

## 5. Subsampled dataset 1

Dataset (no. taxa)	# Genes	Length (bp)	Grouping	ML	BEAST		BEAST (no OG)	
				bootstrap	posterior	Bayes factor	posterior	Bayes factor
1*. (38 <i>sp</i> ) full	5	4732	Palaeoptera	0.48	<b>0.93</b>	---	<b>0.65</b>	---
			Chiastomyaria	<b>0.49</b>	0.07	6.6	0.17	1.90
			Metapterygota	0.03	<0.01	<b>445.4</b>	0.18	1.71
	4	4372	Palaeoptera	0.43	<b>0.85</b>	---	<b>0.76</b>	---
			Chiastomyaria	<b>0.55</b>	0.15	2.76	0.12	3.15
			Metapterygota	0.02	<0.01	<b>37.47</b>	0.12	2.90
	3	3935	Palaeoptera	<b>0.61</b>	<b>0.94</b>	---	<b>0.77</b>	---
			Chiastomyaria	0.38	0.05	<b>9.94</b>	0.12	3.31
			Metapterygota	0.01	0.01	<b>51.41</b>	0.11	3.31

*Note.* Values indicate bootstrap support (ML) or posterior probability (BEAST) for the specified clade. Maximum likelihood or maximum posterior groupings are shown in bold.