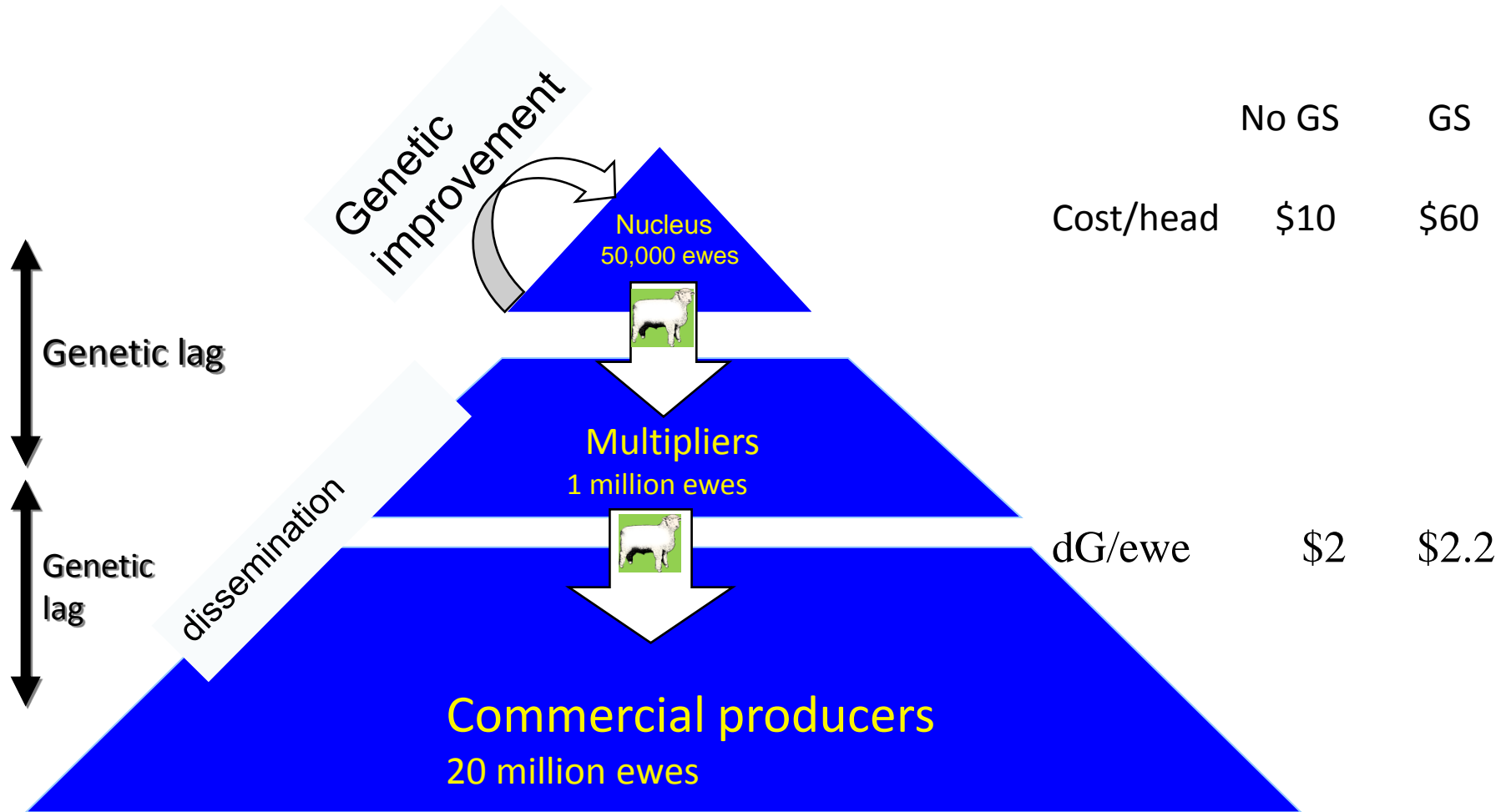


# Optimizing Breeding Programs

## COST-BENEFIT

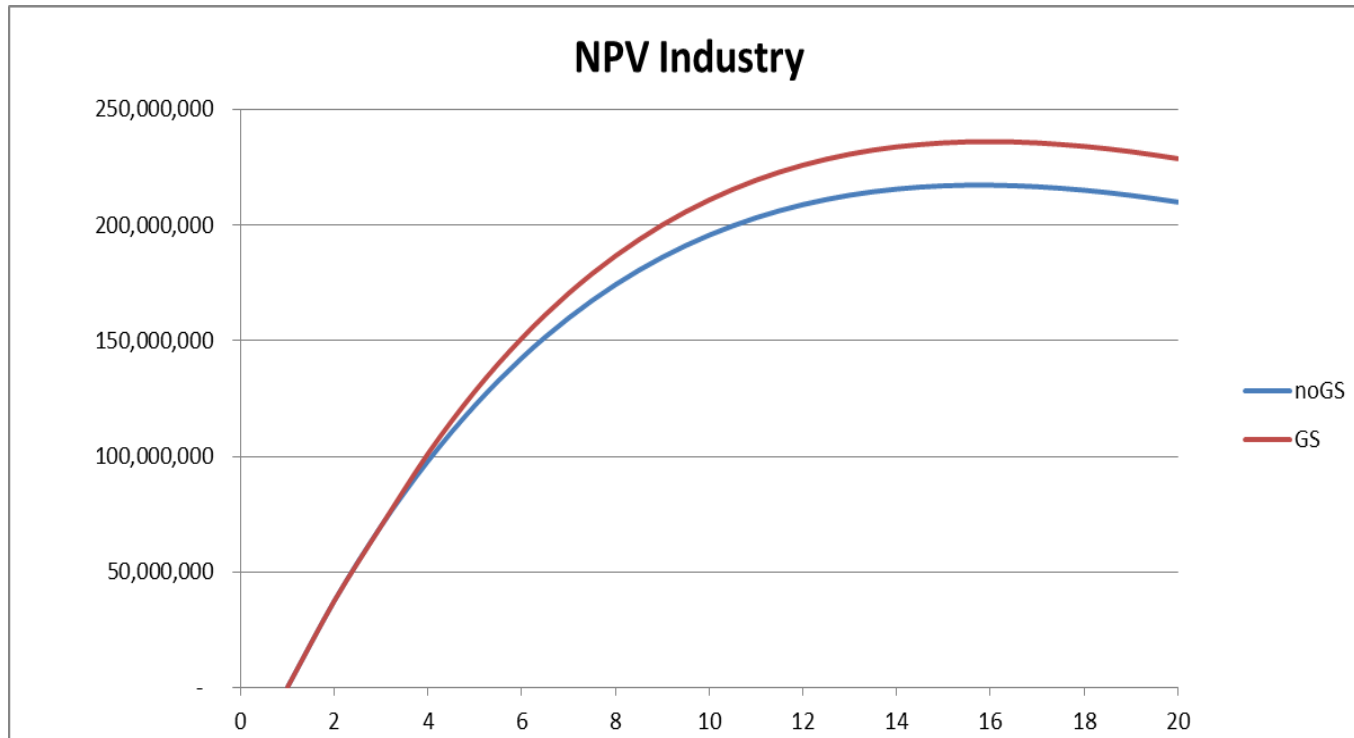
Armidale Animal Breeding Summer Course 2014

# Cost - Benefit



# Cost-Benefit industry wide

	<u>No GS</u>	<u>GS</u>
Cost	\$0.5 M	\$ 1.65 M
dG	\$40 M	\$ 44 M

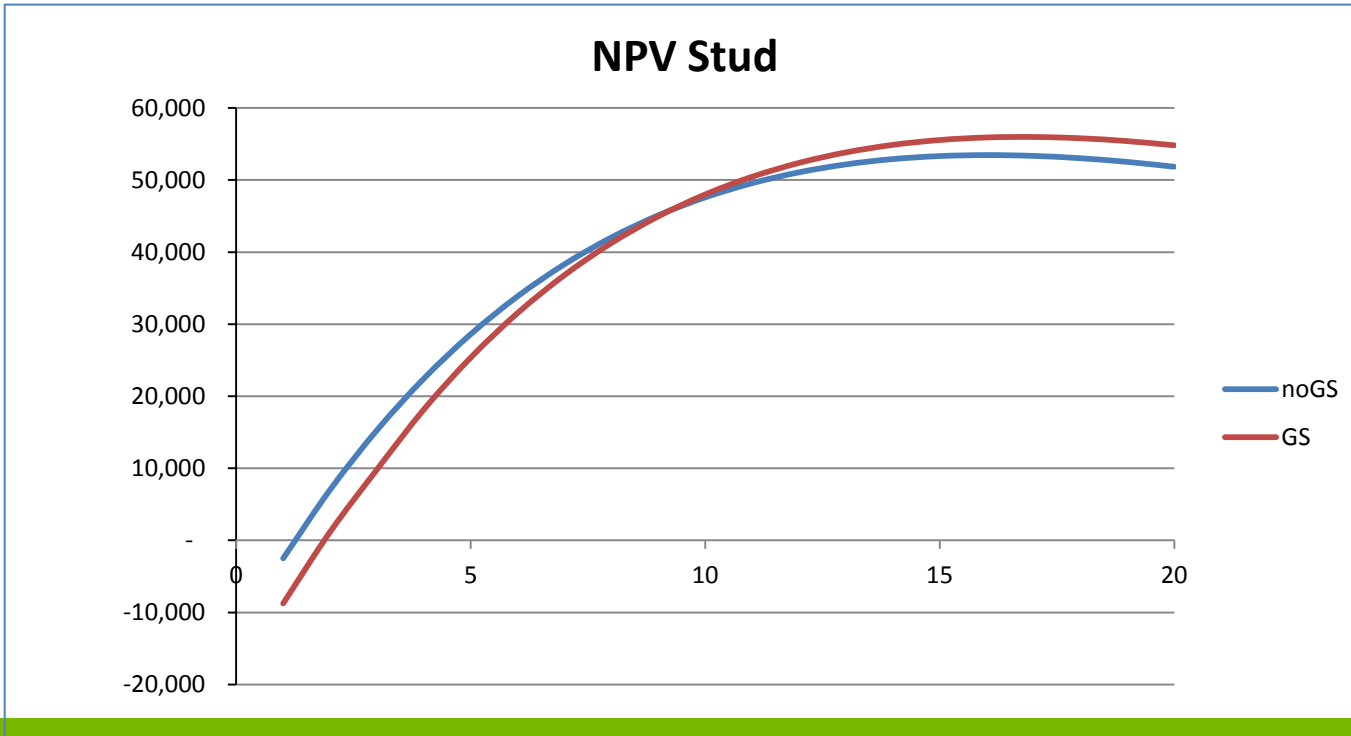


50k Nuc ewes  
20M Comm

3 tier benefit

# Cost-Benefit Stud

	No GS	GS
Cost	\$ 5 k	\$17.5 k
dG	\$20 k	\$ 22 k



500 Nuc ewes  
10k Comm

2 tier benefit

# Outline

- Economic value of genetic improvement
  - Value difference between two rams
  - Value of selecting better rams
    - Rams sold to Commercial
    - Rams used in Stud
  - Value of genetic improvement – whole flock

# Two Commercial Rams

## ASBV PWWT

Ram 1: Kevin

+10 kg

Ram 2: Tony

+15 kg

Nr Progeny:

100

Value of 1 kg PWWT

\$4

Difference in progeny

2.5 kg

Difference in value:

$5 * \$4$

$* 100$

$* 0.5$

as commercial rams

Selection  
Difference

Nr of  
Progeny

Expression  
per progeny

= \$1000.-

# Two Commercial Rams

\$Index

Ram 1: Kevin

+190

Ram 2: Tony

+180

Nr Progeny:

100

Difference in progeny

\$5

Difference in value:  
as commercial rams

\$10

\* 100

\* 0.5

Selection  
Difference

Nr of  
Progeny

Expression  
per progeny

= \$500.-

# Selecting Better Rams

			<u>\$Index</u>
Average of 100 rams sold:	With Genomics		+182
	No Genomics		+180
Nr Progeny:	100 per ram		
Difference in progeny	\$1.0		
Difference in value: as commercial rams	\$2	* 100	* 0.5
	Selection Difference	Nr of Progeny	Expression per progeny
	= \$100.- * 100 rams = \$10,000.		



# So principles are

Value of a superior ram

= Selection Difference \* Nr.Progeny \* expressions per progeny

We look at all expressions in commercial progeny

To evaluate benefit we need to predict

- the extra Selection Difference we can get  
*this will depend a lot on extra accuracy*
- the number of expressions

# How about selection of stud rams?

## Value of a superior ram

= Selection Difference \* Nr.Progeny \* expression per progeny



Progeny in commercial,  
so for a stud ram these  
are actually  
grand progeny,  
great grand progeny, etc

# GENEFLOW

males to males	females to males
males to females	females to females

Donors of genes

		Sires of Nucleus					Dams of Nucleus									
P matrix		1	2	3	4	5	1	2	3	4	5	6	7	8	9	10
Recipients of genes	1	0	0.5	0	0	0	0	0.166667	0.166667	0.166667	0	0	0	0	0	0
	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
	5	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	6	0	0.5	0	0	0	0	0.166667	0.166667	0.166667	0	0	0	0	0	0
	7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
	8	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
	9	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

# GENEFLOW

## Donors of genes

Recipients of genes

Sn<Sn	Sn<Dn	Sn<Sc	Sn<Cm	Sn<Cf	Sn	Sires of Nucleus		
Dn<Sn	Dn<Dn	Sf<Sc	Dn<Cm	Dn<Cf	Dn	Dams of Nucleus		
Sc<Sn	Sc<Dn	Sc<Sc	Sc<Cm	Sc<Cf	Sc	Stud born males to sire commercial		
Cm<Sn	Cm<Dn	Cm<Sc	Cm<Cm	Cm<Cf	Cm	Commercial born males		
Cf<Sn	Cf<Dn	Cf<Sc	Cf<Cm	Cf<Cf	Cf	Commercial born females		



# GENEFLOW

- R = a matrix defining gene transmission of some superiority (or particular allele)
- Q = a matrix describing aging
- P = matrix describing transmission of genes
  - $P=R+Q$

$$m_t = P m_{t-1} + R n_{t-1}$$

- m vector of allele frequency in each age class
- n vector to describe inserting allele or superiority



# Cumulative Discounted Expressions CDE

Value (V) in year t is worth now  $V.c$  where  $c=1/(1+d)^t$

d = discount rate

c = discount factor

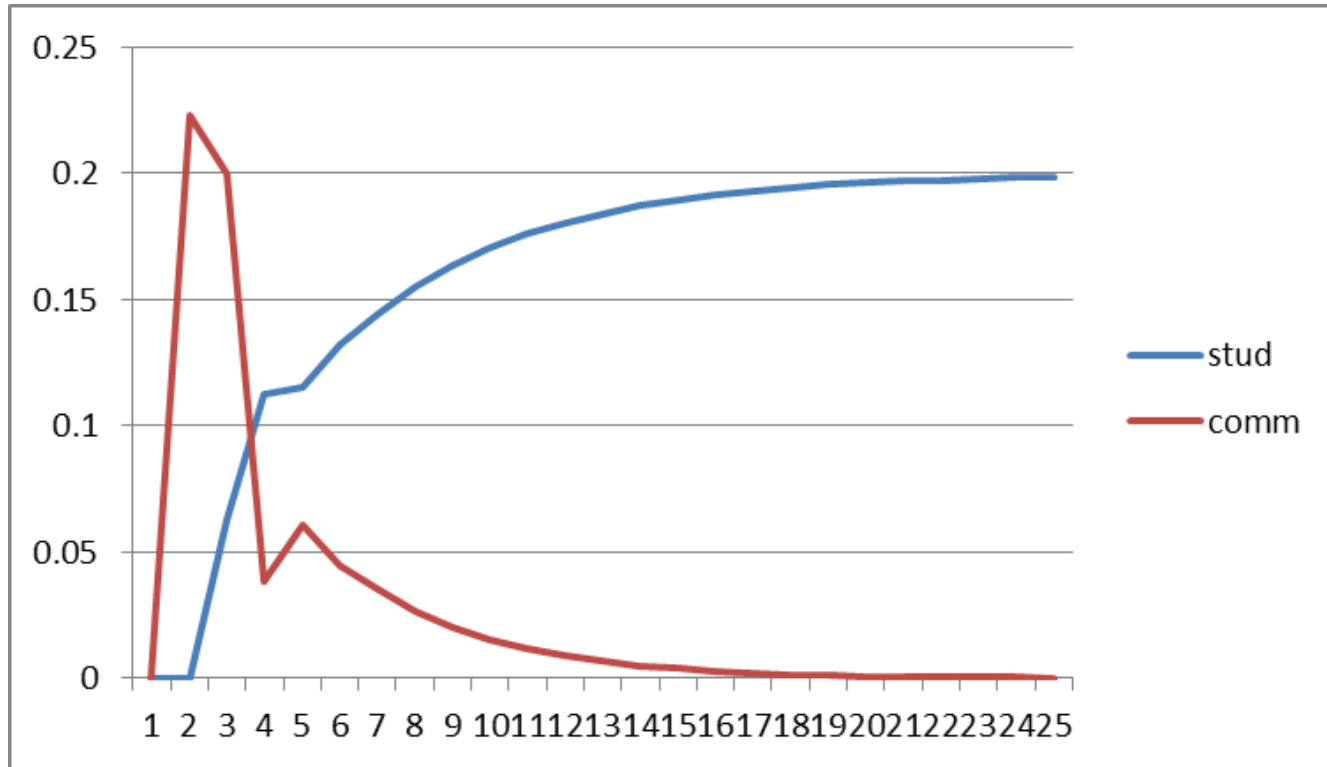
Expression in age class i in year t is  $m(i)_t = E_{it}$

Net Present Value of Sum of expression over 25 years

$$CDE = \sum_{t=1}^{25} \sum_{i=1}^{nac} E_{it} c_t$$



# (allele) frequency of one unit of superiority as expressed in commercial flock

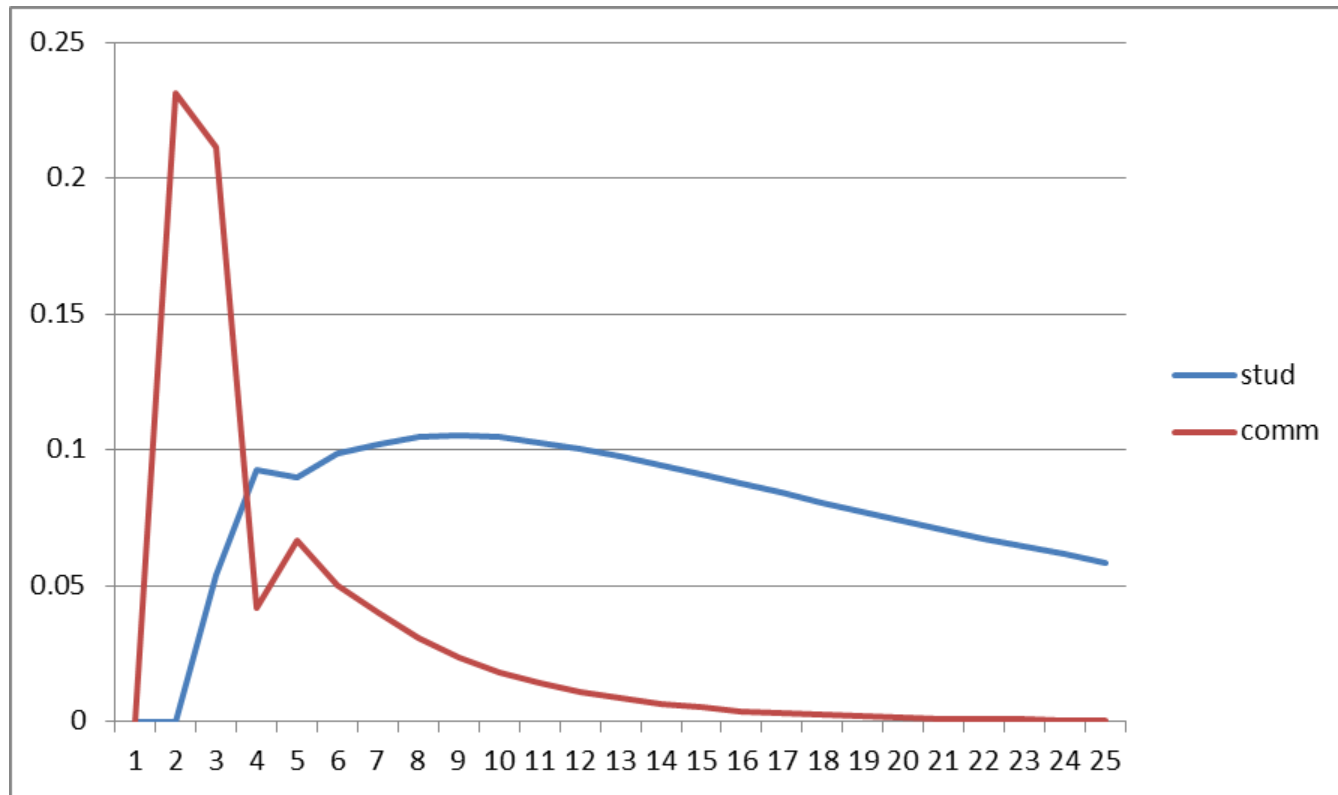


Discount rate  
0  
0.05  
0.08

CDE flock rams  
0.99  
0.78  
0.68

CDE stud rams  
3.93  
1.96  
1.37

# (allele) frequency of one unit of superiority as expressed in commercial flock



<u>Discount rate</u>	<u>CDE flock rams</u>	<u>CDE stud rams</u>
0	0.99	3.93
0.05	0.78	1.96
0.08	0.68	1.37

# Value of selecting Stud Rams and Flock Rams

Value of a superior ram

$$= \text{Selection Difference} * \text{Nr.Progeny} * \text{expression per progeny}$$

CDE

Flock Ram	+ 1.4	100	0.55	= \$ 77
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Stud Ram	+ 3.0	400	1.35	= \$ 1,620
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# Flock structure

	Nr Sheep Commercial Flock	12,000
	Comm Dams/sire	50
	Comm Sire replacem. rate	0.5
	Comm Weaning rate	1
	Nr new rams needed for comm flock/yr	120
	Nr lifetime Progeny per commercial sire	100
	Prop. Nucl.Males sold as breeding ram	0.2000
	Nucleus weaning rate	1
	Nucleus dams/sire	40
	Nr Nucleus females	1200
	Nr. Nucleus born progeny tested/yr	600
	Nr. of Nucleus sires needed/yr	30

100 prog/flock ram

400prog/stud ram

# Some real data

Commerical Flock	Nr Sheep Commercial Flock	34,280	
	Comm Dams/sire	40	
	Comm Sire replacem. rate	0.33333	
	Comm Weaning rate	1.1	
	Nr new rams needed for comm flock/yr	286	
	Nr lifetime Progeny per commercial sire		132

Stud Flock	Prop. Stud.Males sold as breeding ram	40%	
	Stud weaning rate	1.28	
	Stud dams/sire	20	
	Nr stud breeding ewes	1116	
	Nr. Of stud sires	56	
	Nr of flock rams sold per year	286	
	Nr of commercial rams sold per Stud male	5.12	
	Nr of commercial progeny receiving genes from a stud male		676

# Value of selecting Stud Rams and Flock Rams

Value of a superior ram = Selection Difference \* Nr.Progeny \* CDE

- Selection differential within the cohort: “The result of one round of selection”

Breeding performance						
			SD of breeding Objective	10.82		
			Male Selection intensity	2.06		
			Female Selection intensity	0.2		
			Male Selection accuracy <i>without</i> genomics	0.358	increase	
			Male Selection accuracy <i>with</i> genomics	0.432	21%	
			Female Selection accuracy	0.358		
			Generation Interval Stud males	1.53		
			Generation Interval stud females	2.97		
	approximalely	1.90	CDE stud sires	1.90		
			CDE flock sires	0.6		
				no GS	GS	
			Sire superiority	7.979534	9.628934	
			Dam Superiority	0.774712	0.774712	increase
			Rate of gain/year	1.945	2.312	19%

# Comparing geneflow with dG/year method

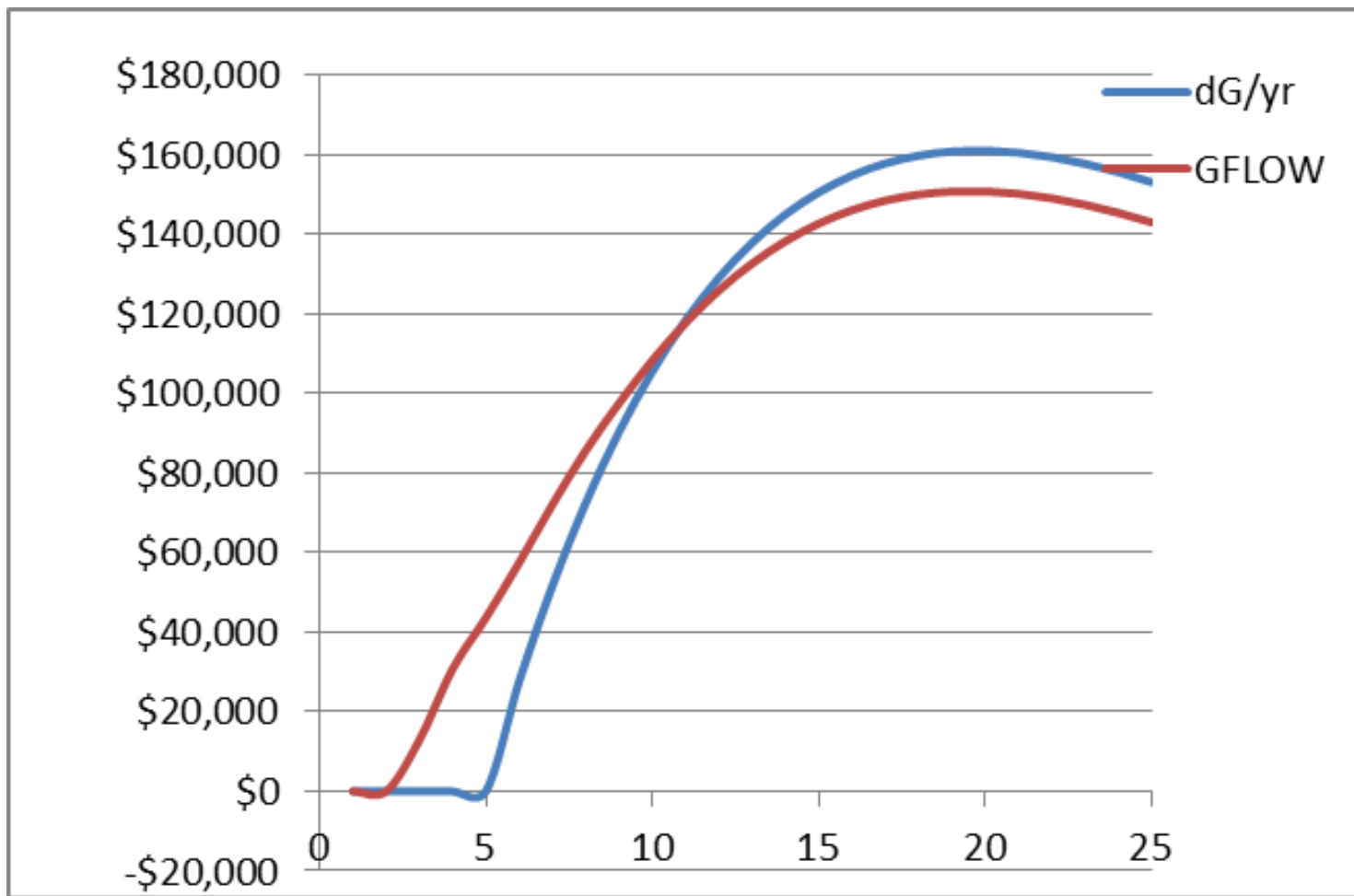
group	int	acc		Sup	L		dG/year
sires	2.1543	0.53		10.27622255	1.0		3.233294535
dams	0.7979	0.37		2.656955587	3.0		

Calculations based on dG/year							calculations based on GFLOW				
dG/gen							sire	dam			
3.23							selection	selection			
dG/yr							superiority	10.2762	2.6570	GFLOW	
year	disc fact	genetic mean	cum benefit	cost	disc retruns	superiority	Expr_SS	Expr_DS	cum benefit	disc retruns	
1	1.000	0	\$ -	\$0	\$0		0.000	0.000	\$ -	\$ -	
2	0.935	0	\$ -	\$0	\$0		0.000	0.000	\$ -	\$ -	
3	0.873	0	\$ -	\$0	\$0		0.119	0.000	\$ 14,694	\$ 12,834	
4	0.816	0	\$ -	\$0	\$0		0.174	0.048	\$ 37,679	\$ 30,757	
5	0.763	0	\$ -	\$0	\$0		0.131	0.105	\$ 57,158	\$ 43,606	
6	0.713	\$3.23	\$ 38,800	\$0	\$27,664		0.157	0.128	\$ 80,610	\$ 57,474	
7	0.666	\$6.47	\$ 77,599	\$0	\$51,708		0.185	0.149	\$ 108,155	\$ 72,068	
8	0.623	\$9.70	\$ 116,399	\$0	\$72,487		0.196	0.165	\$ 137,537	\$ 85,651	
9	0.582	\$12.93	\$ 155,198	\$0	\$90,327		0.197	0.178	\$ 167,514	\$ 97,494	
10	0.544	\$16.17	\$ 193,998	\$0	\$105,522		0.206	0.190	\$ 198,976	\$ 108,230	
11	0.508	\$19.40	\$ 232,797	\$0	\$118,342		0.213	0.199	\$ 231,559	\$ 117,713	
12	0.475	\$22.63	\$ 271,597	\$0	\$129,034		0.217	0.206	\$ 264,833	\$ 125,820	
13	0.444	\$25.87	\$ 310,396	\$0	\$137,820		0.220	0.211	\$ 298,645	\$ 132,602	
14	0.415	\$29.10	\$ 349,196	\$0	\$144,904		0.223	0.216	\$ 332,996	\$ 138,182	
15	0.388	\$32.33	\$ 387,995	\$0	\$150,471		0.225	0.220	\$ 367,735	\$ 142,614	
16	0.362	\$35.57	\$ 426,795	\$0	\$154,690		0.227	0.222	\$ 402,772	\$ 145,983	
17	0.339	\$38.80	\$ 465,594	\$0	\$157,713		0.228	0.225	\$ 438,053	\$ 148,384	
18	0.317	\$42.03	\$ 504,394	\$0	\$159,678		0.229	0.226	\$ 473,539	\$ 149,910	
19	0.296	\$45.27	\$ 543,193	\$0	\$160,711		0.230	0.228	\$ 509,179	\$ 150,648	
20	0.277	\$48.50	\$ 581,993	\$0	\$160,926		0.231	0.229	\$ 544,943	\$ 150,681	
21	0.258	\$51.73	\$ 620,793	\$0	\$160,425		0.231	0.230	\$ 580,808	\$ 150,092	
22	0.242	\$54.97	\$ 659,592	\$0	\$159,300		0.232	0.231	\$ 616,754	\$ 148,954	
23	0.226	\$58.20	\$ 698,392	\$0	\$157,636		0.232	0.231	\$ 652,763	\$ 147,337	
24	0.211	\$61.43	\$ 737,191	\$0	\$155,508		0.232	0.232	\$ 688,823	\$ 145,305	
25	0.197	\$64.67	\$ 775,991	\$0	\$152,984		0.233	0.232	\$ 724,923	\$ 142,916	
				NPV	\$2,607,849				NPV	\$ 2,645,255	

Expressed in  
12,000 ewes

20 nucleus sires

i.e. 600 per sire







# Cost benefit analysis

- Extra benefit  $120 * \$11 + 30 * \$216 = \$ 7,800$
- If all young stud males tested: 600
- Break even:  $\$13.00$  per DNA test

# Merino: Breakeven (\$) for testing

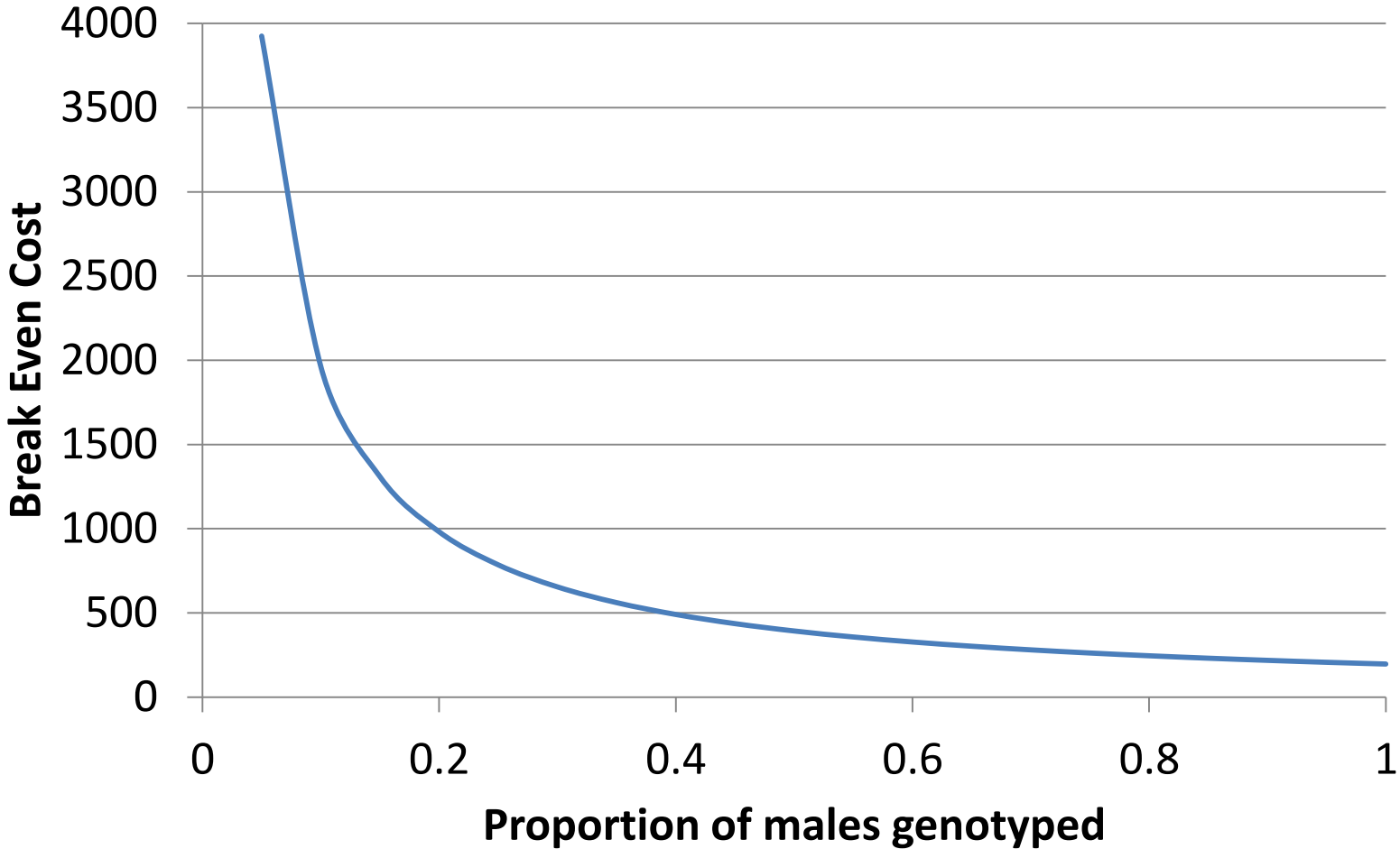
Proportion tested	100%		20%	
Age at first progeny	1yo	2yo	1yo	2yo
Breakeven (\$/test)	196	83	981	415

- assumes 40% males sold as rams

% males born sold as rams	40%		20%	
Age at first progeny	1yo	2yo	1yo	2yo
Breakeven (\$/test)	196	83	98	41

- assumes 100% of males tested

Breakeven cost and proportion genotyped (no loss assumed!)



1yo male, 2yo female, Fine10% + SS, 40% males sold as rams

# What increase in price received per ram sold do you need to cover costs?

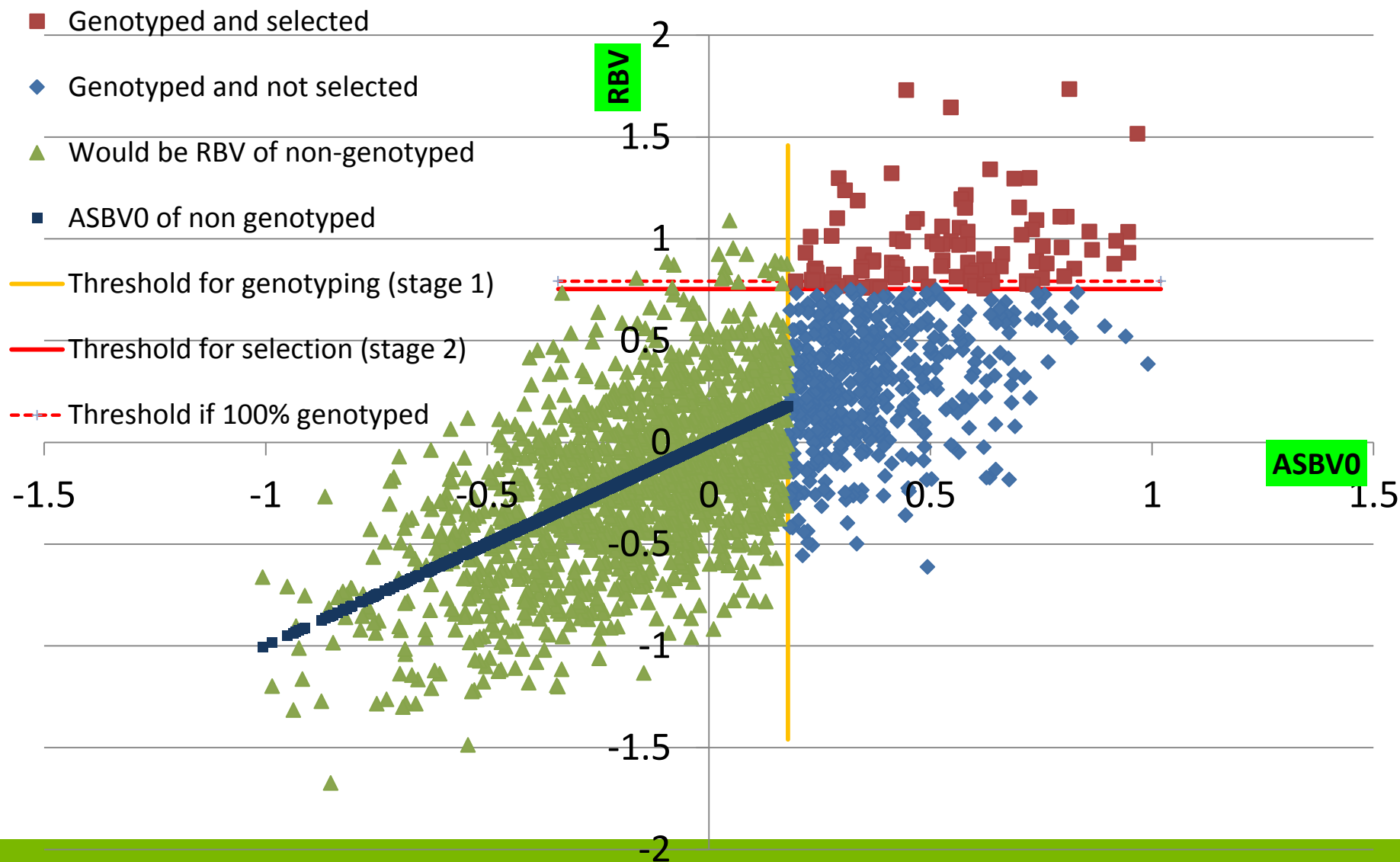
- total cost of genotyping/total nr of rams sold
  - 444 ewes @ 0.9 weaning rate = 200 ram lambs
  - Assume \$50 genotype cost
  - Doesn't account for collection costs etc.

<b>Total ram lambs weaned</b>	<b>200</b>	<b>200</b>	<b>200</b>	<b>200</b>
% tested	20	100	20	100
nr tested (for use in nucleus)	40	200	40	200
Total test cost	2000	10000	2000	10000
% sold as flock rams	20	20	40	40
nr rams sold	40	40	80	80
Cost of test per ram sold	\$50	\$250	\$25	\$125

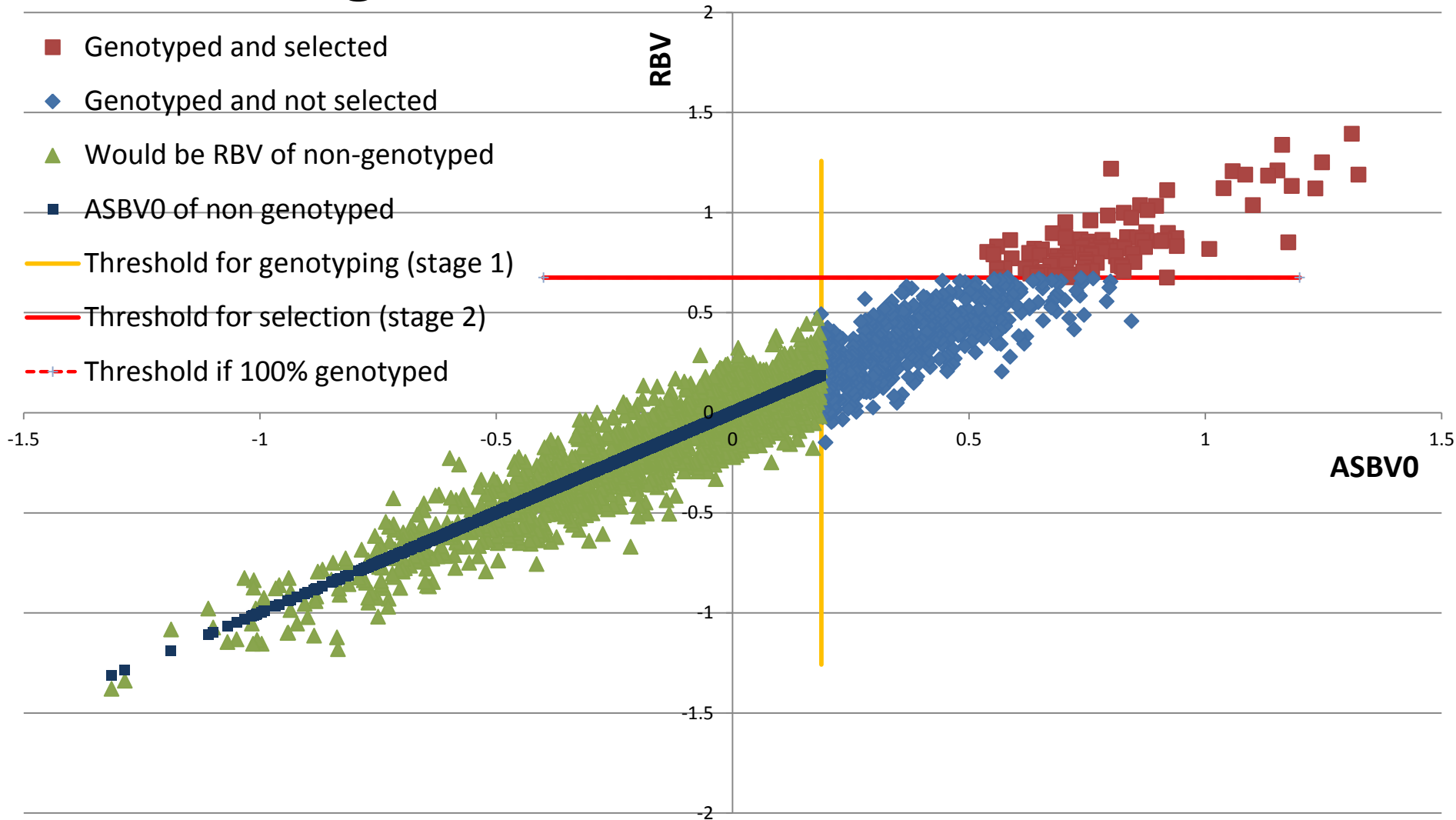
# 2 stage selection

How many rams to genotype?

# 30% genotyped, 5% selected, correlation ASBV to RBV of 0.7

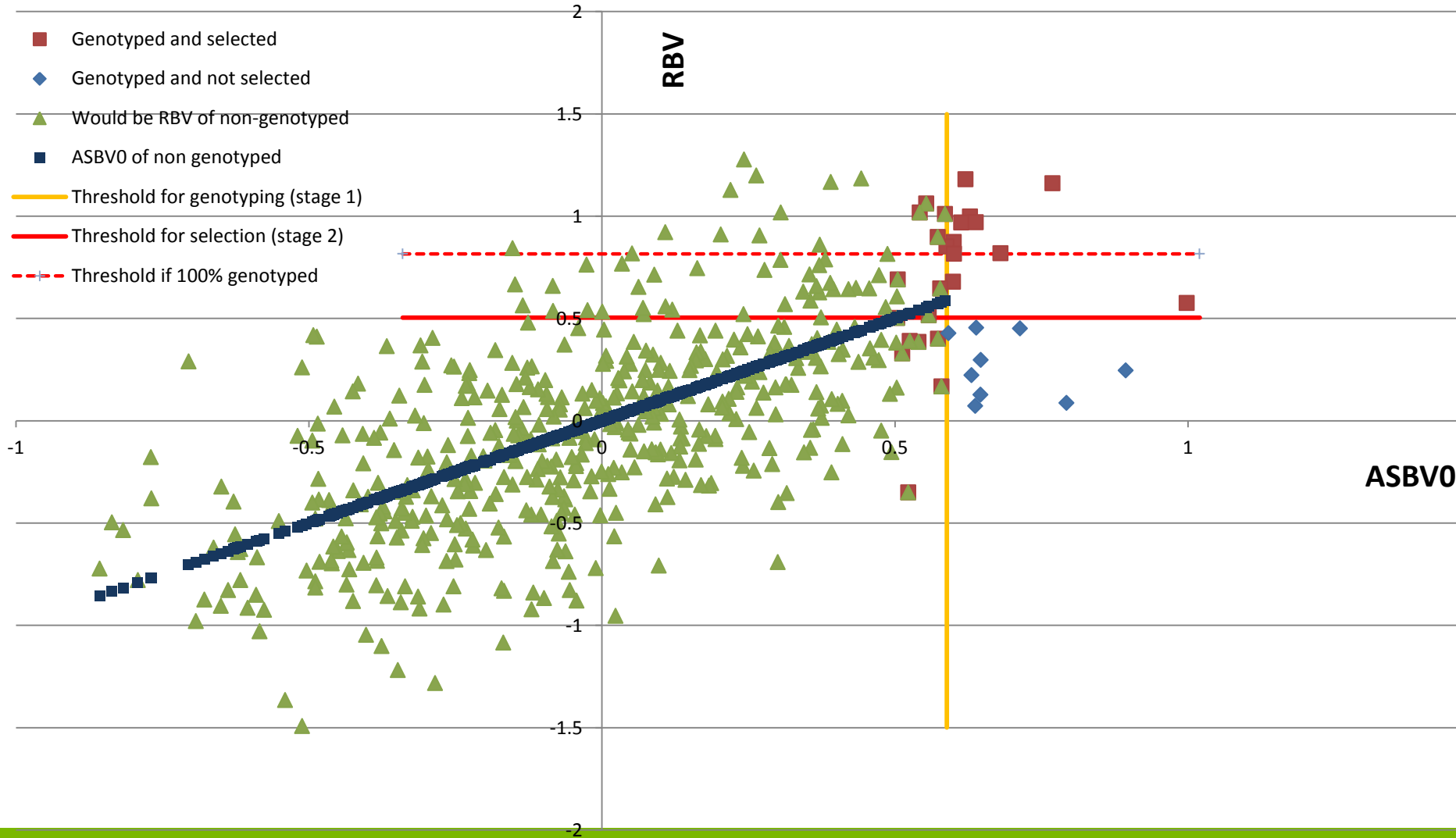


# 30% genotyped, 5% selected with very high correlation ASBV to RBV

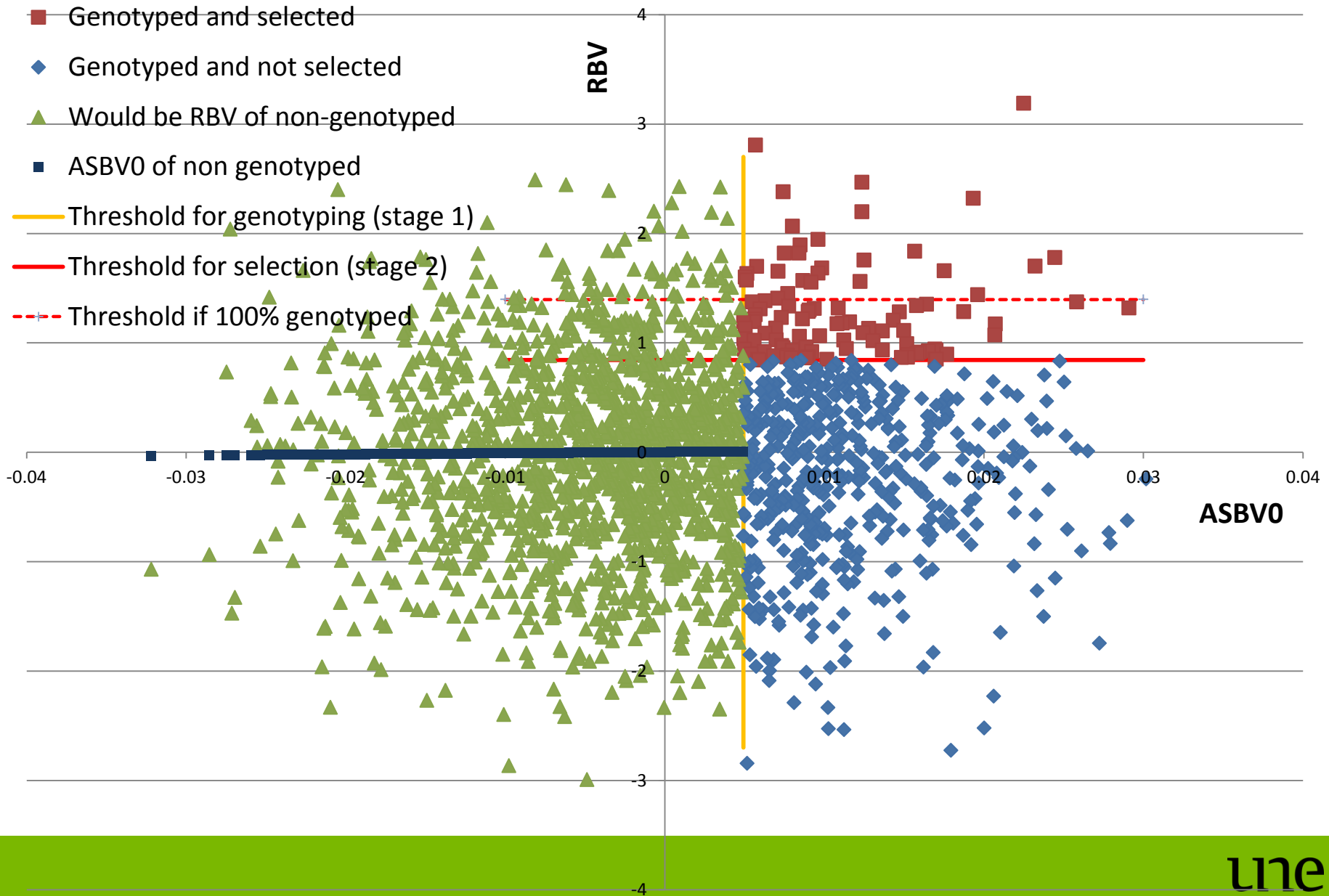




# Very low proportion tested



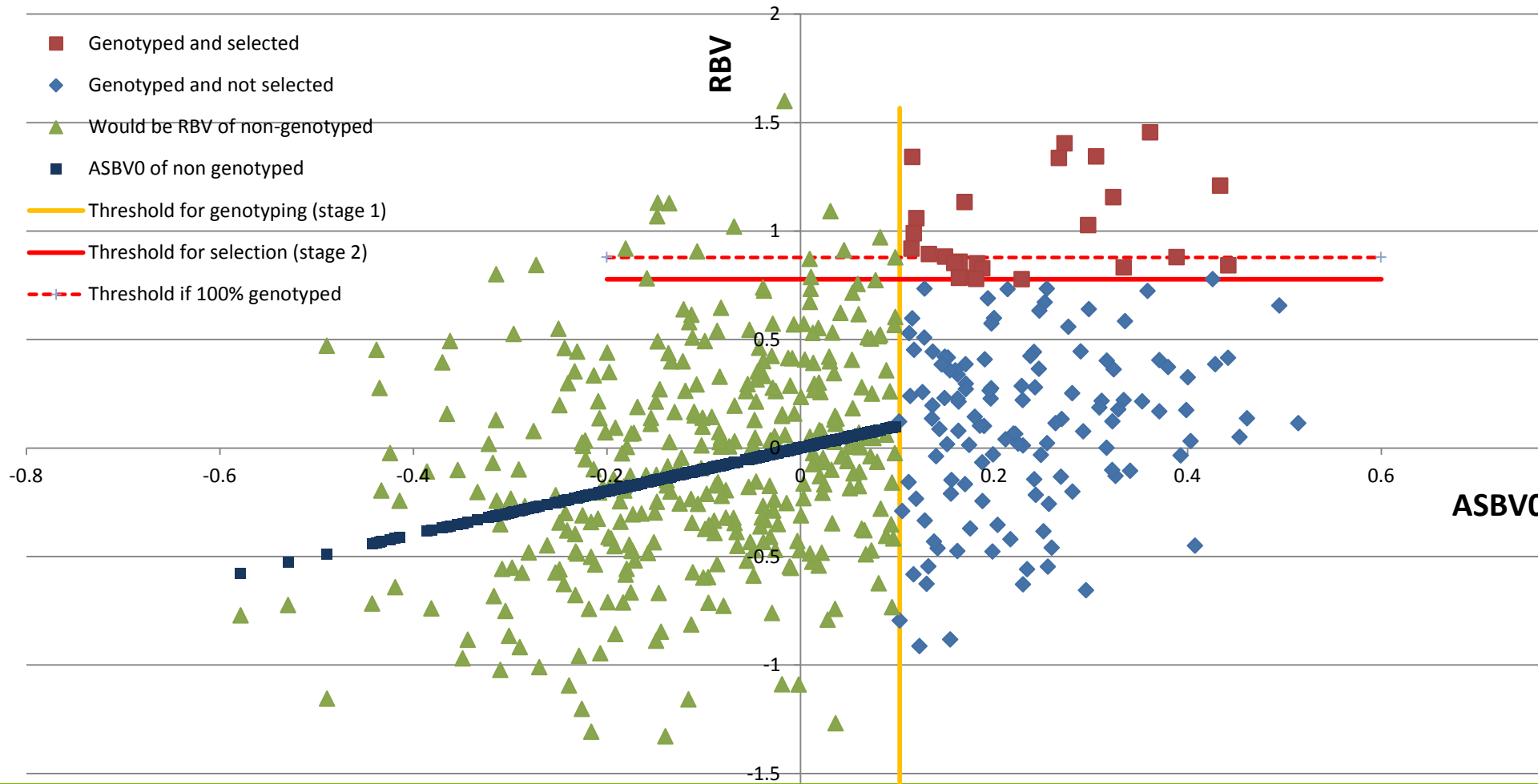
# 0.01 ASBV, 0.90 GBV, $r = 0.9$



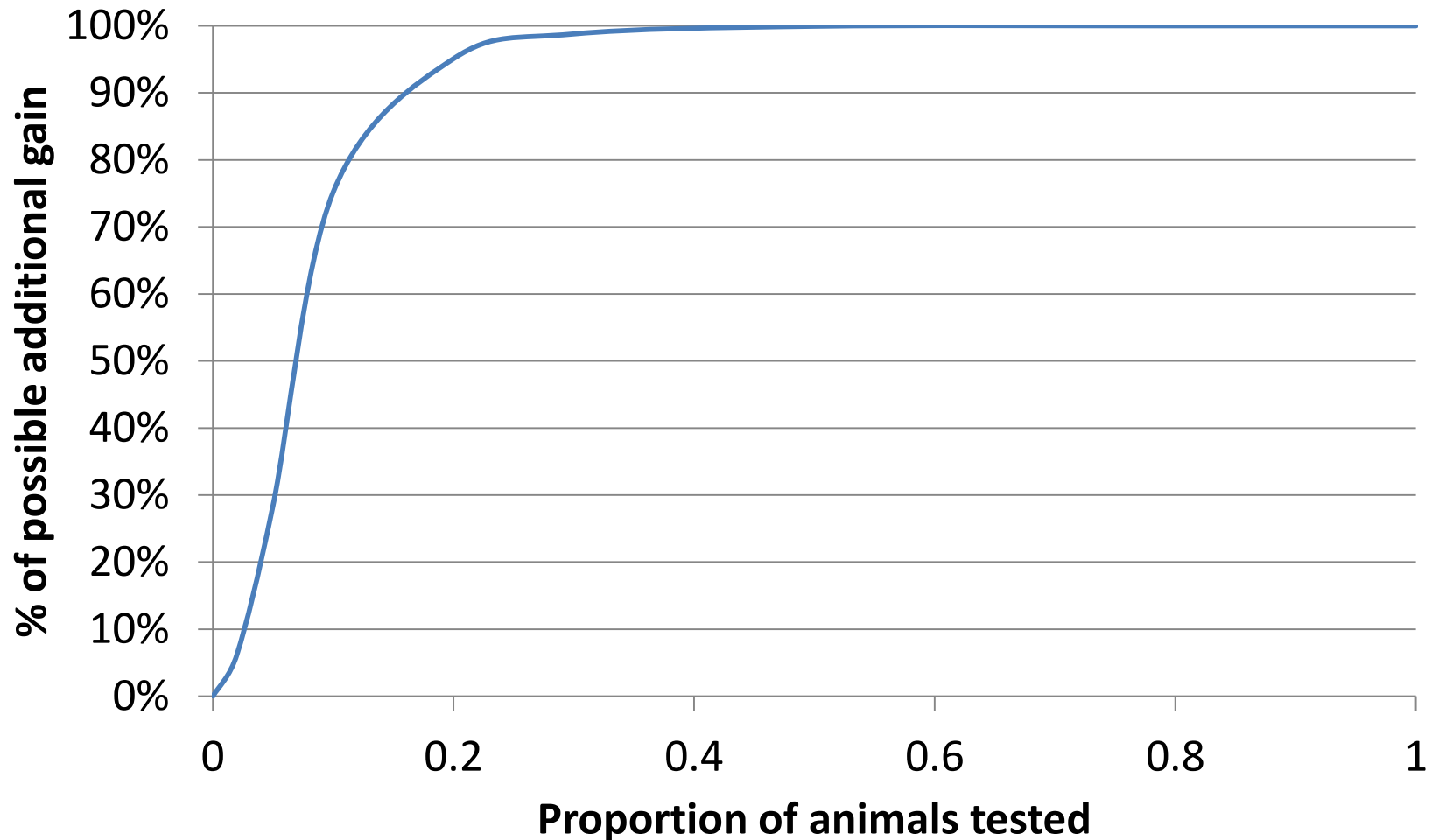
# Low ASBV acc% & high GBV

ASBV0	0.20
GBV	0.50
RBV	0.52
correlation ASBV0-RBV	0.38
prop genotyped	0.3
prop selected final	0.05
Selection Differential	0.96
SelDiff 100% genotyping	1.08
SelDiff 0% genotyping	0.40
% of possible additional gain	82%

# Low ASBVO acc% & high GBV

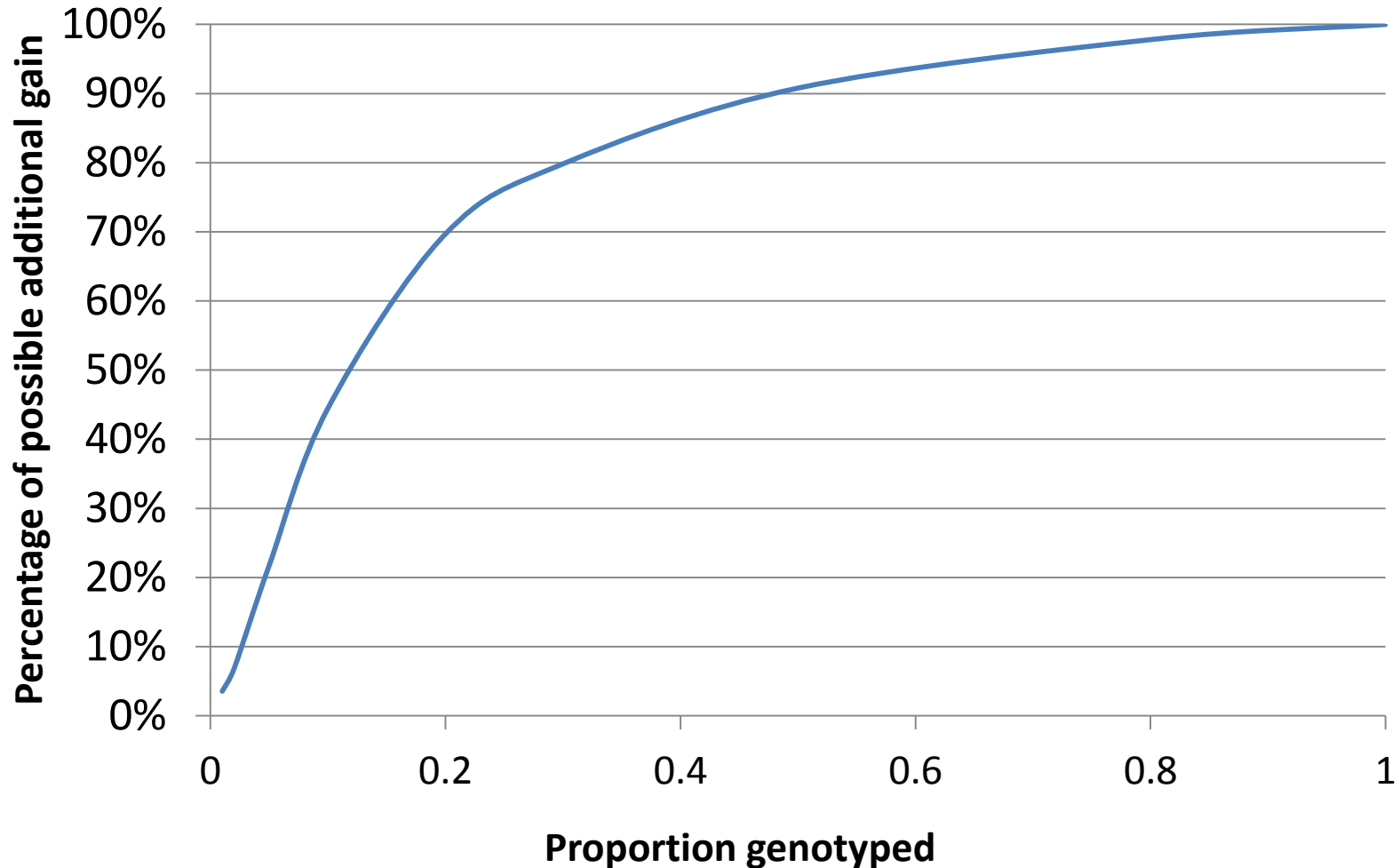


% gain compared with 100% genotyping  
ASBV 0.34, GBV 0.39, RBV = 0.50,  $r = 0.7$



At high(ish) correlation between ASBV and RBV only need to genotype ~20%

% gain compared with 100% genotyping  
ASBV 0.10, GBV = 0.39, RBV 0.40,  $r = 0.25$



At low(er) correlation between ASBV and RBV need to genotype more **the**

## summary

- Can calculate additional gain on a per ram basis, assuming returns in commercial progeny
- Those figures depend on
  - Additional accuracy
  - Age structure
  - Flock parameters such as weaning rate, mating rate, prop. Sold
  - Can have strategies to save costs, e.g. test top 50%
  - Sonja will show many more examples