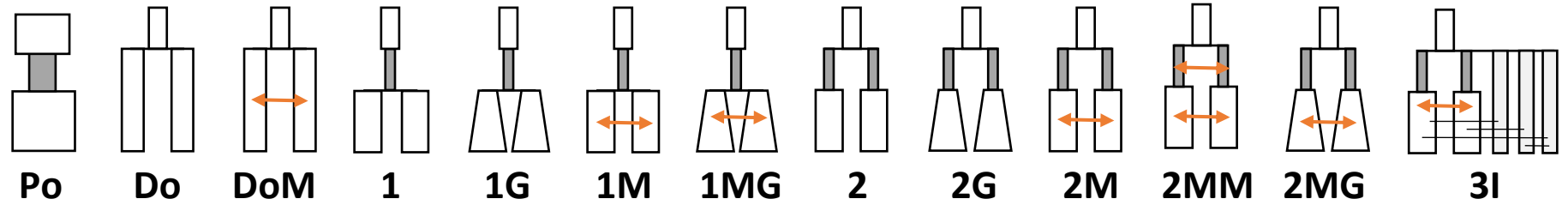


**S4 Table. Non spatial demo-genomic model comparison.** Maximum composite likelihoods, AICs and evidence ratios for the 13 tested demo-genomic models.



<b>ln(L)<sup>a</sup></b>	-1269285	-1175486	-1170663	-1175141	-1174252	-1170585	-1169175	-1174292	-1174221	-1168256	-1168293	-1168546	-1168180
<b>AIC</b>	2538583	2350983	2341339	2350297	2348522	2341188	2338372	2348601	2348462	2336532	2336610	2337115	2336384
<b>w<sub>1</sub><sup>b</sup></b>	0	0	0	0	0	0	0	0	0	1	1.15E-17	2.53E-127	
<b>w<sub>2</sub><sup>b</sup></b>	0	0	0	0	0	0	0	0	0	7.28E-33	8.41E-50	1.84E-159	1

<sup>a</sup> Logarithm of the maximum composite likelihood of the fittest run for each model.

<sup>b</sup> Evidence ratio ( $w_1$ ) including the **3I** model; ( $w_2$ ) or not. The formula to calculate the evidence ratio is:

$$w_i = e^{-\Delta_i/2} \div \sum_{m=1}^M e^{-\Delta_m/2}$$

with  $m$  the model index and  $\Delta_i = AIC_i - AIC_{min}$ , where  $AIC_{min}$  is the overall minimum AIC across all independent runs and candidate models.