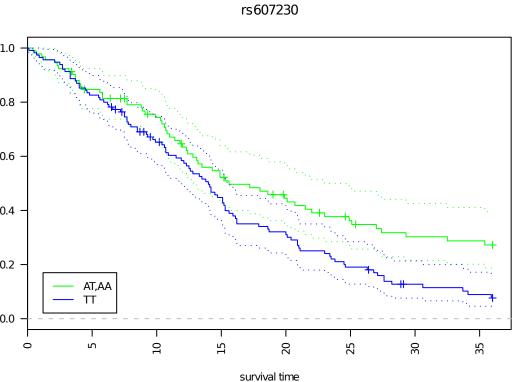
This marker has a genotype specific effect with a p-value of 5.356426e-03. Odds ratios have been estimated using logistic regression at $t \approx 36$:

$$\frac{P(\text{event}|\text{AT},\text{AA})/P(\neg \text{event}|\text{AT},\text{AA})}{P(\text{event}|\text{TT})/P(\neg \text{event}|\text{TT})} \approx 0.354.$$

genotype	total N	events	censored
TT	115	96 (0.835)	19 (0.165)
AT,AA	92	59 (0.641)	33 (0.359)



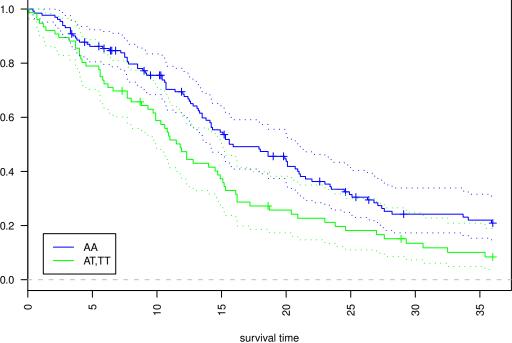
This marker has a genotype specific effect with a p-value of 3.726115e-03.

Odds ratios have been estimated using logistic regression at $t \approx 36$:

Odds ratios have been estimated using logistic regression a	$\iota\iota\iota\iota\sim\iota$
$\frac{P(\text{event} AT,TT)/P(\neg\text{event} AT,TT)}{P(\neg\text{event} AA)/P(\neg\text{event} AA)} \approx 2.692.$	
$P(\text{event} AA)/P(\text{\neg event} AA)$	

genotype	total N	events	censored
AA	131	90 (0.687)	41 (0.313)
AT,TT	76	$65 \ (0.855)$	$11 \ (0.145)$

rs17532679



censored

36 (0.298)

This marker has a genotype specific effect with a p-value of 9.466737e-03. Total of 1 observation deleted due to missingness. Odds ratios have been estimated using logistic regression at $t \approx 36$: $\frac{P(\text{event}|\text{AT,TT})/P(\neg \text{event}|\text{AT,TT})}{P(\text{event}|\text{AA})/P(\neg \text{event}|\text{AA})} \approx 1.826.$

events

85 (0.702)

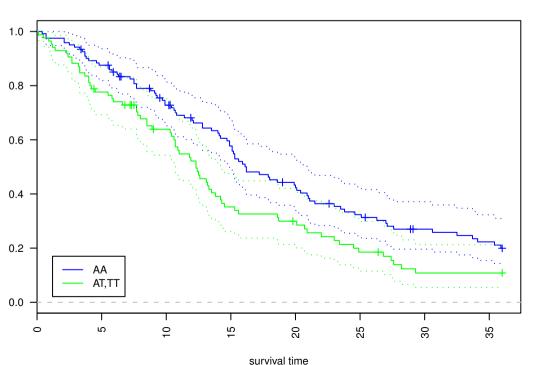
total N

genotype

AA

_	AT,TT	85	69 (0.812)	$16 \ (0.188)$
			154238	

121



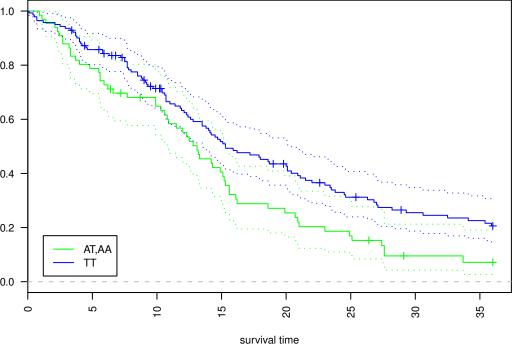
This marker has a genotype specific effect with a p-value of 7.774728e-03.

Odds ratios have been estimated using logistic regression at $t\thickapprox36$:

$$\frac{\text{P (event|AT,AA)/P (\neg event|AT,AA)}}{\text{P (event|TT)/P (\neg event|TT)}} \thickapprox 2.779.$$

genotype	total N	events	censored
TT	141	98 (0.695)	43 (0.305)
AT,AA	66	57 (0.864)	9(0.136)





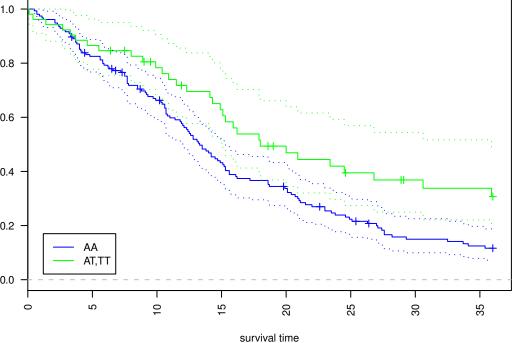
This marker has a genotype specific effect with a p-value of $7.135140 \mathrm{e}\text{-}03$.

Odds ratios have been estimated using logistic regression at $t\thickapprox 36$:

$$\frac{\text{P (event|AT,TT)/P (\neg event|AT,TT)}}{\text{P (event|AA)/P (\neg event|AA)}} \approx 0.369.$$

genotype	total N	events	censored
AA	155	124 (0.8)	31 (0.2)
AT,TT	52	$31\ (0.596)$	21 (0.404)

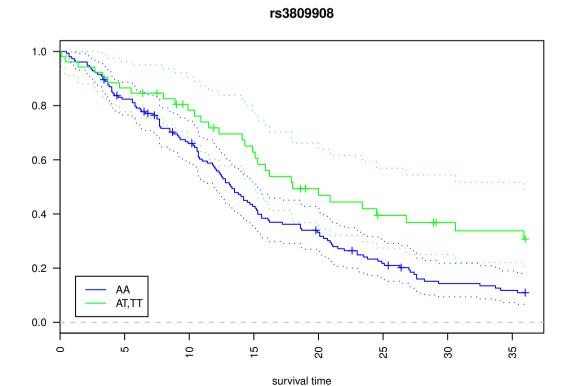




This marker has a genotype specific effect with a p-value of 5.311930e-03. Total of 1 observation deleted due to missingness. Odds ratios have been estimated using logistic regression at $t \approx 36$:

$$\frac{\text{P (event|AT,TT)/P (\neg event|AT,TT)}}{\text{P (event|AA)/P (\neg event|AA)}} \approx 0.357.$$

genotype	total N	events	censored
AA	154	124 (0.805)	30 (0.195)
AT,TT	52	$31\ (0.596)$	21 (0.404)



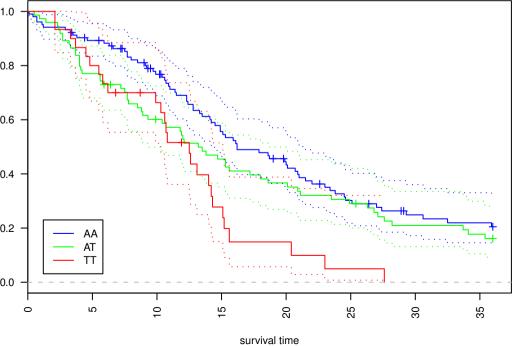
This marker has a genotype specific effect with a p-value of $3.812266\mathrm{e}\text{-}03.$

Odds ratios have been estimated using logistic regression at $t\thickapprox36$:

$$\frac{P(\text{event}|\text{AT})/P(\neg \text{event}|\text{AT})}{P(\text{event}|\text{AA})/P(\neg \text{event}|\text{AA})} \approx 1.634 \text{ and } \frac{P(\text{event}|\text{TT})/P(\neg \text{event}|\text{TT})}{P(\text{event}|\text{AA})/P(\neg \text{event}|\text{AA})} \approx 2.93.$$

genotype	total N	events	censored
AA	103	71 (0.689)	32 (0.311)
AT	74	58 (0.784)	16(0.216)
$_{-}$ TT	30	$26 \ (0.867)$	4(0.133)

rs6077759

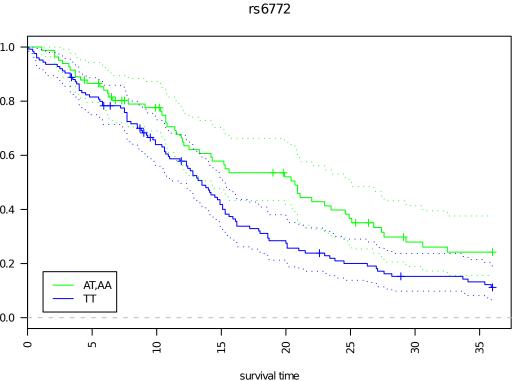


This marker has a genotype specific effect with a p-value of 7.746774e-03.

Odds ratios have been estimated using logistic regression at t \approx 36:

$$\frac{P(\text{event}|\text{AT},\text{AA})/P(\neg \text{event}|\text{AT},\text{AA})}{P(\text{event}|\text{TT})/P(\neg \text{event}|\text{TT})} \approx 0.412.$$

genotype	total N	events	censored
TT	125	102 (0.816)	23 (0.184)
AT,AA	82	53 (0.646)	29 (0.354)



This marker has a genotype specific effect with a p-value of 7.062309e-03.

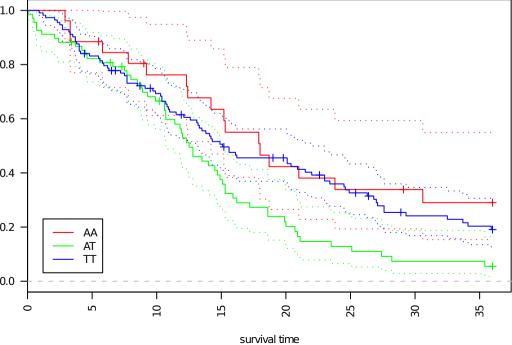
Odds ratios have been estimated using logistic regression at t \approx 36:

P (eventIAT) / P (¬eventIAT)

$\frac{P \text{ (event AT)}/P \text{ (}\neg\text{event AT)}}{P \text{ (event TT)}/P \text{ (}\neg\text{event TT)}} \approx 2.047 \text{ and}$	$P (\text{event} AA) / P (\neg \text{event} AA) \sim 0.746$
$P(\text{event} TT)/P(\neg \text{event} TT) \sim 2.047 \text{ and}$	$P(\text{event} TT)/P(\neg \text{event} TT)$ ~ 0.740.

genotype	total N	events	censored
TT	113	81 (0.717)	32 (0.283)
AT	68	57 (0.838)	11 (0.162)
AA	26	17 (0.654)	9 (0.346)

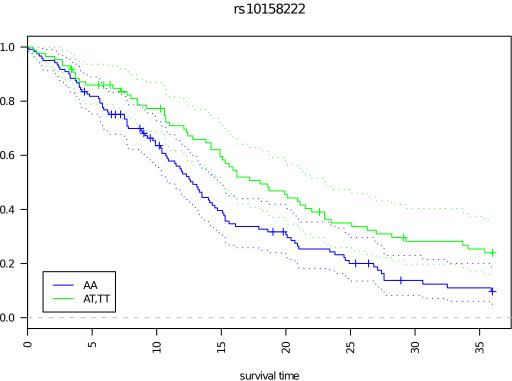
rs11242316



This marker has a genotype specific effect with a p-value of 4.042413e-03. Odds ratios have been estimated using logistic regression at $t \approx 36$:

$$\frac{\text{P (event|AT,TT)/P (\neg event|AT,TT)}}{\text{P (event|AA)/P (\neg event|AA)}} \approx 0.632.$$

genotype	total N	events	censored
AA	121	95 (0.785)	26 (0.215)
AT,TT	86	60 (0.698)	26 (0.302)

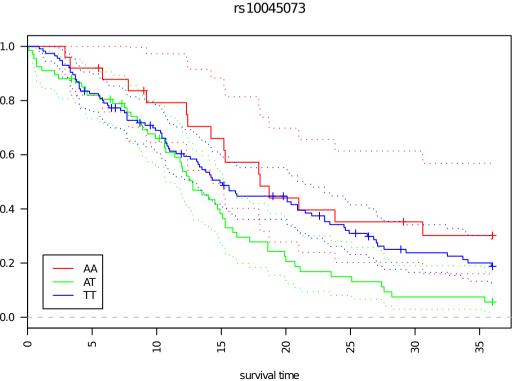


This marker has a genotype specific effect with a p-value of 9.680628e-03.

Odds ratios have been estimated using logistic regression at $t \approx 36$:

 $\frac{P \, (\text{event} | \text{AT}) / \, P \, (\neg \text{event} | \text{AT})}{P \, (\text{event} | \text{TT}) / \, P \, (\neg \text{event} | \text{TT})} \, \approx \, 1.963 \, \, \text{and} \, \, \frac{P \, (\text{event} | \text{AA}) / \, P \, (\neg \text{event} | \text{AA})}{P \, (\text{event} | \text{TT}) / \, P \, (\neg \text{event} | \text{TT})} \, \approx \, 0.685.$

genotype	total N	events	censored
TT	115	83 (0.722)	32 (0.278)
AT	67	56 (0.836)	11 (0.164)
AA	25	16 (0.64)	9 (0.36)



This marker has a genotype specific effect with a p-value of 4.849804e-03. Total of 1 observation deleted due to missingness. Odds ratios have been estimated using logistic regression at $t \approx 36$:

$$\frac{P\left(\text{event}|\text{AT,AA}\right)/P\left(\neg\text{event}|\text{AT,AA}\right)}{P\left(\text{event}|\text{TT}\right)/P\left(\neg\text{event}|\text{TT}\right)} \approx 0.554.$$

total N

136

70

genotype

AT,AA

rs7107335	
No.	
Call Mark Aller	

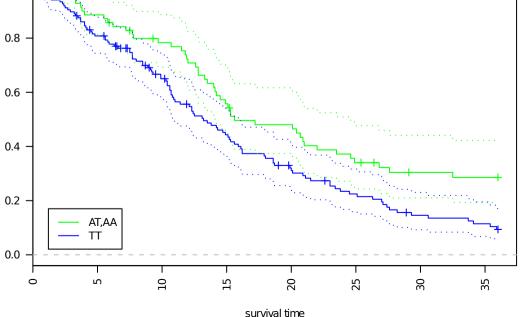
events

107 (0.787)

47 (0.671)

censored 29 (0.213)

23 (0.329)



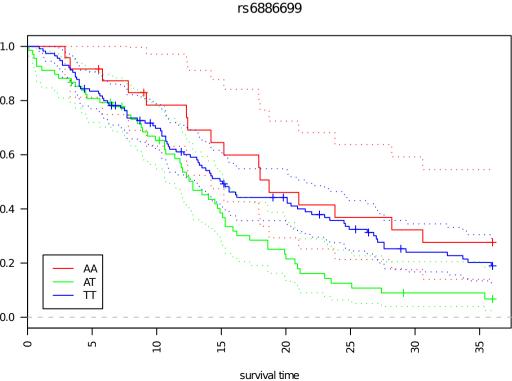
This marker has a genotype specific effect with a p-value of 9.597962e-03.

Odds ratios have been estimated using logistic regression at t \approx 36:

P(oventIAT)/P(-oventIAT)

 $\frac{\frac{P\;(\text{event}|\text{AT}\,)/\,P\;(\neg\text{event}|\text{AT}\,)}{P\;(\text{event}|\text{TT}\,)/\,P\;(\neg\text{event}|\text{TT}\,)}}{\approx 2.085\;\text{and}\;\; \frac{P\;(\text{event}|\text{AA}\,)/\,P\;(\neg\text{event}|\text{AA}\,)}{P\;(\text{event}|\text{TT}\,)/\,P\;(\neg\text{event}|\text{TT}\,)}\approx 0.805.$

genotype	total N	events	censored
TT	115	82 (0.713)	33 (0.287)
AT	68	57 (0.838)	11 (0.162)
AA	24	16 (0.667)	8 (0.333)



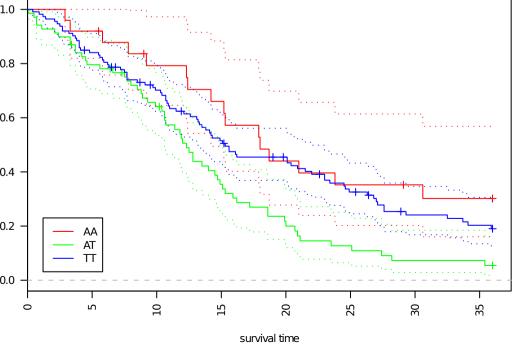
This marker has a genotype specific effect with a p-value of 2.445427e-03.

Odds ratios have been estimated using logistic regression at $t \approx 36$:

P (event AT)/P (¬event AT)		$P(avantl \Lambda \Lambda)/P(-avantl \Lambda \Lambda)$	
i (eventia i)/ i ('eventia i)	~ 2.083 and	i (eventina)/ i (eventina)	~ 0.702
D (oventITT)/D(-oventITT)	~ 2.005 and	D (oventITT)/D(-oventITT)	~ 0.702.

genotype	total N	events	censored
TT	113	81 (0.717)	32 (0.283)
AT	69	58 (0.841)	11 (0.159)
AA	25	16 (0.64)	9 (0.36)

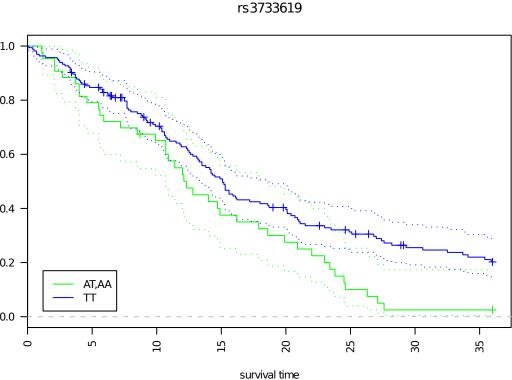
rs3734125



This marker has a genotype specific effect with a p-value of 6.766583e-03. Odds ratios have been estimated using logistic regression at $t \approx 36$:

$$\frac{P\left(\text{event}|\text{AT,AA}\right)/P\left(\neg\text{event}|\text{AT,AA}\right)}{P\left(\text{event}|\text{TT}\right)/P\left(\neg\text{event}|\text{TT}\right)} \approx 5.681.$$

genotype	total N	events	censored
TT	164	115 (0.701)	49 (0.299)
AT,AA	43	40 (0.93)	3 (0.0698)



This marker has a genotype specific effect with a p-value of 5.246671e-03. Odds ratios have been estimated using logistic regression at $t \approx 36$:

$$\frac{P (\text{event}|\text{AT},\text{AA})/P (\neg \text{event}|\text{AT},\text{AA})}{P (\text{event}|\text{TT})/P (\neg \text{event}|\text{TT})} \approx 0.412.$$

genotype	total N	events	censored
TT	125	102 (0.816)	23 (0.184)
AT,AA	82	53 (0.646)	29 (0.354)

