WE CLAIM:

1. A method of asymmetric PCR comprising:
- providing a nucleic acid sample to be used as a target template
- performing a polymerase chain reaction, utilizing highly or partly complementary primers referring to primers that are complementary to each other and will under previously known conditions bind to each other , and as a consequence compete with target sequence binding, wherein either the forward or the reverse primer concentration is decreased to unblock the PCR reaction by initially promoting linear amplification which will progressively shift towards exponential amplification by the COMplementary-Primer-ASymmetric (COMPAS)-PCR;

- identifying the amplified nucleotide target sequence(s);

2. The method of claim 1 wherein the highly complementary primers have a common overlapping DNA target sequence or a different DNA target sequence.

3. The method of claim 2 wherein the overlapping DNA target sequence is direct tandem repeats.

4. The method of any one of claims 3 wherein the direct tandem repeat target is in the 5S-rDNA region.

5. The method of any one of claims 1-4 wherein the assessment of the PCR specificity is performed by a melting curve analysis of the PCR product or by electrophoresis analysis.

6. A method for detecting, identification or monitoring salmonid species comprising: - providing a nucleic acid sample from salmonid to be used as (a) target template(s); - performing a polymerase chain reaction (PCR) applying COMplementary-Primer-ASymmetric (COMPAS)-PCR according to any one of claims 1-4, to amplify a nucleic acid target sequence of the template (s), utilizing a set) of highly complementary primer pair(s) capable of priming said target(s); -
identifying the amplified nucleotide target sequence(s); -
determining the species.

7. The method of claim 6 wherein the determination of the species is performed by a melting curve analysis of the PCR product or by electrophoresis analysis.

8. The method of any one of claims 1-6 wherein the forward primer is extended in the 3´ end to favor priming to the target and not to the reverse primer.

9. The method of any one of claims 1-8 wherein the reverse primer is extended in the 3´ end to favor priming to the target and not to the forward primer.

10. The method of any one of claims 1-9 wherein either the reverse or the forward primer has a SNP at its 3' end.

11. The method of any one of claims 1-10 wherein the primers in the primer pair are oligonucleotides each having a length of about 12 to about 30, preferably about 20 bp.

12. The method of any one of any one of claims 1-11, wherein the complementary set of primers is selected from a set of primer pair (s) wherein the forward primer is selected from Table 1 or a complementary sequence thereof and the reverse primer is selected from Table 2 or a complementary sequence thereof.

13. The method of claims 6-12, wherein said salmonid comprises *Salmo trutta, Salmo salar* and hybrids thereof.

14. Kit for detecting and identification of salmonid species, comprising a collection of oligonucleotide primer pairs selected from Tables 1 and 2 or complementary sequences thereof, capable of detecting salmonid species by the method of any one of claims 1-13.

15. Use of a method of any one of claims 1-13.

16. Use of the kit of claim 14.

FIGURES

Figure 1

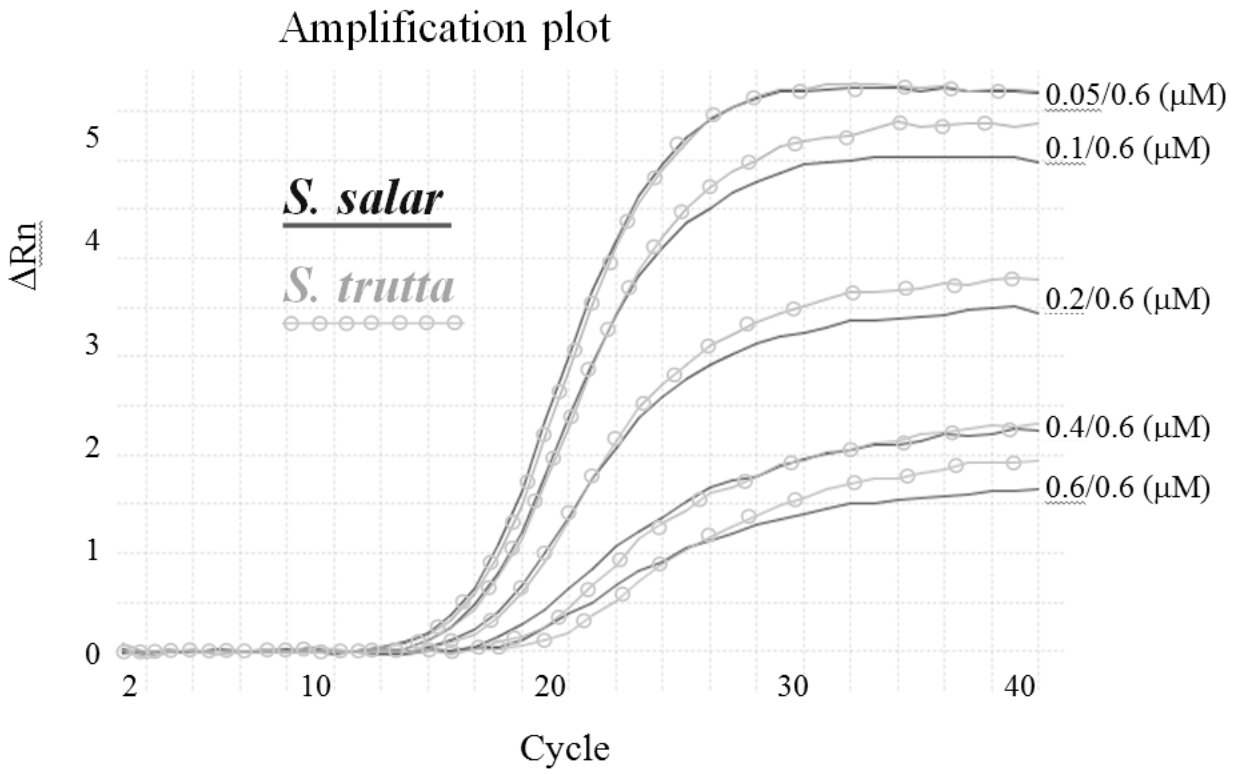

Figure 2

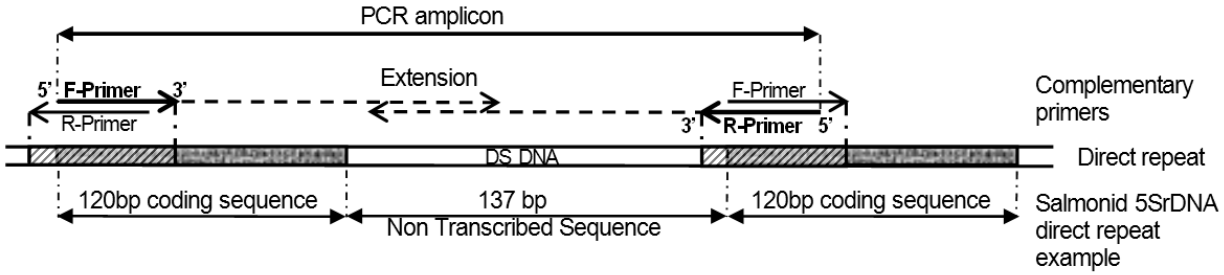

Figure 3

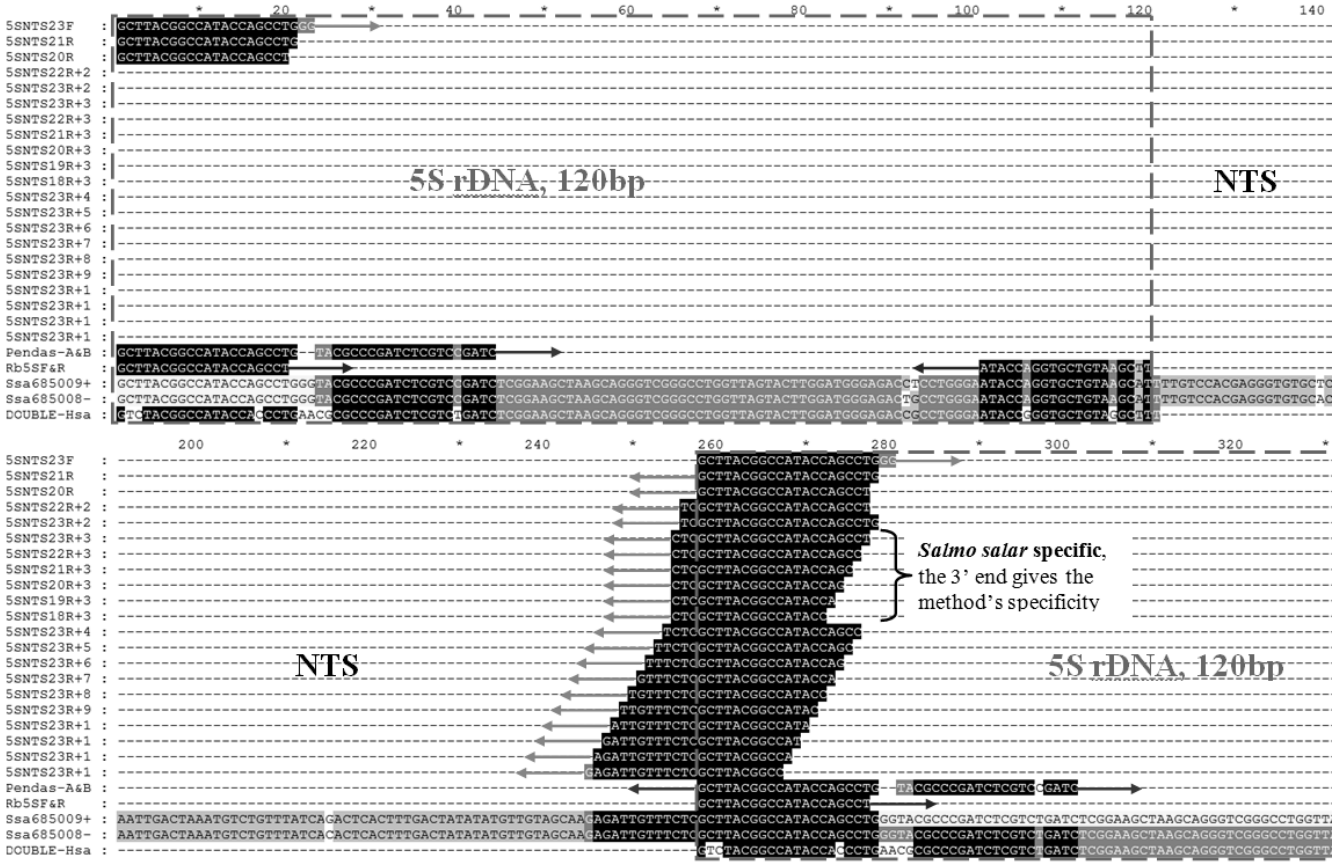

Figure 4

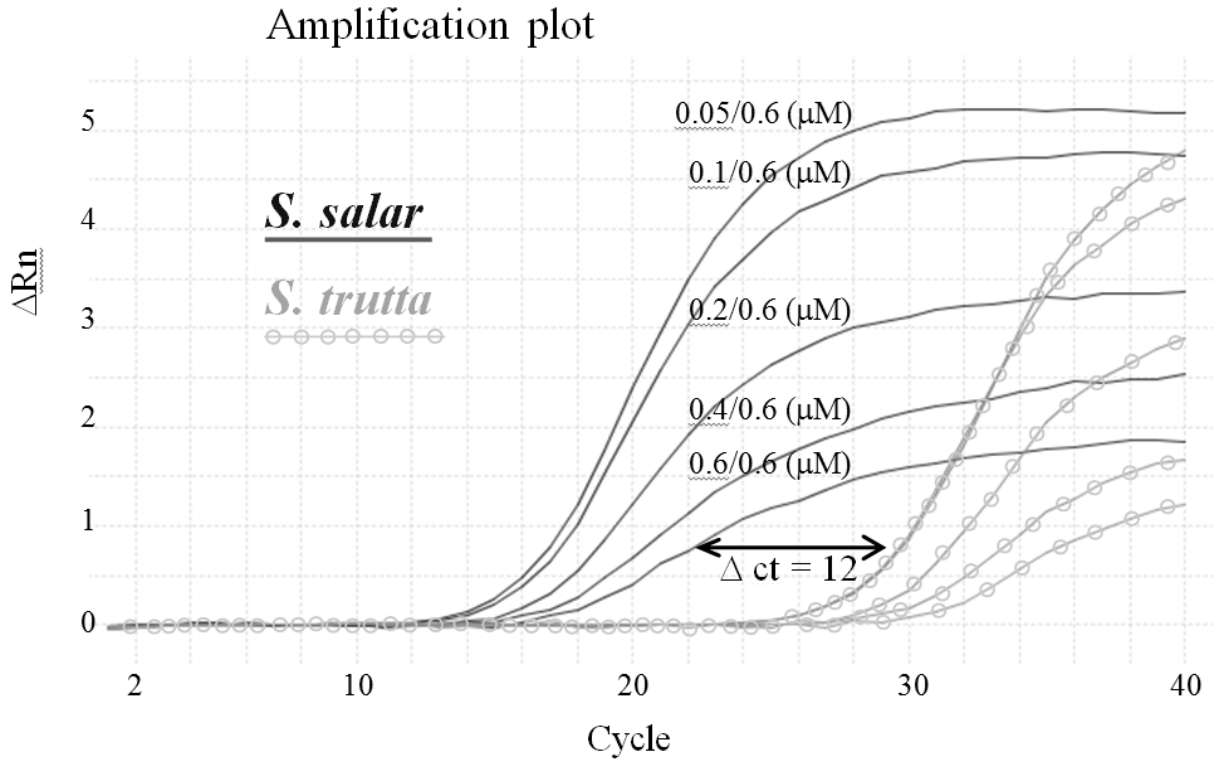

Figure 5

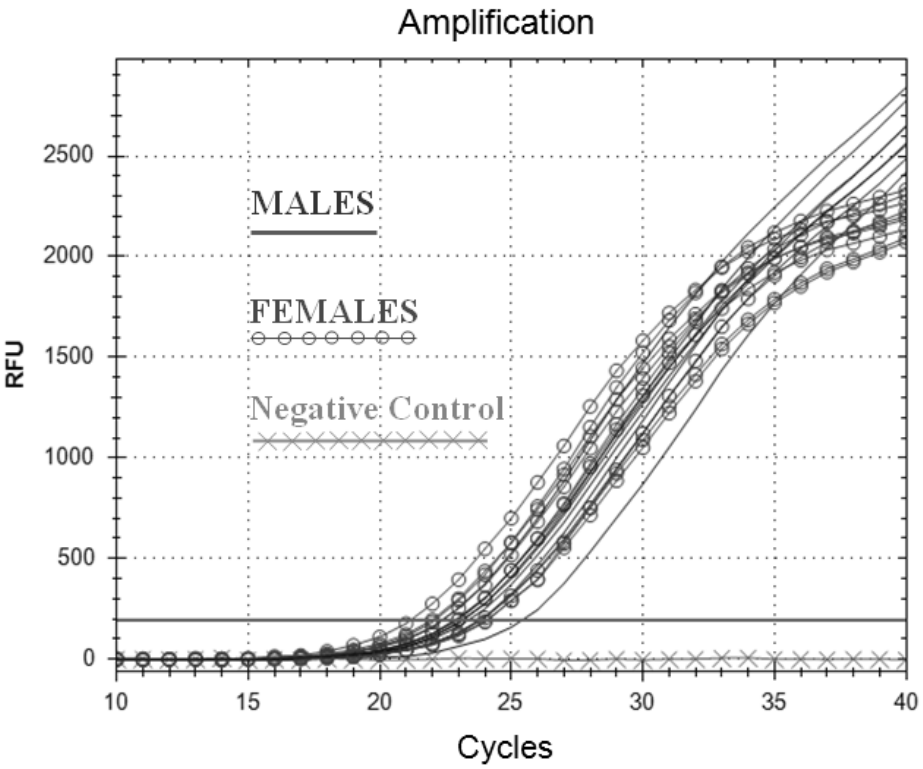

Figure 6

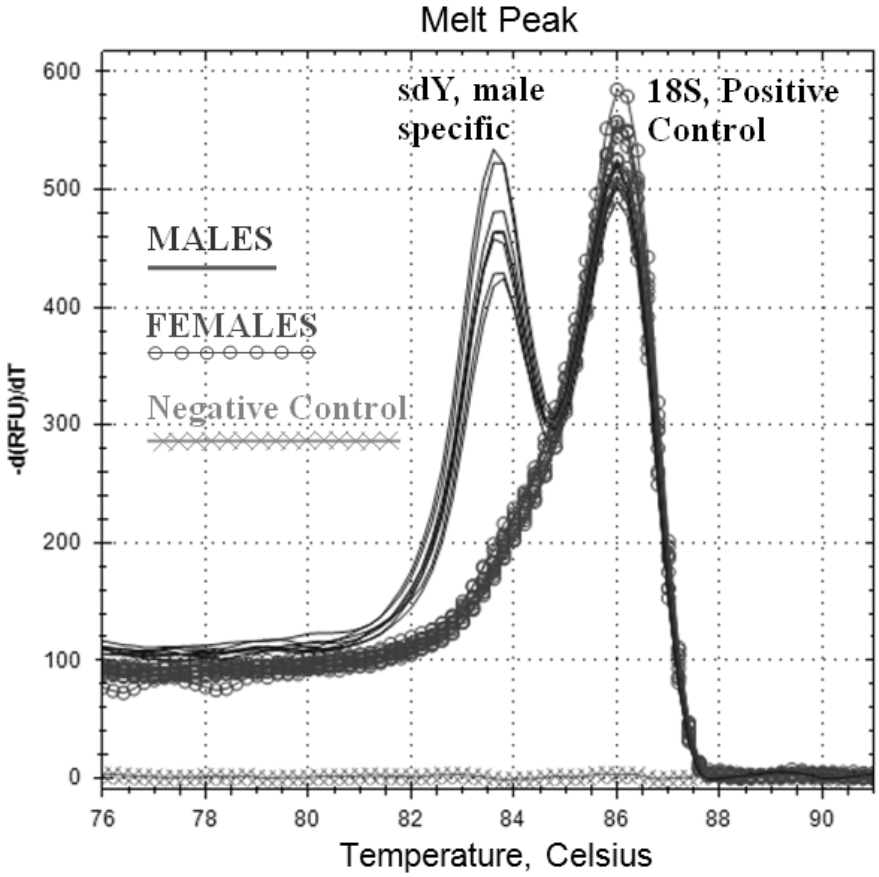

Figure 7

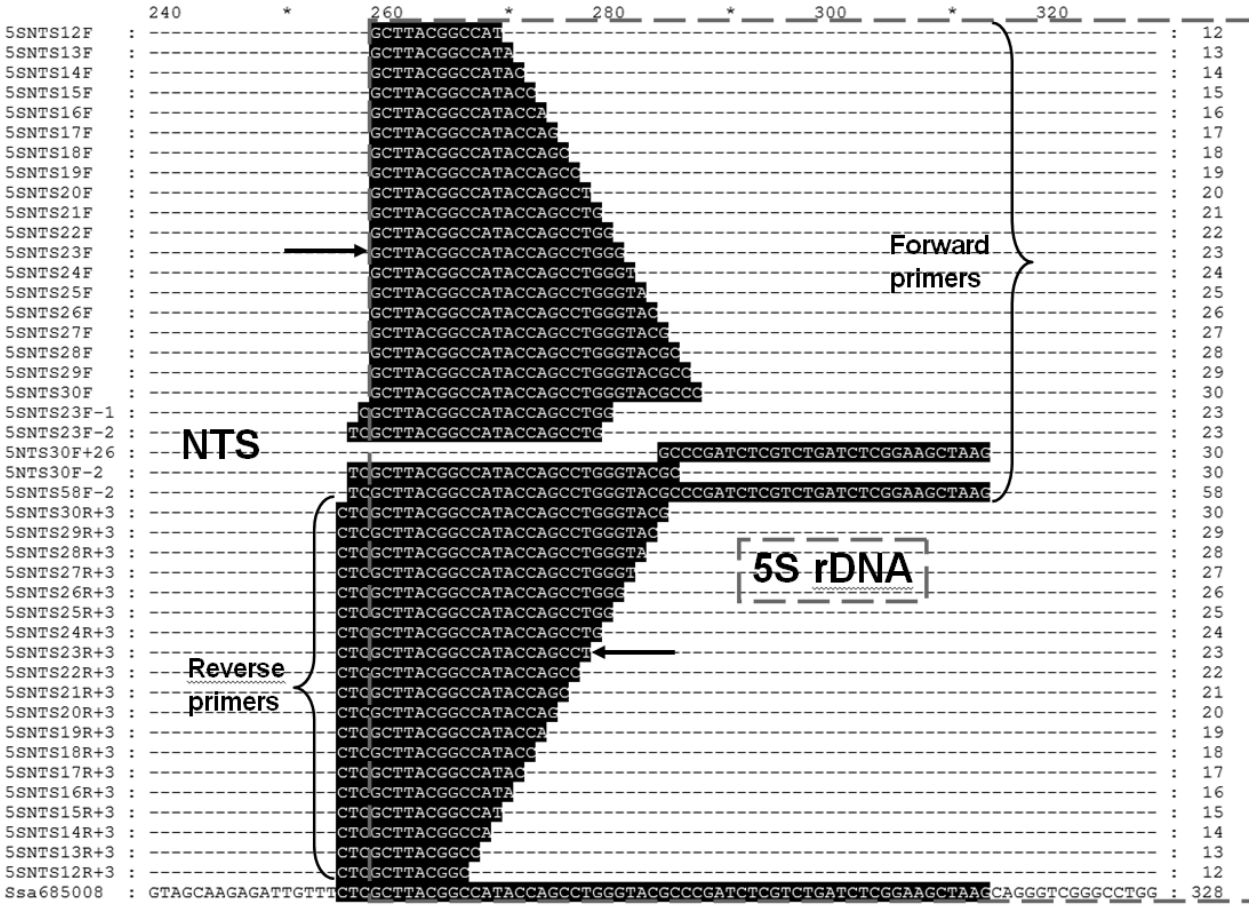

Figure 8

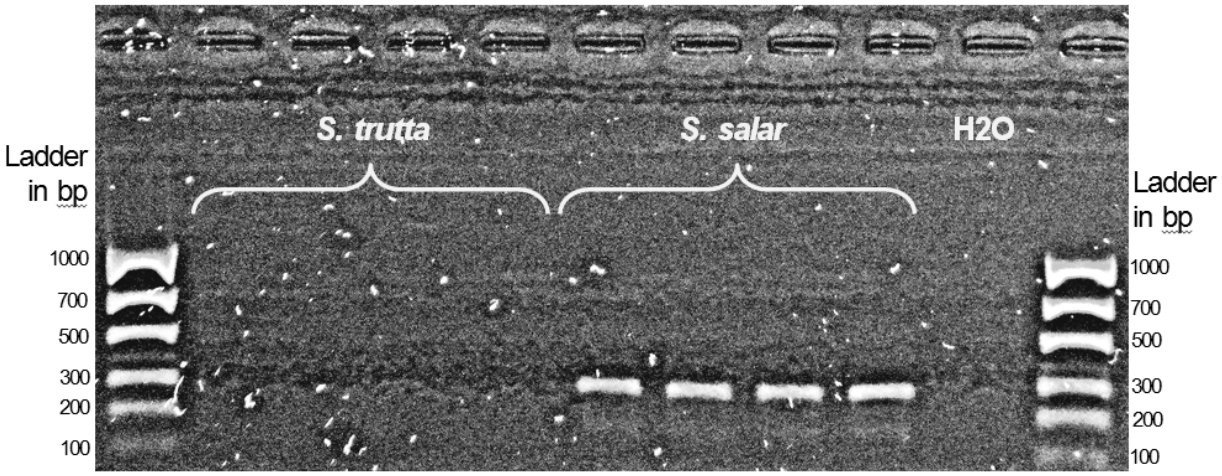
S. trutta
S. salar
H2O
Ladder in bp
1000
700
500
300
200
100
Ladder in bp
1000
700
500
300
200
100

Table 1: Salmonid specie identification; forward primers all indicated in 5' to 3'

Name	Sequence	SEQ ID NO :
5SNTS12F	GCTTACGGCCAT	**1**
5SNTS13F	GCTTACGGCCATA	**2**
5SNTS14F	GCTTACGGCCATAC	**3**
5SNTS15F	GCTTACGGCCATACC	**4**
5SNTS16F	GCTTACGGCCATACCA	**5**
5SNTS17F	GCTTACGGCCATACCAG	**6**
5SNTS18F	GCTTACGGCCATACCAGC	**7**
Ssa5SNTS19F	GCTTACGGCCATACCAGCC	**8**
5SNTS20F	GCTTACGGCCATACCAGCCT	**9**
5SNTS21F	GCTTACGGCCATACCAGCCTG	**10**
5SNTS22F	GCTTACGGCCATACCAGCCTGG	**11**
5SNTS23F	GCTTACGGCCATACCAGCCTGGG	**12**
5SNTS24F	GCTTACGGCCATACCAGCCTGGGT	**13**
5SNTS25F	GCTTACGGCCATACCAGCCTGGGTA	**14**
5SNTS26F	GCTTACGGCCATACCAGCCTGGGTAC	**15**
5SNTS27F	GCTTACGGCCATACCAGCCTGGGTACG	**16**
5SNTS28F	GCTTACGGCCATACCAGCCTGGGTACGC	**17**
5SNTS29F	GCTTACGGCCATACCAGCCTGGGTACGCC	**18**
5SNTS30F	GCTTACGGCCATACCAGCCTGGGTACGCCC	**19**
5SNTS23F-1	CGCTTACGGCCATACCAGCCTGG	**20**
5SNTS23F-2	TCGCTTACGGCCATACCAGCCTG	**21**

5NTS30F+26	GCCCGATCTCGTCTGATCTCGGAAGCTAAG	**22**
5NTS30F-2	TCGCTTACGGCCATACCAGCCTGGGTACGC	**23**
5SNTS58F-2	TCGCTTACGGCCATACCAGCCTGGGTACGC CCGATCTCGTCTGATCTCGGAAGCTAAG	**24**

Table 2 : Salmonid specie identification; reverse primers all indicated in 5' to 3'

Name	**Sequence**	**SEQ ID NO :**
5SNTS30R+3	CGTACCCAGGCTGGTATGGCCGTAAGCGAG	**25**
5SNTS29R+3	GTACCCAGGCTGGTATGGCCGTAAGCGAG	**26**
5SNTS28R+3	TACCCAGGCTGGTATGGCCGTAAGCGAG	**27**
5SNTS27R+3	ACCCAGGCTGGTATGGCCGTAAGCGAG	**28**
5SNTS26R+3	CCCAGGCTGGTATGGCCGTAAGCGAG	**29**
5SNTS25R+3	CCAGGCTGGTATGGCCGTAAGCGAG	**30**
5SNTS24R+3	CAGGCTGGTATGGCCGTAAGCGAG	**31**
5SNTS23R+3	AGGCTGGTATGGCCGTAAGCGAG	**32**
5SNTS22R+3	GGCTGGTATGGCCGTAAGCGAG	**33**
5SNTS21R+3	GCTGGTATGGCCGTAAGCGAG	**34**
5SNTS20R+3	CTGGTATGGCCGTAAGCGAG	**35**
5SNTS19R+3	TGGTATGGCCGTAAGCGAG	**36**
5SNTS18R+3	GGTATGGCCGTAAGCGAG	**37**
5SNTS17R+3	GTATGGCCGTAAGCGAG	**38**
5SNTS16R+3	TATGGCCGTAAGCGAG	**39**

5SNTS15R+3	ATGGCCGTAAGCGAG	**40**
5SNTS14R+3	TGGCCGTAAGCGAG	**41**
5SNTS13R+3	GGCCGTAAGCGAG	**42**
5SNTS12R+3	GCCGTAAGCGAG	**43**

Table 3: Salmonid gender identification; forward and reverse primers all indicated in 5' to 3'

Name	**Sequence**
SdY-Fw	CCCAGCACTGTTTTCTTGTCTCA
SdY-Rev2	CTTAAAACCACTCCACCCTCCAT
18S-FwA	GT**C**CGAAGACGATCAGATACCGT
18S-FwB	GT**T**CGAAGACGATCAGATACCGT
18S-Rv	CCGCATAACTAGTTAGCATGCCG