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Coevolution of Positively Selected IZUMO1 and CD9 in Rodents: Evidence of Interaction Between Gamete Fusion Proteins?

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Supplemental Data

Files in this data supplement:

Supplemental Figure S1. Amino acid alignment of IZUMO1. Positively selected sites with a Bayesian posterior probability > 0.95 (*) are shown. *Rattus norvegicus* was used as outgroup lineage.

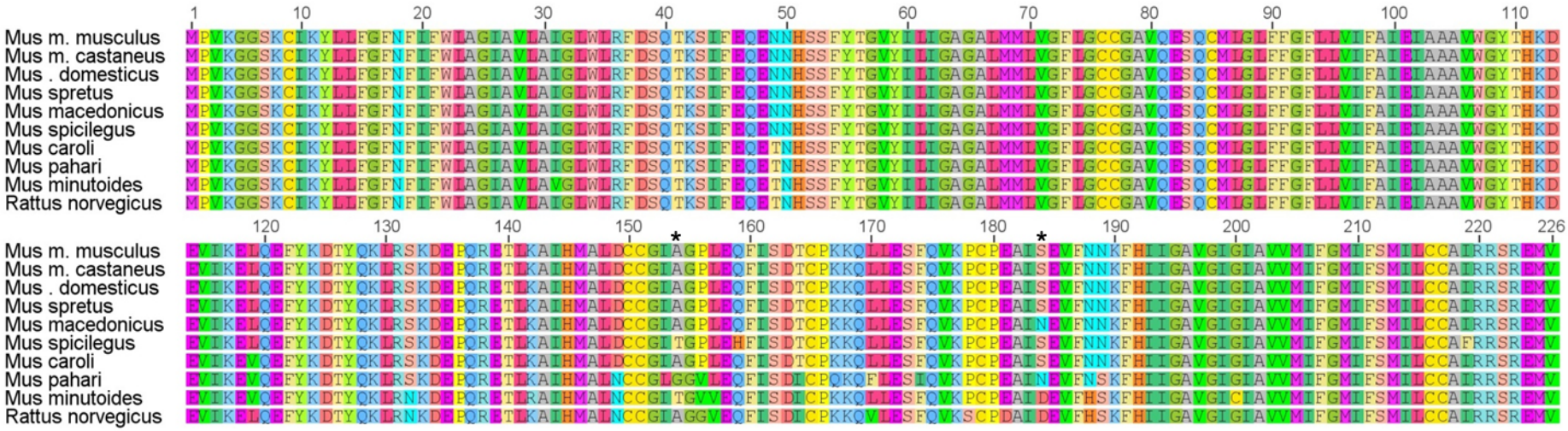
Supplemental Figure S2. Amino acid alignment of CD9. Positively selected sites with a Bayesian posterior probability > 0.95 (*) are shown. *Rattus norvegicus* was used as outgroup lineage.

Supplemental Figure S3. Phylogenetic reconstructions of *Izumo1* gene using Maximum Likelihood (**A**) and Bayesian Inference (**B**) methods. Node labels indicate *P*-values from bootstrap analyses of 1000 simulations and Bayesian posterior probabilities, respectively.

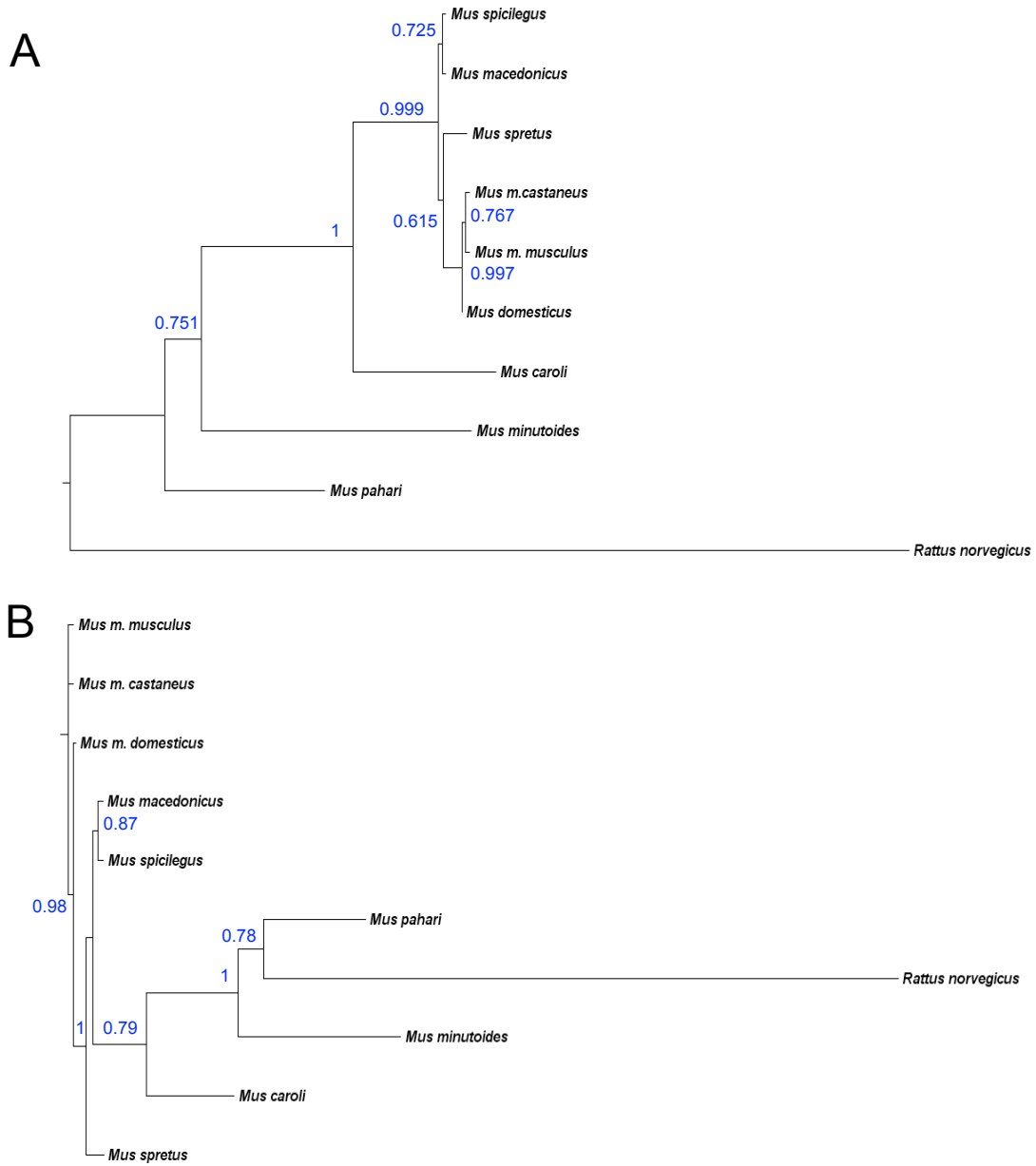
Supplemental Figure S4. Phylogenetic reconstructions of *Cd9* gene using Maximum Likelihood (**A**) and Bayesian Inference (**B**) methods. Node labels indicate *P*-values from bootstrap analyses of 1000 simulations and Bayesian posterior probabilities, respectively.

Supplemental Figure S5. Analyses of robustness for alternative phylogenetic trees. Statistical results for each alternative topology are shown.

Supplemental Figure S1. Amino acid alignment of IZUMO1. Positively selected sites with a Bayesian posterior probability > 0.95 (*) are shown. *Rattus norvegicus* was used as outgroup lineage.



Supplemental Figure S2. Amino acid alignment of CD9. Positively selected sites with a Bayesian posterior probability > 0.95 (*) are shown. *Rattus norvegicus* was used as outgroup lineage.



Supplemental Figure S3. Phylogenetic reconstructions of *Izumo1* gene using Maximum Likelihood (**A**) and Bayesian Inference (**B**) methods. Node labels indicate *P*-values from bootstrap analyses of 1000 simulations and Bayesian posterior probabilities, respectively.

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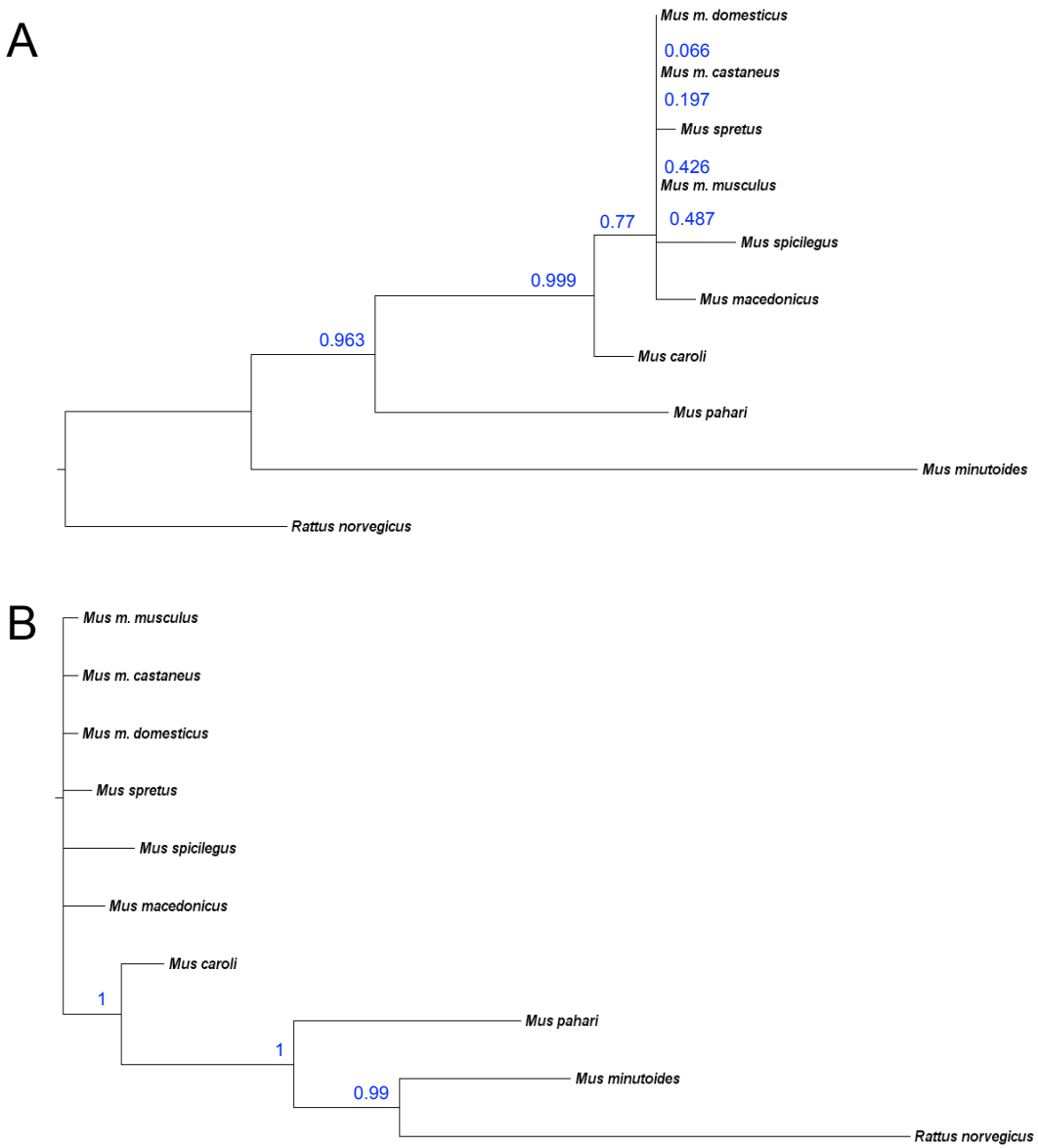
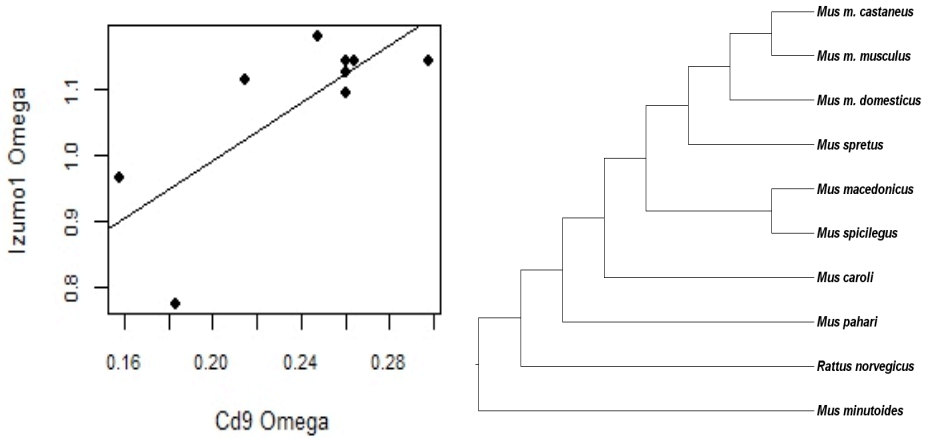
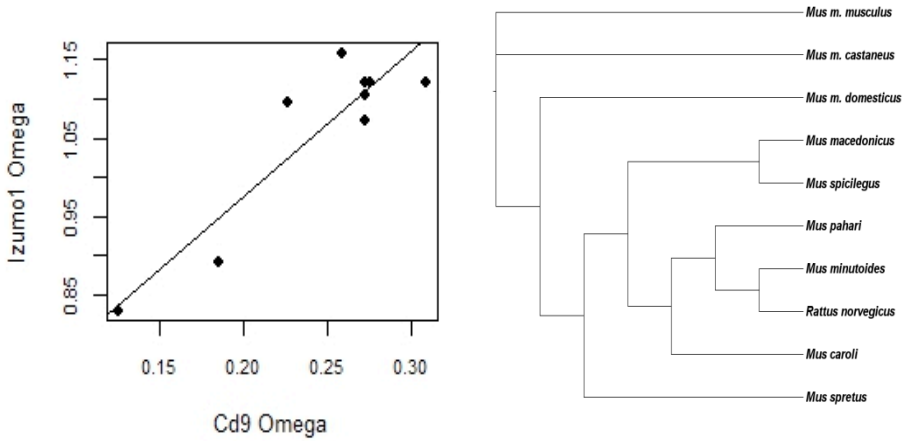


Supplemental Figure S4. Phylogenetic reconstructions of *Cd9* gene using Maximum Likelihood (**A**) and Bayesian Inference (**B**) methods. Node labels indicate *P*-values from bootstrap analyses of 1000 simulations and Bayesian posterior probabilities, respectively.

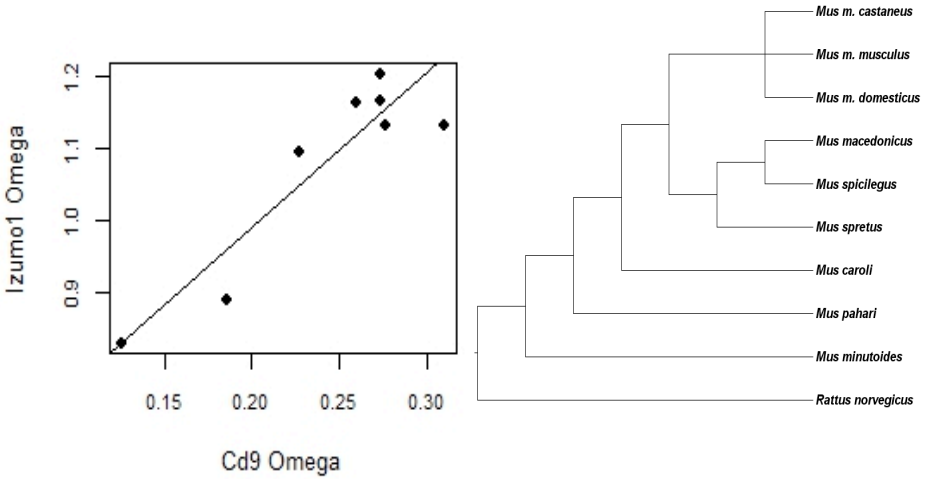
Alternative tree 1 (Maximum Likelihood)



Alternative tree 2 (Bayesian inference)



Alternative tree 3 (Mus musculus polytomy)



Tree	Intercept	Slope	R	*F*	*P*
1	0.5606	2.167	0.5655	9.109	**0.01944**
2	0.60632	1.84677	0.8264	33.33	**0.0007**
3	0.55712	2.16053	0.8426	37.49	**0.0005**

Supplemental Figure S5. Analyses of robustness for alternative phylogenetic trees. Statistical results for each alternative topology are shown.