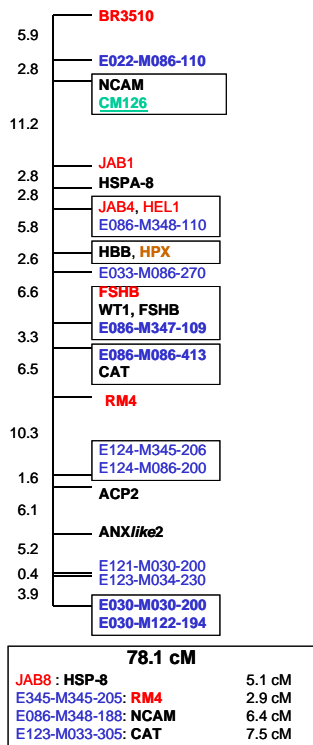


## ELECTRONIC FIGURE

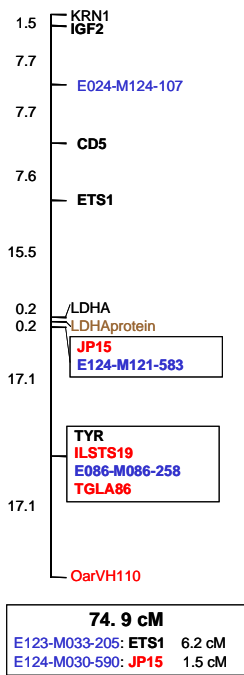
The deer (subfamily *Cervinae*) genetic map. Linkage groups 1-33 and the pseudoautosomal region of the Y chromosome are shown. Map distances are given in Kosambi centimorgans. RFLVs for gene probes are in black font, ESTs green, microsatellite loci red, protein loci brown and AFLPs blue. Where marker order was determined with support  $\text{LOD} \geq 3.0$ , the relevant markers are shown in bold font. Markers that were assigned to a linkage group, but with uncertain location are placed below the linkage group with the distance to the nearest ordered marker indicated. Underlined ESTs represent markers where the map location and predicted location from COMPASS were concordant.

AFLP loci are named such that the primer sequences and product size can be inferred. The following codes refer to specific sequences added to restriction site and adapter recognising primers: 021 = AAA, 022 = AAC, 023 = AAG, 024 = AAT, 030 = AGC, 033 = ATA, 034 = ATC, 035 = ATG, 036 = ATT, 086 = AAAC, 121 = AGCA, 122 = AGCC, 123 = AGCG, 124 = AGCT, 345 = AAACA, 346 = AAACC, 347 = AAACG, 348 = AAACT, 538 = ATACC. Thus, the locus E021-M345-200 would be a 200bp product amplified by one primer that recognises the *EcoRI* site plus adapter plus sequence AAA and another primer that recognises the *MseI* site plus adapter plus sequence AAACA.

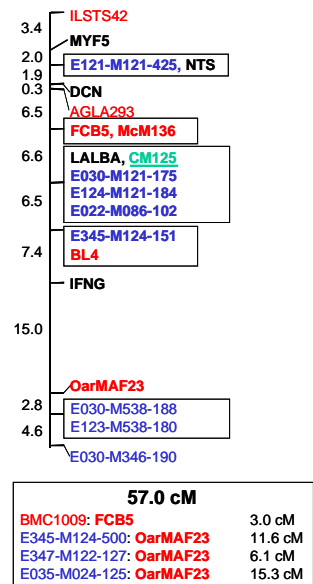
**Linkage Group 1**  
*Bta15, Oar15, Hsa11*



**Linkage Group 2**  
*Bta29, Oar21, Hsa11*



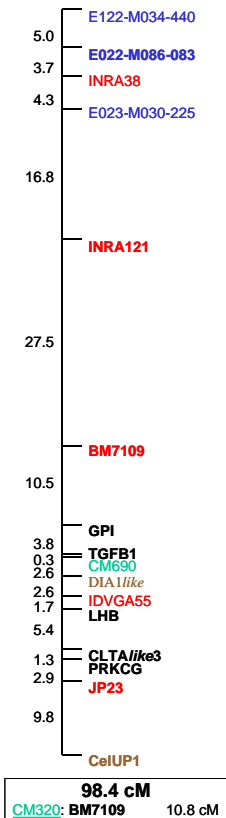
**Linkage Group 3**  
*Bta5, Oar3, Hsa12*



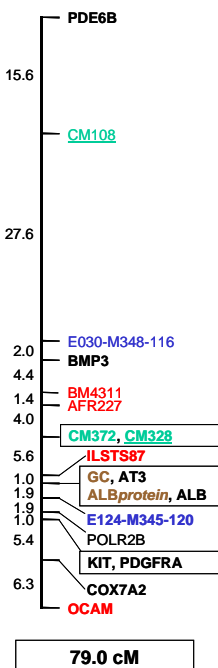
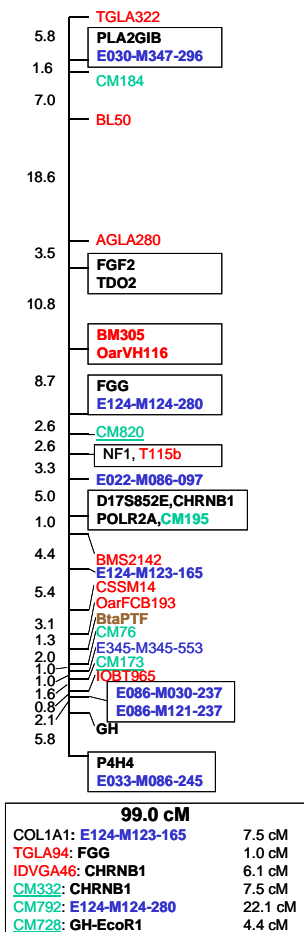
**Linkage Group 5**

*Bta17 & 19, Oar17 & 11, Hsa4, 12 & 17*

**Linkage Group 4**  
*Bta18, Oar14, Hsa19*

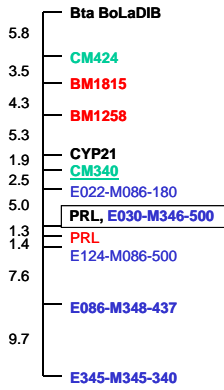


**Linkage Group 6**  
*Bta6, Oar6, Hsa4*



### Linkage Group 7

*Bta23, Oar20, Hsa6*

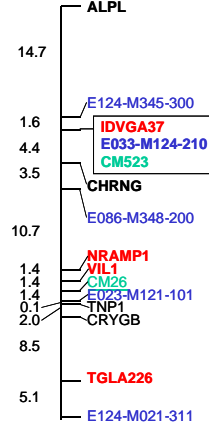


**48.2 cM**

BM1818: PRL	6.3 cM
Delta14: PRL	27.5cM
E124-M346-500: PRL	13.2 cM
E030-M122-074: Bta BoLaDIB	14.7 cM
E030-M086-512: PRL	11.3 cM
E023-M030-318: PRL	10.5 cM

### Linkage Group 8

*Bta2, Oar2, Hsa1 & 2*

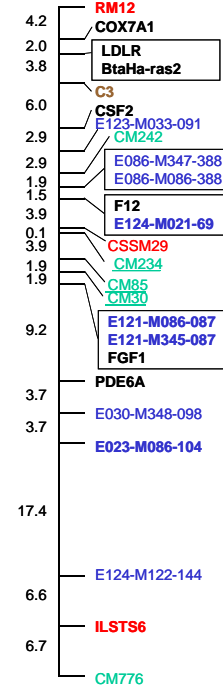


**54.8 cM**

FN1: VIL1	5.9 cM
CM369: CHRNG	9.2 cM
CM669: CHRNG	15.8 cM

### Linkage Group 9

*Bta7, Oar 5, Hsa5 & 19*

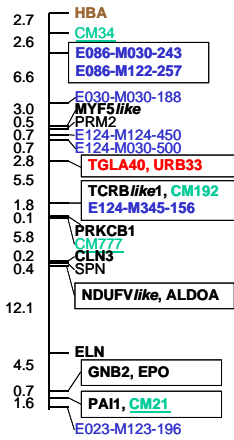


**84.7 cM**

SPARC: PDE6A	2.4 cM
CM73: PDE6A	8.0 cM
E033-M124-085: ILSTS6	5.8 cM

### Linkage Group 10

*Bta25, Oar24, Hsa7 & 16*

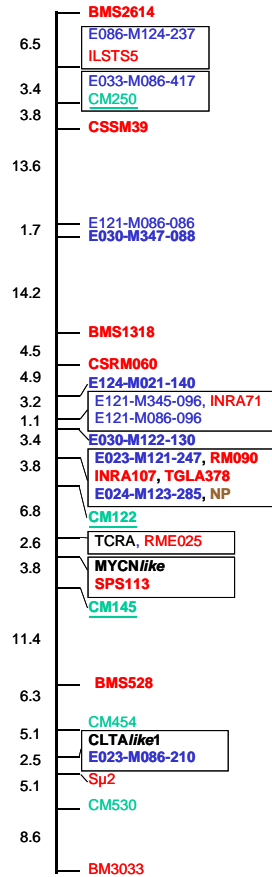


**52.5 cM**

CM31: HBA	14.7 cM
E121-M030-182: TGLA40	4.3 cM

### Linkage Group 12

*Bta10, Oar7, Hsa14 & 15*

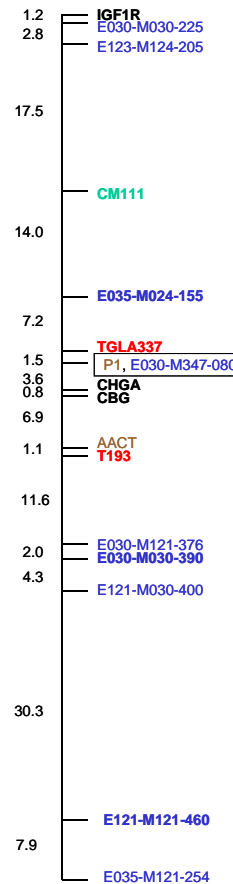


**116.4 cM**

SPTB: CSRM060	5.7 cM
INRA37: CSRM60	13.4 cM
BM898: E030-M122-130	1.5 cM
RT23: INRA107	2.9 cM
CM694: E023-M086-210	12.1 cM
E086-M122-231: E030-M347-088	8.4 cM
E034-M121-082: CLTA like1	6.4 cM

### Linkage Group 13

*Bta21, Oar18, Hsa14 & 15*

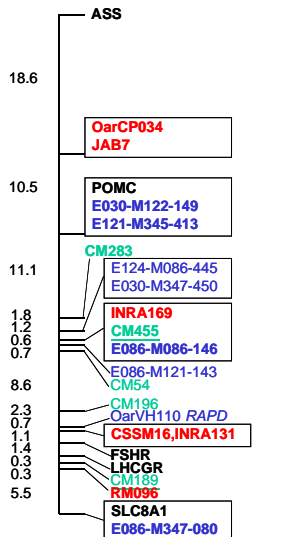


**112.5 cM**

OarCP134: CM111	28.1 cM
OarVH054: IGF1R	14.7 cM
CM837: CHGA	27.5 cM
E124-M346-100: T193	29.6 cM
E030-M121-450: E121-M121-460	15.3 cM
E030-M121-376: E030-M030-390	1.8 cM

### Linkage Group 11

*Bta11, Oar3, Hsa2 & 9*

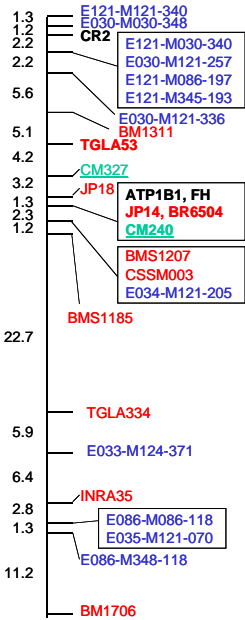


**64.3 cM**

PTGS1: ASS	17.1 cM
E022-M036-110: SCLA81	15.6 cM

### Linkage Group 14

*Bta16, Oar12, Hsa1*

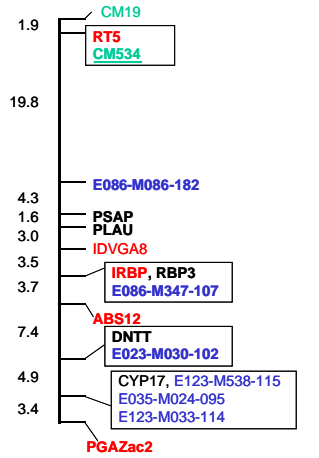


**80.2 cM**

E030-M086-194: CR2 6.3 cM  
E030-M345-195: CR2 4.5 cM

### Linkage Group 15

*Bta 26 & 28, Oar22 & 25, Hsa1 & 10*

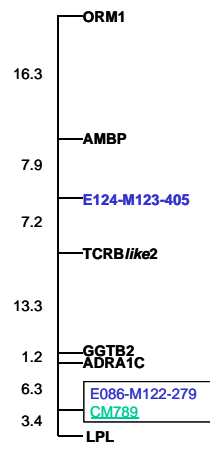


**53.8 cM**

BM4005: E086-M086-182 4.1 cM  
E033-M124-290: PGAZac2 14.4 cM

### Linkage Group 16

*Bta8, Oar2, Hsa8 & 9*

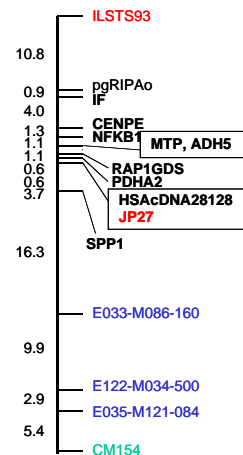


**55.6 cM**

E123-M034-185: E124-M123-405 3.5 cM

### Linkage Group 17

*Bta6, Oar6, Hsa4*

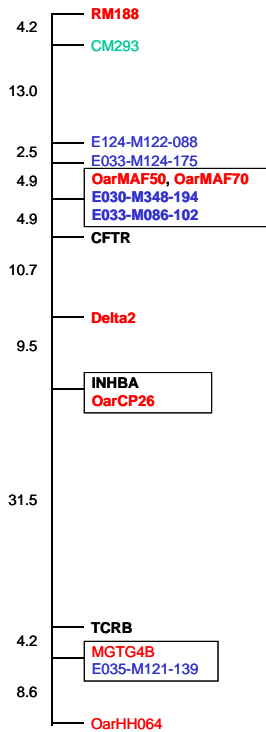


**58.7 cM**

BM1329: ADH5 2.9 cM

### Linkage Group 18

*Bta4, Oar4, Hsa7*

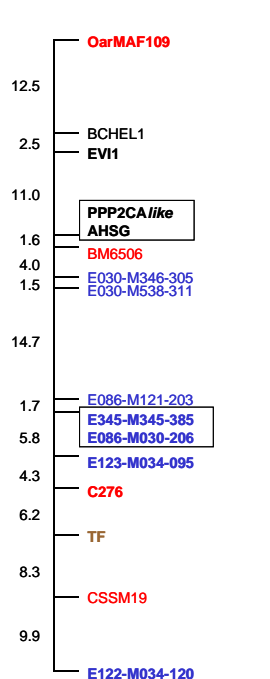


**97.2 cM**

CSSM65: OarCP26 21.8 cM  
pV18: TCRB 17.7 cM  
E030-M348-169: CFTR 25.9 cM

### Linkage Group 19

*Bta1, Oar1, Hsa3 & 21*

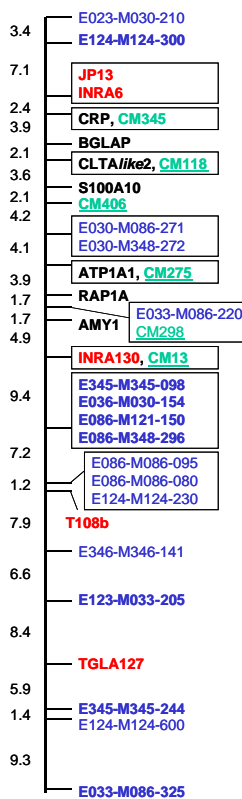


**83.9 cM**

Sl: OarMAF109 17.0 cM  
CSSM32: EVI1 10.1 cM  
RT6: E345-M345-385 6.0 cM  
E035-M024-151: PPP2CA-like 10.5 cM  
INRA11: E086-M030-206 1.3 cM

### Linkage Group 20

*Bta3, Oar1, Hsa1*

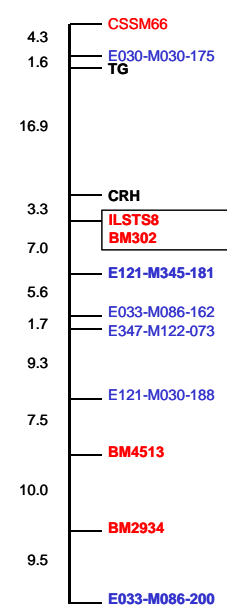


**102.6 cM**

TSHB: RAP1A 3.5 cM  
HUJI177: T108b 10.1 cM  
CM11: E345-M345-244 14.7 cM  
CM755: E033-M086-325 21.6 cM  
CM762: E345-M345-244 23.2 cM  
CM693: CM275 10.8 cM  
CM286: INRA6 3.0 cM  
E124-M030-625: E345-M345-244 8.2 cM  
E121-M086-270: RAP1A 12.0 cM

### Linkage Group 21

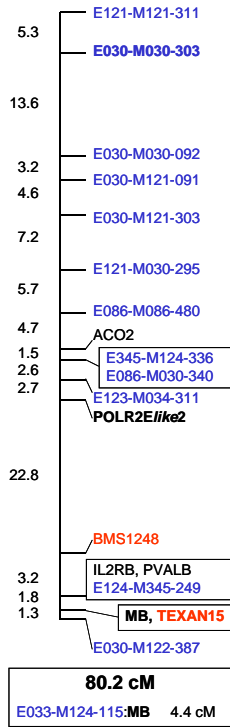
*Bta14, Oar9, Hsa8*



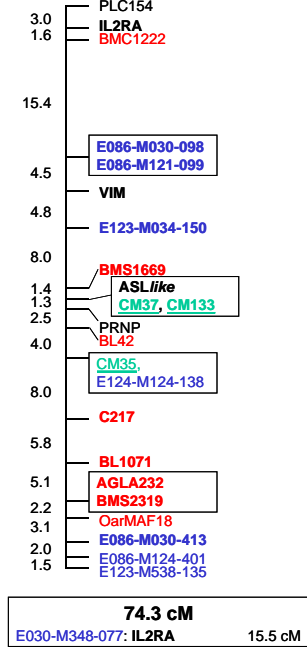
**76.8 cM**

E030-M121-165: TG 4.4 cM

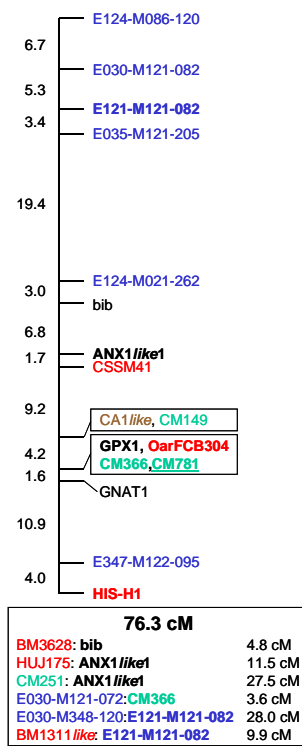
**Linkage Group 22**  
*Bta5, Oar3, Hsa22*



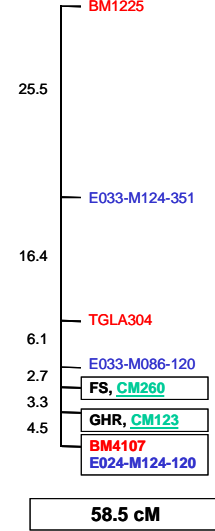
**Linkage Group 23**  
*Bta13, Oar13, Hsa10 & 20*



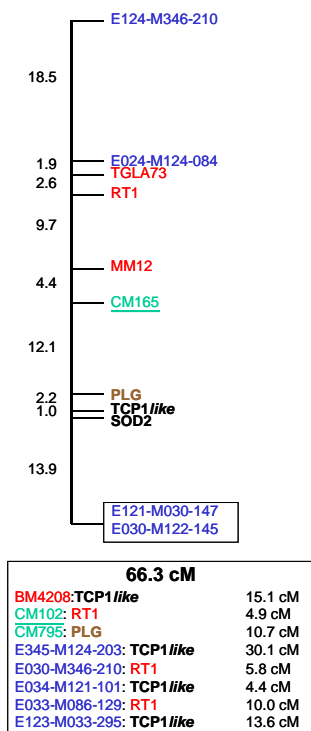
**Linkage Group 24**  
*Bta22, Oar19, Hsa3*



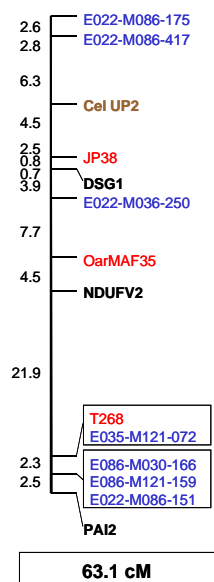
**Linkage Group 25**  
*Bta20, Oar16, Hsa5*



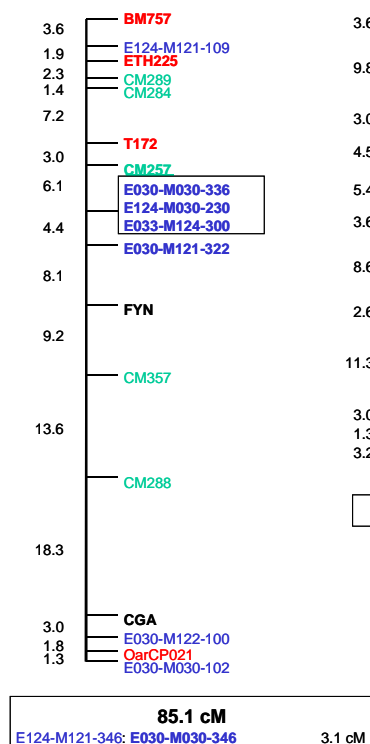
**Linkage Group 26**  
*Bta9, Oar8, Hsa6*



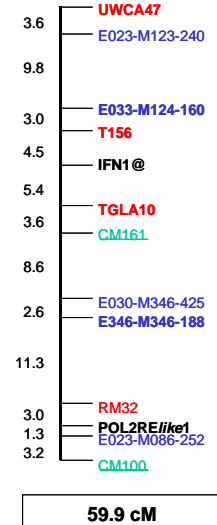
**Linkage Group 27**  
*Bta24, Oar23, Hsa18*



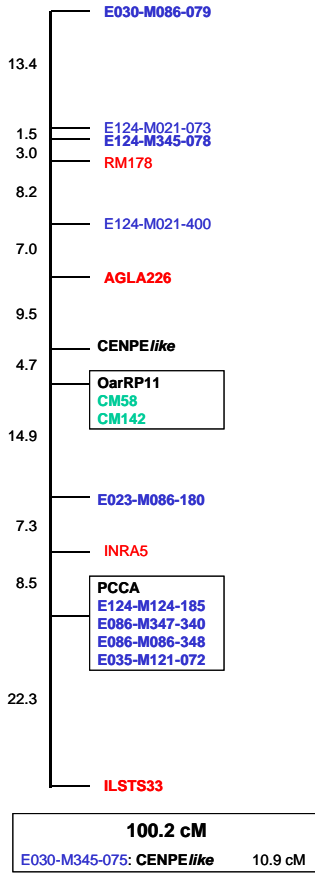
**Linkage Group 28**  
*Bta9, Oar8 & 9, Hsa6*



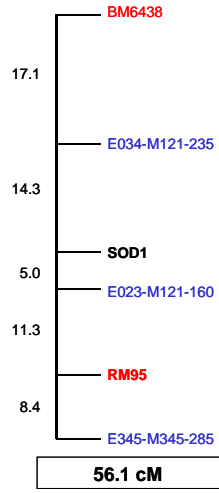
**Linkage Group 29**  
*Bta8, Oar2, Hsa9*



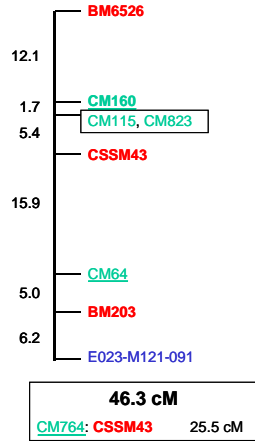
**Linkage Group 30**  
Bta12, Oar10, Hsa13



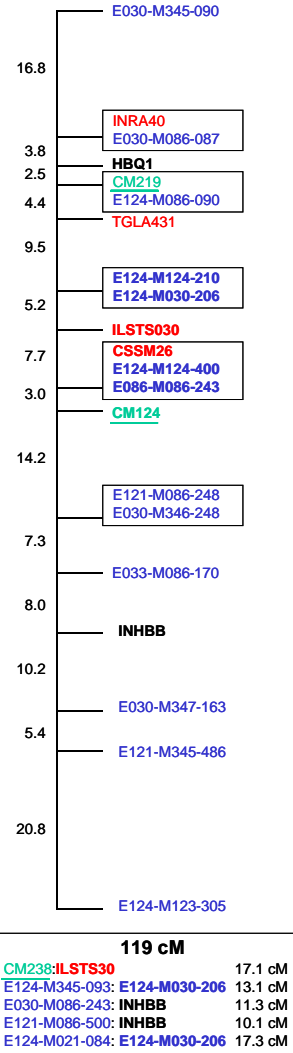
**Linkage Group 31**  
Bta1, Oar1, Hsa21



**Linkage Group 32**  
Bta27, Oar26, Hsa 4 & 8



**Linkage Group 33**  
Bta2 & 22, Oar2, Hsa2 & 3



**Linkage Group X / Y**

