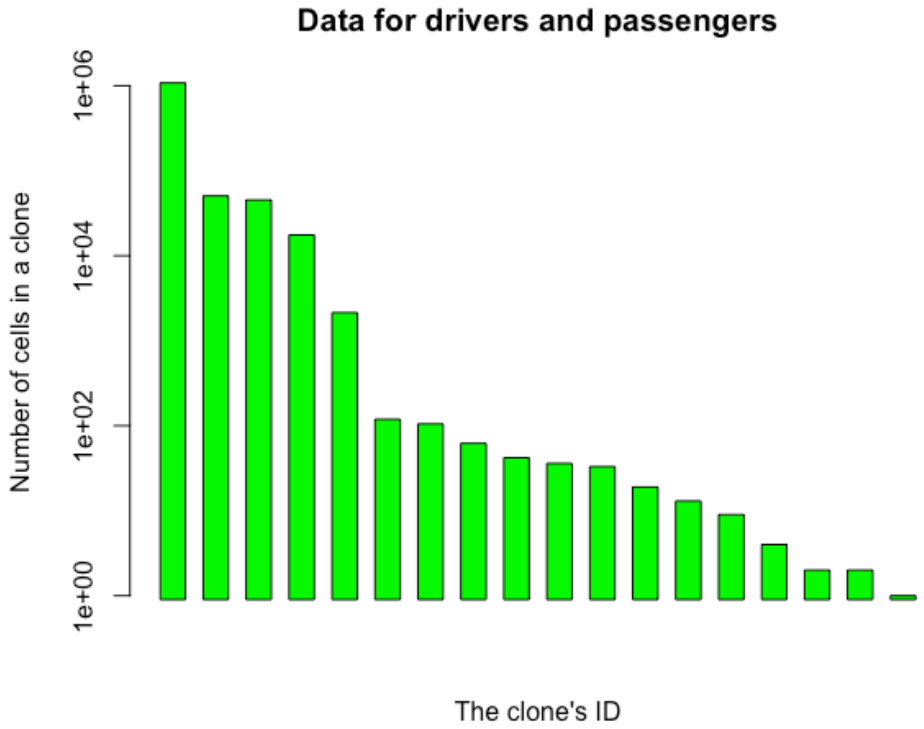

Data for drivers and passengers
Number of cells in a clone
0e+00
4e+05
8e+05
The clone's ID


Data for drivers and passengers
Number of cells in a clone
1e+00
1e+02
1e+04
1e+06
The clone's ID

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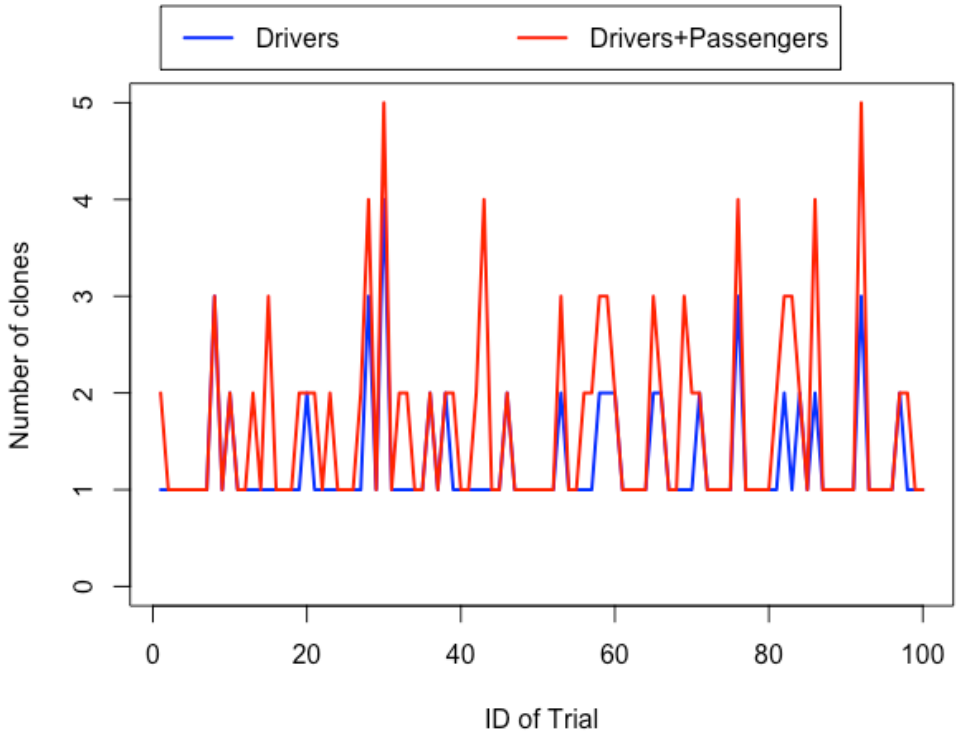
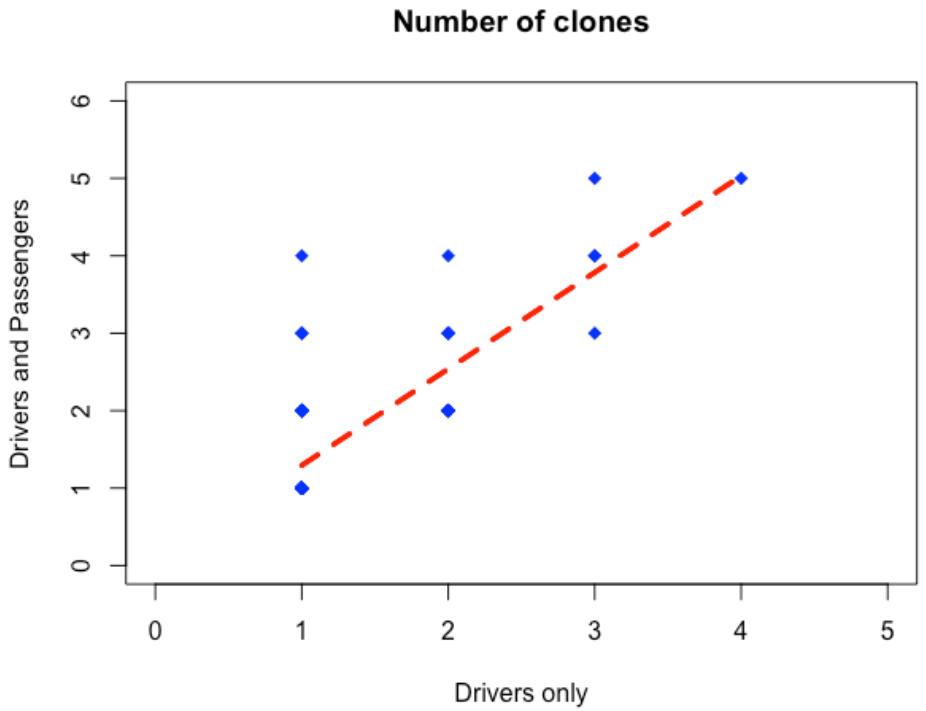

Drivers
Drivers+Passengers
Number of clones
ID of Trial
0
20
40
60
80
100
0
1
2
3
4
5


Number of clones
Drivers and Passengers
Drivers only
0
1
2
3
4
5
6

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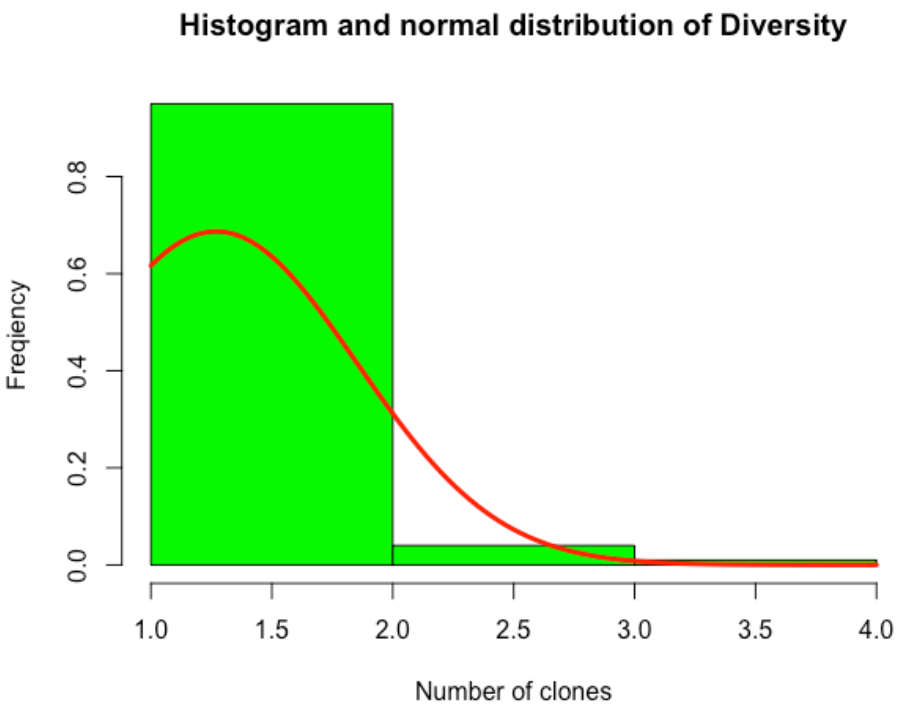
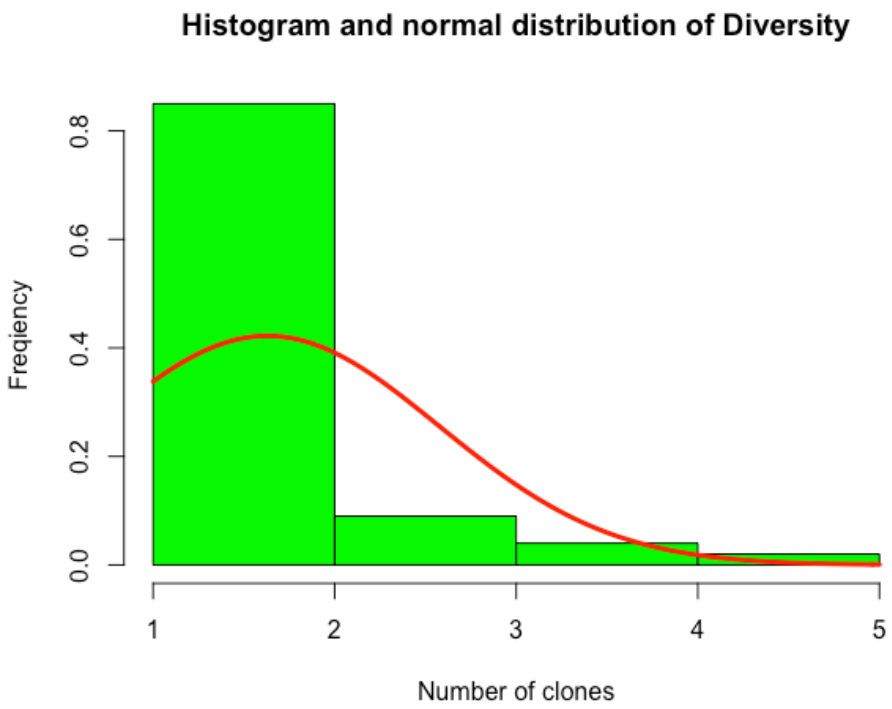
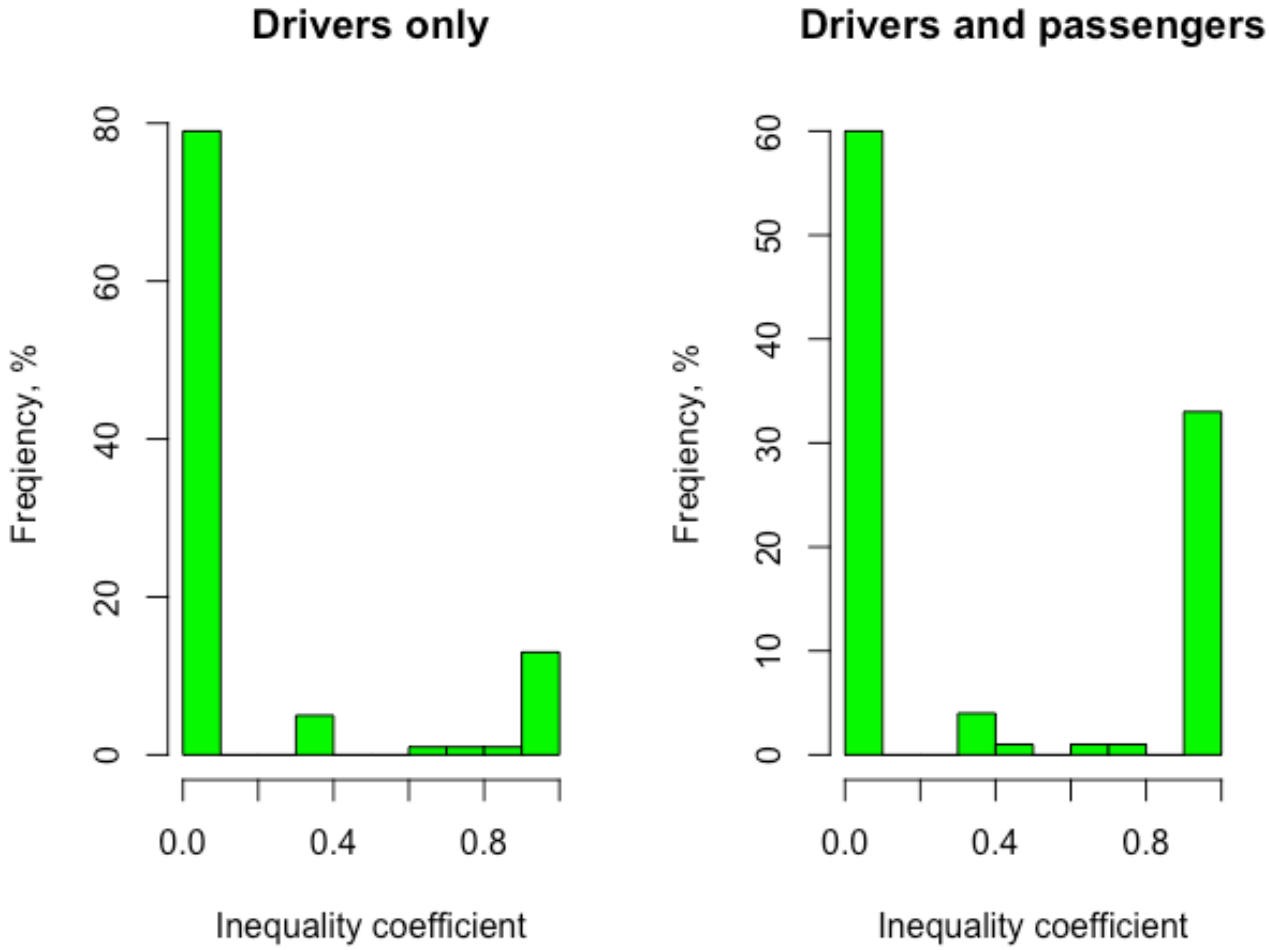
DRIVERS ONLY



Drivers and Passengers




Drivers only
Freqiency, %
0
20
40
60
80
0.0
0.4
0.8
Inequality coefficient
Drivers and passengers
Freqiency, %
0
10
20
30
40
50
60
0.0
0.4
0.8
Inequality coefficient

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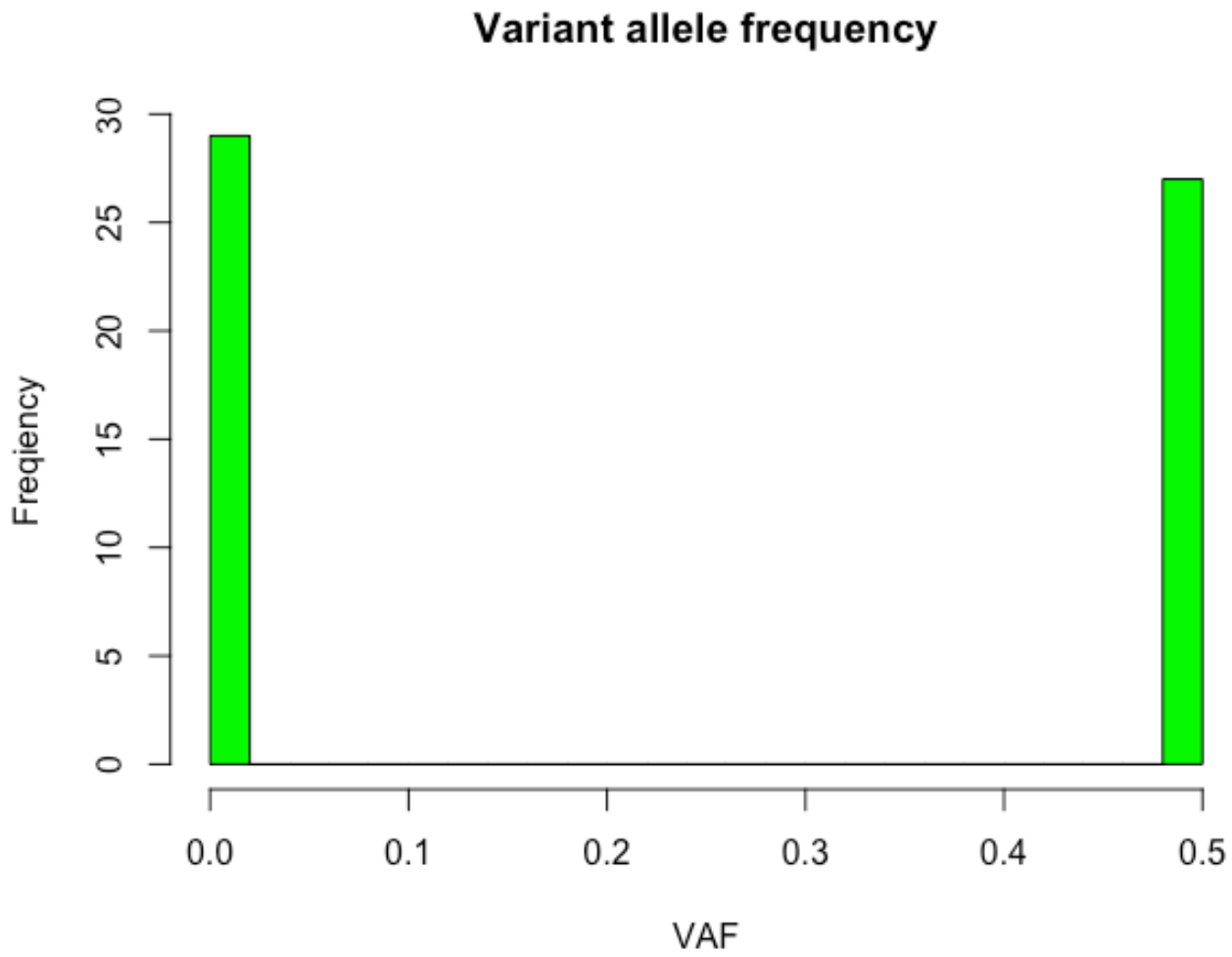
Variant allele frequency
Freqiency
0
5
10
15
20
25
30
0.0
0.1
0.2
0.3
0.4
0.5
VAF

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ORDER of GENE DYSFUNCTIONS		
[1] "GA - 50494"		
[1] "GB - 45303"		
[1] "GIM - 17603"		
[1] "GD - 2140"		
[1] "GA->GI - 119"		
[1] "GI - 105"		
[1] "GA->GIM - 4"		
[1] "GIM->GB - 2"		

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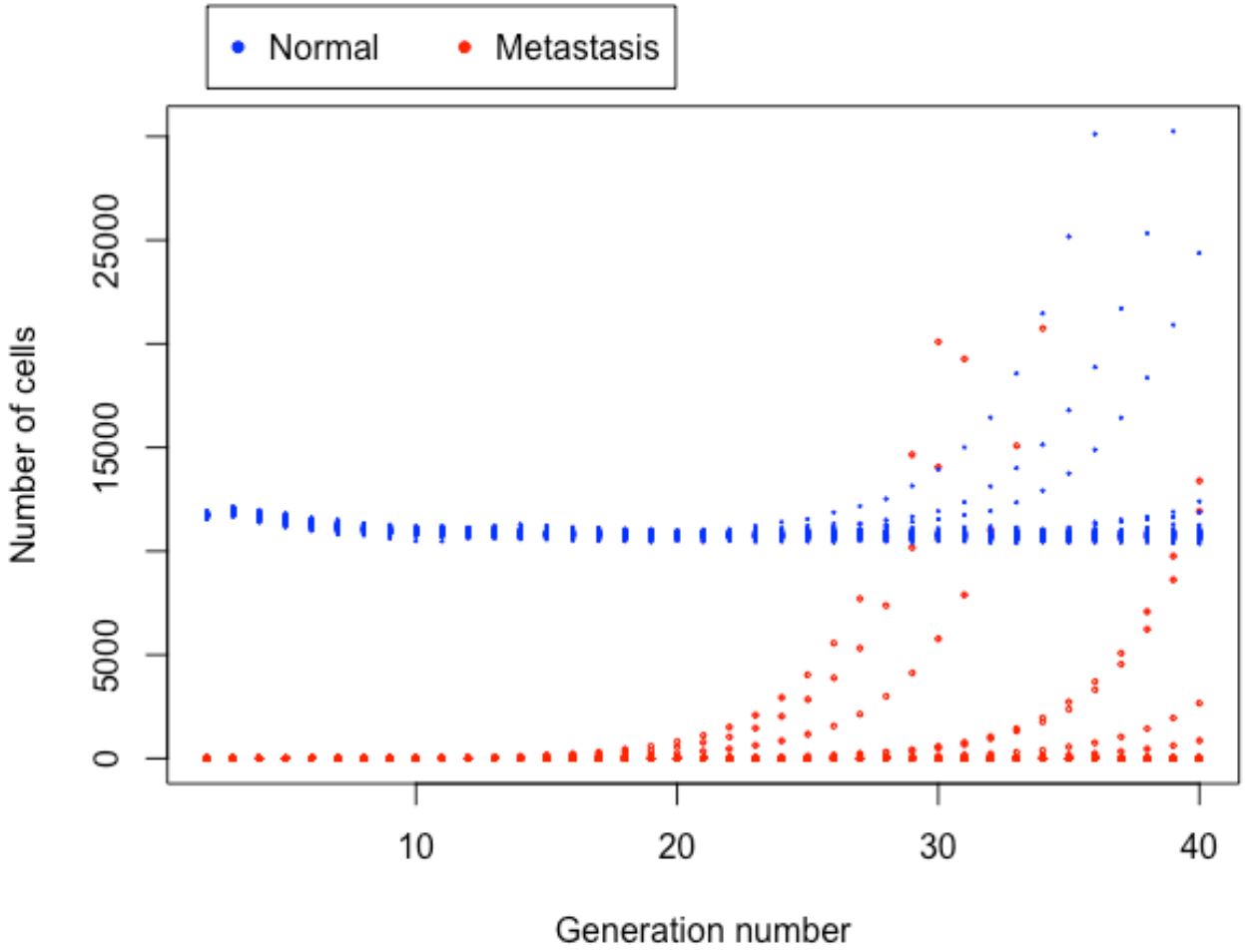
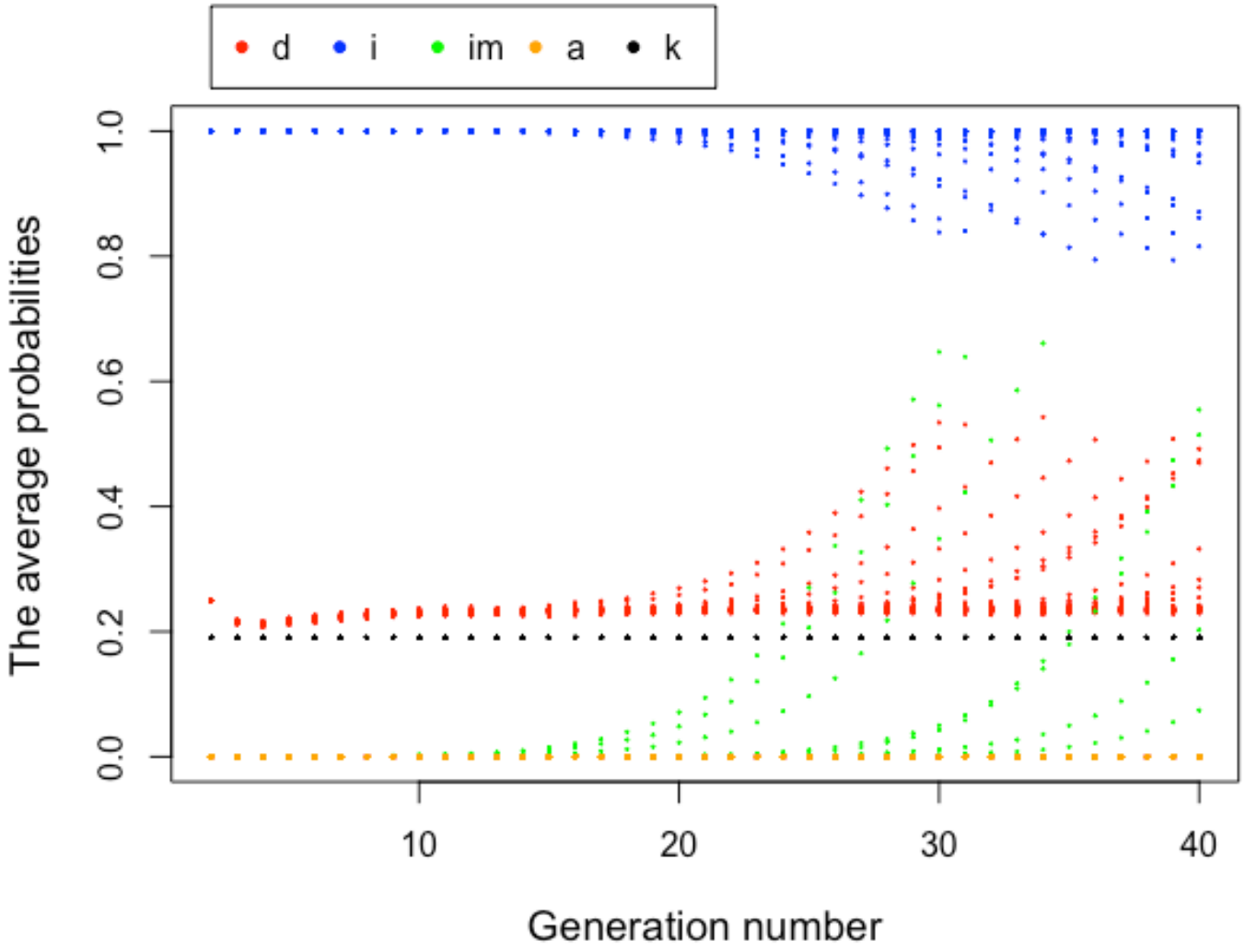
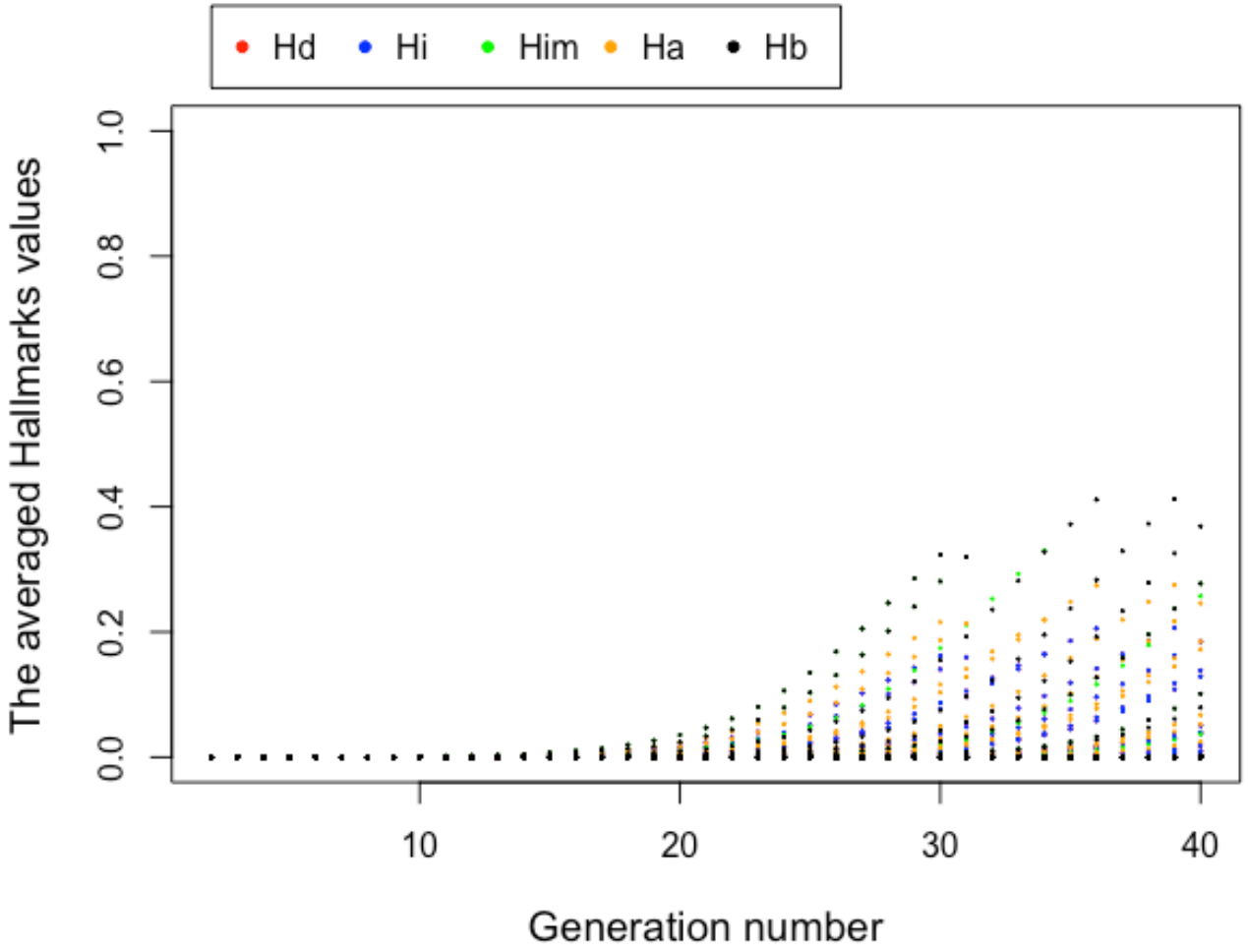
III. More realistic case (colorectal cancer data)

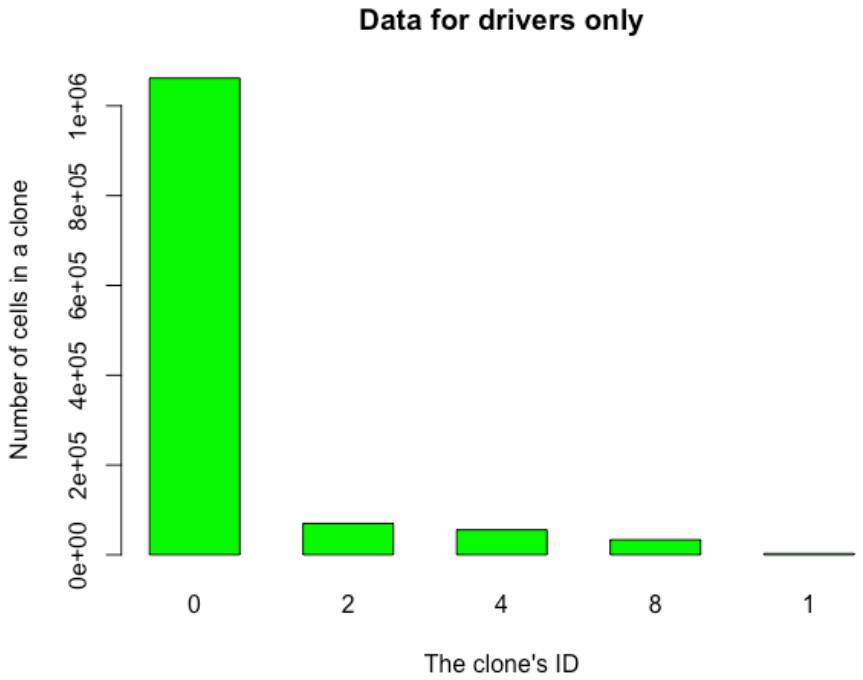


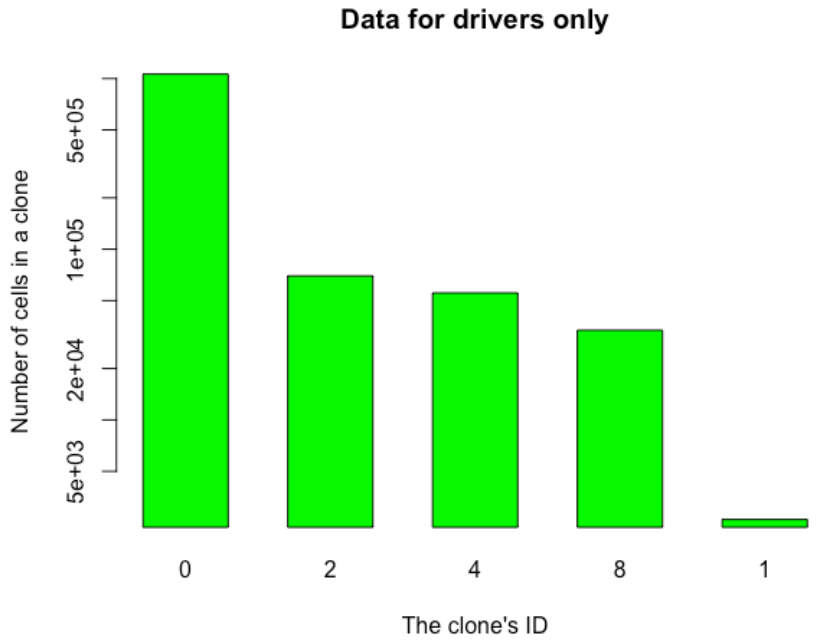

d
i
im
a
k
The average probabilities
0.0
0.2
0.4
0.6
0.8
1.0
10
20
30
40
Generation number

25.02.19


Hd
Hi
Him
Ha
Hb
The averaged Hallmarks values
0.0
0.2
0.4
0.6
0.8
1.0
10
20
30
40
Generation number

25.02.19


Data for drivers only
Number of cells in a clone
0e+00
2e+05
4e+05
6e+05
8e+05
1e+06
0
2
4
8
1
The clone's ID


Data for drivers only
Number of cells in a clone
5e+03
2e+04
1e+05
5e+05
0
2
4
8
1
The clone's ID

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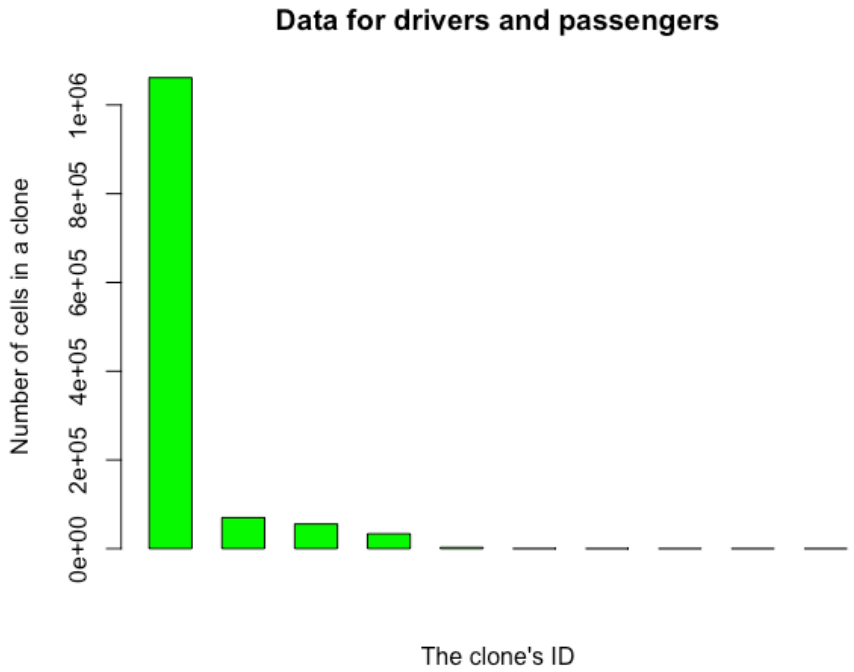
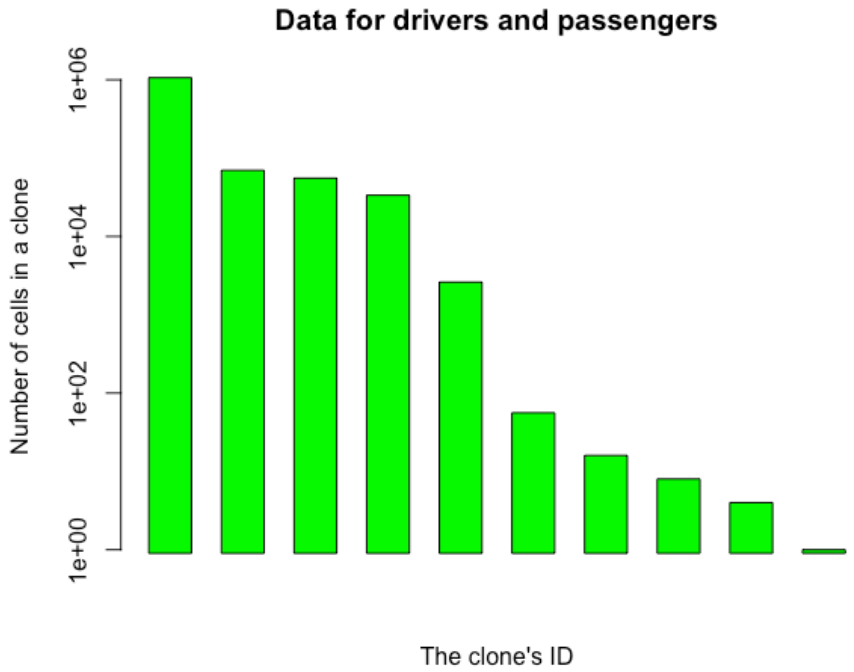

Data for drivers and passengers
Number of cells in a clone
0e+00
2e+05
4e+05
6e+05
8e+05
1e+06
The clone's ID


Data for drivers and passengers
Number of cells in a clone
1e+00
1e+02
1e+04
1e+06
The clone's ID

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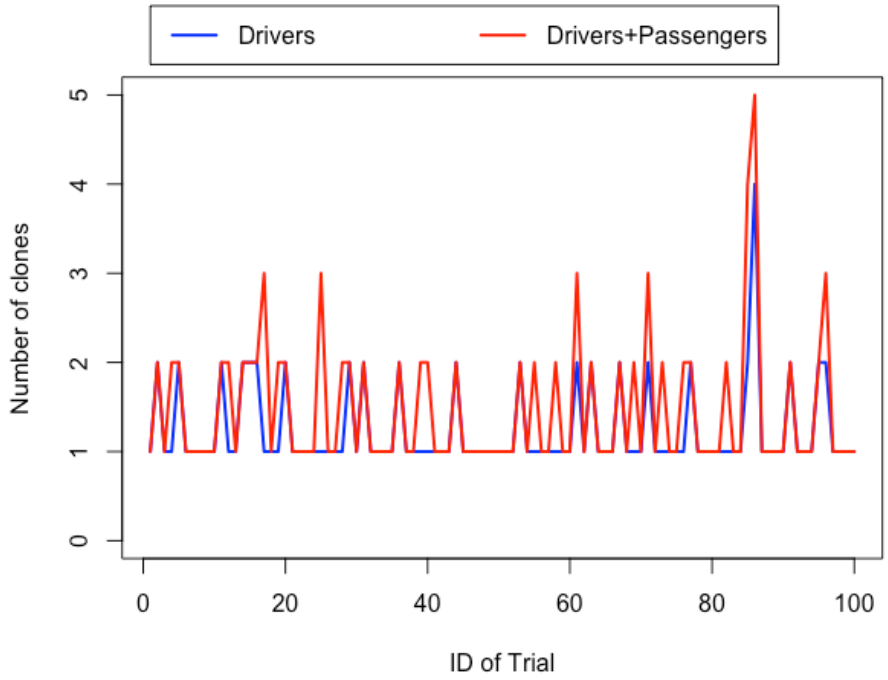
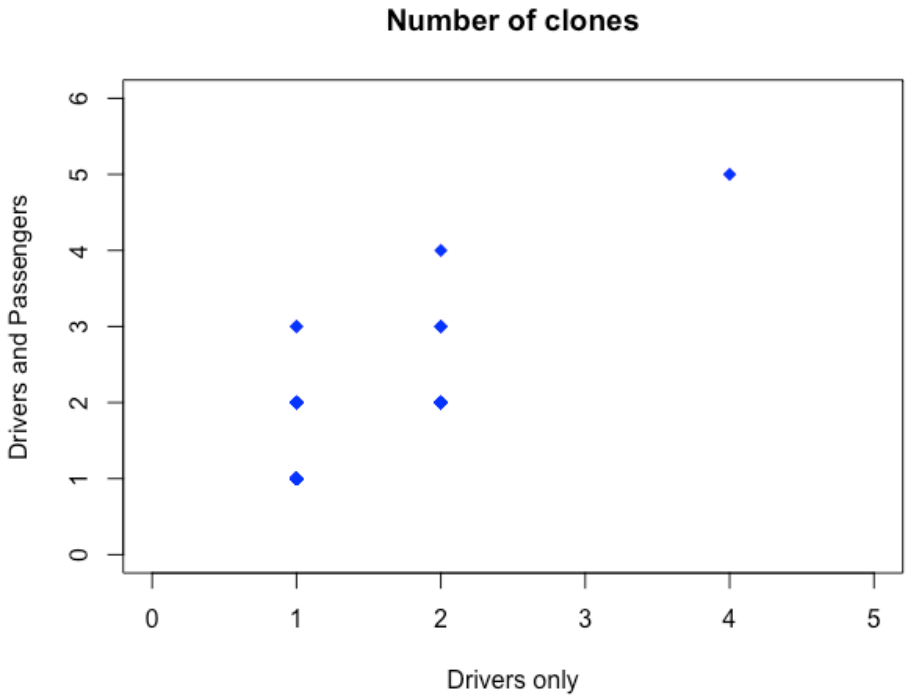

Drivers
Drivers+Passengers
Number of clones
ID of Trial
0
20
40
60
80
100
0
1
2
3
4
5


Number of clones
Drivers and Passengers
Drivers only
0
1
2
3
4
5
6

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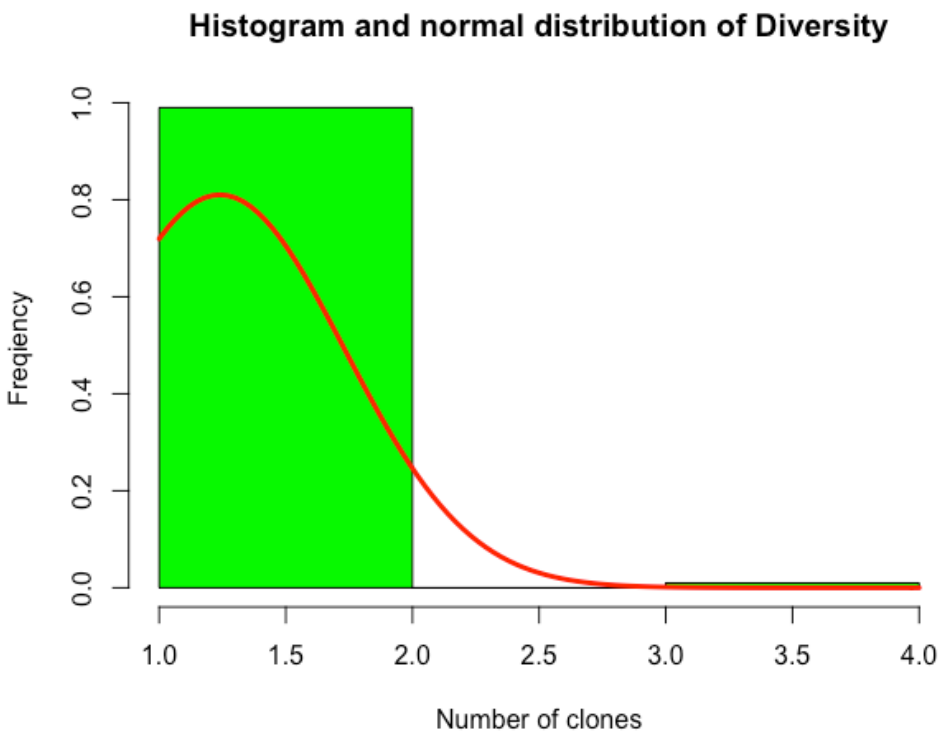
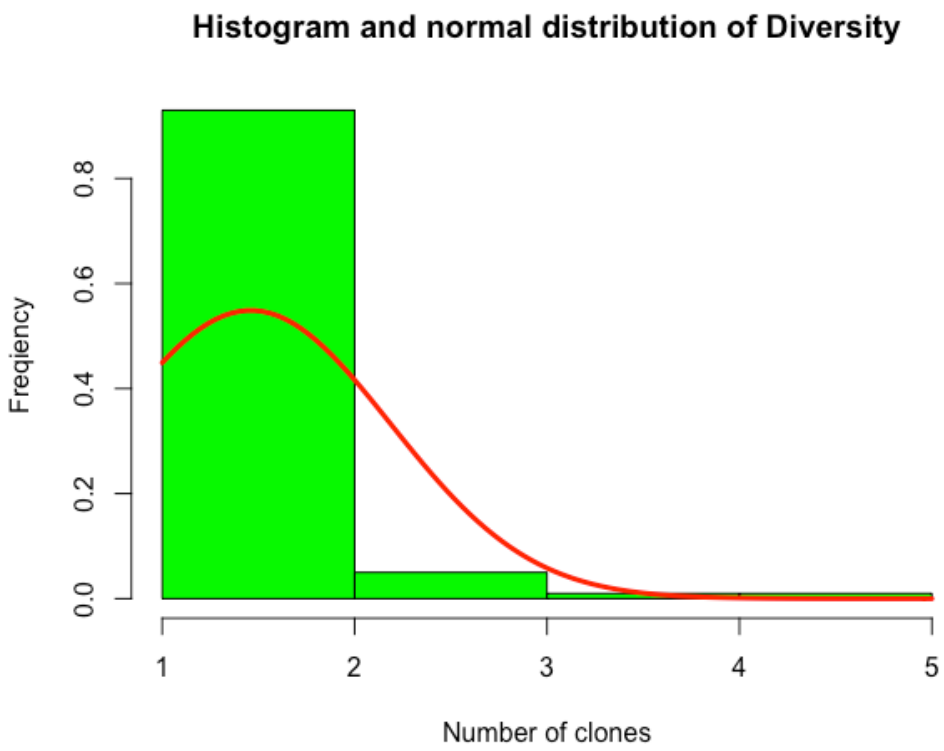
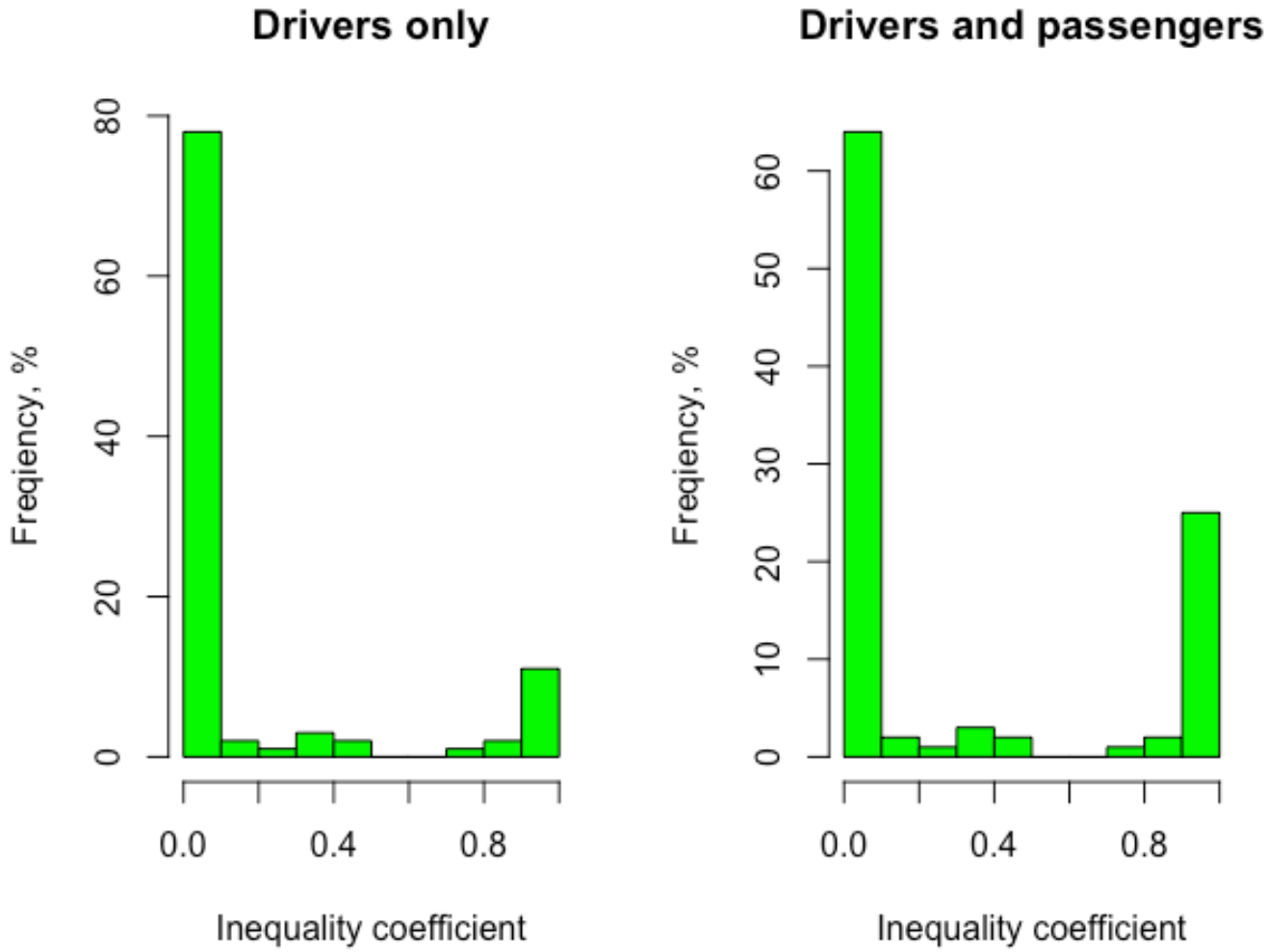
DRIVERS ONLY



Drivers and Passengers




Drivers only
Freqiency, %
0
20
40
60
80
0.0
0.4
0.8
Inequality coefficient
Drivers and passengers
Freqiency, %
0
10
20
30
40
50
60
0.0
0.4
0.8
Inequality coefficient

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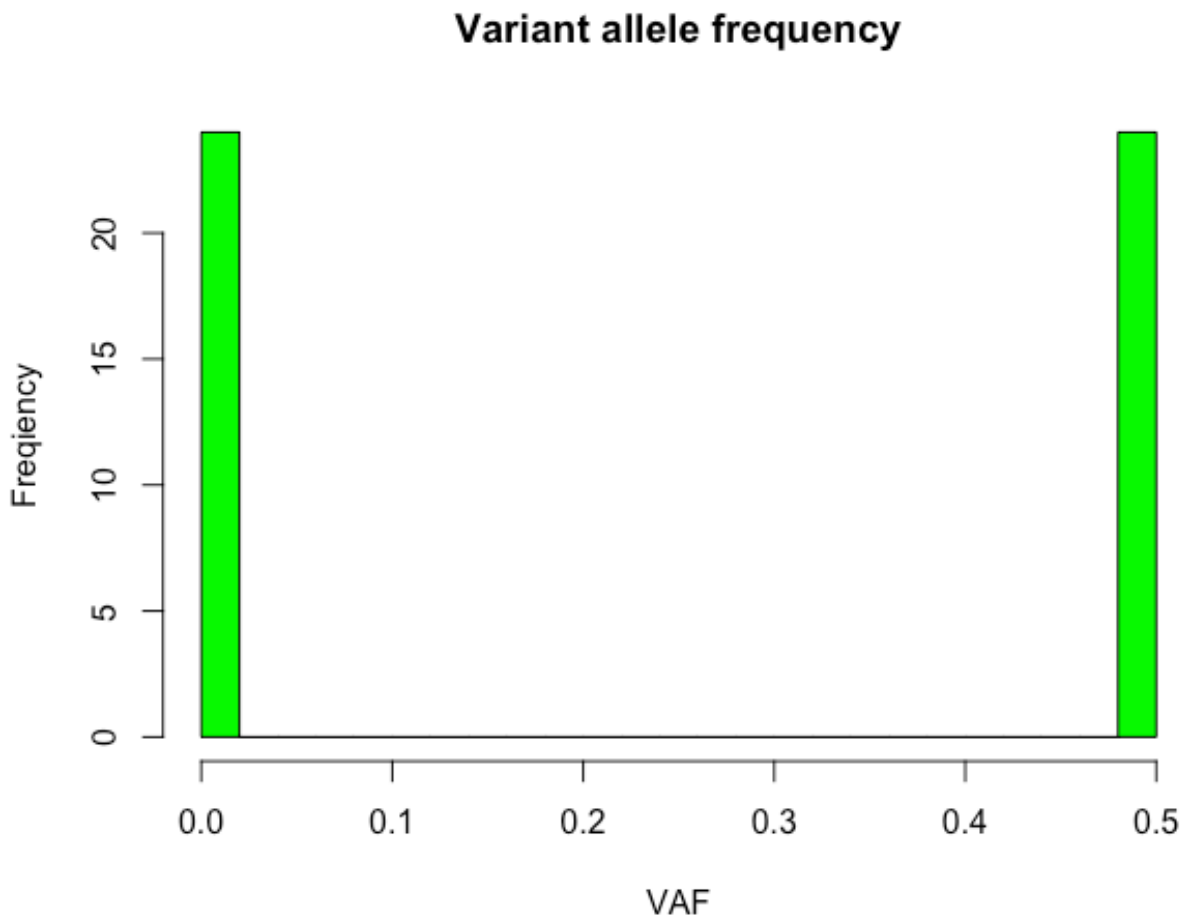
Variant allele frequency
Freqiency
0
5
10
15
20
0.0
0.1
0.2
0.3
0.4
0.5
VAF

25.02.19

ORDER of GENE DYSFUNCTIONS		
[1] "TP53 - 69799"		
[1] "KRAS - 55445"		
[1] "APC - 33535"		
[1] "PIK3CA - 2610"		