

Additional Data File 8. Estimates of unique genes in the genomes of close relatives under three different criteria: h_u , the number of unmapped BESs that matched nr proteins; h_m , the number of mapped BESs that matched nr proteins; n_u , the number of genes in the close relatives-specific regions. Because the numbers of unique genes depend on the ratio of h_u to h_m , we examined two other thresholds for similarity searches against the nr database, E -value of $< 1.0 \times 10^{-20}$ and $< 1.0 \times 10^{-50}$, in addition to an E -value of $< 1.0 \times 10^{-10}$. Although the ratios slightly decreased with stringent thresholds, the numbers of unique genes did not drastically change, suggesting that the three close relatives possess $\sim 1,000$ unique genes that are missing from the genomes of *Oj* and *Oi*.

		h_u / h_m				n_u	
E -value		1.0×10^{-10}	1.0×10^{-20}	1.0×10^{-50}	1.0×10^{-10}	1.0×10^{-20}	1.0×10^{-50}
	<i>On</i>	0.0332	0.0313	0.0302	1,360	1,287	1,243
<i>Oj</i>	<i>Or</i>	0.0231	0.0216	0.0188	934	877	766
	<i>Og</i>	0.0367	0.0361	0.0298	1,260	1,239	1,028
	<i>On</i>	0.0268	0.0247	0.0227	1,105	1,022	942
<i>Oi</i>	<i>Or</i>	0.0213	0.0194	0.0182	865	789	741
	<i>Og</i>	0.0427	0.0418	0.0364	1,456	1,425	1,248