Sex Determination in Tasmanian Atlantic Salmon

by

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Abstract

Although male heterogamety controls Atlantic salmon sex, hormone treatment can induce sex reversal. In Australia where Atlantic salmon males are unmarketable, sex reversed females (neo-males) are crossed with females to produce all female stock. However, neo-males are indistinguishable from males making early male culling difficult. Therefore, a sex-specific genetic marker was needed to make this distinction. With no such marker available offspring sex was predicted via familial microsatellite analysis. Markers from Chromosome 2 (Ssa02), where the sex locus (*SEX*) previously mapped, predicted test family offspring sex inaccurately. A 64 SNP genome-wide scan suggested Chromosome 6 (Ssa06) housed *SEX* instead. Analysis of 38 male lineages revealed three sex loci on Ssa02, Ssa06 and Ssa03 with 34, 22 and 2 representative families respectively. An exon PCR test for the rainbow trout master sex-determining gene (*sdY*) was consistent with a single sex-determining gene that jumps around the genome in Atlantic salmon.

Keywords: Atlantic salmon; sex loci; genetic mapping; *sdY*; jumping gene

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1. Introduction

Regardless of how or why sexual reproduction arose, vertebrates today consequently exist primarily as male, female (gonochoristic species) or some combination of the two (hermaphrodism) (Devlin and Nagahama 2002). In gonochorists, an individual develops as either male or female and remains male or female for its lifetime. Hermaphroditic individuals can be either sequential or synchronous. As the terms imply sequential hermaphrodites develop first as one sex (male–protoandrous / female-protogynous) and later convert to the opposite sex while synchronous hermaphrodites produce and maintain functional male and female gametes simultaneously throughout their life (Devlin and Nagahama 2002). However, in some synchronous animals like the Poey (*Rivulus marmoratus*) self-fertilization has been taken to an extreme resulting in clonal reproduction of totally homozygous offspring (Kallman and Harrington 1964, Devlin and Nagahama 2002).

1.1. Sex determination morphology and implications

In either case the general pathway leading to male or female gonads consists of two main stages: i. development of the urogenital ridge and subsequent bipotential gonad and ii. morphological differentiation of the bipotential gonad to form either male or female gonads (Shoemaker and Crews 2009). The latter of the two stages differs minimally between highly diverse vertebrates suggesting that the underlying pathways of sex differentiation are conserved (Graves and Peichel 2010). However, the mechanisms that determine whether an individual will become male or female are highly diverse including a wide array of environmental and genetic determinants. Although this diversity exists across many different eukaryotes, all these systems can be observed in a single group, fish (Devlin and Nagahama 2002, Volff et al. 2007). Moreover, any one of these systems is labile to environmental influences that may alter sex phenotype even after a particular sex determination pathway has been initiated, particularly if certain factors are not maintained (Devlin and Nagahama 2002). Fish sex determination and

differentiation in particular can be highly influenced by exogenous steroid and pollutants in the environment (Devlin and Nagahama 2002, Hewitt et al. 2008).

1.2. Sex determination and sex differentiation

Before continuing, it is important to distinguish between sex determination and sex differentiation. Due to the great variety in factors and mechanisms that govern sex determination it is difficult to give a black and white definition for this term. In general sex is considered determined when the bipotential gonad begins to follow a stable pathway leading to morphological development of either female or male gonads. For example, in mammals, a high mobility group (HMG) transcription factor, the sex-determining region Y (*Sry*) gene (Sinclair et al. 1990, Koopman et al. 1990) sets off a cascade that ultimately results in male development (Munger and Capel 2012). Sry, similar to other HMG transcription factors alters transcription of target genes by bending bound DNA (Hsiao et al. 2003). In this case sex is considered to be determined upon fusion of gametes because *Sry* is either present or absent in the genome of the resulting individual. Alternatively in many reptiles the incubation temperature during a short window determines the sex of the offspring. In this case it is unknown what the temperature during the window will be until that window period arrives and thus sex is determined in this short window (Shoemaker and Crews 2009). In yet other cases sex determination can be considered to occur multiple times. For example, in sequential hermaphrodites intrinsic or extrinsic factors initiate a male determining pathway, which later may convert to a female pathway due to further environmental factors. This flexibility in sex determination makes the definition of sex determination as well flexible (Devlin and Nagahama 2002). Therefore, the term sex determination here will refer to the presence or absence of any factor that initiates a temporarily stable sexual differentiation pathway. Thus, this allows sex determination to occur multiple times followed by a particular differentiation pathway and the timing of sex determination is therefore also flexible.

1.3. Sex determination in mammals

Because the pathways of sex determination and sex differentiation share many conserved components among vertebrates the analysis of the sex-determining pathway in one vertebrate can provide insight to the pathways of many other vertebrates (Devlin and Nagahama 2002, Graves and Peichel 2010). Of course the sex-determining and differentiation pathways are most extensively studied in mammals and thus are the choice for review here.

Today evidence suggests the development of the urogenital ridge and bipotential gonad in mammals is controlled and maintained by a multitude of male and female factors that act antagonistic to one another in a tug a war fashion. Thus the bipotential gonad remains in an undifferentiated state until this scale is tipped (by the presence or absence of *Sry*) in favour of the male or female pathway (Figure 1.1, Munger and Capel 2012).

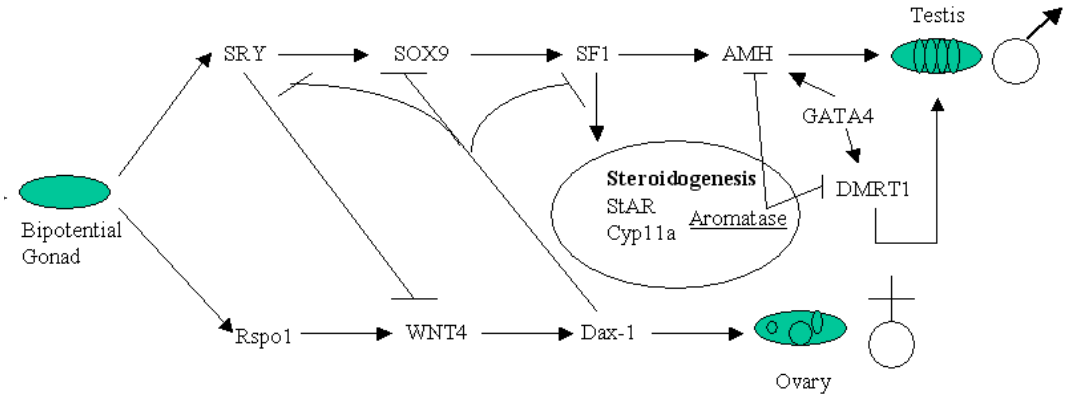


Figure 1.1. A simplified model highlighting some important factors in male and female sex determination and differentiation pathways. Initially the bipotential gonad is primed to develop into testis or ovaries. Figure taken from Li 2010.

In the presence of sex determining region Y (*Sry*) female factors such as Wingless related MMTV integration site 4, (Wnt4) are inhibited tipping the scale in favour of the male pathway. Sry binds the promoter of sex determining region box Y-box 9 (*Sox9*) which in turn binds its own promoter with higher affinity in addition to inducing expression of many other male promoting genes ultimately leading to testis formation. If *Sry* is absent the female pathway dominates, *Sox9* is not upregulated due to inhibition by female promoting genes such as dosage-sensitive sex reversal, adrenal hypoplasia critical region, on chromosome X, gene 1 (dax1) and ovaries develop. SF1: steroidogenic factor 1; AMH: anti-Mullerian hormone; Aromatase: cytochrome P450, family19; GATA4: GATA binding protein 4.

It is important to remember that even though a gonad is initially undifferentiated the sex of the individual has already been determined by the presence or absence of *Sry*. Several antagonistic factors are expressed in what seems like a gradient fashion where, for instance wingless related MMTV integration site 4 (*Wnt4*), a female promoting gene is predominantly expressed at one end of the gonad while, Fibroblast growth factor 9 (*Fgf9*), a male promoting gene is predominantly expressed at the other (Munger and Capel 2012). Both of these antagonistic proteins can act extracellularly influencing neighbouring cells indirectly via respective pathways initiated by the appropriate receptor (Bernard et al. 2012, Eggers and Sinclair 2012). As a result, the region where the expression of these two genes meets, each of their independent expression levels is decreased and the gonad remains undifferentiated. The mechanisms as to how each cell chooses which side to be on is likely dependent upon several external factors from surrounding cells, however there is also evidence that the tug of war between the male and female genes occurs within cells (Munger and Capel 2012). Moreover the finding that both male and female pathways appear to be primed to go in both XX or XY embryos suggests the gonad is capable of becoming male or female even in the absence of *Sry* (Jameson et al. 2012). In the absence of *Sry* the female pathway becomes dominant after a short window (~1.5 days in mice) and as a result is termed the default pathway (Hiramatsu et al. 2009).

It is not known what exactly controls *Sry* expression but loss of function experiments suggest a number of factors that may be involved (Munger and Capel 2012). Moreover, due to the sweeping pattern of *Sry* expression initiated at the center of the gonad and progressing outward committing cells to a pre-sertoli state, it is likely that up regulation of *Sry* in one cell may influence surrounding cells to adopt a similar fate. However, if *Sry* is expressed within the narrow window, the resulting HMG box transcription factor, Sry, up regulates another downstream HMG box transcription factor, *Sox9*. In turn Sox9 binds the promoters of a multitude of other genes involved in the male determining pathway many of which, including *Fgf9* (Kim et al. 2006) and intracellular prostaglandin D_2 synthase (PGD_2S) (Wilhelm et al. 2005), function in feed forward loops to further upregulate *Sox9* as well. Both Fgf9 (mentioned previously) and PGD_2S exert their actions indirectly. PGD_2S converts prostaglandin H_2 (PGH_2) to PGD_2, which in turn is thought to stimulate *Sox9* indirectly via a cell surface receptor (Wilhelm

et al. 2005). Moreover Sox9 binds its own promoter with higher affinity than *Sry* further upregulating itself (Sekido and Lovell-Badge 2008). It is not currently known whether or not Sox9 inhibits the expression of *Sry* (Munger and Capel 2012).

The feed forward loops initiated by *Sry* tip the tug of war in favour of male development and the potentially antagonistic genes from the female pathway such as *Wnt4, Rspo1* (Rspondin homolog 1), β-catenin, and *Foxl2* (forkhead box L2), can no longer keep *Sox9* expression at basal levels to maintain the bipotential gonad (Kim et al. 2006, Uhlenhaut et al. 2009). Wnt4, Rspo1 and β-catenin operate in the same pathway to suppress *Sox9* expression via β-catenin competing antagonistically with Sf1 for the testis specific enhancer (Tesco) (Bernard et al. 2012). For the Foxl2 transcription factor the target is also Tesco (Eggers and Sinclair 2012). The level of Sox9 appears to be dose dependent and is critical for determining differentiation of the support cells of the gonad (Morrish and Sinclair 2002). If Sox9 does not reach a pre-determined threshold, supporting cells will adopt an ovarian state (Munger and Capel 2012). It appears that even after a particular pathway has been chosen that pathway must still be maintained and therefore Sox9 and other male promoting factors must continually repress ovarian promoting genes and likewise the reverse is true for maintenance of ovaries in females (Uhlenhaut et al. 2009, Matson et al. 2011). It should be noted that not all cells that initially express Sry reach critical levels of Sox9 to adopt a pre-sertoli state and as the short window closes before the ovarian pathway takes over, a minimum number of pre-sertoli cells expressing Sox9 above threshold level must be reached before the gonad commits to the male pathway. If too few cells are present the female pathway is adopted (Munger and Capel 2012).

1.4. Environmental sex determination

Several physiological factors within the environment are capable of influencing offspring sex. These influencing factors include temperature as seen in many reptiles (Shoemaker and Crews 2009), exogenous chemicals typically affecting fish (Devlin and Nagahama 2002), and social behavioural interactions and cues generally observed in hermaphroditic species (Devlin and Nagahama 2002). In particular, poikliotherms including both reptiles and fish are subject to temperature changes due to the many enzymes involved in sex determination and differentiation pathways. It is well known

that enzyme activity is highly dependant upon temperature (Devlin and Nagahama 2002).

1.4.1. Temperature dependent sex determination

In many reptiles including turtles, crocodilians, tuataras and some lizards sex is determined by incubation temperature of the developing embryo (Shoemaker and Crews 2009). This phenomenon, termed temperature dependent sex determination, occurs in a narrow window of time for which the embryo is temperature sensitive. The effects of temperature during this sensitive period are unique to each species. For example, during the temperature sensitive period in the red-eared slider turtle (*Trachemys scripta*) an increase in incubation temperature from 26^{o}C to 31^{o}C promotes female development while the American alligator (*Alligator mississippiensis*) exhibits a narrow male promoting temperature range (32.5^{o}C – 33^{o}C) flanked by female promoting temperatures (Shoemaker and Crews 2009). In addition to the different responses to changes in temperature, the timing of the temperature sensitive period differs as well depending on the species chosen.

It is important to note that many of the factors involved in genetic sex-determining mechanisms such as Sf1, Sox9, Sox8, Fgf9, Mis (amh) (see below) are also present in individuals with temperature dependant sex-determining mechanisms; however, their roles are not necessarily the same. For instance, while Sox9 is a key regulator of testis formation in mammals, in reptiles (sea turtle *Lepidochelys olivacea*, as an example), Sox9 is expressed early at both male and female promoting temperatures but at the end of the temperature sensing window is present only in males (Torres-Maldonado et al. 2001, Torres-Maldonado et al. 2002). In addition, shifts from the male promoting temperatures to female promoting temperatures during the sensitive window, resulted in *Sox9* expression and protein level down regulation and vice versa for female to male promoting temperature shifts (Torres-Maldonado et al. 2001, Moreno-Mendoza et al. 2001). The same pattern was observed in 3 other reptiles, *T. scripta* (Shoemaker et al. 2007), *Chelydra serpentina* (Rhen et al. 2007) and *Eublepharis macularius* (Valleley et al. 2001), but not the American alligator where Sox9 is absent until the end of the temperature-sensing period (Western et al. 1999). Therefore Sox9 can be considered an important factor involved in commitment to the male pathway, although other

molecules affected by temperature are likely responsible for the early stages of sex determination and directly or indirectly regulate *Sox9* expression.

Of the other genetic factors involved in vertebrate sex determination, Sf1 shows the greatest potential as a temperature-sensing molecule as it is expressed early in the bipotential gonad of two turtle species (*Trachemys scripta* and *Chrysemys picta*) (Fleming et al. 1999). In these species, *Sf1* expression increased at male promoting temperatures and decreased at female promoting temperatures (Fleming et al. 1999, Valenzuela et al. 2006). However, in the American alligator and other turtle species tested this was not the case, and in fact, Sf1 levels went up during the female promoting temperature (Shoemaker and Crews 2009). Thus, Sf1 may be responsible for testis development in the two turtle species in addition to its apparent more conserved role in development of the bipotential gonad discovered in mammals (Luo et al. 1994, Shoemaker and Crews 2009).

These two genes are merely examples. For a full discussion about genes involved in sex-determining pathways and their comparisons between organisms with genetic and temperature dependent sex-determining mechanisms, please see Shoemaker and Crews (2009).

The above examples of temperature sex determination in reptiles are illustrative of gonochoristic species where the individual's sex remains more or less fixed following the temperature sensitive window. However, in fish species temperature influences can also be present in conjunction with other sex-determining mechanisms, such as in genetic sex determination, and will be discussed further later.

1.4.2. Behavioural sex determination

In hermaphroditic species, sex determination may occur multiple times and sex differentiation may proceed down either a male or female promoting pathway dependent upon environmental cues. Most important is the lack of a sex-determining window, outside of which sex becomes fixed. Consequently, sex determination seems to remain pliable throughout an individual's life and social and behavioural cues related to status within a population determine an individual's sex (Devlin and Nagahama 2002).

Ultimately, an individual's status is controlled by level of dominance with respect to others in the population (Fishelson 1970), size compared to others in the population (Devlin and Nagahama 2002), number of individuals of the same sex in the population and potential pheromones or chemical stimuli present (Devlin and Nagahama 2002). For example, in the protogynous species *Anthias squamipinnis* the presence of a dominant male prevents sex reversal of the larger group of females (Fishelson 1970). When the male is removed from the tank one of the larger females in the group will sex reverse to become male (Fishelson 1970). Similar patterns can be observed for several protogynous and protoandrous species (Devlin and Nagahama 2002). However, other less dominant individuals in a population may sex reverse even in the presence of a dominant individual (Moyer and Zaiser 1984).

1.4.3. Exogenous steroids

Exogenous steroids are used routinely in aquaculture to manipulate offspring sex creating monosex stock (Davidson et al. 2009). This will be discussed further in later sections. However, there are several examples of sex reversal or cases of intersex individuals in wild populations of fish that have been directly affected by steroid containing pollutants and this has also been extensively reviewed in (Devlin and Nagahama 2002, Hewitt et al. 2008, Söffker and Tyler 2012).

1.4.4. Parthenogenesis

In some species a female individual may give birth to offspring in the absence of fertilization by male sperm. These instances and variations of unisexual reproduction, including activation by, and exclusion of, male genetic material from the developing embryo are termed parthenogenesis (Hubbs and Hubbs 1932, Neaves and Baumann 2011). The incidence of parthenogenesis was originally thought to be rare among vertebrates but it is becoming clear that this mode of reproduction is much more common than originally thought with incidence observed in about 80 taxa of unisexual taxa and more still observed today (Neaves and Baumann 2011). For a full review of parthenogenesis please see (Devlin and Nagahama 2002, Neaves and Baumann 2011).

1.5. Genetic sex determination

Genetic sex determination encompasses male heterogamety, as in mammals, female heterogamety, common to birds, XO systems, observed in the mole-vole (*Ellobius lutescens*), and allele specific mechanisms identified in two fish, *Takifugu rubripes* (Kamiya et al. 2012) and *Oryzias luzonensis* (Myosho et al. 2012). Although many of the components of the downstream pathways initiated by these master sex-determining genes are conserved, the way the components fit together can be unique (Kikuchi and Hamaguchi 2013).

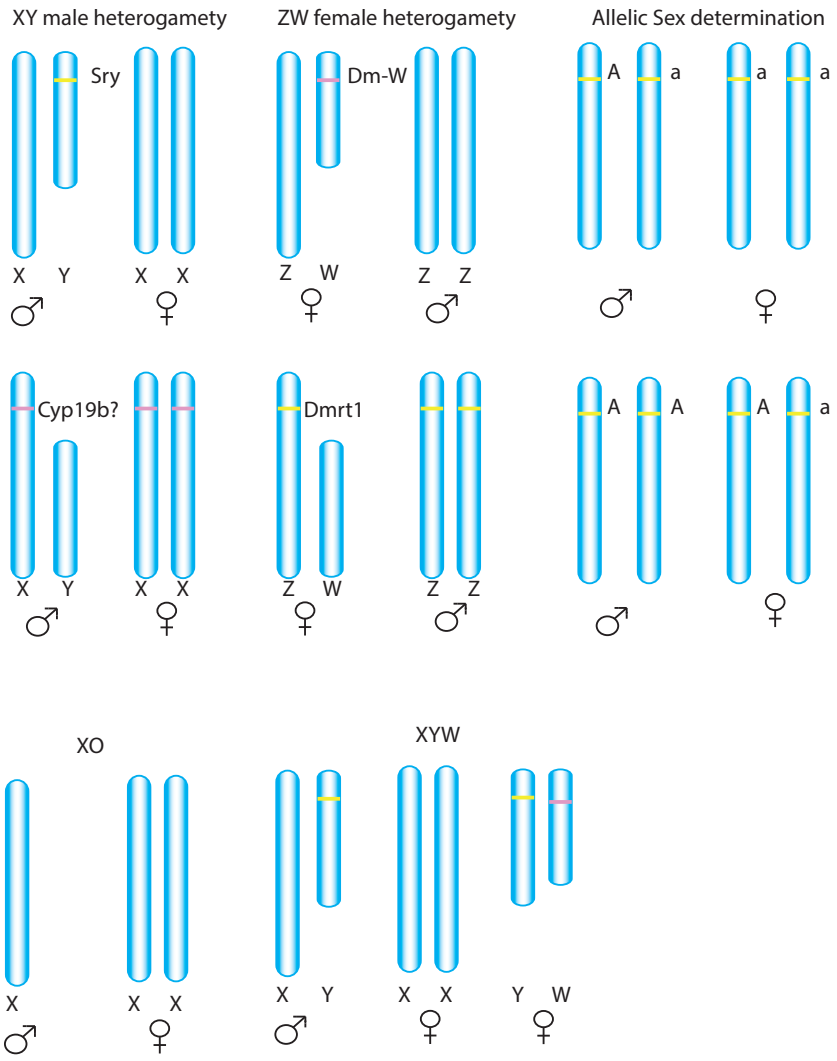


Figure 1.2. Summary of genetic sex determining mechanisms.

For both male heterogamety and female heterogamety individual sex is determined by the presence or absence of a single male or female promoting factor (e.g. *Sry* and *Dm-W)* or in a dosage dependent manner (e.g. *Dmrt1* and possibly *Cyp19b*). Alternatively sex can be determined by a single nucleotide change within a gene as observed in allelic sex determination. Other less common mechanisms include an XO system where the Y chromosome has been deleted all together and an XYW system where Y and W compete for dominance. A yellow band denotes a male promoting gene while a pink band denotes a female promoting gene with the exception of allelic sex determination where the yellow band denotes a gene present in both males and females. Although distinct heteromorphic chromosomes are illustrated for male and female heterogamety in this figure, in reality the difference between these two chromosomes only needs to be a single gene. For example, rainbow trout possess a male heterogametic sex determining system, but cryptic differences between the X and Y cannot be seen under the microscope.

1.5.1. Male heterogamety

Of all the vertebrate sex-determining mechanisms known the most thoroughly studied is our own; a genetic male (XY) heterogametic sex-determining system (Figure 1.2). In this case males will always be the heterogametic sex. This mechanism can exist in one of two forms (Figure 1.2): i. A female sex-determining factor on the X chromosome is required in a dosage dependent manner where two copies are required for female gonad development or ii. A male sex-determining factor on the Y initiates the male pathway. Of course we are most familiar with the latter case due to the discovery of *Sry* in mammals (Koopman et al. 1990, Sinclair et al. 1990).

However, the male determining factor, which may be an activator of a male pathway (as *Sry* is in mammals) or an inhibitor of a female pathway or both, is not conserved among vertebrates (Devlin and Nagahama 2002, Kikuchi and Hamaguchi 2013). For example, the master sex-determining gene *Dmy* in medaka (*Oryzias latipes*) is not found in many closely related species that also possess a male heterogametic sex-determining system (Konodo et al. 2003, Myosho et al. 2012). Although the sex-determining genes in one other medaka related species has been identified (Myosho et al. 2012) many more species of the *Oryzias* genus lack a known sex-determining gene even through they have an identified male or female (see below) heterogametic sex-determining system (Takehana et al. 2005, Takehana et al. 2008). Even though several more fish and other animal species are also known to have a male heterogametic sex-determining system, none of them until recently in a few exceptions, have identified sex-determining genes. The Patagonian perjerry (*Odontesthes hatcheri*), which possesses a duplicated Y-linked anti-mullerian hormone gene (*amhy*), is one of these few (Hattori et al. 2012). In contrast to *Sry* and *Dmy*, which both code for transcription factors, *amhy* is the first master sex-determining gene to dictate phenotypic sex at the hormone level (Hattori et al. 2012). However, all three of these examples consist of a single male promoting gene linked on the Y chromosome of the respective species and to date no male heterogametic systems are known to possess a female promoting master sex-determining gene that operates in a dosage dependant manner (Figure 1.2, Cutting et al. 2013).

The three-spine stickleback may be a promising candidate to identify such a mechanism. Evidence suggests that the three-spine stickleback possess a male heterogametic genetic sex-determining mechanism (Peichel et al. 2004). Yet this system appears to be labile to exogenous hormone treatment and thus the stickleback can be used as a model to study endocrine disruption caused by synthetic human pollutants (Hahlbeck et al. 2004). In addition, this species serves as an important reference for evolutionary studies of other fish species such as Atlantic salmon and rainbow trout (Danzmann et al. 2008, Lien et al. 2011), which have both economic and societal value (Thorgaard et al. 2002). Despite an abundance of resources including the three-spine stickleback reference genome (Jones et al. 2012), the master sex-determining switch in the three-spine stickleback remains a mystery.

Although much work has been done to identify sex linked markers and sex-determining systems in stickleback (see Urton et al. (2011) for review), no one has yet identified a master sex-determining gene. The complex nature and diversity of sex-determining mechanisms, including both male and female heterogametic systems as well as the influence of environmental factors, may be confounding the identification of a single genetic factor controlling sex determination (Urton et al. 2011). Even within the three-spine stickleback two different male heterogametic systems have been observed (Peichel et al. 2004, Ross and Peichel 2008, Kitano et al. 2009, Urton et al. 2011, Ocalewicz et al. 2011). In addition to the different systems, XXY and XY, within the XY system the genetic map produced by Peichel et al. (2004) does not match the deletion observed by Ross and Peichel (2008). Two markers Stn191 and Stn192, are present in the male map of Peichel et al. (2004) but are deleted from the Y in Ross and Peichel (2008). The differences here may be attributed to the differences in populations chosen for analysis and collectively imply different origins of sex-determining genes and mechanisms among different stickleback populations. This is not unlikely given the wide range of freshwater and saltwater habitats this fish has colonized (Jones et al. 2012). In particular, many of the freshwater habitats formed from receding glaciers, have isolated a number of stickleback populations and it begs the question how similar these populations of three-spine stickleback really are to one another. Although it appears the three-spine stickleback have repeatedly evolved similar adaptations to make the transition from saltwater to fresh water (Jones et al. 2012), the flexibility in the number of

ways in which sex can be determined allows the possibility of novel sex-determining factors to arise in each population.

The best candidate in the marine Pacific three-spine stickleback species is the *Cyp19b* gene, which is absent from the Y chromosome (Ross and Peichel 2008). *Cyp19b* codes for aromatase, the terminal enzyme in the pathway responsible for the conversion of androgens into oestradiol (E2), which promotes female development in many species including stickleback (Hahlbeck et al. 2004, Kroon et al. 2005). Thus, this would lead to a dosage dependent male heterogametic sex-determining mechanism where two copies of aromatase are necessary for female development. Consistent with this hypothesis is evidence that sex reversal of sticklebacks via synthetic oestrogens is dose dependent (Hahlbeck et al. 2004).

1.5.2. Female heterogamety

In contrast to the absence of an identified dosage dependent male heterogametic system, birds display a female heterogametic (ZZ/ZW) system in which a male promoting gene *Dmrt1* does act in a dosage dependent manner where two copies are required for the male phenotype to develop (Figure 1.2, Smith et al. 2007, Smith et al. 2009). Alternatively, a single copy of *Dmrt1* results in female development. It should be noted that *Dmrt1* function has not been tested in birds other than the chicken although its conserved presence on the Z and absence from the W across birds suggest a conserved function across birds (Smith et al. 2009, Chue and Smith 2011). Yet the possibility of other master sex-determining genes in birds should not be excluded despite what seems to be a widespread conservation of the ZZ/ZW female activating system (Smith et al. 2009).

Other examples of female heterogamety are seen in *Xenopus laevis*, which possesses a female promoting master sex-determining gene (*Dm-W*) (Yoshimoto et al. 2008). This case is both analogous and opposite to the examples of male heterogamety observed in mammals (Figure 1.2). Therefore females are heterozygous ZW and males are homozygous ZZ where *Dm-W* is on the W chromosome.

1.5.3. Allelic sex determination

Until recently, evidence suggested master sex-determining genes were either single copy genes that operated analogous to *Dm-W* (Yoshimoto et al. 2008) or *Sry* (Koopman et al. 1990, Sinclair et al. 1990), or dosage dependent genes such as *Dmrt1* (Smith et al. 2009). In contrast to this belief two recent publications have shown genetic master sex determinants do not have to be an entire gene but rather can be a single base pair change in a gene (Figure 1.2). The first is an allele of *Amhr2* in the tiger puffer fish (*Takifugu rubripes*) where the presence of a G/C SNP denotes male phenotype while C/C denotes female phenotype (Kamiya et al. 2012). This is the second case, *amhy* in *O. hatcheri* being the first (Hattori et al. 2012), where the anti-Mullerian hormone pathway has been involved in sex determination. However, in this case it is a single amino acid change (His/Asp384) in the target of amh, anti-Mullerian hormone receptor 2, that plays the role in sex determination (Kamiya et al. 2012). Similarly in *Oryzias luzonensis*, a closely related species to medaka described earlier, *Dmy* is absent and instead an allele of *gsdf* (gonadal soma derived growth factor) controls maleness (Myosho et al. 2012). Moreover, interspecific transgenic experiments between *O. luzonensis* and medaka provide the first example for the evolution of a new master sex-determining gene via a mutation in a downstream player which subsequently takes over the downstream pathway in the absence of the original master sex-determining gene (*Dmy* in this case) (Myosho et al. 2012, Kikuchi and Hamaguchi 2013). However, in both cases the master sex-determining genes, *Amrh2* and *gsdf*, of *O. hatcheri* and *O. luzonensis,* respectively are present on both the X and Y chromosome and it is only small changes within these genes that differ between Y and X chromosome.

1.6. Other vertebrate sex-determining systems

It is quite remarkable to find that only a single base pair change in an entire genome can dictate the sex of an organism. Yet in some organisms even less is required to become male. For example the mole vole (*Ellobius lutescens*) has lost the Y chromosome all together and thus females are XO while males are $X^{H\text{-}Y}O$ (Figure 1.2, Yukifumi and Ohno 1977). The process by which this likely evolved suggests the H-Y antigen, which would have been on a previous Y chromosome, jumped to the X

chromosome removing the need for a Y. At the same time there must have been selection to remove individuals with XX^{H-Y} since these individuals will be sterile (Yukifumi and Ohno 1977). In this case H-Y represents the male determining factor.

Another exception among mammals is the platypus, which like other extant monotremes exhibits multiple sex chromosomes as opposed to just X and Y (Tsend-Ayush et al. 2012). In the case of the platypus there are 5X and 5Y chromosomes and unlike other mammals *Sry* is absent among monotremes (Tsend-Ayush et al. 2012). Instead, it has recently been suggested that *Crspy* and *Crspx* genes may be able to activate the testis-specific enhancer element and thus *Crspy*, which is located on Y chromosome 5, serves as a master sex-determining gene candidate among monotremes (Tsend-Ayush et al. 2012).

The platyfish (*Xiphophorus maculatus*) utilizes an out of the ordinary mode of sex determination by merging both the ordinary female heterogametic ZW and ordinary male heterogametic XY systems (Figure 1.2). In this system X, Y and W chromosomes are all present. All three of these chromosomes are thought to contain male-determining factors but it appears only the allele on the Y is expressed while the alleles on the X and W are suppressed by autosomal influences (Volff and Schartl 2001, Schartl and Volff 2002). As a result males can be XY or YY while XX, XW and WY individuals are female (Volff and Schartl 2001, Schartl and Volff 2002). In this case WY fish are female because the W chromosome has an additional suppressor that is specific for the male determining allele on the Y (Volff and Schartl 2001). This intriguing system allows the observation of the relationship of male heterogamety and female heterogamety and insight to evolutionary transitions between male and female heterogamety (Ezaz et al. 2006). The idea that sex chromosomes systems can flip back and forth is consistent with the observation of both male and female heterogametic systems observed among the species of the previously discussed stickleback and *Oryzias* (Urton et al. 2011, Myosho et al. 2012). To date no master sex-determining gene has been identified in the platyfish and thus the above proposed sex determining system remains as a model; however, this model is consistent with genetic results observed from atypical crosses resulting in spontaneous XX, XW, YW, and WW males and XY and YY females (Volff and Schartl 2001). The recent publication of the platyfish genome (Schartl et al. 2013) will certainly be an asset in the search for a master sex-determining gene in this species.

Although the sex-determining mechanism used by the platyfish is extraordinary, it is not quite so rare as the Cichlid fish, *Metriaclima pyrsonotus,* was found to possess a similar mechanism as well (Ser et al. 2010). In *M. pyrsonotus*, *SEX* (the sex locus) is linked to LG7 in the XY system and LG5 in the ZW system (Ser et al. 2010). Once again it appears the W dominates the Y and WY individuals are female. More interesting in this case is the observation of female skewed families in *M. pyrsonotus* that operate in similar manner to but are absent of the LG5 ZW system thus suggesting a second dominant W locus (Ser et al. 2010). From an evolutionary standpoint the identification of multiple sex loci between and within Cichlid fish species in this case appears to be the result of recruitment of novel sex-determining genes as opposed to a single mobile gene (Ser et al. 2010). This is similar to the case in medaka where closely related species do not share the same master sex-determining gene (Konodo et al. 2003).

1.7. Genome duplication and sex in fish

Since it was first proposed by (Ohno 1970), genome duplication has long been argued as a means for speciation and radiation. In addition to the proposed two rounds of whole genome duplication (WGD) known as the 2R hypothesis (Sidow 1996, Kasahara et al. 2007) a third WGD is though to have given rise to the teleost lineage (Christoffels et al. 2004, Meyer and Van der Peer 2005). Consistent with these proposed hypotheses is the observation that mammals have four HOX gene clusters while invertebrates have only one (Amores et al. 1998, Naruse et al. 2000). By this logic teleosts should have eight clusters of HOX genes. The identification of only seven clusters in turn implies loss of one of the clusters (Hoegg et al. 2008). An additional so called 4R genome duplication is thought to have occurred approximately 25-100 million years ago in the common ancestor leading to radiation of the salmonids (Allendorf and Thorgaard 1984) and this is well supported by several independent observations. In addition to the identification of approximately twice as many members, compared to teleosts, of fatty acid binding proteins in salmon (Lai et al. 2012), both Atlantic salmon and rainbow trout contain 13 Hox gene clusters, approximately twice that found in zebrafish and medaka (Moghadam et al. 2005a, Moghadam et al. 2005b). Salmonids not only also contain approximately twice as much DNA as found in other teleosts but

twice as many chromosome arms as well (Phillips and Rab 2001, Mank and Avise 2006, Phillips et al. 2009).

It is well established that genome duplication plays some role at least in driving evolution but how does such an event drive this process? It has been proposed that once a whole genome duplication has occurred the resulting paralogous (duplicated) genes may: i. become silenced or lost (nonfunctionalization), ii. acquire a new beneficial function(s) (neofunctionalization), or iii. divide the load each contributing part of the function carried out by the ancestral gene (subfunctionalization) (Innan and Kondrashov 2010). Put simply, the idea is that once the genome has become duplicated since only one gene is necessary for survival the other is free to accumulate mutations and thus face one of the three fates above. However, these affects are slow acting across entire chromosomes and thus much homology exists between paralogous chromosomes as is evident by quadravalent meiotic pairing observed in Atlantic salmon (Wright et al. 1983). In turn this allows one to identify paralogous chromosomes by mapping markers from the chromosomes of one species to an ancestral species. This is the means by which homeologous chromosomes have been identified in Atlantic salmon (Lien et al. 2011).

Following genome duplication one of the major problems facing an organism is sex determination (Davidson et al. 2009). However, the same three fates can face a duplicated master sex-determining gene that face any other duplicated gene in the genome. Currently evidence for neofunctionalization can be observed in medaka where a duplicate of *Dmrt1* (*Dmy*) assumed the sex-determining role. Alternatively, one of the sex-determining genes may be pseudogenized or lost as it now seems in rainbow trout (Yano et al. 2012). Note this hypothesis assumes *sdY* was the master sex-determining gene in the common ancestor of the salmonids.

1.8. Sex determination in Salmonidae

In contrast to mammals in which a male heterogametic sex determination system dominates, sex determination in fish includes all of the various systems described in the previous sections (Devlin and Nagahama 2002). Moreover, due to their labiality to surrounding temperature changes, fish sex chromosomes are much more susceptible to turnover, and thus are not only ideal for studying the process by which chromosomes

turnover but also the early stages of sex chromosome evolution (Devlin and Nagahama 2002). Due to their economic and societal value, the Salmonidae (salmon, trout, charr, grayling and freshwater whitefish; Nelson 2006) have received a great deal of attention (Thorgaard et al. 2002, Davidson et al. 2010). Moreover, the Salmonidae are of great interest to the scientific community due to an autotetraploidization event making them ideal candidates for the study of early stages of sex chromosome evolution (Thorgaard et al. 2002, Davidson et al. 2009).

Sex determination operates primarily via a male heterogametic system in several members of the Salmonidae (Davidson et al. 2009). This has been shown via crosses between sex reversed males (XY females) with normal males (XY) males which yield a 3:1 ratio of male to female offspring, while crossing sex reversed females (XX males) with normal females produces all female offspring (Davidson et al. 2009).

Although male heterogamety is conserved among salmonids, there has been great debate as to whether or not a single master sex gene dominates, similar to *Sry* in mammals (Sinclair et al. 1990, Koopman et al. 1990), or if each species of this family possesses their own master sex-determining gene as seen in the genus *Oryzias* (Myosho et al. 2012) and stickleback (Urton et al. 2011). The observation that genetic markers linked to the sex-determining locus (*SEX*) in one species (e.g. Atlantic salmon) map to autosomal chromosomes in brown trout (*Salmo trutta*), rainbow trout and Arctic charr (*Salvelinus alpinus*) by Woram et al. (2003) suggested multiple genes exist possibly as a result of an autotetraploidization event in the common ancestor of the salmonids (Allendorf and Thorgaard 1984). However, it was also argued that a single sex-determining gene exists and has moved about the genome, giving rise to the interspecific sex chromosome polymorphisms observed between members of this family (Phillips et al. 2001, Davidson et al. 2009). The discovery by Yano et al. (2012) of the master sex-determining gene in rainbow trout (*sdY*) and its presence in other salmonid species suggest that the latter hypothesis is correct (Yano et al. 2013).

1.9. Sex and Aquaculture

Sex manipulation is commonly practiced in aquaculture as females are often preferred for production purposes. The Tasmanian Atlantic salmon aquaculture industry

relies on all female production stock because the relatively warm Tasmanian seawater leads to rapid sexual development in males, which gives rise to poorer flesh quality and increased disease susceptibility (Aksnes et al. 1986, Elliott and Kube 2009). The strategy is to treat some females with 17-α-methyl-testosterone at an early age, which makes them develop as phenotypic males. Crossing these sex-reversed females (neo-males) with normal females produces all female offspring (Johnstone and Youngson 1984). Phenotypic differentiation of sex-reversed females from true males is not feasible until the fish become sexually mature, and even then only with destructive sampling. A male-specific genetic marker would overcome this problem and enable the culling of surplus genetic males at an early age, thus reducing the cost associated with tank space and feed.

1.10. Project aims

Although sex-specific (i.e., male) genetic markers had been identified in *Onchorhynchus* sp. including:OP-P9/ OmyP9 in rainbow trout (*O. mykiss*) (Iturra et al. 1997); OtY1 (OTY8) and OtY2 in Chinook salmon (*O. tshawytscha*) (Devlin et al. 1991, Devlin et al. 1998, Brunelli and Thorgaard 2004); and a growth hormone pseudogene in Chinook, coho (*O. kisutch*), chum (*O. keta*) and pink (*O. gorbuscha*) salmon (Zhang et al. 2001), none had been identified in Atlantic salmon (*Salmo salar*) (McGowan and Davidson 1998) at the start of this project. Therefore, the aim of this project was to identify a genetic marker that could consistently be used to accurately predict offspring sex in Tasmanian Atlantic salmon. Subsequent aims of this project were:

i. To generate a comprehensive data set that identifies maintained male lineages within the SALTAS Tasmanian Atlantic salmon selective breeding population as having SEX on either chromosome 2, chromosome 3 or chromosome 6.
ii. Determine if the rainbow trout master sex-determining gene (*sdY*) is present in all three male lineages identified.
iii. Determine the relationship between the three identified sex loci and identify individuals in which the proposed master sex-determining gene may have jumped.

2. Methods

2.1. SALTAS Atlantic salmon population samples

All Atlantic salmon samples used in this study come from the SALTAS selective breeding program population. Historically the origins of this population can be traced to the River Philip in Nova Scotia, Canada. The first stocks from this source were initially imported to Garden, New South Wales in 1965 to 1967, for sport fishing, and later transferred to Tasmania between 1984-1986. Until 2004, when the SALTAS selective breeding program was initiated, the population was managed with the primary goal of maintaining genetic diversity. The objectives and desirable traits selected in the program are described in (Elliott and Kube 2009).

A subset of 47 out of 152 families from the 2009 year class were chosen for analysis in this study based on criteria described later. This subset representing a total 38 of the 50 maintained sire lineages constitutes 1128 individuals of the sixth year class of the selective breeding program. The 47 families and the male lineages to which they belong are shown in Supplementary Table S1. Families chosen were the result of crosses between 44 sires and 36 dams where some parents were used in multiple matings. For instance one sire crossed to two different dams. The sires belong to the 2005, 2006 and 2007 year classes, with 57% one generation from founding stock and 43% two generations from founders. The dams belong to the 2005 and 2006 year classes, where 92% were one generation from founders and 8% two generations from founders.

Families were chosen to maximize the number of sire lineages represented in the data set and confined to a minimum of 15 individuals per family. Individuals were also excluded from the final data set if a confident genotype or phenotype call could not be made. As a result the number of individuals per family in the final data set ranged from 11-54 with between 4-23 males and 4-29 females per family. Sex phenotypes were recorded at either 23 months post fertilization during culling of early maturing individuals

or 29 months post fertilization when final harvest assessment is conducted. All sex phenotypes were assessed by gonad inspection at slaughter.

2.2. Genotyping analyses

Microsatellite and SNP (single nucleotide polymorphism) based linkage analyzes were used to identify *SEX* in Atlantic salmon. In order for a microsatellite or SNP marker to be useful for sexing offspring (informative), the sire of the family must be heterozygous for the given marker while the dam of the family may be homozygous or heterozygous but cannot have a genotype identical to the sire. These methods are described previously in (Danzmann et al. 2008); however, details will be described here and Figure 2.1 provides an example of how offspring can be sexed via this method.

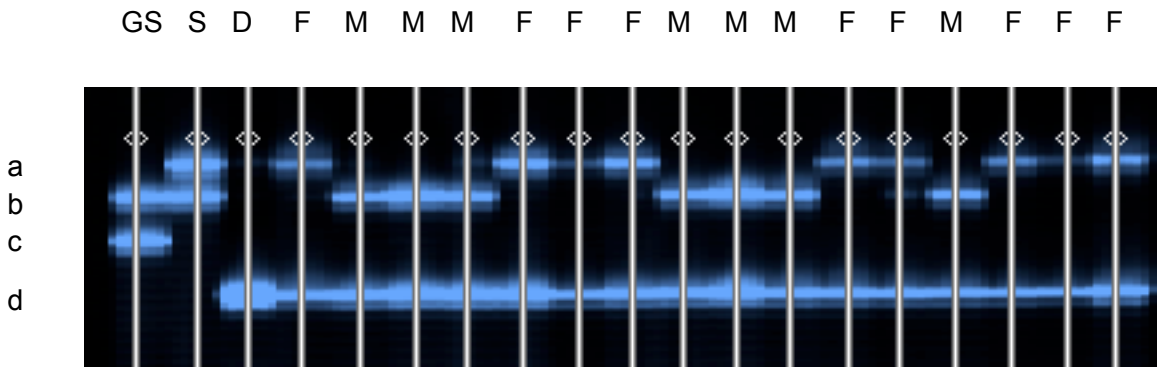


Figure 2.1. An example of genotype analysis using a single marker linked to the sex locus.

The paternal or male allele b is passed from the Grandsire (GS) to the sire (S) to all male (M) offspring. Predicted males and females are indicated with an M and F while a D denotes D the dam. The alleles are denoted a, b, c and d arbitrarily.

Each 6 µl PCR reaction contained 4.05 µl nuclease free water (IDT technologies) 0.19 µM M13 tailed forward primer, 0.43 µM reverse primer and Fam or Hex (M13 tail shown below), 0.18 µM dNTP's (Invitrogen), 0.579 µl 10X Coral buffer (QIAGEN) (15 mM $MgCl_2$), 0.29 U of Taq (Roche) and 0.5 µl of genomic DNA (15 ng/µl).

M13 tail: TGTAAAACGACGGCCAGT, on individuals where the *sdY* exon based PCR test did not agree with sex phenotype.

All primers used in this project were synthesized by IDT Technologies. PCR reactions were carried out in either a T1, T personal, or T3000 Biometra thermocycler. Thermocycler conditions included an initial denaturation at 94^{o}C (2min) followed by a touchdown involving 10 cycles of 94^{o}C (30s), 60^{o}C-50^{o}C touch down (30s) and 72^{o}C (30s). An additional 24 cycles with annealing temperature 55^{o}C followed.

Two µl of formamide loading dye (ABI) was added to 2 µl of each PCR reaction. The mix was denatured at 94^{0}C for 5min in a T1 Biometra thermocycler and subsequently placed on ice before loading on to a 7% urea polyacrylamide gel run on a 377 ABI sequencer. Detailed information for the microsatellite and SNP markers, along with respective integrated linkage maps are available at www.asalbase.org. For the first seven 2009YC families (Figure 2.2) DNA, extracted from an adipose fin clip, was obtained from Agresearch (www.agresearch.co.nz). For all other 2009YC families, DNA was provided by Landcatch Natural Selection Ltd. (www.landcatch.co.uk).

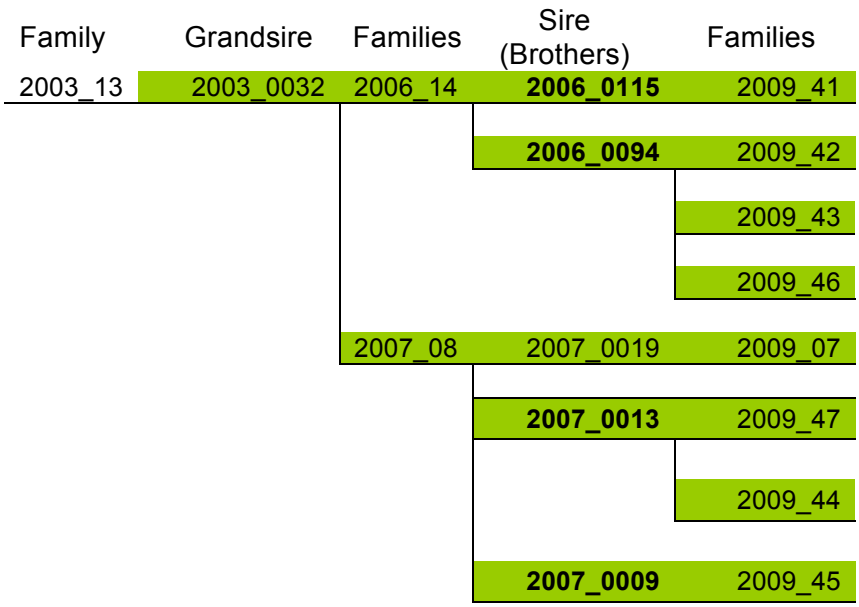


Figure 2.2. Lineage containing the four sires of the seven families in the initial pilot study.

All of these families were identified to have the sex-determining gene located on Ssa06. Individuals (males) are shown in the format, Year class (YC),_, individual ID, (e.g. 2003_0032; YC 2003, ID 0032). Families are classified in the same way (e.g. 2003_13; YC 2003, family ID 13). Pedigrees of all 40 lineages can be found in Supplementary Figure S1. The four sires are shown in bold.

A TaqMan 64 SNP genome wide assay (Applied Biosystems) was conducted in 10 µl reactions on the 2009YC families. Each 10 µl TaqMan PCR reaction contained, 5 µl 2x genotyping master mix (Applied Biosystems), 0.25 µl of 40x genotyping assay mix (Applied biosystems), 3.75 µl Nuclease Free Water (IDT Technologies) and 1 µl DNA (15 ng/µl). Initial denaturation at 95^0C was held for 10minutes followed by 40 cycles of 95^0C 15 sec and 60^0C 1 min. Although reactions could be carried out in either a 7900HT Fast Real-Time PCR system (ABI) machine or a Biometra T1 thermocycler, all reactions had to be analyzed on the ABI machine. Figure 2.3 shows an example of an informative family genotyped using this method. The 64 SNP markers are listed in Supplementary Table S2. Additional SNP data related to *SEX* from the 2005YC and 2006YC (Dominik et al. 2010, Lien et al. 2011) were used to predict the sex locus of unknown lineages. Genotypes were compared to male and female phenotypic calls to assess linkage to *SEX.*

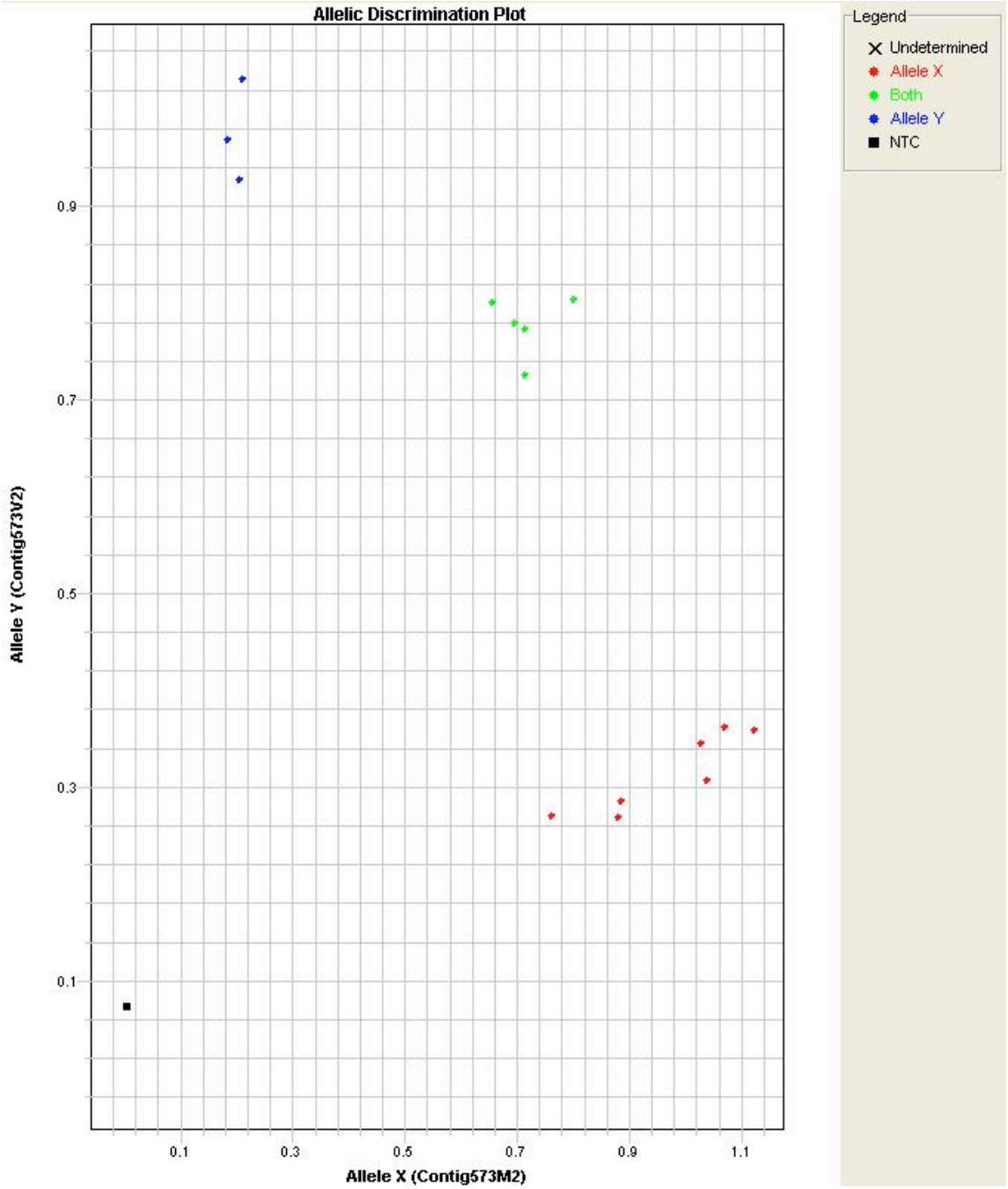


Figure 2.3. An example of the TaqMan probe marker genotyping result.

Alleles are color coded as indicated in the legend. NTC represents the negative control. "Allele X" and "allele Y" represent homozygous individuals while, "both" represents individuals who are heterozygote or XY.

SALTAS personnel made phenotype calls at harvest, maturation grading and spawning. Fish with questionable phenotypes are indicated in Supplementary Table S3. To determine the chromosomal location of *SEX* in each family, the following criteria were set: (1) at least one marker from Ssa02, Ssa03 or Ssa06 accurately predicts offspring sex; and (2) at least one marker from each of the other loci does not predict offspring sex accurately (negative confirmation). For markers with duplicate loci each informative locus was distinguished by the addition of /1 and /2 to the marker name to indicate locus 1 and 2, respectively (Danzmann et al. 2008). In cases where the grandsire and sire genotype were identical, the male allele was inferred based on the comparison between genotype and phenotype of the offspring.

Logarithm of Odds (LOD) scores (Morton 1962) were calculated individually for each family marker combination in Maple 16 using the following equation.

$$Z = \log_{10} \frac{(1-\theta)^x \theta^y}{0.5^{(x+y)}}$$

Where the LOD score Z is given as a function of the number of non recombinant offspring *x* and the number of recombinant offspring *y* for a given recombination rate θ. Cases where the sex phenotype predicted by genotype was 100% accurate were considered to be significant regardless of LOD score.

2.3. PCR-based *sdY* test for Atlantic salmon males

Yano et al. (2012) recently identified a male specific master sex-determining gene, *sdY*, (sexually dimorphic on the Y chromosome) in rainbow trout. Two primer pairs, one specific for exon two and the other specific for exon four of the *sdY* gene, were designed based on an alignment (not shown) of Atlantic salmon *sdY* (Palibroda *et al*., in preparation) with Danube salmon (*Hucho hucho*), Chinook salmon (OTY-3), rainbow trout Y chromosome genomic sequence, and rainbow trout sdY. GenBank accession numbers for the Danube salmon, Chinook salmon, rainbow trout Y and rainbow trout sdY sequences are JF951962.1, DQ393568.1, EU081756.1 and AB626896.1, respectively. A triplex PCR reaction was developed to screen the parents and offspring of the tested 2009YC families, with the following primers (IDT Technologies):

Exon 2:

Forward: TGATGGATGGGATCCCCGTCATCTCTCTCCCAAAG
Reverse: TCCCTCATGGAGGGTGGAGTGGTTTTAAGCTCTA

Exon 4:

Forward: AGTTGGAACGCTTCAGCAGAGCAGATGG
Reverse: GGACAAGACTCATCACTCAGTGCACCAATCT

Fabp6b (DNA quality control; Y. Lai, personal communication):

Forward: AATTACGATGAGTTTCTGGAGGCAA
Reverse: CTTTCCGATGGTGAATTTGTTAGTCAA

Each 8.7 µl reaction contained 2.25 µl nuclease free water (IDT technologies) 1 µl of DNA (~50 ng/µl), 0.3 µl DMSO (100%) (New England Bio Labs), 1 µl dNTPs (Invitrogen) (10µM), 1 µl 10X Coral buffer (QIAGEN) (15 mM $MgCl_2$), 0.15 µl of Taq (Roche) (5 U/µl) and forward and reverse primers of: Exon 2 (0.15 µl at 10 µM), Exon 4 (1 µl at 10 µM) and Fabp6b (0.35 µl at 10 µM). When 15 ng/µl DNA working stocks were used, 4 µl of DNA was added to each reaction (total volume 11.7 µl). PCR conditions, run on a Biometra T1 Thermocyler machine, were 94^{o}C for 2 min followed by 36 cycles of 94^{o}C for 30 s, 60^{o}C for 30 s, 68^{o}C for 30 s. A final extension of 68^{o}C for 10 min was used. The parents and offspring of the 2009YC families were screened with this multiplex and PCR products were separated on a 1.5% 1 X TBE agarose gel and visualized using ethidium bromide.

Exon 3 was tested, using primers:

Forward: AGTTGGAACGGCTTCAGCAGAGCAGAT and

Reverse: AGATTGGTGCACTGAGTGATGAGTCTTGTCC

on individuals where the *sdY* exon based PCR test did not agree with sex phenotype. Here each reaction contained 6.85 µl nuclease free water (IDT technologies), 0.5 µl forward primer and reverse primer (IDT technologies), 1 µl 10X Coral buffer (QIAGEN) (15 mM $MgCl_2$), 1 µl dNTPs (2 µM) 0.15 µl of Taq (Roche). Thermocyler conditions were as above except the extension temperature was 70^{0}C.

3. Results

3.1. Screening Tasmanian Atlantic salmon with microsatellite markers on Ssa02

SEX was previously mapped to Atlantic salmon linkage group 1 (LG1) (Woram et al. 2003), and Artieri et al. (2006) showed that this corresponds to chromosome 2 (Ssa02). Therefore, to identify a sex-linked genetic marker, which could be used to predict males in the Tasmanian Atlantic salmon population, seven pilot test families from the SALTAS breeding population with microsatellite markers from Ssa02 were screened first (www.asalbase.org; Figure 2.2, Supplementary Table S1 and Table S3). However, *SEX* was not associated with any alleles from these loci, which suggested that *SEX* was not on Ssa02 in these families.

3.2. Mapping of *SEX* to Ssa06 in Tasmanian Atlantic salmon

A screen of these seven Tasmanian Atlantic salmon families using 64 SNP markers, distributed across the genome, indicated that *SEX* resided on Ssa06 in these families (Supplementary Table S1, Table S2 and Table S3). Linkage analysis using microsatellite markers from Ssa06 confirmed this prediction (Supplementary Table S3 and Table S4). An examination of the pedigree records of the SALTAS breeding program revealed that these seven Atlantic salmon families had a common grandsire, and thus represented a single male lineage in the SALTAS population (Figure 2.2). Therefore, some additional 2009YC families from different ancestral male lineages in the SALTAS Atlantic salmon breeding population were screened with microsatellite markers from Ssa06. Although these markers predicted the gender of offspring accurately in some families, in other families there was no association between the genotypic results and offspring sex phenotypes (Supplementary Table S3, Table S4 and Table S5). For non-Ssa06 *SEX* linked families, accurate sex predictions were obtained using genetic markers from Ssa02 (Supplementary Table S5).

3.3. Screening the SALTAS Atlantic salmon broodstock with Ssa02 and Ssa06 genetic markers

With evidence for two sex-determining loci in the SALTAS Atlantic salmon broodstock, a total of 40 families from 34 male lineages with representatives in the 2009YC of the selective breeding program were screened for *SEX* linked to Ssa02 or Ssa06. SNP markers associated with *SEX* from Dominik *et al*. (2010) and Lien *et al*. (2011) predicted a number of male lineages to have *SEX* associated with Ssa02 (data not shown). This increased the number of male lineages with an identified *SEX* locus to 38 (Supplementary Table S1). *SEX* was predominantly associated with Ssa02, being found in 34 of 58 families, which corresponds to 25 of the 38 male lineages. In contrast, *SEX* was associated with Ssa06 in 22 of the 58 families, representing 11 of the 38 identified male lineages (Supplementary Table S4 and Table S5).

Although confident in the assignment of *SEX* to Ssa02 or Ssa06 in 56 of 58 families, a lack of consistency was observed between sex phenotype predictions made by markers mapping to either of these chromosomes for two families (2009_32 and 2009_37), containing 35 and 17 offspring, respectively. These results suggested the presence of a third sex-determining locus in Tasmanian Atlantic salmon. Colleagues at CIGENE, Norway recently identified *SEX* on Ssa03 in some European Atlantic salmon (S. Lien, personal communication). Therefore, genetic markers from Ssa03 were used to screen these two Tasmanian families. In both families, 2009_32 and 2009_37, there was linkage between sex phenotype and Ssa03 (LOD scores of 5.3 and 3.2, respectively) (Supplementary Table S6).

Although there was evidence for association of sex phenotype with three different chromosomes, there were some instances when sex phenotypes and genotype predictions did not match. For example, in one family (2009_32) with 35 offspring, in which the sex phenotype was linked to Ssa03, sex predictions using six Ssa03 markers were inconsistent for four individuals (Figure 3.1 and Supplementary Table S3). Of these four individuals, three carried a Y specific allele passed from grandsire to sire (predicted males), but were found to be female at harvest. Two of these three predicted males (phenotypic females) gave PCR product only for exon 3 of the potential master sex gene, *sdY*, by PCR (see below) whereas the other one gave PCR products for exon 3

and exon 4, but not exon 2 (Figure 3.1. and Supplementary Table S3). Exon 3 of *sdY* was tested only on individuals in which the presence or absence of *sdY* did not agree with the phenotype assessment of the fish (Supplementary Table S7). The other individual, which had a female microsatellite haplotype and male phenotype, gave a positive PCR result for exons 2, 3 and 4 of the *sdY* gene (Supplementary Table S3).

2009_32 Ssa03

parents and *sdY* agree 100%

	AS1-2002_0013	AS2	S1-2007_0001	S2	2009_0598	2009_0967	2009_0279	2009_0558	2009_0636	2009_0137	2009_0609	2009_0470
Ssa0649BSFU	2	1	2	1	2	2	2	2	2	1	2	1
Ssa0017BSFU	3	2	3	1	3	3	3	3	3	1	1	1
Ssa0368BSFU	1	3	1	4	1	1	1	1	1	4	4	4
Ssa0516BSFU	3	3	3	4	3	3	3	3	3	4	4	4
OMM5019	2	1	2	1	2	2	2	2	?	1	1	1
OMM1267	1	3	1	2	1	1	?	?	1	2	2	?
SsaD144BSFU	1	3	1	2	1	1	1	1	1	2	2	2
			sdY	Exon 2	1	1	0	0	0	0	0	1
				Exon 4	1	0	1	0	0	0	0	1
				Fabp6b	1	0	1	1	1	1	1	1
			Sex call from Phenotype		Male	Male	Female	Female	Female	Female	Female	Male

Figure 3.1. An abstract of the second largest family (2009_32), in which the sex locus mapped Ssa03, to illustrate the comparisons of phenotype to sdY phenotype predictions and haplotype predictions of phenotype.

AS-1 (ancestral sire-1) represents the paternal or Y linked allele housed by the grandsire (2002_0013) while AS-2 represent the maternal or X linked allele housed by the grandsire. Likewise S-1 (sire-1), inherited from the AS, and S-2, inherited from the ancestral dam (AD) represent the Y linked and X linked alleles housed by the sire (2007_0001) respectively. Offspring ID's run in the same row where Individual ID's are shown in the format year class_IDXXXX (e.g. 2009_0598 is the 2009 Year class ID 0598. Haplotype offspring sex predictions that do no match the sex call from phenotype are highlighted green. The *sdY* predictions are based on the presence of Exon 2 and Exon 4 (predicting male) indicated by a 1 or absence indicated by a 0. *Fabp6b* represents a quality control of DNA where a 1 indicates presence and 0 indicates absence of an amplified product. Full details of this family can be found in Supplementary Table S3.

Seventeen phenotypic males from 10 other families also tested positive for exons 2 and 4 of *sdY* even through they carried the sire's maternally inherited haplotype (Table 3.1; Supplementary Table S3). We also found additional inconsistencies among predicted sex phenotype based on haplotype analysis, sex phenotype observed at harvest and the presence of the *sdY* gene, and these are summarized in Table 3.2 and Supplementary Table S7. Unfortunately none of these fish were used as broodstock, and therefore they have no associated offspring of their own that could be analyzed.

Table 3.1. Phenotypic male individuals from the 2009 year class in which SEX may have moved by recombination, translocation or transposition (see Figure 4.1 for details).

[1]Individual ID	Number of markers predicting female haplotype	*sdY* positive	Chromosome housing (*SEX*) in family
2009_0756	2	Yes	2
2009_0582	3	Yes	2
2009_0013	1	Yes	2
2009_0252	1	Yes	2
2009_0316	1	Yes	2
2009_0604	1	Yes	2
2009_0953	2	Yes	2
2009_0947	1	Yes	6
2009_0924	1	Yes	6
2009_0192	1	Yes	6
2009_0528	3	Yes	6
2009_0390	1	Yes	6
2009_0641	1	Yes	6
2009_0982	2	Yes	6
2009_0369	2	Yes	6
2009_1080	5	Yes	6
2009_0470	4	Yes	3
2009_0578	4	Yes	3

[1]Individual IDs are shown in the format year class_ individual ID, for example, 2009_0756 for 2009 year class _ ID 0756

Table 3.2. Some explanations of inconsistent outcomes between phenotype, genotype and sdY. For a fuller discussion see Figure 4.1.

Phenotype	Haplotype	*sdY* test	Total # of individuals	Possible Explanation
Female	Male	Male	1	Phenotype miscall or loss of function of *sdY*
Female	Female	Male	3	
Female	Male	Female	7	Movement of marker or *sdY*
Male	Female	Male	20	Movement of marker or *sdY*
Male	Female	Female	12	Temperature dependent sex reversal or phenotype miscall (King *et al.* 2012)
Male	Male	Female	4	

3.4. Development of a PCR-based test to identify Tasmanian Atlantic salmon males

The recent publication of the male-specific sex-determining gene in rainbow trout, *sdY*, by Yano *et al.* 2013 enabled us to design two pairs of Atlantic salmon specific primers, one from exon 2 and the other from exon 4, to screen the Tasmanian Atlantic salmon for the presence or absence of the *sdY* gene using a PCR based assay (Figure 3.2).

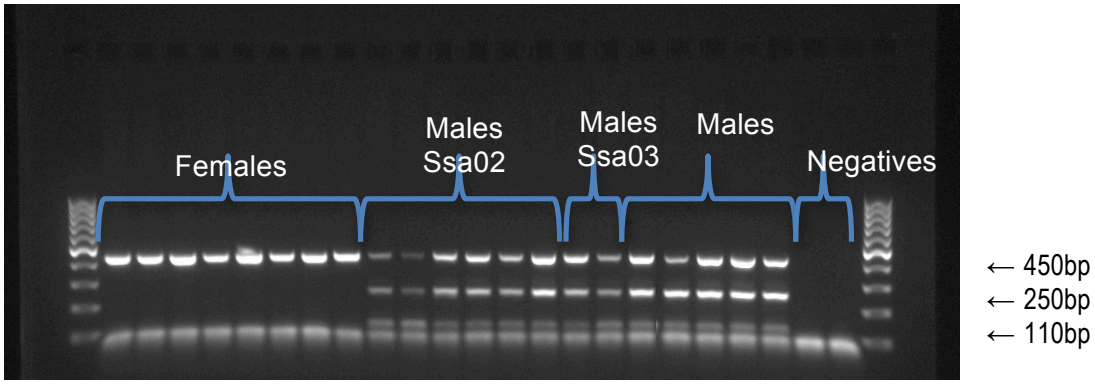


Figure 3.2. sdY triplex PCR test with primers (see methods) from exon 2 (~110 bp) exon 4 (~250 bp) and fabp6b (~450 bp) (Y. Lai personal communication).

Sires are compared to dams from families with *SEX* on Ssa02/ Linkage group 1, Ssa06/ Linkage group 4 and Ssa03/Linkage group 11. The 100 bp ladder is shown in the first and last lanes.

Since both exon 2 and exon 4 should be present in a fully functional *sdY* gene, any individuals in which only one of these two exons amplified were designated as predicted females (e.g. 2009_0279; Figure 3.1) with the following exception: the absence of the quality control *Fabp6b* amplicon, which is indicative of DNA degradation, but presence of the exon 2 product (e.g. 2009_0967; Figure 3.1). In this particular case a male designation was assigned. A full list of the 19 individuals with only an exon 2 or exon 4 amplicon present can be found in Supplementary Table S9. All the parents in the tested 2009YC families were screened using these primer pairs for *sdY*, and there was 100% agreement between parent phenotype and the presence or absence of *sdY* PCR products (Figure 3.1; Supplementary Table S3). Expanding the sample set to include all offspring from the 47 families, yielded a concordance between *sdY* and phenotype to 539/567 for males and 405/409 for females (Supplementary Table S3 and Table S8). Of the total 957 offspring *sdY* test results that were consistent with sex phenotype, 27 disagreed with sex predictions based on genotype (Figure 2.2; Supplementary Table S3 and Table S8). For eleven individuals, in which *sdY* predictions did not match phenotype calls, microsatellite haplotype predictions agreed with predictions made by the *sdY* test (Supplementary Table S8). Figure 3.1 illustrates the examples of most of these instances that have been observed within a single family (2009_32).

4. Discussion

4.1. Multiple sex loci within a species is rare

Fish do not share conservation of a master sex-determining gene, and even closely related species can have different sex-determining genes (Konodo et al. 2003, Myosho et al. 2012, Kikuchi and Hamaguchi 2013). However, it is rare to find this phenomenon within orders of other vertebrates such as mammals and birds. The observation of different master sex-determining genes within a species has not been reported. Although rare, multiple sex-determining gene loci, as shown here for Atlantic salmon, have been described previously in Arctic charr (Moghadam et al. 2007, Küttner et al. 2011).

4.2. A single conserved sex-determining gene

The occurrence of multiple sex linkage groups in salmonid species led to two competing hypothesis: either a single conserved sex-determining gene that can jump between chromosomes exists; or different sex loci represent unique sex-determining genes (Woram et al. 2003, Phillips et al. 2001, Davidson et al. 2009). The recent reports of Yano et al. (2012, 2013) suggest the former hypothesis is correct. Likewise the PCR based survey here, using primers designed from exon 2 and exon 4 of the *sdY* gene, suggests that *sdY* is present in all three male lineages identified in the Tasmanian Atlantic salmon population. However, in a number of individuals, the inherited microsatellite and SNP marker haplotype, the presence or absence of the *sdY* gene and the sex phenotype did not agree. The single individual (2009_0838) that was positive for exon 2 and exon 4 of the *sdY* gene and carried a male haplotype but was phenotypically assessed to be female may represent an error in phenotype assignment. Likewise the same explanation is possible for the eleven *sdY* negative individuals that possessed a female haplotype but were assessed to be phenotypically male (Table 3.2 and Supplementary Table S7). Phenotype assessment can be difficult to make due to variation in gonadal tissue and human error. Human error could have also been

introduced through mix up of samples during DNA extraction; however, because genotyping and *sdY* tests were conducted on the same samples, observed inconsistencies between these two data sets are unlikely to have resulted from this type of error. Alternatively, a male phenotype could be observed when both *sdY* and haplotype tests predict female phenotype due to temperature dependent sex reversal, which has been reported in Tasmanian Atlantic salmon (King et al. 2012). Table 3.2 summarizes explanations for the inconsistencies between *sdY* sex predictions and phenotype while Figure 4.1 summarizes the explanations for possible inconsistent outcomes between *sdY* and phenotypic sex predicted by haplotype. The simplest of these explanations to explain inconsistencies between phenotypic sex predicted by haplotype and the *sdY* test is homologous recombination between the Y and X chromosome (Figure 4.1). Although this study was not set up to test this explanation, which is consistent with the lack of morphological differences between the Y and X (Davidson et al. 2009), six instances of a crossover between the Y chromosome and the X chromosome were observed in individuals 2009_0439, 2009_0090, 2009_0784, 2009_0609, 2009_1089 and 2009_1095 (Supplementary Table S3), one of which, 2009_0609 is also shown in Figure 3.1. Due to the criteria set to assign *SEX* to a particular chromosome (see methods) the depth of coverage of markers from any one linkage group for any one family is too small to assess how often this event actually occurs. However, because recombination is suppressed on the male Y chromosome (Woram et al. 2003, Lien et al. 2011), whether it be chromosome 2, 3 or 6, the rate of crossover is expected to be low. In addition, only a single recombination between the Y and X chromosomes was observed in Family 2009_32 (Figure 3.1, Supplementary Table S3), the second largest family with a male haplotype comprised of markers mapping from 3.1 cM to 113.5 cM on the female linkage map (www.asalbase.org). To date, the function of *sdY* is unknown, but the protein product is predicted to contain an association domain while lacking a DNA binding domain (Figure 4.2, Yano et al. 2012).

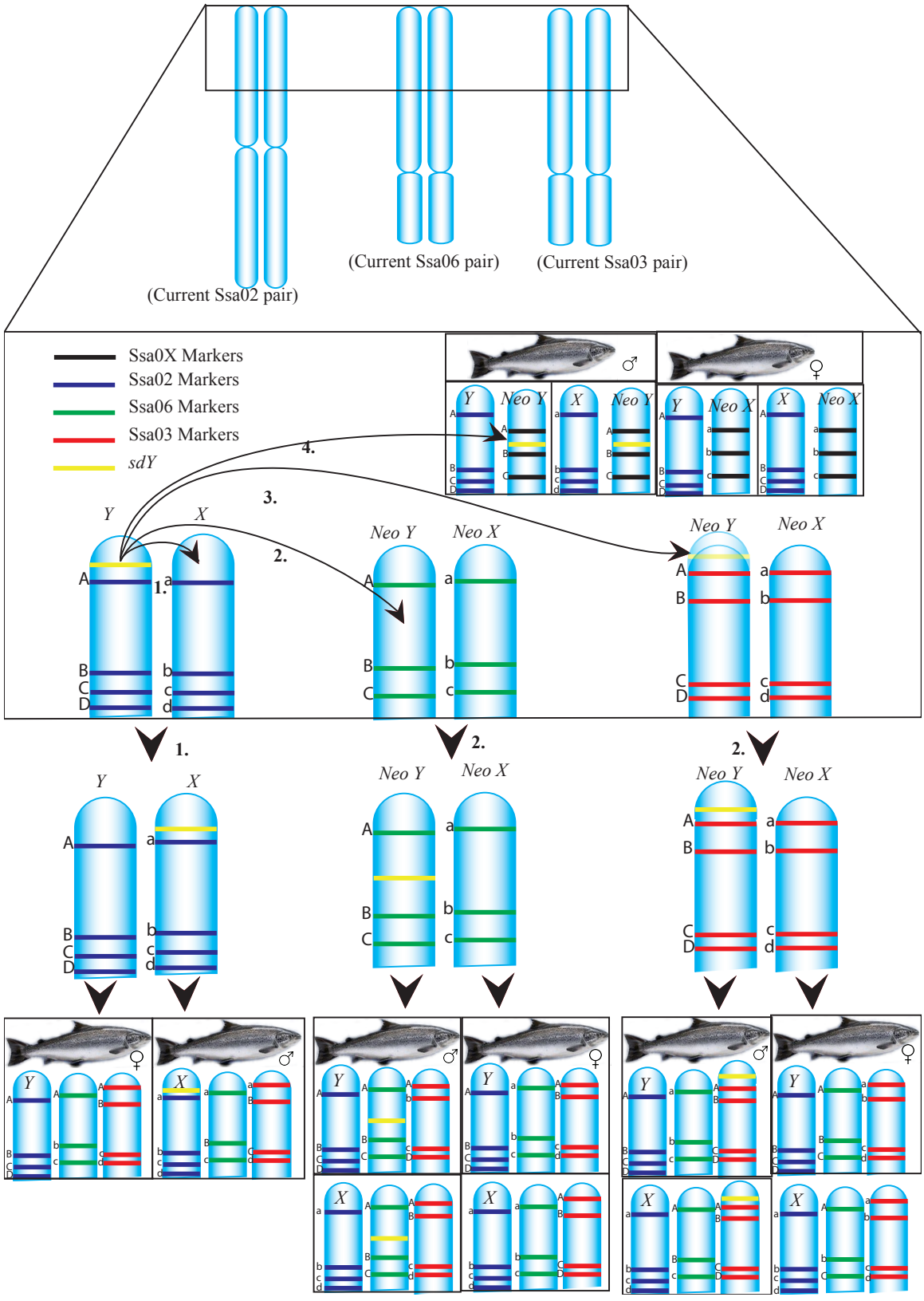

(Current Ssa02 pair)
(Current Ssa06 pair)
(Current Ssa03 pair)
Ssa0X Markers
Ssa02 Markers
Ssa06 Markers
Ssa03 Markers
sdY
1.
2.
3.
4.
Y
X
Neo Y
Neo X

Figure 4.1. Mechanisms of sdY movement during meiosis of a sire with SEX located on Ssa02.

Each major pathway is designated a different number: (1). Homologous recombination including *sdY* between X and Y; (2). Transposition or (3). Translocation of *sdY* to Ssa03 or Ssa06; or (4). Translocation or transposition of sdY to another chromosome within the genome (labeled N). Upon transposition to a new chromosome e.g. Ssa06 or Ssa03 the homologous pair becomes a new X and Y (designated neo X and neo Y) after which point segregation can produce different phenotype/*sdY*/genotype predictions. Note that case 4 could not be observed because individuals in which sex likely jumped were harvested and thus had no offspring that could be analyzed. Following any of these three major events chromosomal segregation further alters the haplotype / *sdY* / phenotype sex predictions (shown at bottom). Homeologous recombination could also occur between the paralogous chromosomes Ssa06 and Ssa03 (outcomes the same as in 2.) This figure also does not include sex-reversal due to temperature (see Table 3.2).

Figure 4.2. Predicted structure of the sdY protein (green ribbon) based on sequence similarity to Interferon regulatory factor 3 association domain (white ribbon: 1QWT) and the well conserved DNA binding domain (blue ribbon 1T2K). Note the orientation of the DNA binding domain is not positioned physiologically with respect to the association domain.

Therefore, because interferon proteins have been shown to inhibit testosterone production, and important factor in male differentiation and development, in leydig cells

it is likely that *sdY* may function as an inhibitor of this action via binding to the interferon regulatory factors (Yano et al. 2012). Since interferon regulatory factors act as a dimer (Chen et al. 2008) an inactive heterodimer may formed between, the *sdY*, lacking a DNA binding domain and the interferon regulatory factor. Alternatively, *sdY* may have a completely new function via interaction with another factor involved in sex determination and this could add another level of complexity to the relationship of the presence of the *sdY* gene, the familial *SEX* genotype and the sex phenotype. Consistent with the idea of a completely novel function is the observation that functionally as a sex determinant *sdY* is lineage specific despite sequence similarity to interferon like proteins in other vertebrates (Yano et al. 2012, 2013). However, the proposed mechanism above is still a novel function compared to the interferon regulatory factors. Along the line of increased complexity in salmonid sex determination, changes in any of several other factors including modifier genes and other key genes in the Atlantic salmon sex-determining pathway could result in naturally observed changes to sex phenotype as is found in some human sex reversal disorders (Eggers and Sinclair 2012). In addition, autosomal influences from what seems to be a weaker sex locus has been observed to sex reverse some rainbow trout females to males in all female populations generated by gynogenesis (Quillet et al. 2002, Valdivia et al. 2013). Therefore, the possibility that *sdY* is not the master sex-determining gene in Atlantic salmon but rather an important downstream player that can alter the sex phenotype should not be ruled out. However, the presence or absence of the *sdY* gene did show 100% concordance with the sex phenotypes of the parents. These individuals have the most accurate sex phenotype calls because progeny have been reared from them.

4.3. Mechanisms of *sdY* movement from one chromosome to another

With a seemingly conserved sex-determining gene (*sdY*) identified in the Tasmanian Atlantic salmon that exhibit three *SEX* loci on different chromosomes, I sought to identify mechanisms by which the *sdY* gene could move about the genome. Given the large regions of homology between the homeologous chromosomes Ssa03 (LG11) and Ssa06 (LG4) in European Atlantic salmon (Lien et al. 2011), recombination between homeologous regions may allow *sdY* movement between Ssa03 and Ssa06. However,

SNP markers did not detect homeology between Ssa02 (LG1) and Ssa03 or Ssa06 (Lien et al. 2011). Rather, Ssa02 shares large homeologous regions with Ssa05 and Ssa12 (Lien et al. 2011). Therefore, it is suggested that the *sdY* gene likely moves by a chromosomal translocation between Ssa02 and Ssa03 or Ssa06. Alternatively, the gene may be able to jump via transposition events (Davidson et al. 2009). At this time it can only be speculated which of these potential mechanisms may have been involved in producing the multiple sex-determining loci observed in Tasmanian Atlantic salmon.

4.4. Why these three loci?

Although the possibility that more than three sex loci exist in Atlantic salmon, it is interesting to speculate why only three loci were observed. Is it merely a coincidence? Has the gene only had the opportunity to jump once or twice? Is there some ancestral homology between chromosomes 2, 3 and 6? or is there some selective advantage to having *SEX* on one of these three chromosomes? The first two questions will require expansion to larger sample sets including families from Europe and North America and thus cannot be answered here.

The third question poses the hypothesis that chromosome 2 is the ancestral locus while chromosomes 3 and 6 which represent few lineages in the sample set may have arisen more recently. Consistent with this hypothesis is the observed slight homology between the Arctic charr sex linkage group 1/21 and Atlantic salmon linkage group 1/6 (Küttner et al. 2011). Linkage group 1 and Linkage group 6 correspond to chromosome 2 (Ssa02) and chromosome 12 (Ssa12) in Atlantic salmon, respectively. In fact comparative homology with stickleback by Lien et al. (2011) showed Ssa02 and Ssa12 q arms were paralogous. However, the homology observed between Atlantic salmon and Arctic char chromosomes constitutes only a single marker and no homology could be found between Atlantic salmon chromosomes 2 and 3 and 6 by ancestral genome comparison method. Therefore at the present moment no deep homology can be found that would have acted as a means for *SEX* movement from Ssa02 to Ssa03 or Ssa06.

What if not all chromosomes are equally good at being sex chromosomes and some are in fact predisposed to carrying out such a role? Such chromosomes house a

collection of sex-determining and differentiation factors (Brelsford et al. 2013). One gene in particular that appears to have deep homology among vertebrates is *Dmrt1* (Brelsford et al. 2013). This gene and or its duplicates seem to continually show up on vertebrate sex chromosomes studied including birds (Smith et al. 2009), mammals (Matson et al. 2011), medaka (Nanda et al. 2002), *Bufotes siculus* (Sicilian green toad)*, Hyla arborea* (European tree frog)*, Rana temporaria* (common frog) *and X. tropicalis* (Yoshimoto et al. 2008, Brelsford et al. 2013). Could it be possible then that this gene and other important sex-determining or differentiating factors are located on these three chromosomes? FISH analysis using bacterial artificial chromosomes (BACs) containing *Dmrt1* and thirteen other characterized sex determination and differentiation factors did not hybridize to any of the three chromosomes identified here (Li 2010). Therefore it seems unlikely that these three chromosomes were predisposed to becoming sex chromosomes in Atlantic salmon.

In summary, all of these different speculations require further testing with the exception of the last hypothesis, which can likely be ruled out. Characterization of the region surrounding *sdY* in the three male lineages would indeed be most valuable to answer the question if deep homology exists between the three sex chromosomes identified here or if a mobile element constitutes the entire homology between Ssa02 and Ssa06 or Ssa03.

4.5. Are there more than three *SEX* loci in Atlantic salmon?

It is surprizing how little genetic mapping of sex-determining loci has actually been carried out in salmonids, particularly Atlantic salmon. For example, only two SALMAP mapping families with parents from the River Tay, Scotland were used in the identification of LG1 (Ssa02) as the *SEX* containing linkage group in Atlantic salmon (Woram et al. 2003, Danzmann et al. 2008). Subsequent genetic mapping studies involving Atlantic salmon, including those using predominantly SNP markers (Lien et al. 2011, Brenna-Hansen et al. 2012), did not incorporate the sex phenotype as a variable when genetic maps were constructed. In Arctic charr two genetic mapping families were initially used to assign *SEX* to LG4 (Woram et al. 2003), and it was not until mapping studies were conducted on other families of Arctic charr that evidence for additional sex-determining loci in this species was reported (Moghadam et al. 2007, Küttner et al.

2011). This rather unexpected observation, coupled with the results reported here, indicate the importance of using many families when mapping *SEX* in salmonid species.

The Tasmanian Atlantic salmon ancestral population came from the River Phillip, Nova Scotia, Canada. Given the chromosomal differences and sub species status of Scottish (European) and Tasmanian (North American derived) Atlantic salmon it was not so surprising to find that *SEX* mapped to a different locus in each strain (Brenna-Hansen et al. 2012). What was astonishing was that three *SEX* loci were found in the Tasmanian population. This population was founded by three introductions in consecutive years in the 1960s. It begs questions then concerning year class differences in the ancestral population, and how many *SEX* loci there are in Atlantic salmon and how these *SEX* loci are distributed across the species range. Moreover, as mentioned earlier, is it possible to identify the ancestral *SEX* locus in *Salmo salar*, and if so does this provide a clue how the *SEX* locus moves about the genome? Based on linkage analysis in four families, *SEX* was mapped to LG28 in brown trout, the sister species to Atlantic salmon in the genus *Salmo* (Woram et al. 2003). Brown trout LG28 corresponds to LG8 (Ssa15) in Atlantic salmon (Li et al. 2011). Thus, no common ancestral *SEX* locus is obvious for the genus *Salmo*. As with Atlantic salmon, it may be worth mapping the sex-determining gene in families of brown trout from several different geographical populations.

5. Conclusions

In summary, three sex loci lineages were identified in the SALTAS Tasmanian Atlantic salmon breeding population, all of which show evidence for the presence of *sdY*. However, at this point it can only be speculated which chromosome houses the ancestral locus and how *sdY* might be moving between these three chromosomes. Characterization of the genomic sequence surrounding the *sdY* gene as well as further linkage analysis to identify individuals in which *sdY* may have jumped are necessary to provide answers for these questions. It still remains unknown how many sex loci there are in Atlantic salmon and if there are any constraints on which chromosomes are appropriate hosts for the sex-determining gene. Thus, further *SEX* linkage analysis across the entire species range of Atlantic salmon should be conducted.

References

Aksnes A., B. Gjerde, and S. O. Roald. 1986. Biological, chemical and organoleptic changes during maturation of farmed Atlantic salmon, *Salmo salar*. Aquaculture 53:7-20.

Allendorf F. W., G. H. Thorgaard. 1984. Tetraploidy and the evolution of salmonid fishes. Pages 1-53 *In* B. J. Turner, editor. Evolutionary Genetics of Fishes, Plenum Publishing, New York.

Amores A., A. Force, Y. L. Yan, L. Joly, C. Amemiya, and A. Fritz. 1998. Zebrafish *hox* clusters and vertebrate genome evolution. Science 282:1711-1714.

Artieria C. G., L. A. Mitchella, S. H. S. Nga, S. E. Parisottoa, R. G. Danzmannb, B. Hoyheimc, R. B. Phillipsd, M. Moraschd, B. F. Koope, and W. S. Davidson. 2006. Identification of the sex-determining locus of Atlantic salmon *(Salmo salar)* on chromosome 2. Cytogenet Genome Res 112:152-159.

Bernard, P., J. Ryan, H. Sim, D.P. Czech, A.H. Sinclair, P. Koopman and V.R. Harley. 2012. Wnt signalling in ovarian development inhibits Sf1 activation of Sox9 via the Tesco enhancer. Endocrinology 153:901-912.

Brelsford A., M. Stöck, C. Betto-Colliard, S. Dubey, C. Dufresnes, H. Jourdan-Pineau, et al. 2013. Homologous sex chromosomes in three deeply divergent anuran species. Evolution 10.1111/evo.12151.

Brenna-Hansen S., J. Li, M. P. Kent, E. G. Boulding, S. Dominik, W. S. Davidson, et al. 2012. Chromosomal differences between European and North American Atlantic salmon discovered by linkage mapping and supported by fluorescence in situ hybridization analysis. Genomics 13:432.

Brunelli J. P., G. H. Thorgaard. 2004. A new Y-chromosome-specific marker for Pacific salmon. Trans Am Fish Soc 133:1247-1253.

Chen W., Lam S.S., Srinath H., Jiang Z., Correia J.J., Schiffer C.A., et al. 2008. Insights into interferon regulatory factor activation from the crystal structure of dimeric IRF5. Nat Struct Mol Biol 11:1213-1220.

Christoffels A., E. G. L. Koh, J. Chia, S. Brenner, S. Aparicio, and B. Venkatesh. 2004. Fugu Genome Analysis Provides Evidence for a Whole-Genome Duplication Early During the Evolution of Ray-Finned Fishes. Mol Biol Evol 21:1146-1151.

Chue J., C. A. Smith. 2011. Sex determination and sexual differentiation in the avian model. FEBS 278:1027-1034.

Cutting A., J. Chue, and C. A. Smith. 2013. Just how conserved is vertebrate sex determination. Dev Dyn 242:380-387.

Danzmann R. G., E. A. Davidson, M. M. Ferguson, K. Gharbi, B. F. Koop, B. Hoyheim, and et al. 2008. Distribution of ancestral proto-Actinopterygian chromosome arms within the genomes of 4R-derivative salmonid fishes (Rainbow trout and Atlantic salmon). BMC Genomics 9:557.

Davidson W. S., T. Huang, K. Fujiki, K. R. von Schalburg, and B. F. Koop. 2009. The Sex-determining Loci and Sex Chromosomes in the Family Salmonidae. Sex Dev 3:78-87.

Davidson W. S., B. F. Koop, S. J. M. Jones, P. Iturra, R. Vidal, A. Maass, and et al. 2010. Sequencing the genome of the Atlantic salmon (*Salmo salar*). Genome Biol 11:403.

Devlin R. H., G. W. Stone, and D. E. Smailus. 1998. Extensive direct tandem organization of a long repeat DNA sequence on the Y-chromosome of chinook salmon (*Oncorhynchus tshawytscha*). J Mol Evol 46: 277–287 46:277-287.

Devlin R. H., B. K. McNeil, T. D. D. Groves, and E. M. Donaldson. 1991. Isolation of a Y-chromosomal DNA probe capable of determining genetic sex in Chinook salmon (*Oncorhynchus tshawytscha*). Can J Fish Aquat Sci 48:1606-1612.

Devlin R. H., Y. Nagahama. 2002. Sex determination and sex differentiation in fish: an overview of genetic, physiological, and environmental influences. Aquaculture 208:191-364.

Dominik S., J. M. Henshall, P. D. Kube, H. King, S. Lien, and M. P. Kent. 2010. Evaluation of an Atlantic salmon SNP chip as a genomic tool for the application in a Tasmanian Atlantic salmon (*Salmo salar*) breeding population. Aquaculture 308:S56-S61.

Eggers S., A. Sinclair. 2012. Mammalian sex determination –insights from humans and mice. Chromosome Res 20:215-238.

Elliott N., P. Kube. 2009. Developement and early results of the Tasmanian Atlantic salmon breeding program. Proc Assoc Advmt Anim Breed Genet 18:362-365.

Ezaz T., R. Stiglec, F. Veyrunes, and J. A. M. Graves. 2006. Relationships between vertebrate ZW and XY sex chromosome systems. Curr Biol 16:R736-R743.

Fishelson L. 1970. Protogynous sex reversal in the fish Anthias squamipinnis (Teleostei, Anthiidae) regulated by the presence or absence of a male fish. Nature 227:90-91.

Fleming A., T. Wibbels, J. K. Skipper, and D. Crews. 1999. Developmental expression of*steroidogenic factor 1* in a turtle with temperature-dependent sex determination. Gen Comp Endocrinol 116:336-346.

Graves J. A. M., C. Peichel. 2010. Are homologies in vertebrate sex determination due to shared ancestry or to limited options? Genome Biol 11:205.

Hahlbeck E., R. Griffiths, and B. E. Bengtsson. 2004. The juvenile three-spined stickleback (*Gasterosteus aculeatus L.*) as a model organism for endocrine disruption. I. Sexual differentiation. Aquat Toxicol 70:287-310.

Hattori R. S., Y. Murai, M. Oura, S. Masuda, S. K. Majhi, T. Sakamoto, et al. 2012. A Y-linked anti-Mullerian hormone duplication takes over a critical role in sex determination. Proc Natl Acad Sci USA 109:2955-2959.

Hewitt L. M., T. G. Kovacs, M. G. Dube, D. L. Maclatchy, P. H. Martel, M. E. McMaster, et al. 2008. Altered reproduction in fish exposed to pulp and paper mill effluents: roles of individual compounds and mill operating conditions. Environ Toxicol and Chem 3:682-697.

Hsiao, N., Samuel, D., Liu, Y., Chen L., Yang, T., Jayaraman, G., et al. 2003. Mutagenesis study on the zebra fish Sox9 high-mobility group: comparison of sequence and non-sequence specific HMG domains. Biochemistry 42:11183-11193.

Hiramatsu R., S. Matoba, M. Kanai-Azuma, N. Tsunekawa, Y. Katoah-Fukui, M. Kurohmaru, et al. 2009. A critical time window of Sry action in gonadal sex determination in mice. Development 136:129-138.

Hoegg S., J. L. Boore, J. V. Kuehl, and A. Meyer. 2008. Comparative phylogenomic analysis of telost fish Hox gene clusters: lessons from the cichlid fish. Astatotilapia burtoni. BMC Genomics 8:317.

Hubbs C. L., L. C. Hubbs. 1932. Apparent parthenogenesis in nature in a form of fish of hybrid origin. Science 76:628-630.

Innan H., F. Kondrashov. 2010. The evolution of gene duplications: classifying and distinguishing between models. Nat Rev Genet 11:97-108.

Iturra P., J. F. Medrano, M. Bagley, N. Lam, N. Vergara, and J. C. Marin. 1997. Identification of sex chromosome molecular markers using RAPDs and fluorescent in situ hybridization in rainbow trout. Genetica 101:209-213.

Jameson S. A., A. Natarajan, J. Cool, T. Defalco, D. M. Maatouk, L. Mork, et al. 2012. Temporal transcriptional profiling of somatic and germ cells reveals biased lineage priming of sexual fate in the fetal mouse gonad. PLoS Genetics 8:e1002575.

Johnstone R., A. F. Youngson. 1984. The progeny of sex-inverted female Atlantic salmon (Salmo salar L.). Aquaculture 37:179-182.

Jones F. C., M. G. Grabherr, Y. F. Chan, P. R. Russell, E. Mauceli, J. Johnson, et al. 2012. The genomic basis of adaptive evolution in threespine sticklebacks. Nature 484:55-61.

Kallman K. D., J. R. Harrington. 1964. Evidence for the existence of homozygous clones in the self fertilizing teleost *Rivulus marmoratus* (Poey). Biol Bull 126:101-114.

Kamiya T., W. Kai, S. Tasumi, A. Oka, T. Matsunaga, N. Mizuno, et al. 2012. A trans-species missense SNP in Amhr2 is associated with sex determination in the tiger pufferfish, *Takifugu rubripes* (fugu). PLoS Genetics 8:e1002798.

Kasahara M., K. Naruse, S. Sasaki, Y. Nakatani, W. Qu, and B. Ahsan. 2007. The medaka draft genome and insights into vertebrate genome evolution. Nature 447:714-719.

Kikuchi K., S. Hamaguchi. 2013. Novel sex-determining genes in fish and sex chromosome evolution. Dev Dyn 242:339-353.

Kim Y., T. Kobayashi, R. Sekido, L. DiNapoli, J. Brennan, M. C. Chaboissier, et al. 2006. Fgf9 and Wnt4 act as antagonistic signals to regulate mammalian sex determination. PLoS Genetics 4:e.187.

King H., N. Ruff, B. Evans, and N. Elliott. 2012. Evidence that sex differentiation in Atlantic salmon is thermolabile. ICISB, Oslo P-018.

Kitano J., J. A. Ross, S. Mori, M. Kume, F. C. Jones, et al. 2009. A role for a neo-sex chromosome in stickleback speciation. Nature 461:1079-1083.

Konodo M., I. Nanda, U. Hornung, S. Asakawa, N. Shimizu, H. Mitani, et al. 2003. Absence of the candidate male sex-determining gene *dmrt1b(Y)* of medaka from other fish species. Curr Biol 13:416-420.

Koopman P., A. Munsterber, B. Capel, N. Vivian, and R. Lovell-Badge. 1990. Expression of a candidate sex-determining gene during mouse testis differentiation. Nature 348:450-452.

Kroon F. J., P. L. Munday, D. A. Westcott, J. P. Hobbs, and N. R. Liley. 2005. Aromatase pathway mediates sex change in each direction. Proc Biol Sci 272:1399-1405.

Küttner E., J. Nilsson, S. Skúlason, S. Gunnarsson, M. M. Ferguson, and R. G. Danzmann. 2011. Sex chromosome polymorphisms in arctic charr and their evolutionary origins. Genome 54:852-861.

Lai Y. Y. Y., K. P. Lubieniecki, B. F. Koop, and W. S. Davidson. 2012. Characterization of the Atlantic salmon (*Salmo salar*) brain type fatty acid binding protein (*fabp7)* genes reveals the fates of teleost fabp7 genes following whole genome duplications. Gene 504:253-261.

Li J. 2010. Sex determination in the genus Salmo. Simon Fraser University Masters Thesis.

Li J., R. B. Phillips, A. S. Harwood, B. F. Koop, and W. S. Davidson. 2011. Identification of the sex chromosomes of brown trout *(Salmo trutta)* and their comparison with the corresponding chromosomes in Atlantic salmon *(Salmo salar)* and rainbow trout (*Oncorhynchus mykiss*). Cytogenet Genome Res 133:25-33.

Lien S., L. Gidskehaug, T. Moen, B. J. Hayes, P. R. Berg, W. S. Davidson, S. W. Omholt, and M. P. Kent. 2011. A dense SNP-based linkage map for Atlantic salmon (*Salmo salar*) reveals extended chromosome homeologies and striking differences in sex-specific recombination patterns. BMC Genomics 12:615.

Luo X., Y. Ikeda, and K. L. Parker. 1994. A cell-specific nuclear receptor is essential for adrenal and gonadal development and sexual differentiation. Cell 77:481-490.

Mank J. E., J. C. Avise. 2006. Phylogenetic conservation of chromosome numbers in Actinopterygiian fishes. Genetica 127:321-327.

Matson C. K., M. W. Murphy, A. L. Saver, M. D. Griswold, V. J. Bardwell, and D. Zarkower. 2011. DMRT1 prevents female reprogramming in the postnatal mammalian testis. Nature 476:101-104.

McGowan C., W. S. Davidson. 1998. The RAPD technique fails to detect a male-specific genetic marker in Atlantic salmon. J Fish Biol 53:1134-1136.

Meyer A., Y. Van der Peer. 2005. From 2R to 3R: evidence for a fish-specific genome duplication (FSGD). Bioessays 27:937-945.

Moghadam H. K., M. M. Ferguson, and R. G. Danzmann. 2007. Linkage variation at the sex-determining locus within Fraser strain Arctic charr *Salvelinus alpinus*. J Fish Biol 71:294-301.

Moghadam H. K., M. M. Ferguson, and M. M. Danzmann. 2005a. Evolution of *Hox* clusters in Salmonidae: A comparative analysis between Atlantic salmon (*Salmo salar*) and rainbow trout (*Oncorhynchus mykiss*). J Mol Evol 61:636-649.

Moghadam H. K., M. M. Ferguson, and R. G. Danzmann. 2005b. Evidence for *Hox* gene duplication in rainbow trout (*Onchorhynchus mykiss*): A tetraploid model species. J Mol Evol 61:804-818.

Moreno-Mendoza N., V. R. Harley, and H. Merchant-Larios. 2001. Temperature regulates SOX9 expression in cultured gonads of *Lepidochelys olivacea*, a species with temperature sex determination. Dev Biol 229:319-326.

Morrish B. C., A. H. Sinclair. 2002. Vertebrate sex determination: many means to an end. Reproduction 124:447-457.

Morton N. E. 1962. Segregation and Linkage. Pages 17-52 *In* W. J. Burdette, editor. Methodology in Human Genetics, Holden Day, San Francisco.

Moyer J. T., M. J. Zaiser. 1984. Early sex change: a possible mating strategy of Centropyge angelfishes (Pisces: Pomacanthidae). J Ethol 2:63-67.

Munger S. C., B. Capel. 2012. Sex and the circuitry: progress toward systems-level understanding of vertebrate sex determination. WIREs Syst Biol Med 4:401-412.

Myosho T., H. Otake, H. Masuyama, M. Matsuda, Y. Kuroki, A. Fujiyama, et al. 2012. Tracing the emergence of a novel sex-determining gene in Medaka*, Oryzias luzonensis*. Genetics 191:163-170.

Nanda I., M. Kondo, U. Hornung, S. Asakawa, C. Winkler, A. Shimizu, et al. 2002. A duplicated copy of DMRT1 in the sex-determining region of the Y chromosome of the medaka, *Oryzias latipes*. Proc Natl Acad Sci U S A 99:11778-11783.

Naruse K., S. Fukamachi, H. Mitani, M. Konodo, T. Matsuoka, S. Kondo, et al. 2000. A Detailed Linkage Map of Medaka, *Oryzias latipes*: Comparative Genomics and Genome Evolution. Genetics 154:1773-1784.

Neaves W. B., P. Baumann. 2011. Unisexual reproduction among vertebrates. Trends in Genetics 27:81-88.

Nelson J. S. 2006. *Fishes of the World*. John Wiley and Sons, New York.

Ocalewicz K., P. Woznicki, G. Furgala-Selezniow, and M. Jankun. 2011. Chromosomal location of Ag/ CMA3-NORs, 5S rDNA and telomeric repeats in two stickleback species. Ital J Zool 78:12-19.

Ohno S. 1970. Evolution by gene duplication. Springer Verlag, New York.

Peichel C. L., J. A. Ross, C. K. Matson, M. Dickson, J. Grimwood, J. Schmutz, R. M. Myers, S. Mori, D. Schluter, and D. M. Kingsley. 2004. The Master Sex-Determination Locus in threespine sticklebacks is on a nascent Y chromosome. Curr Biol 14:1416-1424.

Phillips R. B., P. Rab. 2001. Chromosome evolution in the Salmonidae (Pisces): An update. Biol Rev 76:1-25.

Phillips R. B., K. A. Keatley, M. R. Morasch, A. B. Ventura, K. P. Lubieniecki, and B. F. Koop. 2009. Assignment of Atlantic salmon (*Salmo salar)* linkage groups to specific chromosomes: Conservation of large syntenic blocks corresponding to whole chromosome arms in rainbow trout (*Oncorhynchus mykiss*). BMC Genetics 10:46.

Phillips R. B., N. R. Konkol, K. M. Reed, and J. D. Stein. 2001. Chromosome painting supports lack of homology among sex chromosomes in *Oncorhynchus, Salmo*, and *Salvelinus* (Salmonidae). Genetica 111:119-123.

Quillet, E., G. Aubard, and I. Quéau. 2002. Mutation in a sex-determining gene in rainbow trout: detection and genetic analysis. J Hered 93:91-9.

Rhen T., K. Metzger, A. Schroeder, and R. Woodward. 2007. Expression of putative sex-determining genes during the thermosensitive period of gonad development in the snapping turtle, *Chelydra serpentina*. Sex Dev 1:255-270.

Ross J. A., C. L. Peichel. 2008. Molecular cytogenetic evidence of rearrangements on the Y chromosome of the threespine stickleback fish. Genetics 179:2173-2182.

Schartl M., J. N. Volff. 2002. Sex determination and sex chromosome evolution in the medaka *Oryzias latipes*, and the platyfish, *Xiphophorus maculatus*. Cytogenet Genome Res 99:170-177.

Schartl M., R. B. Walter, Y. Shen, T. Garcia, J. Catchen, A. Amores, et al. 2013. the genome of the platyfish, *Xiphorphorus maculatus*, provides insights into evolutionary adaptation and several complex traits. Nature Genetics 45:567-572.

Sekido R., R. Lovell-Badge. 2008. Sex determination involves synergistic action of SRY and SF1 on a specific Sox9 enhancer. Nature 453:930-934.

Ser J. R., R. B. Roberts, and T. D. Kocher. 2010. Multiple Interacting loci control sex determination in Lake Malawi Cichlid fishes. Evolution 64:486-501.

Shoemaker C. M., D. Crews. 2009. Analyzing the coordinated gene network underlying temperature-dependent sex determination in reptiles. Semin Cell Dev Biol 20:293-303.

Shoemaker C. M., J. Queen, and D. Crews. 2007. Response of candidate sex-determining genes to changes in temperature reveals their involvement in the molecular network underlying temperature-dependent sex determination. Mol Endocrinol 21:2750-2763.

Sidow A. 1996. Gen(om)e duplications in the evolution of early vertebrates. Current Opinion Genet Develop 6:715-722.

Sinclair A. H., P. Berta, M. S. Palmer, J. R. Hawkins, B. L. Griffiths, and M. J. Smith. 1990. A gene from the human sex-determining region encodes a protein with homology to a conserved DNA-binding motif. Nature 346:240-244.

Smith C. A., K. N. Roeszier, Q. J. Hudson, and A. H. Sinclair. 2007. Avian sex determination: what, when and where. Cytogenet Genome Res 117:165-173.

Smith C. A., K. N. Roesier, T. Ohnesorg, D. M. Cummins, P. G. Farlie, T. J. Doran, and et al. 2009. The avian Z-linked gene DMRT1 is required for male sex determination in the chicken. Nature 461:267-271.

Söffker M., C. R. Tyler. 2012. Endocrine disrupting chemicals and sexual behaviors in fish – a critical review on effects and possible consequences. Crit Rev Toxicol 42:653-668.

Takehana Y., S. Hamaguchi, and M. Sakaizumi. 2008. Different origins of ZZ/ZW sex chromosomes in closely related medaka fishes, *Oryzias javanicus* and *O. hubbsi* . Chromosome Res 16:801-811.

Takehana Y., K. Naruse, and M. Sakaizumi. 2005. Molecular phylogeny of the medaka fishes genus *Oryzias* (Beloniformes: Adrianichthyidae) based on nuclear and mitochondrial DNA sequences . Mol Phylogenet Evol 36:417-428.

Thorgaard G. H., G. S. Bailey, D. Williams, D. R. Buhler, S. L. Kaattan, S. S. Ristow, et al. 2002. Status and opportunities for genomics research with rainbow trout. Comp Biochem Physiol B Biochem Mol Biol 133:609-646.

Torres-Maldonado L., N. Moreno-Mendoza, A. Landa, and H. Merchant-Larios. 2001. Timing of SOX9 down regulation and female sex determination in gonads of the sea turtle *Lepidochelys olivacea*. J Exp Zool 290:498-503.

Torres-Maldonado L. C., A. Landa Piedra, N. Moreno-Mendoza, A. Marmolejo-Valencia, A. Meza Martıınez, and H. Merchant-Larios. 2002. Expression profiles of *Dax1, Dmrt1*, and *Sox9* during temperature sex determination in gonads of the sea turtle *Lepidochelys olivacea*. Gen Comp Endocrinol 129:20-26.

Tsend-Ayush E., R. D. Kortschak, P. Bernard, S. L. Lim, J. Ryan, R. Rosenkranz, et al. 2012. Identification of mediator complex 26 (Crsp7) gametologs on platypus X1 and Y5 sex chromosomes: a candidate testis-determining gene in monotremes? Chromosome Res 20:127-128.

Uhlenhaut N. H., S. Jakob, K. Anlag, T. Eisenberger, R. Seikido, J. Kress, et al. 2009. Somatic sex reprogramming of adult ovaries to testes by FOXL2 ablation. Cell 139:1130-1142.

Urton J. R., S. R. McCanna, and C. L. Peichela. 2011. Karyotype Differentiation between Two Stickleback Species (Gasterosteidae). Cytogenet Genome Res 135:150-159.

Valdivia, K., B. Mourot., E. Jouanno., J.-N. Volff., D. Galiana-Arnoux., Guyomard, R., et al. 2013. Sex differentiation in an all-female (XX) rainbow trout population with a genetically governed masculinization phenotype. Sex Dev 7:196-206.

Valenzuela N., A. LeClere, and t. Shikano. 2006. Comparative gene expression of *steroidogenic factor 1* in *Chrysemys picta* and *Apalone mutica* turtles with temperature-dependent and genotypic sex determination. Evol Dev 8:424-432.

Valleley E. M., E. J. Cartwright, N. J. Croft, A. F. Markham, and P. L. Coletta. 2001. Characterization and expression of *Sox9* in the Leopard gecko, *Eublepharis macularius*. J Exp Zool 291:85-91.

Volff J. N., M. Schartl. 2001. Variability of genetic sex determination in poeciiid fishes. Genetica 111:101-110.

Volff J. N., I. Nanda, M. Schmid, and M. Schartl. 2007. Governing sex determination in fish: regulatory putsches and ephemeral dictators. Sex Dev 1:85-99.

Western P. S., J. L. Harry, J. A. M. Graves, and A. H. Sinclair. 1999. Temperature dependent sex determination: upregulation of SOX9 expression after commitment to male development. Dev Dyn 214:171-177.

Wilhelm D., F. Martinson, S. Bradford, M. J. Wilson, A. N. Combes, A. Beverdam, et al. 2005. Sertoli cell differentiation is induced both cell-autonomously and through prostaglandin signalling during mammalian sex determination. Dev Biol 287:111-124.

Woram R. A., K. Gharbi, T. Sakamoto, B. Hoyheim, L. E. Holm, K. Naish, C. McGowan, M. M. Ferguson, R. B. Phillips, J. Stein, R. Guyomard, M. Cairney, J. B. Taggart, R. Powell, W. Davidson, and R. G. Danzmann. 2003. Comparative genome analysis of the primary sex-determining locus in salmonid fishes. Genome Res 13:272-280.

Wright J. E., K. Johnson, A. Hollister, and B. May. 1983. Chromosome pairing in tetraploid derivative salmonid genomes. Isozymes Curr Top Biol Med Res. 10:239-260.

Yano A., B. Nicol, E. Jouanno, E. Quillet, A. Fostier, R. Guyomard, et al. 2013. The sexually dimorphic on the Y-chromosome gene (*sdY*) is a conserved male-specific Y-chromosome sequence in many salmonids. Evol Applic 6: 486-496.

Yano A., R. Guyomard, B. Nicol, E. Jouanno, E. Quillet, C. Klopp, et al. 2012. An immune-related gene evolved into the master sex-determining gene in rainbow trout, *Oncorhynchus mykiss*. Curr Biol 22:1-6.

Yoshimoto S., E. Okada, H. Umemoto, K. Tamura, Y. Uno, C. Nishida-Umehara, et al. 2008. A W-linked DM-domain gene, DM-W, participates in primary ovary development in *Xenopus laevis*. Proc Natl Acad Sci U S A 105:2469-2474.

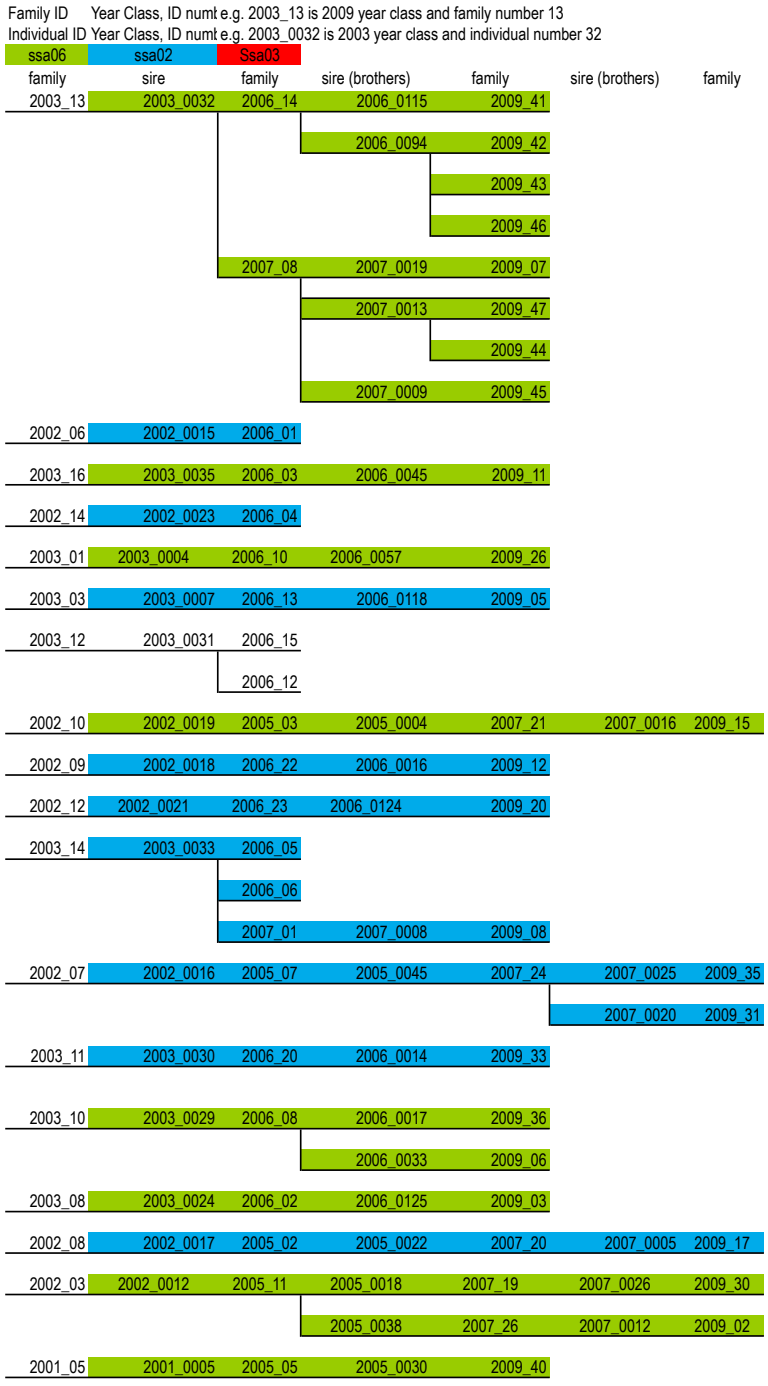
Yukifumi N., S. Ohno. 1977. Testis-Determining H-Y Antigen in X0 Males of the Mole-Vole (*Ellobius lutescens*). Cell 10:729-732.

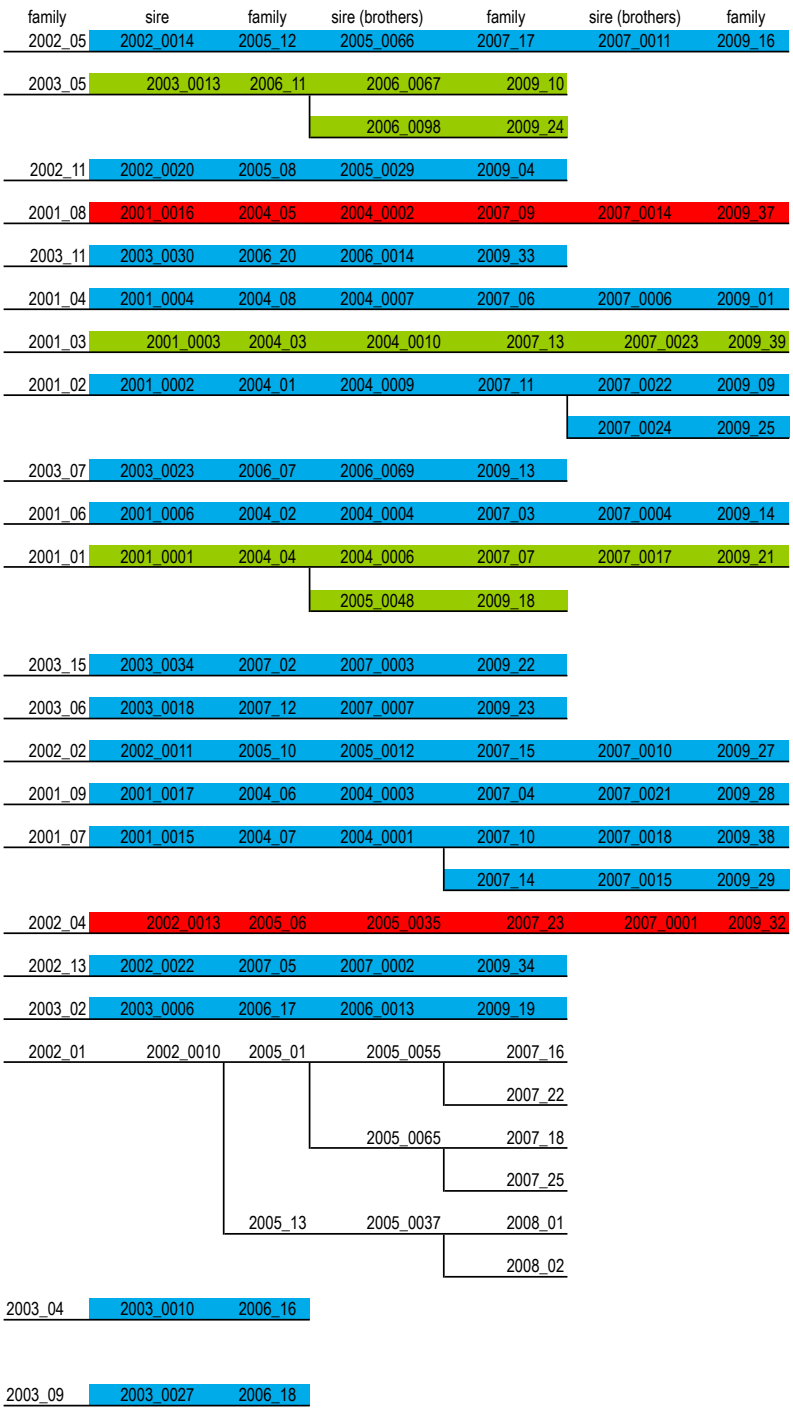
Zhang Q., I. Nakayama, A. Fujiwara, T. Kobayashi, I. Oohara, and T. Masaoka. 2001. Sex identification by male-specific growth hormone pseudogene (GH-ψ) in *Oncorhynchus masou* complex and a related hybrid. Genetica 111:111-118.

Appendix.

Supplementary Tables and Figures

Supplementary Table S1.
Pedigree of the lineages with representation in the 2009 year class




family
sire
family
sire (brothers)
family
sire (brothers)
family
2002_05
2002_0014
2005_12
2005_0066
2007_17
2007_0011
2009_16
2003_05
2003_0013
2006_11
2006_0067
2009_10
2006_0098
2009_24
2002_11
2002_0020
2005_08
2005_0029
2009_04
2001_08
2001_0016
2004_05
2004_0002
2007_09
2007_0014
2009_37
2003_11
2003_0030
2006_20
2006_0014
2009_33
2001_04
2001_0004
2004_08
2004_0007
2007_06
2007_0006
2009_01
2001_03
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2004_0010
2007_13
2007_0023
2009_39
2001_02
2001_0002
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2004_0009
2007_11
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2007_0024
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2003_07
2003_0023
2006_07
2006_0069
2009_13
2001_06
2001_0006
2004_02
2004_0004
2007_03
2007_0004
2009_14
2001_01
2001_0001
2004_04
2004_0006
2007_07
2007_0017
2009_21
2005_0048
2009_18
2003_15
2003_0034
2007_02
2007_0003
2009_22
2003_06
2003_0018
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2001_0017
2004_06
2004_0003
2007_04
2007_0021
2009_28
2001_07
2001_0015
2004_07
2004_0001
2007_10
2007_0018
2009_38
2007_14
2007_0015
2009_29
2002_04
2002_0013
2005_06
2005_0035
2007_23
2007_0001
2009_32
2002_13
2002_0022
2007_05
2007_0002
2009_34
2003_02
2003_0006
2006_17
2006_0013
2009_19
2002_01
2002_0010
2005_01
2005_0055
2007_16
2007_22
2005_0065
2007_18
2007_25
2005_13
2005_0037
2008_01
2008_02
2003_04
2003_0010
2006_16
2003_09
2003_0027
2006_18

Supplementary Table S2.
The 64 SNPs chosen for the genome wide scan. Detailed linkage groups (LG)s can also be found at www.asalbase.org. Additional SNP information is available online at www.asalbase.org

SNPs taken from across the genome.	ID	Alternate ID
LG2	Ssa0193ECIG	16654_489
LG3 only Moen map	Ssa0169aECIG	16265_112
LG4	Ssa0074ECIG	14686_659
LG5	Ssa0131aECIG	15686_402
LG13 only Moen map	Ssa0258ECIG	17495_0157
LG21	Ssa0063cECIG	14392_0452
LG6	Ssa0156ECIG	16129_0239
LG17 only Moen map	Ssa0064ECIG	14468_0119
LG19	Ssa0158ECIG	16147_0613
LG24	Ssa0030ECIG	13579_599
LG28 only Moen map	Ssa0023ECIG	13197_0590
LG33	Ssa0099ECIG	15153_346
LG11	Ssa0137ECIG	15804_0172
LG13 only Moen map	Ssa0142ECIG	15912_0572
LG18	Ssa0082ECIG	14834_0524
LG18	Ssa0052ECIG	14186_163
LG23	Ssa0045ECIG	14053_0820
LG25 only Moen map	Ssa0037ECIG	13907_0121
LG16	Ssa0207ECIG	16791_0446
LG14 only Moen map	Ssa0214ECIG	16856_0321
LG20	Ssa0244ECIG	17230_430
LG31	Ssa0172ECIG	16317_0150
LG15	Ssa0205ECIG	16783_0060
LG7	Ssa0194ECIG	16677_0620
LG23	Ssa154SSFU	Contig925
LG18	Ssa150SSFU	Contig831
LG1 only Moen map	Ssa0182ECIG	16475_1011
LG2	Ssa0078ECIG	14746_388
LG8	Ssa0218ECIG	16903_662
LG9	Ssa0081ECIG	14800_360
LG9	Ssa0028ECIG	Contig13513_0493
LG5	Ssa0170ECIG	Contig16294_0244
LG8	Ssa0217ECIG	Contig16890_1072
LG15	Ssa0248ECIG	Contig17293_0832
LG3	Ssa0250ECIG	Contig17321_0691
LG25	Ssa0147SSFU	Contig 573
LG11	Ssa0062ECIG	Contig14389_0361
LG2	Ssa0072ECIG	Contig14649_80
LG12	Ssa0079bECIG	Contig14757_562
LG20	Ssa0109ECIG	Contig15309_266
LG16	Ssa0119ECIG	Contig15513_384
LG10	Ssa0126aECIG	Contig15610_504

SNPs taken from across the genome.	ID	Alternate ID
LG18	Ssa0157ECIG	Contig16140_0475
LG24	Ssa0167ECIG	Contig16258_0579
LG25	Ssa0168ECIG	Contig16260_0757
LG23	Ssa0004ECIG	Contig11981_0368
LG19	Ssa0091ECIG	Contig15004_0676
LG14	Ssa0257ECIG	Contig17489_0078
LG22	Ssa0005ECIG	Contig12000_0548
LG21	Ssa0019ECIG	Contig12869_0119
LG28	Ssa0044ECIG	Contig14035_0356
LG17	Ssa0055ECIG	Contig14230_0080
LG31	Ssa0127ECIG	Contig15618_92
LG13	Ssa0190ECIG	Contig16609_0285
LG32	Ssa0032bECIG	Contig13615_543
LG6	Ssa0049ECIG	Contig14161_559
LG33	Ssa0087ECIG	Contig14962_456
LG4	Ssa0103aECIG	Contig15190_1379
LG1	Ssa0166ECIG	Contig16240_0204
LG10 only Moen map	Ssa0093ECIG	15042_307
LG2	Ssa1SSFU	Contig94
LG25	Ssa147SSFU	Contig573
LG2	Ssa10SSFU	Contig1167
LG6	Ssa158SSFU	Contig1062

Supplementary Table S3. Comprehensive Survey of the 2009 Year class. Microsatellite SNP and sdY raw data is organized by families.

Legend: AS-Ancestral sire | S1 or S2 is sire | D1 or D2 is dam | Unknown | Known Male | Predicted male | Known female | Predicted female | Discrepancy | sex predicted for this family | sdY presence and absence indicated by 1 and 0 respectively for:

Markers: Ssa02/LG1 | Ssa06/LG4 | Ssa03/LG11 — Actual known phenotypes are displayed in the" Sex call from Pheotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class_Family 5. Individual ID in format Year class_Individual number e.g. 2003_0007 = 2003 Year class_Individual 0007

Exon 2 | Exon 4 | Fabp6 (DNA quality control)

Family 2009_05 — Ssa02 parents and sdY agree 100%

	AS1-2003_0007	AS2	S1-2006_0118	S2	2009_0048	2009_0181	2009_0542	2009_0280	2009_0326	2009_0585	2009_0810	2009_0046	2009_0152	2009_0161	2009_0196	2009_0197	2009_0433	2009_0483	2009_0648	2009_0729	2009_0742	2009_0796	2009_0232
Ssa0055BSFU	5	5	5	11	5	5	5	5	5	5	11	5	11	5	5	6 or 11?	5	11	11	5	5	11	11
Ssa0350BSFU	6	3	6	4	4	6	4	4	4	6	6	6	6	6	6	4	6	6	6	4	6	4	6
Ssa0818BSFU	1	3	1	3	1	1	1	1	1	1	3	3	3	3	3	3	3	3	1	1	3	3	1

			D1-2005_0011	D2	2009_0048	2009_0181	2009_0542	2009_0280	2009_0326	2009_0585	2009_0810	2009_0046	2009_0152	2009_0161	2009_0196	2009_0197	2009_0433	2009_0483	2009_0648	2009_0729	2009_0742	2009_0796	2009_0232
Ssa0055BSFU			2	6	6	6	2	2	6	2	2	6	6	2	2	2	6	6	6	2	2	6	2
Ssa0350BSFU			4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Ssa0818BSFU			1	2	1	1	1	1	2	2	2	1	2	1	1	2	1	1	2	2	1	2	2
Exon 2					0	1	1	1	1	1	0	1	0	1	1	0	1	0	0	1	1	0	0
Exon 4					1	1	1	1	1	1	0	1	0	1	1	0	1	0	0	1	1	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype Match?	Male	Male	Male	Male	Male	Male	Not present	Male	No Gonad	Not present	Male	No call	Not present	Female	Female	Male	Male	Female	Female

Family 2009_08 — Ssa02 parents and sdY agree 100%

	AS1-2003_0033	AS2	S1-2007_0008	S2	2009_0054	2009_0057	2009_0439	2009_0681	2009_0746	2009_0820	2009_0870	2009_0937	2009_0956	2009_0587	2009_0539	2009_0300	2009_0132	2009_0205	2009_0319	2009_0351	2009_0373	2009_0445	2009_0491	2009_0516	2009_0560	2009_0602	2009_0638	2009_0666	2009_0768	2009_0941	2009_0963	2009_0978	2009_0545
Ssa0055BSFU	8	3	5	8	6	6	8	6	6	6	6	6	6	6	6	6	8	8	8	8	6	8	5	5	6	8	5	5	8	6	8	8	8
Ssa0183BSFU	3	6	3	2	3	3	3	3	3	3	3	3	3	3	3	3	2	2	2	2	3	2	3	3	3	2	3	3	2	3	2	2	2
Ssa0350BSFU	4	5	4	5	4	4	4	5	5	5	5	5	4	4	5	5	4	4	4	5	5	5	5	4	5	5	4	4	4	4	5	5	5
Ssa0368BSFU	5	2	5	2	5	5	2	2	3?	5	2	5	5	2	2	5	2	2	2	5	5	5	5	5	5	5	2	2	5	5	2	2	2

			D1-2005_0006	D2	2009_0054	2009_0057	2009_0439	2009_0681	2009_0746	2009_0820	2009_0870	2009_0937	2009_0956	2009_0587	2009_0539	2009_0300	2009_0132	2009_0205	2009_0319	2009_0351	2009_0373	2009_0445	2009_0491	2009_0516	2009_0560	2009_0602	2009_0638	2009_0666	2009_0768	2009_0941	2009_0963	2009_0978	2009_0545
Ssa0055BSFU			1	5	5	5	1	1	5	5	5	5	5	1	1	1	5	5	5	1	1	5	1	5	5	1	1	1	5	1	5	5	5
Ssa0183BSFU			2	6	6	6	2	2	6	6	6	6	6	2	2	2	6	6	6	2	2	6	2	6	6	2	2	2	6	2	6	6	6
Ssa0350BSFU			3	6	3	3	3	6	6	6	6	6	6	3	3	3	6	6	3	3	6	3	3	6	6	3	6	3	6	3	6	3	6
Ssa0368BSFU			4	5	5	4	5	5	5	5	4	5	5	5	5	4	4	4	4	4	4	4	5	4	4	4	5	5	5	5	5	5	5
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	1	1	0	1	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	1	1	0	1	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype Match?	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Not Present	Female	Female	Female	Female	Female	Male	Male	Male	Female	Male	Male	Female	Male	Not present	Female	Female

Family 2009_12 — Ssa02 parents and sdY agree 100%

	AS1-2002_0018	AS2	S1-2006_0016	S2	2009_0225	2009_0342	2009_0398	2009_0447	2009_0934	2009_0116	2009_0323	2009_0769	2009_0266	2009_0115	2009_0146	2009_0553	2009_0078	2009_0443	2009_0356	2009_0341	2009_0971	2009_0716	2009_0725	2009_0736	2009_0313	2009_0973	2009_1010	2009_0536
Ssa0233BSFU	1	3	1	3	1	1	1	1	1	1	1	1	1	1	3?	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0769BSFU	2	4	2	3	2	2	3	2	3	3	2	3	2	2	3	3	3	3	2	3	3	2	2	3	2	2	2	3
Ssa0212BSFU	1	1	1	2	1	2	1	1	1	2	1	1	2	1	2	2	2	1	2?	1	1	1	1?	1	1	1	2	1

			D1-2005_0054	D2	2009_0225	2009_0342	2009_0398	2009_0447	2009_0934	2009_0116	2009_0323	2009_0769	2009_0266	2009_0115	2009_0146	2009_0553	2009_0078	2009_0443	2009_0356	2009_0341	2009_0971	2009_0716	2009_0725	2009_0736	2009_0313	2009_0973	2009_1010	2009_0536
Ssa0233BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0769BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0212BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1	1	1	1	1
Exon 2					1	0	1	1	1	?	1	1	1	1	0	?	0	0	0	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	?	1	1	1	1	0	?	0	0	0	0	0	0	1	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype Match?	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female

Family 2009_19 — Ssa02 parents and sdY agree 100%

	AS1-2003_0026	AS2	S1-2006_0013	S2	2009_0001	2009_0044	2009_0098	2009_0109	2009_0133	2009_0182	2009_0215	2009_0273	2009_0463	2009_0512	2009_0754	2009_0777	2009_0837	2009_0896	2009_0250	2009_0606
Ssa0055BSFU	5	3	5	10	5	5	10	10	5	10	5	10	5	10	5	10	5	5	10	10
Ssa0769BSFU	1	1	1	4	4	4	4	4	1	4	4	1	1	4	1	4	1	4	4	1
SsaD144	3	2	3	4	4	3	3	3	4	4	4	3	3	3	4	4	3	4	4	4

			D1-2005_0057	D2	2009_0001	2009_0044	2009_0098	2009_0109	2009_0133	2009_0182	2009_0215	2009_0273	2009_0463	2009_0512	2009_0754	2009_0777	2009_0837	2009_0896	2009_0250	2009_0606
Ssa0055BSFU			2	5	2	2	5	5	2	5	2	5	5	5	5	5	2	5	5	5
Ssa0769BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
SsaD144			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Exon 2					1	1	0	0	1	0	1	0	1	0	1	0	1	1	0	0
Exon 4					1	1	0	0	1	0	1	0	1	0	1	0	1	1	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype Match?	Male	Not Present	Female	Female	Male	Not Present	Male	Female	Male	Female	Not Present	Female	Not Present	Male	Female	Female

Family 2009_31 — Ssa02 parents and sdY agree 100%

	AS1-2002_0016	AS2	S1-2007_0020	S2	2009_0003	2009_0236	2009_0244	2009_0276	2009_0720	2009_0756	2009_0930	2009_1004	2009_0119	2009_0451	2009_0730	2009_0657	2009_0600	2009_0970	2009_0249	2009_0271	2009_0278	2009_0290	2009_0575	2009_0630	2009_0658	2009_0803	2009_0811	2009_0878	2009_0919	2009_0976	2009_0979	2009_0959
Ssa0055BSFU	1	5	1	5	1	1	1	1	1	6	1	1	1	1	1	1	1	1	6	6	6	6	6	6	6	6	6	6	6	6	6	6
Ssa0183BSFU	2	1	2	6	2	2	2	2	2	6	2	2	2	2	2	2	2	2	2	2	6	6	6	6	6	2	6	6	6	6	6	6
Ssa0769BSFU	1	1	1	2	1	3	1	3	1	3	1	3	1	1	1	3	3	1	1	?	1	1	1	1	1	1	1	3	?	1	1
Ssa0368BSFU	4	5	4	3	3	3	3	3	3	3	3	3	3	3	3	4	3	4	3	3	4	3	3	3	4	3	3	3	4	3	3	3

			D1-2006_0083	D2	2009_0003	2009_0236	2009_0244	2009_0276	2009_0720	2009_0756	2009_0930	2009_1004	2009_0119	2009_0451	2009_0730	2009_0657	2009_0600	2009_0970	2009_0249	2009_0271	2009_0278	2009_0290	2009_0575	2009_0630	2009_0658	2009_0803	2009_0811	2009_0878	2009_0919	2009_0976	2009_0979	2009_0959
Ssa0055BSFU			10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Ssa0183BSFU			2	3	2	2	2	3	2	3	2	3	3	3	3	3	3	2	3	3	3	3	2	2	2	3	2	2	2	2	3	2
Ssa0769BSFU			1	3	1	1	4	4	1	1	1	4	1	1	1	4	4	4	4	?	4	1	4	1	4	1	1	4	?	1	4
Ssa0368BSFU			3	6	6	6	3	3	6	6	3	6	6	6	3	6	3	3	6	3	3	6	6	6	6	6	6	6	3	3	6
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	0	0	0	1	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	0	0	0	1	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype Match?	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Not Present	Not Present	Male	Female	Female	Not Present	Not Present	Female	Female	Female

Family 2009_33 — Ssa02 parents and sdY agree 100%

	AS1-2003_0030	AS2	S1-2006_0014	S2	2009_0149	2009_0305	2009_0389	2009_1001	2009_0898	2009_0138	2009_0335	2009_0511	2009_0788	2009_0861	2009_0912	2009_0530	2009_0564	2009_0322	2009_0223	2009_0257	2009_0180	2009_0093	2009_0307	2009_0235	2009_0362	2009_0574	2009_0682	2009_0694	2009_0757
Ssa0055BSFU	8	12	8	3	8	8	8	8	8	8	8	8	8	3	3	3	3	3	8	3	3	3	3	3	3	3	3	3
Ssa0233BSFU	1	3	1	3	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa1209BSFU	3	2	3	1	1	1	3	3	1	3	1	1	1	1	1	3	3	3	3	3	1	1	3	3	1	3	3	3	1
Ssa0368BSFU	6	4	6	4	6	4	6	6	4	6	4	6	6	4	4	6	6	4	4	6	6	6	6	4	4	4	4	4

			D1-2006_0088	D2	2009_0149	2009_0305	2009_0389	2009_1001	2009_0898	2009_0138	2009_0335	2009_0511	2009_0788	2009_0861	2009_0912	2009_0530	2009_0564	2009_0322	2009_0223	2009_0257	2009_0180	2009_0093	2009_0307	2009_0235	2009_0362	2009_0574	2009_0682	2009_0694	2009_0757
Ssa0055BSFU			5	8	8	5	8	5	5	8	8	5	5	5	8	8	5	5	5	8	5	5	5	8	8	5	5	5
Ssa0233BSFU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa1209BSFU			1	2	1	1	2	2	2	2	2	1	1	1	1	2	2	1	2	1	1	1	2	1	1	2	1	2	2
Ssa0368BSFU			1	4	4	1	4	1	1	1	4	4?	4	1	1	1	4	4	4	1	4	1	1	4	1	1	4	1	1
Exon 2					1	1	1	1	1	1	1	1	1	0	0	?	0	0	1	0	0	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	0	0	?	0	0	1	0	0	0	0	0	0	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype Match?	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Not Present	Female	Female	Not Present	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female

Legend	AS-Ancestral sire	S1 or S2 is sire	D1 or D2 is dam	Unknown	Known Male	Predicted male	Known female	Predicted female	Discrepancy	sex predicted for this family	sdY presence and absence indicated by 1 and 0 respectively for:
Markers	Ssa02/LG1										Exon 2
	Ssa06/LG4	Actual known phenotypes are displayed in the" Sex call from Pheotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class_Family 5.									Exon 4
	Ssa03/LG11	Individual ID in format Year class_Individual number e.g. 2003_0007 = 2003 Year class_Individual 0007									Fabp6 (DNA quality control)

Match?

2009_35 Ssa02 parents and *sdY* agree 100%

	AS1-2002_0016	AS2	S1-2007_0025	S2	2009_0317	2009_0382	2009_0420	2009_0429	2009_0478	2009_0776	2009_0580	2009_0833	2009_0974	2009_0345	2009_0822	2009_0582	2009_0396	2009_0068	2009_0186	2009_0203	2009_0212	2009_0246	2009_0260	2009_0344	2009_0354	2009_0503	2009_0569	2009_0662	2009_0858	2009_0891	2009_0960	2009_0566	2009_0850
Ssa1077BSFU	10	3	10	7	10	10	10	10	10	10	10	10	10	10	10	7	10	7	7	10	7	7	10	10	10	10	10	7	10	7	10	7	7
Ssa0055BSFU	1	1	1	10	1	1	1	1	1	1	1	1	1	1	1	10	1	10	10	1	10	10	1	1	1	1	1	10	1	10	1	10	10
Ssa0183BSFU	2	2	2	4	2	2	2	2	2	2	2	2	?	2	2	4	2	4	4	2	4	4	2	2	2	2	2	4	2	4	2	4	4
Ssa1299BSFU	3	3	3	2	3	2	2	2	2	2	3	3	3	2	2	2	3	2	2	2	2	3	2	3	3	2	3	2	3	2	3	3	2
Ssa0368BSFU	4	6	4	6	4	4	6	6	6	?	6	4	4	4	4	4	6	6	6	4	6	6	6	4	4	4	4	6	4	6	4	4	6
			D1-2005_0059	D2	2009_0317	2009_0382	2009_0420	2009_0429	2009_0478	2009_0776	2009_0580	2009_0833	2009_0974	2009_0345	2009_0822	2009_0582	2009_0396	2009_0068	2009_0186	2009_0203	2009_0212	2009_0246	2009_0260	2009_0344	2009_0354	2009_0503	2009_0569	2009_0662	2009_0858	2009_0891	2009_0960	2009_0566	2009_0850
Ssa1077BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0055BSFU			11	12	11	12	12	12	12	12	11	12	11	11	12	12	12	11	12	11	11	11	12	11	12	11	11	11	12	11	11	11	12
Ssa0183BSFU			3	3	3	3	3	3	3	3	3	3	?	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa1299BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0368BSFU			2	7	7	2	2	2	7	?	7	7	3?	2	2	2	2	7	7	2	2	2	2	2	2	7	2	2	2	2	2	7	2
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0	1	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	1	1?	0	1	0	0	1	1	1	1	1	0	1	0	1	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Male	Female	Female	Male	Male	Male	Male	Male	Female	Male	Female	Male	Female	Female
Match?																																	

2009_17 Ssa02 100% parents and *sdY* agree 100%

	AS1-2002_0017	AS2	S1-2007_0005	S2	2009_0065	2009_0350	2009_0291	2009_0938	2009_0007	2009_0009	2009_0095	2009_0131	2009_0285	2009_0286	2009_0302	2009_0329	2009_0339	2009_0428	2009_0452	2009_0489	2009_0498	2009_0549	2009_0591	2009_0617	2009_0872	2009_0935	2009_1000	2009_0809	2009_0828	2009_1006	2009_0856
Ssa0055BSFU	8	13	8	4	8	8	8	8	4	8	8	4	8	8	4	8	8	4	4	4	8	4	8	4	8	4	4	4	4	4	4
Ssa1299BSFU	1	3	1	3	3	3	3	3	3	3	1	1	3	3	3	3	3	1	1	1	3	1	1	1	3	1	3	3	3	1	3
Ssa0017BSFU	3	6	3	6	3	3	6	3	3	?	3	6	3	6	3	3	3	3	3	3	6	6	6	3	3	6	3	6	6	6	3
			D1-2005_0043	D2	2009_0065	2009_0350	2009_0291	2009_0938	2009_0007	2009_0009	2009_0095	2009_0131	2009_0285	2009_0286	2009_0302	2009_0329	2009_0339	2009_0428	2009_0452	2009_0489	2009_0498	2009_0549	2009_0591	2009_0617	2009_0872	2009_0935	2009_1000	2009_0809	2009_0828	2009_1006	2009_0856
Ssa0055BSFU			4	5	4	5	5	4	5	4	4	5	4	5	5	5	4	5	5	4	4	5	5	5	4	5	5	4	5	4	5
Ssa1299BSFU			1	2	2	1	1	1	1	1	2	2	2	1	1	2	2	2	2	2	1	2	2	2	1	2	2	1	1	2	1
Ssa0017BSFU			3	4	4	3	3	4	4	?	4	4	4	4	3	3	3	4	4	3	4	4	3	3	4	3	3	4	4	4	4
Exon 2					1	1	1	1	0	1	1	0	1	1	0	1	1	0	0	0	1	0	1	0	1	0	0	0	0	0	0
Exon 4					1	1	1	1	0	0	1	0	1	1	0	1	1	0	0	0	1	0	1	0	1	0	0	0	0	0	0
Fabp6b					1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Not present	Male	Male	Female	Male	Male	Female	Male	Male	Female	Not Present	Female	Male	Female	Male	Female	Male	Female	Female	Female	Female	Female	Female
Match?																															

2009_20 Confirmed Ssa02 parents and *sdY* agree 100%

	AS1-2002_0021	AS2	S1-2006_0124	S2	2009_0002	2009_0026	2009_0056	2009_0113	2009_0178	2009_0179	2009_0308	2009_0376	2009_0471	2009_0475	2009_0649	2009_0661	2009_0672	2009_0693	2009_0866	2009_0977	2009_1002	2009_0189	2009_0502	2009_0717	2009_0081	2009_0064	2009_0082	2009_0108	2009_0228	2009_0268	2009_0371	2009_0523	2009_0616	2009_0678	2009_0679	2009_0689	2009_0706	2009_0867	2009_0943	2009_0989	2009_0122	2009_0265	2009_0476	2009_0687	2009_0819	2009_0876	2009_0916	2009_0928	2009_0964	2009_1027	2009_0781	2009_0731	2009_0510	2009_0990	2009_0835	2009_0614	2009_0991	2009_1008
Ssa0055BSFU	12	9	12	9	12	12	12	12	12	12	12	12	12	12	12	12	9	12	12	12	12	12	12	12	12	12	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	12	9	9	9	9	9	9	9?	12
OMM5037/1	5	8	5	2	2	2	5	5	5	2	5	5	2	5	2	2	5	5	5	2	5	5	5	5	5	2	5	2	5	5	5	5	2	2	5	2	2	5	5	2	5	2	2	2	5	2	5	5	5	5	5	5	5	5	2	2	2	5
Ssa0368BSFU	3	4	3	7	3	7	3	7	3	3	3	3	3	7	3	7	3	7	7	3	3	7	7	7	3	?	3	3	3	?	3	3	7	3	7	3	3	3	3	3	3	3	3	7	3	7	3	3	3	3	3	3	7	3	7	7	3	7
			D1-2005_0057	D2	2009_0002	2009_0026	2009_0056	2009_0113	2009_0178	2009_0179	2009_0308	2009_0376	2009_0471	2009_0475	2009_0649	2009_0661	2009_0672	2009_0693	2009_0866	2009_0977	2009_1002	2009_0189	2009_0502	2009_0717	2009_0081	2009_0064	2009_0082	2009_0108	2009_0228	2009_0268	2009_0371	2009_0523	2009_0616	2009_0678	2009_0679	2009_0689	2009_0706	2009_0867	2009_0943	2009_0989	2009_0122	2009_0265	2009_0476	2009_0687	2009_0819	2009_0876	2009_0916	2009_0928	2009_0964	2009_1027	2009_0781	2009_0731	2009_0510	2009_0990	2009_0835	2009_0614	2009_0991	2009_1008
Ssa0055BSFU			3	5	3	3	3	5	3	5	3	5	3	5	3	3	5	5	5	3	5	3	3	5	3	5	5	3	5	3	5	5	5	3	5	5	3	3	5	5	5	5	3	5	3	3	3	3	3	3	3	3	3	5	5?	3	5	5
OMM5037/1			4	7	7	7	7	4	4	4	7	7	7	4	4	4	4	4	4	7	4	4	4	7	4	4	4	7	7	4	4	7	7	4	4	4	7	7	4	7	4	7	4	7	7	4	7	7	7	7	4	7	7	4	7	7	4	7
Ssa0368BSFU			5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	?	5	5	5	?	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Not present	Female	Female	Female	Not Present	Female	Not Present	Female	Female	Female	Female	Female	Female	Not Present	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female
Match?																																																										

2009_04 Ssa02 parents and *sdY* agree 100%

	AS1-2002_0020	AS2	S1-2005_0029	S2	2009_0013	2009_0053	2009_0073	2009_0233	2009_0252	2009_0294	2009_0407	2009_0408	2009_0469	2009_0556	2009_0589	2009_0744	2009_0948	2009_0945	2009_0016	2009_0385	2009_0043	2009_0063	2009_0211	2009_0296	2009_0321	2009_0325	2009_0336	2009_0353	2009_0442	2009_0488	2009_0515	2009_0628	2009_0633	2009_0696	2009_0708	2009_0831	2009_0892	2009_0968	2009_0995	2009_1023	2009_0334	2009_0444	2009_0366	2009_1012
Ssa0055BSFU	12	6	12	4	4	4	?	12	4	12	12	12	12	12	12	12	12	12	12	12	12	12	12	4	4	12	4	4	12	12	4	4	4	4	4	4	4	12	12	12	4	4	4	12 or 4?
Ssa0752BSFU	2	2	2	3	2	2	3	2	2	2	2	3	2	2	2	3	3	2	3	2	2	2	2	2	3	3	2	2	2	3	2	3	3	3	2	2	2	3	2	2	2	2	2	3
Ssa0343BSFU	3	1	3	2	?	?	?	?	3	3	?	2	3	?	2	2	2	2	2	3	?	2	3	3	2	2	2	?	2	3	3	3	3	3	3	2	2	3	3	2	3	3	2	4
			D1-2006_0089	D2	2009_0013	2009_0053	2009_0073	2009_0233	2009_0252	2009_0294	2009_0407	2009_0408	2009_0469	2009_0556	2009_0589	2009_0744	2009_0948	2009_0945	2009_0016	2009_0385	2009_0043	2009_0063	2009_0211	2009_0296	2009_0321	2009_0325	2009_0336	2009_0353	2009_0442	2009_0488	2009_0515	2009_0628	2009_0633	2009_0696	2009_0708	2009_0831	2009_0892	2009_0968	2009_0995	2009_1023	2009_0334	2009_0444	2009_0366	2009_1012
Ssa0055BSFU			6	6	6	6	?	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	?
Ssa0752BSFU			1	4	4	1	?	1	1	1	1	4	1	4	4	4	1	4	4	1	4	4	4	1	4	1	4	1	4	4	1	1	1	4	1	1	4	1	1	1	4	4	1	1
Ssa0343BSFU			2	2	2	2	?	2	2	2	?	2	2	?	2	2	2	2	2	2	2	2	2	2	2	2	2	?	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1?
Exon 2					1	0	?	1	1	1	1	0	1	?	1	1	1	1	1	1	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1	1	1	0	0	0	1
Exon 4					1	0	?	1	1	1	1	0	1	?	1	1	1	1	1	1	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1	1	1	0	0	0	1
Fabp6b					1	1	?	1	1	1	1	1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Not Present	Male	Not Present	Not Present	Male	Hermaphrodite	Female	Not Present	Male	Not present	Not Present	Female	Female	Female	Female	Not Present	Male	Male	Male	Female	Female	Female	female
Match?																																												

2009_02 Ssa06 parents and *sdY* agree 100%

	AS1-2002_0012	AS2	S1-2007_0012	S2	2009_0066	2009_0071	2009_0085	2009_0399	2009_0421	2009_0816	2009_0983	2009_0192	2009_0677	2009_0462	2009_0141	2009_0187	2009_0843	2009_0853	2009_0869	2009_1025	2009_0454	2009_0128	2009_0668	2009_0712
Ssa1299BSFU	1	3	1	3	1	1	1	1	1	1	1	3	1	1	3	3	3	1	1	3	3	3	3	3
Ssa0055BSFU	2	11	2	5	5	5	5	5	5?	2	2	2	5	2	5	2	5	2	5	5	5	5?	2	5
Ssa0183BSFU	3	6	3	6	3	3	3	6	6	6	6	6	6	6	3	6	6	6	3	6	3	6	6	3
Ssa0818BSFU	1	2	2	4	4	2	4	4	2	2	4	4	2	2	2	4	2	2	4	2	4	4	2	4
			D1-2006_0133	D2	2009_0066	2009_0071	2009_0085	2009_0399	2009_0421	2009_0816	2009_0983	2009_0192	2009_0677	2009_0462	2009_0141	2009_0187	2009_0843	2009_0853	2009_0869	2009_1025	2009_0454	2009_0128	2009_0668	2009_0712
Ssa1299BSFU			1	2	1	1	2	1	1	2	2	1	2	2	2	1	1	1	1	1	2	2	2	2
Ssa0055BSFU			6	11	11	6	11	11	11	6	6?	6	11	6	11	6	11	6	11	11	11	11	6	11
Ssa0183BSFU			3	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Ssa0818BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Exon 2					1	1	1	1	1	1	1	0	1	1	0	0	0	1	1	?	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	0	0	0	1	1	?	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Not Present	Not Present	Female	Female	Female	Female	Female
Match?																								

2009_07 Ssa06 parents and *sdY* agree 100%

	AS1-2003_0032	AS2	S1-2007_0019	S2	2009_0105	2009_0094	2009_0238	2009_0551	2009_0700	2009_0710	2009_0841	2009_0144	2009_0202	2009_0255	2009_0295	2009_0370	2009_0543	2009_0552	2009_0612	2009_0623	2009_0705	2009_0802	2009_0103	2009_0324	2009_0387	2009_0416	2009_0438	2009_0832	2009_0840	2009_0844	2009_0873	2009_0584	2009_0911	2009_0423	2009_0194	2009_0147	2009_0248	2009_0017
Ssa0376BSFU	3	2	3	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1
Ssa0183BSFU	2	3	2	3	2	2	2	3	2	2	2	3	2	2	2	2	3	2	3	2	3	3	3	3	3	2	3	3	3	3	2	3	2	3	2	3	2	3
Ssa0055BSFU	10	2	10	4	4	4	4	10	4	4	4	10	4	4	4	4	10	4	10	4	10	10	10	10	10	4	10	10	10	10	4	10	4	10	4	10	4	10
Ssa0368BSFU	6	6	6	2	2	6	6	6	6	6	6	6	2	2	2	2	2	6	2	2	2	6	2	2	6	6	6	2	2	2	6	2	6	6	f	2	2	2
			D1-2006_0025	D2	2009_0105	2009_0094	2009_0238	2009_0551	2009_0700	2009_0710	2009_0841	2009_0144	2009_0202	2009_0255	2009_0295	2009_0370	2009_0543	2009_0552	2009_0612	2009_0623	2009_0705	2009_0802	2009_0103	2009_0324	2009_0387	2009_0416	2009_0438	2009_0832	2009_0840	2009_0844	2009_0873	2009_0584	2009_0911	2009_0423	2009_0194	2009_0147	2009_0248	2009_0017
Ssa0376BSFU			3	7	3	3	7	7	3	7	3	3	7	3	3	7	3	3	3	3	3	3	3	7	7	3	3	7	7	3	3	7	7	7	7	7	7	7
Ssa0183BSFU			2	6	2	2	6	6	2	2	6	2	6	2	2	2	6	2	2	2	2	2	2	2	2	6	6	2	6	2	2	2	6	2	6	6	6	2
Ssa0055BSFU			11	4	4	4	11	11	4	4	11	4	11	4	4	4	11	4	4	4	4	4	4	4	4	11	11	4	11	4	4	4	11	4	11	11	11	4
Ssa0368BSFU			3	5	5	3	5?	3	5	5	5	3	5	3	5	5	3	5	3	5	5	3	5	3	3	3	3	3	3	5	3	5	5	3		3	3	3
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	1	0	0	0	1	0	1?	1?	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female????	Female	Female	Female	Female	Female	Male	Female	Not Present	Female	Female	Female	Female	Female	Female	Female
Match?																																						

2009_11 Ssa06 parents and *sdY* agree 100%

	AS1-2003_0035	AS2	S1-2006_0045	S2	2009_0301	2009_0110	2009_0234	2009_0473	2009_0619	2009_0129	2009_0088	2009_0640	2009_0714	2009_0818	2009_0914	2009_0994	2009_0610	2009_0724	2009_0849	2009_0986
Ssa0376BSFU	3	1	3	2	3	3	3	3	3	3	3	2	2	?	3	2	2	2	2	2
Ssa0183BSFU	5	6	4	2	4	4	4	4	2	2	2	2	2	2	2	2	2	2	2	4
Ssa0818BSFU	3	2	3	2	2	2	3	3	?	3	?	2	3	2	?	2	3	2	3	2
			D1-2006_0131	D2	2009_0301	2009_0110	2009_0234	2009_0473	2009_0619	2009_0129	2009_0088	2009_0640	2009_0714	2009_0818	2009_0914	2009_0994	2009_0610	2009_0724	2009_0849	2009_0986
Ssa0376BSFU			1	2	2	2	2	2	2	2	1	2	1	?	1	1	2	2	1	1
Ssa0183BSFU			3	4	4	3	4	4	4	4	4	4	4	4	4	4	4	3	4	4
Ssa0818BSFU			1	2	1	1	2	1	?	2	?	1	2	2	?	2	2	1	2	1
Exon 2					1	1	1	1	1	1	1	0	0	0	1	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	0	0	0	1	0	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	No Gonad	Female	Female	Not present	Not Present	Female	Female	Female	Female	Female
Match?																				

2009_15 Ssa06 parents and *sdY* agree 100%

	AS1-2002_0019	AS2	S1-2007_0016	S2	2009_0183	2009_0528	2009_0594	2009_0333	2009_0440	2009_0015	2009_0634	2009_0101	2009_0118	2009_0126	2009_0191	2009_0417	2009_0427	2009_0815	2009_0794	2009_0909	2009_0883
Ssa0789BSFU	3	1	3	1	3	1	3	3	3	3	3	1	3	1	3	1	1	1	1	1	1
Ssa0350BSFU	5	5	5	3	5	3	5	5	5	5	5	3	5	3	5	3	3	3	3	3	3
Ssa0752BSFU	2	1	2	1	2	1	2	2	2	2	2	1	2	1	2	1	1	1	1	1	1
Ssa0055BSFU	4	3	4	9	9	4	4	9	9	4	9	4	4	9	9	4	9	9	9	4	9
Ssa0368BSFU	?	?	1	5	1	5	1	1	1	5	5	1	5	1	1	1	1	5	5	5	1
			D1-2006_0055	D2	2009_0183	2009_0528	2009_0594	2009_0333	2009_0440	2009_0015	2009_0634	2009_0101	2009_0118	2009_0126	2009_0191	2009_0417	2009_0427	2009_0815	2009_0794	2009_0909	2009_0883
Ssa0789BSFU			2	5	5	5	5	5	2	2	5	2	5	2	5	5	5	2	2	5	5
Ssa0350BSFU			4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Ssa0752BSFU			2	4	4	4	2	2	2	2	4	2	4	2	4	4	4	2	2	4	4
Ssa0055BSFU			3	13	13	13	3	13	3	13	3	13	3	3	3	13	13	3	13	13	3
Ssa0368BSFU			6	7	6	7	6	7	6	6	6	6	6	7	6	6	7	6	7	6	6
Exon 2					1	1	1	1	1	1	1	0	1	0	1	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	0	1	0	1	0	0	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Female	Male	Not Present	Male	Female	Male	Female	Female	Female	Female
Match?																					

2009_30 Ssa06 parents and *sdY* agree 100%

	AS1-2002_0012	AS2	S1-2007_0026	S2	2009_0166	2009_0145	2009_0169	2009_0210	2009_0237	2009_0292	2009_0297	2009_0701	2009_0738	2009_0813	2009_0663	2009_0156	2009_0262	2009_0697	2009_0962	2009_0456	2009_0577	2009_0642	2009_0595	2009_0400	2009_0670	2009_0834	2009_0201	2009_0021	2009_0355	2009_0404	2009_0432
Ssa0074ECIG	M	M	M	V	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	V	V	V	V	V	V	V	V	V
Ssa0376BSFU	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3	3	3	3	3
Ssa0055BSFU	4	10	4	6	6	6	4	6	4	6	4	6	4	4	4	4	4	4	6	6	4	4	4	6	4	6	4	4	4	6	6
Ssa0818BSFU	2	1	2	3	3	3	2	2	2	3	3	2	3?	3	2	3	3	3	3	3	3	2	3	3	3	2	3	3	2	3	2
			D1-2006_0117	D2	2009_0166	2009_0145	2009_0169	2009_0210	2009_0237	2009_0292	2009_0297	2009_0701	2009_0738	2009_0813	2009_0663	2009_0156	2009_0262	2009_0697	2009_0962	2009_0456	2009_0577	2009_0642	2009_0595	2009_0400	2009_0670	2009_0834	2009_0201	2009_0021	2009_0355	2009_0404	2009_0432
Ssa0074ECIG			V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0055BSFU			11	13	11	11	11	13	11	11	13	11	11	13	13	12?? Adopted	13	13	13	11	13	11	11	13	13	13	13	13	11	13	13
Ssa0818BSFU			1	3	3	3	1	3	3	3	1	1	3?	3	3	3	3	1	3	1	1	3	1	1	1	1	3	1	3	1	1
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	0	?	?	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	0	?	?	1	1	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	?	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	not Present	Male	Male	Male	Male	Male	Not Present	Female	Female	Female	Female	Female	Female	Female	Female	Female
Match?																															

2009_40 Ssa06 parents and *sdY* agree 100%

	AS1-2001_0005	AS2	S1-2005_0030	S2	2009_0114	2009_0220	2009_0288	2009_0745	2009_0826	2009_0264	2009_0795	2009_0901	2009_0148	2009_0155	2009_0386	2009_0966	2009_0851	2009_0405	2009_0019	2009_0897	2009_0349	2009_1032	2009_0198	2009_0758	2009_0184
Ssa0103aECIG	M	M	M	V	M	M	M	M	M	M	M	M	M	M	M	M	M	V	V	V	V	V	V	V	V
Ssa0376BSFU	1	1	1	3	1	1	1	1	1	1	1	1	1	1	f	1	1	f	3	3	f	3	3	3	3
Ssa0055BSFU	5	5	5	6	6	6	6	5	6	6	5	5	5	5	5	6	5	5	5	5	6	6	5	6	6
Ssa0343BSFU	1	3	1	4	4	1	1	4	1	4	4	4	4	4	1	1	1	4	1	1	1	?	1	1	1
			D1-2006_0062	D2	2009_0114	2009_0220	2009_0288	2009_0745	2009_0826	2009_0264	2009_0795	2009_0901	2009_0148	2009_0155	2009_0386	2009_0966	2009_0851	2009_0405	2009_0019	2009_0897	2009_0349	2009_1032	2009_0198	2009_0758	2009_0184
Ssa0103aECIG			M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
Ssa0376BSFU			1	2	1	1	1	1	1	2	2	2	1	1	f	1	1	f	2	2	f	2	1	1	2
Ssa0055BSFU			1 or 5	10	1	10	1	10	10	10	1	1	10	10	1	1	1	1	10	10	10	10	10	10	1
Ssa0343BSFU			4	5	4	4	5	5	4	4	5	4	5	4	5	4	5	5	4	5	5	?	5	5	5
Exon 2					?	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	?	0	0	0	0
Exon 4					?	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	?	0	0	0	0
Fabp6b					?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1?	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Female	Female	Female	Not Present	Not Present
Match?																									

Legend
Markers

AS-Ancestral sire
Ssa02/LG1
Ssa05/LG4
Ssa03/LG11

S1 or S2 is sire

D1 or D2 is dam

Unknown | Known Male | Predicted male | Known female | Predicted female | Discrepancy | sex predicted for this family

Actual known phenotypes are displayed in the" Sex call from Pheotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class_Family 5.

Individual ID in format Year class_Individual number e.g. 2003_0007 = 2003 Year class_Individual 0007

sdY presence and absence indicated by 1 and 0 respectively for:
Exon 2
Exon 4
Fabp6 (DNA quality control)

2009_06 Ssa06
parents and sdY agree 100%

	AS1-2003_0029	AS2	S1-2006_0033	S2	2009_0031	2009_0059	2009_0337	2009_0126	2009_0363	2009_0406	2009_0505	2009_0561	2009_0562	2009_0597	2009_0644	2009_0573	2009_0072	2009_0310	2009_0764	2009_0770	2009_0306	2009_0367	2009_0309	2009_0320	2009_0325	2009_0326	2009_0304	2009_0384	2009_0519	2009_0626	2009_0639	2009_0772	2009_0624
Ssa0074EC5G	1	1	1	1	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	V	V	V	V	V	V	V	V	V	V
Ssa0055B5FU	3	2	3	4	3	3	4	3	4	4	4	3	4	4	3	3	4	4	4	4	4	3	4	4	3	3	4	4	3	3	4	3	3
Ssa0055B5FU	5	5	5	3	3	2	5	2	5	2	5	5	5	2	3	2	5	2	5	2	5	2	5	5	5	2	5	5	2	5	5	2	57

			D1-2006_0074	D2	2009_0031	2009_0059	2009_0337	2009_0126	2009_0363	2009_0406	2009_0505	2009_0561	2009_0562	2009_0597	2009_0644	2009_0573	2009_0072	2009_0310	2009_0764	2009_0770	2009_0306	2009_0367	2009_0309	2009_0320	2009_0325	2009_0326	2009_0304	2009_0384	2009_0519	2009_0626	2009_0639	2009_0772	2009_0624
Ssa0074EC5G			V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V
Ssa0055B5FU			3	10	3	3	3	3	10	3	10	10	3	3	10	10	3	10	10	10	3	10	3	3	10	10	3	3	3	3	3	10
Ssa0055B5FU			5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	57
Exon 2					1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	?	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	17	0	0	0	?	17	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Not Present	Not Present	Not Present	Male	Not Present	Not Present	Female	Female	Female	Female	Female	Not Present	Not Present	Not Present	Female	Female	Female
Match?																																

2009_26 Ssa06
parents and sdY agree 100%

	AS1-2003_0004	AS2	S1-2006_0057	S2	2009_0030	2009_0090	2009_0499	2009_0784	2009_0060	2009_0270	2009_0338	2009_0453	2009_0562	2009_0761	2009_0847	2009_0001	2009_0998	2009_0996	2009_1003	2009_0076	2009_0036	2009_0136	2009_0507	2009_0751	2009_0800	2009_0620	2009_0405	2009_0391	2009_0446	2009_0502	2009_0217
Ssa0074EC5G	1	1	1	1	M	M	M	M	V	V	V	V	V	V	V	?	M	M	V	?	M	M	M	M	V	V	V	?	?	M	?
Ssa0376B5FU	2	3	2	1	2	2	1	27	2	2	2	2	2	2	2	2	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1
Ssa0129B5FU	3	2	3	2	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	3	1	1	1	1	1	3	3	3	1	1	1
Ssa0055B5FU	5	4	5	4	12 adopted?	5	5	5	5	5	5	5	5	5	4	5	4	4	4	5	5	5	5	5	5	5	5	4	5	5	5
Ssa1027B5FU	10	10	10	8	8	8	8	8	8	8	8	8	8	8	8	10	8	10	10	10	8	8	8	8	8	8	8	8	10	8	8	8
Ssa0017B5FU	5	5	5	3	3	5	5	3	3	3	3	3	3	3	?	5	3	5	5	5	5	3	3	3	3	3	3	3	3	3	3	3

			D1-2006_0727	D2	2009_0030	2009_0090	2009_0499	2009_0784	2009_0060	2009_0270	2009_0338	2009_0453	2009_0562	2009_0761	2009_0847	2009_0001	2009_0998	2009_0996	2009_1003	2009_0076	2009_0036	2009_0136	2009_0507	2009_0751	2009_0800	2009_0620	2009_0405	2009_0391	2009_0446	2009_0502	2009_0217
Ssa0074EC5G			V	V	M? this is not a pol	V	V	V	V	V	V	V	V	?	V	V	M	?	V	V	V	V	V	V	V	V	V	V	V	V	V
Ssa0376B5FU			1	1	1	1	1	1	1	1	3	3	3	1	3	1	3	1	3	3	1	1	1	1	1	3	3	3	3	3	3
Ssa1129B5FU			2	3	3	3	3	2	2	2	2	2	2	2	3	3	3	3	2	2	2	3	2	2	3	2	2	2	2	3	3
Ssa0055B5FU			1	3	higher 37 Adopted	1	1	3	3	1	1	3	1	1	1	1	1	3	1	1	? lower? Adopted?	3	1	1	1	1	3	3 or 1	3	1	3
Ssa1027B5FU			10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Ssa0017B5FU			2	5	5	5	5	5	2	5	5	5	2	5	2	5	5	5	5	5	2	2	5	2	2	2	5	2	5	2	2	2
Exon 2					1	1	0	1	1	1	1	1	1	1	1	1	13	0	0	0	0	1	0	0	1	1	1	1	0	0	0
Exon 4					1	1	0	1	1	1	1	1	1	1	1	1	19	0	0	0	0	1	0	0	1	1	1	1	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Female/????	Not present	Not Present	Not Present	Female	Female	Male	Male	Not Present	Male	Not Present	Female	Female
Match?																																

2009_36 Ssa06
parents and sdY agree 100%

	AS1-2003_0029	AS2	S1-2006_0017	S2	2009_0012	2009_0079	2009_0217	2009_0113	2009_0256	2009_0426	2009_0493	2009_0579	2009_1011	2009_0733	2009_0792	2009_0885	2009_0947	2009_0901	2009_0739	2009_0364	2009_0726	2009_0637	2009_0125	2009_0185	2009_0596	2009_0652	2009_0520	2009_0740	2009_0767
Ssa0074EC5G	1	1	1	1	M	M	M	M	M	M	M	M	M	M	M	M	F	M	M	M	V	V	V	V	V	V	V	V	V
Ssa0055B5FU	3	2	3	3	3	5	3	5	5	6?	3	3	5	6	5	3	5	3	5	5	5	5	3	5	3	5	5	5	5
Ssa0055B5FU	5	4	5	5	3	5	5	5	5	3	3	5	5	5	5	5	3	5	3	3	5	5	5	5	5	5	5	5	5

			D1-2006_0034	D2	2009_0012	2009_0079	2009_0217	2009_0113	2009_0256	2009_0426	2009_0493	2009_0579	2009_1011	2009_0733	2009_0792	2009_0885	2009_0947	2009_0901	2009_0739	2009_0364	2009_0726	2009_0637	2009_0125	2009_0185	2009_0596	2009_0652	2009_0520	2009_0740	2009_0767
Ssa0074EC5G			V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V
Ssa0055B5FU			3	10	3	3	3	3	3	3	10	3	67	107	57	3	10	10	67	3	10	10	3	3	10	10	10	57
Ssa0055B5FU			4	6	6	4	4	4	4	6	6	4	6	4	6	6	4	6	6	4	6	4	6	4	6	6	4	6
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Not Present	Male	Not Present	Female	Not Present	Female	Female	Female	Female	Female	Not Present	Female
Match?																													

2009_01 Ssa02
parents and sdY agree 100%

	AS1-2001_0004	AS2	S1-2007_0006	S2	2009_0588	2009_0713	2009_0880	2009_1013	2009_0262	2009_0696	2009_0463	2009_0151	2009_0522	2009_0038	2009_0014	2009_0104	2009_0316	2009_0359	2009_0497	2009_0604	2009_0713	2009_0750	2009_0981	2009_0998	2009_0529	2009_0404	2009_0534
Ssa1027B5FU	1	6	1	6	1	1	1	1	1	1	1	1	1	1	6	6	6	6	6	6	1	1	6	1	6	6	6
OMM03317	5	6	5	5	9	5	9	9	9	9	9	9	9	9	9	9	5	9	9	5	5	9	5	5	9	9	9
OMM1272	4	3	4	4	4	2	2	2	2	2	4	4	?	4	2	4	2	4	?	4	2	4	2	?	4	4	2

			D1-2005_0053	D2	2009_0588	2009_0713	2009_0880	2009_1013	2009_0262	2009_0696	2009_0463	2009_0151	2009_0522	2009_0038	2009_0014	2009_0104	2009_0316	2009_0359	2009_0497	2009_0604	2009_0713	2009_0750	2009_0981	2009_0998	2009_0529	2009_0404	2009_0534
Ssa1027B5FU			3	11	11	11	11	11	3	11	3	11	11	3	11	3	11	3	11	11	11	3	11	11	11	11	11
OMM03317			5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
OMM1272			4	1	4	1	1	1	1	4	2	?	1	4	1	1	1	?	4	1	4	1	?	4	1	1	1
Exon 2					1	1	1	1	1	1	1	1	1	1	0	0	1	0	?	1	1	1	0	1	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	0	0	1	0	?	1	1	1	0	1	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1	1	1	1	?	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Male	Female	Female	Male	Male	Male	Female	Female	Female	Female	Female
Match?																											

2009_03 Ssa06
parents and sdY agree 100%

	AS1-2003_0024	AS2	S1-2006_0125	S2	2009_0709	2009_0732	2009_0921	2009_0940	2009_0946	2009_1033	2009_0992	2009_0643	2009_0920	2009_0884	2009_0805	2009_0024	2009_0448	2009_0541	2009_1028	2009_1026
Ssa0074EC5G	1	1	1	1	M	M	M	M	M	M	?	V	V	V	V	V	V	V	V	?
Ssa0376B5FU	1	4	1	2	1	17	1	2	1	1	1	2	2	2	27	2	2	2	2	2
Ssa0129B5FU	4	5	4	2	4	7	2	4	4	2	4	2	4	2	2	4	4	4	4	2
Ssa0017B5FU	6	5	6	5	5	6	6	5	6	5	5	5	5	6	6	5	5	5	5	5

			D1-2006_0133	D2	2009_0709	2009_0732	2009_0921	2009_0940	2009_0946	2009_1033	2009_0992	2009_0643	2009_0920	2009_0884	2009_0805	2009_0024	2009_0448	2009_0541	2009_1028	2009_1026
Ssa0074EC5G			V	V	V	V	V	V	V	V	V	V	V	V	V	V	?	?	V	V
Ssa0376B5FU			1	3	1	37	1	17	1	3	1	1	7	1	3	3	3	1	1	1
Ssa1027B5FU			3	10	3	3	3	10	10	3	10	10	3	3	3	3	3	3	10	
Ssa0017B5FU			6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
Exon 2					1	1	1	1	1	1	1	0	0	0	0	0	0	0	1	
Exon 4					1	1	1	1	1	1	1	0	0	0	0	0	0	0	1	
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Female??	Female	Female	Female	Female	Not Present
Match?																				

2009_09 Ssa02
parents and sdY agree 100%

	AS1-2001_0002	AS2	S1-2007_0022	S2	2009_0139	2009_0224	2009_0068	2009_0150	2009_0529	2009_0414	2009_0401	2009_0505	2009_0808	2009_0852	2009_0112	2009_0127	2009_0006	2009_0171	2009_0188	2009_0897	2009_0293	2009_0477	2009_0506	2009_0807	2009_0857	2009_0274
Ssa0055B5FU	1	1	1	1	9	9	9	9	7	9	9	9	9	9	9	9	9	7	9	9	7	9	9	9	7	7
Ssa0043B5FU	3	1	3	4	4	3	3	4	4	3	4	3	3	4	3	3	4	37	3	3	3	47	3	4	4	4
Ssa0376B5FU	2	6	2	3	2	3	3	2	3	3	2	3	3	2	3	3	2	2	3	2	3	2 and 37	3	2	2	2
Ssa0618B5FU	2	4	2	4	2	4	2	2	2	2	4	2	2	4	2	4?	4	4	4	4	2	4	4	2	4	2

			D1-2005_0006	D2	2009_0139	2009_0224	2009_0068	2009_0150	2009_0529	2009_0414	2009_0401	2009_0505	2009_0808	2009_0852	2009_0112	2009_0127	2009_0006	2009_0171	2009_0188	2009_0897	2009_0293	2009_0477	2009_0506	2009_0807	2009_0857	2009_0274
Ssa0055B5FU			1	4	1	1	1	1	?	4	4	1	1	4	1	1	1	4	1	4	4	4	1	4	4
Ssa0043B5FU			2	3	3	2	2	3	2	2	3	2	2	3	2	2	37	2	3	2	37	5?	2	3	3
Ssa0376B5FU			1	6	6	1	6	6	1	1	6	1	1	6	1	1	1	6	6	1	1	6	67	6	6
Ssa0618B5FU			4	4	4	4	4	4	4	4	4	4	4	4	4	4?	4	4	4	4	4	4	4	7	4
Exon 2					1	1	1	1	1	1	1	1	0	0	0	1	1	0	0	1	1	0	1	0	0
Exon 4					1	1	1	1	1	1	1	1	0	0	0	1	1	0	0	1	1	0	1	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Male	Not Present	Female	Female	Female	Male	Male	Female	Male	Female	Female
Match?																										

2009_10 Ssa06
parents and sdY agree 100%

	AS1-2003_0013	AS2	S1-2006_0067	S2	2009_0659	2009_0718	2009_0859	2009_0672	2009_0928	2009_0121	2009_0226	2009_0267	2009_0308	2009_0222	2009_0735	2009_0927	2009_0984	2009_1019	2009_0508	2005_0524	2009_0625	2009_0306	2009_0347	2009_0102	2009_0111	2009_0924
Ssa0376B5FU	3	4	3	1	3	3	3	3	3	3	3	3	3	1	1	1	1	1	2	1	1	3	1	2	1	1
Ssa0023B5FU	3	3	3	2	2	2	3	3	2	2	2	2	2	2	2	2	2	3	2	2	2	2	2	2	2	2
Ssa0618B5FU	4	3	4	2	4	2	2	2	2	2	2	2	2	4	4	4	4	2	2	2	4	4	2	2	2	4

			D1-2006_0079	D2	2009_0659	2009_0718	2009_0859	2009_0672	2009_0928	2009_0121	2009_0226	2009_0267	2009_0308	2009_0222	2009_0735	2009_0927	2009_0984	2009_1019	2009_0508	2005_0524	2009_0625	2009_0306	2009_0347	2009_0102	2009_0111	2009_0924
Ssa0376B5FU			1	2	2	2	2	2	2	1	2	1	2	2	2	2	2	2	2	2	2	1	2	2	1
Ssa0023B5FU			3	4	3	3	4	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	3	4	2	3
Ssa0618B5FU			2	5	5	2	2	2	5	2	2	2	5	2	5	5	5	5	2	2	2	5	5	2	5	5
Exon 2					1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	1	1	0	1	0	1	0
Exon 4					1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	1	1	0	2	1	0	
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Male	Female	Not Present	Female	Male	Male	Female	Male	Male	Female
Match?																										

2009_13 Ssa02
parents and sdY agree 100%

	AS1-2003_0023	AS2	S1-2006_0069	S2	2009_0281	2009_0343	2009_0645	2009_0904	2009_0647	2009_0583	2009_0600	2009_0986	2009_0480	2009_0379	2009_0395	2009_0499	2009_0521	2009_0570	2009_0605	2009_0309	2009_0660	2009_0664	2009_0993	2009_1009	2009_0360	2009_0022	2009_0140	2009_0165	2009_0575	2009_0125	2009_0385	2009_0905	2009_0075
Ssa0055B5FU	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0233B5FU	2	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa0376B5FU	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa1129B5FU	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0366B5FU	1	2	1	1	7	7	7	7	1	1	7	1	?	7	?	7	?	7	7	7	1	1	1	?	1	1	7	1	7	7	1	7

			D1-2006_0088	D2	2009_0281	2009_0343	2009_0645	2009_0904	2009_0647	2009_0583	2009_0600	2009_0986	2009_0480	2009_0379	2009_0395	2009_0499	2009_0521	2009_0570	2009_0605	2009_0309	2009_0660	2009_0664	2009_0993	2009_1009	2009_0360	2009_0022	2009_0140	2009_0165	2009_0575	2009_0125	2009_0385	2009_0905	2009_0075
Ssa0055B5FU			3	9	9	9	3 and 9?	9	3	9	3	3	9	9	9	9	3	9	9	3	9	3	9	9	3	3	9	9	9	3	9	9
Ssa0233B5FU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa0376B5FU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa1129B5FU			1	3	3	3	3	3	3	3	3	3	1	1	3	3	3	3	3	3	3	3	3	1	3	3	3	3	1	1	3	1
Ssa0366B5FU			5	6	5	?	7	7	6	6	5	6	6	?	?	7	?	7	6	6	6	5	6	5	7	6	5	6	6	6	6	6	5
Exon 2					1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
Fabp6B					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Male	Not Present	Not Present	Female	Female	Male	Male	Female	Male	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female
Match?																																

Legend	AS-Ancestral sire	S1 or S2 is sire	D1 or D2 is dam	Unknown	Known Male	Predicted male	Known female	Predicted female	Discrepancy	sex predicted for this family	sdY presence and absence indicated by 1 and 0 respectively for:
Markers	Ssa02/LG1										Exon 2
	Ssa06/LG4	Actual known phenotypes are displayed in the" Sex call from Pheotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class_Family 5.									Exon 4
	Ssa03/LG11	Individual ID in format Year class_Individual number e.g. 2003_0007 = 2003 Year class_Individual 0007									Fabp6 (DNA quality control)

2009_14 Ssa02
parents and *sdY* agree 100%

	AS1-2001_0006	AS2	S1-2007_0004	S2	2009_0049	2009_0817	2009_0864	2009_0899	2009_0949	2009_0199	2009_0830	2009_0845	2009_0752	2009_0786	2009_0455	2009_0492	2009_0514	2009_0748	2009_0685	2009_0434	2009_0646
Ssa202DU	4	1	4	5	4	4	?	4	4	4	4	4	5	4	5	4	5	5	5	5	5
Ssa1454BSFU	2	2	2	3	3	3	2	3	2	2	2	3	3	2	3	2	3	2	3	3	3
Ssa0376BSFU	2	1	2	3	3	3	2	3	2	2	2	3	3	2	3	2	3	2	3	3	3
Ssa0350BSFU	3	5	3	5	5	5	3	5	3	3	3	5	5	3	5	3	5	3	5	5	5
Ssa0752BSFU	1	1	1	4	4	4	1	4	1	1	1	4	4	1	1 or 4?	1	4	1	4	4	4
Ssa0368BSFU	3	6	3	6	6	6	3	6	?	?	3	6	6	6	6	6	6	6	3	6	6
			D1-2006_0032	D2	2009_0049	2009_0817	2009_0864	2009_0899	2009_0949	2009_0199	2009_0830	2009_0845	2009_0752	2009_0786	2009_0455	2009_0492	2009_0514	2009_0748	2009_0685	2009_0434	2009_0646
Ssa202DU			2	3	2	3	?	2	3	2	2	2	2	3	3	2	3	3	3	2	2
Ssa1454BSFU			1	4	4	4	1	1	4	4	4	4	4	1	1	4	4	4	1	1	1
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0350BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0752BSFU			1	2	2	2	1	1	2	1	2	1	2	2	2	1	1	2	2	1	1
Ssa0368BSFU			3	7	7	7	7	7	7	7	7	7	7	7	3	7	3	7	7	7	3
					1	1	1	1	1	1	1	1	0	1	?	1	0	0	0	0	0
					1	1	1	1	1	1	1	1	0	1	?	1	0	0	0	0	0
					1	1	1	1	1	1	1	1	1	1	?	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Not Present	Male	Female???	Not Present	Female	Female	Female	Female	Female
				Match?																	

2009_16 Ssa02
parents and *sdY* agree 100%

	AS1-2002_0014	AS2	S1-2007_0011	S2	2009_0737	2009_0368	2009_0430	2009_0654	2009_1031	2009_0741	2009_0177	2009_0254	2009_0029	2009_0410	2009_0091	2009_0656	2009_0671	2009_0195	2009_0868	2009_0231
Ssa0055BSFU	6	5	6	4	?	6	6	6	?	4	4	4	4	6	4	?	4	6	6	6
Ssa0074ECIG	M	V	M	V	M	V	?	M	M	M	M	V	V	V	V	V	V	V	V	?
Ssa0789BSFU	1	3	1	4	4	1	4	1	4	4	1	1	1	1	1	1	1	1	1	1
Ssa0818BSFU	3	4	3	4	3	3	4	3	3	3	3?	4	3	3	4	4	4	4	3	3
			D1-2005_0032	D2	2009_0737	2009_0368	2009_0430	2009_0654	2009_1031	2009_0741	2009_0177	2009_0254	2009_0029	2009_0410	2009_0091	2009_0656	2009_0671	2009_0195	2009_0868	2009_0231
Ssa0055BSFU			3	10	3	3	5?	4?	3	?	10	3	3	3	10	3	3	3	3	3
Ssa0074ECIG			M	M	M	M	M	M	?	M	M	M	?	M	M	M	M	M	M	M
Ssa0789BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0818BSFU			4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Exon 2					1	1	1	1	0	0	0	0	0	1	1	0	0	1	1	1
Exon 4					1	1	1	1	0	0	0	0	?	1	0	0	0	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	?	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Not Present	Female	Not Present	Not Present	Female	Female	Male	female	Female	Female	Male	Not Present	Male
				Match?																

2009_18 Ssa06
parents and *sdY* agree 100%

	AS1-2001_0001	AS2	S1-2005_0048	S2	2009_0773	2009_0025	2009_0027	2009_0084	2009_0167	2009_0299	2009_0312	2009_0388	2009_0390	2009_0509	2009_0532	2009_0568	2009_0590	2009_0665	2009_0676	2009_0863	2009_0871	2009_0879	2009_0881	2009_0910	2009_0954	2009_1024	2009_1034	2009_0159
Ssa0789BSFU	3	1	3	5	3	5	5	3	5	5	3	5	5	5	3	?	5	3	5	3	3	5	5	3	3	5	?	5
Ssa0055BSFU	4	6	4	2	4	4	2	4	4	2	4	4	2	4	4	4	2	2	2	4	2	4	4	4	4	2	4	4
Ssa0368BSFU	2	2	2	7	7	2	7	2	7	7	2	7	7	2	7	2	2	2	2	2	7	7	2	2	7	2	?	2
			D1-2005_0043	D2	2009_0773	2009_0025	2009_0027	2009_0084	2009_0167	2009_0299	2009_0312	2009_0388	2009_0390	2009_0509	2009_0532	2009_0568	2009_0590	2009_0665	2009_0676	2009_0863	2009_0871	2009_0879	2009_0881	2009_0910	2009_0954	2009_1024	2009_1034	2009_0159
Ssa0789BSFU			1	1	1	1	2	1	1	2	2	1	1	1	2	1	1	2	1	1	2	1	1	1	2	1	?	1
Ssa0055BSFU			3	5	3	3	5	3	3	3	3	3	5	3	3	3	5	5	3	3	3	3	3	5	3	5	3	3
Ssa0368BSFU			3	5	3	3	5	3	3, 5?	5	5	5	3	3	5	5	3	3	5	3	5	3	3	5	3	5	?	5
Exon 2					1	0	0	1	0	0	1	0	1	1	1	0	0	1	0	1	1	0	0	1	1	0	?	0
Exon 4					1	0	0	1	0	0	1	0	1	1	1	0	0	1	0	1	1	0	0	1	1	0	?	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1
				Sex call from Phenotype	Male	Female	Not Present	Male	No Gonad	Female	Male	Female	Male	Not Present	Male	Male	Not Present	Male	Not Present	Male	Male	Female	Female	Male	Not Present	Female	Male	Female
				Match?																								

2009_21 Ssa06
parents and *sdY* agree 100%

	AS1-2001_0001	AS2	S1-2007_0017	S2	2009_0018	2009_0069	2009_0130	2009_0263	2009_0272	2009_0315	2009_0340	2009_0375	2009_0437	2009_0533	2009_0969	2009_0692	2009_0520	2009_0893	2009_0889	2009_0926	2009_0051	2009_1029	2009_0571	2009_0143	2009_0162	2009_0298	2009_0357	2009_0377	2009_0383	2009_0413	2009_0419	2009_0466	2009_0629	2009_0680	2009_0747	2009_0801	2009_0875	2009_0925	2009_0931	2009_0951	2009_0955	2009_0160	2009_0411	2009_0624
OMM5037/1	4	2	4	7	4	4	4	4	4	4	4	7	4	4	4	4	4?	4	7	4	4	4	4?	7	7	7	4	7	7	7	7	7	7	7	7	7	7	7	7	7	4	7	7 or 4?	7
Ssa0055BSFU	7	8	7	1	7	7	7	7	1	7	7	1	1	7	7	1	7	7	7	7	1	7	7	1	1	1	1	1	1	7	1	1	1	1	1	1	1	7	1	1	7	7	7	1
Ssa0368BSFU	2	2	2	1	2	2	2	2	1	1	1	1	2	2	2	2	2	2	1	2	2	2	1	2	1	2	2	2	2	2	2	2	1	2	2	2	1	2	2	1	2	2	1	2
			D1-2006_0071	D2	2009_0018	2009_0069	2009_0130	2009_0263	2009_0272	2009_0315	2009_0340	2009_0375	2009_0437	2009_0533	2009_0969	2009_0692	2009_0520	2009_0893	2009_0889	2009_0926	2009_0051	2009_1029	2009_0571	2009_0143	2009_0162	2009_0298	2009_0357	2009_0377	2009_0383	2009_0413	2009_0419	2009_0466	2009_0629	2009_0680	2009_0747	2009_0801	2009_0875	2009_0925	2009_0931	2009_0951	2009_0955	2009_0160	2009_0411	2009_0624
OMM5037/1			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa0055BSFU			12	8	8	12	8	8	8	12	8	8	12	8	8	12	8	12	12	12	12	12	12	8	12	8	8	12	8	12	8	12	8	8	8	12	12	12	8	12	8	8	12	8
Ssa0368BSFU			5	6	5	5	6	5	5	5	5	5	6	5	6	5	6	5	5	6	6	6	5	6	5	5	6	6	6	6	5	5	6	5	5	6	5	6	6	5	5	5	5	5
Exon 2					1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Exon 4					1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Not Present	Female	Female	Not Present	Not Present	Female	Female	Female	Not Present	Female	Female	Not Present	Female	Not Present	Male	Female	Female	Female
				Match?																																								

2009_22 Ssa02
parents and *sdY* agree 100%

	AS1-2003_0034	AS2	S1-2007_0003	S2	2009_0352	2009_0040	2009_0799	2009_0086	2009_0283	2009_0328	2009_0067	2009_0525	2009_0839	2009_0782	2009_0836	2009_0269	2009_0050	2009_1014	2009_0163	2009_0527	2009_0890	2009_0058
Ssa1077BSFU	3	2	3	10	10	3	3	3	3	3	10	3	10	10	10	10	10	10	10	10	10	10
Ssa0376BSFU	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3
Ssa0368BSFU	3	3	3	5	3	3	3	5	5	3	5	5	5	3	5	5	5	5	5	3	3	5
			D1-2006_0052	D2	2009_0352	2009_0040	2009_0799	2009_0086	2009_0283	2009_0328	2009_0067	2009_0525	2009_0839	2009_0782	2009_0836	2009_0269	2009_0050	2009_1014	2009_0163	2009_0527	2009_0890	2009_0058
Ssa1077BSFU			9	2	2	9	2	2	9	9	2	9	9	2	2	2	2	9	9	2	2	2
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	3
Ssa0368BSFU			4	7	4	4	4	7	7	7	7	7	7	7	7	7	7	4	7	4	4	4
					0	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0
					0	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0
					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Female	Male	Female	Female	Female	Female	Female	Female	Female	Not Present	Female	Female
				Match?																		

2009_23 Ssa02
parents and *sdY* agree 100%

	AS1-2003_0018	AS2	S1-2007_0007	S2	2009_0042	2009_0107	2009_0124	2009_0153	2009_0174	2009_0402	2009_0559	2009_0318	2009_0089	2009_0431	2009_0798	2009_0607	2009_0005	2009_0047	2009_0207	2009_0517	2009_0535	2009_0586	2009_0618	2009_0688	2009_0704	2009_0715	2009_0812	2009_1036	2009_0763	2009_0766	2009_0961
Ssa0055BSFU	6	13	6	2	6	6	6	6	6	6	2	6	6	6	6	6	6	2	6	2	2	2	2	6	2	2	2	2	2	2	2
OMM5037/1	4	4	4	5	5	5	5	4	5	4	5	4	5	4	?	5	5	4	4	4	4	5	4	5	5	4	5	4	4	5	5
Ssa0368BSFU	2	3	2	7	2	7	7	7	2	2	7	2	2	7	7	2	7	2	7	2	2	2	2	2	7	7	7	?	2	7	2
			D1-2006_0060	D2	2009_0042	2009_0107	2009_0124	2009_0153	2009_0174	2009_0402	2009_0559	2009_0318	2009_0089	2009_0431	2009_0798	2009_0607	2009_0005	2009_0047	2009_0207	2009_0517	2009_0535	2009_0586	2009_0618	2009_0688	2009_0704	2009_0715	2009_0812	2009_1036	2009_0763	2009_0766	2009_0961
Ssa055BSFU			6	7	6	6	6	6	7	7	7	7	6	7	6	7	7	7	6	6	6	7	6	6	6	7	7	6	7	6	6
OMM5037/1			5	8	8	8	8	8	5	8	5	5	5	5	?	8	5	8	5	8	8	5	5	8	5	5	5	4?	8	5	5
Ssa0368BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	?	3	3	3
Exon 2					1	1	1	1	1	1	0	1	1	1	1	1	1	1?	1	0	0	0	0	1	0	0	0	?	0	0	0
Exon 4					1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	0	0	0	0	1	0	0	0	?	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Male	Female	Male	not Present	female	Male	Female	Not Present	Female	Female	Female	female	Female
				Match?																											

2009_24 Ssa06
parents and *sdY* agree 100%

	AS1-2003_0013	AS2	S1-2006_0098	S2	2009_0062	2009_0939	2009_0154	2009_0176	2009_0227	2009_0621	2009_0641	2009_0902	2009_0924	2009_0572	2009_0615	2009_0650	2009_0727	2009_0123	2009_0372	2009_0526	2009_0230	2009_0206	2009_0134
Ssa0376BSFU	2	3	2	1	2	2	2	2	2	2	1	2	2	1	1	1	1	?	1	1	1	1	?
Ssa0055BSFU	6	11	6	11	11	11	6	11	6	11	11	6	6	11	6	6	11	11	11	11	6	6	11
Ssa0368BSFU	7	7	7	5	7	5	7	7	7	7	7	7	5	5	5	5	5	5	5	5	7	7	5
			D1-2006_0041	D2	2009_0062	2009_0939	2009_0154	2009_0176	2009_0227	2009_0621	2009_0641	2009_0902	2009_0924	2009_0572	2009_0615	2009_0650	2009_0727	2009_0123	2009_0372	2009_0526	2009_0230	2009_0206	2009_0134
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0055BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0368BSFU			2	6	6	2	6	2	2	2	6	2	2	2	6	2	2	2	6	2	2	6	6
					1	1	1	1	1	1	1	1	1	0	?	0	0	0	0	0	1	0	1
					1	1	1	1	0	1	1	1	1	0	?	0	0	0	0	0	0	0	1
					1	1	1	1	0	1	1	1	1	1	?	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Female	Female	Not Present	Female	Female	Female	Not Present
				Match?																			

2009_25 Ssa02
parents and *sdY* agree 100%

	AS1-2001_0002	AS2	S1-2007_0024	S2	2009_0055	2009_0214	2009_0418	2009_0486	2009_0787	2009_0806	2009_0099	2009_0240	2009_0239	2009_0655	2009_0023	2009_0100	2009_0277	2009_0314	2009_0394	2009_0415	2009_0496	2009_0554	2009_0675	2009_0785	2009_0865	2009_0895	2009_0952	2009_0965	2009_0172	2009_0838	2009_0631	2009_0449
Ssa0055BSFU	9	4	9	7	9	9	9	9	9	9	9	9	9	9	9	7	7	9	9	9	9	9	7	9	9	7	7	9	7	9	7	7
Ssa0350BSFU			7	5	7	7	7	7	5	5	7	7	5	7	7	5	7	7	5	7	5	5	5	7	7	7	7	5	5	7	7	7
OMM1272	1	1	1	2	2	1?	2	1	2	1	1	2	1	2	1	2	2	1	1	2	2	2?	2	2	1	2	2	2	1	1	2	1
			D1-2006_0123	D2	2009_0055	2009_0214	2009_0418	2009_0486	2009_0787	2009_0806	2009_0099	2009_0240	2009_0239	2009_0655	2009_0023	2009_0100	2009_0277	2009_0314	2009_0394	2009_0415	2009_0496	2009_0554	2009_0675	2009_0785	2009_0865	2009_0895	2009_0952	2009_0965	2009_0172	2009_0838	2009_0631	2009_0449
Ssa0055BSFU			1	4	1	1	1	1	1	1	4	4	1	1	1	1	1	1	4	1	4	4	4	1	1	1	4	4	4	1	4	4
Ssa0350BSFU			7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
OMM1272			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Exon 2					1	1	1	1	1	1	1	1	1	1	1	0	?	1	1	1	1	1	0	1	1	0	0	1	0	1	0	0
Exon 4					1	1	1	1	1	1	1	1	1	1	1	0	?	1	1	1	1	1	0	1	1	0	0	1	0	1	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Not Present	Female	Female	Not Present	Male	Male	Male	Male	Female	Not Present	Male	Female	Female	Male	Female	Female	Female	Female
				Match?																												

2009_27 Ssa02
parents and *sdY* agree 100%

	AS1-2002_0011	AS2	S1-2007_0010	S2	2009_0208	2009_0037	2009_0480	2009_0565	2009_0581	2009_0933	2009_0936	2009_0468	2009_0487	2009_0548	2009_0683	2009_0034	2009_0219	2009_0035	2009_0193	2009_0707	2009_0779	2009_0495	2009_0204	2009_0464	2009_0538	2009_0760	2009_0158	2009_0441	2009_0106	2009_0467	2009_0950	2009_0412	2009_0425	2009_0567	2009_1007	2009_1015
Ssa0055BSFU	3	4	3	2	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2	2	2	2	2	3	2	2	2	2	2	2	2	2	2
Ssa0103aECIG	M	V	M	V	V	V	V	V	V	V	V	M	M	M	M	M	M	M	M	M	M	M	M	M	V	V	V	V	V	V	V	M	M	M	M	M
Ssa0368BSFU	7	7	7	5	5	7	5	5	7	5	5	7	5	5	5	5	7	5	7	7	7	5	7	5	7	7	7	5	5	7	5	7	7	5	7	7
			D1-2006_0037	D2	2009_0208	2009_0037	2009_0480	2009_0565	2009_0581	2009_0933	2009_0936	2009_0468	2009_0487	2009_0548	2009_0683	2009_0034	2009_0219	2009_0035	2009_0193	2009_0707	2009_0779	2009_0495	2009_0204	2009_0464	2009_0538	2009_0760	2009_0158	2009_0441	2009_0106	2009_0467	2009_0950	2009_0412	2009_0425	2009_0567	2009_1007	2009_1015
Ssa0055BSFU			5	6	5	5	5	6	5	6	6	6	6	6	5	6	5	6	6	6	5	5	5	5	5	5	5	6	5	5	6	5	6	5	6	5
Ssa0103aECIG			M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
Ssa0368BSFU			4	6	6	4	4	4	4?	6	6	4	4	6	4	6	6	6	4	4	6	6	6	6	4	4	6	6	6	4	4	6	6 or 4?	4?	6	4
Exon 2					1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	0	0	?	0	0	0	?	0
Exon 4					1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	0	0	?	0	0	0	?	0
Fabp6b					1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	1	1	1	?	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	No Gonad	Female	female	Female	Male	Female	Female	Female	Female	Female	Female	Female	Female	Female

Legend	AS-Ancestral sire	S1 or S2 is sire	D1 or D2 is dam	Unknown	Known Male	Predicted male	Known female	Predicted female	Discrepancy	sex predicted for this family	sdY presence and absence indicated by 1 and 0 respectively for:
Markers	Ssa02/LG1										Exon 2
	Ssa06/LG4	Actual known phenotypes are displayed in the" Sex call from Pheotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class_Family 5.									Exon 4
	Ssa03/LG11	Individual ID in format Year class_Individual number e.g. 2003_0007 = 2003 Year class_Individual 0007									Fabp6 (DNA quality control)

2009_28 Ssa02
parents and *sdY* agree 100%

	AS1-2001_0017	AS2	S1-2007_0021	S2	2009_0793	2009_0918	2009_0484	2009_0070	2009_0087	2009_0117	2009_0142	2009_0213	2009_0168	2009_0221	2009_0275	2009_0472	2009_0479	2009_0041	2009_0501	2009_0563	2009_0599	2009_0627	2009_0667	2009_0723	2009_0753	2009_0821	2009_1016	2009_0045	2009_0061	2009_0576
Ssa0183BSFU	3	4	3	4	3	3	3	3	3	3	4	3	4	4	4	4	3	3	4	4	4	4	4	3	3	3	3	4	3	4
Ssa0376BSFU	1	1	1	6	1	1	1	6	1	1	6	6	6	6?	6	6	6	1	1	1	6	1	6	1?	1	1	1	1	6	1?
Ssa0818BSFU	4	3	4	2	4	4	4	2	2	2	4	4	4	2	2	4	2	2	2	2	2	2	4	2	2	2	4	4	2	2

			D1-2006_0129	D2	2009_0793	2009_0918	2009_0484	2009_0070	2009_0087	2009_0117	2009_0142	2009_0213	2009_0168	2009_0221	2009_0275	2009_0472	2009_0479	2009_0041	2009_0501	2009_0563	2009_0599	2009_0627	2009_0667	2009_0723	2009_0753	2009_0821	2009_1016	2009_0045	2009_0061	2009_0576
Ssa0183BSFU			2	6	6	2	6	6	2	2	2	2	2	6	2	2	6	2	2	2	6	2	2	6	2	2	2	2	2	6
Ssa0376BSFU			1	7	1	7	7	1	7	7?	1	1	1	1?	1	1	1	1	7	7	1	7	1	1	1	1	1	7	1	7?
Ssa0818BSFU			2	3	2	2	2	3	3	2	3	2	3	3	2	2	3	3	3	2	3	2	2	3	2	3	3	3	2	2
Exon 2					1	1	1	1	1	1	0	1	0	0	0	0	1	1	0	0	0	0	0	1	1	1	1	0	1	0
Exon 4					1	1	1	1	1	1	0	1	0	0	0	0	1	1	0	0	0	0	0	1	1	1	1	0	1	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Female	Male	Female	Not Present	Female	Female	Not Present	Male	Not Present	Female	Male	Female	Female	Male	Not Present	Male	Male	Female	Male	female
				Match?																										

2009_29 Ssa02
parents and *sdY* agree 100%

	AS1-2001_0015	AS2	S1-2007_0015	S2	2009_0011	2009_0033	2009_0284	2009_0409	2009_0457	2009_0485	2009_0783	2009_0888	2009_0241	2009_0330	2009_0540	2009_0877	2009_0374	2009_0245	2009_0593	2009_0814	2009_0922	2009_0216	2009_0958	2009_0436	2009_0632	2009_0644	2009_0546	2009_0039	2009_1022	2009_0080
Ssa0182ECIG	M	M	M	V	M	M	M	M	M	M	M	M	M	M	M	M	M	V	V	V	V	V	V	V	V	V	V	V	V	V
Ssa0055BSFU	4	2	4	6	4	4	4	4	4	4	4	4	4	4	4	4	4	6	6	6	6	6	6	6	6	6	6	6	6	6
Ssa0789BSFU	1	3	1	4	1	4	4	4	4	4	4	1	1	1	4	4	4	4	1	4	1	1	1	4	1	4	1	4	1	1
Ssa0368BSFU	6	1	6	4	4	4	4	6	4	6	6	6	4	6	6	6	6	6	4	6	6	6	6	4	6	4	4	4	4	6

			D1-2006_0113	D2	2009_0011	2009_0033	2009_0284	2009_0409	2009_0457	2009_0485	2009_0783	2009_0888	2009_0241	2009_0330	2009_0540	2009_0877	2009_0374	2009_0245	2009_0593	2009_0814	2009_0922	2009_0216	2009_0958	2009_0436	2009_0632	2009_0644	2009_0546	2009_0039	2009_1022	2009_0080
Ssa0182ECIG			M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
Ssa0055BSFU			4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Ssa0789BSFU			4	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0368BSFU			1	5	1	5?	5?	5	5?	5	5	1	5	5	5	5	5	5	5	5	5	5	1	1	5	1	1	1	5	5
Exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Exon 4					1	1	1	1	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Fabp6b					1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Female	Female	Female	Female	Female	Not Present	Female	Not Present	Female	Not Present	Female
				Match?																										

2009_32 Ssa03
parents and *sdY* agree 100%

	AS1-2002_0013	AS2	S1-2007_0001	S2	2009_0253	2009_0598	2009_0311	2009_0531	2009_0200	2009_0243	2009_0258	2009_0332	2009_0967	2009_0734	2009_0673	2009_0749	2009_0722	2009_0997	2009_0279	2009_0558	2009_0611	2009_0942	2009_0608	2009_0636	2009_0137	2009_0494	2009_0513	2009_0609	2009_0915	2009_0259	2009_0422	2009_0686	2009_0702	2009_0771	2009_0083	2009_0229	2009_0363	2009_0397	2009_0424	2009_0470	2009_0827
Ssa0649BSFU	2	1	2	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	?	1	2	1	1	1	2	1	1	1	1	1	?	2	1	1	1	1	1	1
Ssa0017BSFU	3	2	3	1	3	3	3	3	3	3	3	3	3	?	3	3	3	3	3	3	3	1	1	3	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1
Ssa0368BSFU	1	3	1	4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	4	4	1	4	4	4	4	4	4	4	4	4	4	1	4	4	4	?	4	4
Ssa0516BSFU	3	3	3	4	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	?	4	3	4	4	4	4	4	4	4	4	4	4	3	4	4	4	4	4	4
OMM5019	2	1	2	1	2	2	2	2	2	2	?	2	2	2	2	2	2	2	2	2	2	?	1	?	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1
OMM1267	1	3	1	2	?	1	1	1	?	1	1	?	1	1	1	1	1	1	?	?	1	?	2	1	2	?	?	2	2	2	2	2	2	2	1	2	2	2	2	?	?
SsaD144BSFU	1	3	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	2	2	2	2	2	2	2	2	2	?	1	2	2	2	2	2	2
Ssa1077BSFU	11	7	11	7	11	11	11	11	11	7	11	11	11	11	11	11	11	11	7	7	11	7	11	11	7	7	11	11	11	7	7	7	7	7	11	7	11	11	7	11	7
OMM5037/1	1?	9?	4	2	4	4	4	4	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Ssa0103aECIG	V	V	V	M	V	V	V	V	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V

			D1-2006_0026	D2	2009_0253	2009_0598	2009_0311	2009_0531	2009_0200	2009_0243	2009_0258	2009_0332	2009_0967	2009_0734	2009_0673	2009_0749	2009_0722	2009_0997	2009_0279	2009_0558	2009_0611	2009_0942	2009_0608	2009_0636	2009_0137	2009_0494	2009_0513	2009_0609	2009_0915	2009_0259	2009_0422	2009_0686	2009_0702	2009_0771	2009_0083	2009_0229	2009_0363	2009_0397	2009_0424	2009_0470	2009_0827
Ssa0649BSFU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	?	2	2	2	2	2	2	2	2	2	2	2	?	2	2	2	2	2	2	2
Ssa0017BSFU			4	4	4	4	4	4	4	4	4	4	4	?	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Ssa0368BSFU			2	4	2	?	4	2	4	4	4	4	4	2	4	4	4	4	2	2	4	2	2	4	2	4	4	4	4	2	2	2	2	4	4	2	2	4	?	4	2
Ssa0516BSFU			1	2	2	1	1	1	1	2	1	2	2	2	2	2	1	2	1	1	1	?	2	2	1	1	1	2	2	1	1	1	2	1	2	1	2	1	1	1	2
OMM5019			1	1	1	1	1	1	1	1	?	1	1	1	1	1	1	1	1	1	1	?	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
OMM1267			3	4	?	4	4	4	?	3	4	?	3	3	3	3	4	3	?	?	4	?	3	3	3	?	?	3	3	4	4	4	3	4	3	4	3	4	4	?	?
SsaD144BSFU			3	4	4	2	4	4	4	4	4	4	?	3	4	3	3	4	4	4	4	?	4	4	3	4	3	4	4	3	4	4	4	?	3	3	4	4	4	4	3
Ssa1077BSFU			10	8	10	10	10	8	8	10	10	8	8	8	10	8	8	10	8	10	8	10	8	8	8	10	10	10	8	8	10	8	8	8	8	10	10	8	8	8	10
OMM5037/1			1	4	4	4	4	1	1	1	1	4	4	1	1	1	4	4	4	1	1	1	1	4	1	4	1	4	4	1	4	1	4	1	1	1	4	1	1	1	1
Ssa0103aECIG			M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
exon 2					1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	?	?	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
exon 4					1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	?	?	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Fabp6b					1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	?	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Female	Male	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Male	Female	female	Not present	Not Present	Male	Female
				Match?																																					

2009_34 Ssa02
parents and *sdY* agree 100%
Calls for Ssa0233Checked

	AS1-2002_0022	AS2	S1-2007_0002	S2	2009_0052	2009_0157	2009_0164	2009_0170	2009_0282	2009_0380	2009_0458	2009_0791	2009_0932	2009_0894	2009_0913	2009_0699	2009_0096	2009_0135	2009_0348	2009_0953	2009_1018	2009_0848	2009_0789	2009_0403	2009_0557	2009_0855	2009_0435	2009_0613	2009_0635	2009_0923	2009_0074	2009_0287	2009_0381	2009_1030
Ssa0055BSFU	4	3	5	10	5	5	5	5	5	5	5	5	5	5	10	5	5	10	10	10	5	10	10	10	10	6?	10	10	10	10	10	10	10	10
Ssa0233BSFU	2	3	2	1	2	2	2	2	2	2	2	?	2	?	?	?	2	1	?	1	2	?	?	?	1	?	1	1	1	?	1	1	1	1
Ssa0074ECIG	M	V	M	V	M	M	M	V	V	V	V	V	V	M	M	M	M	M	M	V	V	V	V	V	V	?	V	V	V	V	M	M	M	?
Ssa0350BSFU	6	8	6	5	5	5	5	6	6	6	6	6	6	5	5	5	5	5	5	6	6	6	6	6	6	5	6	6	6	6	5	5	5	5
OMM1272	1	1	1	2	2	1	2	1	1	1	1	2	2	1	1	1	1	2	2	2	1	1	2	?	1	?	1	1	2	2	2	1	2	2

			D1-2006_0088	D2	2009_0052	2009_0157	2009_0164	2009_0170	2009_0282	2009_0380	2009_0458	2009_0791	2009_0932	2009_0894	2009_0913	2009_0699	2009_0096	2009_0135	2009_0348	2009_0953	2009_1018	2009_0848	2009_0789	2009_0403	2009_0557	2009_0855	2009_0435	2009_0613	2009_0635	2009_0923	2009_0074	2009_0287	2009_0381	2009_1030
Ssa0055BSFU			4	5	4	4	4	5	5	5	5	4	5	5	5	4	5	4	5	5	5	4	5	5	4	1?	4	4	4	5	5	4	4	4
Ssa0233BSFU			2	3	2	2	2	3	3	2	3	?	3	?	?	?	3	2	?	3	3	?	?	?	2	?	2	3	3	?	3	2	2	2
Ssa0074ECIG			M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	?	M	M	M	M	M	M	?	M	M	M	M	M	M	M	M
Ssa0350BSFU			8	6	6	6	8	8	8	8	6	8	6	8	6	6	8	6	8	8	6	8	8	6	6	8	8	8	8	8	8	6	6	6
OMM1272			1	3	1	3	1	1	1	3	3	3	1	1	3	3	1	1	3	3	3	1	3	?	3	?	1	3	1	3	1	1	3	1
Exon 2					1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	1	1	0	0	0	0	?	0	0	0	0	0	0	0	1
Exon 4					1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	1	1	0	0	0	0	?	0	0	0	0	0	0	0	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1?	1	?	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Female	Male	Male	Not Present	Female	Male	Not Present	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female
				Match?																														

2009_37 Ssa03
parents and *sdY* agree 100%

	AS1-2001_0016	AS2	S1-2007_0014	S2	2009_0218	2009_0378	2009_0547	2009_0854	2009_1005	2009_0327	2009_0550	2009_0578	2009_0361	2009_0743	2009_0762	2009_1021	2009_0622	2009_0774	2009_0887	2009_0755	2009_0944	2009_1020	2009_0190	2009_0537	2009_0726	2009_0797
Ssa0017BSFU	1	1	3	2	3	3	3	3	3	3	3	2	3	2	2	2	2?	2	3	2	2	?	2	2	2	2
Ssa0516BSFU	1	4	1	3	1	1	1	1?	1	1	1	3	3	3	3	3	1	3	1	3	3	?	3	3	3	3
OMM1267	2	1	3	2	3	3	3	3	3	3	3?	2	3	2	2	2	3?	?	3	2	2	?	2	2?	2	2
Ssa0074ECIG	M	V	M	V	M	M	M	M	M	V	V	V	M	M	M	M	V	V	V	V	V	V	M	M	M	M
Ssa1299BSFU	1	3	1	3	1	1	1	1	1	3	3	3	1	1	1	1	1	3	3	3	3	3	1	1	1	1
Ssa202DU	1	3	1	4	4	1	4	1	1	4	4	1	4	1	4	4	1	1	4	4	4	4	4	4	4	4

			D1-2006_0003	D2	2009_0218	2009_0378	2009_0547	2009_0854	2009_1005	2009_0327	2009_0550	2009_0578	2009_0361	2009_0743	2009_0762	2009_1021	2009_0622	2009_0774	2009_0887	2009_0755	2009_0944	2009_1020	2009_0190	2009_0537	2009_0726	2009_0797
Ssa0017BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	?	3	3	3	3
Ssa0516BSFU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	?	2	2	2	2
OMM1267			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	?	2	2	2	?	2	2	2	2
Ssa0074ECIG			V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V
Ssa1299BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa202DU			1	2	2	1	1	2	2	1	2	2	1	2	1	2	1	1	2	2	1	1	1	1	1	1
Exon 2					1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0
Exon 4					1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	0	?	?	1	1	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?	?	1	1	1	1
				Sex call from Phenotype	Male	Male	male	Male	Male	Male	Male	Male	Not Present	Not Present	Female	Female	Not Present	Not Present	Not present	Female	Female	Female	Female	Female	Female	Female
				Match?																						

2009_38 Ssa02
parents and *sdY* agree 100%

	AS1-2001_0015	AS2	S1-2007_0018	S2	2009_0261	2009_0077	2009_0209	2009_0242	2009_0247	2009_0500	2009_0518	2009_0695	2009_0999	2009_0075	2009_0481	2009_0690	2009_0691	2009_0251	2009_0703	2009_0759	2009_0765	2009_0823	2009_0862	2009_0886	2009_0004	2009_0684	2009_0905	2009_0267	2009_0674	2009_0780	2009_0907
Ssa0055BSFU	8	2	8	7	7	8	8	8	8	8	8	8	8	8	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7
Ssa0376BSFU	3	2	3	4	4	4	4	4	4	4	4	4	3	4	4	4 or 3	3	4	4	4	4	4	4	3	3	3	4	3	4	3 and 5?	4
Ssa0350BSFU	8	4	8	5	5	5	5	5	5	5	5	5	8	5	5	5	8	5	8	5	5	5	5	8	8	8	5	8	5	8	5
Ssa0368BSFU	4	1	4	3	3	4	3	4	3	3	4	4	4	4	3	4	4	4	3	3	4	3	3	4	3	4	4	3	3	4	3

			D1-2006_0012	D2	2009_0261	2009_0077	2009_0209	2009_0242	2009_0247	2009_0500	2009_0518	2009_0695	2009_0999	2009_0075	2009_0481	2009_0690	2009_0691	2009_0251	2009_0703	2009_0759	2009_0765	2009_0823	2009_0862	2009_0886	2009_0004	2009_0684	2009_0905	2009_0267	2009_0674	2009_0780	2009_0907
Ssa0055BSFU			2	11	11	11	2	2	2	11	11	2	11	11	2	11	11	2	11	11	2	2	11	2	11	2	11	11	2	2	2
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0350BSFU			4	6	4	4	6	6	4	6	6	6	4	6	6	4	6	4	6	6	6	6	6	6	6	6	4	4	6	4	6
Ssa0368BSFU			2	5	2	5	2	2	2	2	5	2	5	5	5	2	5	2	5	5	5	2	5	2	5	2	5	2	2	5	2
Exon 2					0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Exon 4					0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	Male	Male	Male	male	Male	Not Present	Female	Female	Female	Female	Female	Female	Not Present	Female	Not Present	Male	female	Female	Female	Female	Female	Female
				Match?																											

2009_39 Ssa06
parents and *sdY* agree 100%

	AS1-2001_0003	AS2	S1-2007_0023	S2	2009_0842	2009_0846	2009_0653	2009_0289	2009_0721	2009_0917	2009_0982	2009_0369	2009_0460	2009_0603	2009_0303	2009_0669	2009_0719	2009_0008	2009_0778	2009_0825	2009_0010	2009_0032	2009_0860	2009_0874	2009_0882	2009_0331	2009_0392	2009_0474	2009_0346	2009_0790	2009_0450	2009_0482
Ssa0376BSFU	1	1	1	4	1	1	1	1	1	1	4	4	1	4	4	1	1	1	4	4	4	4	4	4	1	4	4	4	1	4	4	4
Ssa0789BSFU	3	1	3	4	3	3	3	3	3	3	4	4	3	4	4	3	3	3	4	4	4	4	4	4	3	4	4	4	3	4	4	4
Ssa1077BSFU	3	10	3	7	?	3	3	7	7	3	3	3	3	7	7	3	7	3	7	7	7	7	7	3	3	7	3	3	7	7	7	7
Ssa0183BSFU	1?	2?	3	6	?	3	3	6	6	3	3	3	3	6	6	3	6	6	6	6	6	6	6	3	3	6	3	3	6	6	6	6
OMM1272	1	3	1	2	?	1	2	2	2	2	2	1	1	1	1	1	1	1	2	2	2	1	1	2	1	1	1	2	2	2	1	2

			D1-2006_0062	D2	2009_0842	2009_0846	2009_0653	2009_0289	2009_0721	2009_0917	2009_0982	2009_0369	2009_0460	2009_0603	2009_0303	2009_0669	2009_0719	2009_0008	2009_0778	2009_0825	2009_0010	2009_0032	2009_0860	2009_0874	2009_0882	2009_0331	2009_0392	2009_0474	2009_0346	2009_0790	2009_0450	2009_0482
Ssa0376BSFU			1	2	1	2	1	1	2	1	2	1	1	2	2	1	2	2	2	2	2	2	2	1	1	1	1	2	2	2	1	2
Ssa0789BSFU			1	4	1	4	1	1	4	1	4	1	1	4	4	1	4	4	4	4	4	1	4	4	1	1	1	1	1	4	1	4
Ssa1077BSFU			10	10	?	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Ssa0183BSFU			2	4	?	2	4	4	2	2	4	2	4	4	2	4	2	4	2	4	2	2	2	2	2	4	2	2	4	4	4	2
OMM1272			2	3	?	3	2	2	3	3	2	3	2	2	2	3	2	2	2	2	3	2	2	2	3	2	3	3	2	3	3	2
Exon 2					?	1	1	1	1	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0
Exon 4					?	1	1	1	1	1	1	?	1	0	0	1	1	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0
Fabp6b					?	1	1	1	1	1	1	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
				Sex call from Phenotype	Male	Male	Male	Male	Male	male	Male	Male	Male	Female	Female	Male	Not Present	Male	Female	Female	Not Present	Female	Female	Female	Not Present	Female	Female	Female	Male	Female	Female	Female
				Match?																												

Legend
Markers

AS-Ancestral sire | S1 or S2 is sire | D1 or D2 is dam | Unknown | Known Male | Predicted male | Known female | Predicted female | Recapture | sex predicted for this family | sdY+ presence and absence indicated by 1 and 0 respectively for: Exon 2, Exon 4, Fabp6 (DNA quality control)

Ssa02/L/01
Ssa06/L/04
Ssa03/L/011

Actual known phenotypes are displayed in the" Sex call from Phenotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class_Family 5.
Individual ID in format Year class_Individual number e.g. 2003_0007 = 2003 Year class_Individual 0007

2009_42 Ssa06
parents and *sdY* agree 100%

	AS-12003_0032	AS2	S1-2006_0094	S2	S40974 2009_1044	S41000 2009_1047	S41085 2009_1066	S41253 2009_1099	S41324 2009_1112	S41084 2009_1065	S41053 2009_1058	S41153 2009_1079	S41196 2009_1088	S41209 2009_1090	S41217 2009_1093	S41276 2009_1104	S41332 2009_1113	S41348 2009_1115
OMM5037/1	7		7	3	3	3	3	3	3	3	7	7	7	7	7	7	7	7
Ssa0376BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
Ssa0789BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
Ssa0142BSFU	2		2	4	4	4	4	4	4	4	2	2	2	2	2	2	2	2
Ssa0350BSFU	1		1	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1
Ssa0055BSFU	2	1	2	1	1	1	1	1	1?	1	2	2	2	1	2	2	2	1
Ssa0368BSFU	4	4	4	1	4	1	1	1	1	4	4	4	4	4	1	1	1	1

			D1-2006_0081	D2	S40974 2009_1044	S41000 2009_1047	S41085 2009_1066	S41253 2009_1099	S41324 2009_1112	S41084 2009_1065	S41053 2009_1058	S41153 2009_1079	S41196 2009_1088	S41209 2009_1090	S41217 2009_1093	S41276 2009_1104	S41332 2009_1113	S41348 2009_1115
OMM5037/1			2	5	5	5	5	5	5	2	5	5	2	2	2	5	?	2
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0789BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0142BSFU			5	4	4	4	4	4	4	5	5	4	4	4	5	4	4	5
Ssa0350BSFU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa0055BSFU			2	2	2	2	2	2	2	2	2	2	2	?	2	2	2	2
Ssa0368BSFU			4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Exon 2					0	0	0	0	0	0	1	1	1	1	1	1	1	1
Exon 4					0	0	0	0	0	0	1	1	1	1	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1
Sex call from Phenotype					female	female	female	female	female	female	male	male	male	male	male	male	male	male

2009_47 Ssa06
parents and *sdY* agree 100%

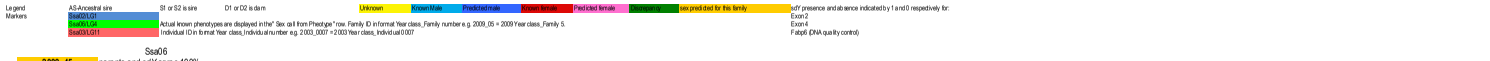
	AS-12003_0032	AS2	S1-2007_0013	S2	S41289 2009_1106	S41309 2009_1110	S40954 2009_1039	S41073 2009_1063	S41186 2009_1085	S41304 2009_1109	S41315 2009_1111	S41088 2009_1068	S41268 2009_1102	S40945 2009_1037	S41294 2009_1108
OMM5037/1	7		7	6	6	6	6	6	6	6	6	7	7	7	7
Ssa0043BSFU	4		4	2	2	2	2	?	2	2	4	4	4	4	4
Ssa0376BSFU	2		2	1	1	1	1	1	1	1	1	2	2	2	2
Ssa0789BSFU	2		2	1	1	1	1	1	1	1	?	2	2	2	2
Ssa0142BSFU	2		2	1	1	1	1	1	1	1	1	2	2	2	2
Ssa0350BSFU	1		1	4	4	4	4	4	4	4	4	1	1	1	1
Ssa0752BSFU	1		1	2	?	2	2	2	2	2	2	1	1	1	1
Ssa1299BSFU	3		3	1	1	1	1	1	1	1	1	3	3	3	3
Ssa0183BSFU	1	2	1	2	2	2	1	1	2	2	2	1	1	1	1
Ssa0818BSFU	3	2	3	4	4	3	3	3	3	3	4	4	4	4	4

			D1-2005_0042		S41289 2009_1106	S41309 2009_1110	S40954 2009_1039	S41073 2009_1063	S41186 2009_1085	S41304 2009_1109	S41315 2009_1111	S41088 2009_1068	S41268 2009_1102	S40945 2009_1037	S41294 2009_1108
OMM5037/1			3	4	3	3	4	4	4	4	3	3	3	3	3
Ssa0043BSFU			3	3	3	3	3	?	3	3	3	3	3	3	3
Ssa0376BSFU			3	1	1	1	3	1	3	1	3	3	3	1	3
Ssa0789BSFU			1	1	1	1	1	1	1	1	?	1	1	1	1
Ssa0142BSFU			4	2	4	2	4	2	4	2	2	4	4	2	4
Ssa0350BSFU			3	2	2	3	3	2	2	2	3	3	3	3	3
Ssa0752BSFU			1	1	?	1	1	1	1	1	1	1	1	1	1
Ssa1299BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0183BSFU			1	4	4	4	1	1	1	1	4	adopted?	1	1	
Ssa0818BSFU			1	3	1	3	1	3	3	1	3	3	1	1	1
Exon 2					0	0	0	0	0	0	0	1	1	1	1
Exon 4					0	0	0	0	0	0	0	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1
					female	female	female	female	female	female	female	male	male	male	male

2009_41 Ssa06
parents and *sdY* agree 100%

	AS-12003_0032	AS2	S1-2006_0115	S2	S40964 2009_1042	S41408 2009_1125	S41377 2009_1119	S41292 2009_1107	S41121 2009_1073	S41157 2009_1080	S41365 2009_1117	S41402 2009_1123	S41087 2009_1067	S41144 2009_1076	S41214 2009_1091	S41168 2009_1083	S41336 2009_1114	S40959 2009_1040	S41013 2009_1048	S41412 2009_1126
OMM5037/1	3		3	2	2	2	2	2	3	2	3	3	3	3	3	3	7	3	3	3
Ssa0376BSFU	2		2	1	1	1	1	1	2	1	2	2	2	2	2	2	2	2	2	2
Ssa0789BSFU	4		4	3	3	3	3	3	4	3	4	?	4	4	4	4	4	4	4	4
Ssa0142BSFU	2		2	1	1	1	1	1	2	1	2	2	2	2	2	2	2	2	2	?
Ssa0350BSFU	1		1	2	2	2	2	2	1	2	1	1	1	1	1	1	1	1	1	1
Ssa0055BSFU	2	2	2	1	1	2	1	1	2	2	2	2	2	2	2	2	1	1	1	1
Ssa0818BSFU	2	3	2	1	1	2	1	2	1	2	1	2	1	2	1	1	2	1	2	1

			D1-2006_0081	D2	S40964 2009_1042	S41408 2009_1125	S41377 2009_1119	S41292 2009_1107	S41121 2009_1073	S41157 2009_1080	S41365 2009_1117	S41402 2009_1123	S41087 2009_1067	S41144 2009_1076	S41214 2009_1091	S41168 2009_1083	S41336 2009_1114	S40959 2009_1040	S41013 2009_1048	S41412 2009_1126
OMM5037/1			2	1	2	2	1	2	1	1	?	1	1	1	1	1	?	1	1	2
Ssa0376BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0789BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0142BSFU			3	4	4	4	3	4	4	4	4	3	4	3	3	4	3	?	4	?
Ssa0350BSFU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa0055BSFU			2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Ssa0818BSFU			1	4	1	1	1	1	4	4	4	1	4	4	4	1	4	1	4	1
Exon 2					0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1
Exon 4					0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
					female	female	female	female	male	male	male	male (precocious)	male	male	male	male	male	male	male	male



Ssa06

2009_45 parents and sdY agree 100%

					S41058	S41197	S41215	S41264	S41221	S41239	S41368	S40993	S41036	S41046	S41102	S41106	S41116	S41233	S41064
	AS-12003_0032	AS2	S1-2007_0009	S2	2009_1059	2009_1089	2009_1092	2009_1101	2009_1095	2009_1097	2009_1118	2009_1046	2009_1052	2009_1057	2009_1070	2009_1071	2009_1072	2009_1096	2009_1061
OMM5037/1	7		7	1	1	1	1	1	1	1	1	7	7	7	7	7	7	7	7
Ssa0043BSFU	4		4	3	3	3	3	3	3	3	3	4	4	4	4	4	?	4	?
Ssa0376BSFU	2		2	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
Ssa0789BSFU	2		2	3	3	3	3	3	3	3	3	?	2	2	2	2	2	2	2
Ssa0142BSFU	2		2	3	3	2	?	3	2	?	3	2	2	2	2	2	2	2	2
Ssa0350BSFU	1		1	3	3	?	?	?	?	3	3	?	?	?	?	?	1	?	?
OMM5037/III	1		1	2	2	1	2	2	2	1	2	2	1	1	2	2	1	2	?
OMM1272	3	3	3	2	2	3	2	2	2	3	2	2	3	3	2	2	3	2	3
Ssa202DU	6	6	6	3	3	3	6	6	6	?	6	3	3	6	6	3	3	?	3

					S41058	S41197	S41215	S41264	S41221	S41239	S41368	S40993	S41036	S41046	S41102	S41106	S41116	S41233	S41064
			D1-2005_0042		2009_1059	2009_1089	2009_1092	2009_1101	2009_1095	2009_1097	2009_1118	2009_1046	2009_1052	2009_1057	2009_1070	2009_1071	2009_1072	2009_1096	2009_1061
OMM5037/1			3	4	3	4	3	4	4	3	3	3	3	3	3	3	3	4	3
Ssa0043BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	?	3	?
Ssa0376BSFU			3	1	3	1	1	3	1	3	3	1	3	3	3	1	1	1	1
Ssa0789BSFU			1	1	1	1	1	1	1	1	1	?	1	1	1	1	1	1	1
Ssa0142BSFU			2	4	4	3?	?	4	3?	?	4	2	4	4	4	2	2	2	2
Ssa0350BSFU			1	3	3	?	?	?	?	3	3	?	?	?	?	?	1	?	?
OMM5037/III			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	?
OMM1272			1	2	2	1	1	1	1	2	2	2	1	2	2	1	1	2	2
Ssa202DU			1	3	1	1	1	1	3	?	3	1	1	1	1	1	1	?	3
Exon 2					0	0	0	0	0	0	0	1	1	1	1	1	1	1	1
Exon 4					0	0	0	0	0	0	0	1	1	1	1	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
					female	female	female	female	female	female	female	male	male	male	male	male	male	male	male

Ssa06

2009_43 sdY and parents agree 100%

					S40950	S41038	S41394	S41023	S41251	S40962	S41061	S41082	S41125	S41163	S41396	S41286
	AS-12003_0032	AS2	S1-2006_0094	S2	2009_1038	2009_1054	2009_1121	2009_1049	2009_1098	2009_1041	2009_1060	2009_1064	2009_1074	2009_1081	2009_1122	2009_1105
OMM5037/1	7		7	3	3	3	3	3	3	7	7	7	7	7	7	7
Ssa0043BSFU	4		4	3	?	3	3	3	3	4	4	4	4	4	4	4
Ssa0376BSFU	2		2	1	1	1	1	1	1	2	2	2	2	2	2	2
Ssa0789BSFU	2		2	1	?	1	1	1	1	2	2	2	2	2	2	2
Ssa0142BSFU	2		2	4	4	4	4	4	4	2	2	2	2	2	2	2
Ssa0350BSFU	1		1	3	3	3	3	3	3	1	1	1	1	1	1	1
Ssa0752BSFU	1		1	2	2	2	2	2	2	1	1	1	1	1	?	1
Ssa1299BSFU	3		3	1	1	1	1	1	1	3	3	3	3	3	3	3
Ssa202DU	6	6	6	3	3	6	3	6	6	3	6	6	3	3	6	3
Ssa0368BSFU	4	4	4	1	4	4	4	4	1	4	1	4	1	4	4	4

					S40950	S41038	S41394	S41023	S41251	S40962	S41061	S41082	S41125	S41163	S41396	S41286
			D1-2005_0019	D2	2009_1038	2009_1054	2009_1121	2009_1049	2009_1098	2009_1041	2009_1060	2009_1064	2009_1074	2009_1081	2009_1122	2009_1105
OMM5037/1			6	2	2	2	2	6	2	6	6	6	6	2	2	6
Ssa0043BSFU			1	4	?	1	4	4	1	1	1	4	1	1	1	1
Ssa0376BSFU			3	1	1	1	1	1	1	3	3	1	3	3	1	3
Ssa0789BSFU			3	1	?	1	1	1	3	3	3	1	3	3	1	3
Ssa0142BSFU			4	5	5	5	5	5	5	5	4	4	4	4	4	4
Ssa0350BSFU			1	2	2	2	2	1	2	1	1	2	2	1	2	1
Ssa0752BSFU			3	2	2	2	2	2	2	3	2	2	2	3	?	3
Ssa1299BSFU			2	1	1	1	1	1	1	1	1	1	1	1	1	2
Ssa202DU			2	5	2	2	5	5	5	2	2	2	2	2	2	5
Ssa0368BSFU			4	6	4	6	4	4	4	4	6	4	6	4	6	4
Exon 2					0	0	0	0	0	1	1	1	1	1	1	1
Exon 4					0	0	0	0	0	1	1	1	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1
					female	female	female	female	female	male	male	male	male	male	male	male

Ssa06

2009_46 sdY and parents agree 100%

					S41254	S41068	S41188	S41220	S41413	S41415	S40970	S40978	S41150	S41039	S41129	S41151	S41360
	AS-12003_0032	AS-2	S1-2006_0094	S-2	2009_1100	2009_1062	2009_1086	2009_1094	2009_1127	2009_1128	2009_1043	2009_1045	2009_1077	2009_1055	2009_1075	2009_1078	2009_1116
OMM5037/1	7		7	3	3	3	3	3	3	3	7	7	7	?	7	7	7
Ssa0043BSFU	4		4	3	3	3	3	3	3	3	4	4	4	4	4	4	4
Ssa0376BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2	2	2
Ssa0789BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2	2	2
Ssa0142BSFU	2		2	4	?	4	?	4	?	?	2	2	2	2	2	?	?
Ssa0350BSFU	1		1	3	?	3	?	?	?	3	?	?	1	?	1	?	1
Ssa0752BSFU	1		1	2	2	2	2	2	2	2	1	1	1	1	1	1	1
Ssa1299BSFU	3		3	1	1	1	1	1	1	?	3	3	3	3	3	3	3
Ssa0368BSFU	4	4	4	1	4	1	4	1	4	1	4	4	4	4	4	?	4
Ssa202DU	6	6	6	3	3	3	3	6	3	?	6	3	6	6	6	6	6

					S41254	S41068	S41188	S41220	S41413	S41415	S40970	S40978	S41150	S41039	S41129	S41151	S41360
			D1-2005_0042	D-2	2009_1100	2009_1062	2009_1086	2009_1094	2009_1127	2009_1128	2009_1043	2009_1045	2009_1077	2009_1055	2009_1075	2009_1078	2009_1116
OMM5037/1			4	3	4	3	4	4	4	3	3	3	3	?	4	3	4
Ssa0043BSFU			3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Ssa0376BSFU			1	3	1	3	1	1	1	3	1	1	1	1	1	3	3
Ssa0789BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa0142BSFU			2	4	?	4	?	4	?	?	2	2	2	2	2	?	?
Ssa0350BSFU			1	3	?	3	?	?	?	3	?	?	1	?	1	?	1
Ssa0752BSFU			1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ssa1299BSFU			3	3	3	3	3	3	3	?	3	3	3	3	3	3	3
Ssa0368BSFU			2	3	3	2	3	2	3	3	3	2	2	2	3	?	3
Ssa202DU			1	3	1	3	3	3	3	?	1	1	3	3	3	3	3
Exon 2					0	0	0	0	0	0	1	1	1	1	1	1	1
Exon 4					0	0	0	0	0	0	1	1	1	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1	1	1
					female	female	female	female	female	female	male	male	male	male	male	male	male

Legend
Markers

AS-Ancestral sire
Ssa06.G31
Ssa18LG14
Ssa03LG11

S1 or S2 is sire

D1 or D2 is dam

Actual known phenotypes are displayed in the" Sex call from Phenotype" row. Family ID in format Year class_Family number e.g. 2009_05 = 2009 Year class, Family 5.

Individual ID in format Year class_Individual number e.g. 2003_0007= 2003 Year class_Individual 0007

Unknown | Known Male | Predicted male | Known female | Predicted female | Incongruency | sex predicted for this family

sdY presence and absence indicated by 1 and 0 respectively for:
Exon 2
Exon 4
Fabp6 (DNA quality control)

2009_44 Ssa06

sdY and parents agree 100%

					S41032	S41042	S41175	S41035	S41096	S41403	S41164	S41037	S41274	S41386	S41193
	AS-12003_0032	**AS2**	S1-2007_0013	**S2**	2009_1050	2009_1056	2009_1084	2009_1051	2009_1069	2009_1124	2009_1082	2009_1053	2009_1103	2009_1120	2009_1087
OMM5037/1	7		7	6	6	6	6	6	6	6	7	7	7	7	?
Ssa0043BSFU	4		4	1	2?	2?	2?	2?	2?	2?	4	4	4	4	4
Ssa0376BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2
Ssa0789BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2
Ssa0142BSFU	2		2	1	1	1	1	1	1	1	2	2	2	2	2
Ssa0350BSFU	1		1	4	4	4	4	4	4	4	1	1	1	1	1
Ssa0752BSFU	1		1	2	2	2	2	2	2	2	?	1	1	1	1
Ssa1299BSFU	3		3	1	1	1	1	1	1	1	3	3	3	3	3
Ssa0818BSFU	3	2	3	4	4	?	3	3	3	3	4	4	3	4	3
Ssa0183BSFU	1	2	1	2	1	1	2	2	2	2	1	1	1	2	2

					S41032	S41042	S41175	S41035	S41096	S41403	S41164	S41037	S41274	S41386	S41193
			D1-2005_0019	**D2**	2009_1050	2009_1056	2009_1084	2009_1051	2009_1069	2009_1124	2009_1082	2009_1053	2009_1103	2009_1120	2009_1087
OMM5037/1			6	2	2	2	6	2	2	6	6	2	2	6	?
Ssa0043BSFU			1	4	4	4	1	4	4	4	1	1	1	1	4
Ssa0376BSFU			3	1	1	1	3	1	1	1	3	3	1	3	1
Ssa0789BSFU			3	1	1	1	3	1	1	1	3	3	1	3	1
Ssa0142BSFU			4	5	4	5	4	5	5	4	4	4	5	4	5
Ssa0350BSFU			1	2	2	2	1	2	2	1	1	1	2	1	1
Ssa0752BSFU			3	2	2	3	3	2	2	2	?	3	2	3	2
Ssa1299BSFU			2	1	1	2	2	1	1	1	2	2	1	2	2
Ssa0818BSFU			1	1	1	?	1	1	1	1	1	1	1	1	1
Ssa0183BSFU			1	3	1	1	1	3	3	3	1	3	3	3	1
Exon 2					0	0	0	0	0	0	1	1	1	1	1
Exon 4					0	0	0	0	0	0	1	1	1	1	1
Fabp6b					1	1	1	1	1	1	1	1	1	1	1
					female	female	female	female	female	female	male	male	male	male	male (precocious)

Supplementary Table S4.
Microsatellite and SNP analysis of SALTAS broodstock families in which the sex-determining gene resides on Ssa06 (AS-4). Markers are arranged in order corresponding to their placement on the female European Atlantic salmon linkage map (See Phillips et al. 2009 for nomenclature) www.asalbase.org. The seven families originally analyzed are highlighted yellow.

	2009_XX[1]																						
Marker	21	18	39	40	30	02	15	26	10	24	03	06	36	07	11	45	44	47	41	42	43	46	total
[2]**Ssa02**																							
Ssa1077BSFU			18/24 (1.4)					6/23 (0)			7/14 (0)												
Ssa0055BSFU	[3]25/33 [4](2.0)	9/17 (0)		8/18 (0)	13/25 (0)	11/18 (-0.2)	7/16 (0.1)	15/22 (0.6)		6/16 (0)		11/21 (0)	6/16 (0)	10/32 (0)					11/16 (0.5)	12/14 (1.7)			
Ssa0183BSFU			17/24 (0.9)			8/18 (0)								21/32 (0.7)	10/13 (0.9)		7/11 (0.2)	9/11 (1.0)					
Ssa202DU																4/13 (0.4)					5/12 (0.1)	10/12 (1.3)	
Ssa0233BSFU									7/21 (0)														
Ssa1265BSFU																							
Ssa0182ECIG																							
Ssa06																							
OMM5037	31/33 (6.6)															15/15 (4.5)	10/10 (3.0)	11/11 (3.3)	14/15 (2.9)	13/13 (3.9)	12/12 (3.6)	12/12 (3.6)	118/121
Ssa0074ECIG					25/25 (7.5)			17/21 (1.9)			14/14 (4.2)	21/21 (6.3)	20/21 (4.6)										97/102
Ssa0376BSFU			23/25 (4.5)	16/16 (4.8)	25/25 (7.5)			21/23 (4.0)	20/21 (4.6)	14/16 (3.2)	14/14 (4.2)			32/32 (9.6)	13/13 (3.9)	15/15 (4.5)	11/11 (3.3)	11/11 (3.3)	15/16 (3.2)	14/14 (4.2)	12/12 (3.6)	13/13 (3.9)	269/277
Ssa0789BSFU		16/16 (2.9)	23/25 (4.5)				14/16 (3.2)									14/14 (4.2)	11/11 (3.3)	10/10 (3.0)	14/15 (2.9)	14/14 (4.2)	11/11 (3.3)	13/13 (3.9)	140/145
Ssa0043BSFU																11/13 (1.5)	5/5 (1.5)	10/10 (3.0)	14/16 (3.2)		11/11 (3.3)	13/13 (3.9)	64/68
Ssa0103aECIG				19/19 (5.4)																			19/19
Ssa0142BSFU																13/13 (3.9)	11/11 (3.3)	11/11 (3.3)	14/15 (2.9)	14/14 (4.2)	12/12 (3.6)	7/7 (2.1)	82/83
Ssa0350BSFU							14/16 (3.2)									4/4 (1.2)	11/11 (3.3)	11/11 (3.3)	15/16 (3.2)	14/14 (4.2)	12/12 (3.6)	5/5 (1.5)	86/89
Ssa1299BSFU						17/18 (3.7)		21/22 (4.8)									11/11 (3.3)	11/11 (3.3)			12/12 (3.6)	12/12 (3.6)	84/86
Ssa0752BSFU							14/16 (3.2)										10/10 (3.0)	10/10 (3.0)			11/11 (3.3)	13/13 (3.9)	58/60
Ssa03																							
Ssa0649BSFU																							
Ssa0343BSFU				6/19 (0.6)																			
OMM1272			11/24 (0)													9/15 (0.1)							
Ssa0017BSFU								8/22 (0.3)			8/15 (0)												
ESTNV_29224_109																							
Ssa0368BSFU	18/34 (0)	9/17 (0)					9/16 (0.1)			14/17 (1.7)		10/21 (0)	11/21 (0.01)	17/31 (0.1)						8/14 (0.1)	6/12 (0)	9/12 (0.7)	
Ssa0818BSFU					11/25 (0.1)	10/20 (0)			6/21 (0.9)						7/12 (0.1)		3/10 (0.4)	4/11 (0.2)	8/16 (0)				
Ssa0212BSFU																							
Ssa0516BSFU																							
OMM5019																							
OMM1267																							
SsaD144																							
OMM5037/2																8/14 (0.1)							

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Ssa06	LOD	theta
OMM5037	30.3	0.02
Ssa0074ECIG	22	0.05
Ssa0376BSFU	67.6	0.03
Ssa0789BSFU	34.2	0.03
Ssa0043BSFU	13.9	0.06
E15190_1379	5.7	0
Ssa0142BSFU	22.6	0.01
Ssa0350BSFU	21.1	0.03
Ssa1299BSFU	21.8	0.02
Ssa0752BSFU	14.2	0.03

[1]Family (2009 year class where family ID's are given as XX, values below). [2] Chromosome number shown in Ssa0X. [3]Number of offspring for which genotype/phenotype agreee / total number of offspring with genotype/phenotype. [4]LOD score corresponding to the ratio of correct genotype/phenotype matches:incorrect genotype/pheotype matches in a given family.

Supplementary Table S5.
Microsatellite and SNP analysis of SALTAS broodstock families in which the sex-determining gene housed on Ssa02 (AS-1). Markers are arranged in order corresponding to their placement on the female European Atlantic salmon linkage map (www.asalbase.org).

Marker	Families 2009_XX[1] 25	9	1	29	38	28	27	16	31	35	17	12	04	20	34	19	05	23	13	33	08	22	14	Total	98 102 LOD	Theta	Ssa02
Ssa02[2]																											
Ssa1077BSFU			21/23[3] (4.0)[4]							28/29 (6.8)												16/17 (3.4)		65/69	14.1	0.06	Ssa1077BSFU
Ssa0055BSFU	24/25 (5.7)	20/20 (6.0)		23/23 (6.9)	23/24 (5.4)		31/31 (9.3)	9/9 (2.7)	23/24 (5.4)	28/29 (6.8)	25/25 (7.5)		27/30 (4.8)	46/50 (9.0)	26/27 (6.2)	12/12 (3.6)	14/14 (4.2)	23/25 (4.5)	26/26 (7.7)	23/23 (6.9)	25/27 (5.0)			428/444	103.7	0.04	Ssa0055BSFU
Ssa0183BSFU						21/22 (4.9)			23/24 (5.4)	28/29 (6.8)											26/27 (6.3)			98/102	23.4	0.04	Ssa0183BSFU
Ssa202DU																							14/14 (4.2)	14/14	4.2	0	Ssa202DU
Ssa0233BSFU												23/23 (6.9)			17/18 (3.7)				26/26 (7.7)	23/23 (6.9)				89/90	24.7	0.01	Ssa0233BSFU
Ssa0182ECIG				23/23 (6.9)																				23/23	6.9	0	Ssa0182ECIG
Ssa06																											
OMM5037			13/23 (0.1)											26/50 (0)				10/24 (0.1)									
Ssa0074ECIG								6/10 (0.1)							17/26 (0.5)												
ESTNV_21223_122																											
Ssa0376BSFU		7/20 (0)			10/24 (0)														15/26 (0.1)			11/17 (-0.1)	10/15 (0.36)				
Ssa0789BSFU				10/23 (0)				4/12 (0)	11/22 (0)			14/23 (0.2)				7/12 (0.1)											
Ssa0043BSFU		8/20 (0)																									
Ssa0103aECIG							16/31 (0)																				
Ssa0142BSFU																											
Ssa0350BSFU	6/14 (0)														14/28 (0)		6/14 (0.1)				14/27 (0)						
Ssa1299BSFU					10/24 (0)					16/29 (0.1)	8/25 (0)								15/26 (0.1)	9/23 (0.2)							
Ssa0752BSFU													20/33 (0.3)														
Ssa03																											
Ssa0649BSFU																											
Ssa0343BSFU													11/25 (0.1)														
OMM1272	13/25 (0)		8/20 (0.2)												15/26 (0.1)												
Ssa0017BSFU											10/24 (0.1)																
ESTNV_29224_109																											
Ssa0368BSFU				11/23 (0)	14/24 (0.2)		14/31 (0.1)		6/24 (1.6)	21/29 (1.3)				29/48 (0.5)				10/25 (0.2)	11/20 (0)	13/23 (0.1)	16/26 (0.3)	12/17 (0.6)	7/13 (0)				
Ssa0818BSFU		15/21 (0.9)				8/22 (0.4)		8/12 (0.3)									10/14 (0.6)										
Ssa0212BSFU												12/23 (0)															
Ssa0516BSFU																											
OMM5019																											
OMM1267																											
SsaD144																4/12 (0.3)											

[1]Family (2009 year class where family ID's are given as XX, values below). [2] Chromosome number shown in Ssa0X. [3]Number of offspring for which genotype/phenotype agreee / total number of offspring with genotype/phenotype. [4]LOD score corresponding to the ratio of correct genotype/phenotype matches:incorrect genotype/pheotype matches in a given family.

Supplementary Table S6.
Microsatellite and SNP analysis of SALTAS broodstock families in which the sex-determining gene housed on Ssa03 (AS-11). Markers are arranged in order corresponding to their placement on the female European Atlantic salmon linkage map. www.asalbase.org

Marker	2009_32[1]	2009_37	Total	LOD	Theta	
Ssa02[2]						
Ssa1077BSFU	28/35[3] (2.9)[4]					
Ssa0055BSFU						
Ssa0183BSFU						
Ssa202DU		13/17 (1.1)				
Ssa0233BSFU						
Ssa1265BSFU						
Ssa0182ECIG						
Ssa06						
OMM5037	16/35 (0)					
Ssa0074ECIG		10/17 (0.1)				
Ssa0376BSFU						
Ssa0789BSFU						
Ssa0043BSFU						
Ssa0103aECIG	12/35 (0)					
Ssa0142BSFU						
Ssa0350BSFU						
Ssa1299BSFU		8/17 (0)				
Ssa0752BSFU						
Ssa03						
Ssa0649BSFU	28/33 (3.8)		28/33	3.8	0.15	Ssa0649BSFU
Ssa0017BSFU	30/34 (4.9)	15/16 (3.2)	45/50	8	0.1	Ssa0017BSFU
Ssa0368BSFU	31/35 (5.1)		31/35	5.1	0.11	Ssa0368BSFU
OMM1267	24/25 (5.7)	14/15 (2.9)	38/40	8.6	0.05	OMM1267
Ssa0516BSFU	30/34 (4.9)	15/16 (3.2)	45/50	8	0.1	Ssa0516BSFU
OMM5019	29/32 (5.3)		29/32	5.3	0.09	OMM5019
SsaD144	30/34 (4.9)					

[1]Family (2009 year class where family ID's are given as XX, values below). [2] Chromosome number shown in Ssa0X.

[3](Number of offspring for which genotype and phenotype agree) / (total number of offspring with genotype and phenotype). [4]LOD score corresponding to the ratio of correct genotype and phenotype matches:incorrect genotype and pheotype matches in a given family.

Supplementary Table S7.
Summary of individuals in which *sdY* call, phenotype call and/ or genotype call do not agree. Discrepancies are highlighted green.

			Phenotypic sex predicted by:		
[1]Family ID	[2]Individual ID	Phenotype	Haplotype	[7]* *sdY* test	Exon 3
2009_32	2009_0558	[4]F	M	[3]F	[5]N
2009_20	2009_0064	F	M	F	[6]Y
2009_20	2009_1027	F	M	F	Y
2009_20	2009_1008	F	M	F	Y
2009_32	2009_0636	F	M	F	N
2009_24	2009_0924	M	F	M	Y
2009_20	2009_0672	M	F	F	Y
2009_08	2009_0373	F	M	F	N
2009_04	2009_0053	M	F	F	N
2009_15	2009_0427	M	F	F	N
2009_38	2009_0261	M	F	F	N
2009_22	2009_0352	M	F	F	N
2009_26	2009_0459	M	F	F	Y
2009_10	2009_0102	M	F	F	Y
2009_23	2009_0559	M	F	F	Y
2009_28	2009_0599	M	F	F	Y
2009_23	2009_0535	M	F	F	N
2009_04	2009_0408	M	M	F	N
2009_05	2009_0048	M	M	F	Y
2009_12	2009_0342	M	M	F	Y
2009_06	2009_0406	M	M	F	Y
2009_41	2009_1080	M	F	M	Y
2009_30	2009_0400	F	F	M	Y
2009_34	2009_1030	F	F	M	Y
2009_26	2009_0988	F	F	M	Y
2009_25	2009_0838	F	M	M	Y
2009_32	2009_0279	F	M	F	N
2009_08	2009_0439	M	F	M	Y
2009_31	2009_0756	M	F	M	Y
2009_35	2009_0582	M	F	M	Y
2009_04	2009_0013	M	F	M	Y
2009_04	2009_0252	M	F	M	Y
2009_02	2009_0192	M	F	M	Y
2009_15	2009_0528	M	F	M	Y

			Phenotypic sex predicted by:		
[1]Family ID	[2]Individual ID	Phenotype	Haplotype	[7]* *sdY* test	Exon 3
2009_32	2009_0470	M	F	M	Y
2009_01	2009_0316	M	F	M	Y
2009_01	2009_0604	M	F	M	Y
2009_18	2009_0390	M	F	M	Y
2009_03	2009_0940	M	F	M	Y
2009_24	2009_0641	M	F	M	Y
2009_34	2009_0953	M	F	M	Y
2009_37	2009_0578	M	F	M	Y
2009_39	2009_0982	M	F	M	Y
2009_39	2009_0369	M	F	M	Y
2009_36	2009_0947	M	F	M	Y

1 Family ID in format Year class _ID e.g. 2009_ 01 = 2009 Year class_family 01

2 Individual ID in format Year class_ID e.g. 2009_0001 = 2009 year class_ individual 01

3 F= female

4 M= Male

5 N= No (Call does not agree with *sdY* call)

6 Y= yes (call agrees with *sdY* call)

7 *sdY* call based on multiplex

* For *sdY* multiplex tests exon 2 and exon 4 must be present for a male call. Note a male call was given if only Exon 2 showed up but the Fabp6b quality control did not amplify (see Supplementary Table S9 for details).

Supplementary Table S8.
Concordance of sdY with genotype and phenotype of the 2009 year class (YC) families.

Family ID	phenotype and genotypes avialable	Total correct calls		Total miscalls				Phenotype of miscalls sdY		Phenotype miscalls genotype	
		agree with genotype	disagree with genotype	agree with genotype	disagree with genotype	total with only one representative exon 2 or 4	male	female	male	female
2009_05[1]	14	13	0	0	1	1		1		
2009_08	27	25	2	0	0	0				1
2009_12	21	20	0	0	1	2		1	1	
2009_19	12	12	0	0	0	0				
2009_31	24	23	1	0	0	0			1	
2009_33	23	23	0	0	0	0				
2009_35	29	28	1	0	0	1			1	
2009_17	25	25	0	0	0	1				
2009_20	50	46	3	1	0	0		1		3
2009_04	29	25	2	1	1	0		2	3	
2009_02	17	16	1	0	0	0			1	
2009_07	32	32	0	0	0	3				
2009_11	13	13	0	0	0	0				
2009_15	16	15	1	1	0	0		1	2	
2009_30	23	22	0	0	1	2	1			
2009_40	15	15	0	0	0	0				
2009_06	20	19	0	0	1	3		1		
2009_26	23	21	0	1	1	0	1	1	1	
2009_36	21	20	1	0	0	0			1	
2009_01	22	20	2	0	0	0			2	
2009_03	14	13	1	0	0	0			1	
2009_09	21	21	0	0	0	0				
2009_10	21	20	0	1	0	0		1	1	
2009_13	26	26	0	0	0	0				
2009_14	14	14	0	0	0	0				
2009_16	8	8	0	0	0	1				
2009_18	16	15	1	0	0	0			1	
2009_21	33	31	0	2	0	0		2	2	
2009_22	17	16	0	1	0	0		1	1	
2009_23	24	22	0	2	0	0		2	2	
2009_24	15	13	2	0	0	1			1	1
2009_25	24	23	0	1	0	0	1			1
2009_27	28	28	0	0	0	0				
2009_28	22	21	0	1	0	0		1	1	
2009_29	23	23	0	0	0	1				
2009_32	33	29	4	0	0	2			1	3
2009_34	26	24	1	0	1	0	1		1	
2009_37	15	14	1	0	0	2			1	
2009_38	24	23	0	1	0	0		1		
2009_39	24	22	2	0	0	0			1	
*2009_42	14	14	0	0	0	0				
*2009_41	16	15	1	0	0	0			1	
*2009_47	11	11	0	0	0	0				
*2009_45	15	15	0	0	0	0				
*2009_43	12	12	0	0	0	0				
*2009_46	13	13	0	0	0	0				
*2009_44	11	11	0	0	0	0				
Totals	976	930	27	13	7	20		16	4	31	9

Total males	Total correct males	Total females	Total correct females	Total correct calls
567	539	409	405	957

[1] Family ID shown as Year class _ family number e.g. 2009_01 = 2009 Year class_ family 01

Supplementary Table S9.
Individuals in which only a single exon of sdY (exon 2 or exon 4) was present. A 1 indicates the presence of a particular condition (Fabp6b, No Fabp6b).

	Individuals only carrying exon 4 of *sdY*		Individuals only carrying exon 2 of *sdY*		Phenotype
Individual	No Fabp6b	Fabp6b	No Fabp6b	Fabp6b	
[1]2009_0048		1			male
2009_0342		1			male
2009_0725		1			female
2009_0068		1			female
2009_0009			1		male
2009_0911				1	female
2009_0147				1	female
2009_0355		1			female
2009_0404		1			female
2009_0304		1			female
2009_0772		1			female
2009_0227			1		male
2009_0457			1		male
2009_0279		1			female
2009_0967			1		male
2009_0091				1	female
2009_0190		1			female
2009_0537		1			female
2009_0406		1			female
Total:		12	4	3	

[1]Individual ID given as year class _XXXX e.g. 2009_0048 is 2009 yearclass individual 0048