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(71) Applicants *(for all designated States except US)*: **AARHUS UNIVERSITET** [DK/DK]; Nordre Ringgade 1, DK-8000 Århus C (DK). **KVÆGAVLSFORENINGEN DANSIRE** [DK/DK]; Ebeltoftvej 16, DK-8900 Randers (DK).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **LUND, Mogens, Sandø** [DK/DK]; Vestergade 7, Ørum, DK-8830 Tjele (DK). **BENDIXEN, Christian** [DK/DK]; Amstrupvej 7, DK-8860 Ulstrup (DK). **JENSEN, Helle** [DK/DK]; Middagshøjvej 38, 1., DK-8800 Viborg (DK). **THOMSEN, Bo** [DK/DK]; Ryhaven 49, DK-8210 Århus V (DK). **SØRENSEN, Peter** [DK/DK]; Baldersvej 13, DK-8800 Viborg (DK). **SVENDSEN, Søren** [DK/DK]; Rindsvej 13, st. tv., DK-8900 Randers (DK). **THOMASEN, Jørn, Rind** [DK/DK]; Nørre Hvamvej 2, Hvam, DK-7500 Holstebro (DK). **NIELSEN, Vivi, Hunnicke** [DK/DK]; Veldsparken 72, Ørum, DK-8830 Tjele (DK). **MAJGREN, Bente, Flügel** [DK/DK]; Slåenvej 10, Hørby, DK-9500 Hobro (DK). **GULDBRANDTSEN, Bernt** [DK/DK]; Fjældevænget 124, 1. th., DK-8210 Århus V (DK).

(74) Agent: **HØIBERG A/S**; Store Kongensgade 59 A, DK-1264 Copenhagen K (DK).

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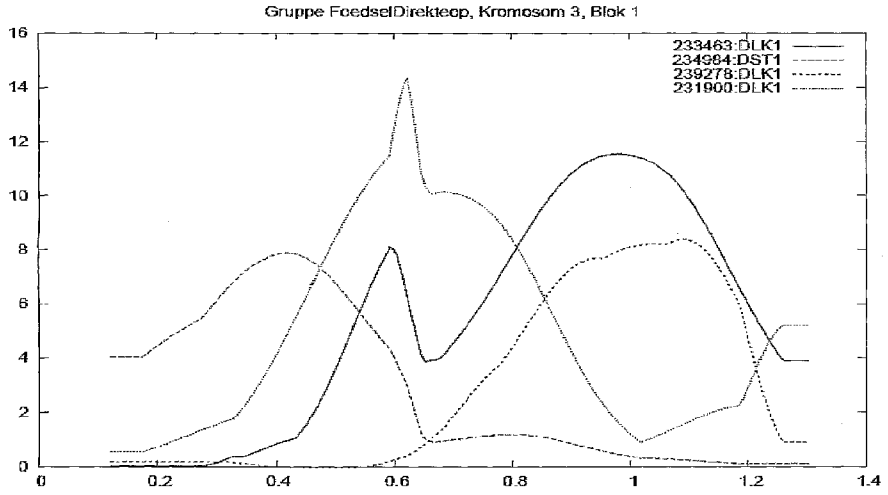
(54) Title: CALVING CHARACTERISTICS



(57) Abstract: The invention relates to a method for determining calving characteristics in bovine subjects, wherein calving characteristics comprise stillbirth, calving difficulty and calf size at birth, which are all economically important factors. In particular, the method of the invention involves identification of genetic markers and/or Quantitative Trait Locus (QTL) for the determination of calving characteristics in a bovine subject. The determination of calving characteristics involves resolution of the specific microsatellite status. Furthermore, the invention relates to a diagnostic kit for detection of genetic marker(s) associated with calving characteristics. The method and kit of the present invention can be applied for selection of bovine subjects for breeding purposes. Thus, the invention provides a method of genetically selecting bovine subjects with calving characteristics that will yield cows less prone to stillbirth, calving difficulties and undesired calf size at birth.

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Calving characteristics

Field of invention

The present invention relates to calving characteristics in bovine subjects. In particular, the invention relates to genetic markers for the determination of calving characteristics in a bovine subject and a diagnostic kit for detection of genetic marker(s) associated with calving characteristics.

Background of invention

Stillbirth, calving difficulty and calf size at birth are economic important calving traits, which are included in the Danish dairy cattle breeding program (Pedersen et al., 2003). The incidence of stillbirths for Holstein cattle has increased in several Holstein populations during the last two decades (Hansen et al., 2004). The increased incidence of stillbirths reduces the potential number of replacement heifers in dairy cattle herds and is associated with ethical problems.

Both direct and maternal genetic components are associated with the calving traits. In Danish Holstein, the heritability (h^2) estimates of the calving traits, measured as a direct sire effect (h^2=0.05-0.19) are higher than the heritability estimates of the calving traits measured as a maternal grand sire effect (h^2=0.04-0.06). The genetic correlation between calving traits measured as a direct sire effect (0.69-0.93) are markedly higher than the genetic correlation between calving traits measured as a maternal grand sire effect (0.01-0.62). The genetic component associated with the calving traits may be due to the segregation of one or more quantitative trait loci (QTL).

Quantitative trait locus (QTL) is a region of DNA that is associated with a particular trait (e.g. a disease or calving characteristics). A QTL is not necessarily a gene itself, but rather a DNA region that is closely linked to the genes that underlie the trait in question. Most likely, a QTL is a set of genes that collectively encode a quantitative trait that varies continuously across a population. Thus, the allelic variation of the QTL is associated with variation in a quantitative trait. The presence of QTL is inferred from genetic mapping, in which the genetic location of the QTL is determined relative to known genetic markers.

The identification of genetic markers that are linked to a particular phenotype, such as calving traits or to a heritable disease, has been facilitated by the discovery of microsatellite markers as a source of polymorphic markers and single nucleotide polymorphisms linked to a mutation causing a specific phenotype. Markers linked to the mutation or the mutation itself causing a specific phenotype of interest are localised by use of genetic analysis in pedigrees and also by exploiting linkage disequilibrium (LD) when looking at populations

Linkage disequilibrium reflects recombination events dating back in history and the use of LD mapping within families increases the resolution of mapping. LD exists when observed haplotypes in a population do not agree with the haplotype frequencies predicted by multiplying together the frequency of individual genetic markers in each haplotype. In this respect the term haplotype means a set of closely linked genetic markers present on one chromosome which tend to be inherited together.
In order for LD mapping to be efficient the density of genetic markers needs to be compatible with the distance across which LD extends in the given population. In a study of LD in dairy cattle population using a high number of genetic markers (284 autosomal microsatellite markers) it was demonstrated that LD extends over several tens of centimorgans for intrachromosomal markers (Farnir et al. 2000). Similarly, Georges, M (2000) reported that the location of a genetic marker that is linked to a particular phenotype in livestock typically has a confidence interval of 20-30 cM (corresponding to maybe 500-1000 genes) (Georges, M., 2000). The existence of linkage disequilibrium is taken into account in order to use maps of particular regions of interest with high confidence.

Several QTL have been detected for calving traits in other Holstein populations (e.g. Kühn et al., 2003; Schrooten et al., 2000; Elo et al., 1999). Some QTL may affect more than one trait, and some QTL may even be located at the same chromosomal position for different traits. If the QTL affects multiple traits then it is important, for e.g. selection purposes, to test if it is a pleiotropic or linked QTL affecting the traits.

Calving traits such as stillbirth, calving difficulty and calf size are not easily predicted. The use of genetic analysis and genetic selection appears to be a possible method for prognostication of these calving traits. Once mapped, a QTL can be usefully applied in marker assisted selection.

Summary of invention

It is an object of the present invention to provide an application method for marker assisted selection of polymorphisms in the bovine genome, wherein polymorphisms are associated with calving trait characteristics, such as still birth, calving difficulties, and calf size; and/or provide genetic markers for use in such a method, and/or to provide animals selected using the method of the invention.

One aspect of the present invention relates to a method of determining calving characteristics in a bovine subject, comprising detecting in a sample from said bovine subject the presence or absence of at least one genetic marker that is linked to at least one trait indicative of increased risk of stillbirth and/or increased risk of calving difficulties and/or increased risk of non-desired calf size, wherein said at least one genetic marker is located on the bovine chromosome BTA3 in a region flanked by and including polymorphic microsatellite markers INRA006 and BM7225 and/or

BTA4 in the region flanked by and including polymorphic microsatellite markers BMS1788 and MGTG4B and/or,

BTA5 in the region flanked by and including polymorphic microsatellite markers BMS1095 and BM2830 and/or,

BTA7 in a region flanked by and including polymorphic microsatellite markers BM7160 and BL1043 and/or,

BTA8 in a region flanked by and including polymorphic microsatellite markers IDVGA-11 and BMS836 and/or,

BTA9 in a region flanked by and including polymorphic microsatellite markers BMS2151 and BMS1967 and/or,

BTA10 in a region flanked by and including polymorphic microsatellite markers DIK2658 and BMS2614 and/or,

BTA11 in the region flanked by and including polymorphic microsatellite markers BM716 and HEL13 and/or,

BTA12 in a region flanked by and including polymorphic microsatellite markers BMS410 and BMS2724 and/or,

BTA15 in a region flanked by and including polymorphic microsatellite markers BR3510 and BMS429 and/or,

BTA18 in a region flanked by and including polymorphic microsatellite markers IDVGA-31 and DIK4013 and/or,

BTA19 in a region flanked by and including polymorphic microsatellite markers BM9202 and BMS601 and/or,
BTA20 in a region flanked by and including polymorphic microsatellite markers BM3517 and UWCA26 and/or,
BTA21 in a region flanked by and including polymorphic microsatellite markers DIK5182 and IDVGA-30 and/or,
BTA22 in a region flanked by and including polymorphic microsatellite markers CSSM26 and BM4102 and/or,
BTA24 in a region flanked by and including polymorphic microsatellite markers BMS917 and BMS3024 and/or,
BTA25 in a region flanked by and including polymorphic microsatellite markers ILSTS102 and AF5 and/or,
BTA26 in a region flanked by and including polymorphic microsatellite markers BMS651 and BM7237 and/or,
BTA28 in a region flanked by and including polymorphic microsatellite markers, BMC6020 and BMC2208, , wherein the presence of said at least one genetic marker is indicative of calving characteristics of said bovine subject and/or off-spring therefrom.

A second aspect of the present invention relates to diagnostic kit for use in detecting the presence in a bovine subject of at least one genetic marker associated with bovine calving characteristics, comprising at least one oligonucleotide sequence, wherein the nucleotide sequences are selected from any of SEQ ID NO.: 1 to SEQ ID NO.: 558 and/or any combination thereof.

Description of drawings

Fig. 1: Genome scan of BTA3 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 2: Genome scan of BTA4 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 3: Genome scan of BTA7 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 4: Genome scan of BTA7 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 5: Genome scan of BTA8 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL

analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 6: Genome scan of BTA8 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 7: Genome scan of BTA9 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 8: Genome scan of BTA10 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 9: Genome scan of BTA12 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the

positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 10: Genome scan of BTA12 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 11: Genome scan of BTA15 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 12: Genome scan of BTA18 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 13: Genome scan of BTA18 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis

represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 14: Genome scan of BTA18 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 15: Genome scan of BTA18 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 16: Genome scan of BTA19 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 17: Genome scan of BTA20 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in

calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 18: Genome scan of BTA21 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 19: Genome scan of BTA22 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 20: Genome scan of BTA22 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 21: Genome scan of BTA24 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL

correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 22: Genome scan of BTA25 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 23: Genome scan of BTA25 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 24: Genome scan of BTA26 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 25: Genome scan of BTA26 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are

designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 26: Genome scan of BTA26 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 27: Genome scan of BTA28 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. Calving parameters are designated by D: Direct effect, M Maternal effect, while LK corresponds to stillbirth, FL correspond to calving difficulty, and ST correspond to calf size. The number 1 in calving parameter designates that data is derived from first calving. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 28: Genome scan of BTA5 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Fig. 29: Genome scan of BTA11 in relation to calving characteristics. Numbers refer to 'herdbook number' and calving parameter, respectively. The X-axis represents the distance of the chromosome expressed in Morgan according to the positions employed in this analysis. The Y-axis represents the test-statistics of the QTL analysis expressed

in the F-value. High F-values are indicative of genes, which affect the investigated calving traits.

Detailed description of the invention

The present invention relates to genetic determinants of calving characteristics in dairy cattle. Calving traits, such as calving difficulties, stillbirths and calf size are economically important factors in the dairy industry. Therefore, it is of economic interest to identity those bovine subjects that have a genetic predisposition for specific calving characteristics. Bovine subjects with genetic predisposition for calving characteristics are carriers of non-desired traits, which both complicate calving, and can be passed on to their offspring.

The term "bovine subject" refers to cattle of any breed and is meant to include both cows and bulls, whether adult or newborn animals. No particular age of the animals are denoted by this term. One example of a bovine subject is a member of the Holstein breed. In one embodiment, the bovine subject is a member of the Holstein-Friesian cattle population. In another embodiment, the bovine subject is a member of the Holstein Swartbont cattle population. In another embodiment, the bovine subject is a member of the Deutsche Holstein Schwarzbunt cattle population. In another embodiment, the bovine subject is a member of the US Holstein cattle population. In one embodiment, the bovine subject is a member of the Red and White Holstein breed. In another embodiment, the bovine subject is a member of the Deutsche Holstein Schwarzbunt cattle population. In one embodiment, the bovine subject is a member of any family, which include members of the Holstein breed. In one embodiment the bovine subject is a member of the Danish Red population. In another embodiment the bovine subject is a member of the Finnish Ayrshire population. In yet another embodiment the bovine subject is a member of the Swedish Red population. In a further embodiment the bovine subject is a member of the Danish Holstein population. In another embodiment, the bovine subject is a member of the Swedish Red and White population. In yet another embodiment, the bovine subject is a member of the Nordic Red population.

In one embodiment of the present invention, the bovine subject is selected from the group consisting of Swedish Red and White, Danish Red, Finnish Ayrshire, Holstein-Friesian, Danish Holstein and Nordic Red. In another embodiment of the present

invention, the bovine subject is selected from the group consisting of Finnish Ayrshire and Swedish Red cattle. In another embodiment of the present invention, the bovine subject is selected from the group consisting of Finnish Ayrshire and Swedish Red cattle.

In one embodiment, the bovine subject is selected from the group of breeds shown in table 1a

Table 1a Breed names and breed codes assigned by ICAR (International Committee for Animal Recording)

Breed	Breed Code	National Breed Names Annex
Abondance	AB	-
Tyrol Grey	AL	2.2
Angus	AN	2.1
Aubrac	AU	
Ayrshire	AY	2.1
Belgian Blue	BB	
Blonde d'Aquitaine	BD	
Beefmaster	BM	
Braford	BO	
Brahman	BR	
Brangus	BN	
Brown Swiss	BS	2.1
Chianina	CA	
Charolais	CH	
Dexter	DR	
Galloway	GA	2.2
Guernsey	GU	
Gelbvieh	GV	
Hereford, horned	HH	
Hereford, polled	HP	
Highland Cattle	HI	
Holstein	HO	2.2
Jersey	JE	
Limousin	LM	
Maine-Anjou	MA	
Murray-Grey	MG	
Montbéliard	MO	
Marchigiana	MR	
Normandy	NO**	
Piedmont	PI	2.2
Pinzgau	PZ	
European Red Dairy Breed	[RE]*	2.1, 2.2
Romagnola	RN	
Holstein, Red and White	RW***	2.2
Salers	SL**	
Santa Gertrudis	SG	
South Devon	SD	
Shorthorn	[SH]*	2.2
Simmental	SM	2.2
Sahiwal	SW	
Tarentaise	TA	
Welsh Black	WB	
Buffalo (Bubalis bubalis)	BF	

* *new breed code*
** *change from earlier code because of existing code in France*
*** US proposal WW

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In one embodiment, the bovine subject is a member of a breed selected from the group of breeds shown in table 1b

Table 1b Breed names

National Breed Names		
English Name	National names	
Angus	Including	Aberdeen Angus Canadian Angus American Angus German Angus
Ayrshire	Including	Ayrshire in Australia Canada Colombia Czech Republic Finland Kenya New Zealand Norway (NRF) Russia South Africa Sweden (SRB) and SAB UK US Zimbabwe
Belgian Blue	French: Flemish:	Blanc-bleu Belge Witblauw Ras van Belgie
Brown Swiss	German: Italian: French: Spanish: Serbo-Croatian: Czech: Romanian: Russian: Bulgarian:	Brauvieh Razza Bruna Brune Bruna, Parda Alpina Slovenacko belo Hnedy Karpatsky Shvitskaja Bruna B'ljarska kafyava
European Red Dairy Breed	Including	Danish Red Angeln Swedish Red and White Norwegian Red and White Estonian Red Latvian Brown Lithuanian Red Byelorus Red Polish Red Lowland

In one embodiment, the bovine subject is a member of a breed selected from the group of breeds shown in table 1c

Table 1c Breed names

National Breed Names		
English Name	National names	
European Red Dairy Breed (continued)		Ukrainian Polish Red (French Rouge Flamande?) (Belgian Flamande Rouge?)
Galloway:	Including	Black and Dun Galloway Belted Galloway Red Galloway White Galloway
Holstein, Black and White:	Dutch:	Holstein Swartbont
	German:	Deutsche Holstein, schwarzbunt
	Danish:	Sortbroget Dansk Malkekvaeg
	British:	Holstein Friesian
	Swedish:	Svensk Låglands Boskaap
	French:	Prim Holstein
	Italian:	Holstein Frisona
	Spanish:	Holstein Frisona
Holstein, Red and White	Dutch:	Holstein, roodbunt
	German:	Holstein, rotbunt
	Danish:	Roedbroget Dansk Malkekvaeg
Piedmont	Italian:	Piemontese
Shorthorn	Including	Dairy Shorthorn Beef Shorthorn Polled Shorthorn
Simmental	Including dual purpose and beef use	
	German:	Fleckvieh
	French:	Simmental Française
	Italian:	Razza Pezzata Rossa
	Czech:	Cesky strakatý
	Slovakian:	Slovensky strakaty
	Romanian:	Baltata românească
	Russian:	Simmentalskaja
Tyrol Grey	German:	Tiroler Grauvieh Oberinntaler Grauvieh Rätisches Grauvieh
	Italian:	Razza Grigia Alpina

The term "genetic marker" refers to a variable nucleotide sequence (polymorphism) of the DNA on the bovine chromosome. The variable nucleotide sequence can be identified by methods known to a person skilled in the art, for example by using specific oligonucleotides in for example amplification methods and/or hybridization techniques and/or observation of a size difference. However, the variable nucleotide sequence may also be detected by sequencing or for example restriction fragment length polymorphism analysis. The variable nucleotide sequence may be represented by a deletion, an insertion, repeats, and/or a point mutation. Thus, a genetic marker comprises a variable number of polymorphic alleles.

One type of genetic marker is a microsatellite marker that is linked to a quantitative trait locus. Microsatellite markers refer to short sequences repeated after each other. In short sequences are for example one nucleotide, such as two nucleotides, for example three nucleotides, such as four nucleotides, for example five nucleotides, such as six nucleotides, for example seven nucleotides, such as eight nucleotides, for example nine nucleotides, such as ten nucleotides. However, changes sometimes occur and the number of repeats may increase or decrease. The specific definition and locus of the polymorphic microsatellite markers can be found in the USDA genetic map (Kappes et al. 1997; or by following the link to U.S. Meat Animal Research Center http://www.marc.usda.gov/).

In one embodiment of the present invention, specific marker alleles are linked to quantitative trait loci affecting calving characteristics.

It is furthermore appreciated that the nucleotide sequences of the genetic markers of the present invention are genetically linked to traits for calving in a bovine subject. Consequently, it is also understood that a number of genetic markers may be generated from the nucleotide sequence of the DNA region(s) flanked by and including the genetic markers according to the method of the present invention.

Calving trait characteristics

Calving in a bovine subject is affected by a number of characteristics. Traits that affect calving according to the present invention are for example the occurrence of stillbirth (SB), calving difficulty (CD) and the size of the calf at birth (CS). The traits are assessed by a direct effect (D) of the sire in the calf. However, the traits are also assessed as a maternal effect (M) of the sire in the mother of the calf.

By the term calving characteristics is meant traits which affect calving in the bovine subject or its off-spring. Thus, calving characteristics of a bull are physically manifested by its off-spring – both female and male.

In the present invention calving characteristics comprise the traits SB, CD, and CS, which refer to the following characteristics:

SB: Designates stillbirths.

CS: Size of calves.

CD: Calving difficulties, which are based on registrations from the farmers where it is subjectively registered how difficult the calving is. The calving difficulties consist of four categories:

1: easy with no help
2: easy with assistance
3: difficult but without veterinary assistance
4: difficult with veterinary assistance

In one embodiment of the present invention, the method and kit described herein relates to still births, calving difficulties as categorized herein and/or calf size. In one embodiment of the present invention, the method and kit described herein relates to still births. In another embodiment, the method and kit of the present invention pertains to calving difficulties, such as detected by the calving difficulty categories described above. In yet another embodiment, the method and kit of the present invention relates to calf size. In another embodiment of the present invention, the method and kit described herein relates to any combination of still birth, calving difficulties and/or calf size.

Granddaughter design

The granddaughter design includes analysing data from DNA-based markers for grandsires that have been used extensively in breeding and for sons of grandsires where the sons have produced offspring. The phenotypic data that are to be used together with the DNA-marker data are derived from the daughters of the sons. Such phenotypic data could be for example milk production features, features relating to calving, meat quality, or disease. One group of daughters has inherited one allele from their father whereas a second group of daughters has inherited the other allele from their father. By comparing data from the two groups information can be gained whether a fragment of a particular chromosome is harbouring one or more genes that affect the trait in question. It may be concluded whether a QTL is present within this fragment of the chromosome.

A prerequisite for performing a granddaughter design is the availability of detailed phenotypic data. In the present invention such data have been available (http://www.lr.dk/kvaeg/diverse/principles.pdf).

In contrast, DNA markers can be used directly to provide information of the traits passed on from parents to one or more of their offspring when a number of DNA markers on a chromosome have been determined for one or both parents and their offspring. The markers may be used to calculate the genetic history of the chromosome linked to the DNA markers.

Frequency of recombination

The frequency of recombination is the likelihood that a recombination event will occur between two genes or two markers. The frequency of recombination may be calculated as the genetic distance between the two genes or the two markers. Genetic distance is measured in units of centiMorgan (cM). One centiMorgan is equal to a 1% chance that a marker at one genetic locus will be separated from a marker at a second locus due to crossing over in a single generation. One centiMorgan is equivalent, on average, to one million base pairs.

Chromosomal regions and markers

BTA is short for *Bos taurus* autosome.

One aspect of the present invention relates to a method of determining calving characteristics in a bovine subject, comprising detecting in a sample from said bovine subject the presence or absence of at least one genetic marker that is linked to at least one trait indicative of increased risk of stillbirth and/or increased risk of calving difficulties and/or increased risk of non-desired calf size, wherein said at least one genetic marker is located on the bovine chromosome BTA3 in a region flanked by and including polymorphic microsatellite markers INRA006 and BM7225 and/or BTA4 in the region flanked by and including polymorphic microsatellite markers BMS1788 and MGTG4B and/or, BTA5 in the region flanked by and including polymorphic microsatellite markers BMS1095 and BM2830 and/or, BTA7 in a region flanked by and including polymorphic microsatellite markers BM7160 and BL1043 and/or, BTA8 in a region flanked by and including polymorphic microsatellite markers IDVGA-11 and BMS836 and/or, BTA9 in a region flanked by and including polymorphic microsatellite markers BMS2151 and BMS1967 and/or, BTA10 in a region flanked by and including polymorphic microsatellite markers DIK2658 and BMS2614 and/or, BTA11 in the region flanked by and including polymorphic microsatellite markers BM716 and HEL13 and/or, BTA12 in a region flanked by and including polymorphic microsatellite markers BMS410 and BMS2724 and/or, BTA15 in a region flanked by and including

polymorphic microsatellite markers BR3510 and BMS429 and/or, BTA18 in a region flanked by and including polymorphic microsatellite markers IDVGA-31 and DIK4013 and/or, BTA19 in a region flanked by and including polymorphic microsatellite markers BM9202 and BMS601 and/or, BTA20 in a region flanked by and including polymorphic microsatellite markers BM3517 and UWCA26 and/or, BTA21 in a region flanked by and including polymorphic microsatellite markers DIK5182 and IDVGA-30 and/or, BTA22 in a region flanked by and including polymorphic microsatellite markers CSSM26 and BM4102 and/or, BTA24 in a region flanked by and including polymorphic microsatellite markers BMS917 and BMS3024 and/or, BTA25 in a region flanked by and including polymorphic microsatellite markers ILSTS102 and AF5 and/or, BTA26 in a region flanked by and including polymorphic microsatellite markers BMS651 and BM7237 and/or, BTA28 in a region flanked by and including polymorphic microsatellite markers, BMC6020 and BMC2208, , wherein the presence of said at least one genetic marker is indicative of calving characteristics of said bovine subject and/or off-spring therefrom.

In order to determine calving characteristics in a bovine subject, wherein the at least one genetic marker is located on a bovine chromosome in the region flanked by and including the polymorphic microsatellite marker, it is appreciated that more than one genetic marker may be employed in the present invention. For example the at least one genetic marker may be a combination of at least two or more genetic markers such that the accuracy may be increased, such as at least three genetic markers, for example four genetic markers, such as at least five genetic markers, for example six genetic markers, such as at least seven genetic markers, for example eight genetic markers, such as at least nine genetic markers, for example ten genetic markers.

The at least one genetic marker may be located on at least one bovine chromosome, such as two chromosomes, for example three chromosomes, such as four chromosomes, for example five chromosomes, and/or such as six chromosomes.

In a preferred embodiment the at least one marker is selected from any of the individual markers of the tables shown herein.

BTA3

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA3. In one specific embodiment of the present invention, the at

least one genetic marker is located in the region from about 17.1 cM to about 101.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers INRA006 and BM7225. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 2a:

Table 2a

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/
INRA006	17.1
UWCA7	17.4
ILSTS096	27.4
DIK4403	32.5
RME23	32.5
BMS963	32.9
BMS819	33.5
FCGR1	34.6
BL41	43.3
DIK4353	52.5
INRA003	59.4
BMS2790	62.4
ILSTS029	64.9
BM220	66.3
INRA123	66.3
BMS862	67.4
HUJ246	68.0
BMS937	68.0
DIK4664	68.3
DIK2702	77.6
HUJII77	87.3
DIK2686	95.5

BM7225	101.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 34.6 cM to about 87.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers FCGR1 and HUJII77. The at least one genetic marker is selected from the group of markers shown in Table 2b:

Table 2b

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/
FCGR1	34.6
BL41	43.3
DIK4353	52.5
INRA003	59.4
BMS2790	62.4
ILSTS029	64.9
BM220	66.3
INRA123	66.3
BMS862	67.4
HUJ246	68.0
BMS937	68.0
DIK4664	68.3
DIK2702	77.6
HUJII77	87.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 32.5 cM to about 59.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers DIK4403and INRA003. The at least one genetic marker is selected from the group of markers shown in Table 2c:

Table 2c

Marker on BTA3	Relative position (cM)

	http://www.marc.usda.gov/
DIK4403	32.5
RME23	32.5
BMS963	32.9
BMS819	33.5
FCGR1	34.6
BL41	43.3
DIK4353	52.5
INRA003	59.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 77.6 cM to about 101.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers DIK2702 and BM7225. The at least one genetic marker is selected from the group of markers shown in Table 2d:

Table 2d

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/
DIK2702	77.6
HUJII77	87.3
DIK2686	95.5
BM7225	101.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 52.5 cM to about 68.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers DIK4353and DIK4664. The at least one genetic marker is selected from the group of markers shown in Table 2e:

Table 2e

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/
DIK4353	52.5

INRA003	59.4
BMS2790	62.4
ILSTS029	64.9
BM220	66.3
INRA123	66.3
BMS862	67.4
HUJ246	68.0
BMS937	68.0
DIK4664	68.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 59.4 cM to about 66.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers INRA003 and INRA123. The at least one genetic marker is selected from the group of markers shown in Table 2f:

Table 2f

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/
INRA003	59.4
BMS2790	62.4
ILSTS029	64.9
BM220	66.3
INRA123	66.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 32.5 cM to about 52.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the markers DIK4403 and DIK4353. The at least one genetic marker is selected from the group of markers shown in Table 2g:

Table 2g

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/

DIK4403	32.5
RME23	32.5
BMS963	32.9
BMS819	33.5
FCGR1	34.6
BL41	43.3
DIK4353	52.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 77.6 cM to 101.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA3. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA3 in the region flanked by and including the marker FCGR1 and HUJII77. The at least one genetic marker is selected from the group of markers shown in Table 2h:

Table 2h

Marker on BTA3	Relative position (cM) http://www.marc.usda.gov/
DIK2702	77.6
HUJII77	87.3
DIK2686	95.5
BM7225	101.8

BTA4

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA4. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 12.5 cM to about 112.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers BMS1788 and MGTG4B. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 3a:

Table 3a

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
BMS1788	12.5
BMS2646	43.2
TGLA116	52.5
INRA072	63.0
BM8233	73.4
BMS648	91.2
BR6303	104.9
MGTG4B	112.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 12.5 cM to about 91.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers BMS1788 and BMS648. The at least one genetic marker is selected from the group of markers shown in Table 3b:

Table 3b

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
BMS1788	12.5
BMS2646	43.2
TGLA116	52.5
INRA072	63.0
BM8233	73.4
BMS648	91.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 43.2 cM to about 91.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers BMS2646 and BMS648. The at least one genetic marker is selected from the group of markers shown in Table 3c:

Table 3c

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
BMS2646	43.2
TGLA116	52.5
INRA072	63.0
BM8233	73.4
BMS648	91.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 43.2 cM to about 63.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers BMS2646 and INRA072. The at least one genetic marker is selected from the group of markers shown in Table 3d:

Table 3d

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
BMS2646	43.2
TGLA116	52.5
INRA072	63.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 52.2 cM to about 73.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers TGLA116 and BM8233. The at least one genetic marker is selected from the group of markers shown in Table 3e:

Table 3e

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
TGLA116	52.5
INRA072	63.0
BM8233	73.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 63.0 cM to about 91.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers INRA072 and BMS648. The at least one genetic marker is selected from the group of markers shown in Table 3f:

Table 3f

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
INRA072	63.0
BM8233	73.4
BMS648	91.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 63.0 cM to about 73.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA4. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA4 in the region flanked by and including the markers INRA072 and BM8233. The at least one genetic marker is selected from the group of markers shown in Table 3g:

Table 3g

Marker on BTA4	Relative position (cM) http://www.marc.usda.gov/
INRA072	63.0
BM8233	73.4

BTA5

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA5. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 116.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers BMS1095 and BM2830. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is

significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 4a:

Table 4a

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
BMS1095	0.0
BM6026	6.0
MNB-33	7.4
BMS610	12.0
BP1	17.3
DIK4747	18.3
DIK2718	30.1
AGLA293	32.3
DIK5002	33.7
DIK4759	40.3
BMC1009	41.7
CSSM034	45.5
RM500	56.3
BMS1617	56.3
DIK5046	66.2
ETH10	71.8
CSSM022	74.2
BMS1216	78.2
DIK2943	82.9
BMS1248	90.8
BM315	103.2
BMS1658	105.7
BM2830	116.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.0 cM to about 103.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers BMS1095 and BM315. The at least one genetic marker is selected from the group of markers shown in Table 4b:

Table 4b

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
BMS1095	0.0
BM6026	6.0
MNB-33	7.4
BMS610	12.0
BP1	17.3
DIK4747	18.3
DIK2718	30.1
AGLA293	32.3
DIK5002	33.7
DIK4759	40.3
BMC1009	41.7
CSSM034	45.5
RM500	56.3
BMS1617	56.3
DIK5046	66.2
ETH10	71.8
CSSM022	74.2
BMS1216	78.2
DIK2943	82.9
BMS1248	90.8
BM315	103.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.1 cM to about 103.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers DIK2718 and BM315. The at least one genetic marker is selected from the group of markers shown in Table 4c:

Table 4c

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/

DIK2718	30.1
AGLA293	32.3
DIK5002	33.7
DIK4759	40.3
BMC1009	41.7
CSSM034	45.5
RM500	56.3
BMS1617	56.3
DIK5046	66.2
ETH10	71.8
CSSM022	74.2
BMS1216	78.2
DIK2943	82.9
BMS1248	90.8
BM315	103.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.1 cM to about 78.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers DIK2718 and BMS1216. The at least one genetic marker is selected from the group of markers shown in Table 4d:

Table 4d

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
DIK2718	30.1
AGLA293	32.3
DIK5002	33.7
DIK4759	40.3
BMC1009	41.7
CSSM034	45.5
RM500	56.3
BMS1617	56.3
DIK5046	66.2

ETH10	71.8
CSSM022	74.2
BMS1216	78.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 18.3 cM to about 56.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers DIK4747 and RM500. The at least one genetic marker is selected from the group of markers shown in Table 4e:

Table 4e

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
DIK4747	18.3
DIK2718	30.1
AGLA293	32.3
DIK5002	33.7
DIK4759	40.3
BMC1009	41.7
CSSM034	45.5
RM500	56.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 17.3 cM to about 33.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers BP1 and DIK5002. The at least one genetic marker is selected from the group of markers shown in Table 4f:

Table 4f

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
BP1	17.3
DIK4747	18.3
DIK2718	30.1

AGLA293	32.3
DIK5002	33.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 45.5 cM to about 82.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers CSSM034 and DIK2943. The at least one genetic marker is selected from the group of markers shown in Table 4g:

Table 4g

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
CSSM034	45.5
RM500	56.3
BMS1617	56.3
DIK5046	66.2
ETH10	71.8
CSSM022	74.2
BMS1216	78.2
DIK2943	82.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 45.5 cM to about 66.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers CSSM034 and DIK5046. The at least one genetic marker is selected from the group of markers shown in Table 4h:

Table 4h

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
CSSM034	45.5
RM500	56.3
BMS1617	56.3
DIK5046	66.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 66.2 cM to about 82.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers DIK5046 and DIK2943. The at least one genetic marker is selected from the group of markers shown in Table 4i:

Table 4i

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
DIK5046	66.2
ETH10	71.8
CSSM022	74.2
BMS1216	78.2
DIK2943	82.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 71.8 cM to about 90.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA5. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA5 in the region flanked by and including the markers ETH10 and BMS1248. The at least one genetic marker is selected from the group of markers shown in Table 4j:

Table 4j

Marker on BTA5	Relative position (cM) http://www.marc.usda.gov/
ETH10	71.8
CSSM022	74.2
BMS1216	78.2
DIK2943	82.9
BMS1248	90.8

BTA7

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA7. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 135.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the

at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers BM7160 and BL1043. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 5a:

Table 5a

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
BM7160	0.0
BL1067	14.7
BMS713	16.8
DIK5321	22.3
DIK4421	22.7
DIK2207	26.7
DIK5412	30.2
IL4	32.0
BM6105	37.9
TGLA303	39.3
DIK2819	47.9
DIK4606	55.3
BM7247	57.3
UWCA20	58.6
BM6117	62.2
BMS2840	65.3
DIK2915	76.2
BMS2258	77.2
OARAE129	95.9
DIK2895	103.1
ILSTS006	116.6
BL1043	135.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.2 cM to about 95.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers DIK5412 and OARAE129. The at least one genetic marker is selected from the group of markers shown in Table 5b:

Table 5b

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
DIK5412	30.2
IL4	32.0
BM6105	37.9
TGLA303	39.3
DIK2819	47.9
DIK4606	55.3
BM7247	57.3
UWCA20	58.6
BM6117	62.2
BMS2840	65.3
DIK2915	76.2
BMS2258	77.2
OARAE129	95.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.2 cM to about 55.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers DIK5412 and DIK4606. The at least one genetic marker is selected from the group of markers shown in Table 5c:

Table 5c

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
DIK5412	30.2
IL4	32.0

BM6105	37.9
TGLA303	39.3
DIK2819	47.9
DIK4606	55.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 58.6 cM to about 95.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers UWCA20 and OARAE129. The at least one genetic marker is selected from the group of markers shown in Table 5d:

Table 5d

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
UWCA20	58.6
BM6117	62.2
BMS2840	65.3
DIK2915	76.2
BMS2258	77.2
OARAE129	95.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 77.2 cM to about 135.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers BMS2258 and BL1043. The at least one genetic marker is selected from the group of markers shown in Table 5e:

Table 5e

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
BMS2258	77.2
OARAE129	95.9
DIK2895	103.1
ILSTS006	116.6

BL1043	135.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 77.2 cM to about 116.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers BMS2258 and ILSTS006. The at least one genetic marker is selected from the group of markers shown in Table 5f:

Table 5f

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
BMS2258	77.2
OARAE129	95.9
DIK2895	103.1
ILSTS006	116.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 77.2 cM to about 95.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA7. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA7 in the region flanked by and including the markers BMS2258 and OARAE129. The at least one genetic marker is selected from the group of markers shown in Table 5g:

Table 5g

Marker on BTA7	Relative position (cM) http://www.marc.usda.gov/
BMS2258	77.2
OARAE129	95.9

BTA8

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA8. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 11.3 cM to about 122.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA8. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA8 in the region flanked by and including the markers IDVGA-11 and BMS836. The at least one genetic

marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 6a:

Table 6a

Marker on BTA8	Relative position (cM) http://www.marc.usda.gov/
IDVGA-11	11.3
BMS1591	31.4
BMS678	41.6
INRA129	54.6
BMS2072	66.0
BMS887	68.5
URB037	69.0
MCM64	71.1
CSSM047	118.7
BMS836	122.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 11.3 cM to about 71.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA8. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA8 in the region flanked by and including the markers IDVGA-11 and MCM64. The at least one genetic marker is selected from the group of markers shown in Table 6b:

Table 6b

Marker on BTA8	Relative position (cM) http://www.marc.usda.gov/
IDVGA-11	11.3
BMS1591	31.4
BMS678	41.6
INRA129	54.6
BMS2072	66.0
BMS887	68.5

URB037	69.0
MCM64	71.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 41.6 cM to about 66.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA8. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA8 in the region flanked by and including the markers BMS678 and BMS2072. The at least one genetic marker is selected from the group of markers shown in Table 6c:

Table 6c

Marker on BTA8	Relative position (cM) http://www.marc.usda.gov/
BMS678	41.6
INRA129	54.6
BMS2072	66.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 71.1 cM to about 122.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA8. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA8 in the region flanked by and including the markers MCM64 and BMS836. The at least one genetic marker is selected from the group of markers shown in Table 6d:

Table 6d

Marker on BTA8	Relative position (cM) http://www.marc.usda.gov/
MCM64	71.1
CSSM047	118.7
BMS836	122.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 11.3 cM to about 41.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA8. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA8 in the region flanked by and including the markers IDVGA-11 and BMS678. The at least one genetic marker is selected from the group of markers shown in Table 6e:

Table 6e

Marker on BTA8	Relative position (cM) http://www.marc.usda.gov/
IDVGA-11	11.3
BMS1591	31.4
BMS678	41.6

BTA9

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA9. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 8,49 cM to about 109.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers BMS2151 and BMS1967. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 7a:

Table 7a

Marker on BTA9	Relative position (cM) http://www.marc.usda.gov/
BMS2151	8.49
ETH225	12.8
ILSTS037	26.3
BM2504	30.9
DIK2892	30.9
DIK3003	36.5
DIK3002	36.5
BMS1267	38.7
DIK5142	43.8
BMS555	43.8
DIK5364	45.7
UWCA9	50.0

DIK4720	54.0
BMS1290	64.9
DIK2816	68.1
BM6436	77.6
BMS2753	79.2
BM4208	90.7
BMS2819	91.0
BMS2295	98.6
BMS1967	109.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 12.8 cM to about 90.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers ETH225 and BM4208. The at least one genetic marker is selected from the group of markers shown in Table 7b:

Table 7b

Marker on BTA9	Relative position (cM) http://www.marc.usda.gov/
ETH225	12.8
ILSTS037	26.3
BM2504	30.9
DIK2892	30.9
DIK3003	36.5
DIK3002	36.5
BMS1267	38.7
DIK5142	43.8
BMS555	43.8
DIK5364	45.7
UWCA9	50.0
DIK4720	54.0
BMS1290	64.9
DIK2816	68.1
BM6436	77.6

BMS2753	79.2
BM4208	90.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 12.8 cM to about 64.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers ETH225 and BMS1290. The at least one genetic marker is selected from the group of markers shown in Table 7c:

Table 7c

Marker on BTA9	Relative position (cM) http://www.marc.usda.gov/
ETH225	12.8
ILSTS037	26.3
BM2504	30.9
DIK2892	30.9
DIK3003	36.5
DIK3002	36.5
BMS1267	38.7
DIK5142	43.8
BMS555	43.8
DIK5364	45.7
UWCA9	50.0
DIK4720	54.0
BMS1290	64.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 50.0 cM to about 91.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers UWCA9 and BMS2819. The at least one genetic marker is selected from the group of markers shown in Table 7d:

Table 7d

Marker on BTA9	Relative position (cM)

	http://www.marc.usda.gov/
UWCA9	50.0
DIK4720	54.0
BMS1290	64.9
DIK2816	68.1
BM6436	77.6
BMS2753	79.2
BM4208	90.7
BMS2819	91.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 50.0 cM to about 79.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers UWCA9 and BMS2753. The at least one genetic marker is selected from the group of markers shown in Table 7e:

Table 7e

Marker on BTA9	Relative position (cM) http://www.marc.usda.gov/
UWCA9	50.0
DIK4720	54.0
BMS1290	64.9
DIK2816	68.1
BM6436	77.6
BMS2753	79.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 45.7 cM to about 68.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers DIK5364 and DIK2816. The at least one genetic marker is selected from the group of markers shown in Table 7f:

Table 7f

Marker on BTA9	Relative position (cM)

	http://www.marc.usda.gov/
DIK5364	45.7
UWCA9	50.0
DIK4720	54.0
BMS1290	64.9
DIK2816	68.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 12.8 cM to about 43.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA9. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA9 in the region flanked by and including the markers ETH225 and DIK5142. The at least one genetic marker is selected from the group of markers shown in Table 7g:

Table 7g

Marker on BTA9	Relative position (cM) http://www.marc.usda.gov/
ETH225	12.8
ILSTS037	26.3
BM2504	30.9
DIK2892	30.9
DIK3003	36.5
DIK3002	36.5
BMS1267	38.7
DIK5142	43.8

BTA10

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA10. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 2.7 cM to about 104.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers DIK2658 and BMS2614. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least

one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 8a:

Table 8a

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
DIK2658	2.7
DIK2503	9.0
CSSM38	11.0
BMS528	24.0
BM1237	24.7
MB077	35.1
DIK2000	37.5
BMS2742	44.3
BMS529	55.6
DIK2361	56.5
BM888	60.0
TGLA433	74.0
INRA037	79.0
BMS1620	80.4
ILSTS070	81.4
BMS2641	87.5
BMS614	100.0
BMS2614	109.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 9.0 cM to about 35.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers DIK2503 and MB077. The at least one genetic marker is selected from the group of markers shown in Table 8b:

Table 8b

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
DIK2503	9.0

CSSM38	11.0
BMS528	24.0
BM1237	24.7
MB077	35.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 11.0 cM to about 37.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers CSSM38 and DIK2000. The at least one genetic marker is selected from the group of markers shown in Table 8c:

Table 8c

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
CSSM38	11.0
BMS528	24.0
BM1237	24.7
MB077	35.1
DIK2000	37.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 24.0 cM to about 35.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers BMS528 and MB077. The at least one genetic marker is selected from the group of markers shown in Table 8d:

Table 8d

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
BMS528	24.0
BM1237	24.7
MB077	35.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 37.5 cM to about 80.4 cM (http://www.marc.usda.gov/) on the

bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers DIK2000 and BMS1620. The at least one genetic marker is selected from the group of markers shown in Table 8e:

Table 8e

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
DIK2000	37.5
BMS2742	44.3
BMS529	55.6
DIK2361	56.5
BM888	60.0
TGLA433	74.0
INRA037	79.0
BMS1620	80.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 44.3 cM to about 74.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers BMS2742 and TGLA433. The at least one genetic marker is selected from the group of markers shown in Table 8f:

Table 8f

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
BMS2742	44.3
BMS529	55.6
DIK2361	56.5
BM888	60.0
TGLA433	74.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 56.5 cM to about 74.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the

markers DIK2361 and TGLA433. The at least one genetic marker is selected from the group of markers shown in Table 8g:

Table 8g

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
DIK2361	56.5
BM888	60.0
TGLA433	74.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 74.0 cM to about 87.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers TGLA433 and BMS2641. The at least one genetic marker is selected from the group of markers shown in Table 8h:

Table 8h

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
TGLA433	74.0
INRA037	79.0
BMS1620	80.4
ILSTS070	81.4
BMS2641	87.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 87.5 cM to about 109.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA10. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA10 in the region flanked by and including the markers BMS2641 and BMS2614. The at least one genetic marker is selected from the group of markers shown in Table 8i:

Table 8i

Marker on BTA10	Relative position (cM) http://www.marc.usda.gov/
BMS2641	87.5

BMS614	100.0
BMS2614	109.4

BTA11

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA11. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 19.4 cM to about 122.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers BM716 and HEL13. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table9a:

Table 9a

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
BM716	19.4
BMS2569	21.1
BM2818	30.0
INRA177-2	34.8
INRA177	34.8
RM096	40.5
INRA131	47.3
BM7169	50.3
BM6445	61.6
ILSTS036	61.6
BMS1822	65.9
TGLA58	73.1
BMS2047	78.5
HUJV174	92.2
BMS989	92.2
TGLA436	105.2

BMS460	109.4
ILSTS045	114.2
DIK4819	115.0
HEL13	122.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 19.4 cM to about 92.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers BM716 and BMS989. The at least one genetic marker is selected from the group of markers shown in Table 9b:

Table 9b

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
BM716	19.4
BMS2569	21.1
BM2818	30.0
INRA177-2	34.8
INRA177	34.8
RM096	40.5
INRA131	47.3
BM7169	50.3
BM6445	61.6
ILSTS036	61.6
BMS1822	65.9
TGLA58	73.1
BMS2047	78.5
HUJV174	92.2
BMS989	92.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 19.4 cM to about 50.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the

markers BM716 and BM7169. The at least one genetic marker is selected from the group of markers shown in Table 9c:

Table 9c

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
BM716	19.4
BMS2569	21.1
BM2818	30.0
INRA177-2	34.8
INRA177	34.8
RM096	40.5
INRA131	47.3
BM7169	50.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.0 cM to about 50.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers BM2818 and BM7169. The at least one genetic marker is selected from the group of markers shown in Table 9d:

Table 9d

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
BM2818	30.0
INRA177-2	34.8
INRA177	34.8
RM096	40.5
INRA131	47.3
BM7169	50.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 34.8 cM to about 47.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the

markers INRA177-2 and INRA131. The at least one genetic marker is selected from the group of markers shown in Table 9e:

Table 9e

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
INRA177-2	34.8
INRA177	34.8
RM096	40.5
INRA131	47.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 50.3 cM to about 92.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers BM7169 and BMS989. The at least one genetic marker is selected from the group of markers shown in Table 9f:

Table 9f

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
BM7169	50.3
BM6445	61.6
ILSTS036	61.6
BMS1822	65.9
TGLA58	73.1
BMS2047	78.5
HUJV174	92.2
BMS989	92.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 61.6 cM to about 92.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers BM6445 and BMS989. The at least one genetic marker is selected from the group of markers shown in Table 9g:

Table 9g

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
BM6445	61.6
ILSTS036	61.6
BMS1822	65.9
TGLA58	73.1
BMS2047	78.5
HUJV174	92.2
BMS989	92.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 73.3 cM to about 92.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers TGLA58 and BMS989. The at least one genetic marker is selected from the group of markers shown in Table 9h:

Table 9h

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
TGLA58	73.1
BMS2047	78.5
HUJV174	92.2
BMS989	92.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 92.2 cM to about 109.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA11. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA11 in the region flanked by and including the markers HUJV174 and BMS460. The at least one genetic marker is selected from the group of markers shown in Table 9i:

Table 9i

Marker on BTA11	Relative position (cM) http://www.marc.usda.gov/
HUJV174	92.2

BMS989	92.2
TGLA436	105.2
BMS460	109.4

BTA12

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA12. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 109.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA12. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA12 in the region flanked by and including the markers BMS410 and BMS2724. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table 10a:

Table 10a

Marker on BTA12	Relative position (cM) http://www.marc.usda.gov/
BMS410	0.0
BM6108	15.1
BM860	50.4
BMS975	63.8
BMS1316	102.0
BMS2724	109.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 50.4 cM to about 109.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA12. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA12 in the region flanked by and including the markers BM860 and BMS2724. The at least one genetic marker is selected from the group of markers shown in Table 10b:

Table 10b

Marker on BTA12	Relative position (cM) http://www.marc.usda.gov/

BM860	50.4
BMS975	63.8
BMS1316	102.0
BMS2724	109.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 50.4 cM to about 102.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA12. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA12 in the region flanked by and including the markers BM860 and BMS1316. The at least one genetic marker is selected from the group of markers shown in Table 10c:

Table 10c

Marker on BTA12	Relative position (cM) http://www.marc.usda.gov/
BM860	50.4
BMS975	63.8
BMS1316	102.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 63.8 cM to about 102.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA12. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA12 in the region flanked by and including the markers BMS975 and BMS1316. The at least one genetic marker is selected from the group of markers shown in Table 10d:

Table 10d

Marker on BTA12	Relative position (cM) http://www.marc.usda.gov/
BMS975	63.8
BMS1316	102.0

BTA15

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA15. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 9.4 cM to about 109.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one

embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BR3510 and BMS429. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table11a:

Table 11a

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BR3510	9.4
BMS2533	13.9
INRA050	31.1
JAB8	31.2
BMS2684	48.2
DIK1106	51.9
INRA145	67.8
IDVGA-10	67.8
DIK4850	74.1
DIK2768	77.9
ILSTS027	83.4
BMS812	84.9
BMS2076	91.8
BL1095	94.8
BMS820	98.2
BMS927	105.0
BMS429	109.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 48.2 cM to about 109.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS2684 and BMS429. The at least one genetic marker is selected from the group of markers shown in Table 11b:

Table 11b

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BMS2684	48.2
DIK1106	51.9
INRA145	67.8
IDVGA-10	67.8
DIK4850	74.1
DIK2768	77.9
ILSTS027	83.4
BMS812	84.9
BMS2076	91.8
BL1095	94.8
BMS820	98.2
BMS927	105.0
BMS429	109.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 48.2 cM to about 91.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS2684 and BMS2076. The at least one genetic marker is selected from the group of markers shown in Table 11c:

Table 11c

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BMS2684	48.2
DIK1106	51.9
INRA145	67.8
IDVGA-10	67.8
DIK4850	74.1
DIK2768	77.9
ILSTS027	83.4
BMS812	84.9
BMS2076	91.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 77.9 cM to about 109.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers 77.9 and 109.8. The at least one genetic marker is selected from the group of markers shown in Table 11d:

Table 11d

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
DIK2768	77.9
ILSTS027	83.4
BMS812	84.9
BMS2076	91.8
BL1095	94.8
BMS820	98.2
BMS927	105.0
BMS429	109.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 84.9 cM to about 109.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS812 and BMS429. The at least one genetic marker is selected from the group of markers shown in Table 11e:

Table 11e

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BMS812	84.9
BMS2076	91.8
BL1095	94.8
BMS820	98.2
BMS927	105.0
BMS429	109.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 84.9 cM to about 94.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS812 and BL1095. The at least one genetic marker is selected from the group of markers shown in Table 11f:

Table 11f

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BMS812	84.9
BMS2076	91.8
BL1095	94.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 91.8 cM to about 105.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS2076 and BMS927. The at least one genetic marker is selected from the group of markers shown in Table 11g:

Table 11g

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BMS2076	91.8
BL1095	94.8
BMS820	98.2
BMS927	105.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 98.2 cM to about 109.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS820 and BMS429. The at least one genetic marker is selected from the group of markers shown in Table 11h:

Table 11h

Marker on BTA15	Relative position (cM)

	http://www.marc.usda.gov/
BMS820	98.2
BMS927	105.0
BMS429	109.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 105.0 cM to about 109.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA15. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA15 in the region flanked by and including the markers BMS927 and BMS429. The at least one genetic marker is selected from the group of markers shown in Table 11i:

Table 11i

Marker on BTA15	Relative position (cM) http://www.marc.usda.gov/
BMS927	105.0
BMS429	109.8

BTA18

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA18. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 84.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers IDVGA-31 and DIK4013. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table12a:

Table 12a

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
IDVGA-31	0.0
BMS1355	2.9
BMS1322	13.5

TEXAN-10	20.7
BMS2213	24.5
INRA121	30.2
BR4406	33.4
BMS2554	40.2
MNB-27	44.0
BM7109	47.0
INRA063	48.0
ILSTS002	54.7
BMS2639	55.5
DIK4960	56.3
DIK4849	57.0
BMON117	57.6
DIK4232	61.2
BMS2785	72.0
DIK4569	73.8
BM2078	76.8
BM6507	78.8
TGLA227	84.1
DIK4013	84.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.0 cM to about 13.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers IDVGA-31 and BMS1322. The at least one genetic marker is selected from the group of markers shown in Table 12b:

Table 12b

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
IDVGA-31	0.0
BMS1355	2.9
BMS1322	13.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 2.9 cM to about 13.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers BMS1355 and BMS1322. The at least one genetic marker is selected from the group of markers shown in Table 12c:

Table 12c

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BMS1355	2.9
BMS1322	13.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.2 cM to about 61.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers INRA121 and DIK4232. The at least one genetic marker is selected from the group of markers shown in Table 12d:

Table 12d

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
INRA121	30.2
BR4406	33.4
BMS2554	40.2
MNB-27	44.0
BM7109	47.0
INRA063	48.0
ILSTS002	54.7
BMS2639	55.5
DIK4960	56.3
DIK4849	57.0
BMON117	57.6
DIK4232	61.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 33.4 cM to about 54.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers BR4406 and ILSTS002. The at least one genetic marker is selected from the group of markers shown in Table 12e:

Table 12e

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BR4406	33.4
BMS2554	40.2
MNB-27	44.0
BM7109	47.0
INRA063	48.0
ILSTS002	54.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 57.6 cM to about 84.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers BMON117 and DIK4013. The at least one genetic marker is selected from the group of markers shown in Table 12f:

Table 12f

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BMON117	57.6
DIK4232	61.2
BMS2785	72.0
DIK4569	73.8
BM2078	76.8
BM6507	78.8
TGLA227	84.1
DIK4013	84.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 61.2 cM to about 84.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers DIK4232 and DIK4013. The at least one genetic marker is selected from the group of markers shown in Table 12g:

Table 12g

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
DIK4232	61.2
BMS2785	72.0
DIK4569	73.8
BM2078	76.8
BM6507	78.8
TGLA227	84.1
DIK4013	84.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 72.0 cM to about 76.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers BMS2785 and BM2078. The at least one genetic marker is selected from the group of markers shown in Table 12h:

Table 12h

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BMS2785	72.0
DIK4569	73.8
BM2078	76.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 76.8 cM to about 84.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the

markers BM2078 and DIK4013. The at least one genetic marker is selected from the group of markers shown in Table 12i:

Table 12i

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BM2078	76.8
BM6507	78.8
TGLA227	84.1
DIK4013	84.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 76.8 cM to about 78.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers BM2078 and BM6507. The at least one genetic marker is selected from the group of markers shown in Table 12j:

Table 12j

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BM2078	76.8
BM6507	78.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 78.8 cM to about 84.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA18. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA18 in the region flanked by and including the markers BM6507 and DIK4013. The at least one genetic marker is selected from the group of markers shown in Table 12k:

Table 12k

Marker on BTA18	Relative position (cM) http://www.marc.usda.gov/
BM6507	78.8
TGLA227	84.1
DIK4013	84.4

BTA19

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA19. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 108.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the markers BM9202 and BMS601. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table13a:

Table 13a

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
BM9202	0.0
BMS745	16.0
BP20	45.9
IDVGA-46	47.0
BMS2389	52.2
CSSM065	69.8
ETH3	90.0
BMS601	108.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.0 cM to about 90.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the markers BM9202 and ETH3. The at least one genetic marker is selected from the group of markers shown in Table 13b:

Table 13b

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
BM9202	0.0
BMS745	16.0

BP20	45.9
IDVGA-46	47.0
BMS2389	52.2
CSSM065	69.8
ETH3	90.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.0 cM to about 45.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the markers BM9202 and BP20. The at least one genetic marker is selected from the group of markers shown in Table 13c:

Table 13c

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
BM9202	0.0
BMS745	16.0
BP20	45.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 16.0 cM to about 45.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the markers BMS745 and BP20. The at least one genetic marker is selected from the group of markers shown in Table 13d:

Table 13d

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
BMS745	16.0
BP20	45.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 47.0 cM to about 90.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the

markers IDVGA-46 and ETH3. The at least one genetic marker is selected from the group of markers shown in Table 13e:

Table 13e

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
IDVGA-46	47.0
BMS2389	52.2
CSSM065	69.8
ETH3	90.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 52.2 cM to about 108.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the markers BMS2389 and BMS601. The at least one genetic marker is selected from the group of markers shown in Table 13f:

Table 13f

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
BMS2389	52.2
CSSM065	69.8
ETH3	90.0
BMS601	108.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 69.8 cM to about 90.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA19. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA19 in the region flanked by and including the markers CSSM065 and ETH3. The at least one genetic marker is selected from the group of markers shown in Table 13g:

Table 13g

Marker on BTA19	Relative position (cM) http://www.marc.usda.gov/
CSSM065	69.8

ETH3	90.0

BTA20

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA20. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 77.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers BM3517 and UWCA26. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table14a:

Table 14a

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
BM3517	0.0
HEL12	0.6
BMS1282	19.1
BMS1754	26.3
TGLA126	31.9
BMS2361	49.7
AGLA29	55.1
BMS703	60.1
BM5004	71.8
UWCA26	77.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.0 cM to about 71.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers BM3517 and BM5004. The at least one genetic marker is selected from the group of markers shown in Table 14b:

Table 14b

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
BM3517	0.0
HEL12	0.6
BMS1282	19.1
BMS1754	26.3
TGLA126	31.9
BMS2361	49.7
AGLA29	55.1
BMS703	60.1
BM5004	71.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.0 cM to about 26.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers BM3517 and BMS1754. The at least one genetic marker is selected from the group of markers shown in Table 14c:

Table 14c

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
BM3517	0.0
HEL12	0.6
BMS1282	19.1
BMS1754	26.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 0.6 cM to about 19.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers HEL12 and BMS1282. The at least one genetic marker is selected from the group of markers shown in Table 14d:

Table 14d

Marker on BTA20	Relative position (cM)

	http://www.marc.usda.gov/
HEL12	0.6
BMS1282	19.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 19.1 cM to about 55.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers BMS1282 and AGLA29. The at least one genetic marker is selected from the group of markers shown in Table 14e:

Table 14e

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
BMS1282	19.1
BMS1754	26.3
TGLA126	31.9
BMS2361	49.7
AGLA29	55.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 31.9 cM to about 49.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers TGLA126 and BMS2361. The at least one genetic marker is selected from the group of markers shown in Table 14f:

Table 14f

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
TGLA126	31.9
BMS2361	49.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 49.7 cM to about 55.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the

markers BMS2361 and AGLA29. The at least one genetic marker is selected from the group of markers shown in Table 14g:

Table 14g

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
BMS2361	49.7
AGLA29	55.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 55.1 cM to about 77.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers AGLA29 and UWCA26. The at least one genetic marker is selected from the group of markers shown in Table 14h:

Table 14h

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
AGLA29	55.1
BMS703	60.1
BM5004	71.8
UWCA26	77.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 60.1 cM to about 71.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA20. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA20 in the region flanked by and including the markers BMS703 and BM5004. The at least one genetic marker is selected from the group of markers shown in Table 14i:

Table 14i

Marker on BTA20	Relative position (cM) http://www.marc.usda.gov/
BMS703	60.1
BM5004	71.8

BTA21

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA21. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 5.6 cM to about 76.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the markers DIK5182 and IDVGA-30. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table15a:

Table 15a

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
DIK5182	5.5
BMS1117	11.0
RM151	12.6
DIK2492	18.3
AGLA233	21.2
ILSTS095	23.7
DIK4602	24.3
BM103	29.8
DIK4001	30.0
IDVGA-45	30.9
DIK2481	33.7
INRA103	35.9
BMS2815	41.7
DIK2842	41.7
DIK3036	47.8
DIK4391	52.1
DIK2913	57.1
BM846	61.2
TGLA122	62.7
ILSTS054	65.8

BMS743	75.3
IDVGA-30	76.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 11.0 cM to about 61.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the markers BMS1117 and BM846. The at least one genetic marker is selected from the group of markers shown in Table 15b:

Table 15b

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
BMS1117	11.0
RM151	12.6
DIK2492	18.3
AGLA233	21.2
ILSTS095	23.7
DIK4602	24.3
BM103	29.8
DIK4001	30.0
IDVGA-45	30.9
DIK2481	33.7
INRA103	35.9
BMS2815	41.7
DIK2842	41.7
DIK3036	47.8
DIK4391	52.1
DIK2913	57.1
BM846	61.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 18.3 cM to about 57.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the

markers DIK2492 and DIK2913. The at least one genetic marker is selected from the group of markers shown in Table 15c:

Table 15c

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
DIK2492	18.3
AGLA233	21.2
ILSTS095	23.7
DIK4602	24.3
BM103	29.8
DIK4001	30.0
IDVGA-45	30.9
DIK2481	33.7
INRA103	35.9
BMS2815	41.7
DIK2842	41.7
DIK3036	47.8
DIK4391	52.1
DIK2913	57.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 18.3 cM to about 30.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the markers DIK2492 and DIK4001. The at least one genetic marker is selected from the group of markers shown in Table 15d:

Table 15d

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
DIK2492	18.3
AGLA233	21.2
ILSTS095	23.7
DIK4602	24.3
BM103	29.8

DIK4001	30.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 30.9 cM to about 47.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the markers IDVGA-45 and DIK3036. The at least one genetic marker is selected from the group of markers shown in Table 15e:

Table 15e

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
IDVGA-45	30.9
DIK2481	33.7
INRA103	35.9
BMS2815	41.7
DIK2842	41.7
DIK3036	47.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 33.7 cM to about 41.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the markers DIK2481 and BMS2815. The at least one genetic marker is selected from the group of markers shown in Table 15f:

Table 15f

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
DIK2481	33.7
INRA103	35.9
BMS2815	41.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 5.5 cM to about 61.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA21. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA21 in the region flanked by and including the

markers DIK5182 and BM846. The at least one genetic marker is selected from the group of markers shown in Table 15g:

Table 15g

Marker on BTA21	Relative position (cM) http://www.marc.usda.gov/
DIK5182	5.5
DIK3036	47.8
DIK4391	52.1
DIK2913	57.1
BM846	61.2

BTA22

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA22. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 0.0 cM to about 82.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the markers CSSM26 and BM4102. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table16a:

Table 16a

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/
CSSM26	0.0
INRA026	2.9
BM1558	19.1
BM3628	47.1
BMS875	64.1
BM4102	82.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 2.9 cM to about 82.9 cM (http://www.marc.usda.gov/) on the

bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the markers INRA026 and BM4102. The at least one genetic marker is selected from the group of markers shown in Table 16b:

Table 16b

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/
INRA026	2.9
BM1558	19.1
BM3628	47.1
BMS875	64.1
BM4102	82.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 2.9 cM to about 47.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the markers INRA026 and BM3628. The at least one genetic marker is selected from the group of markers shown in Table 16c:

Table 16c

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/
INRA026	2.9
BM1558	19.1
BM3628	47.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 19.1 cM to about 47.1 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the markers BM1558 and BM3628. The at least one genetic marker is selected from the group of markers shown in Table 16d:

Table 16d

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/

BM1558	19.1
BM3628	47.1

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 19.1 cM to about 82.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the markers BM1558 and BM4102. The at least one genetic marker is selected from the group of markers shown in Table 16e:

Table 16e

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/
BM1558	19.1
BM3628	47.1
BMS875	64.1
BM4102	82.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 47.1 cM to about 82.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the markers BM3628 and BM4102. The at least one genetic marker is selected from the group of markers shown in Table 16f:

Table 16f

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/
BM3628	47.1
BMS875	64.1
BM4102	82.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 64.1 cM to about 82.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA22. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA22 in the region flanked by and including the

markers BMS875 and BM4102. The at least one genetic marker is selected from the group of markers shown in Table 16g:

Table 16g

Marker on BTA22	Relative position (cM) http://www.marc.usda.gov/
BMS875	64.1
BM4102	82.9

BTA24

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA24. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 6.2 cM to about 65.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers BMS917 and BMS3024. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table17a:

Table 17a

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
BMS917	6.2
BM7151	8.2
BM226	8.2
BMS2526	8.2
TGLA351	11.1
BM7228	19.3
CSSM23	20.6
BMS2270	23.7
ILSTS065	27.4
BMS1862	35.5
BMS466	48.8

INRA090	56.3
BMS1926	61.2
BMS3024	65.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 8.2 cM to about 65.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers BM7151 and BMS3024. The at least one genetic marker is selected from the group of markers shown in Table 17b:

Table 17b

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
BM7151	8.2
BM226	8.2
BMS2526	8.2
TGLA351	11.1
BM7228	19.3
CSSM23	20.6
BMS2270	23.7
ILSTS065	27.4
BMS1862	35.5
BMS466	48.8
INRA090	56.3
BMS1926	61.2
BMS3024	65.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 8.2 cM to about 35.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers BM7151 and BMS1862. The at least one genetic marker is selected from the group of markers shown in Table 17c:

Table 17c

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
BM7151	8.2
BM226	8.2
BMS2526	8.2
TGLA351	11.1
BM7228	19.3
CSSM23	20.6
BMS2270	23.7
ILSTS065	27.4
BMS1862	35.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 11.1 cM to about 23.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers TGLA351 and BMS2270. The at least one genetic marker is selected from the group of markers shown in Table 17d:

Table 17d

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
TGLA351	11.1
BM7228	19.3
CSSM23	20.6
BMS2270	23.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 35.5 cM to about 65.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers BMS1862 and BMS3024. The at least one genetic marker is selected from the group of markers shown in Table 17e:

Table 17e

Marker on BTA24	Relative position (cM)

	http://www.marc.usda.gov/
BMS1862	35.5
BMS466	48.8
INRA090	56.3
BMS1926	61.2
BMS3024	65.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 48.8 cM to about 61.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers BMS466 and BMS1926. The at least one genetic marker is selected from the group of markers shown in Table 17f:

Table 17f

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
BMS466	48.8
INRA090	56.3
BMS1926	61.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 48.8 cM to about 56.3 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA24 in the region flanked by and including the markers BMS466 and INRA090. The at least one genetic marker is selected from the group of markers shown in Table 17g:

Table 17g

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
BMS466	48.8
INRA090	56.3

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 56.3 cM to about 61.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA24. In one embodiment the at least one genetic marker is

located on the bovine chromosome BTA24 in the region flanked by and including the markers INRA090 and BMS1926. The at least one genetic marker is selected from the group of markers shown in Table 17h:

Table 17h

Marker on BTA24	Relative position (cM) http://www.marc.usda.gov/
INRA090	56.3
BMS1926	61.2

BTA25

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA25. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 7.2 cM to about 61.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA25. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA25 in the region flanked by and including the markers ILSTS102 and AF5. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table18a:

Table 18a

Marker on BTA25	Relative position (cM) http://www.marc.usda.gov/
ILSTS102	7.2
BMS2843	22.6
BM737	31.6
ILSTS046	33.3
BMS1353	46.4
AF5	61.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 7.2 cM to about 31.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA25. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA25 in the region flanked by and including the

markers ILSTS102 and BM737. The at least one genetic marker is selected from the group of markers shown in Table 18b:

Table 18b

Marker on BTA25	Relative position (cM) http://www.marc.usda.gov/
ILSTS102	7.2
BMS2843	22.6
BM737	31.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 7.2 cM to about 22.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA25. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA25 in the region flanked by and including the markers ILSTS102 and BMS2843. The at least one genetic marker is selected from the group of markers shown in Table 18c:

Table 18c

Marker on BTA25	Relative position (cM) http://www.marc.usda.gov/
ILSTS102	7.2
BMS2843	22.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 31.6 cM to about 61.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA25. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA25 in the region flanked by and including the markers BM737 and AF5. The at least one genetic marker is selected from the group of markers shown in Table 18d:

Table 18d

Marker on BTA25	Relative position (cM) http://www.marc.usda.gov/
BM737	31.6
ILSTS046	33.3
BMS1353	46.4
AF5	61.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 33.3 cM to about 46.4 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA25. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA25 in the region flanked by and including the markers ILSTS046 and BMS1353. The at least one genetic marker is selected from the group of markers shown in Table 18e:

Table 18e

Marker on BTA25	Relative position (cM) http://www.marc.usda.gov/
ILSTS046	33.3
BMS1353	46.4

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 46.4 cM to about 61.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA25. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA25 in the region flanked by and including the markers BMS1353 and AF5. The at least one genetic marker is selected from the group of markers shown in Table 18f:

Table 18f

Marker on BTA25	Relative position (cM) http://www.marc.usda.gov/
BMS1353	46.4
AF5	61.7

BTA26

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA26. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 2.8 cM to about 66.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers BMS651 and BM7237. The at least one genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one

genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table19a:

Table 19a

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
BMS651	2.8
HEL11	22.9
BMS332	31.7
RM026	37.6
BM9284	41.6
RME40	43.2
IDVGA-59	53.1
BMS882	53.5
BM804	60.5
BM7237	66.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 2.8 cM to about 60.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers BMS651 and BM804. The at least one genetic marker is selected from the group of markers shown in Table 19b:

Table 19b

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
BMS651	2.8
HEL11	22.9
BMS332	31.7
RM026	37.6
BM9284	41.6
RME40	43.2
IDVGA-59	53.1
BMS882	53.5
BM804	60.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 2.8 cM to about 37.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers BMS651 and RM026. The at least one genetic marker is selected from the group of markers shown in Table 19c:

Table 19c

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
BMS651	2.8
HEL11	22.9
BMS332	31.7
RM026	37.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 22.9 cM to about 31.7 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers HEL11 and BMS332. The at least one genetic marker is selected from the group of markers shown in Table 19d:

Table 19d

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
HEL11	22.9
BMS332	31.7

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 31.7 cM to about 41.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers BMS332 and BM9284. The at least one genetic marker is selected from the group of markers shown in Table 19e:

Table 19e

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/

BMS332	31.7
RM026	37.6
BM9284	41.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 37.6 cM to about 66.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers RM026 and BM7237. The at least one genetic marker is selected from the group of markers shown in Table 19f:

Table 19f

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
RM026	37.6
BM9284	41.6
RME40	43.2
IDVGA-59	53.1
BMS882	53.5
BM804	60.5
BM7237	66.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 37.6 cM to about 43.2 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers RM026 and RME40. The at least one genetic marker is selected from the group of markers shown in Table 19g:

Table 19g

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
RM026	37.6
BM9284	41.6
RME40	43.2

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 43.2 cM to about 66.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers RME40 and BM7237. The at least one genetic marker is selected from the group of markers shown in Table 19h:

Table 19h

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
RME40	43.2
IDVGA-59	53.1
BMS882	53.5
BM804	60.5
BM7237	66.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 53.1 cM to about 60.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA26. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA26 in the region flanked by and including the markers IDVGA-59 and BM804. The at least one genetic marker is selected from the group of markers shown in Table 19i:

Table 19i

Marker on BTA26	Relative position (cM) http://www.marc.usda.gov/
IDVGA-59	53.1
BMS882	53.5
BM804	60.5

BTA28

In one embodiment of the invention the at least one genetic marker is located on the bovine chromosome BTA28. In one specific embodiment of the present invention, the at least one genetic marker is located in the region from about 8.0 cM to about 59.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers BMC6020 and BMC2208. The at least one

genetic marker is significant for the calving traits SB, CD and/or CS. In a particular embodiment the at least one genetic marker is significant for for example the trait SB, such as CD, for example CS. However, in a further embodiment the at least one genetic marker is significant for the traits in any combination. The at least one genetic marker is selected from the group of markers shown in Table20a:

Table 20a

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
BMC6020	8.0
ETH1112	16.9
BL25	24.8
DIK2955	38.0
BMS2608	38.5
BMS2658	43.0
DIK713	45.9
BMS1714	49.4
DIK5056	50.5
DIK5323	55.9
DIK4862	59.6
BMC2208	59.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 8.0 cM to about 24.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers BMC6020 and BL25. The at least one genetic marker is selected from the group of markers shown in Table 20b:

Table 20b

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
BMC6020	8.0
ETH1112	16.9
BL25	24.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 16.9 cM to about 24.8 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers ETH1112 and BL25. The at least one genetic marker is selected from the group of markers shown in Table 20c:

Table 20c

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
ETH1112	16.9
BL25	24.8

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 24.8 cM to about 50.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers BL25 and DIK5056. The at least one genetic marker is selected from the group of markers shown in Table 20d:

Table 20d

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
BL25	24.8
DIK2955	38.0
BMS2608	38.5
BMS2658	43.0
DIK713	45.9
BMS1714	49.4
DIK5056	50.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 38.0 cM to about 45.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers DIK2955 and DIK713. The at least one genetic marker is selected from the group of markers shown in Table 20e:

Table 20e

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
DIK2955	38.0
BMS2608	38.5
BMS2658	43.0
DIK713	45.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 38.0 cM to about 43.0 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers DIK2955 and BMS2658. The at least one genetic marker is selected from the group of markers shown in Table 20f:

Table 20f

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
DIK2955	38.0
BMS2608	38.5
BMS2658	43.0

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 43.0 cM to about 59.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers BMS2658 and BMC2208. The at least one genetic marker is selected from the group of markers shown in Table 20g:

Table 20g

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
BMS2658	43.0
DIK713	45.9
BMS1714	49.4
DIK5056	50.5

DIK5323	55.9
DIK4862	59.6
BMC2208	59.6

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 45.9 cM to about 55.9 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers DIK713 and DIK5323. The at least one genetic marker is selected from the group of markers shown in Table 20h:

Table 20h

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
DIK713	45.9
BMS1714	49.4
DIK5056	50.5
DIK5323	55.9

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 49.4 cM to about 50.5 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the markers BMS1714 and DIK5056. The at least one genetic marker is selected from the group of markers shown in Table 20i:

Table 20i

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
BMS1714	49.4
DIK5056	50.5

In a preferred embodiment of the invention, the at least one genetic marker is located in the region from about 55.9 cM to about 59.6 cM (http://www.marc.usda.gov/) on the bovine chromosome BTA28. In one embodiment the at least one genetic marker is located on the bovine chromosome BTA28 in the region flanked by and including the

markers DIK5323 and BMC2208. The at least one genetic marker is selected from the group of markers shown in Table 20j:

Table 20j

Marker on BTA28	Relative position (cM) http://www.marc.usda.gov/
DIK5323	55.9
DIK4862	59.6
BMC2208	59.6

In another embodiment of the present invention, the at least one genetic marker is a combination of markers, as indicated in tables 20k1 to 20k19. It is understood that the term BTA3, BTA4. BTA5, BTA7, BTA8, BTA9, BTA10, BTA11, BTA12, BTA15, BTA18, BTA19, BTA20, BTA21, BTA22, BTA24, BTA25, BTA26, and BTA28 in tables 20k1 to 20k19 is meant to comprise any regions and genetic markers located on the bovine chromosomes, respectively, as described elsewhere herein.

The tables 20k1 to 20k19 show different embodiments, wherein the combination of markers is a multiplicity of bovine chromosomes, wherein the specific chromosome in each embodiment is indicated with X.

Table 20k1.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1	X	X																	
2	X		X																
3	X			X															
4	X				X														
5	X					X													
6	X						X												
7	X							X											
8	X								X										
9	X									X									
10	X										X								
11	X											X							
12	X												X						
13	X													X					
14	X														X				
15	X															X			
16	X																X		
17	X																	X	
18	X																		X
19	X		X		X						X							X	
20	X		X		X						X								

21	X		X		X													
22	X		X								X							
23	X				X						X						X	
24	X										X						X	

Table 20k2.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1		X	X																
2		X		X															
3		X			X														
4		X				X													
5		X					X												
6		X						X											
7		X							X										
8		X								X									
9		X									X								
10		X										X							
11		X											X						
12		X												X					
13		X													X				
14		X														X			
15		X															X		
16		X																X	
17		X																	X
18		X			X			X					X				X		X
19		X	X		X						X							X	
20		X	X		X						X								
21		X	X		X														
22		X	X								X								
23		X			X						X							X	
24		X									X							X	

Table 20k3.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1			X	X															
2			X		X														
3			X			X													
4			X				X												
5			X					X											
6			X						X										
7			X							X									
8			X								X								
9			X									X							
10			X										X						
11			X											X					
12			X												X				
13			X													X			
14			X														X		

15			X														X	
16			X															X
17			X			X		X			X		X		X		X	X	
18			X															
19			X		X						X						X	
20			X		X						X							
21			X		X													
22			X								X							
23			X		X						X						X	
24			X								X						X	

Table 20k4.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1				X	X														
2				X		X													
3				X			X												
4				X				X											
5				X					X										
6				X						X									
7				X							X								
8				X								X							
9				X									X						
10				X										X					
11				X											X				
12				X												X			
13				X													X		
14				X														X	
15		X		X	X		X		X		X				X		X	X	X
16			X	X		X	X	X		X		X		X		X	X		
17		X		X		X		X				X		X	X				
18				X		X		X		X		X				X		X	X
19			X	X	X						X							X	
20			X	X	X						X								
21			X	X	X														
22			X	X							X								
23				X	X						X							X	
24				X							X							X	

Table 20k5.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1					X	X													
2					X		X												
3					X			X											
4					X				X										
5					X					X									
6					X						X								
7					X							X							
8					X								X						

9					X								X					
10					X									X				
11					X										X			
12					X											X		
13					X												X	
14					X													X
15		X		X	X		X		X		X				X		X	X	X
16			X	X	X	X	X	X		X		X		X		X	X		
17		X		X	X	X		X				X		X	X				
18				X	X	X		X		X		X				X		X	X
19			X		X						X							X	
20			X		X						X								
21			X		X														
22			X		X						X								
23					X						X							X	
24					X						X							X	

Table 20k6.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1						X	X												
2						X		X											
3						X			X										
4						X				X									
5						X					X								
6						X						X							
7						X							X						
8						X								X					
9						X									X				
10						X										X			
11						X											X		
12						X												X	
13						X													X
14		X		X	X	X	X		X		X				X		X	X	X
15			X	X	X	X	X	X		X		X		X		X	X		
16		X		X	X	X		X				X		X	X				
17				X	X	X		X		X		X				X		X	X
18		X				X			X		X			X					
19			X		X	X					X							X	
20			X		X	X					X								
21			X		X	X													
22			X			X					X								
23					X	X					X							X	
24						X					X							X	

Table 20k7.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1							X	X											
2							X		X										

3							X			X								
4							X				X							
5							X					X						
6							X						X					
7							X							X				
8							X								X			
9							X									X		
10							X										X	
11							X											X
12							X											X
13		X		X	X	X	X		X		X				X		X	X	X
14			X	X		X	X	X		X		X		X		X	X		
15		X				X	X	X				X		X	X				
16				X	X	X	X	X		X		X				X		X	X
17		X				X	X		X		X			X					
18							X												
19			X		X		X				X							X	
20			X		X		X				X								
21			X		X		X												
22			X				X				X								
23					X		X				X							X	
24							X				X							X	

Table 20k8.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1								X	X										
2								X		X									
3								X			X								
4								X				X							
5								X					X						
6								X						X					
7								X							X				
8								X								X			
9								X									X		
10								X										X	
11								X											X
12		X		X	X	X	X	X	X		X				X		X	X	X
13			X	X		X	X	X		X		X		X		X	X		
14		X				X	X	X				X		X	X				
15				X	X	X	X	X		X		X				X		X	X
16		X				X	X	X	X		X			X					
17			X		X			X					X				X		
18				X	X		X	X		X			X		X		X		
19			X		X			X			X							X	
20			X		X			X			X								
21			X		X			X											
22			X					X			X								
23					X			X			X							X	
24								X			X							X	

Table 20k9.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1									X	X									
2									X		X								
3									X			X							
4									X				X						
5									X					X					
6									X						X				
7									X							X			
8									X								X		
9									X									X	
10									X										X
11					X		X		X	X		X			X		X		X
12		X	X			X		X	X	X	X			X		X		X	
13	X		X		X				X		X							X	
14	X		X		X				X		X								
15	X		X		X				X										
16	X		X						X		X								
17			X		X				X		X							X	
18			X						X										
19			X		X				X		X								
20			X		X				X									X	
21			X						X		X							X	
22			X						X									X	
23					X				X		X								
24	X								X		X							X	

Table 20k10.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1										X	X								
2										X		X							
3										X			X						
4										X				X					
5										X					X				
6										X						X			
7										X							X		
8										X								X	
9										X									X
10					X		X			X		X			X		X		X
11		X	X			X		X		X	X			X		X		X	
12	X		X		X					X	X							X	
13	X		X		X					X	X								
14	X		X		X					X									
15	X		X							X	X								
16			X		X					X	X							X	
17			X							X									
18			X		X					X	X								
19			X		X					X								X	
20			X							X	X							X	
21			X							X								X	

22					X					X	X							
23	X									X	X						X	
24	X									X	X						X	

Table 20k11.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1											X	X							
2											X		X						
3											X			X					
4											X				X				
5											X					X			
6											X						X		
7											X							X	
8											X								X
9		X			X			X		X	X		X		X	X		X	
10	X			X			X		X	X	X	X		X	X		X		
11			X				X		X	X	X		X						X
12		X	X			X		X		X	X			X		X		X	
13	X		X		X						X							X	
14	X		X		X						X								
15	X		X		X						X								
16	X		X								X								
17			X		X						X							X	
18			X								X								
19			X		X						X								
20			X		X						X							X	
21			X								X							X	
22			X								X							X	
23					X						X								
24	X										X							X	

Table 20k12.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1												X	X						
2												X		X					
3												X			X				
4												X				X			
5												X					X		
6												X						X	
7												X							X
8			X	X	X	X	X	X		X		X		X		X	X		
9		X		X	X	X		X				X		X	X				
10				X	X	X		X		X		X				X		X	X
11		X				X			X		X			X					
12			X		X	X					X							X	
13	X		X		X						X	X						X	
14	X		X		X						X	X							
15	X		X		X							X							

16	X		X							X	X							
17			X		X					X	X						X	
18			X								X							
19			X		X					X	X							
20			X		X						X						X	
21			X							X	X						X	
22			X								X						X	
23					X					X	X							
24	X									X	X						X	

Table 20k13.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1													X	X					
2													X		X				
3													X			X			
4													X				X		
5													X					X	
6													X						X
7		X			X			X		X			X		X	X		X	
8	X			X			X		X	X		X	X	X	X		X		
9			X				X		X	X	X		X						X
10		X	X			X		X		X			X	X		X		X	
11	X		X		X						X		X					X	
12	X		X		X						X		X						
13	X		X		X						X		X						
14	X		X								X		X						
15			X		X						X		X					X	
16			X								X		X						
17			X		X								X						
18			X		X								X					X	
19			X										X					X	
20			X								X		X					X	
21					X								X						
22	X										X		X					X	
23					X								X					X	
24													X					X	

Table 20k14.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1														X	X				
2														X		X			
3														X			X		
4														X				X	
5														X					X
6		X			X			X		X			X		X	X		X	
7	X			X			X		X	X		X	X	X	X		X		
8			X				X		X	X	X		X						X
9					X		X					X		X	X		X		X

10		X	X			X		X			X			X		X		X	
11	X		X		X						X			X				X	
12	X		X		X						X			X					
13	X		X		X									X					
14	X		X								X			X					
15			X		X						X			X				X	
16			X											X					
17			X		X						X			X					
18			X		X									X				X	
19			X								X			X				X	
20			X											X				X	
21					X						X			X					
22	X										X			X				X	
23	X										X			X				X	
24											X			X				X	

Table 20k15.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1															X	X			
2															X		X		
3															X			X	
4															X				X
5		X			X			X		X			X		X	X		X	
6	X			X			X		X	X		X	X	X	X		X		
7			X				X		X	X	X		X		X				X
8					X		X					X			X		X		X
9		X	X			X		X			X				X	X		X	
10	X		X		X						X				X			X	
11	X		X		X						X				X				
12	X		X		X										X				
13	X		X								X				X				
14			X		X						X				X			X	
15			X												X				
16			X		X						X				X				
17			X		X										X			X	
18			X								X				X			X	
19			X												X			X	
20					X						X				X				
21	X										X				X			X	
22	X										X				X			X	
23											X				X			X	
24											X				X			X	

Table 20k16.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1																X	X		
2																X		X	
3																X			X

4		X			X			X		X			X			X		X	
5	X			X			X		X	X		X	X	X		X	X		
6			X				X		X	X	X		X			X			X
7					X		X					X				X	X		X
8		X	X			X		X			X					X		X	
9	X		X		X						X					X		X	
10	X		X		X						X					X			
11	X		X		X											X			
12	X		X								X					X			
13			X		X						X					X		X	
14			X													X			
15			X		X						X					X			
16			X		X											X		X	
17			X								X					X		X	
18			X													X		X	
19					X						X					X			
20	X										X					X		X	
21	X										X					X		X	
22											X					X		X	
23											X					X		X	
24											X					X		X	

Table 20k17.

Embodiment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1																	X	X	
2																	X		X
3		X			X			X		X			X				X	X	
4	X			X			X		X	X		X	X	X			X		
5			X				X		X	X	X		X				X		X
6					X		X					X					X		X
7		X	X			X		X			X						X	X	
8	X		X		X						X						X	X	
9	X		X		X						X						X		
10	X		X		X												X		
11	X		X								X						X		
12			X		X						X			X			X	X	
13			X												X		X		
14			X		X						X			X			X		
15			X		X										X	X	X	X	
16			X								X						X	X	
17			X											X		X	X	X	
18					X						X						X		
19	X										X					X	X	X	
20	X										X						X	X	
21		X		X	X						X						X	X	
22							X				X			X			X	X	
23		X	X		X	X					X						X	X	
24	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Table 20k18.

Embod	BTA

iment																			
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1																		X	X
2	X		X		X						X							X	
3	X		X		X						X							X	
4	X		X		X													X	
5	X		X								X							X	
6			X		X						X							X	
7			X		X													X	
8			X								X							X	
9			X		X													X	
10			X								X							X	
11			X															X	
12					X						X							X	
13	X										X							X	
14	X				X						X							X	
15	X		X		X			X		X	X		X		X		X	X	
16	X																	X	
17						X			X		X			X		X		X	
18		X		X			X			X		X			X	X	X	X	
19			X		X						X							X	
20			X		X						X							X	
21			X		X													X	
22			X								X							X	
23		X			X		X	X			X							X	
24							X				X		X		X			X	

Table 20k19.

Embod iment	BTA																		
	3	4	5	7	8	9	10	11	12	15	18	19	20	21	22	24	25	26	28
1		X			X			X		X			X					X	X
2	X			X			X		X	X		X	X	X					X
3			X				X		X	X	X		X						X
4					X		X					X				X			X
5		X	X			X		X			X							X	X
6	X		X		X						X							X	X
7	X		X		X						X								X
8	X		X		X		X		X			X		X		X	X		X
9	X		X								X								X
10			X		X						X			X				X	X
11			X												X				X
12			X		X						X			X					X
13			X		X										X	X		X	X
14			X								X							X	X
15			X											X		X		X	X
16					X						X								X
17	X										X					X		X	X
18	X										X							X	X
19		X		X	X						X							X	X
20							X				X			X				X	X
21		X	X		X	X					X							X	X
22	X		X								X								X

23	X				X					X						X	
24	X									X						X	

Detection

The detection of the presence or absence of a genetic marker allele according to the present invention may be conducted on the DNA sequence of the bovine chromosomes BTA3, BTA4, BTA5, BTA7, BTA8, BTA9, BTA10, BTA11, BTA12, BTA15, BTA18, BTA19, BTA20, BTA21, BTA22, BTA24, BTA25, BTA26, and/or BTA28 specified elsewhere herein according to the present invention or a complementary sequence as well as on transcriptional (mRNA) and translational products (polypeptides, proteins) therefrom.

It will be apparent to the person skilled in the art that there are a large number of analytical procedures which may be used to detect the presence or absence of variant nucleotides at one or more of positions mentioned herein in the specified region. Mutations or polymorphisms within or flanking the specified region can be detected by utilizing a number of techniques. Nucleic acid from any nucleated cell can be used as the starting point for such assay techniques, and may be isolated according to standard nucleic acid preparation procedures that are well known to those of skill in the art. In general, the detection of allelic variation requires a mutation discrimination technique, optionally an amplification reaction and a signal generation system.

A number of mutation detection techniques are listed in Table 21. Some of the methods listed in Table 21 are based on the polymerase chain reaction (PCR), wherein the method according to the present invention includes a step for amplification of the nucleotide sequence of interest in the presence of primers based on the nucleotide sequence of the variable nucleotide sequence. The methods may be used in combination with a number of signal generation systems, a selection of which is also listed in Table 22.

Table 21

General techniques	DNA sequencing, Sequencing by hybridisation, SNAPshot
Scanning techniques	Single-strand conformation polymorphism analysis, Denaturing gradient gel electrophoresis, Temperature gradient gel electrophoresis, Chemical mismatch

	cleavage, cleavage, heteroduplex analysis, enzymatic mismatch cleavage
Hybridisation based techniques	Solid phase hybridisation: Dot blots, Multiple allele specific diagnostic assay (MASDA), Reverse dot blots, Oligonucleotide arrays (DNA Chips) Solution phase hybridisation: Taqman -U.S. Pat. No. 5,210,015 & 5,487,972 (Hoffmann-La Roche), Molecular Beacons -- Tyagi et al (1996), Nature Biotechnology, 14, 303; WO 95/13399 (Public Health Inst., New York), Lightcycler, optionally in combination with Fluorescence resonance energy transfer (FRET).
Extension based techniques	Amplification refractory mutation system (ARMS), Amplification refractory mutation system linear extension (ALEX) - European Patent No. EP 332435 B1 (Zeneca Limited), Competitive oligonucleotide priming system (COPS) - Gibbs et al (1989), Nucleic Acids Research, 17, 2347.
Incorporation based techniques	Mini-sequencing, Arrayed primer extension (APEX)
Restriction Enzyme based techniques	Restriction fragment length polymorphism (RFLP), Restriction site generating PCR
Ligation based techniques	Oligonucleotide ligation assay (OLA)
Other	Invader assay
Various Signal Generation or Detection Systems	Fluorescence: Fluorescence resonance energy transfer (FRET), Fluorescence quenching, Fluorescence polarisation--United Kingdom Patent No. 2228998 (Zeneca Limited)
Other	Chemiluminescence, Electrochemiluminescence, Raman, Radioactivity, Colorimetric, Hybridisation protection assay, Mass spectrometry

Further amplification techniques are listed in Table 2. Many current methods for the detection of allelic variation are reviewed by Nollau et al., Clin. Chem. 43, 1114-1120, 1997; and in standard textbooks, for example "Laboratory Protocols for Mutation Detection", Ed. by U. Landegren, Oxford University Press, 1996 and "PCR", 2nd Edition by Newton & Graham, BIOS Scientific Publishers Limited, 1997.

The detection of genetic markers can according to one embodiment of the present invention be achieved by a number of techniques known to the skilled person, including typing of microsatellites or short tandem repeats (STR), restriction fragment length polymorphisms (RFLP), detection of deletions or insertions, random amplified polymorphic DNA (RAPIDs) or the typing of single nucleotide polymorphisms by methods such as restriction fragment length polymerase chain reaction, allele-specific oligomer hybridisation, oligomer-specific ligation assays, hybridisation with PNA or locked nucleic acids (LNA) probes.

Table 22

Further amplification techniques	Self sustained replication (SSR), Nucleic acid sequence based amplification (NASBA), Ligase chain reaction (LCR), Strand displacement amplification (SDA)

A primer of the present invention is a nucleic acid molecule sufficiently complementary to the sequence on which it is based and of sufficiently length to selectively hybridise to the corresponding region of a nucleic acid molecule intended to be amplified. The primer is able to prime the synthesis of the corresponding region of the intended nucleic acid molecule in the methods described above. Similarly, a probe of the present invention is a molecule for example a nucleic acid molecule of sufficient length and sufficiently complementary to the nucleic acid sequence of interest which selectively binds to the nucleic acid sequence of interest under high or low stringency conditions.

Sample

The method according to the present invention includes analyzing a sample of a bovine subject, wherein said sample may be any suitable sample capable of providing the

bovine genetic material for use in the method. The bovine genetic material may for example be extracted, isolated and purified if necessary from a blood sample, a tissue samples (for example spleen, buccal smears), clipping of a body surface (hairs or nails), milk and/or semen. The samples may be fresh or frozen.

The sequence polymorphisms of the invention comprise at least one nucleotide difference, such as at least two nucleotide differences, for example at least three nucleotide differences, such as at least four nucleotide differences, for example at least five nucleotide differences, such as at least six nucleotide differences, for example at least seven nucleotide differences, such as at least eight nucleotide differences, for example at least nine nucleotide differences, such as 10 nucleotide differences. The nucleotide differences comprise nucleotide differences, deletion and/or insertion or any combination thereof.

Primers

The primers that may be used according to the present invention are shown in Table 22. The in Table 22 specified primer pairs may be used individually or in combination with one or more primer pairs of Table 22.

The design of such primers or probes will be apparent to the molecular biologist of ordinary skill. Such primers are of any convenient length such as up to 50 bases, up to 40 bases, more conveniently up to 30 bases in length, such as for example 8-25 or 8-15 bases in length. In general such primers will comprise base sequences entirely complementary to the corresponding wild type or variant locus in the region. However, if required one or more mismatches may be introduced, provided that the discriminatory power of the oligonucleotide probe is not unduly affected. The primers/probes of the invention may carry one or more labels to facilitate detection.

In one embodiment, the primers and/or probes are capable of hybridizing to and/or amplifying a subsequence hybridizing to a single nucleotide polymorphism containing the sequence delineated by the markers as shown herein.

The primer nucleotide sequences of the invention further include: (a) any nucleotide sequence that hybridizes to a nucleic acid molecule of the delineated region(s) or its complementary sequence or RNA products under stringent conditions, e.g., hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about

45°C followed by one or more washes in 0.2x SSC/0.1% Sodium Dodecyl Sulfate (SDS) at about 50-65°C, or (b) under highly stringent conditions, e.g., hybridization to filter-bound nucleic acid in 6x SSC at about 45°C followed by one or more washes in 0.1x SSC/0.2% SDS at about 68°C, or under other hybridization conditions which are apparent to those of skill in the art (see, for example, Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at pp. 6.3.1-6.3.6 and 2.10.3). Preferably the nucleic acid molecule that hybridizes to the nucleotide sequence of (a) and (b), above, is one that comprises the complement of a nucleic acid molecule of the region s or r or a complementary sequence or RNA product thereof. In a preferred embodiment, nucleic acid molecules comprising the nucleotide sequences of (a) and (b), comprises nucleic acid molecule of RAI or a complementary sequence or RNA product thereof.

Among the nucleic acid molecules of the invention are deoxyoligonucleotides ("oligos") which hybridize under highly stringent or stringent conditions to the nucleic acid molecules described above. In general, for probes between 14 and 70 nucleotides in length the melting temperature (TM) is calculated using the formula:

Tm(°C)=81.5+16.6(log [monovalent cations (molar)])+0.41(% G+C)-(500/N)

where N is the length of the probe. If the hybridization is carried out in a solution containing formamide, the melting temperature is calculated using the equation Tm(°C)=81.5+16.6(log[monovalent cations (molar)])+0.41(% G+C)-(0.61% formamide)-(500/N) where N is the length of the probe. In general, hybridization is carried out at about 20-25 degrees below Tm (for DNA-DNA hybrids) or 10-15 degrees below Tm (for RNA-DNA hybrids).

Exemplary highly stringent conditions may refer for example to washing in 6x SSC/0.05% sodium pyrophosphate at 37°C (for about 14-base oligos), 48°C (for about 17-base oligos), 55°C (for about 20-base oligos), and 60°C (for about 23-base oligos). Accordingly, the invention further provides nucleotide primers or probes which detect the r region polymorphisms of the invention. The assessment may be conducted by means of at least one nucleic acid primer or probe, such as a primer or probe of DNA, RNA or a nucleic acid analogue such as peptide nucleic acid (PNA) or locked nucleic acid (LNA).

According to one aspect of the present invention there is provided an allele-specific oligonucleotide probe capable of detecting a polymorphism at one or more of positions in the delineated regions 1.

The allele-specific oligonucleotide probe is preferably 5-50 nucleotides, more preferably about 5-35 nucleotides, more preferably about 5-30 nucleotides, more preferably at least 9 nucleotides.

Determination of linkage

In order to detect whether the genetic marker is present in the genetic material, standard methods well known to persons skilled in the art may be applied, for example by the use of nucleic acid amplification. In order to determine whether the genetic marker is genetically linked to the calving traits, a permutation test can be applied when the regression method is used (Doerge and Churchill, 1996), or the Piepho-method can be applied (Piepho, 2001) when the variance components method is used. The principle of the permutation test is well described by Doerge and Churchill (1996), whereas the Piepho-method is well described by Piepho (2001). Significant linkage in the within family analysis using the regression method, a 1000 permutations were made using the permutation test (Doerge and Churchill, 1996). A threshold at the 5% chromosome wide level was considered to be significant evidence for linkage between the genetic marker and the calving traits. In addition, the QTL was confirmed in different sire families. For the across family analysis and multi-trait analysis with the variance component method the piepho method was used to determine the significance level (Piepho, 2001). A threshold at the 5% chromosome wide level was considered to be significant evidence for linkage between the genetic marker and the calving traits.

Kit

Another aspect of the present invention relates to a diagnostic kit for use in detecting the presence or absence in a bovine subject of at least one genetic marker associated with bovine calving characteristics, comprising at least one oligonucleotide sequence, wherein the nucleotide sequences are selected from any of SEQ ID NO.: 1 to SEQ ID NO.: 558 and/or any combination thereof.

Genotyping of a bovine subject in order to establish the genetic determinants of calving traits for that subject according to the present invention can be based on the analysis of genomic DNA which can be provided using standard DNA extraction methods as described herein. The genomic DNA may be isolated and amplified using standard techniques such as the polymerase chain reaction using oligonucleotide primers corresponding (complementary) to the polymorphic marker regions. Additional steps of purifying the DNA prior to amplification reaction may be included. Thus, a diagnostic kit for establishing calving characteristics comprises, in a separate packing, at least one oligonucleotide sequence selected from the group of sequences shown in table 23 and any combinations thereof.

Examples

Experimental design

A total genome scan for QTL affecting calving traits, was carried out in the Danish Holstein population. Marker and phenotypic data were collected according to the granddaughter design (Weller et al., 1990), which included 34 sires with 2042 progeny-tested sons. Numbers of sons per sire ranged from 20 to 106. Sires and their sons were genotyped for marker information whereas phenotypic records were taken from granddaughter performances. Numbers of daughters of each son ranged between 70 and 100. The marker data set included a total of 384 microsatellites covering all 29 Bos Taurus chromosomes.

Purification of genomic DNA

Genomic DNA was purified from semen according to the following protocol:

After thawing the semen-straw, both ends of the straw were cut away with a pair of scissors and the content of semen transferred to a 1.5 ml eppendorf tube. 1 ml of 0.9% NaCl was used to flush the straw into the tube. The tube was then centrifuged for 5 minutes at 2000 rpm, followed by removal of the supernatant. This washing step was repeated twice.

Then 300 µl buffer S (10 mM Tris HCl pH 8, 100 mM NaCl, 10 mM EDTA pH 8; 0,5 % SDS), 20 µl 1 M DTT and 20 µl pronase (20 mg/ml) (Boehringer)are added to the tube. After mixing the tubes are incubated over night with slow rotation where after 180 µl saturated NaCl is added followed by vigorous agitation for 15 seconds. The tube is the centrifuged for 15 minutes at 11000 rpm. 0.4 ml of the supernatant is transferred to a 2 ml tube and 1 ml of 96% ethanol is added, mixing is achieved by slow rotation of

the tube. The tube is then centrifuged for 10 minutes at 11000 rpm. Remove the supernatant by pouring away the liquid, wash the pellet with 70% ethanol (0.2 ml) and centrifuge again for 10 minutes at 11000 rpm. Pour away the ethanol, dry the pellet and resuspend in 0.5 ml of TE-buffer) for 30 minutes at 55°C.

Amplification procedures

PCR reactions were run in a volume of 8 µl using TEMPase (GeneChoice) polymerase and reaction buffer I as provided by the supplier (GeneChoice). Usually 5 different markers are included in each multiplex PCR. 1 µl DNA, 0.1 µl TEMPase enzyme, 0.2 mM dNTPs, 1.2 mM MgCl2, 0.3 µM each primer.

The PCR mixtures were subjected to initial denaturation at 94°C for 15 min (for TEMPase). Subsequently, the samples were cycled for 10 cycles with touchdown, i.e. the temperature is lowered 1°C at each cycle (denaturation at 94°C 30", annealing at 67°C 45", elongation 72°C 30"), after which the samples were cycled for 20 cycles with normal PCR conditions (denaturation at 94°C 30", annealing at 58°C 45", elongation 72°C 30) PCR cycling was terminated by 1 cycle at 72°C 30' and the PCR machine was programmed to cooling down the samples at 4°C for 'ever'.

The nucleotide sequence of the primers used for detecting the markers is shown in Table 23. The sequence is listed from the 5' end.

Table 23 Marker name	Forward Primer F Reverse Primer R	SEQ ID NO.:
BTA3:		
INRA006	**F** AGGAATATCTGTATCAACCTCAGTC	SEQ ID NO.: 1
	R CTGAGCTGGGGTGGGAGCTATAAATA	SEQ ID NO.: 2
UWCA7	**F** TGTAGCTCCCTGGAGGAGAA	SEQ ID NO.: 3
	R GCAAATACAACCCAGTCTGGTG	SEQ ID NO.: 4
ILSTS096	**F** GTGACCTGGAGAAGTTTTCC	SEQ ID NO.: 5
	R ACCACGCTCTGACTTGTAGC	SEQ ID NO.: 6
DIK4403	**F** CGTGCTGCAACTGAGAGTTC	SEQ ID NO.: 7
	R GCTGTATAGCAAAGTGACCCAGT	SEQ ID NO.: 8
RME23	**F** AGAACAAATGTGACACTCACA	SEQ ID NO.: 9
	R GTGAGTACAGGCGCTTTCTG	SEQ ID NO.: 10
BMS963	**F** GGAGGATGAAGGAGTCTTTGG	SEQ ID NO.: 11
	R AATTTACCACAGTCCACCGC	SEQ ID NO.: 12

BMS819	F AAAGAATTGGACCTGACTGAGC	SEQ ID NO.: 13
	R GCTTTCACTTCTGCTGGCTT	SEQ ID NO.: 14
FCGR1	F GGTCTTCATTGGTGTTTTCTCC	SEQ ID NO.: 15
	R GAGCTGCCCTAGATGAGGTG	SEQ ID NO.: 16
BL41	F CCTCTGCCATCTTTATTCCG	SEQ ID NO.: 17
	R **AAGATCAACTTATTCCTCACAGTGG**	SEQ ID NO.: 18
DIK4353	F TGAACTTTAGGGCAGCATGA	SEQ ID NO.: 19
	R AAGACTGAGATGTGGGGAAAA	SEQ ID NO.: 20
INRA003	F CTGGAGGTGTGTGAGCCCCATTTA	SEQ ID NO.: 21
	R CTAAGAGTCGAAGGTGTGACTAGG	SEQ ID NO.: 22
BMS2790	F AAGACAAGGACTTTCAGCCC	SEQ ID NO.: 23
	R AAAGAGTCGGACATTACTGAGC	SEQ ID NO.: 24
ILSTS029	F TGTTTTGATGGAACACAGCC	SEQ ID NO.: 25
	R TGGATTTAGACCAGGGTTGG	SEQ ID NO.: 26
BM220	F TTTTCTACTGCCCAACAAAGTG	SEQ ID NO.: 27
	R TAGGTACCATAGCCTAGCCAAG	SEQ ID NO.: 28
INRA123	F TCTAGAGGATCCCCGCTGAC	SEQ ID NO.: 29
	R AGAGAGCAACTCCACTGTGC	SEQ ID NO.: 30
BMS862	F TATAATGCCCTCTAGATCCACTCA	SEQ ID NO.: 31
	R ATGGAAAAATAAGATGTGGTATGTG	SEQ ID NO.: 32
HUJ246	F ACTCCAGTTTTCTTTCCTGGG	SEQ ID NO.: 33
	R TGCCATGTAGTAGCTGTGTGC	SEQ ID NO.: 34
BMS937	F GTAGCCATGGAGACTGGACTG	SEQ ID NO.: 35
	R CATTATCCCCTGTCACACACC	SEQ ID NO.: 36
DIK4664	F AACTGGCTCCAAGGTCAATG	SEQ ID NO.: 37
	R TCCCCTGTCACACACCTGTA	SEQ ID NO.: 38
DIK2702	F TGCGATATTTAATGGATGTCT	SEQ ID NO.: 39
	R TTCCTTTCTCCGAACTGCTC	SEQ ID NO.: 40
HUJII77	F TCCATCAAGTATTTGAGTGCAA	SEQ ID NO.: 41
	R ATAGCCCTACCCACTGTTTCTG	SEQ ID NO.: 42
DIK2686	F ATGTTTTTCAGGCCAATCCA	SEQ ID NO.: 43
	R TGCCCTGATTTCTCATACCC	SEQ ID NO.: 44
BM7225	F GGTGTTATGCATTCTCTAGGTGC	SEQ ID NO.: 45
	R AAGAGTTAGACATGACTGAGCACG	SEQ ID NO.: 46
BTA4:		
BMS1788	F ACGTCCAGATTCAGATTTCTTG	SEQ ID NO.: 47
	R GGAGAGGAATCTTGCAAAGG	SEQ ID NO.: 48
BMS2646	F CAAAGCCATAAGAAGCAATTATG	SEQ ID NO.: 49

BMS2646	R CCTTCTATAGTGTGGTGACTACCC	SEQ ID NO.: 50
	F GCACAGTAATAAGAGTGATGGCAGA	SEQ ID NO.: 51
TGLA116	R TGGAGAAGATTTGGCTGTGTACCCA	SEQ ID NO.: 52
	F CTTAACTCATTCACCTCAACTG	SEQ ID NO.: 53
INRA072	R AGTGATTGAGCACATTGCGCAT	SEQ ID NO.: 54
	F GCATTGGCAAGTGGATTCTT	SEQ ID NO.: 55
BM8233	R AAGGCAATTAACACATACATCACC	SEQ ID NO.: 56
	F ACTTCCCATCCATCCATCAG	SEQ ID NO.: 57
BMS648	R CTTCCATTCTCAGCCATCTAGC	SEQ ID NO.: 58
	F TGAGCCATAGAATTAAGATTCAAGC	SEQ ID NO.: 59
BR6303	R TTTGTTCCTCTTTATTTTCTTCTGC	SEQ ID NO.: 60
	F GAGCAGCTTCTTTCTTTCTCATCTT	SEQ ID NO.: 61
MGTG4B	R GCTCTTGGAAGCTTATTGTATAAAG	SEQ ID NO.: 62
BTA5:		
	F AGGGATTGGTTTATGCTCTCTC	SEQ ID NO.: 63
BMS1095	R GTTGCAGAGTCGGACATGAC	SEQ ID NO.: 64
	F GCAACTAAGACCCAACCAAC	SEQ ID NO.: 65
BM6026	R ACTGATGTGCTCAGGTATGACG	SEQ ID NO.: 66
	F GCTTTGGTACACCCTTTAAGC	SEQ ID NO.: 67
MNB-33	R GAACAAATTCACAAGGGAAAAC	SEQ ID NO.: 68
	F TTTCACTGTCATCTCCCTAGCA	SEQ ID NO.: 69
BMS610	R ATGTATTCATGCACACCACACA	SEQ ID NO.: 70
	F AAAATCCCTTCATAACAGTGCC	SEQ ID NO.: 71
BP1	R CATCGTGAATTCCAGGGTTC	SEQ ID NO.: 72
	F CCAAAAATTCTGGCACCAAT	SEQ ID NO.: 73
DIK4747	R CCTGGGCTTGTGACTAGCAT	SEQ ID NO.: 74
	F AGGAAGGACAAGGACATTGC	SEQ ID NO.: 75
DIK2718	R AGAGGGTCAAAGGCTTAATGG	SEQ ID NO.: 76
	F GAAACTCAACCCAAGACAACTCAAG	SEQ ID NO.: 77
AGLA293	R ATGACTTTATTCTCCACCTAGCAGA	SEQ ID NO.: 78
	F TGTGCTGGAGGTGATAGCTG	SEQ ID NO.: 79
DIK5002	R TGCAGGAATATGAGAGCTGAGA	SEQ ID NO.: 80
	F AGTTGGACCTGCCATTGTTC	SEQ ID NO.: 81
DIK4759	R ACTTATGTGCGTGCGTGCT	SEQ ID NO.: 82
	F GCACCAGCAGAGAGGACATT	SEQ ID NO.: 83
BMC1009	R ACCGGCTATTGTCCATCTTG	SEQ ID NO.: 84
	F CCATAACTCTGGGACTTTTCCTCA	SEQ ID NO.: 557
CSSM034	R ATGTTCAGCCATCTCTCCTGGTCC	SEQ ID NO.: 558

RM500	F CAGACACGACTAAGCGACCA	SEQ ID NO.: 85
	R CCTACAATAAAGCACGGGGA	SEQ ID NO.: 86
BMS1617	F GCCTGCATGTGTCTGTGG	SEQ ID NO.: 87
	R TCTGTGTCGGAATACCCTCC	SEQ ID NO.: 88
DIK5046	F TGAATTGTTTCTGCTTCTTGGA	SEQ ID NO.: 89
	R TGCATGACTCCCCTCTCTCT	SEQ ID NO.: 90
ETH10	F GTTCAGGACTGGCCCTGCTAACA	SEQ ID NO.: 91
	R CCTCCAGCCCACTTTCTCTTCTC	SEQ ID NO.: 92
CSSM022	F TCTCTCTAATGGAGTTGGTTTTTG	SEQ ID NO.: 93
	R ATATCCCACTGAGGATAAGAATTC	SEQ ID NO.: 94
BMS1216	F GAGTAGAACACAACTGAGGACACA	SEQ ID NO.: 95
	R CAATGCTGTGGGTACTGAGG	SEQ ID NO.: 96
DIK2943	F GGTTTCCTCAGGACATGGTG	SEQ ID NO.: 97
	R CAGTCCATGAGGTTGCAGAA	SEQ ID NO.: 98
BMS1248	F GTAATGTAGCCTTTTGTGCCG	SEQ ID NO.: 99
	R TCACCAACATGAGATAGTGTGC	SEQ ID NO.:100
BM315	F TGGTTTAGCAGAGAGCACATG	SEQ ID NO.:101
	R GCTCCTAGCCCTGCACAC	SEQ ID NO.:102
BMS1658	F ATTGATGCTTTATGATCCTCATG	SEQ ID NO.:103
	R CCCACTAAGAGAGGAGGAGG	SEQ ID NO.:104
BM2830	F AATGGGCGTATAAACACAGATG	SEQ ID NO.:105
	R TGAGTCCTGTCACCATCAGC	SEQ ID NO.:106
BTA7:		
BM7160	F TGGATTTTTAAACACAGAATGTGG	SEQ ID NO.:107
	R TCAGCTTCTCTTTAAATTTCTCTGG	SEQ ID NO.:108
BL1067	F AGCCAGTTTCTTCAAATCAACC	SEQ ID NO.:109
	R ATGGTTCCGCAGAGAAACAG	SEQ ID NO.:110
BMS713	F CCAAGGGAGGAAAAATAAGTTAA	SEQ ID NO.:111
	R ACCAGCAGTAGGTTGAGGTTAA	SEQ ID NO.:112
DIK5321	F AACCTTCACAGGCTCCTTCC	SEQ ID NO.:113
	R CCCATCTCTTGTGCCAAATC	SEQ ID NO.:114
DIK4421	F CATCTGAATGGCCAGAATGA	SEQ ID NO.:115
	R GTCCCCTGCATGTGTCTCTC	SEQ ID NO.:116
DIK2207	F ACATTGGCTTACGCTCACACT	SEQ ID NO.:117
	R CCTGTCTGGGTTTGTTTGCT	SEQ ID NO.:118
DIK5412	F ATGGACAGAACAGCCTGACA	SEQ ID NO.:119
	R TGGTGAACTCAGCCTCACTG	SEQ ID NO.:120
IL4	F GTGCTGGACATCTGCAAGTG	SEQ ID NO.:121

	R ACATTCAGGTCTGTGATCCATG	SEQ ID NO.:122
BM6105	F ACTAATAAGAAATTCTGCATGTGTG	SEQ ID NO.:123
	R CCACCATGACTCAGAAGTAGTTC	SEQ ID NO.:124
TGLA303	F TAATCATAAGTCAAAGTAACAGTTT	SEQ ID NO.:125
	R GATCTGGACATACAAAAGTATTAC	SEQ ID NO.:126
DIK2819	F TTACTTTTCGTGGGCCAGAG	SEQ ID NO.:127
	R GGAACTGTGCCACATAGCAA	SEQ ID NO.:128
DIK4606	F TCTTGGAAAGGGGAAAAAGC	SEQ ID NO.:129
	R TGCTTCATAGCACTTATCTCTTCA	SEQ ID NO.:130
BM7247	F AGTAAGGCCTGCAGTATTTATATCC	SEQ ID NO.:131
	R AATCTTTCCCTAGAACTTACAAAGG	SEQ ID NO.:132
UWCA20	F CTGAAACACTCTAAAAGGGTATGC	SEQ ID NO.:133
	R ATCCCAACATCCACCCATTCC	SEQ ID NO.:134
BM6117	F GTTCTGAGGTTTGTAAAGCCC	SEQ ID NO.:135
	R GGTGAGCTACAATCCATAGGG	SEQ ID NO.:136
BMS2840	F AGGAACCCATAGGCAGACAC	SEQ ID NO.:137
	R GCCTGGCAAAGAGAAAATTC	SEQ ID NO.:138
DIK2915	F TCTCACCCTCACATGGTTCA	SEQ ID NO.:139
	R GTGGAGCCAAGGTGAAAGAA	SEQ ID NO.:140
BMS2258	F CCAGCAGAAGAGAAAGATACTGA	SEQ ID NO.:141
	R AGTGGTAGAACTTCCATCTCACA	SEQ ID NO.:142
OARAE129	F AATCCAGTGTGTGAAAGACTAATCCAG	SEQ ID NO.:143
	R GTAGATCAAGATATAGAATATTTTTCAACACC	SEQ ID NO.:144
DIK2895	F CTCAATGACGTTTGGCTTCA	SEQ ID NO.:145
	R GGTGCCTGACTCCAATTGAT	SEQ ID NO.:146
ILSTS006	F TGTCTGTATTTCTGCTGTGG	SEQ ID NO.:147
	R ACACGGAAGCGATCTAAACG	SEQ ID NO.:148
BL1043	F AGTGCCAAAAGGAAGCGC	SEQ ID NO.:149
	R GACTTGACCGTTCCACCTG	SEQ ID NO.:150
BTA8:		
IDVGA-11	F CCTCTGGGTCTATCCATGTTG	SEQ ID NO.:151
	R TGGATGAATGAAGAAGATGCC	SEQ ID NO.:152
BMS1591	F GACAAGATAGGCTTTGCATGA	SEQ ID NO.:153
	R GATAGAAATATACCAGGAGCTCACA	SEQ ID NO.:154
BMS678	F ACCATCTACTGTGCTATGGCTT	SEQ ID NO.:155
	R GCAGAAACACAATACTCAGTGC	SEQ ID NO.:156
INRA129	F GGGTAGCCTGTTAAAATGCAG	SEQ ID NO.:157
	R CAGTGCTGACCTCTGAAGTAAG	SEQ ID NO.:158

BMS2072	F TGTTCAGTGCTTGTCTTAGCTG	SEQ ID NO.:159
	R TCTTCAAAGCCATCAATCATC	SEQ ID NO.:160
BMS887	F AAGCTAACTGATATTCTGCCACA	SEQ ID NO.:161
	R TTCCCTCTCTTCCCTCTCC	SEQ ID NO.:162
URB037	F ACTGGAGACGACTGAAGCAACC	SEQ ID NO.:163
	R GAGTGGCTGTTGCTAAATTTGG	SEQ ID NO.:164
MCM64	F TACAGTCCATGGGGTCACAAGAG	SEQ ID NO.:165
	R TCTGAATCTACTCCCTCCTCAGAGC	SEQ ID NO.:166
CSSM047	F TCTCTGTCTCTATCACTATATGGC	SEQ ID NO.:167
	R CTGGGCACCTGAAACTATCATCAT	SEQ ID NO.:168
BMS836	F GAAACTCTTTTCACTCTGCGC	SEQ ID NO.:169
	R GCTCTTAGGGATTGCTTCACC	SEQ ID NO.:170
BTA9:		
BMS2151	F CCATTAAGAGGAAATTGTGTTCA	SEQ ID NO.:171
	R ATGGAGTCACTGAAAGGTACTGA	SEQ ID NO.:172
ETH225	F GATCACCTTGCCACTATTTCCT	SEQ ID NO.:173
	R ACATGACAGCCAGCTGCTACT	SEQ ID NO.:174
ILSTS037	F TAGGCTATGTACTGACCATGC	SEQ ID NO.:175
	R CTGAACTGAGATGACTTTGGC	SEQ ID NO.:176
BM2504	F CAGCTTTCCATCCCCTTTC	SEQ ID NO.:177
	R CTCCCATCCCAAACACAGAC	SEQ ID NO.:178
DIK2892	F TTGACCCTGAAAGATGTCCA	SEQ ID NO.:179
	R CACGGTTTATCAGCTTGGGTA	SEQ ID NO.:180
DIK3003	F ACTTTCAGTTTTGGGCTGAC	SEQ ID NO.:181
	R TGTCACTAGGTAAATTGGTG	SEQ ID NO.:182
DIK3002	F AAATGGAGGTAATGAAATAAAATA	SEQ ID NO.:183
	R CAAACCCATGGACTGTAACCT	SEQ ID NO.:184
BMS1267	F TTCTGAATTTGATTCCCAACA	SEQ ID NO.:185
	R ACTGTTTCCTTAAAAGCTTCCC	SEQ ID NO.:186
DIK5142	F TGGGTAAGTGGGAAAGGATG	SEQ ID NO.:187
	R CTCAGCCAGGTTGTCCTCTC	SEQ ID NO.:188
BMS555	F GGAAAGAGTAGGTGATTCCCTG	SEQ ID NO.:189
	R ATTTAATTGTCATCCCAGGTGA	SEQ ID NO.:190
DIK5364	F CCTCTGAAACCCCAGACTTG	SEQ ID NO.:191
	R AAAAACCCAAAACAACACACAA	SEQ ID NO.:192
UWCA9	F CCTTCTCTGAATTTTTGTTGAAAGC	SEQ ID NO.:193
	R GGACAGAAGTGAGTGACTGAGA	SEQ ID NO.:194
DIK4720	F CATGATATTTACCCTGTGTGTGC	SEQ ID NO.:195

	R GAGGAGCTGGAGGGCTAAAG	SEQ ID NO.:196
BMS1290	F TTGGCACTTACTACCTCATATGTT	SEQ ID NO.:197
	R TTTTCTGGATGTTGAGCCTATT	SEQ ID NO.:198
DIK2816	F ACCTTGGGAATCAAGGTCAT	SEQ ID NO.:199
	R CCCAGTAGTCCAGTGGCTCA	SEQ ID NO.:200
BM6436	F AAAGACTGCTTGCCTGAAGC	SEQ ID NO.:201
	R CAACCAGTGATGCTGTACTCTG	SEQ ID NO.:202
BMS2753	F TCAAAAAGTTGGACATGACTGA	SEQ ID NO.:203
	R AGGTTTTCAAATGAGAGACTTTTC	SEQ ID NO.:204
BM4208	F TCAGTACACTGGCCACCATG	SEQ ID NO.:205
	R CACTGCATGCTTTTCCAAAC	SEQ ID NO.:206
BMS2819	F GCTCACAGGTTCTGAGGACTC	SEQ ID NO.:207
	R AACTTGAAGAAGGAATGCTGAG	SEQ ID NO.:208
BMS2295	F GCTCTGGTGACCCAGGTG	SEQ ID NO.:209
	R CTGGCAGGAGATGAGAGGAG	SEQ ID NO.:210
BMS1967	F GGGCAGATGTGAGTAATTTTCC	SEQ ID NO.:211
	R AACTGAGCTGTATGGTGGACG	SEQ ID NO.:212
BTA10		
DIK2658	F GCACATTGGGATCTCTCCTG	SEQ ID NO.:213
	R AAAGTCCCATCCCACAATCA	SEQ ID NO.:214
DIK2503	F TCCTTACAACACACCATGCAA	SEQ ID NO.:215
	R CACACCCAGGCATCCATAC	SEQ ID NO.:216
CSSM38	F TTCATATAAGCAGTTTATAAACGC	SEQ ID NO.:217
	R ATAGGATCTGGTAACTTACAGATG	SEQ ID NO.:218
BMS528	F CTCACTCCACTGGGCTTCTC	SEQ ID NO.:219
	R TGTGTTCTCACCTCGACCAC	SEQ ID NO.:220
BM1237	F TCATCTTGGGCATAAGACAGG	SEQ ID NO.:221
	R ATTGTTCCCAGCATCTTAGAGG	SEQ ID NO.:222
MB077	F CACCCGTACCCTCACTGC	SEQ ID NO.:223
	R TCACAACCCTCTTCTCACCC	SEQ ID NO.:224
DIK2000	F TGGCTTGCAACACTGCAC	SEQ ID NO.:225
	R CCCACCTACGACTGGGACTTA	SEQ ID NO.:226
BMS2742	F GCTTCAGTTCTGCTTTTCACC	SEQ ID NO.:227
	R CTTCAGCATCTTGATTGTTGC	SEQ ID NO.:228
BMS529	F CTCCAGGTAAGACAGGCCAC	SEQ ID NO.:229
	R CCCGATCTGTGTGTGGGT	SEQ ID NO.:230
DIK2361	F TGTGGGTTTGATCTCTGAGT	SEQ ID NO.:231
	R TGTGTCCTCCTTTGTGGTAGAA	SEQ ID NO.:232

BM888	F ACTAGGAGGCCATATAGGAGGC	SEQ ID NO.:233
	R GAGCTCAAAACGAGGGACAG	SEQ ID NO.:234
TGLA433	F ATTTCTATGAAGTAGTCTTCTGACT	SEQ ID NO.:235
	R ATTTTAAAACTAGTCACGAGTGCCT	SEQ ID NO.:236
INRA037	F GATCCTGCTTATATTTAACCAC	SEQ ID NO.:237
	R AAAATTCCATGGAGAGAGAAAC	SEQ ID NO.:238
BMS1620	F TATGAACTCACATGGTTACCACA	SEQ ID NO.:239
	R TTGCCCAAAAATAGACCTTAAA	SEQ ID NO.:240
ILSTS070	F GGTATTTTGAGAATGTGGGC	SEQ ID NO.:241
	R TCTTTGACCACTACCTATCC	SEQ ID NO.:242
BMS2641	F GTGCGGAAAGGAACAGAGTC	SEQ ID NO.:243
	R AAAGCCGGACTGGAGTGTC	SEQ ID NO.:244
BMS614	F AATGCGTGGGACTTGTTTT	SEQ ID NO.:245
	R CAATTGCTGAAGCAGTCACA	SEQ ID NO.:246
BMS2614	F ACTTTCTTTTCCTGTGGCTCG	SEQ ID NO.:247
	R CAGAGCTGGCACCAGAGG	SEQ ID NO.:248
BTA11:		
BM716	F AGTACTTGGCTTGCTTTGCTC	SEQ ID NO.:249
	R TTAAATTTCCATCTCACCCTGG	SEQ ID NO.:250
BMS2569	F AGAGAGGCCAAAGCTGGG	SEQ ID NO.:251
	R TTTCCTTGGGCTTCAGGAG	SEQ ID NO.:252
BM2818	F TTCTGTGGTTGAAGAGTGTTCC	SEQ ID NO.:253
	R CAATGGCTAAGAGGTCCAGTG	SEQ ID NO.:254
INRA177-2	F TCCAAAAGTTTCGTGACATATTG	SEQ ID NO.:255
	R CACCAGGCTTCTCTGTTGAA	SEQ ID NO.:256
INRA177	F TCCAAAAGTTTCGTGACATATTG	SEQ ID NO.:257
	R CACCAGGCTTCTCTGTTGAA	SEQ ID NO.:258
RM096	F TCGCAAAAAGTTGGACAAGAC	SEQ ID NO.:259
	R TTAGCAGGGTGCCTGACACTT	SEQ ID NO.:260
INRA131	F GGTAAAATCCTGCAAAACACAG	SEQ ID NO.:261
	R TGACTGTATAGACTGAAGCAAC	SEQ ID NO.:262
BM7169	F TGGTATGTAGTTACAGCAGCCC	SEQ ID NO.:263
	R CCATTGAAACAGACATGAATGC	SEQ ID NO.:264
BM6445	F GTGTCTGTCAAAAGATGAATGG	SEQ ID NO.:265
	R GACAACTGCTTCTCGTTGGG	SEQ ID NO.:266
ILSTS036	F GAGTATTATGCTTGGGAGGC	SEQ ID NO.:267
	R AGACAGGATGGGAAGTCACC	SEQ ID NO.:268
BMS1822	F AAAGGCTTCTATTTGTGGTGG	SEQ ID NO.:269

	R TTGATGCTTTATTGTTTTCCTCT	SEQ ID NO.:270
TGLA58	F TTCTACTCTCCAGCCTCCTCC	SEQ ID NO.:271
	R GTTGGCTCCAAGAGCAAGTC	SEQ ID NO.:272
BMS2047	F ACTATGGACATTTGGGGCAG	SEQ ID NO.:273
	R AGTAGGTGGAGATCAAGGATGC	SEQ ID NO.:274
HUJV174	F CAGACCAGTTTCTCAGACAAGC	SEQ ID NO.:275
	R TCATTCCTGTGTCAATACAGCC	SEQ ID NO.:276
BMS989	F TTTGAGAACTTTTGTTTCTGAGC	SEQ ID NO.:277
	R TTATTTTGCTTTTCTGATTTTGTG	SEQ ID NO.:278
TGLA436	F TGTATGGCTGAATGATATTCCATTT	SEQ ID NO.:279
	R CTACTGACAGATGATTAGATAAAGA	SEQ ID NO.:280
BMS460	F TGCCCCATAGTGTAGTGCTC	SEQ ID NO.:281
	R GCCAGCAGAGAATTGTAGCA	SEQ ID NO.:282
ILSTS045	F TTCTGGCAAACTATTCCACC	SEQ ID NO.:283
	R CATGAAAGACACAGATGACC	SEQ ID NO.:284
DIK4819	F ATTTTTCCCAGCGCCTCTC	SEQ ID NO.:285
	R AAACAGAAGACTCAGGAAGACGA	SEQ ID NO.:286
HEL13	F TAAGGACTTGAGATAAGGAG	SEQ ID NO.:287
	R CCATCTACCTCCATCTTAAC	SEQ ID NO.:288
BTA12:		
BMS410	F GGCTGAAAAGCTGTGGTGTT	SEQ ID NO.:289
	R TTGCCACATTTACCTTCTTTCA	SEQ ID NO.:290
BM6108	F TTCTAATGTAGAGCAAAGTGATTGA	SEQ ID NO.:291
	R TGTAGGAGGGACAGATTGGG	SEQ ID NO.:292
BM860	F ACCAGATTGGTGGTAGTGGTG	SEQ ID NO.:293
	R CATGCCGTGGCTAAGACC	SEQ ID NO.:294
BMS975	F TGGAGCTAAATCAATGCGTG	SEQ ID NO.:295
	R CCCAATGGCCAATTAAGTACC	SEQ ID NO.:296
BMS1316	F CCTTCATGGAAGAAATTTTGTG	SEQ ID NO.:297
	R GGAGTTACAGTCCATGGGTTC	SEQ ID NO.:298
BMS2724	F GGCTGATACACAGAGACATGC	SEQ ID NO.:299
	R CCTCTCTGCCTTCTATCAGGT	SEQ ID NO.:300
BTA15:		
BR3510	F GCTGGTGGGTTGTTTACCAC	SEQ ID NO.:301
	R ACCCCGTGGACTGTAGTCTG	SEQ ID NO.:302
BMS2533	F TGAAGTAAGTAAGCACACAAGCA	SEQ ID NO.:303
	R TTGATCATCTTTAGGTCCATCC	SEQ ID NO.:304
INRA050	F ACAGGCTACAGTCCATGGGGTT	SEQ ID NO.:305

	R TATAGAACAGAAAAATGACTACACG	SEQ ID NO.:306
JAB8	F CACGTCACCCGCTTTCTCTTG	SEQ ID NO.:307
	R GGTGAGTGTAACACCTGTGTGCG	SEQ ID NO.:308
BMS2684	F CCAAGGTCATTGTTGCAGC	SEQ ID NO.:309
	R TGGGGATTTGCTTCTCAGTC	SEQ ID NO.:310
DIK1106	F CAAGAGTCAGACATGACTTAGTGAC	SEQ ID NO.:311
	R TCTACCTTTTGATAGCGTGAGC	SEQ ID NO.:312
INRA145	F TAATAAAACTGGTCCCTCTGGC	SEQ ID NO.:313
	R TGCTGGCTCTCCAGTATGC	SEQ ID NO.:314
IDVGA-10	F TCTCCTGGCTACAGGGCTAA	SEQ ID NO.:315
	R CCCACTGGCCTAGAACCC	SEQ ID NO.:316
DIK4850	F AGGGGCGAAGTGAGGATTA	SEQ ID NO.:317
	R TTGCATGGTTCTGCAGATGT	SEQ ID NO.:318
DIK2768	F AGCCTTCCCAGTACCTGTCA	SEQ ID NO.:319
	R TAAGGGAGCTCAAAACCACA	SEQ ID NO.:320
ILSTS027	F GGTGTGTTGGTTAAGACTGG	SEQ ID NO.:321
	R GAATCATAGACCTGACTTCC	SEQ ID NO.:322
BMS812	F TGGACAGGACTGAGTATGCA	SEQ ID NO.:323
	R AGGTATCCAACTAACACAGCCA	SEQ ID NO.:324
BMS2076	F AGCACCTGTACCATCTGTTCC	SEQ ID NO.:325
	R TCCATAGGCTCACAAAGAGTTG	SEQ ID NO.:326
BL1095	F TCCCTCTACCATATATTTCCCC	SEQ ID NO.:327
	R CATTAGCATGGAAAAACCTCTG	SEQ ID NO.:328
BMS820	F CCACTACTTGCCTCAGGGAG	SEQ ID NO.:329
	R ACAGGACTCTCAAGCATCAGC	SEQ ID NO.:330
BMS927	F GATGATCCACCATAACTACCAGA	SEQ ID NO.:331
	R TGGCTCTCAAAGGTCATTGT	SEQ ID NO.:332
BMS429	F TACATTAACCCCAAAATTAAATGC	SEQ ID NO.:333
	R CCCTTGATTTCTCTCATGAGTATT	SEQ ID NO.:334
BTA18:		
IDVGA-31	F CCTTGAGATGAATGTTTGAGGATG	SEQ ID NO.:335
	R AACGCAGCCAGCAGGGTCAGG	SEQ ID NO.:336
BMS1355	F TAAAACCCCAAAAAGAACCC	SEQ ID NO.:337
	R ATATTTGCGACATTGGATGAA	SEQ ID NO.:338
BMS1322	F TGATGCTGATTGATTTTGTGTG	SEQ ID NO.:339
	R TATCTTTGCTCACTCTTTCCCC	SEQ ID NO.:340
TEXAN-10	F TGTGGCTAGGTTCAAGCTCC	SEQ ID NO.:341
	R TCTCTTCTGGTGCATCCATTG	SEQ ID NO.:342

BMS2213	F ATGGGCAGCTTAGGGATTG	SEQ ID NO.:343
	R CTTCAAGAGCCTTCAGTGGG	SEQ ID NO.:344
INRA121	F GGAAACCCATTGGAGGATTTG	SEQ ID NO.:345
	R CTTCACTATTCCCCACAAAGC	SEQ ID NO.:346
BR4406	F TACCTACCAGTTTTCCAGCACC	SEQ ID NO.:347
	R AGAAGAGCCTGGAGGGCTAC	SEQ ID NO.:348
BMS2554	F GGGCTGTAAAGAGTAGGACACA	SEQ ID NO.:349
	R ATCATCTGCTTCCAGTCACAG	SEQ ID NO.:350
MNB-27	F GAGTAAATAAAGCTGCATGATGTC	SEQ ID NO.:351
	R GGATCAGGAGATTTCAACACAG	SEQ ID NO.:352
BM7109	F CAGGTAAAAGAGCGGCTTTG	SEQ ID NO.:353
	R CAGCTTCATGCCCTAGAAGG	SEQ ID NO.:354
INRA063	F ATTTGCACAAGCTAAATCTAACC	SEQ ID NO.:355
	R AAACCACAGAAATGCTTGGAAG	SEQ ID NO.:356
ILSTS002	F TCTATACACATGTGCTGTGC	SEQ ID NO.:357
	R CTTAGGGGTGAAGTGACACG	SEQ ID NO.:358
BMS2639	F ATATCGTTTTCAGATTTCTTTTGC	SEQ ID NO.:359
	R GAGAGATAAATTGGGAGTTTGAGA	SEQ ID NO.:360
DIK4960	F CGCAACTTCCAAGTCCATCT	SEQ ID NO.:361
	R GGACACCTTCCTGTCCTCAA	SEQ ID NO.:362
DIK4849	F CCATCTTCCCCCATTGTGTA	SEQ ID NO.:363
	R CCCCTCTTCATCTCAAAACA	SEQ ID NO.:364
BMON117	F TAGGGCCGTGATACTGTGT	SEQ ID NO.:365
	R CTCTACCATCCAGCACCCTAAT	SEQ ID NO.:366
DIK4232	F TTGTGAGGTAAAGGGACATGA	SEQ ID NO.:367
	R GCCAGATTTGCCAACTGTTT	SEQ ID NO.:368
BMS2785	F ACAAACCTGTGCGCCTTG	SEQ ID NO.:369
	R GGCAATCAGTCGGACACAC	SEQ ID NO.:370
DIK4569	F TCCCCCTAAGGCTCAGAGTT	SEQ ID NO.:371
	R CTAACTTCCCCTTCGGAACC	SEQ ID NO.:372
BM2078	F CCCAAAAGAAGCCAGGAAG	SEQ ID NO.:373
	R TCAGAGTTTGGGGTCCTCAG	SEQ ID NO.:374
BM6507	F ACTTAGCACAATGCCCTCTAGG	SEQ ID NO.:375
	R ATGTTATTCCATCAGGAGGAGC	SEQ ID NO.:376
TGLA227	F CGAATTCCAAATCTGTTAATTTGCT	SEQ ID NO.:377
	R ACAGACAGAAACTCAATGAAAGCA	SEQ ID NO.:378
DIK4013	F GAAATTTGTGACCCCTGCAT	SEQ ID NO.:379
	R CTAAAGCTCTGCCTCCCAAG	SEQ ID NO.:380

BTA19:		
BM9202	F TCTATGAAGACTTTCAGGACCTTC	SEQ ID NO.:381
	R GCATCCCGGTCTCCTATG	SEQ ID NO.:382
BMS745	F TAGGGACTTGTTACCCGTGG	SEQ ID NO.:383
	R TGCAAGCTGTGAGGAGGAG	SEQ ID NO.:384
BP20	F TCTGTGGGTGAACAAGCAAG	SEQ ID NO.:385
	R GGCTCCCTAAAGACCCACTC	SEQ ID NO.:386
IDVGA-46	F AAATCCTTTCAAGTATGTTTTCA	SEQ ID NO.:387
	R ACTCACTCCAGTATTCTTGTCTG	SEQ ID NO.:388
BMS2389	F AATGTTAGGTTTACATGCAGCC	SEQ ID NO.:389
	R AGGCAATAGGATCTCCACTAGC	SEQ ID NO.:390
CSSM065	F TTCCTGCTTGGTGAAACTTTGAAC	SEQ ID NO.:391
	R CAACTCAAAGCTTCAACAGCAGCC	SEQ ID NO.:392
ETH3	F GAACCTGCCTCTCCTGCATTGG	SEQ ID NO.:393
	R ACTCTGCCTGTGGCCAAGTAGG	SEQ ID NO.:394
BMS601	F CACTAGGACGATGCTCTCAGG	SEQ ID NO.:395
	R TCACAAGAGCAATGACGAGG	SEQ ID NO.:396
BTA20:		
BM3517	F GTGTGTTGGCATCTGGACTG	SEQ ID NO.:397
	R TGTCAAATTCTATGCAGGATGG	SEQ ID NO.:398
HEL12	F GCATTAGGTTCTCCAGAGAA	SEQ ID NO.:399
	R CAGACTTGTCAGACTCCATA	SEQ ID NO.:400
BMS1282	F ACTCTTCCACAGTTGGCCTG	SEQ ID NO.:401
	R CCTCCTTCCTCCAGAGCC	SEQ ID NO.:402
BMS1754	F GCATTATTCTTTGTTCTTTGGG	SEQ ID NO.:403
	R GTTTCTGCTCCTGATCTCCTG	SEQ ID NO.:404
TGLA126	F CTAATTTAGAATGAGAGAGGCTTCT	SEQ ID NO.:405
	R TTGGTCTCTATTCTCTGAATATTCC	SEQ ID NO.:406
BMS2361	F ACACAACCCAAATGTTACCAA	SEQ ID NO.:407
	R ATTGTGCAGAGACCAAGTGC	SEQ ID NO.:408
AGLA29	F AGGAAGCCGAGTGAGATATGTAAGC	SEQ ID NO.:409
	R TTACAGCCTGTGTGAATGTCCTCTA	SEQ ID NO.:410
BMS703	F CAATGAGCTCAGATTGTTGCA	SEQ ID NO.:411
	R ATACATGTAGTCAAAAGGCTCATCC	SEQ ID NO.:412
BM5004	F TCTGGAGTGAATGTTTCTGAGG	SEQ ID NO.:413
	R TTGTGATGAGCACCTGAAGG	SEQ ID NO.:414
UWCA26	F TGGGGTCTAAAAGAGTCAGAG	SEQ ID NO.:415
	R TTCAAGTCTGCCTTTTGGTTTCGT	SEQ ID NO.:416

BTA21:

DIK5182	F CGATGTAAAGGGCAGGTTCT	SEQ ID NO.:417
	R CTCTTAGAATCCTGTTTTAGGG	SEQ ID NO.:418
BMS1117	F TGTGTGCTCTCTCACACATGC	SEQ ID NO.:419
	R AACCAAAGCAGGGATCAGG	SEQ ID NO.:420
RM151	F CCCAGAGGTGACAACATTTCCAG	SEQ ID NO.:421
	R GATCCACCAAAAACCAGCTGGA	SEQ ID NO.:422
DIK2492	F AATCCATCCATTCAGCCTTC	SEQ ID NO.:423
	R GAAATGACAGCCCACTCCAG	SEQ ID NO.:424
AGLA233	F TGCAAACATCCACGTAGCATAAATA	SEQ ID NO.:425
	R GCATGAACAGCCAATAGTGTCATC	SEQ ID NO.:426
ILSTS095	F GAAAGATGTTGCTAGTGGGG	SEQ ID NO.:427
	R ATTCTCCTGTGAACCTCTCC	SEQ ID NO.:428
DIK4602	F GACTGCGACCAGGTCTTTTC	SEQ ID NO.:429
	R AGGCCCATACGCATTTGTTA	SEQ ID NO.:430
BM103	F CTAGCTGCTGGCTACTTGGG	SEQ ID NO.:431
	R GGCTGCTCTGGGCTATTG	SEQ ID NO.:432
DIK4001	F TTCTCCAACCCGGTTATGC	SEQ ID NO.:433
	R CTGATTGGTCACTCCATCCA	SEQ ID NO.:434
IDVGA-45	F GTGGTGGCAAAGAGTCAGA	SEQ ID NO.:435
	R AACAGCCCTGATTTCCATA	SEQ ID NO.:436
DIK2481	F CCGTGTTTGTCTTCCTCTGA	SEQ ID NO.:437
	R TGACAGCAGCCAAGATATGG	SEQ ID NO.:438
INRA103	F TTGTCCAGCCCAGCATTTAGC	SEQ ID NO.:439
	R GGAGAAGACTTATGGGAGC	SEQ ID NO.:440
BMS2815	F TGATATTCAAACTCAATGAACCC	SEQ ID NO.:441
	R CTTGCATATGCTCATCATTATCA	SEQ ID NO.:442
DIK2842	F GGATTTTAGCTGCCATTGCT	SEQ ID NO.:443
	R AATCCCATGGACAGAAAAGC	SEQ ID NO.:444
DIK3036	F TGTGTGGCTTTAGCACAT	SEQ ID NO.:445
	R CAGAAAGGGAAATCACATCC	SEQ ID NO.:446
DIK4391	F CCCTTCCAATAGGCAAATCTC	SEQ ID NO.:447
	R TCCAACAAGCTTTTCCTTCC	SEQ ID NO.:448
DIK2913	F AACGTCCAGTCGCTTCAAAT	SEQ ID NO.:449
	R TCACACACCTGAACTCAAAGC	SEQ ID NO.:450
BM846	F GACCACTGGACCACCAGG	SEQ ID NO.:451
	R CTGGTAAAAAGCAATGATGCC	SEQ ID NO.:452
TGLA122	F CCCTCCTCCAGGTAAATCAGC	SEQ ID NO.:453

	R AATCACATGGCAAATAAGTACATAC	SEQ ID NO.:454
ILSTS054	F GAGGATCTTGATTTTGATGTCC	SEQ ID NO.:455
	R AGGGCCACTATGGTACTTCC	SEQ ID NO.:456
BMS743	F AGCTACCCTGGTATACAACACG	SEQ ID NO.:457
	R GCTCTGAAATTCTGGCAGTG	SEQ ID NO.:458
IDVGA-30	F GCATCTGGGAGCCTCGTATCTC	SEQ ID NO.:459
	R TTGTAAAACTCGGGGCATAAGCA	SEQ ID NO.:460
BTA22:		
CSSM26	F GACTTCTGCTTGTGGTTTCCAAGT	SEQ ID NO.:461
	R TTTTCCCATTATGGTTTATCCCAG	SEQ ID NO.:462
INRA026	F TAGTTCCAATGAGACACGAACA	SEQ ID NO.:463
	R TAGGAGCACGGAGGTAAAACA	SEQ ID NO.:464
BM1558	F TGAGGAAAGCCTTGGCAG	SEQ ID NO.:465
	R ACTGGGCCTAGCTCCTTCTC	SEQ ID NO.:466
BM3628	F CTGAGATGGACTCAGGGAGG	SEQ ID NO.:467
	R GTTGGATTGGAAAGGTTAGGC	SEQ ID NO.:468
BMS875	F TCCAGCTTGAATCCCTTCC	SEQ ID NO.:469
	R AAGCAAAGGCTGGGAACAC	SEQ ID NO.:470
BM4102	F CCAAATTCCACTGTGCTGC	SEQ ID NO.:471
	R GAGCGGCCTATCAACCCTAC	SEQ ID NO.:472
BTA24:		
BMS917	F TAATGCCTCTGGAAGGTTGA	SEQ ID NO.:473
	R CAAGCTGGTTGTTCTTTTGC	SEQ ID NO.:474
BM7151	F AAATGTCCACTGCTCAAAGATG	SEQ ID NO.:475
	R ACTTGGAGATAGAACTGGCAGG	SEQ ID NO.:476
BM226	F ATTGCCTTGTCCGTGTATCC	SEQ ID NO.:477
	R CCGGCTGAATTGCTATAAGC	SEQ ID NO.:478
BMS2526	F CAGGCTCCATGTTGGACAC	SEQ ID NO.:479
	R CATCAGGTTGGCAGAGTCG	SEQ ID NO.:480
TGLA351	F GCACATCTGGTGGCCACATCAG	SEQ ID NO.:481
	R CTCTAGGGGATTTCAGTCTCAGT	SEQ ID NO.:482
BM7228	F TTAAATCCTCAAGTAAAGGAAGGC	SEQ ID NO.:483
	R GCAAACCTAAGAATCCTCATTTC	SEQ ID NO.:484
CSSM23	F CACTGGAGTGGGTTGCCATTGTCT	SEQ ID NO.:485
	R GTTCGCAATATGATCTCTGATTTG	SEQ ID NO.:486
BMS2270	F CTGCGTTAACACCCCACC	SEQ ID NO.:487
	R GCAGGAAGGCTGATGCAC	SEQ ID NO.:488
ILSTS065	F GCTGCAAAGAGTTGAACACC	SEQ ID NO.:489

	R AACTATTACAGGAGGCTCCC	SEQ ID NO.:490
BMS1862	F GCACATGCAATCTTGAAAGG	SEQ ID NO.:491
	R ACCAGAGATGATGAAGAATCCC	SEQ ID NO.:492
BMS466	F AGCAGAGGGCAAATGTTATG	SEQ ID NO.:493
	R GGATGTAAGAGGATGCAGACC	SEQ ID NO.:494
INRA090	F GGTCATTTTCCATTATGACAGCAG	SEQ ID NO.:495
	R GGTGTTACCTTTTTTAGTCTCC	SEQ ID NO.:496
BMS1926	F CAACTAGCTTCTCAATGCCTTT	SEQ ID NO.:497
	R TTCTCCCAATCTGTAACTGCA	SEQ ID NO.:498
BMS3024	F CCAAACCAGTGTGACTGACA	SEQ ID NO.:499
	R TTGCTCATTTAACTTCATTACAACA	SEQ ID NO.:500
BTA25:		
ILSTS102	F CAGGACTGAGTAACTAAGGC	SEQ ID NO.:501
	R AGGAGACAGCTACAAACCCC	SEQ ID NO.:502
BMS2843	F ATCCAAGGAGGTCCCAGG	SEQ ID NO.:503
	R TCCTCCAGTGGGAAATATGG	SEQ ID NO.:504
BM737	F TGGGATAGACCACATTGGAA	SEQ ID NO.:505
	R GAATGCTGTTTGGGAGGGTA	SEQ ID NO.:506
ILSTS046	F TAAAGTCCTGCAAGAGAAGG	SEQ ID NO.:507
	R TTTCTGTCTTGAGTCTCTCC	SEQ ID NO.:508
BMS1353	F TTTCAGGACTAATAGGGCATGG	SEQ ID NO.:509
	R ATTCAGACCTGCCTGGTGAC	SEQ ID NO.:510
AF5	F GCAGAAGGAAAAAGCAATGG	SEQ ID NO.:511
	R GATCCTGCGAGCCACAAG	SEQ ID NO.:512
BTA26:		
BMS651	F AATATGTGAAAACAAGTCAAAGCA	SEQ ID NO.:513
	R CCTGGCAAGCAACAGTTAAT	SEQ ID NO.:514
HEL11	F CTTTGTGGAAGGCTAAGATG	SEQ ID NO.:515
	R TCCCACATGATCTATGGTGC	SEQ ID NO.:516
BMS332	F GACAAAACCCTTTTAGCACAGG	SEQ ID NO.:517
	R AATTGCATGGAAAGTTCTCAGC	SEQ ID NO.:518
RM026	F TTGTACATTTCTGTCAATGCCTT	SEQ ID NO.:519
	R ACAATGTCATTGGTCAATTCATT	SEQ ID NO.:520
BM9284	F AGGTGCTGGAATGGCAAC	SEQ ID NO.:521
	R TGTGATTTTGGTCTTCCTTGC	SEQ ID NO.:522
RME40	F TCTGTGAGCATGTGCAGAAT	SEQ ID NO.:523
	R CTCACAGGTAAATTTGGGTGAT	SEQ ID NO.:524
IDVGA-59	F AACCCAAATATCCATCAATAG	SEQ ID NO.:525

	R CAGTCCCTCAACCCTCTTTTC	SEQ ID NO.:526
BMS882	F TAGTGTCCACCAGAGACCCC	SEQ ID NO.:527
	R CCAAAGACACAGTTTAAAGGGC	SEQ ID NO.:528
BM804	F CCAGCATCAACTGTCAGAGC	SEQ ID NO.:529
	R GGCAGATTCTTTGCCTTCTG	SEQ ID NO.:530
BM7237	F CCAGCATCAACTGTCAGAGC	SEQ ID NO.:531
	R GGCAGATTCTTTGCCTTCTG	SEQ ID NO.:532
BTA28:		
BMC6020	F ATTGCATGTAGCTCTTGGGG	SEQ ID NO.:533
	R AAGTGGGTGGCTTCAACACT	SEQ ID NO.:534
ETH1112	F AGTGGATCCTGCATGTTATGCCG	SEQ ID NO.:535
	R CCAGACGGACCTTTGTGGGCAA	SEQ ID NO.:536
BL25	F AACAGTGGCAATGGAAGTGG	SEQ ID NO.:537
	R AGTCAGGATCTAGTGGGTGAGTG	SEQ ID NO.:538
DIK2955	F CATTGAACACTGAAAGGAAAGC	SEQ ID NO.:539
	R TCACAAGGGCTTTGAAGTGA	SEQ ID NO.:540
BMS2608	F GACTAAGCATATGAACCTGGGC	SEQ ID NO.:541
	R CTGCCCCTTGTCATCTCATC	SEQ ID NO.:542
BMS2658	F TCCCTGGACTTCTTGCAGAG	SEQ ID NO.:543
	R CTGGCCCCAGACACAATC	SEQ ID NO.:544
DIK713	F CACTTTGCTGTGGACCTGAA	SEQ ID NO.:545
	R ACCCAGGAACTGAACCCAT	SEQ ID NO.:546
BMS1714	F TTTATCCCAAGAGGTTCCACC	SEQ ID NO.:547
	R AGGTGCTTGCAGTGAATCTG	SEQ ID NO.:548
DIK5056	F CCACCAGGCTAATGGGTAAA	SEQ ID NO.:549
	R TGGTGTTGCATCTGCATTCT	SEQ ID NO.:550
DIK5323	F CTGGGAAGCCTTTTGATCTG	SEQ ID NO.:551
	R ATGGACCAGATGGTGGAAAT	SEQ ID NO.:552
DIK4862	F CTTTCCCATCCTTTCACCAA	SEQ ID NO.:553
	R AAGTAGGGTGTGTGGGGGTA	SEQ ID NO.:554
BMC2208	F GTTGAGCAGGGGGTAACAAG	SEQ ID NO.:555
	R ACGAGTCCCTGCTGCTCTAC	SEQ ID NO.:556

0.5 µl PCR-product is added to 9.5 µl formamide and analysed on an ABI-3730XL sequencing Instrument (Applied Biosystems Inc.).

Phenotype data

The calving traits considered were stillbirth (SB), calving difficulty (CD) and the size of calf at birth (CS) after first calving. The traits were assessed both as a "direct' effect (D) of the sire in the calf and as a "maternal" effect (M) of the sire in the mother of the calf, giving a total of 6 traits for the QTL analysis. Breeding values for each trait were obtained from the Danish Agricultural Advisory Service database. The breeding values were obtained from the routine breeding value estimation procedure by the exception that information from correlated traits and pedigree information were ignored.

Statistical Analysis

The calving traits were analyzed using the linear regression mapping procedure of Haley & Knott (1992). Significant QTL were found by using permutation tests developed by Churchill & Doerge (1994). In this procedure traits and chromosomes were analyzed separately and tested for the presence of a single QTL affecting a particular trait. If the test: (1) exceeds the 5% chromosome-wise significance threshold and (2) the QTL-region affecting two or more traits, then the QTL is retained for further characterization. The variance component QTL mapping approach was used to test if it is a single pleiotropic QTL affecting two traits or two linked QTL affecting different traits. The QTL is modeled as a random effect in a bivariate linear mixed model that adjusts for polygenenic and overall trait means. The IBD matrices were computed using a recursive algorithm (Sørensen et al., 2003, Wang et al., 1995), conditional on the most likely marker linkage phase in the sire. The IBD matrices were computed for every 2 cM along the chromosomes and used in the subsequent variance component estimation procedure.

Baysian information criterion (BIC) and correlation between the QTL (r_q) were used to compare the pleiotropic and linked model.

Example 1

The chromosome-wise regression test (table 24) showed a total of 27 significant QTL for calving traits in first lactation on 17 different chromosomes. 15 of the QTL were related to direct calving ease and 12 QTL was related to the maternal effects.

Average number of informative markers per grandsire family varied from 3.0 (BTA25) to 8.5 (BTA3) informative markers per chromosome.

Table 24

Chromosome wise regressions analysis across families for calving traits after first calving. QTL are shown for traits that exceed 5 % chromosome wise threshold level. Numbers of segregating families are shown in brackets for each trait and chromosome.

BTA	Inform. Level	D_CD	D_SB	D_CS	M_CD	M_SB	M_CS
BTA3	8.5[a] (34)[b]		0.010[c] (5)[d]				
BTA4	5.0 (19)	0.023 (3)					
BTA7	6.4 (34)		0,003 (6)	0,042 (5)			
BTA8	3.6 (34)	0.042 (2)				0.030 (3)	
BTA9	6.0 (19)						0.027 (3)
BTA10	6.1 (34)				0,035 (3)		
BTA12	5.1 (19)		0.031 (1)			0.028 (2)	
BTA15	6.5 (34)			0,02 (3)			
BTA18	7.0 (34)	0.010 (5)	0.026 (4)	0 (4)		0.015 (7)	
BTA19	5.2 (19)			0.007 (3)			
BTA20	3.5 (19)			0.005 (5)			
BTA21	5.3 (34)				0.044 (2)		
BTA22	4.1 (19)			0.010 (2)			0.029 (3)
BTA24	4.6 (19)					0.041 (2)	
BTA25	3.0 (19)	0.006 (2)		0.002 (4)			
BTA26	4.7 (34)		0.021 (3)			0.00 (7)	
BTA28	3.5 (33)				0.025 (3)	0.045 (0)	

D_CD: direct calving difficulty, D_SB: direct stillbirth, D_CS: direct calf size, M_CD: maternal calving difficulty, M_SB: maternal stillbirth, M_CS: maternal calf size.

[a]: numbers of informative markers, [b] : number of analyzed grandsires, [c] : p-values

Each QTL was detected significant in 0 to 7 Holstein families when the test was performed within family analysis. BTA 28 showed no significant families for M_SB, but four families were candidates to significance ($p<0.10$).

Seven chromosomes showed more than one significant QTL in the same region and were further examined for the presence of pleiotropic or linked QTL. Only BTA 18 showed more than two significant QTL.

Example 2

Table 25 shows results of tests to distinguish between pleiotropic and linked QTL. Two regions (BTA 12, BTA25) indicate QTL with pleiotropic effects with strong correlations

between the traits (close to 1 or –1). For BTA7 and BTA26 the linkage model is in favor with correlations closer to 0 and high BIC-values. The analysis on BTA22 and BTA28 could not clarify whether it is linked or pleiotropic QTL. BTA8 did not give useful results because the likelihood did not converge to a maximum. On BTA 18 there may be a pleiotropic QTL affecting all the direct calving traits and probably one QTL affecting maternal stillbirth (M_SB).

Table 25

Multi-trait analysis with pleiotropic and linked QTL models for calving traits on BTA 7, 8, 12, 18, 22, 25, 26, and 28 where QTL were identified for more than one calving trait in first lactation.

BTA		r_q	Dist (cM)	No. markers[a]	Bayes factor[b]
BTA7	D_SB, D_CS	0.35	26	1.15	0.3
BTA8	D_CD, M_SB	NC	38	1.12	NC
BTA12	D_SB, M_SB	0.99	4	0	27
BTA18	D_CD, D_SB	0.87	0	0	27
	D_CD, D_CS	0.93	0	0	109848
	D_CD, M_SB	0.71	14	1.15	0.7
	D_SB, D_CS	0.95	0	0	1806411
	D_SB, M_SB	NC	14	1.15	NC
	D_CS, M_SB	0.49	14	1.15	0.7
BTA22	D_CS, M_SB	0.72	14	0.68	3.7
BTA25	D_CD, D_CS	1.00	0	0	548
BTA26	D_SB, M_SB	0.1	10	0.32	0.13
BTA28	M_CD, M_SB	0.78	10	0.39	3.7

D_CD: direct calving difficulty, D_SB: direct stillbirth, D_CS: direct calf size, M_CD: maternal calving difficulty, M_SB: maternal stillbirth, M_CS: maternal calf size.

[a] : average number of informative markers between QTL, [b] : probability of a pleiotropic model over the linked model

Several QTL affecting both direct and maternal calving traits were identified. The QTL for D_CD on BTA8 confirmed the result in Ashwell et al (2003) and the QTL for direct and maternal stillbirth on BTA7 and BTA18 confirmed the results in Kühn et al (2003). The multi-trait and multiple QTL variance component approach detected two pleiotropic QTL affecting both direct calving size and calving difficulties, and two pleiotropic QTL

affecting both direct and maternal stillbirth. The identified QTL could have important implications for the Danish Holstein breeding program because of relative high economic weight in the combined selection index. In particular, QTL affecting survival and stillbirth without affecting calf size will be an efficient way to improve genetic progress for calving traits. More marker information is needed to get a more precise characterization of the QTL, before it can be used for effective selection purposes.

Claims

1. A method of determining calving characteristics in a bovine subject, comprising detecting in a sample from said bovine subject the presence or absence of at least one genetic marker that is linked to at least one trait indicative of increased risk of stillbirth and/or increased risk of calving difficulties and/or increased risk of non-desired calf size, wherein said at least one genetic marker is located on the bovine chromosome BTA3 in a region flanked by and including polymorphic microsatellite markers INRA006 and BM7225 and/or
BTA4 in the region flanked by and including polymorphic microsatellite markers BMS1788 and MGTG4B and/or,
BTA5 in the region flanked by and including polymorphic microsatellite markers BMS1095 and BM2830 and/or,
BTA7 in a region flanked by and including polymorphic microsatellite markers BM7160 and BL1043 and/or,
BTA8 in a region flanked by and including polymorphic microsatellite markers IDVGA-11 and BMS836 and/or,
BTA9 in a region flanked by and including polymorphic microsatellite markers BMS2151 and BMS1967 and/or,
BTA10 in a region flanked by and including polymorphic microsatellite markers DIK2658 and BMS2614 and/or,
BTA11 in the region flanked by and including polymorphic microsatellite markers BM716 and HEL13 and/or,
BTA12 in a region flanked by and including polymorphic microsatellite markers BMS410 and BMS2724 and/or,
BTA15 in a region flanked by and including polymorphic microsatellite markers BR3510 and BMS429 and/or,
BTA18 in a region flanked by and including polymorphic microsatellite markers IDVGA-31 and DIK4013 and/or,
BTA19 in a region flanked by and including polymorphic microsatellite markers BM9202 and BMS601 and/or,
BTA20 in a region flanked by and including polymorphic microsatellite markers BM3517 and UWCA26 and/or,
BTA21 in a region flanked by and including polymorphic microsatellite markers DIK5182 and IDVGA-30 and/or,

BTA22 in a region flanked by and including polymorphic microsatellite markers CSSM26 and BM4102 and/or,

BTA24 in a region flanked by and including polymorphic microsatellite markers BMS917 and BMS3024 and/or,

BTA25 in a region flanked by and including polymorphic microsatellite markers ILSTS102 and AF5 and/or,

BTA26 in a region flanked by and including polymorphic microsatellite markers BMS651 and BM7237 and/or,

BTA28 in a region flanked by and including polymorphic microsatellite markers, BMC6020 and BMC2208, , wherein the presence of said at least one genetic marker is indicative of calving characteristics of said bovine subject and/or off-spring therefrom.

1. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA3 in the region from about 17.1 to 101.8 cM, or between genetic markers INRA006 and BM7225.
2. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA4 in the region from about 12.5 to 112.8 cM, or between genetic markers BMS1788 and MGTG4B.
3. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA5 in the region from about 0.0 to 116.9 cM, or between genetic markers BMS1095 and BM2830
4. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA7 in the region from about 0.0 to 135.6 cM, or between genetic markers BM7160 and BL1043.
5. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA8 in the region from about 11.3 to 122.9 cM, or between genetic markers IDVGA-11 and BMS836.
6. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA9 in the region from about 8.49 to 109.3 cM, or between genetic markers BMS2151 and BMS1967.
7. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA10 in the region from about 2.7 to 109.4 cM, or between genetic markers DIK2658 and BMS2614.

8. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA11 in the region from about 19.4 to 122.4 cM, or between genetic markers BM716 and HEL13.
9. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA12 in the region from about 0.0 to 109.0 cM, or between genetic markers BMS410 and BMS2724.
10. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA15 in the region from about 9.4 to 109.8 cM, or between genetic markers BR3510 and BMS429.
11. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA18 in the region from about 0.0 to 84.4 cM, or between genetic markers IDVGA-31 and DIK4013.
12. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA19 in the region from about 0.0 to 108.0 cM, or between genetic markers BM9202 and BMS601.
13. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA20 in the region from about 0.0 to 77.1 cM, or between genetic markers BM3517 and UWCA26.
14. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA21 in the region from about 5.5 to 76.8 cM, or between genetic markers DIK5182 and IDVGA-30.
15. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA22 in the region from about 0.0 to 82.9 cM, or between genetic markers CSSM26 and BM4102.
16. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA24 in the region from about 6.2 to 65.9 cM, or between genetic markers BMS917 and BMS3024.
17. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA25 in the region from about 7.2 to 61.7 cM, or between genetic markers ILSTS102 and AF5.
18. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA26 in the region from about 2.8 to 66.8 cM, or between genetic markers BMS651 and BM7237.

19. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA28 in the region from about 8.0 to 59.6 cM, or between genetic markers BMC6020 and BMC2208.
20. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA3 in the region from about 32.6 to 59.4 cM, or between genetic markers DIK4403 and INRA003.
21. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA3 in the region from about 77.6 to 101.8 cM, or between genetic markers DIK2702 and BM7225.
22. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA4 in the region from about 43.2 to 91.2 cM, or between genetic markers BMS2646 and BMS648.
23. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA4 in the region from about 52.5 to 73.4 cM, or between genetic markers TGLA116 and BM8233.
24. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA5 in the region from about 18.3 to 56.3 cM, or between genetic markers DIK4747 and BMS1617.
25. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA5 in the region from about 45.5 to 82.9 cM, or between genetic markers CSSM034 and BMS1248.
26. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA7 in the region from about 30.2 to 55.3 cM, or between genetic markers DIK5412 and DIK4606.
27. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA7 in the region from about 77.2 to 116.6 cM, or between genetic markers BMS2258 and ILSTS006.
28. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA8 in the region from about 41.6 to 66.0 cM, or between genetic markers BMS678 and BMS2072.
29. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA8 in the region from about 71.1 to 122.9 cM, or between genetic markers MCM64 and BMS836.

30. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA9 in the region from about 12.8 to 64.9 cM, or between genetic markers ETH225 and BMS1290.

31. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA9 in the region from about 50.0 to 79.2 cM, or between genetic markers UWCA9 and bms2753.

32. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA10 in the region from about 11.0 to 37.5 cM, or between genetic markers CSSM38 and DIK2000.

33. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA10 in the region from about 44.3 to 74.0 cM, or between genetic markers BMS2742 and TGLA433.

34. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA10 in the region from about 87.5 to 109.4 cM, or between genetic markers BMS2641 and BMS2614.

35. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA11 in the region from about 19.4 to 50.3 cM, or between genetic markers BM716 and BM7169.

36. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA11 in the region from about 61.6 to 92.2 cM, or between genetic markers BM6445 and BMS989.

37. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA12 in the region from about 50.4 to 109.0 cM, or between genetic markers BM860 and BMS2724.

38. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA12 in the region from about 63.8 to 102.0 cM, or between genetic markers BMS975 and BMS1316.

39. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA15 in the region from about 91.8 to 105.0 cM, or between genetic markers BMS2076 and BMS927.

40. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA15 in the region from about 98.2 to 109.8 cM, or between genetic markers BMS820 and BMS429.

41. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA18 in the region from about 30.2 to 61.2 cM, or between genetic markers INRA121 and DIK4232.
42. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA18 in the region from about 61.2 to 84.4 cM, or between genetic markers DIK4232 and DIK4013.
43. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA19 in the region from about 16.0 to 45.9 cM, or between genetic markers BMS745 and BP20.
44. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA19 in the region from about 47.0 to 90.0 cM, or between genetic markers IDVGA-46 and ETH3.
45. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA20 in the region from about 19.1 to 55.1 cM, or between genetic markers BMS1282 and AGLA29.
46. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA20 in the region from about 55.1 to 77.1 cM, or between genetic markers AGLA29 and UWCA26.
47. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA21 in the region from about 18.3 to 30.0 cM, or between genetic markers DIK2492 and DIK4001.
48. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA21 in the region from about 30.0 to 47.8 cM, or between genetic markers DIK4001 and DIK3036.
49. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA22 in the region from about 2.9 to 47.1 cM, or between genetic markers INRA026 and BM3628.
50. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA22 in the region from about 47.1 to 82.9 cM, or between genetic markers BM3628 and BM4102.
51. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA24 in the region from about 8.2 to 35.5 cM, or between genetic markers BM7151 and BMS1862.

52. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA24 in the region from about 35.5 to 65.9 cM, or between genetic markers BMS1862 and BMS3024.

53. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA25 in the region from about 7.2 to 31.6 cM, or between genetic markers ILSTS102 and BM737.

54. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA25 in the region from about 46.4 to 61.7 cM, or between genetic markers BMS1353 and AF5.

55. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA26 in the region from about 2.8 to 37.6 cM, or between genetic markers BMS651 and RM026.

56. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA26 in the region from about 43.2 to 66.8 cM, or between genetic markers RME40 and BM7237.

57. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA28 in the region from about 24.8 to 50.5 cM, or between genetic markers BL25 and DOK5056.

58. The method according to claim 1, wherein the at least one genetic marker is located in the region of the bovine chromosome BTA28 in the region from about 43.0 to 59.6 cM, or between genetic markers BMS2658 and BMS2208.

59. The method according to claim 1, wherein the at least one marker is a combination of genetic markers.

60. The method according to claim 1, wherein a significance level chromosome wise is at least 5%.

61. A diagnostic kit for use in detecting the presence or absence in a bovine subject of at least one genetic marker associated with bovine calving characteristics, comprising at least one oligonucleotide sequence, wherein the nucleotide sequences are selected from any of SEQ ID NO.: 1 to SEQ ID NO.: 558 and/or any combination thereof.

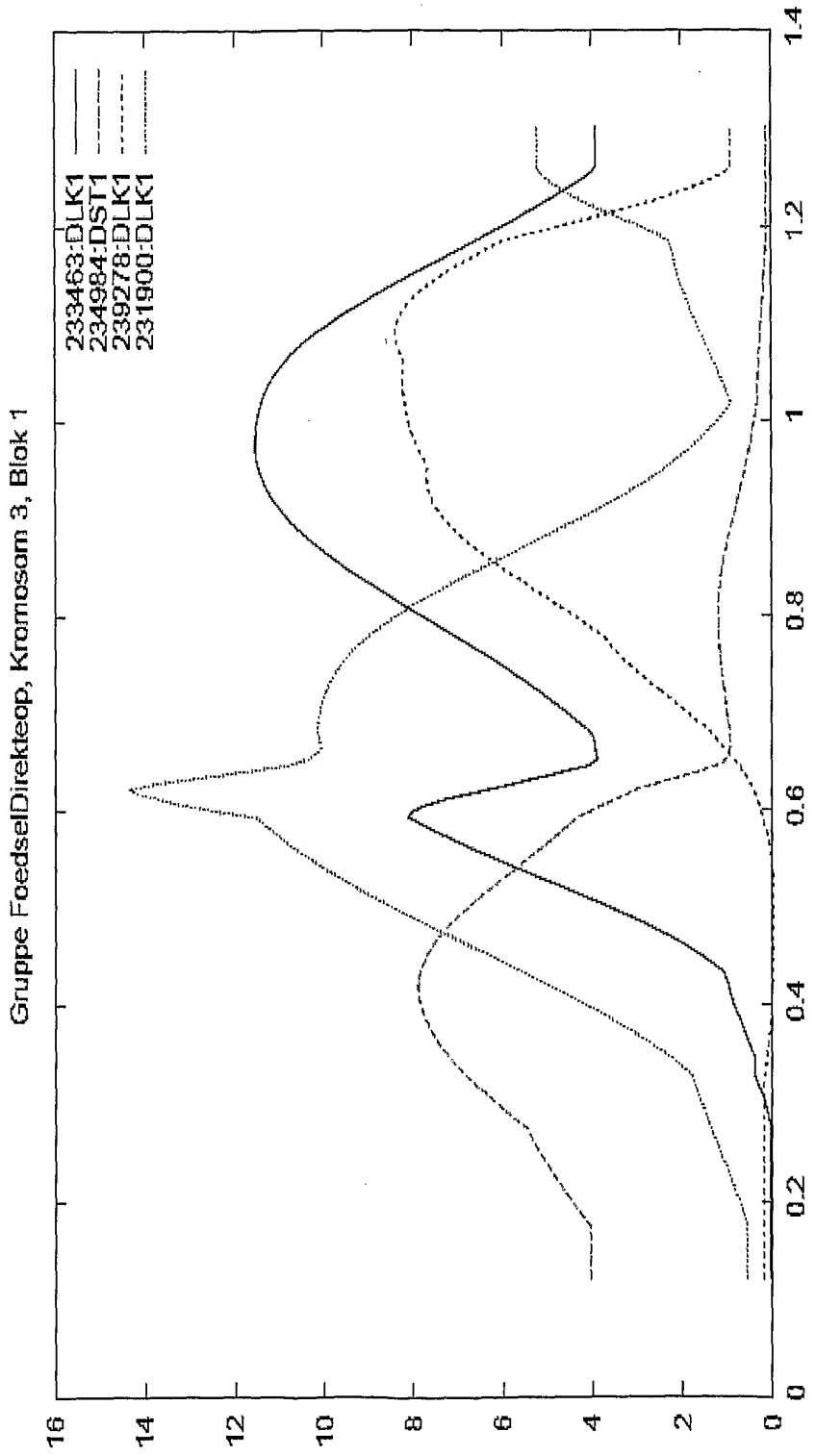

Fig. 1

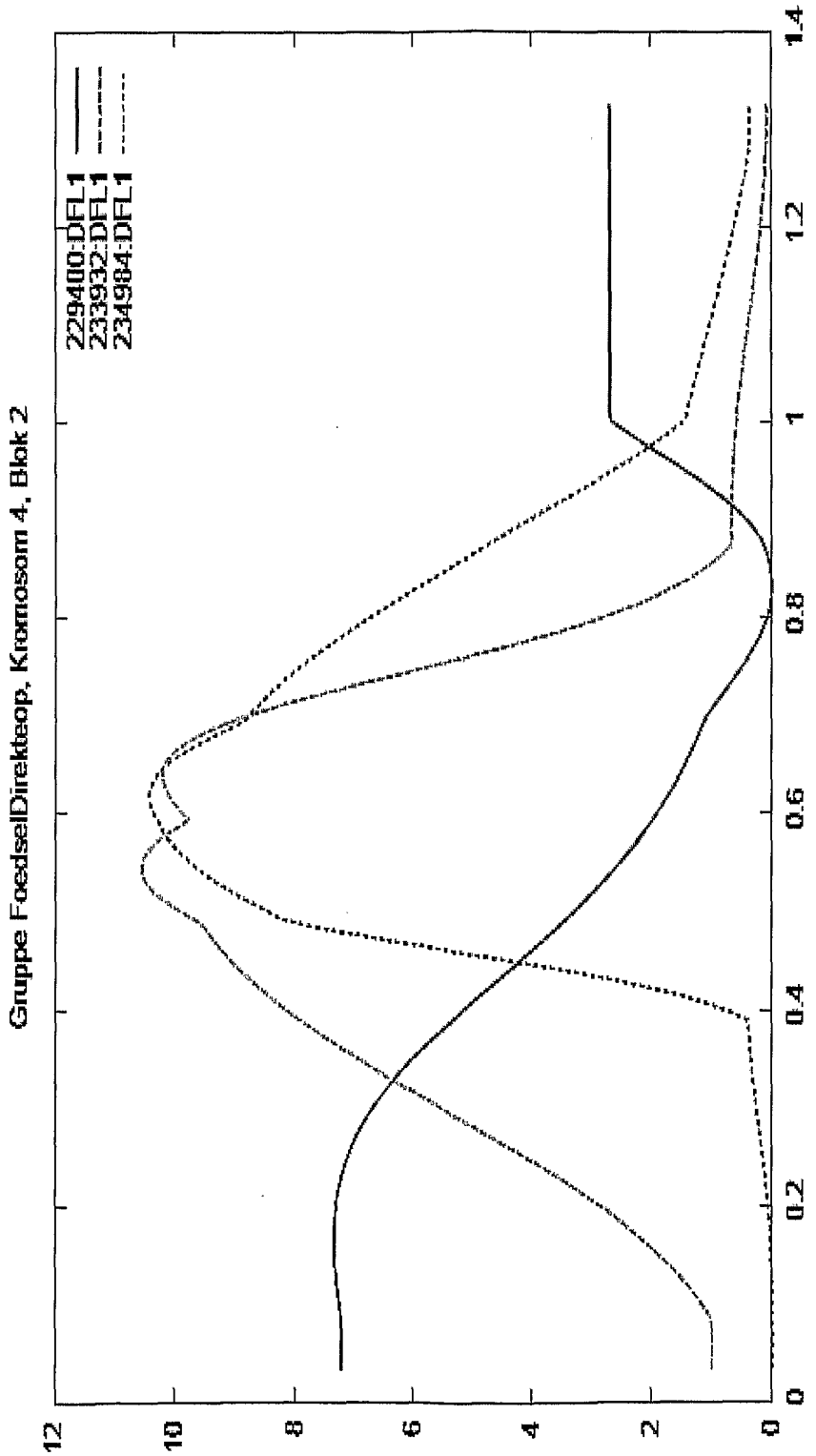

Fig. 2

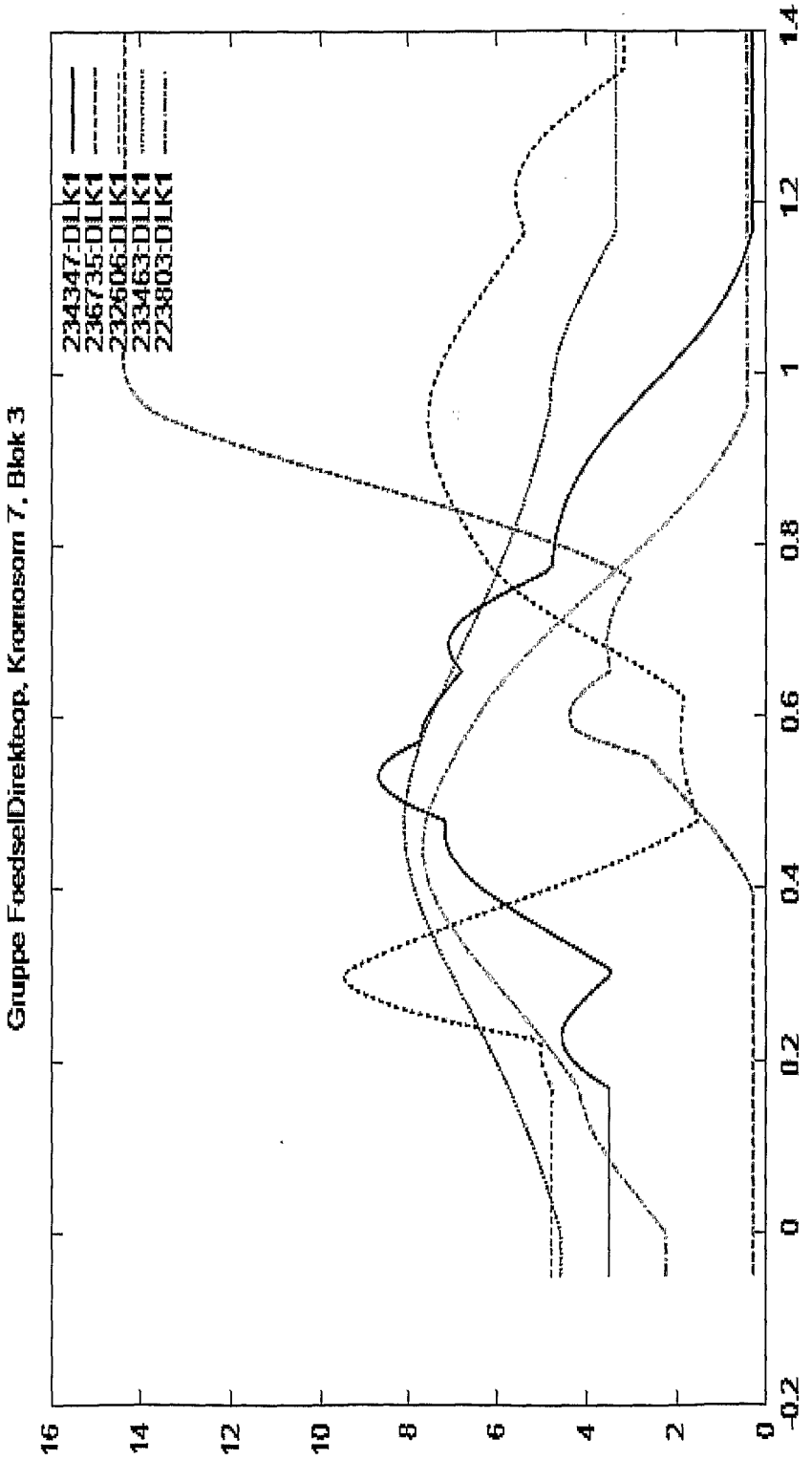

Fig. 3

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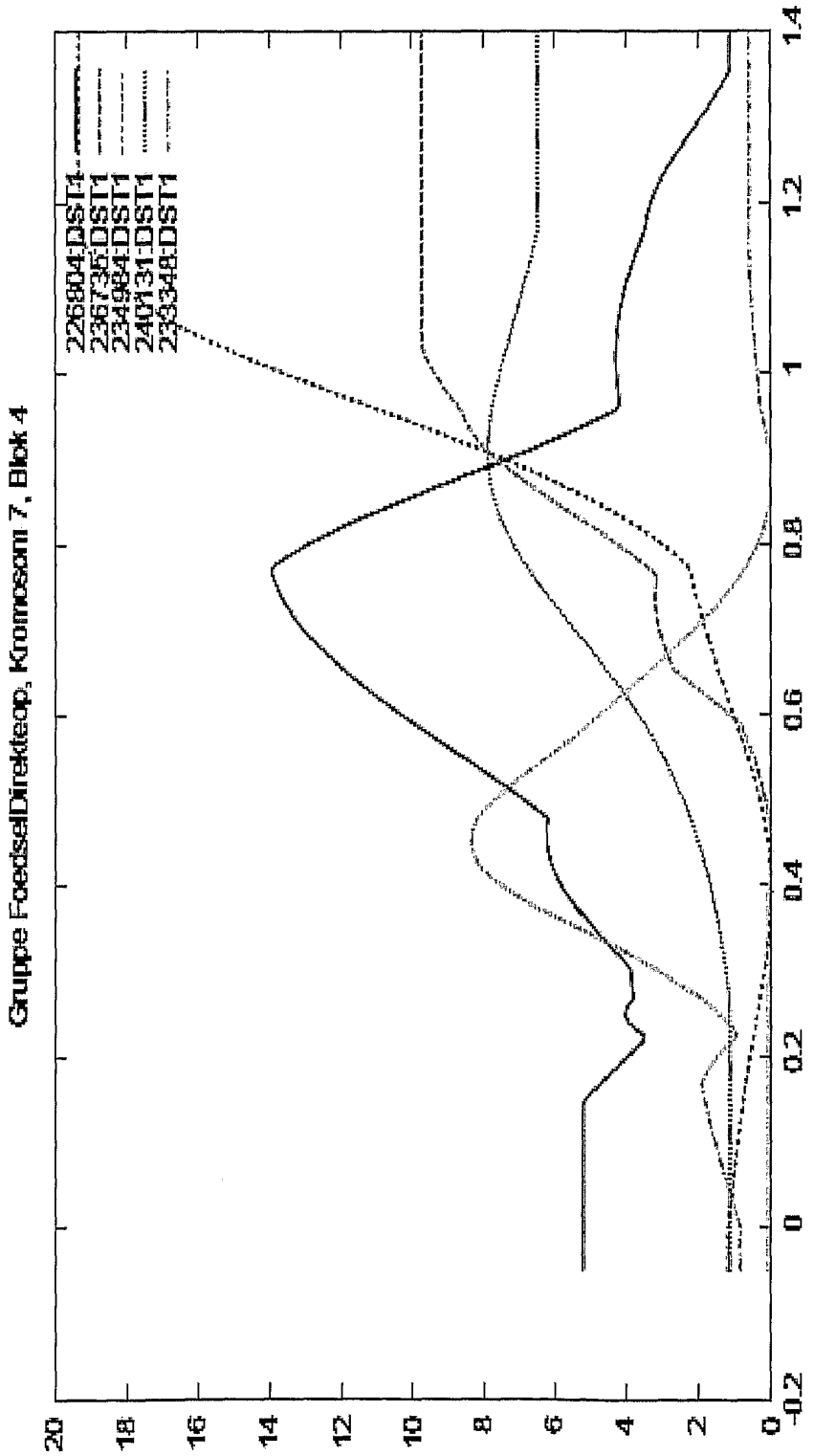

Fig. 4

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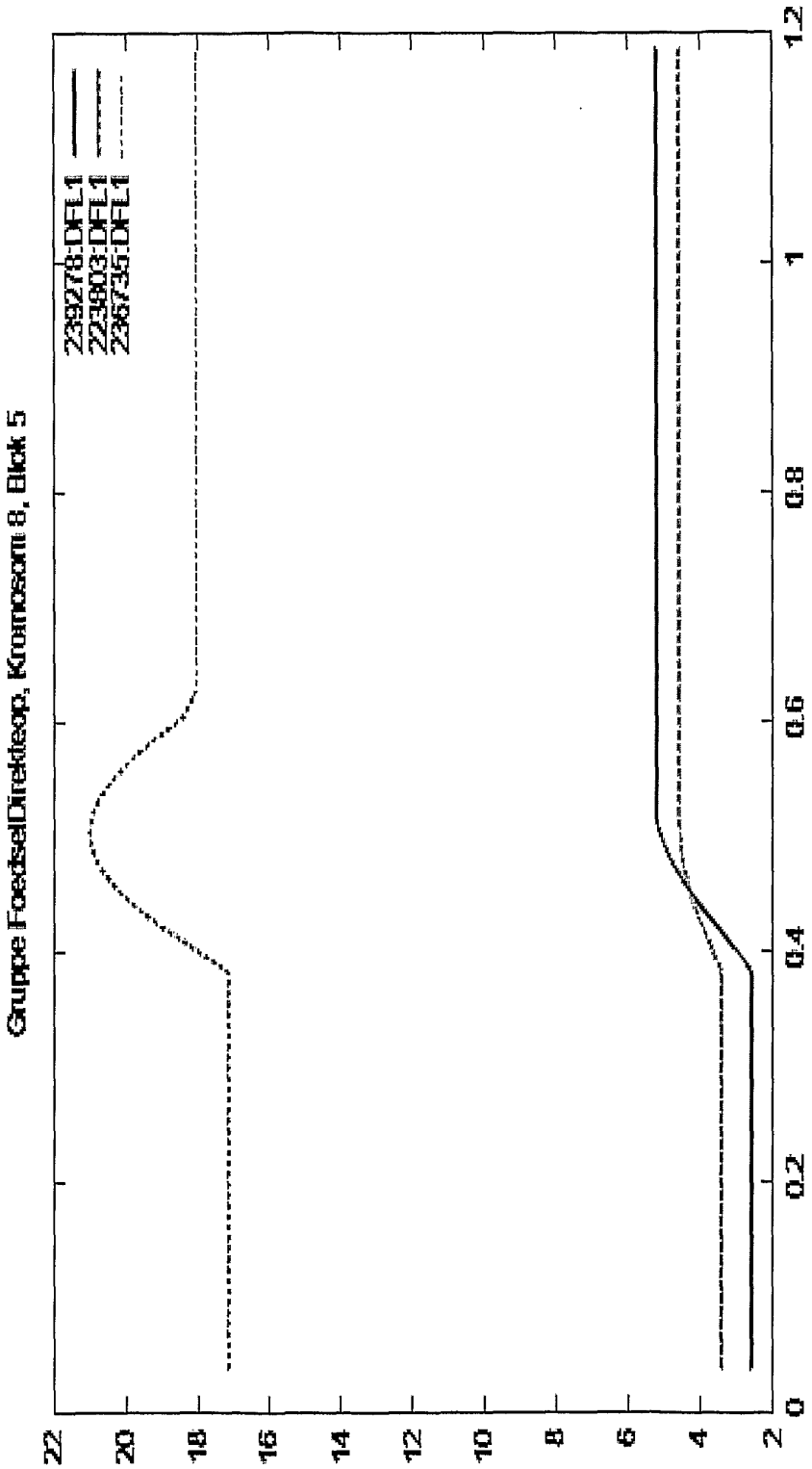

Fig.5

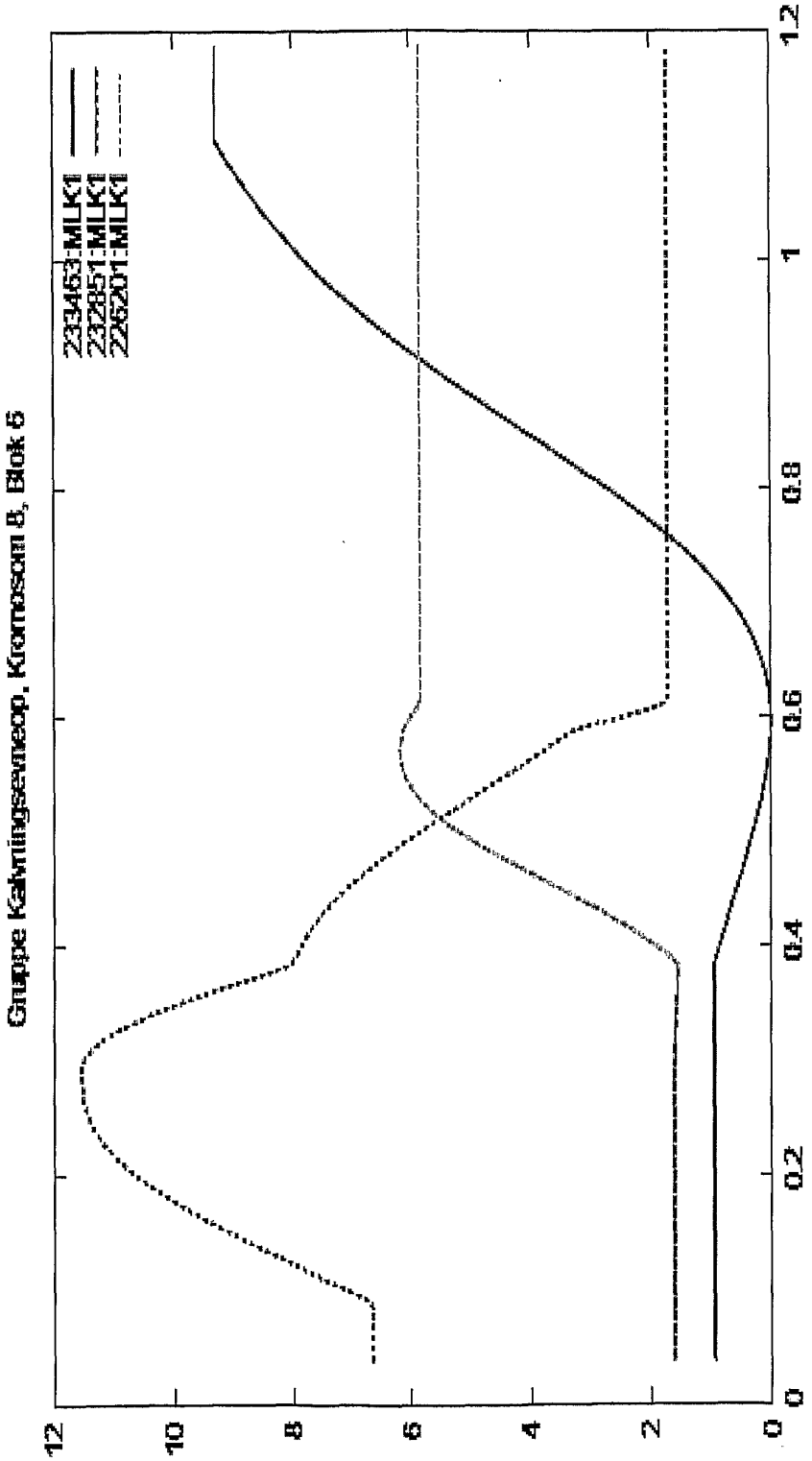

Fig.6

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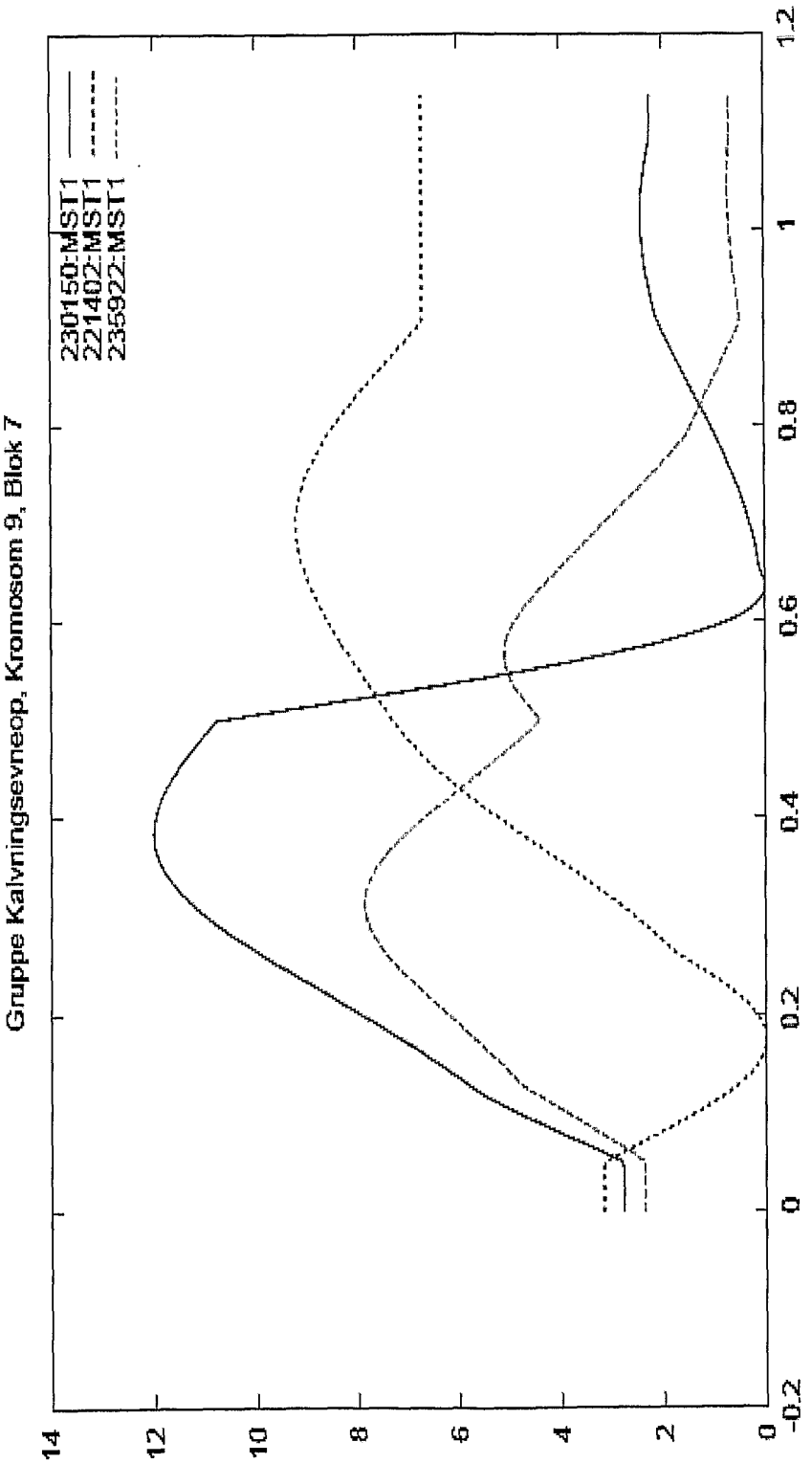

Fig. 7

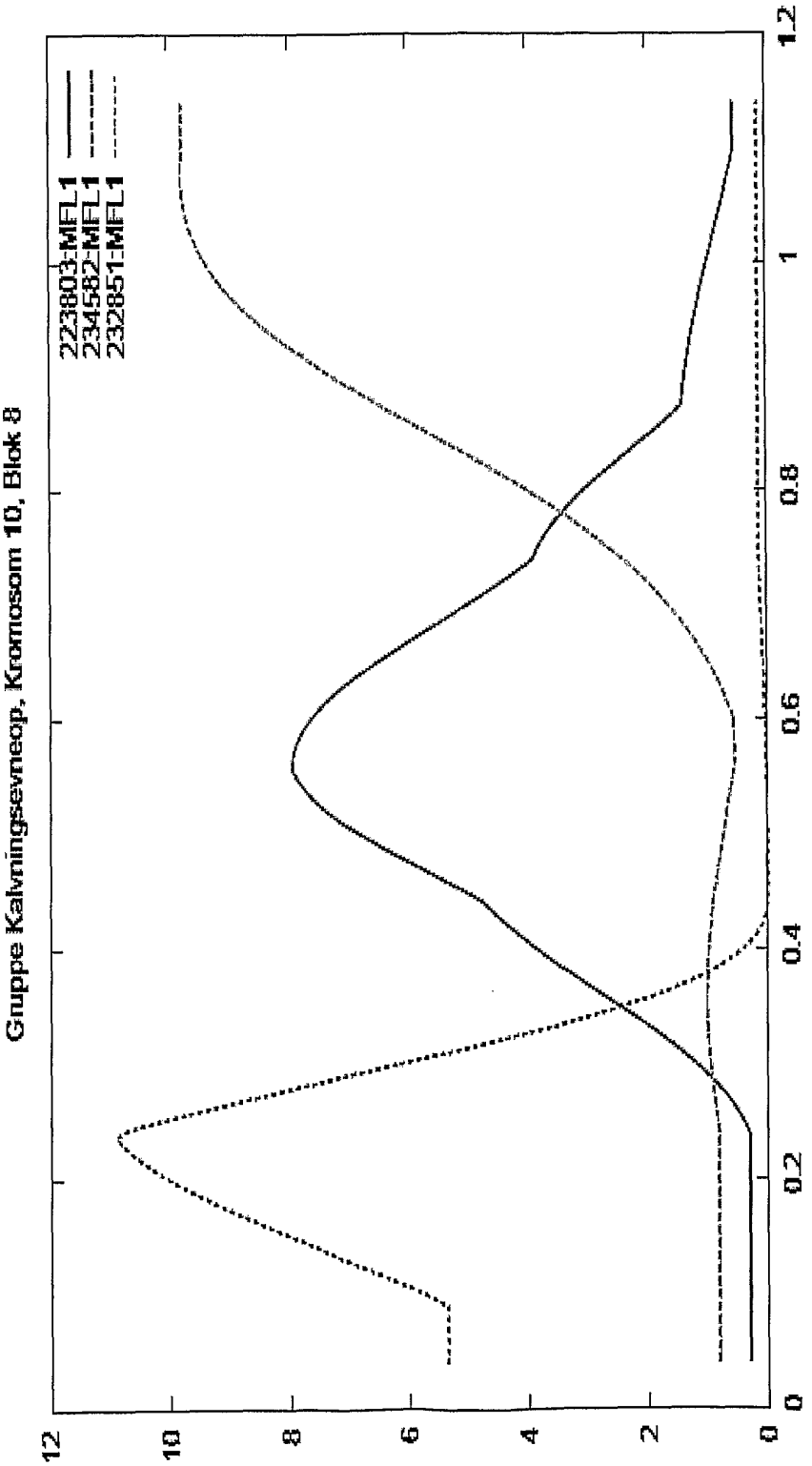

Fig.8

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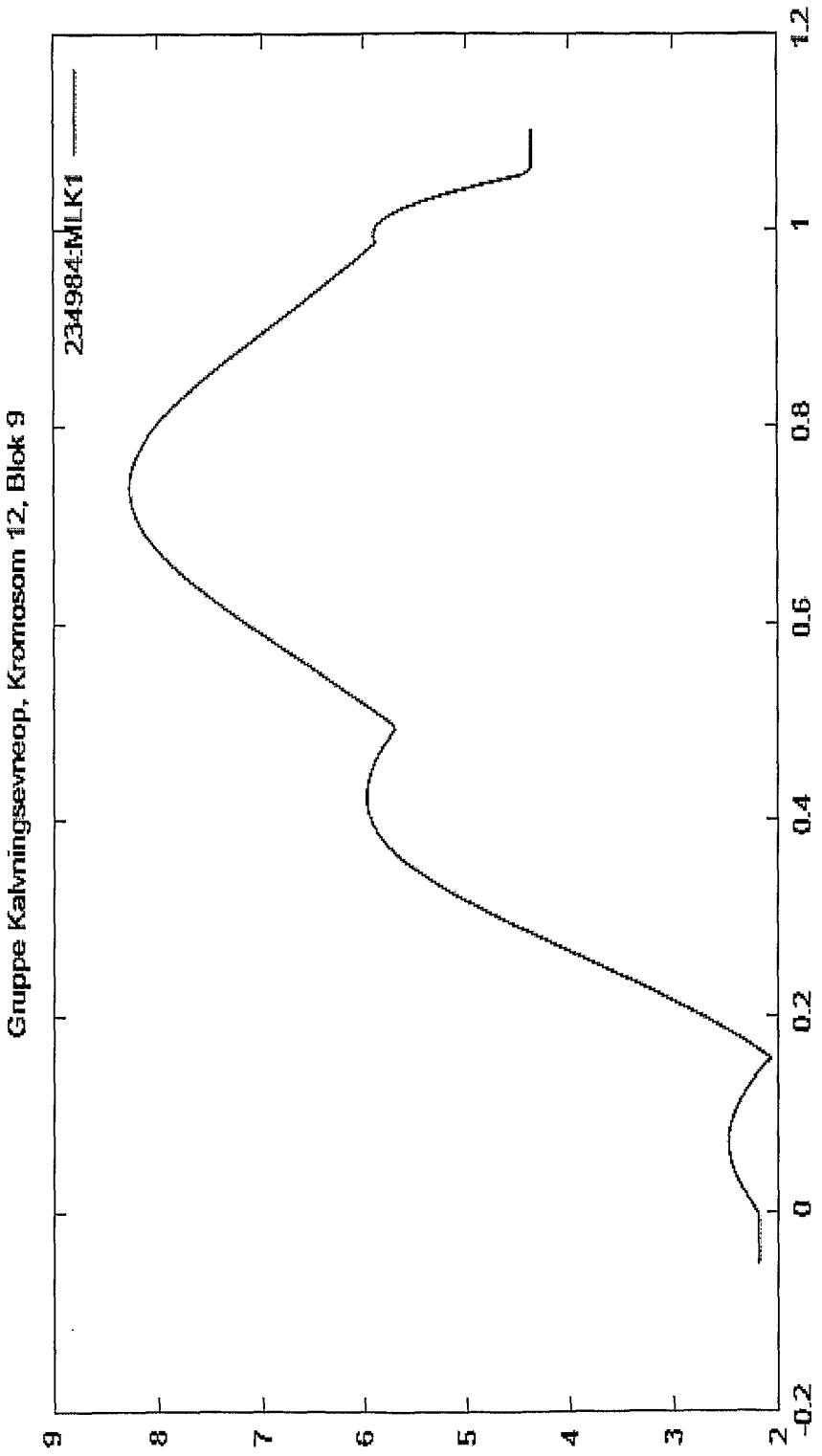

Fig. 9

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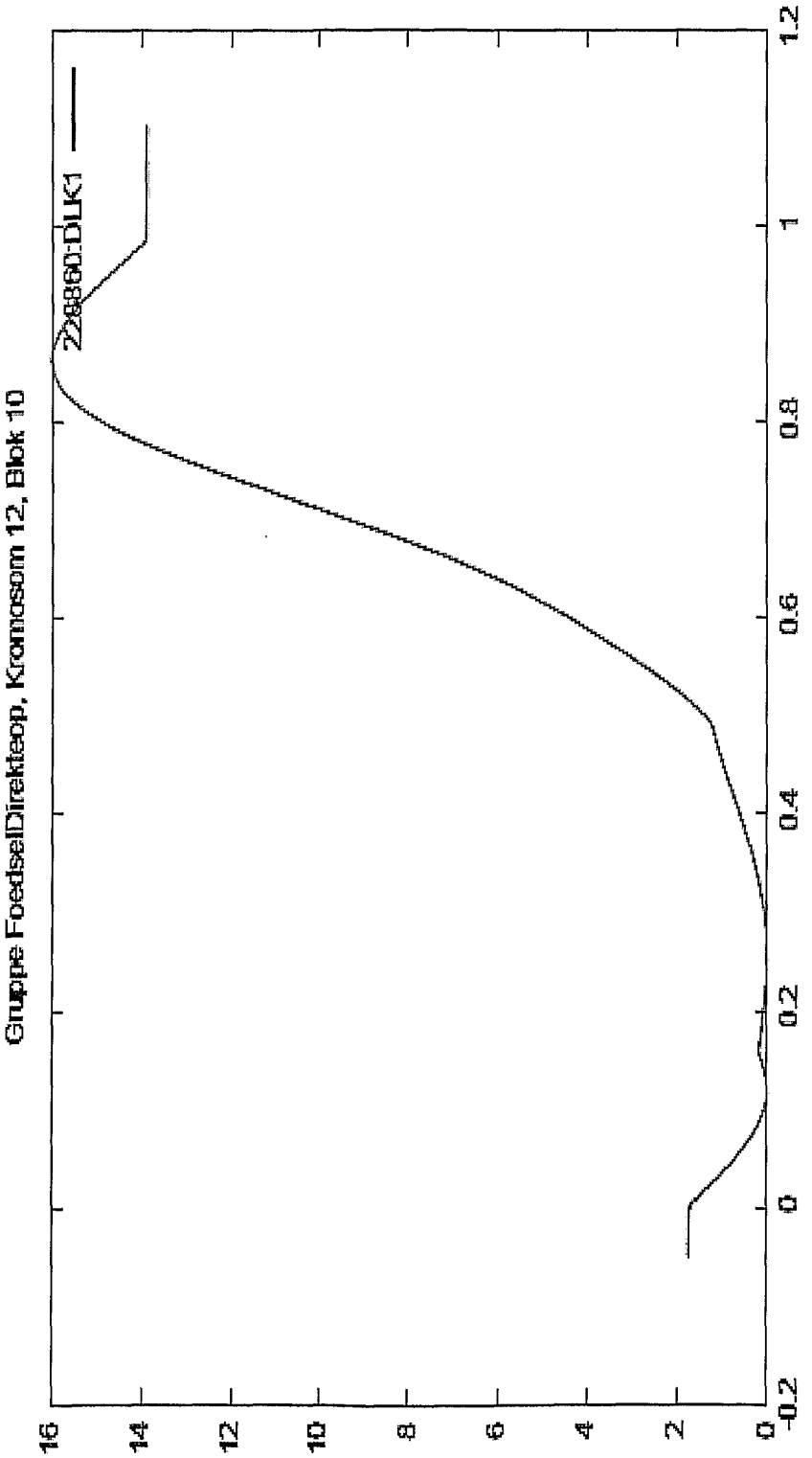

Fig. 10

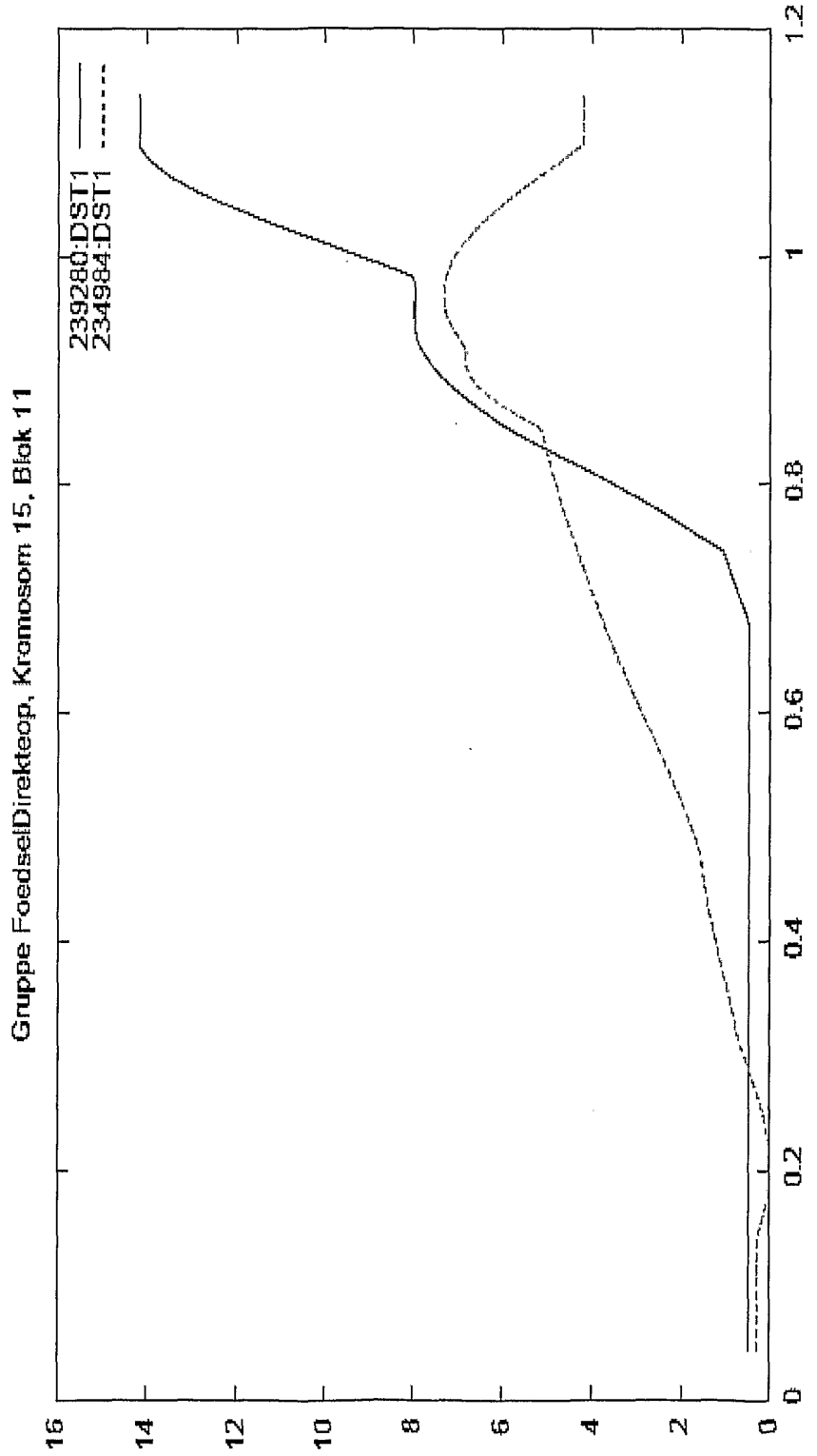

Fig. 11

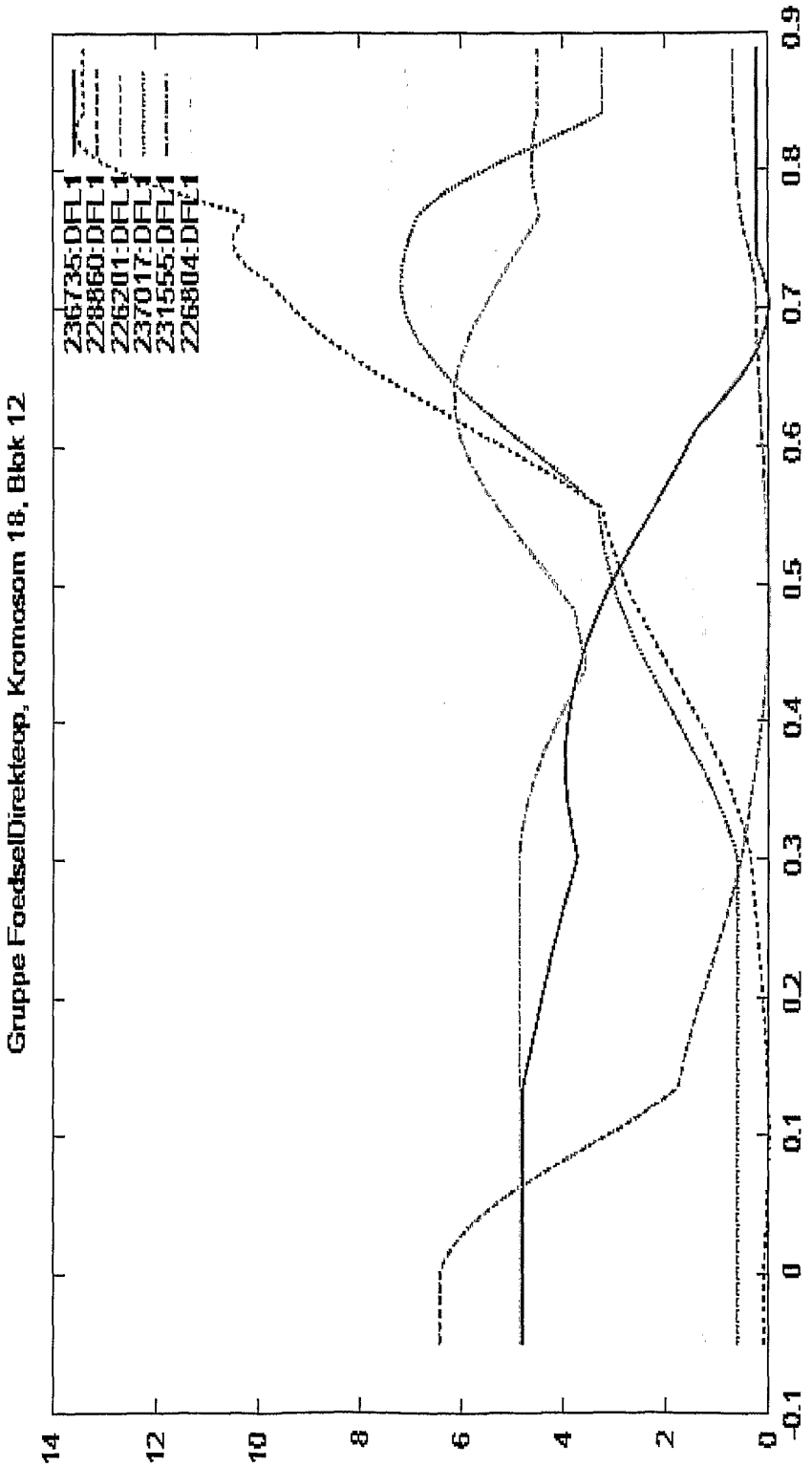

Fig. 12

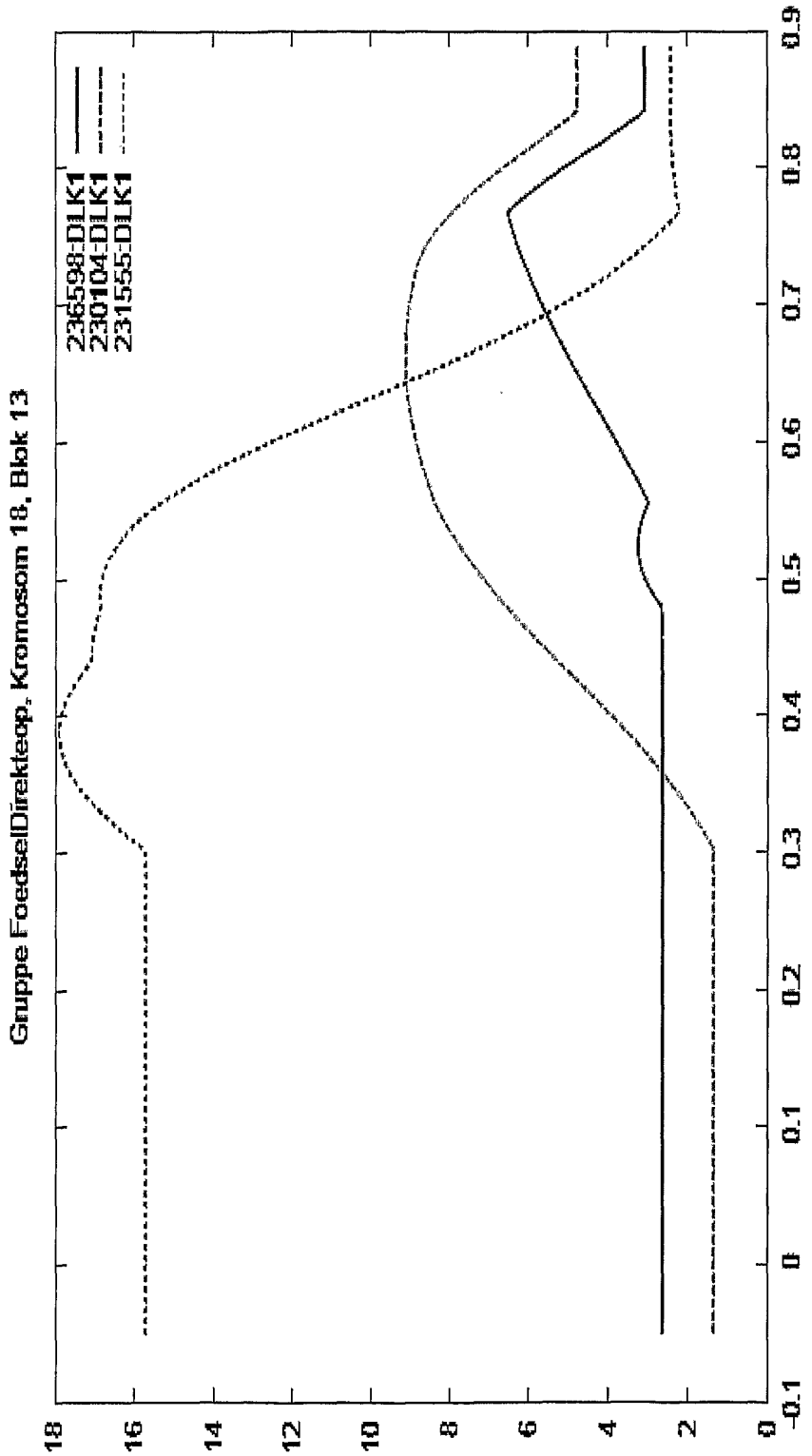

Fig. 13

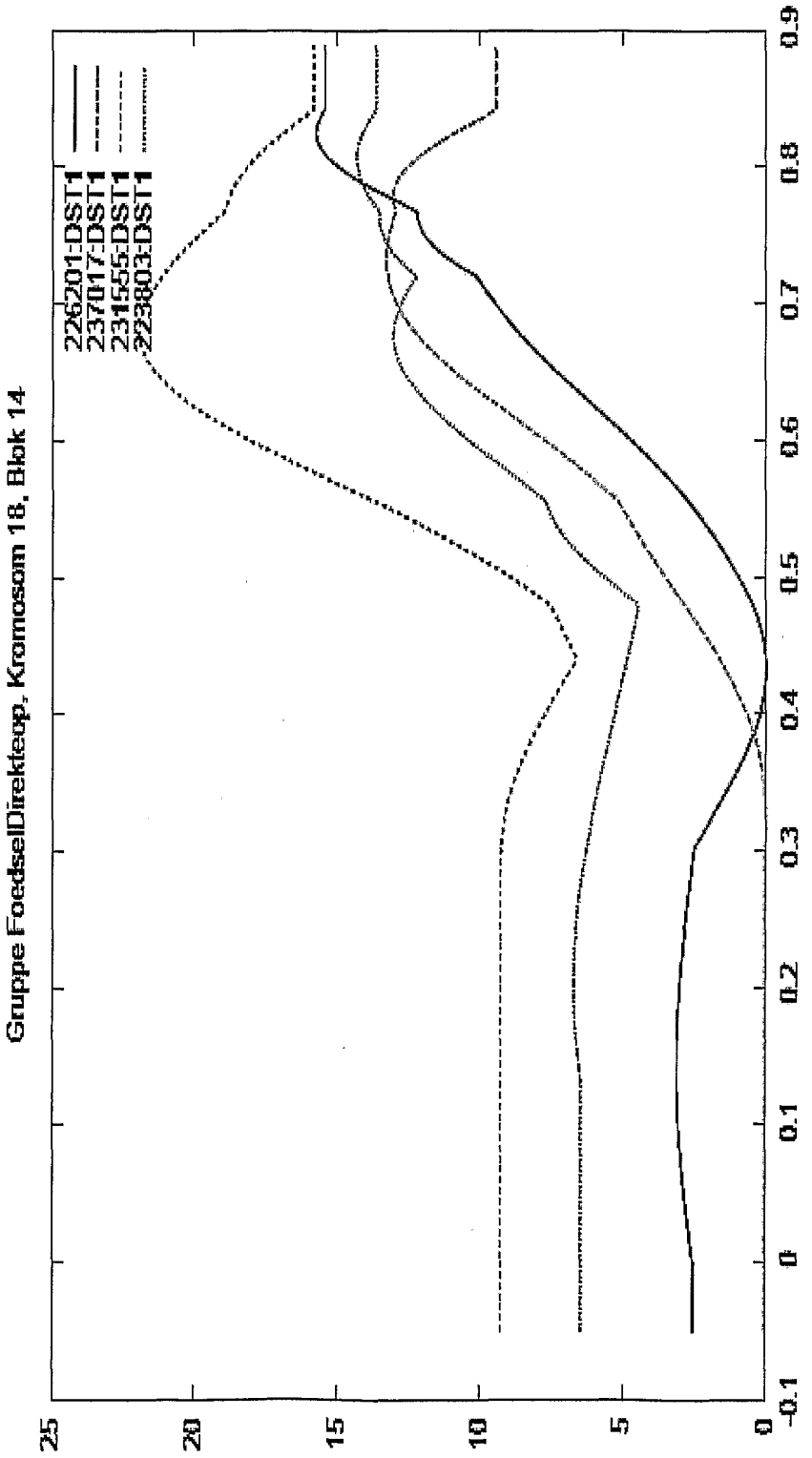

Fig. 14

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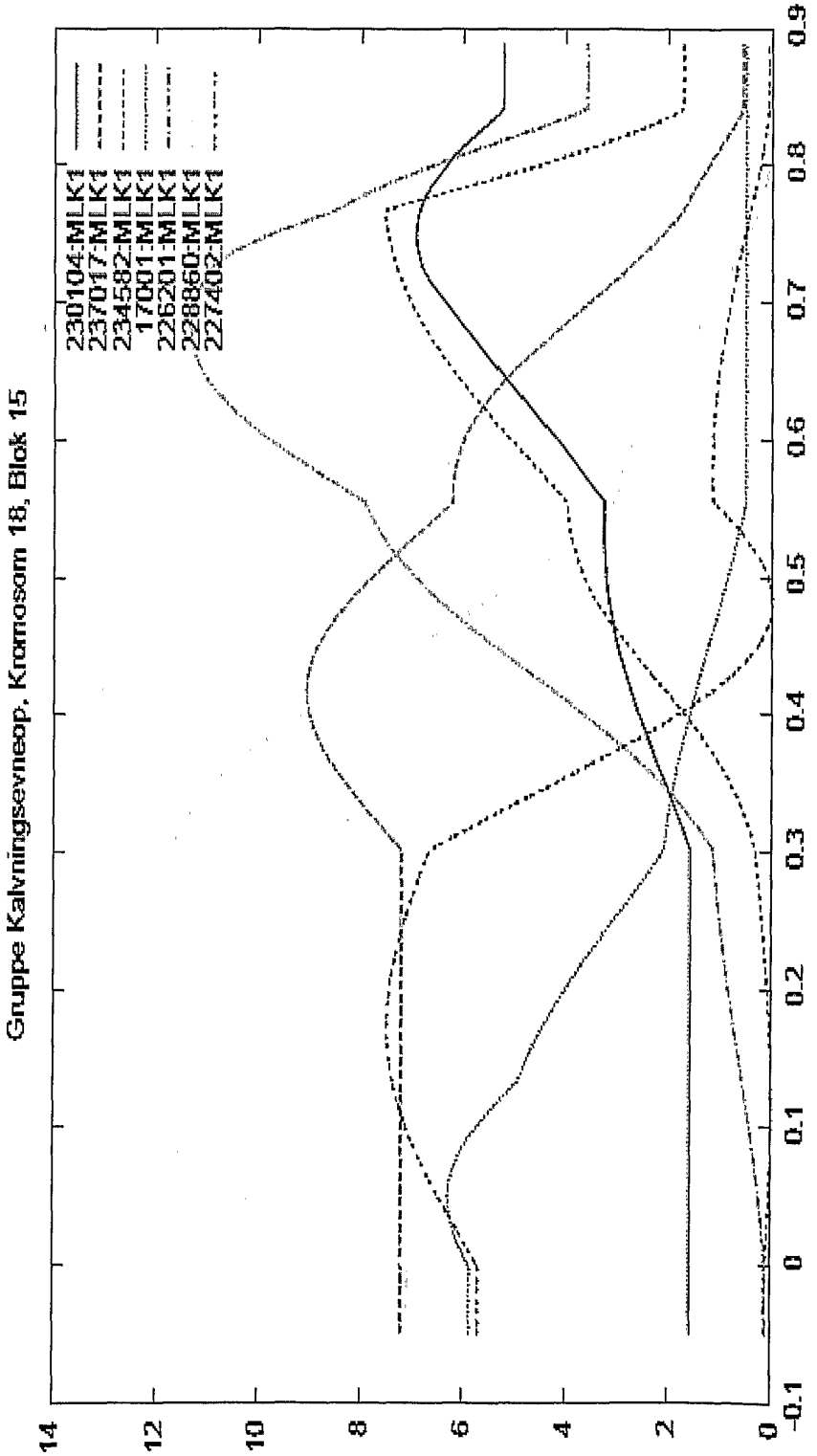

Fig. 15

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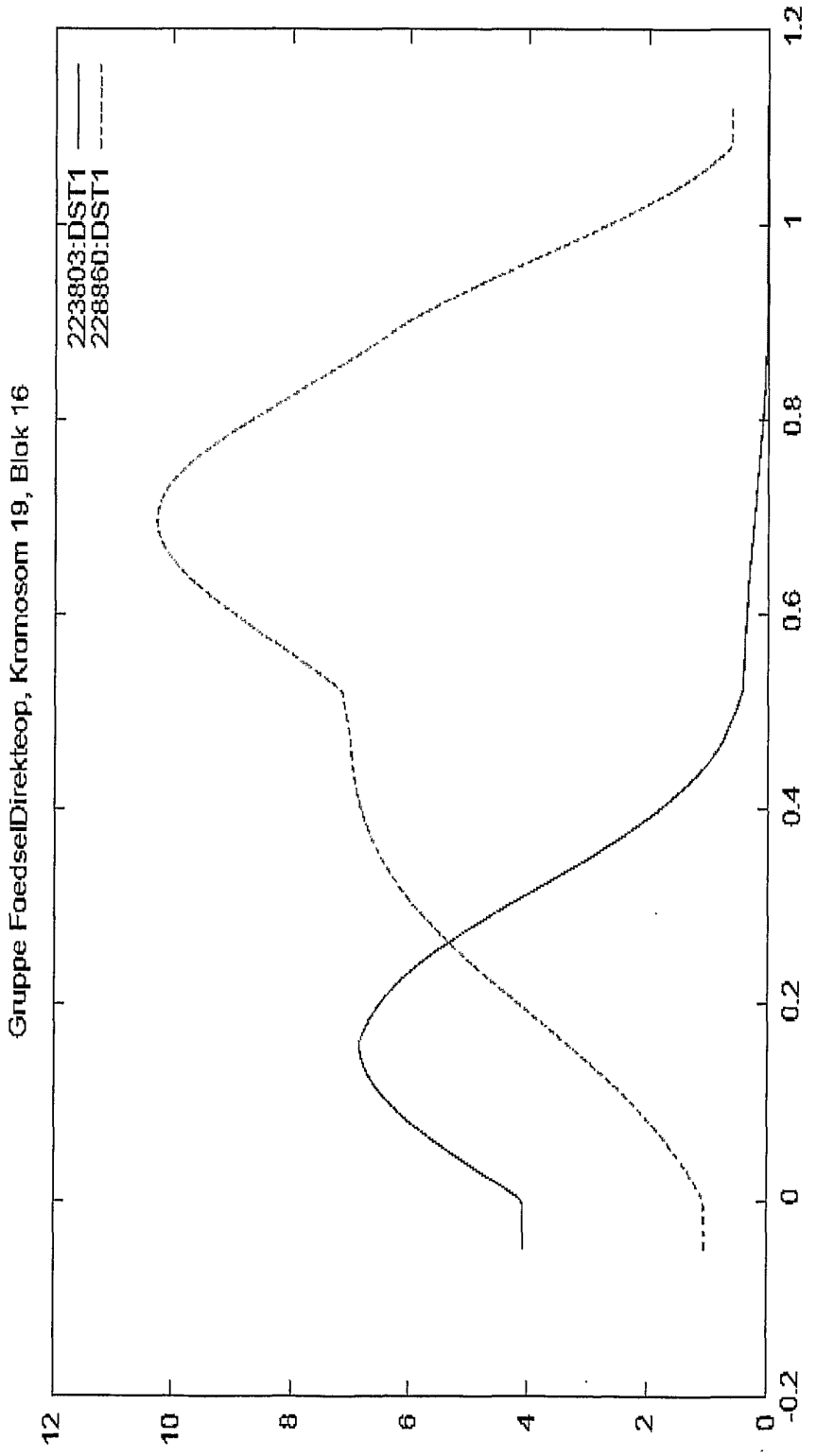

Fig. 16

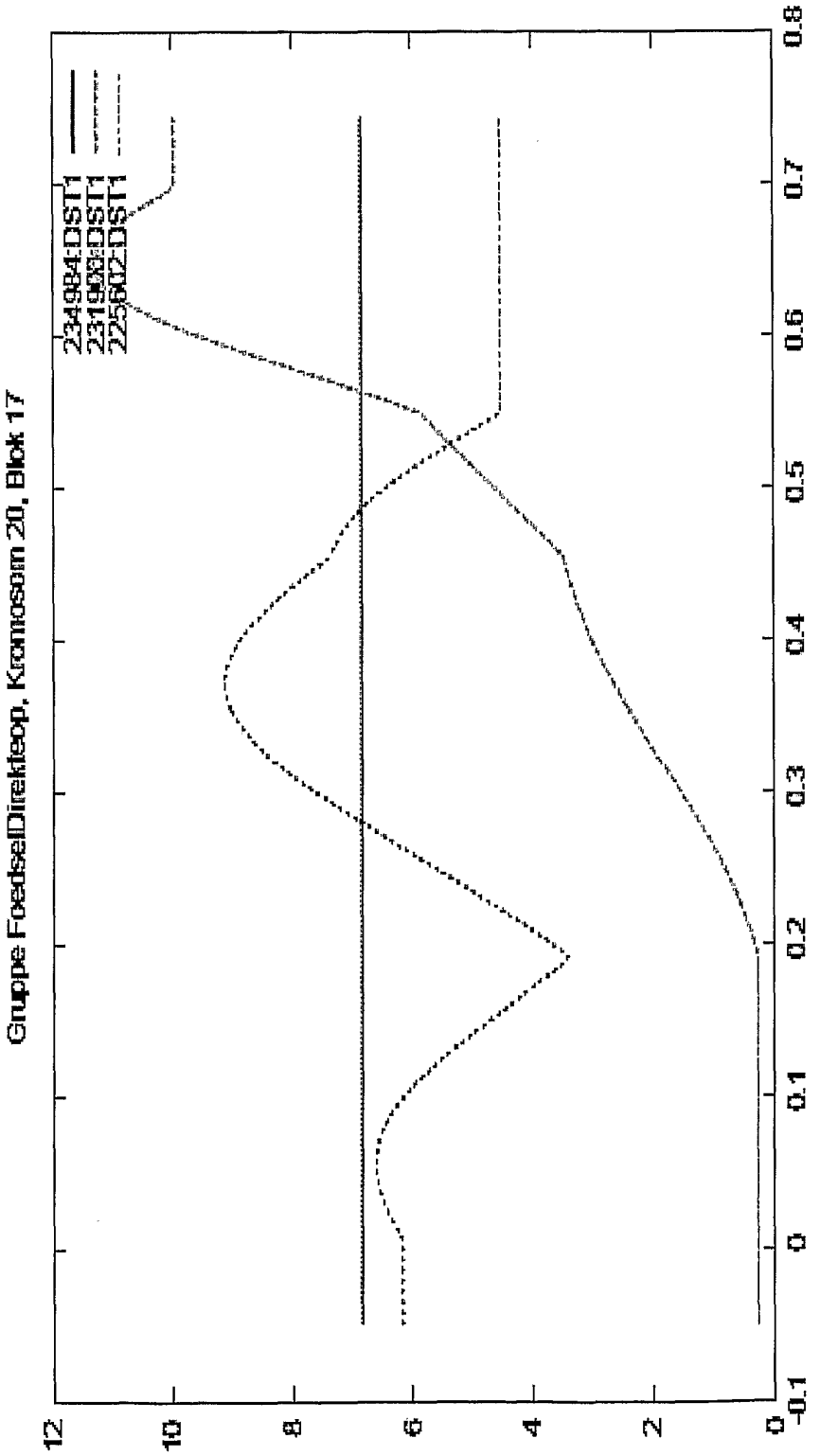

Fig. 17

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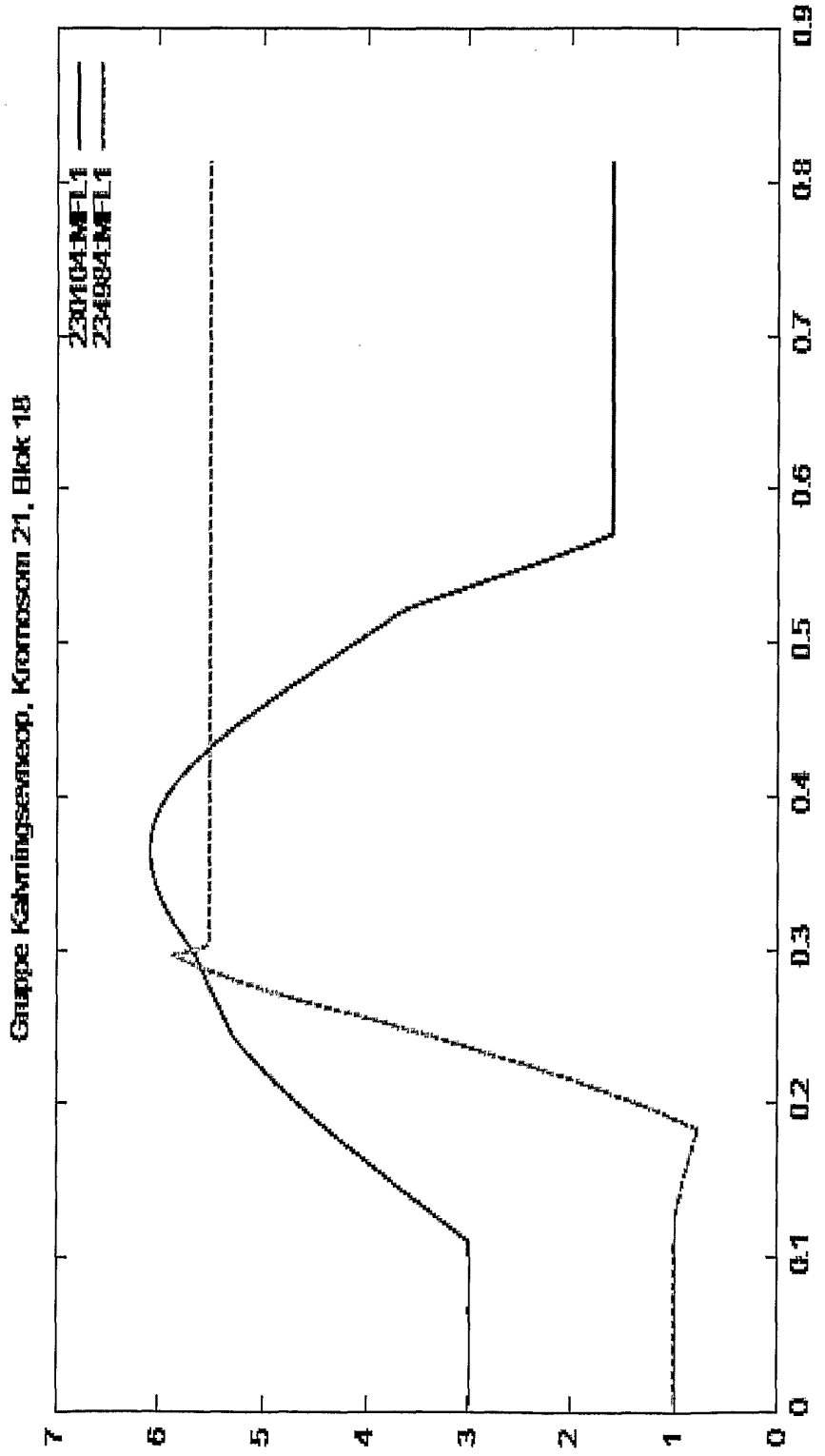

Fig. 18

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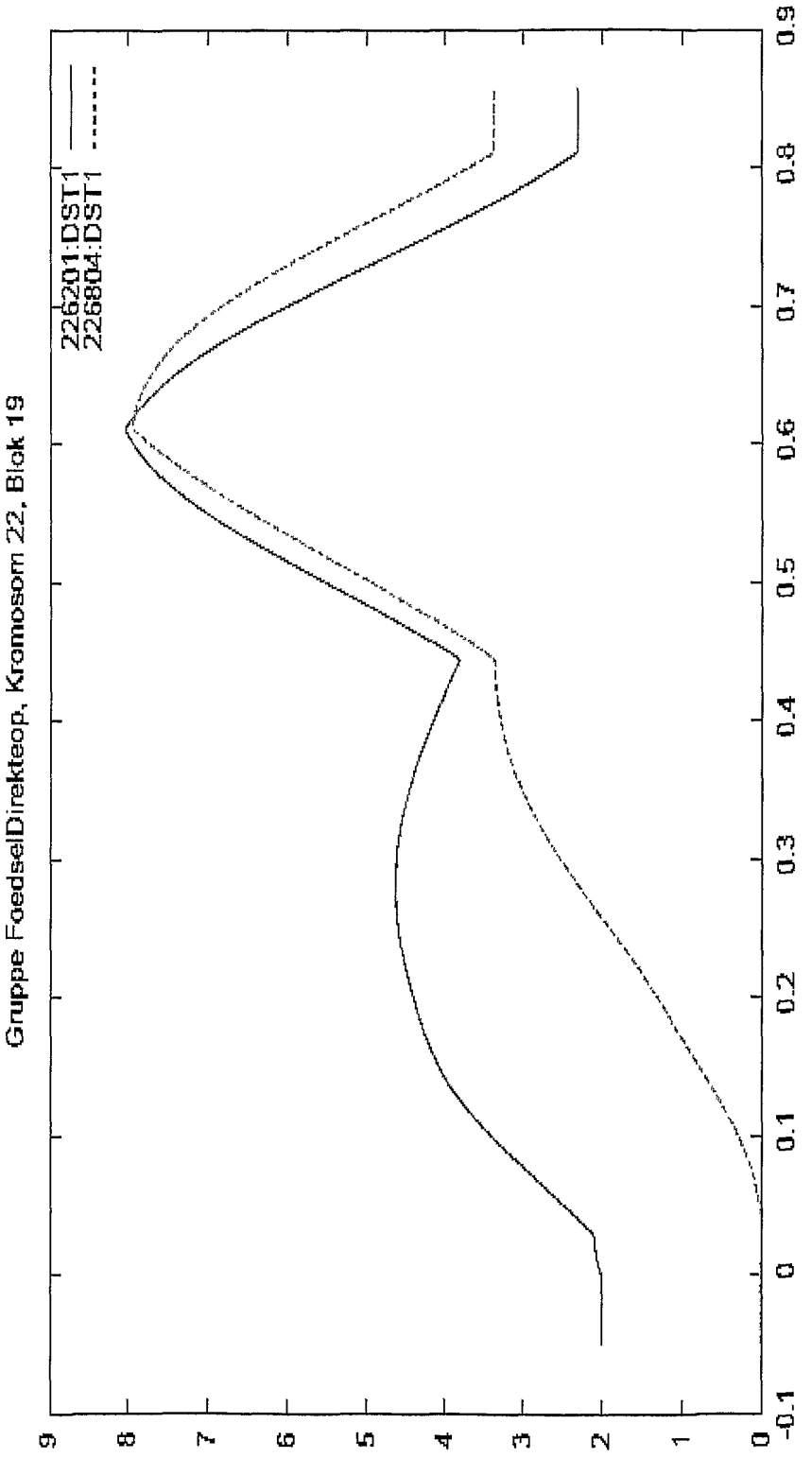

Fig. 19

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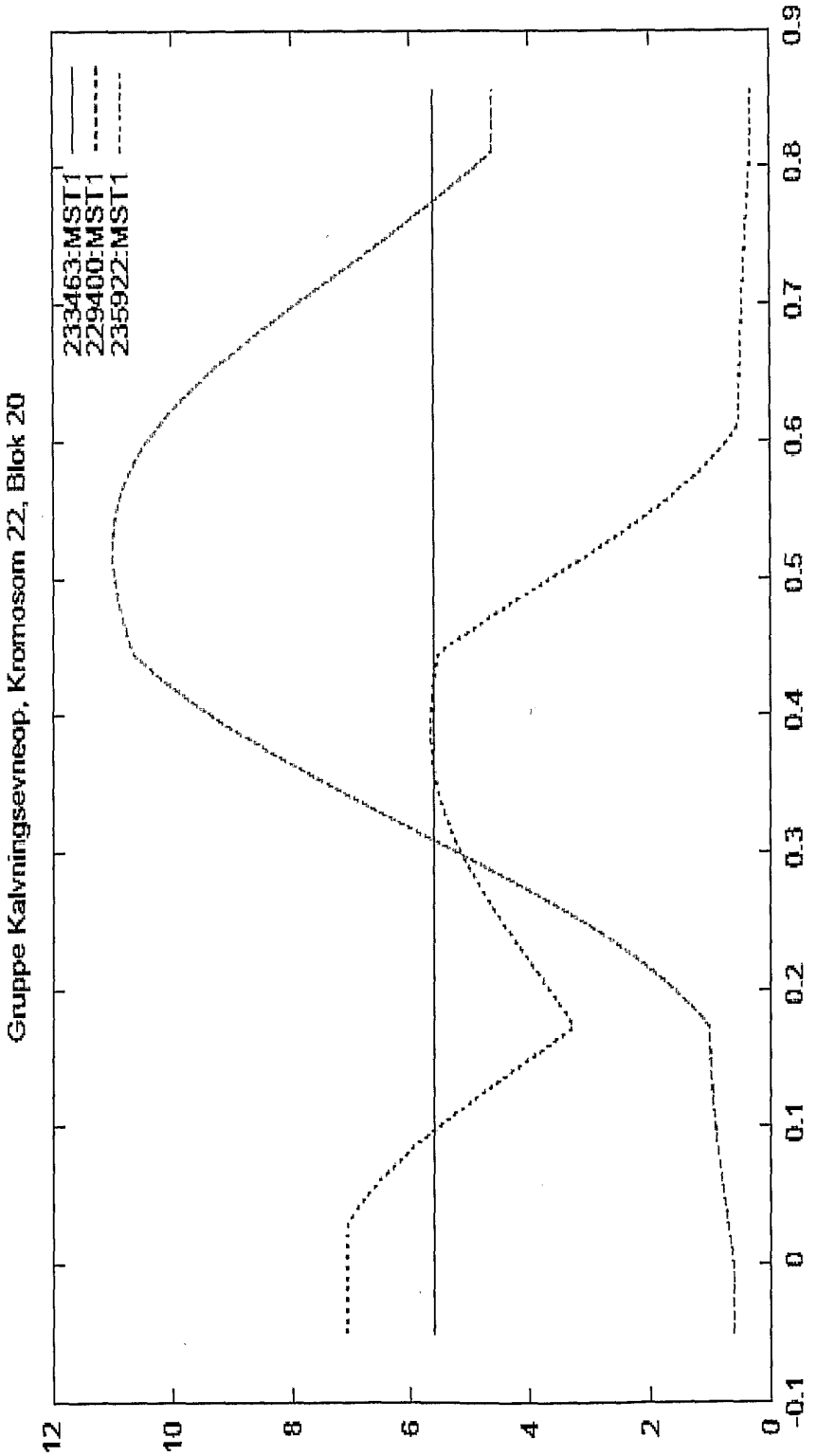

Fig. 20

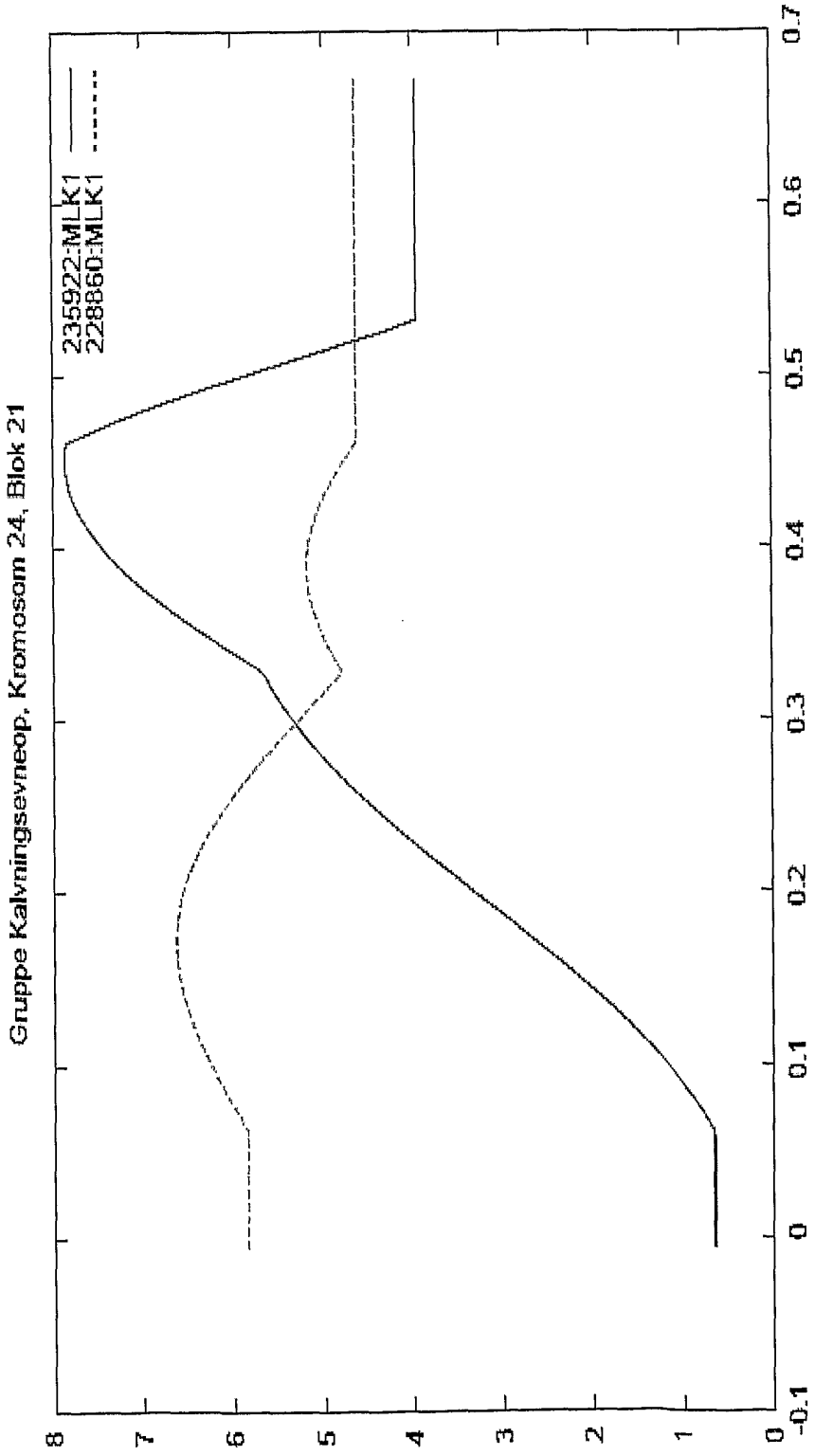

Fig. 21

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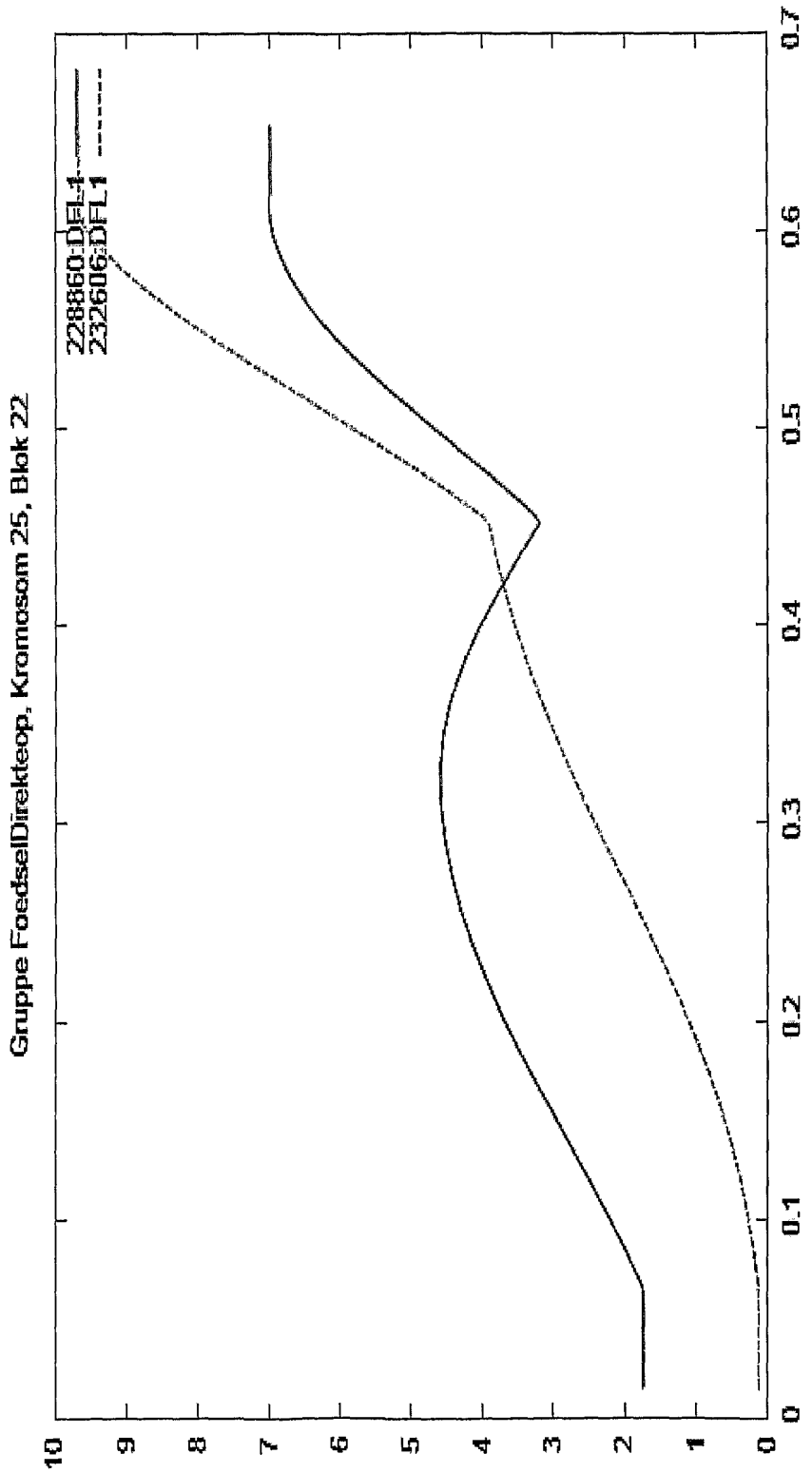

Fig. 22

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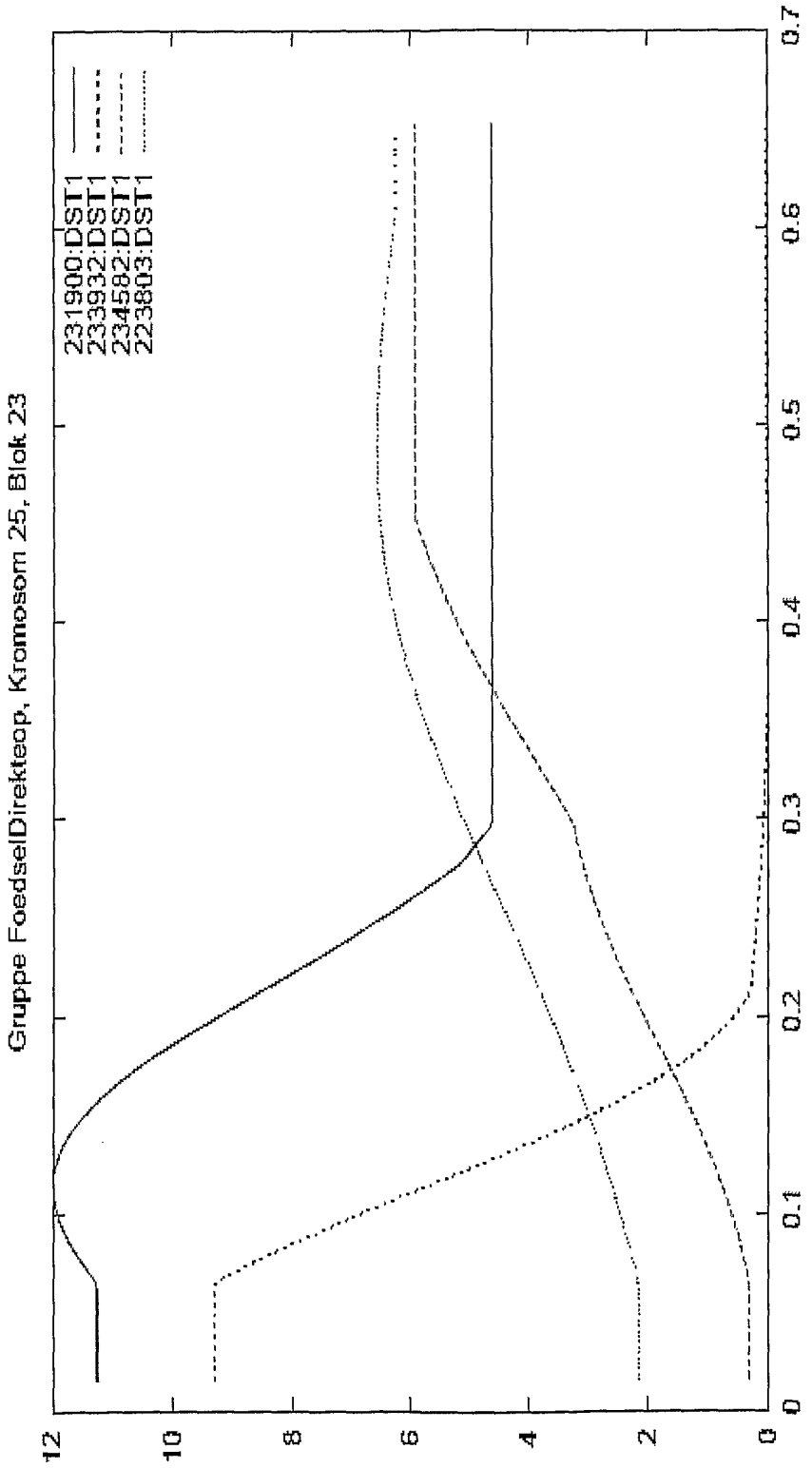

Fig. 23

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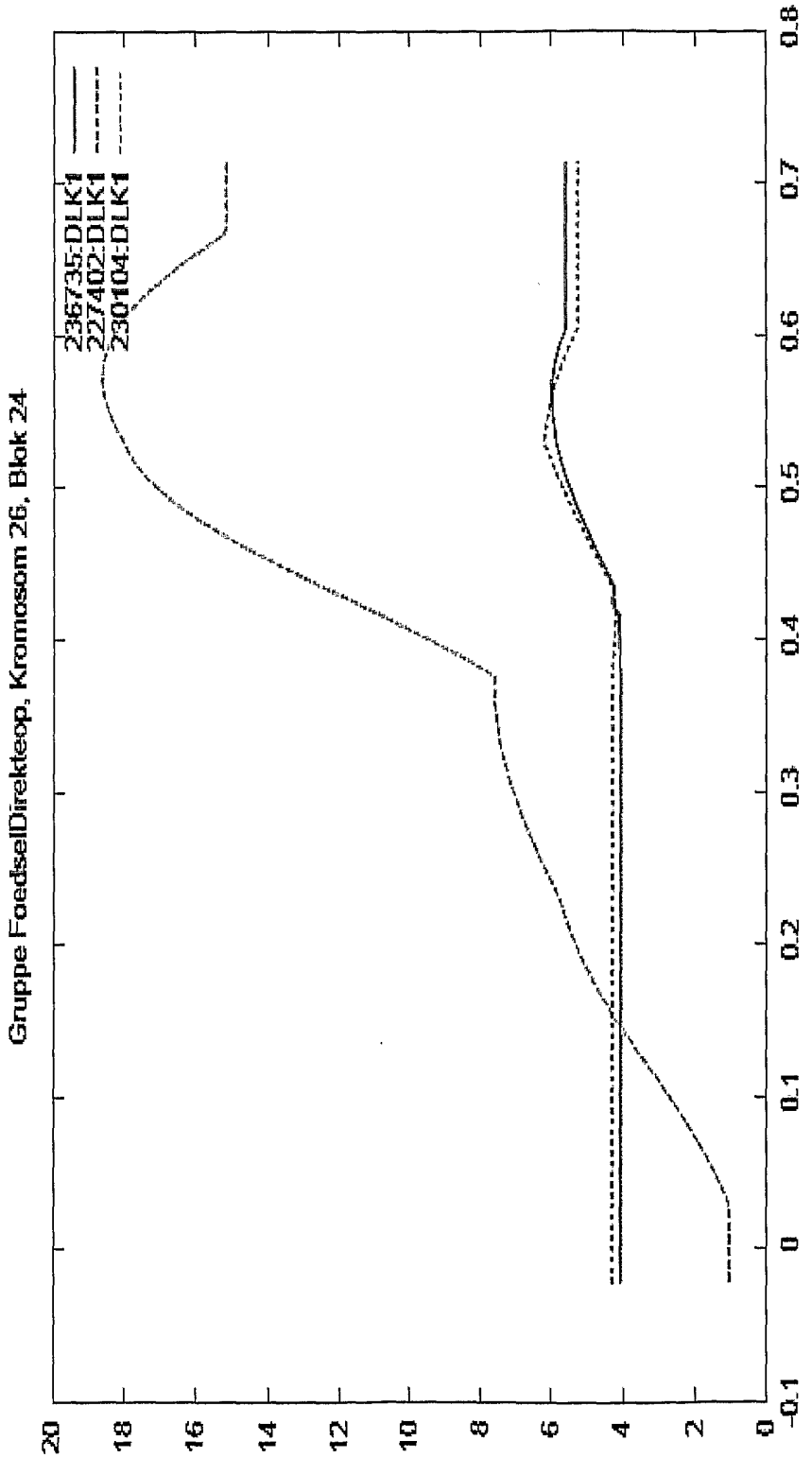

Fig. 24

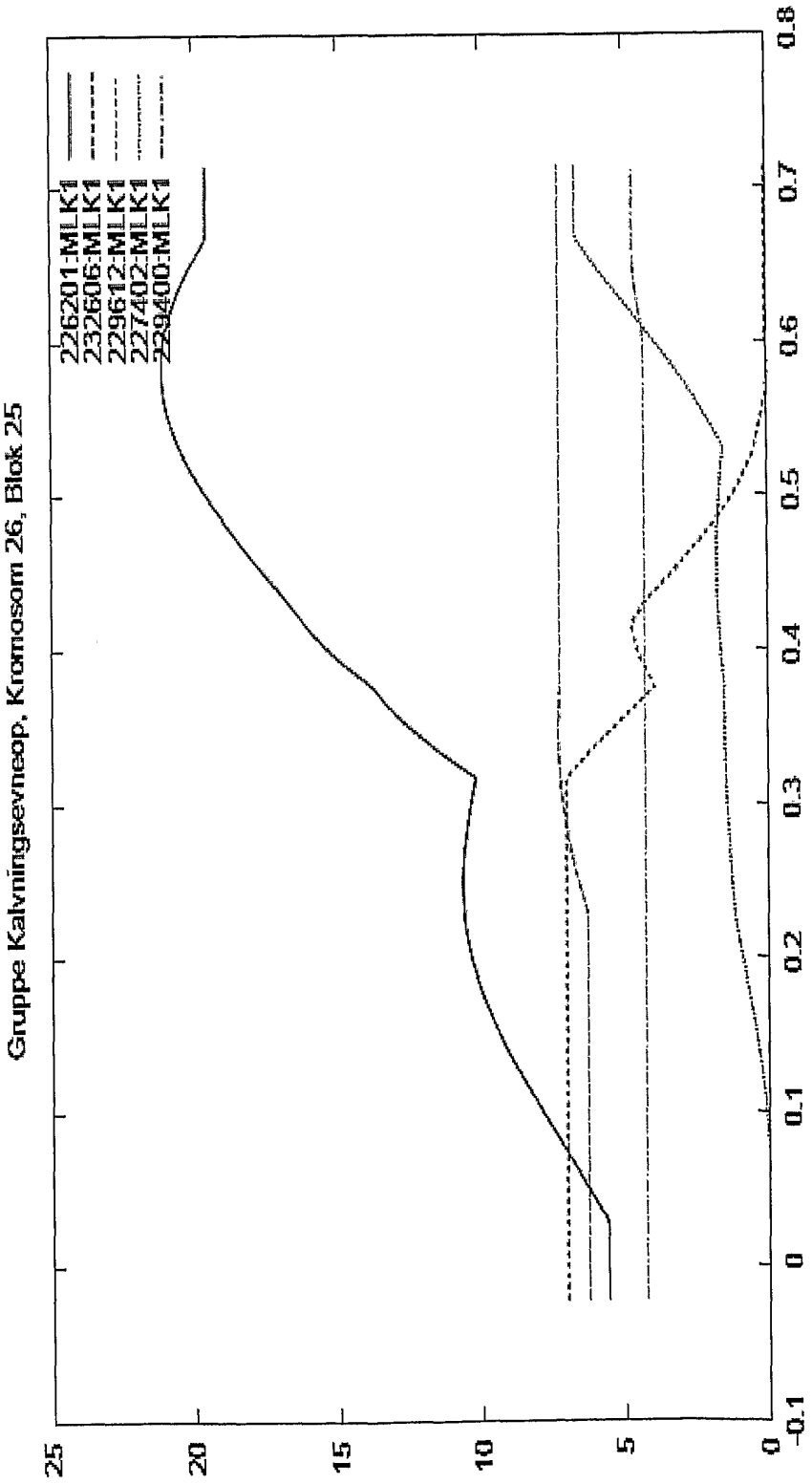

Fig. 25

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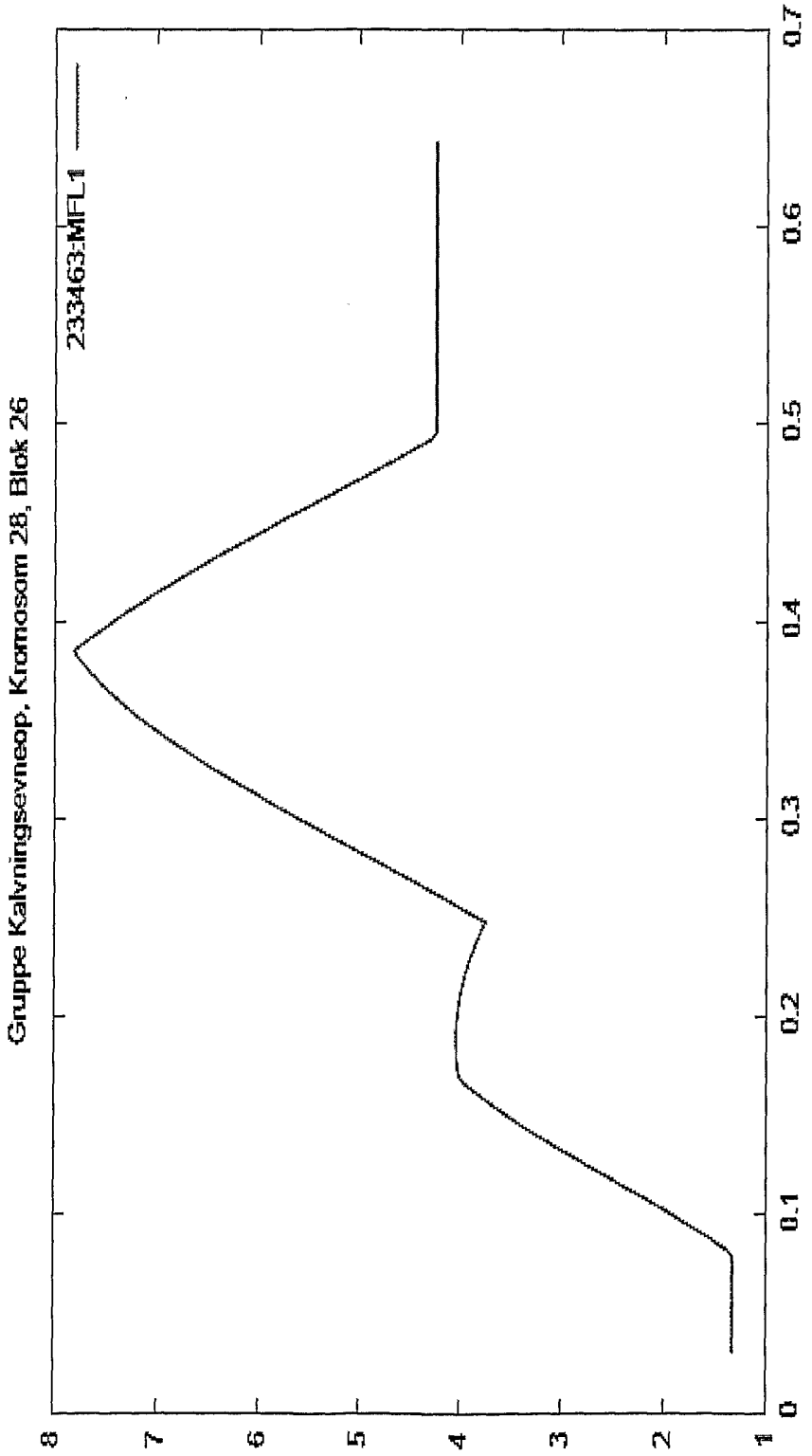

Fig. 26

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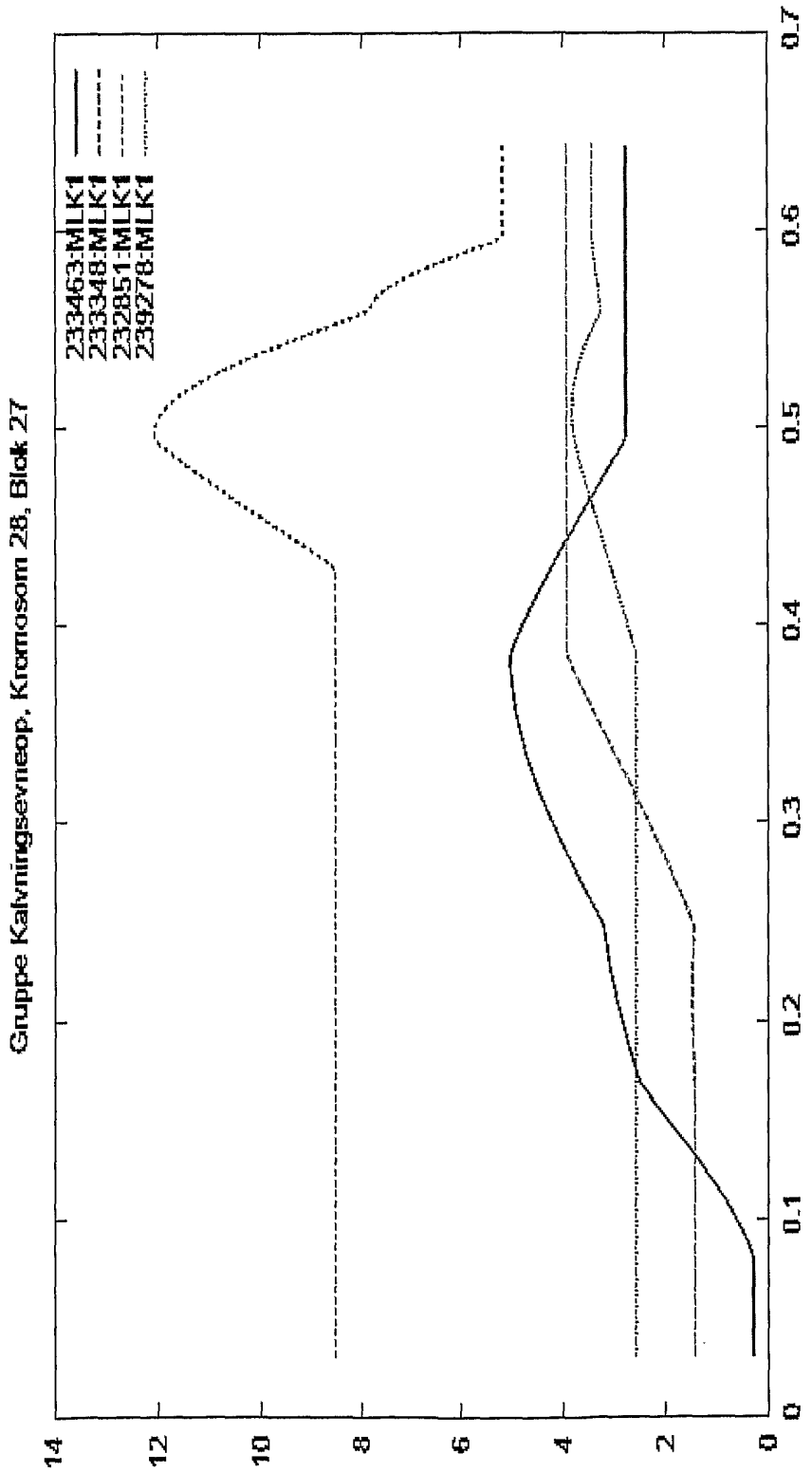

Fig. 27

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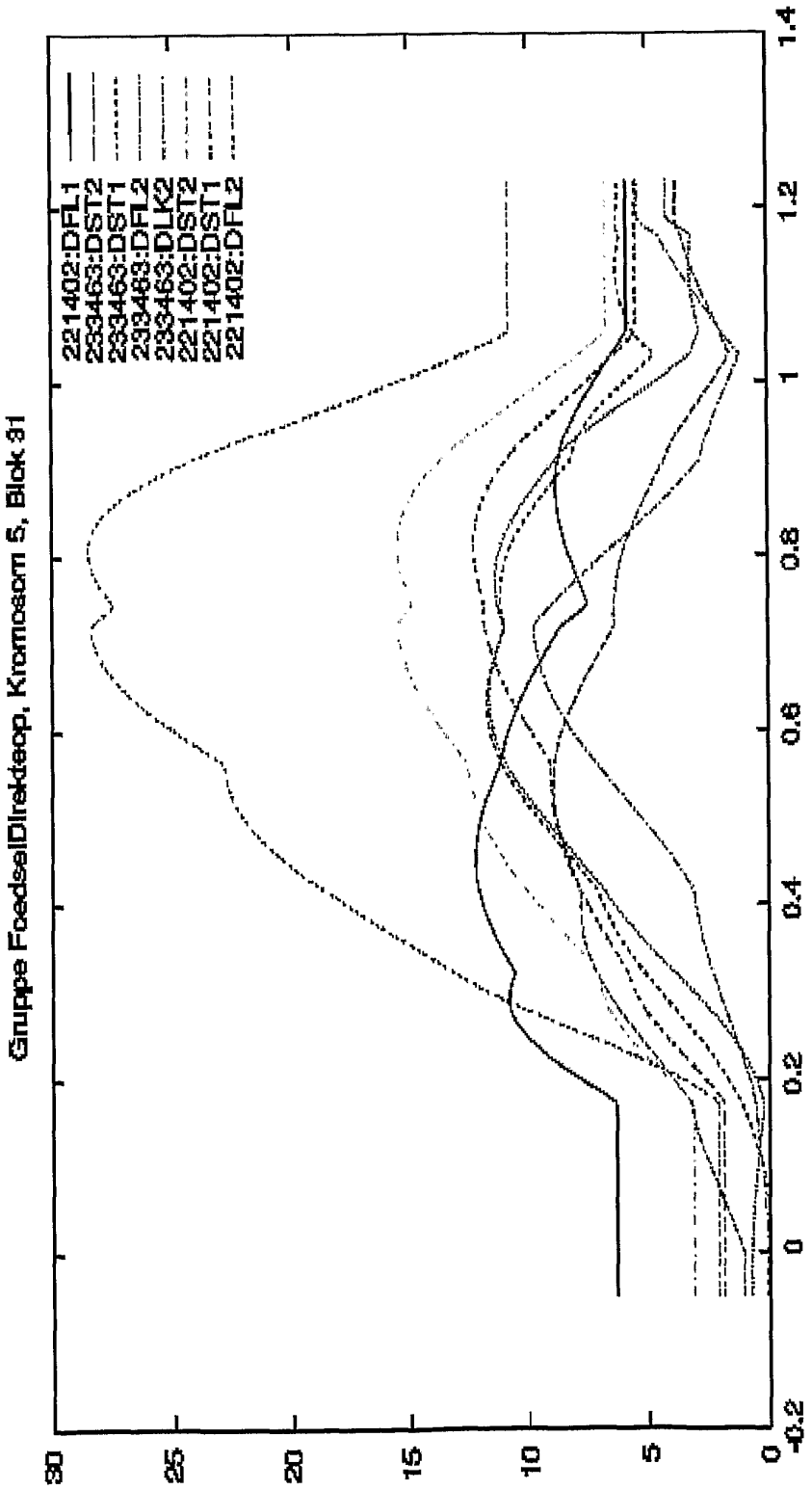

Fig. 28

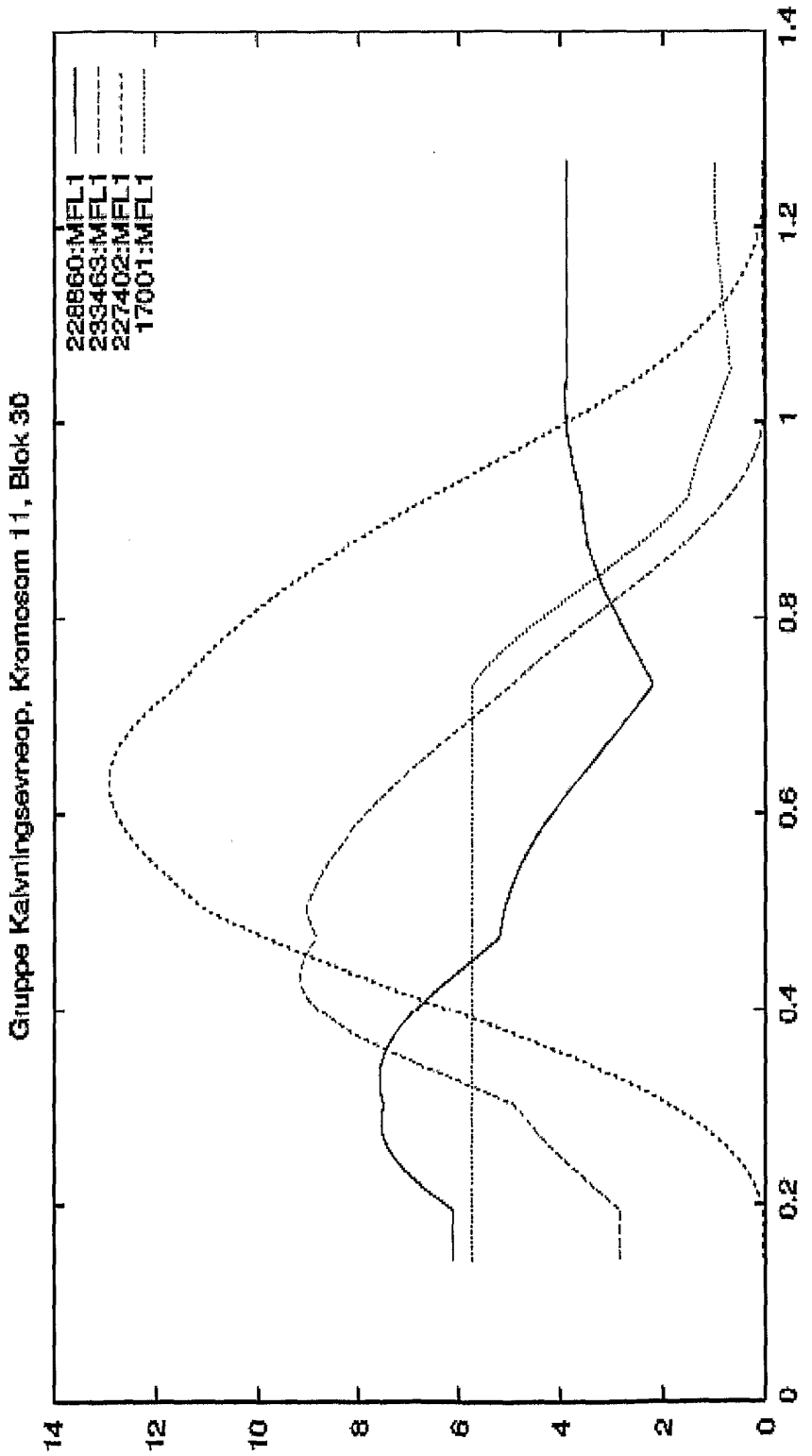

Fig. 29