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**A HIGH DENSITY GENETIC LINKAGE MAP FOR  
RAINBOW TROUT (*Onchorynchus mykiss*)  
CONTAINING 47,839 SNPs**

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# 57K SNP array in Rainbow trout

DataSheet



## Axiom<sup>®</sup> Trout Genotyping Array

A high-density genotyping array for high-resolution genetics research and aquaculture breeding in rainbow trout



# SNP sources and validation rate

Category	DH RADs	Re-Seq	Other	Total*
<b>Total SNPs on the Array</b>	30,032 (52%)	39,159 (68%)	10,964 (19%)	<b>57,501 (100%)</b>
<b>Call Rate &lt;97%</b>	999	1,366	434	<b>2,130</b>
<b>No Minor Homozygotes</b>	526	1,369	459	<b>1,942</b>
<b>Off Target Variant</b>	139	291	73	<b>415</b>
<b>Other</b>	1,084	1,889	615	<b>2,892</b>
<b>Monomorphic High Resolution</b>	223	420	118	<b>654</b>
<b>Polymorphic High Resolution</b>	<b>27,061 (90%)</b>	<b>33,824 (86%)</b>	<b>9,265 (84%)</b>	<b>49,468 (86%)</b>

\* Overlap between sources. ~40% of the SNPs were discovered by two sources

\* Palti et al. 2015, *Molecular Ecology Resources* **E-Published**

# Linkage map utility

- Mapping recombination over chromosomes
- Mapping QTLs
  - Broad/narrow chromosome regions
- Facilitates genomic selection based on linkage
- Valuable tool for assembling genome sequences
  - ‘Glue’ together’ scaffolds and contigs

Linkage map



Sequence contigs



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# Aim

- To produce a high-density SNP based linkage map in Rainbow trout
  - Map QTLs for important commercial traits (IPN)
  - Improve reference genome(s)

# Methods – Linkage analysis

- 57K Affymetrix Rainbow trout SNP array
- 2,464 samples from 56 full-sib families genotyped
  - 46 commercial Norwegian
  - 10 experimental USDA
- 57K SNPs and nearly 2500 animals = software issues
- After trial and error, Lep-MAP was able to handle this dataset
- Worked with the developer to optimise the software
  - Including running multi-threaded
- Steps: Data filtering, twopoint analysis, marker ordering



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# Results – linkage map

- A total of 47,839 SNPs were mapped to 29 linkage groups
  - average of 1,650 SNPs per group
  - 754 to 2,934 SNPs per group
  - Total distances covered by the male and female maps were 2,214 cM and 4,248 cM, respectively
- In all 13 chromosomes known to have homeologous pairing with at least one other chromosome arm, the female/male recombination ratios were  $>2.0$
- In non-duplicated chromosomes the female/male recombination ratio ranged from 1.0 to 2.0
  - with the exception of chromosomes Omy15 and Omy21

# Map summary

Chr	# of SNPs	Chr	# of SNPs
Chr01	2174	Chr16	1915
Chr02	2051	Chr17	1773
Chr03	1871	Chr18	1438
Chr04	2263	Chr19	1354
Chr05	2934	Chr20	1205
Chr06	2048	Chr21	1095
Chr07	1950	Chr22	1314
Chr08	2146	Chr23	1262
Chr09	1701	Chr24	1019
Chr10	1809	Chr25	2010
Chr11	2051	Chr26	754
Chr12	2095	Chr27	1114
Chr13	916	Chr28	1150
Chr14	1912	Chr29	997
Chr15	1518		



# Rainbow trout genome(s)

**NRGene**

Technology & Product

Posted May 20th, 2015 by *nrgene* & filed under .

## ***NRGENE MAPS RAINBOW TROUT GENOME IN COOPERATION WITH U.S. DEPARTMENT OF AGRICULTURE***

***Complete Genome of  
Oncorhynchus mykiss  
Available to Aquaculture  
Researchers & Breeders***

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ard<sup>4,8</sup>,  
Aury<sup>4</sup>,  
Iric Cabau<sup>9</sup>,

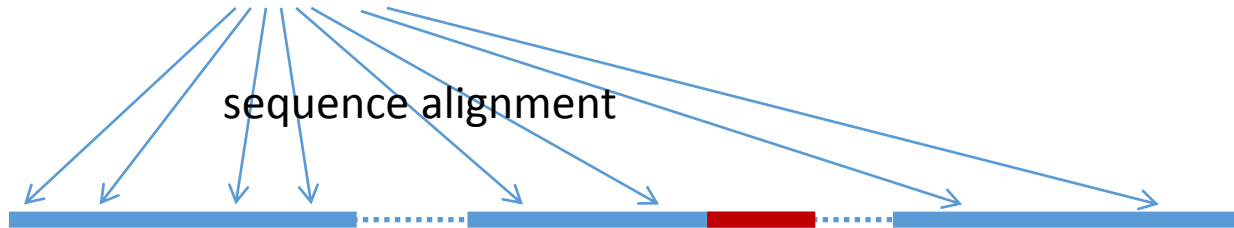
# Atlantic salmon vs rainbow trout comparative mapping

Atlantic salmon chromosome sequence

ssa21



sequence alignment



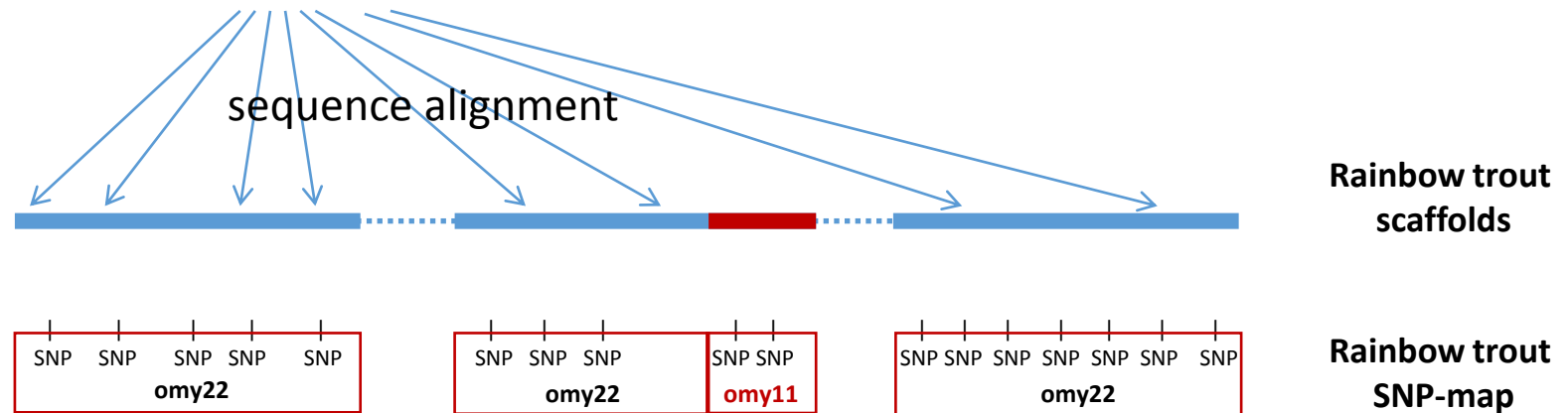
Rainbow trout scaffolds

part of scaffold aligning to  
a different salmon chromosome

# Atlantic salmon vs rainbow trout comparative mapping

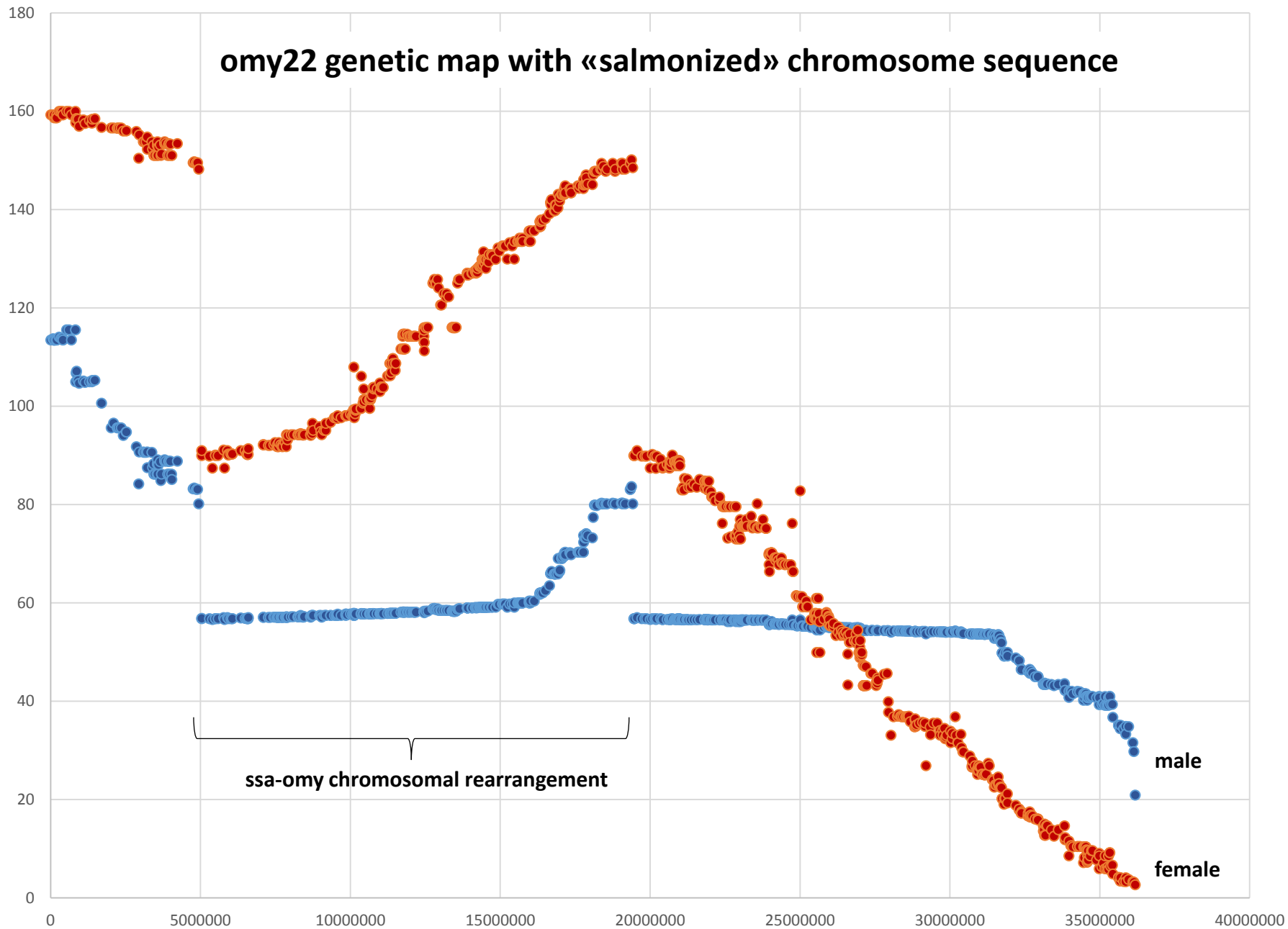
Atlantic salmon chromosome sequence

ssa21

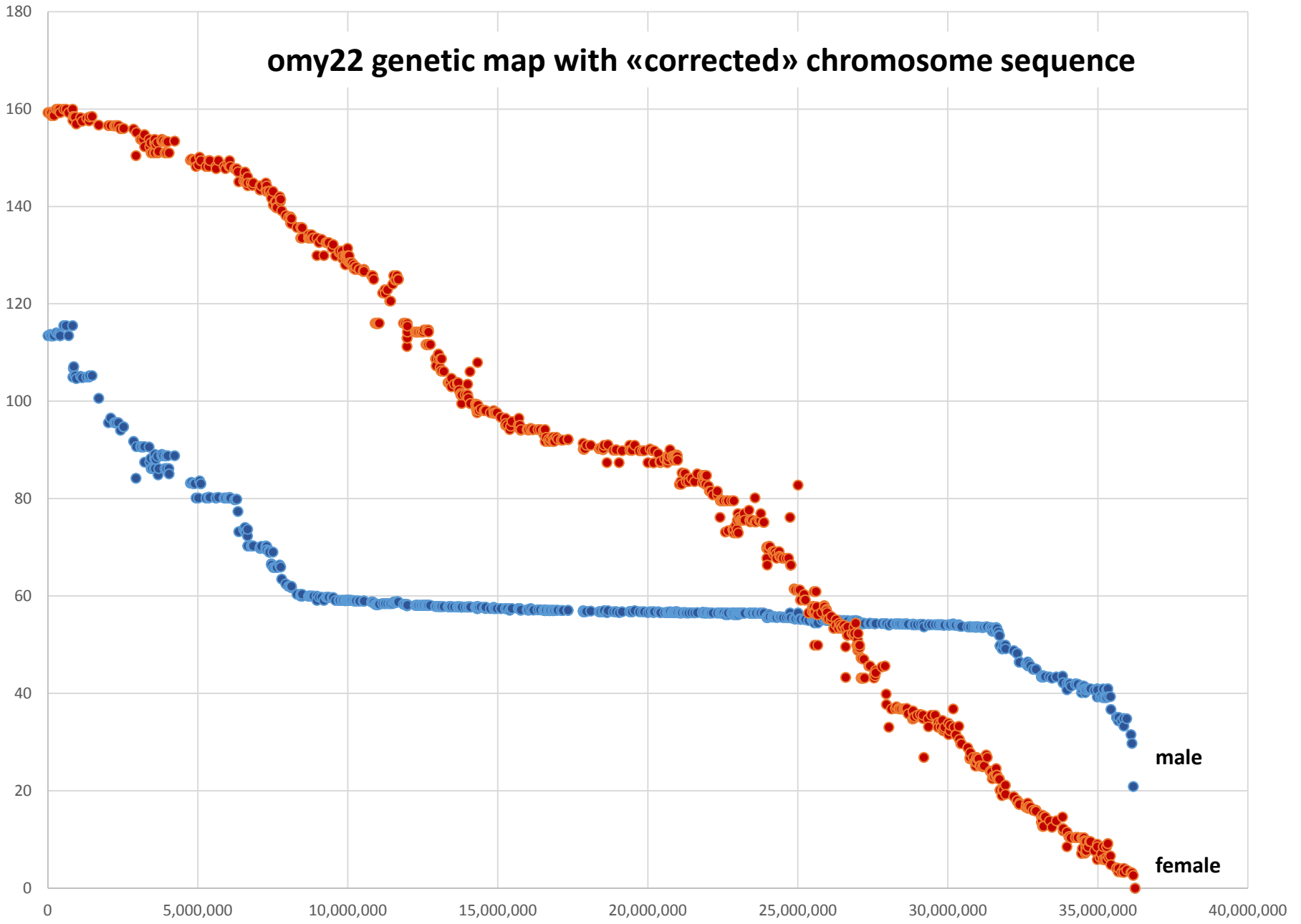


- 1) break erroneous trout scaffolds
- 2) orders and orients trout scaffolds
- 3) compare trout linkage map with salmonized SNP-order
- 4) use linkage map to correct trout chromosome sequences
- 5) build comparative map by aligning Atlantic salmon and rainbow trout chromosome sequences

# omy22 genetic map with «salmonized» chromosome sequence



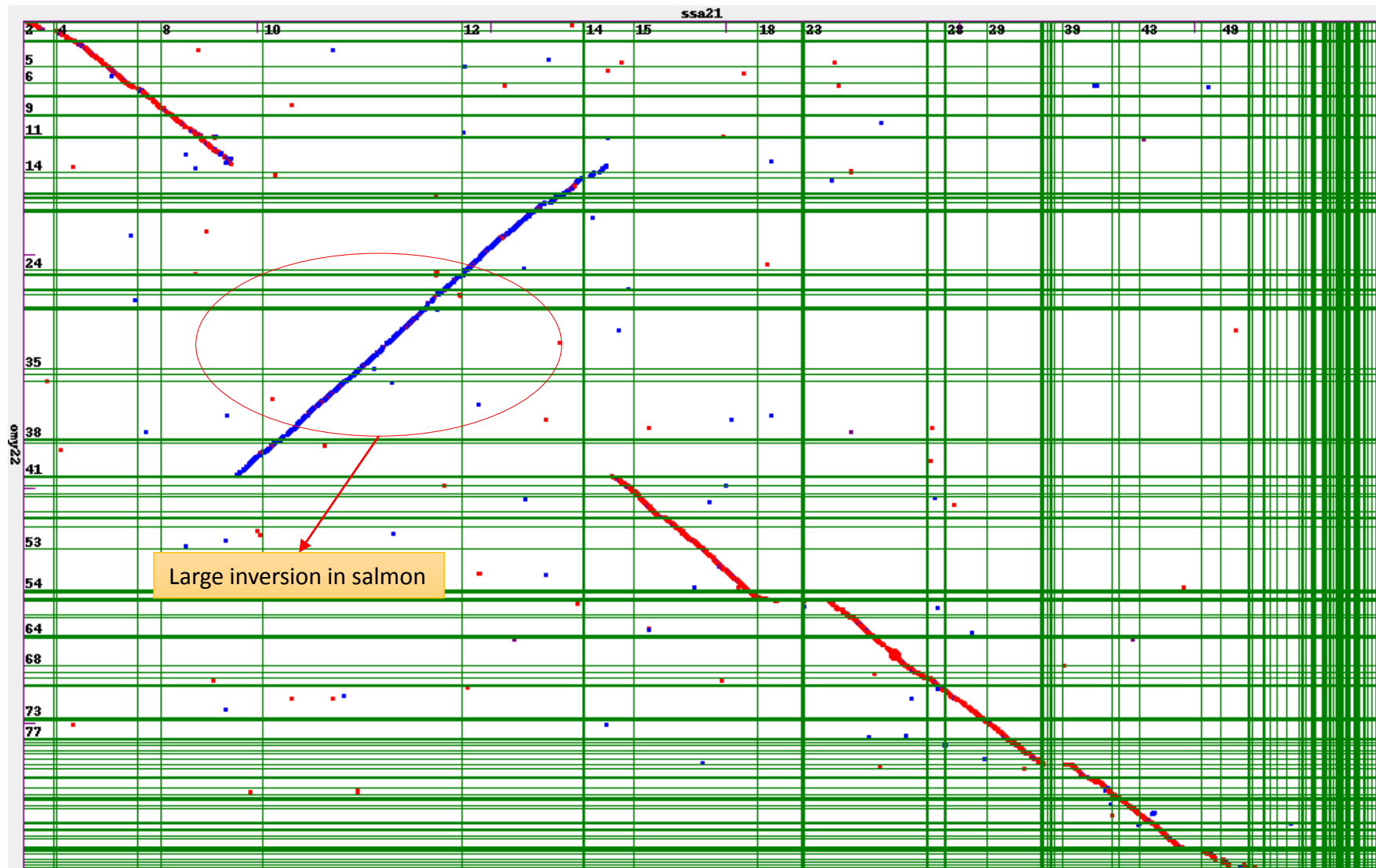
# omy22 genetic map with «corrected» chromosome sequence



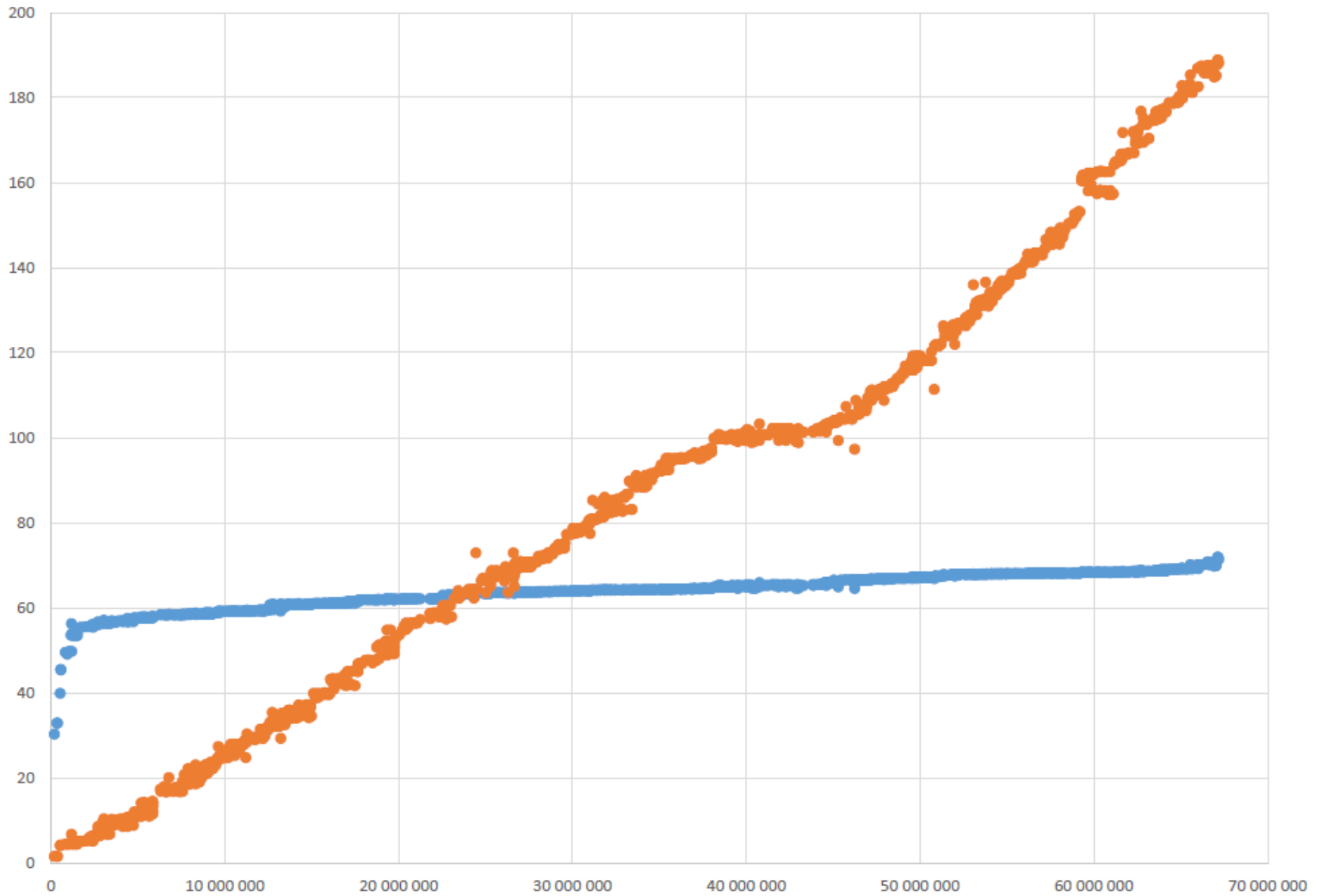
ssa21 vs omy22

ssa21

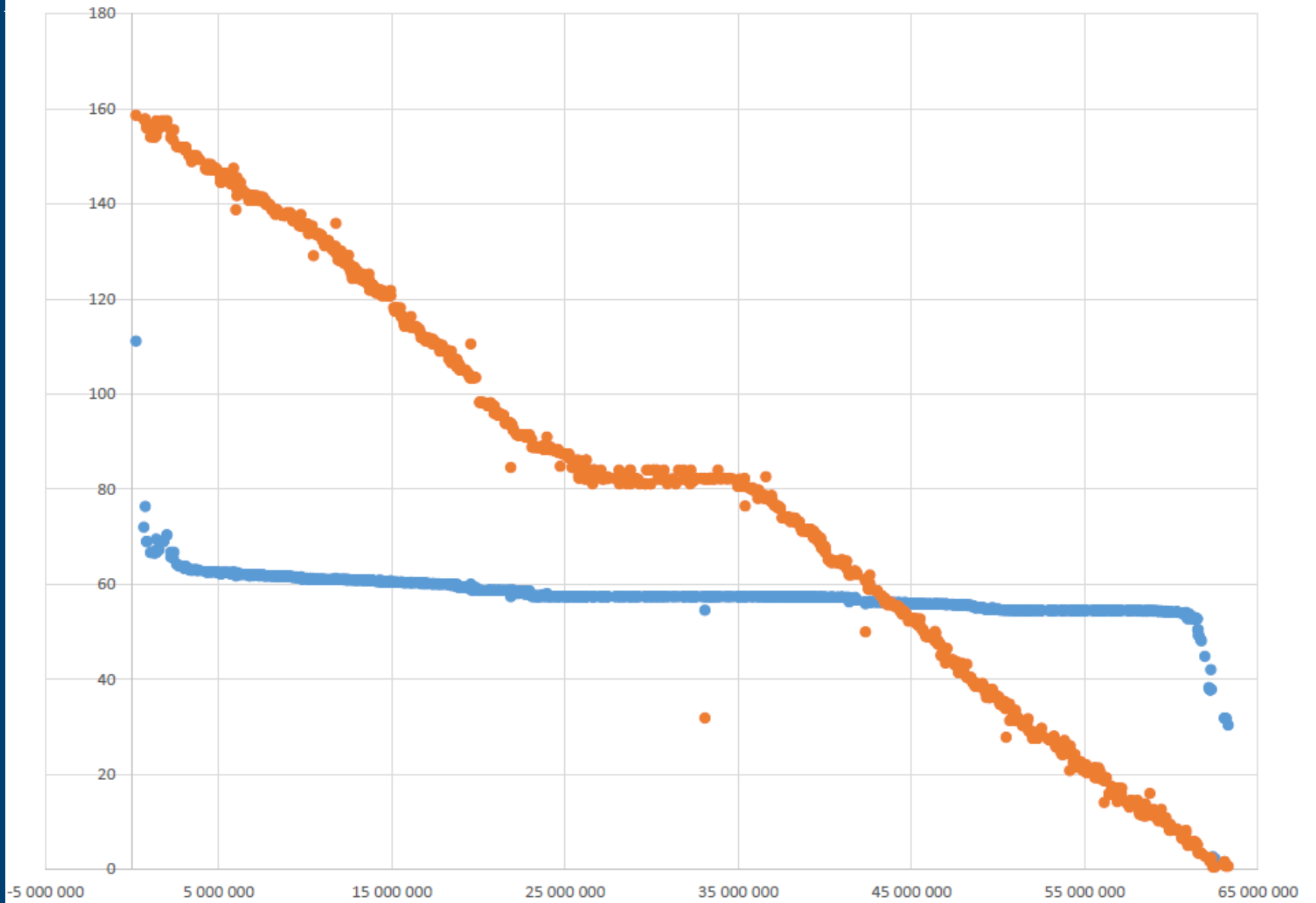
Omy22



omy01



omy08





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# Conclusions

- We mapped nearly 50,000 SNPs to 29 linkage groups
- Map has been used to identify major QTL for IPN resistance
- This map is being integrated together with the salmon and trout genomes
  - SNPs physically ordered on the trout chromosomes
- Misassemblies in published trout scaffolds were identified
- Chromosomal rearrangements between salmon/trout were identified
- Integrated maps/genomes will be of great value for ‘applied’ use
  - More direct transition of QTL/GWAS results to candidate genes and polymorphisms

# Funding Sources



National Research Initiative  
Animal Genome Program

