

# Quantifying prevalence and risk factors of HIV multiple infection in Uganda from cross-sectional population-based deep-sequence data

## Supplementary File 4: Bayesian model fit diagnostics

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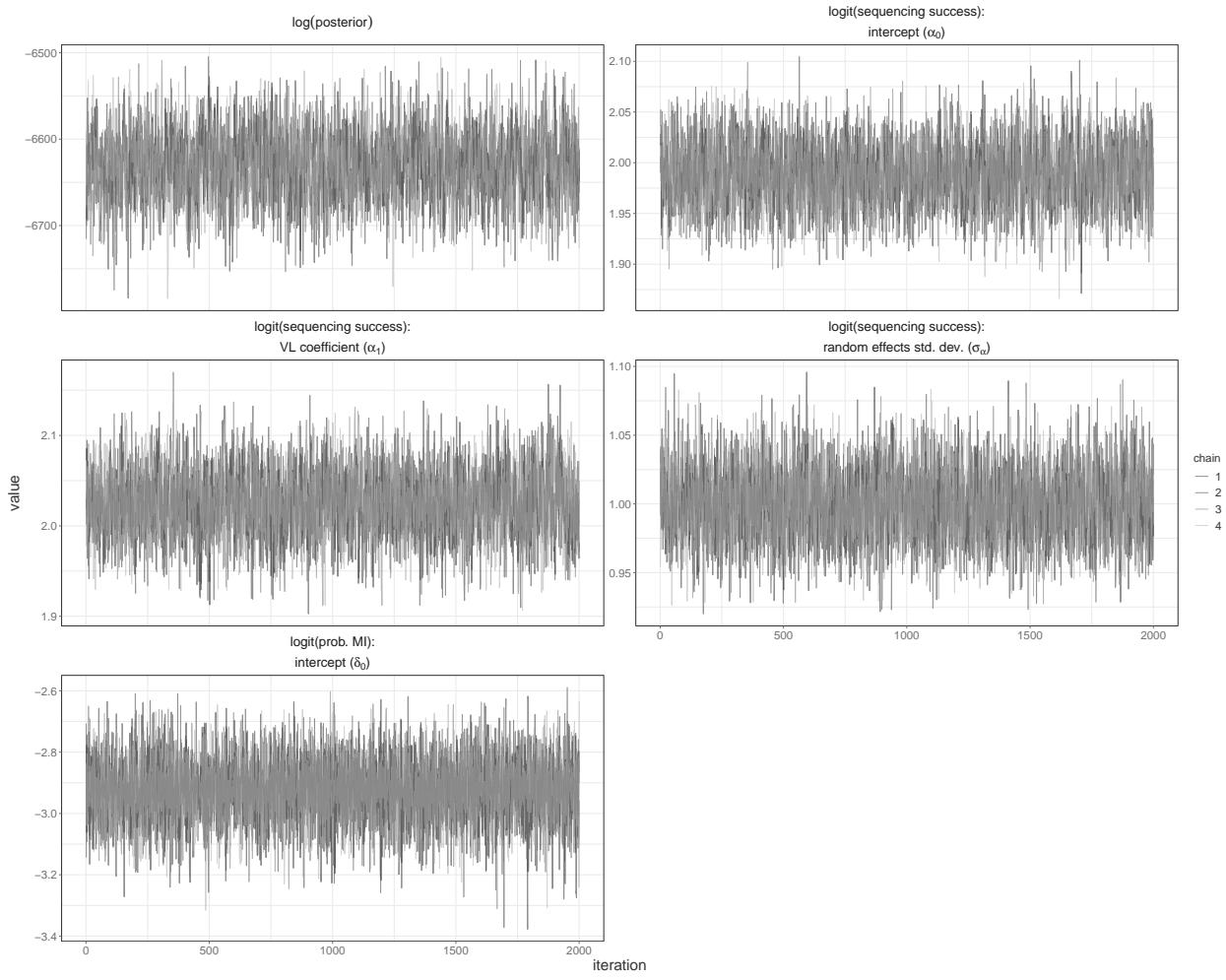
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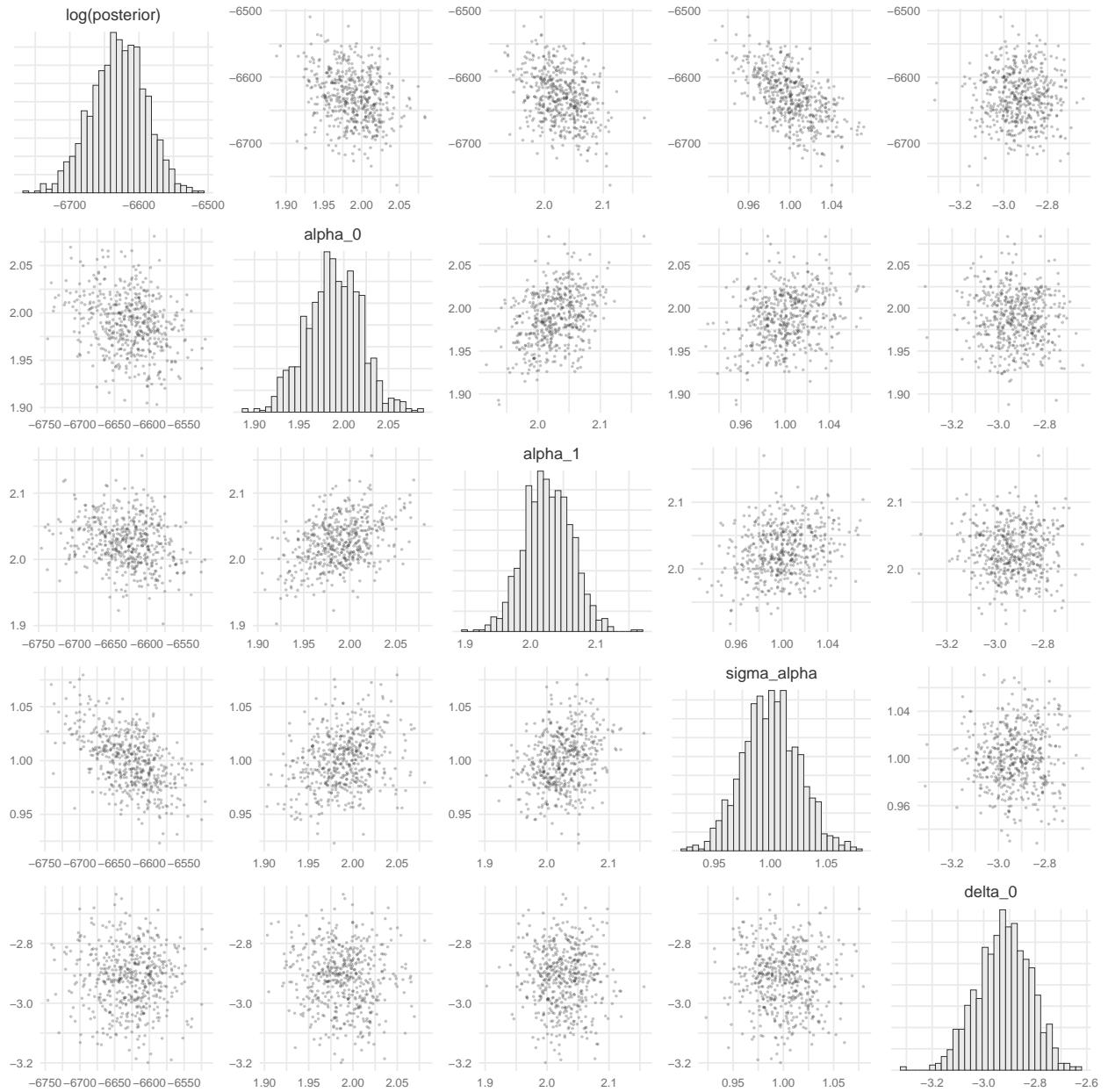
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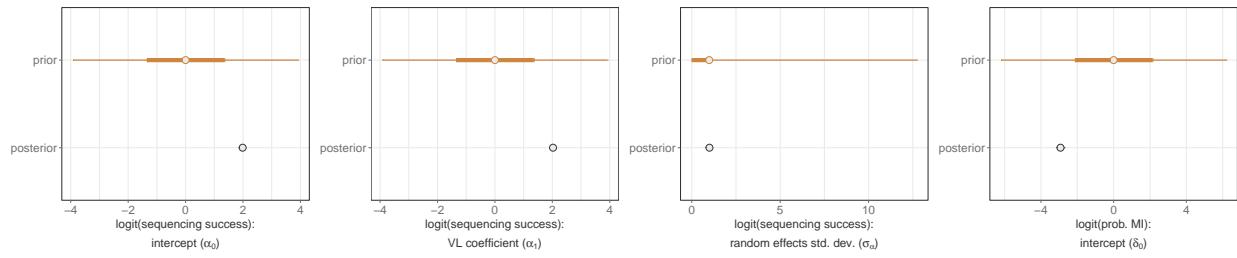


**Fig S.D. 1. MCMC trace plots for parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows.**

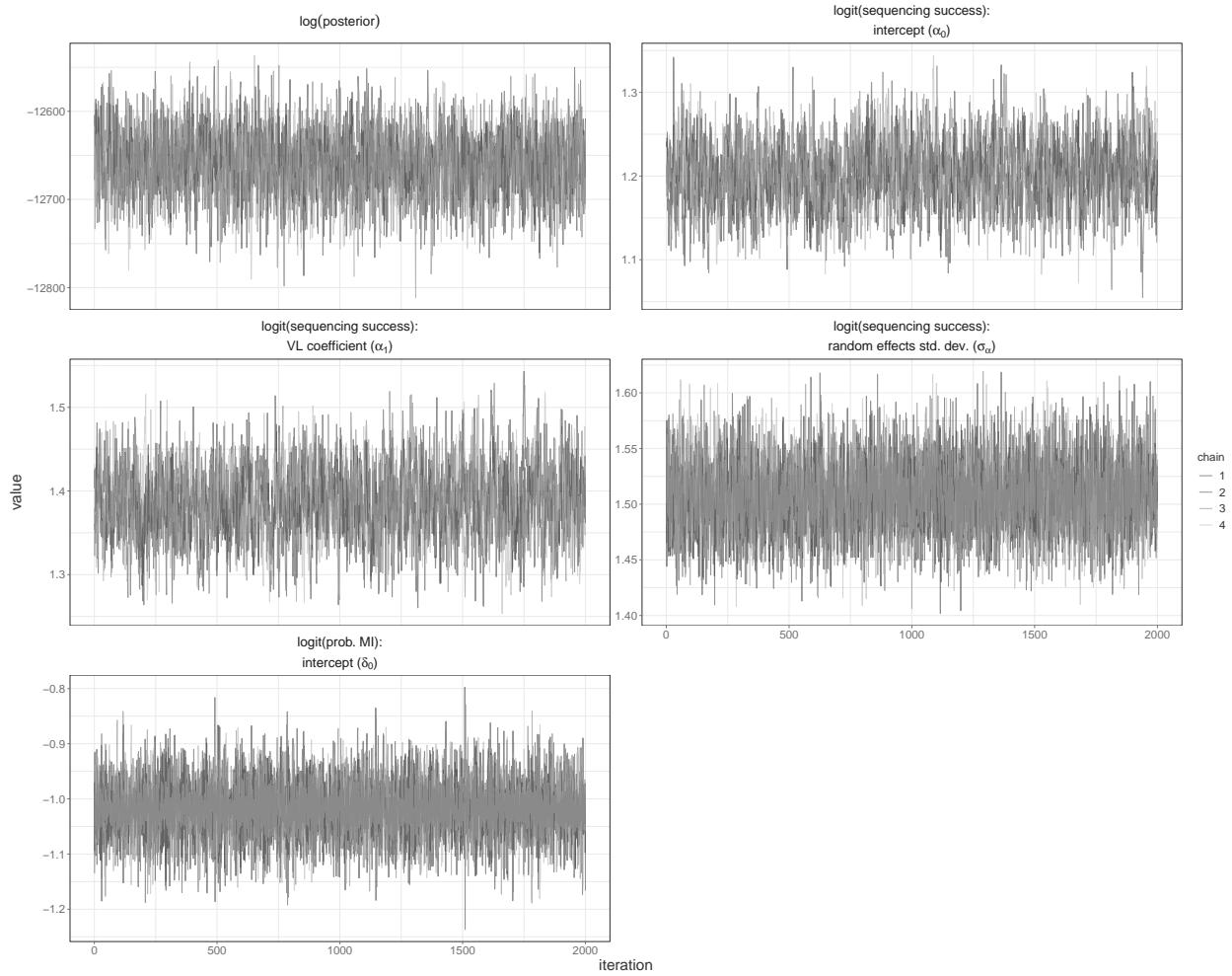
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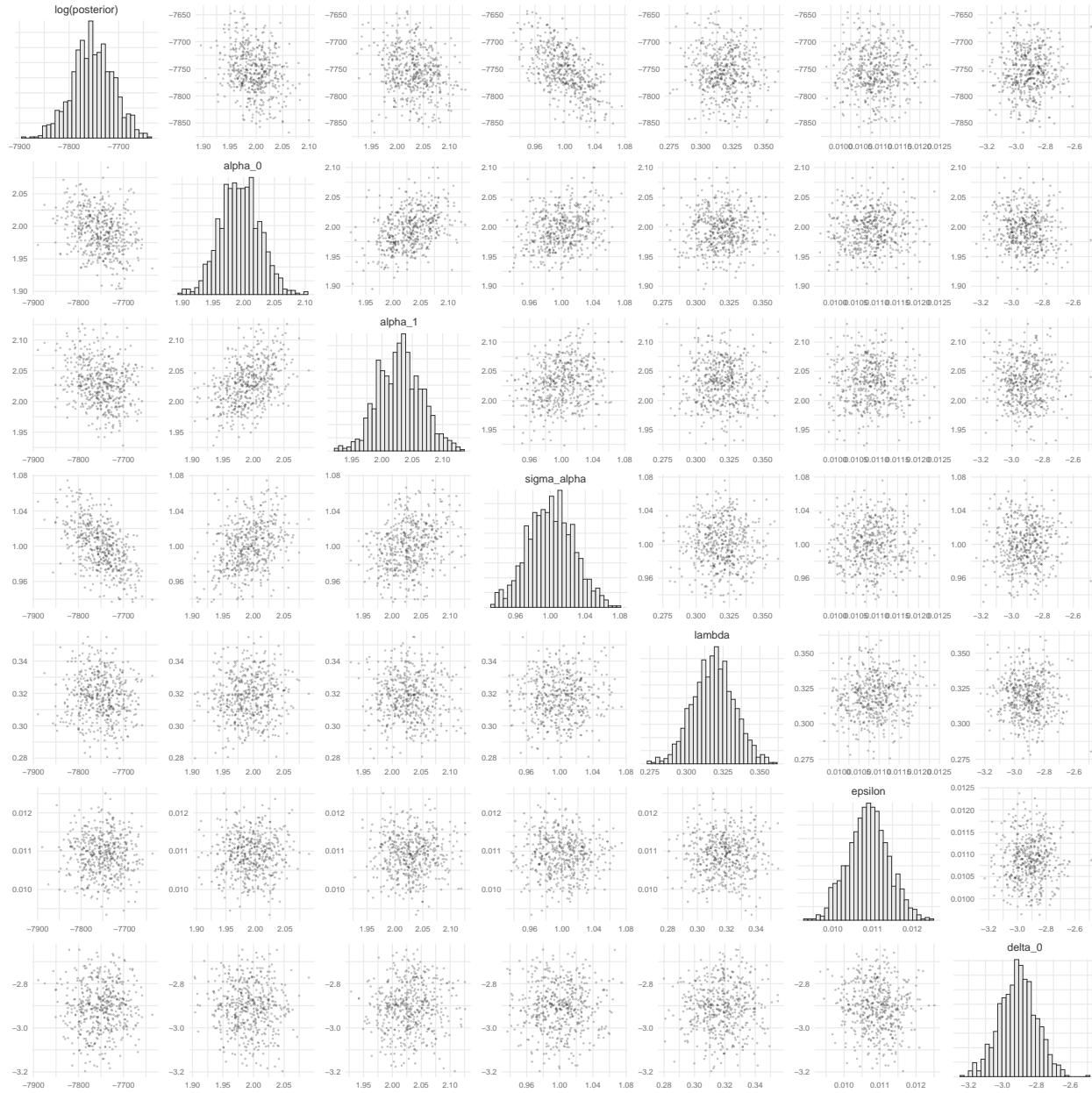
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 Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.



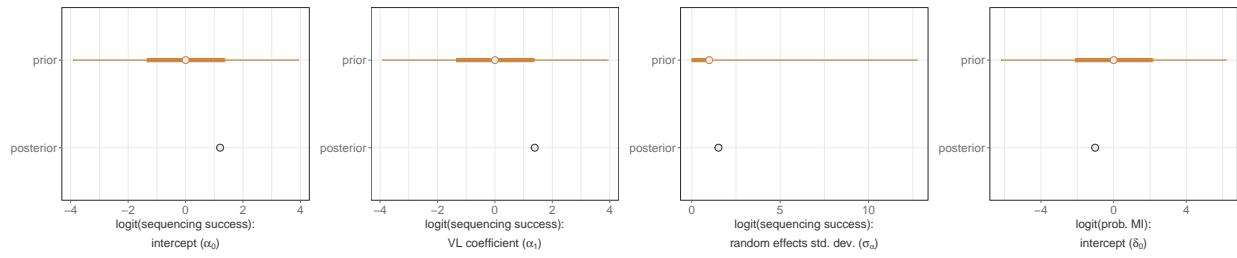
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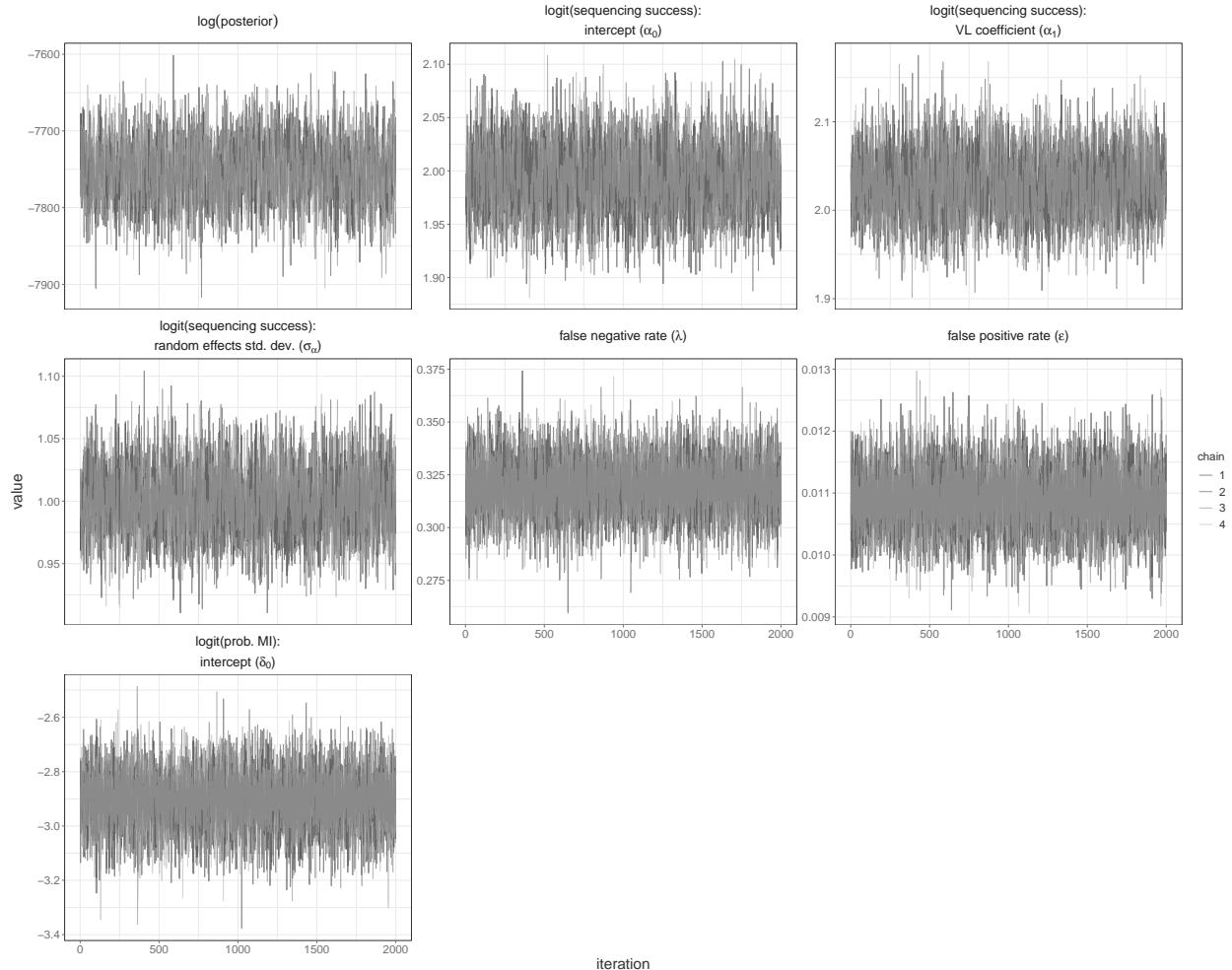
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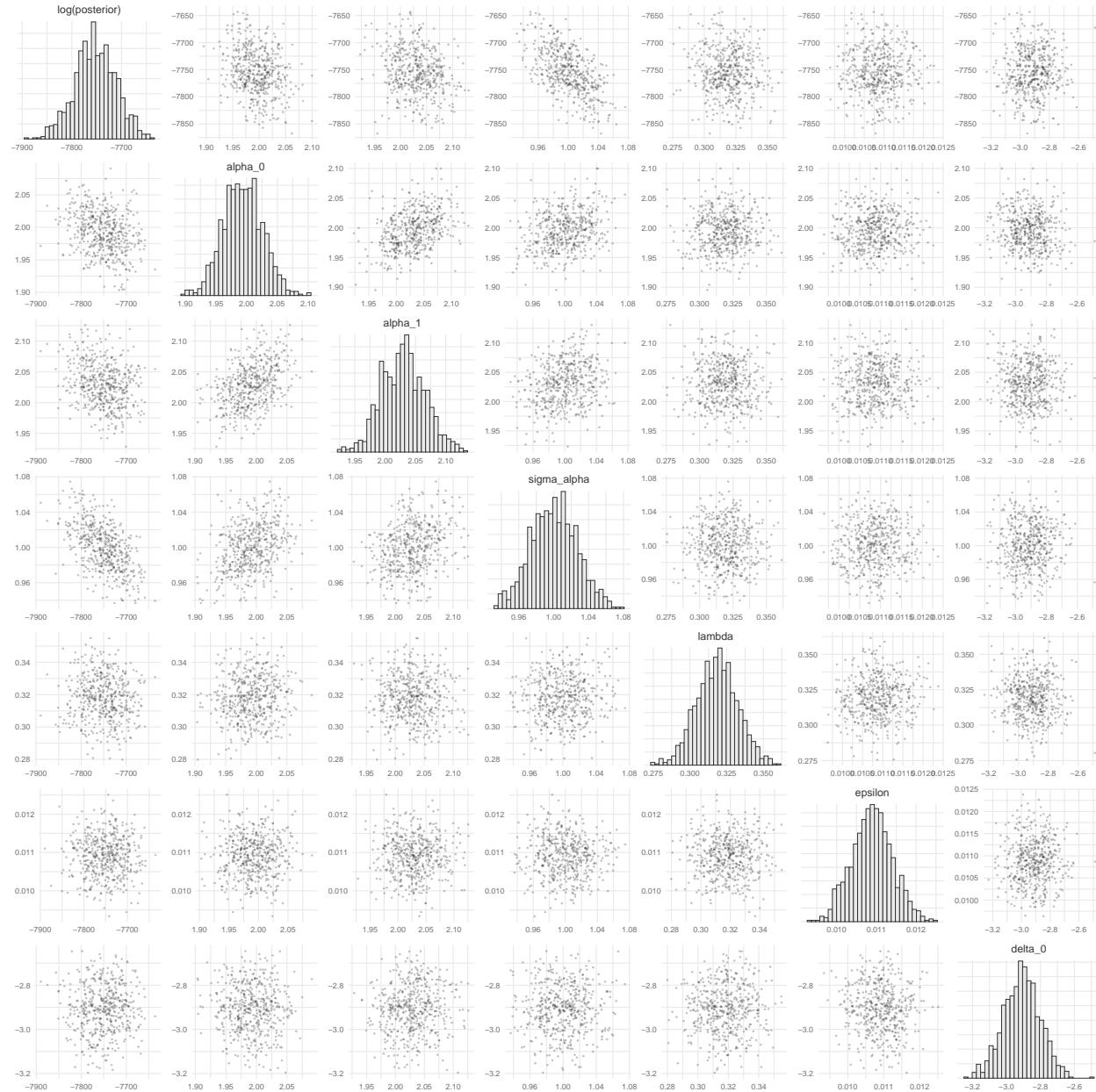
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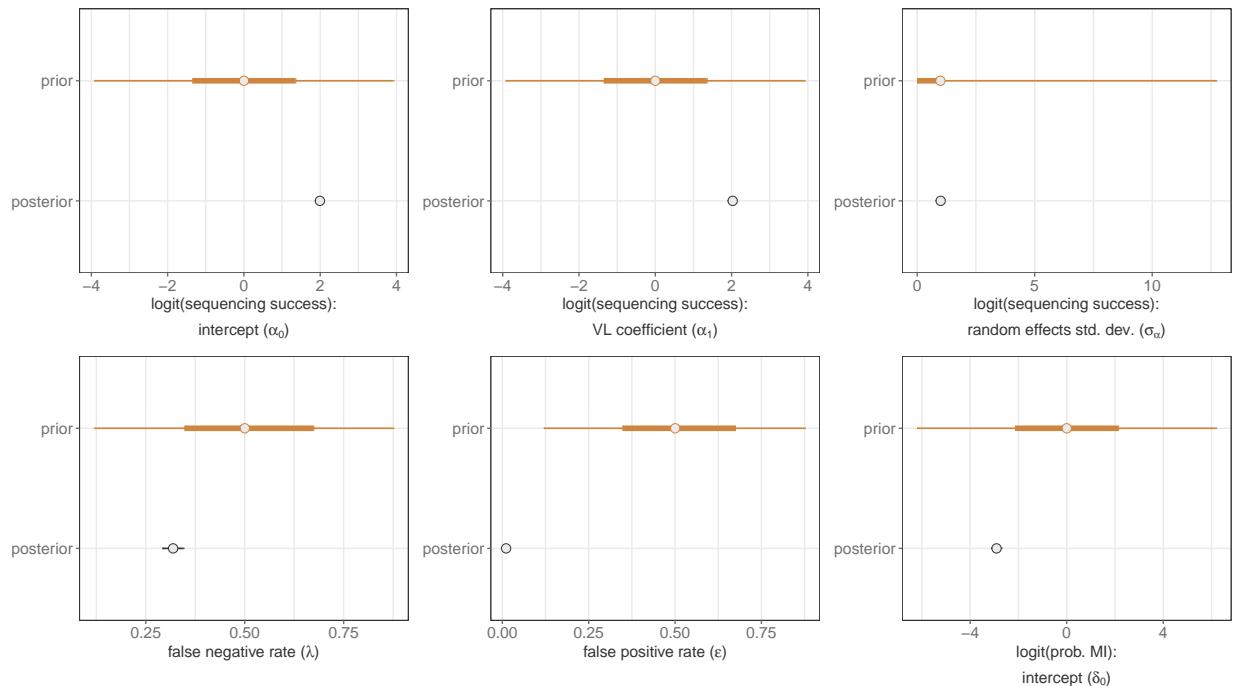
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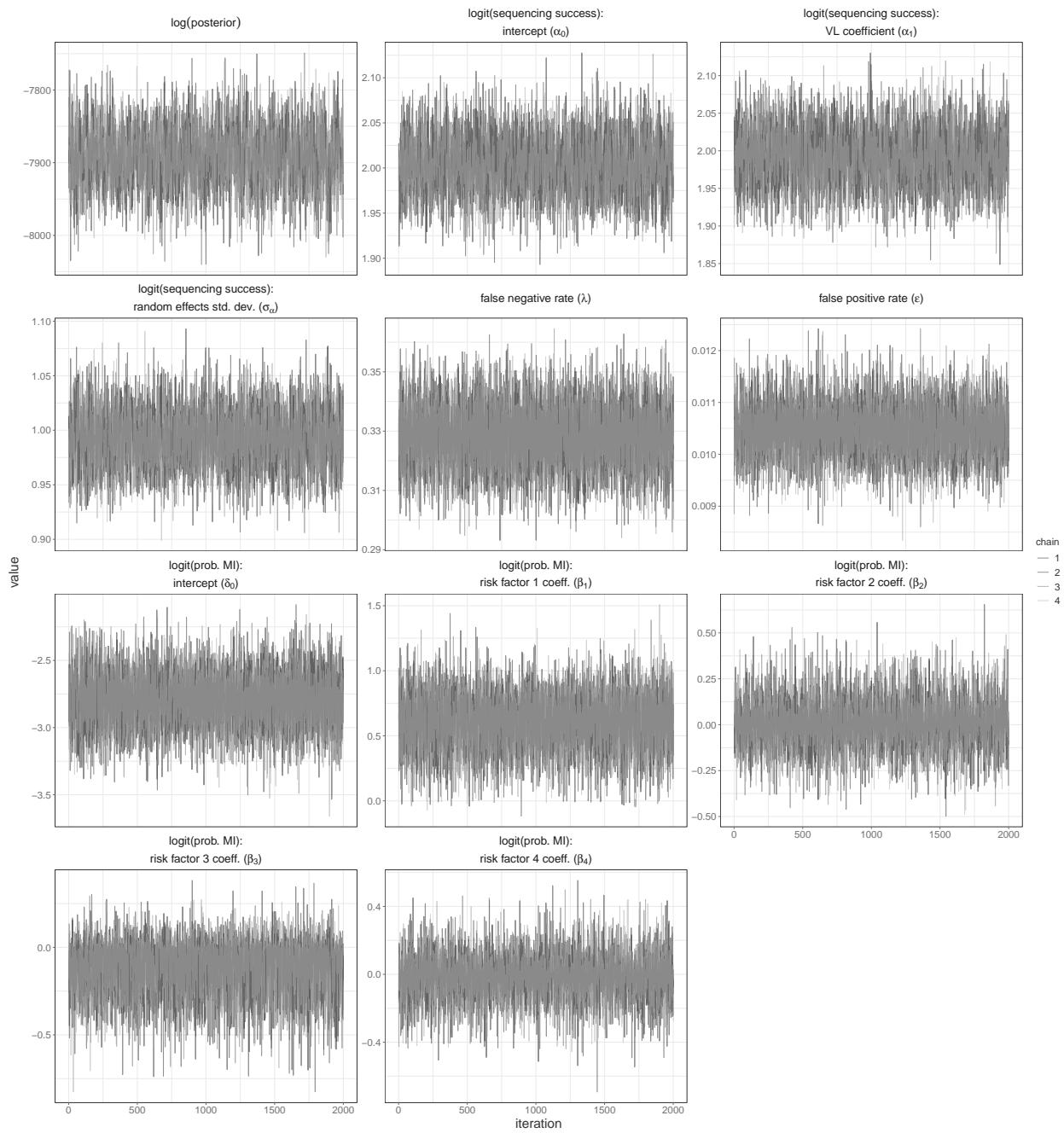
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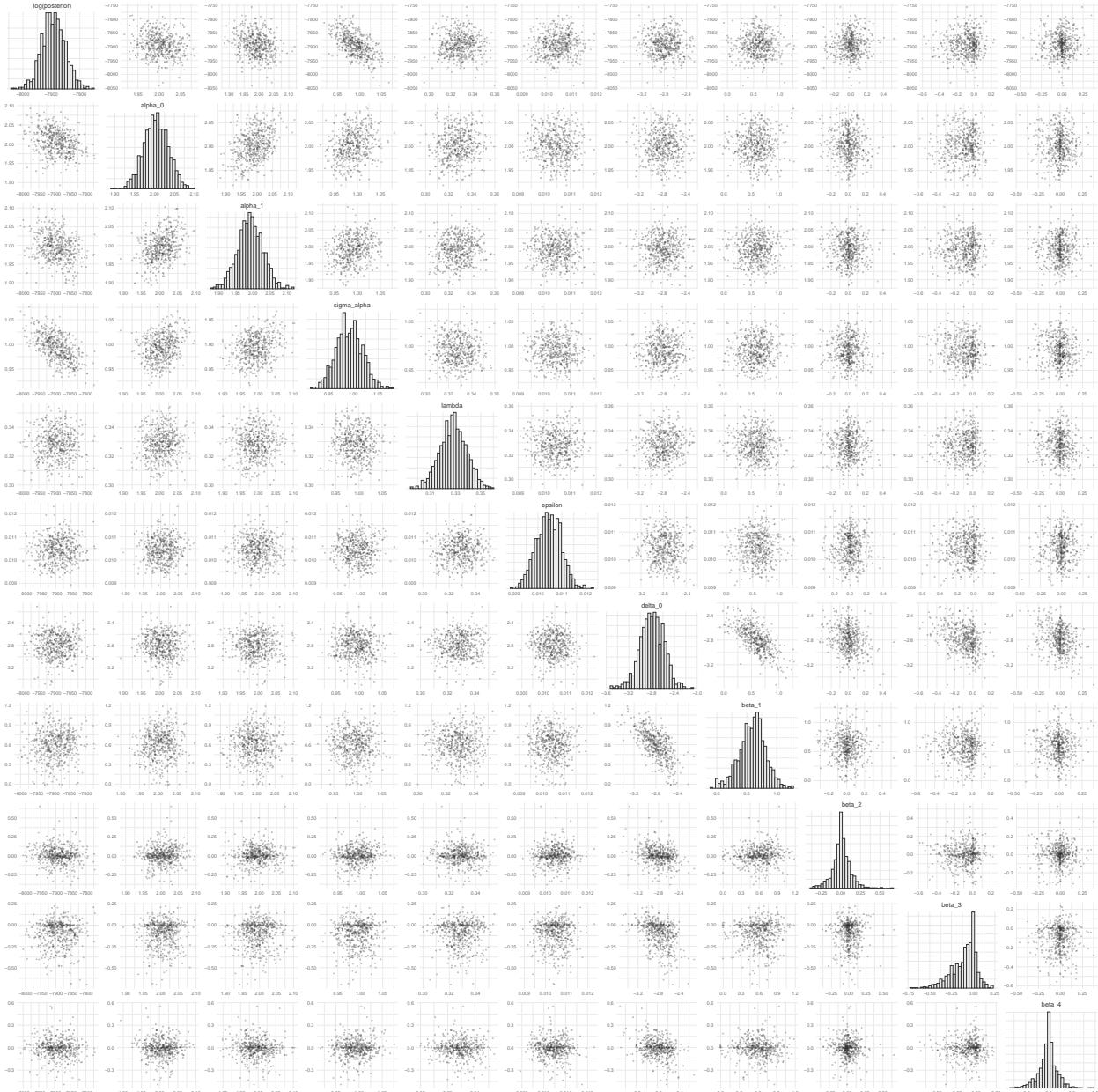
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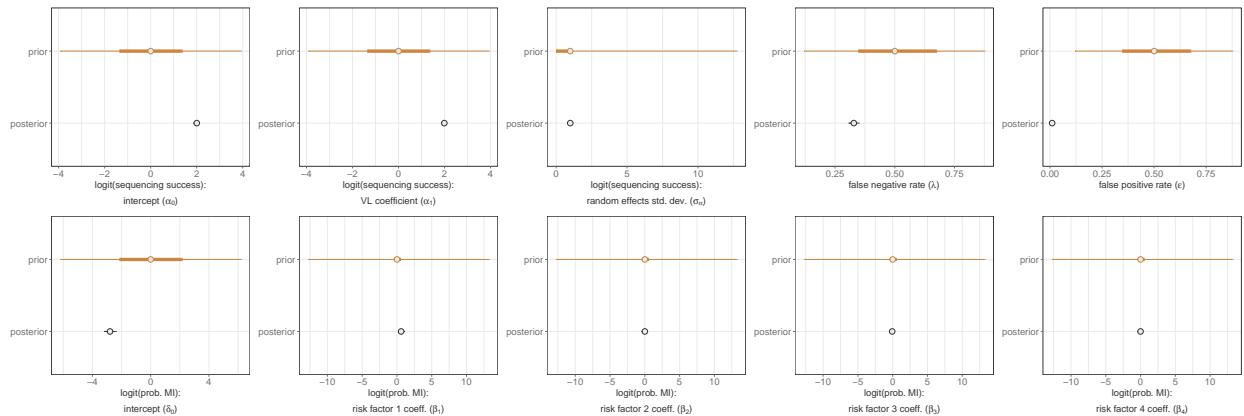
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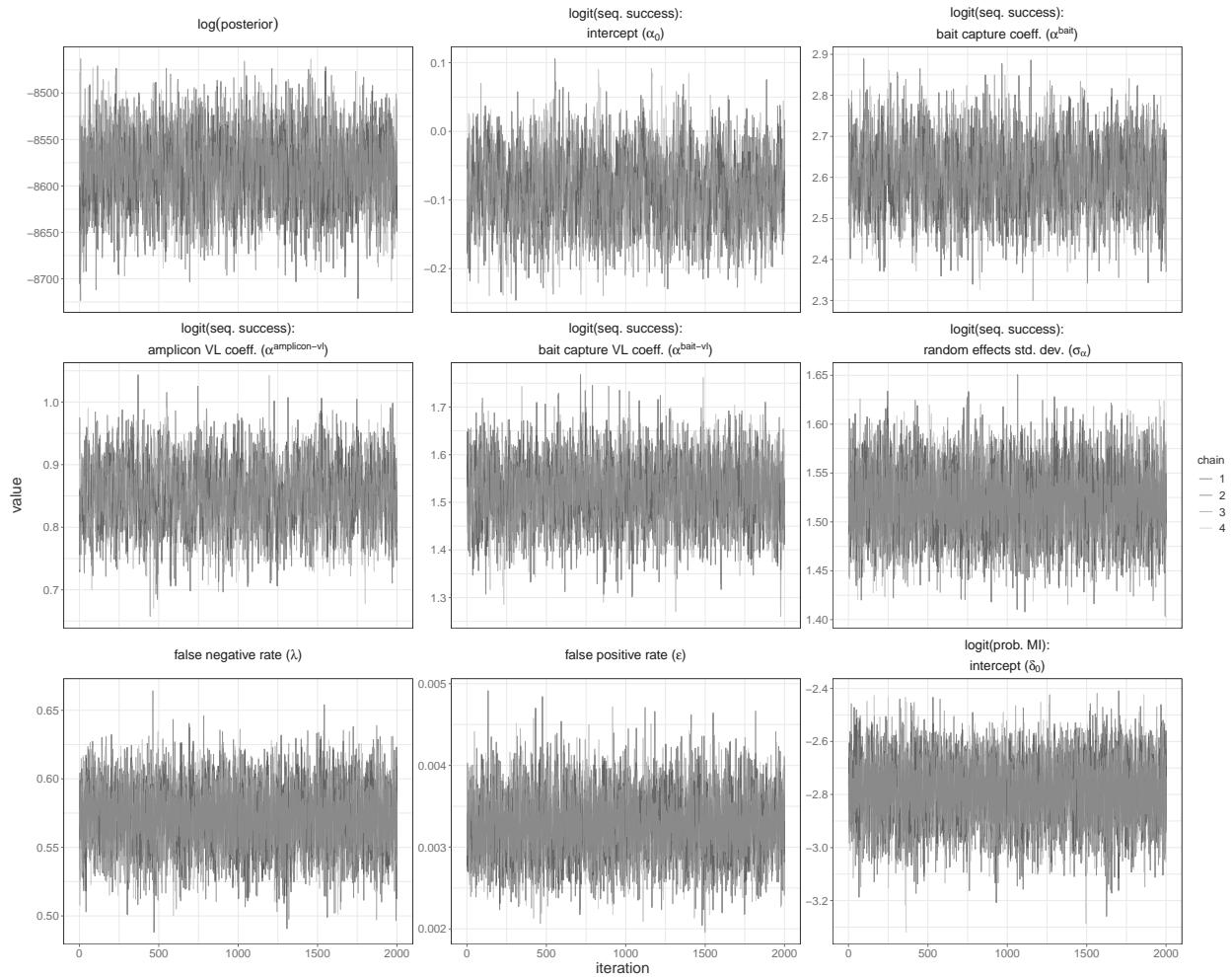
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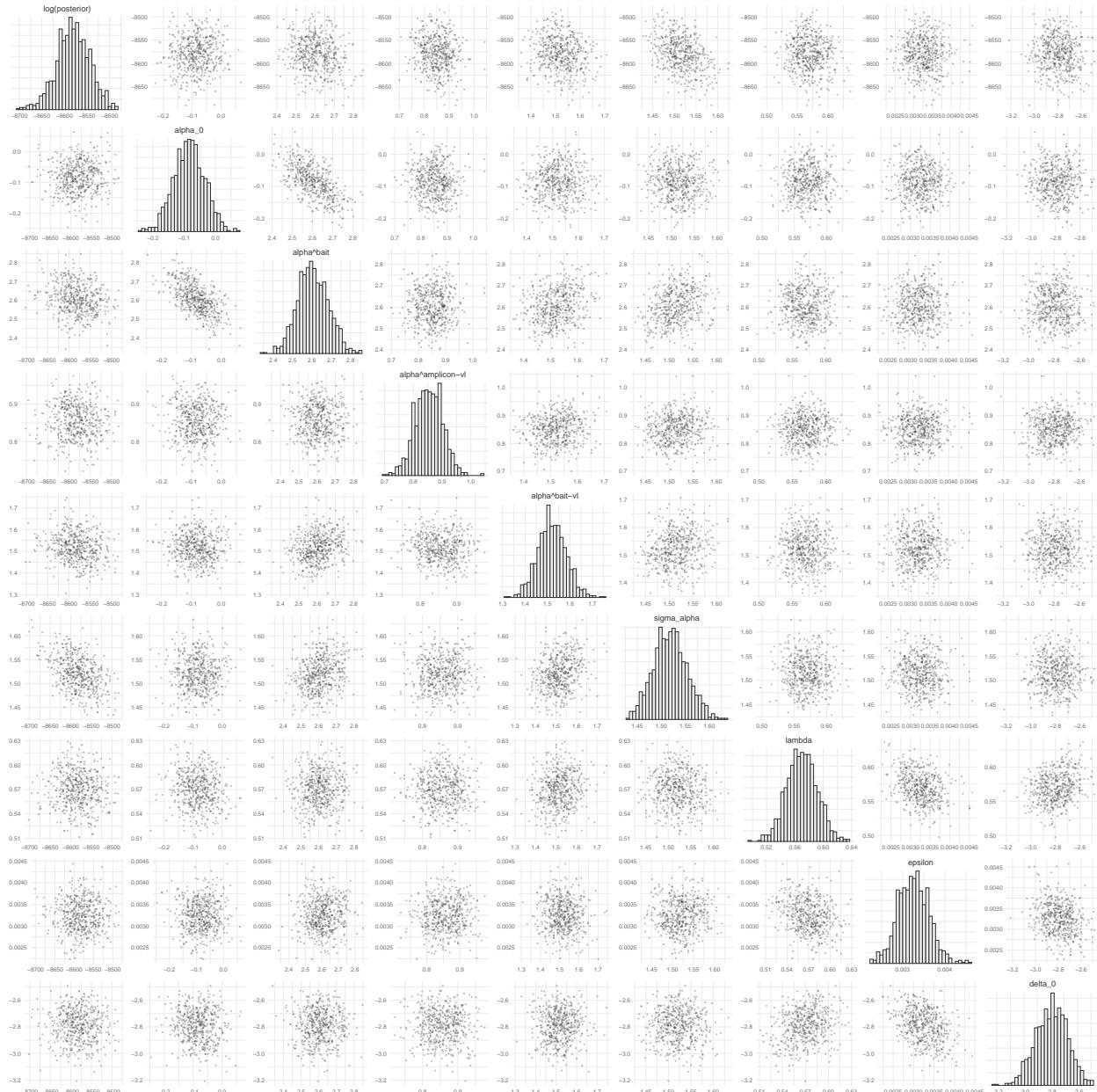
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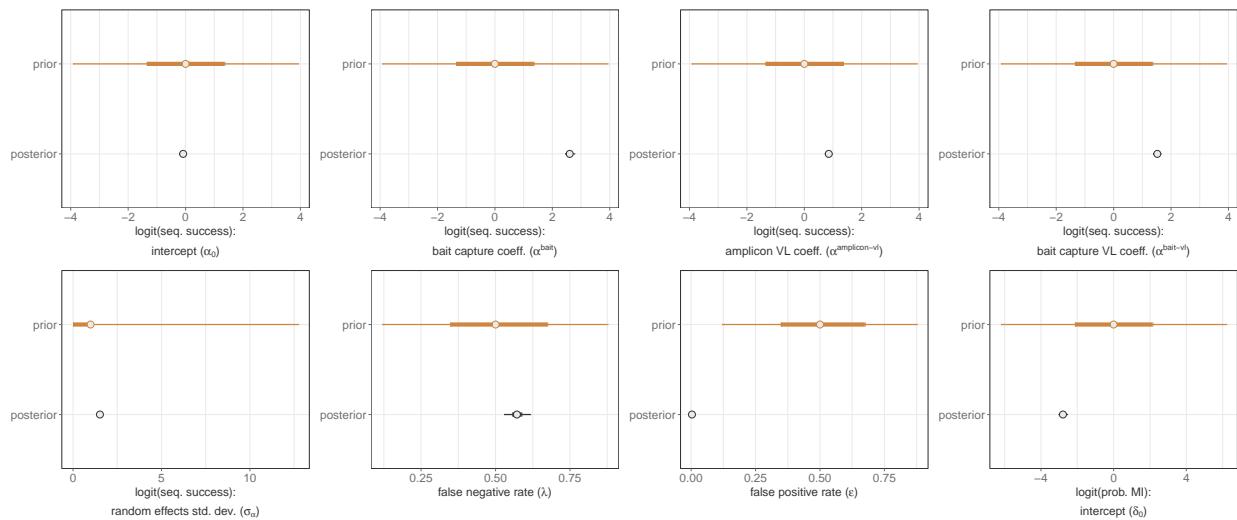
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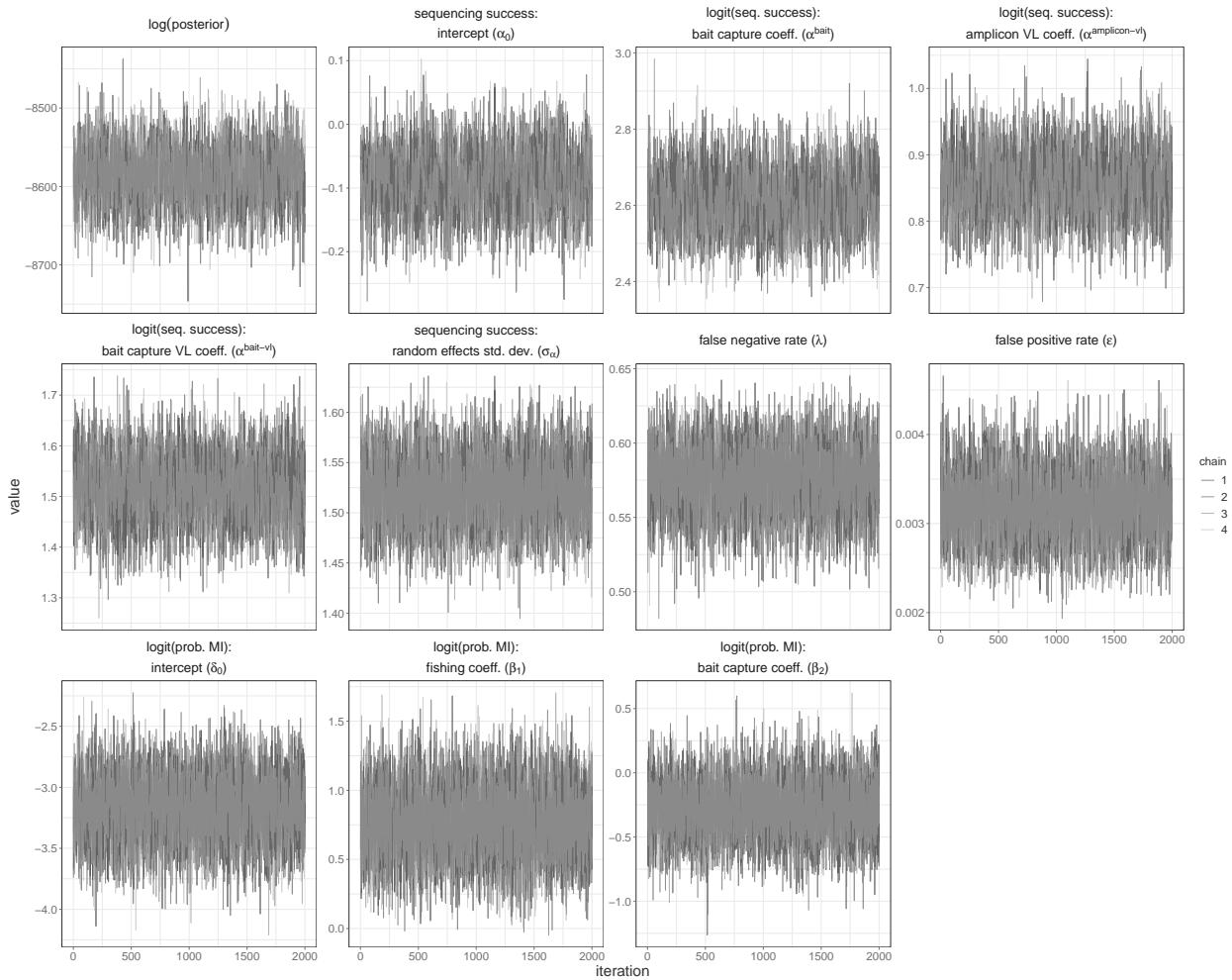
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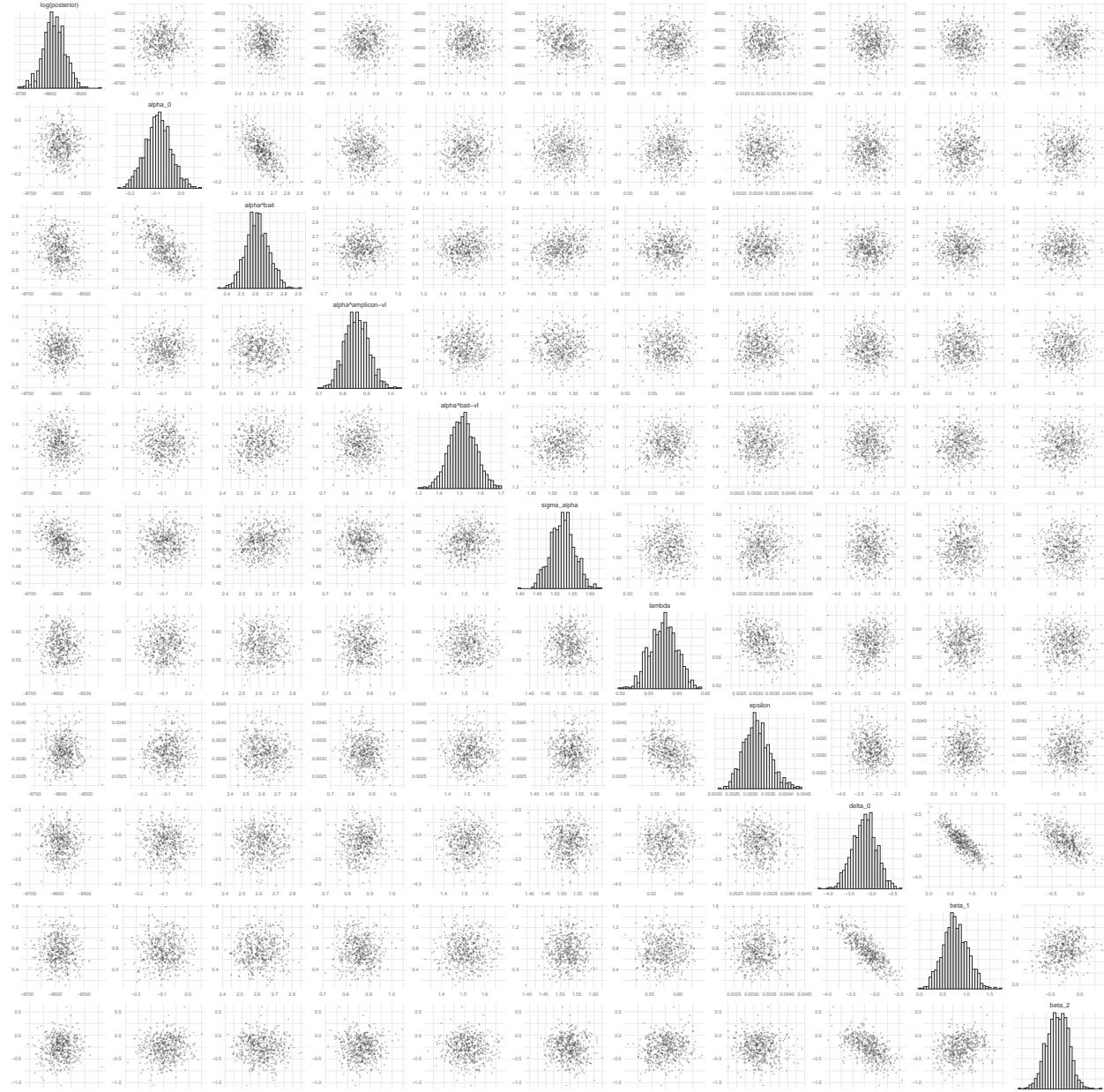
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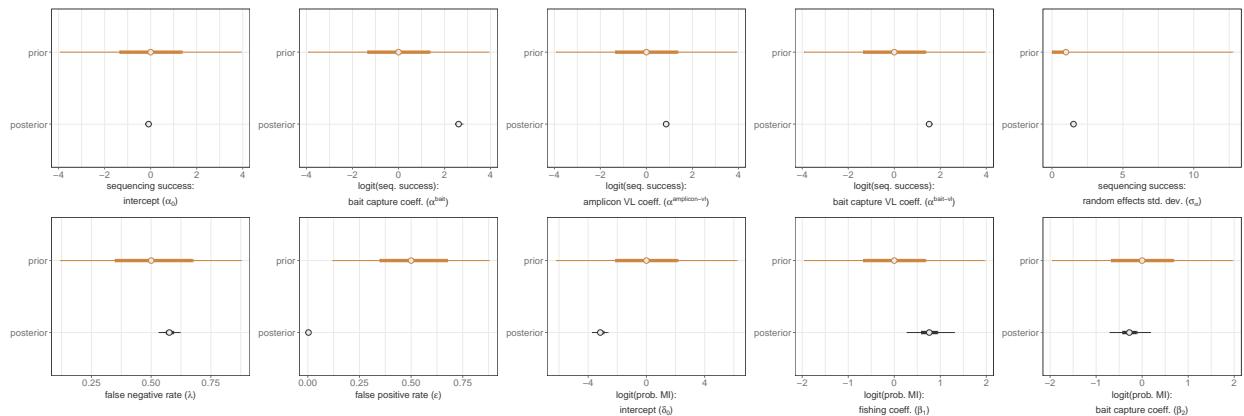
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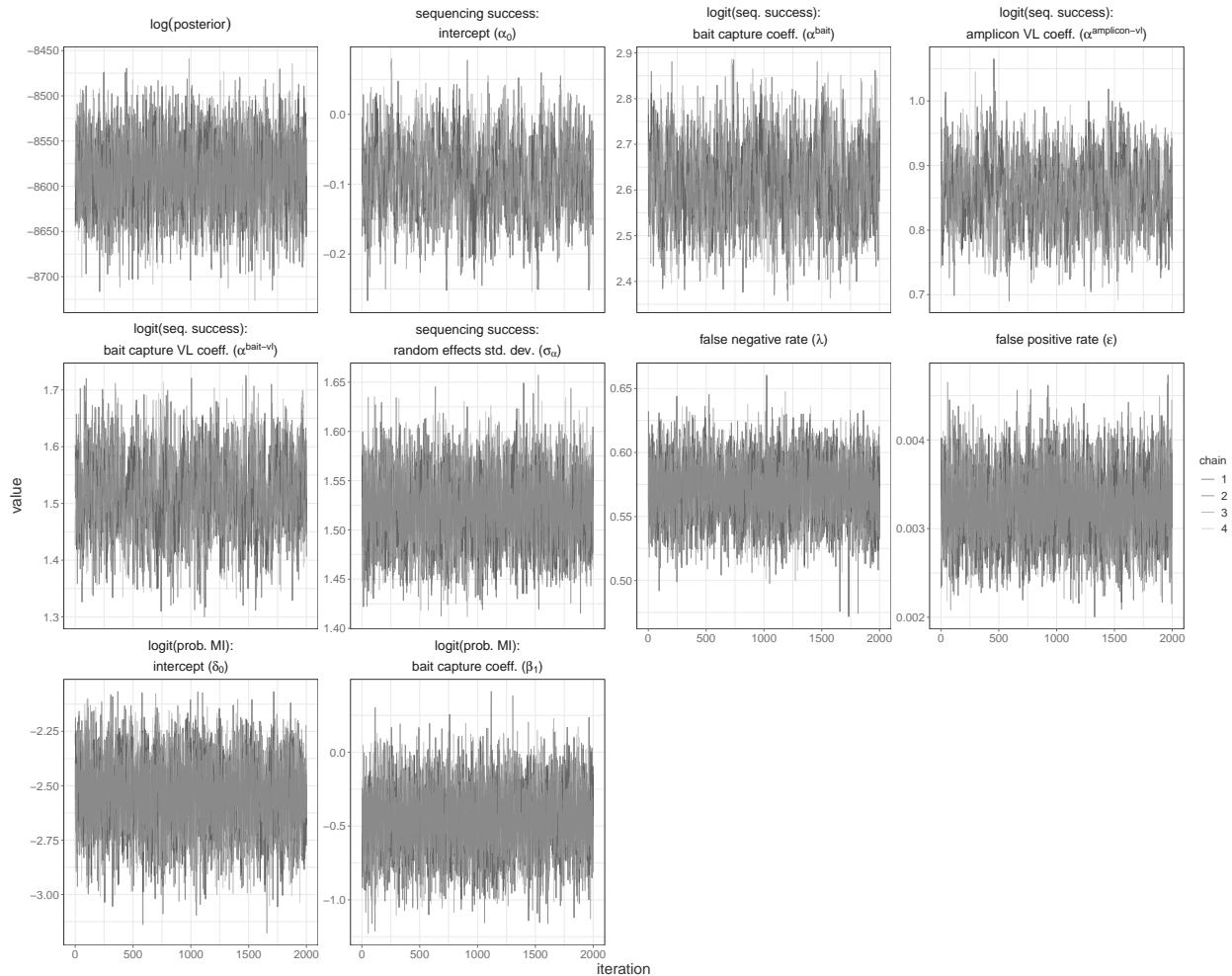
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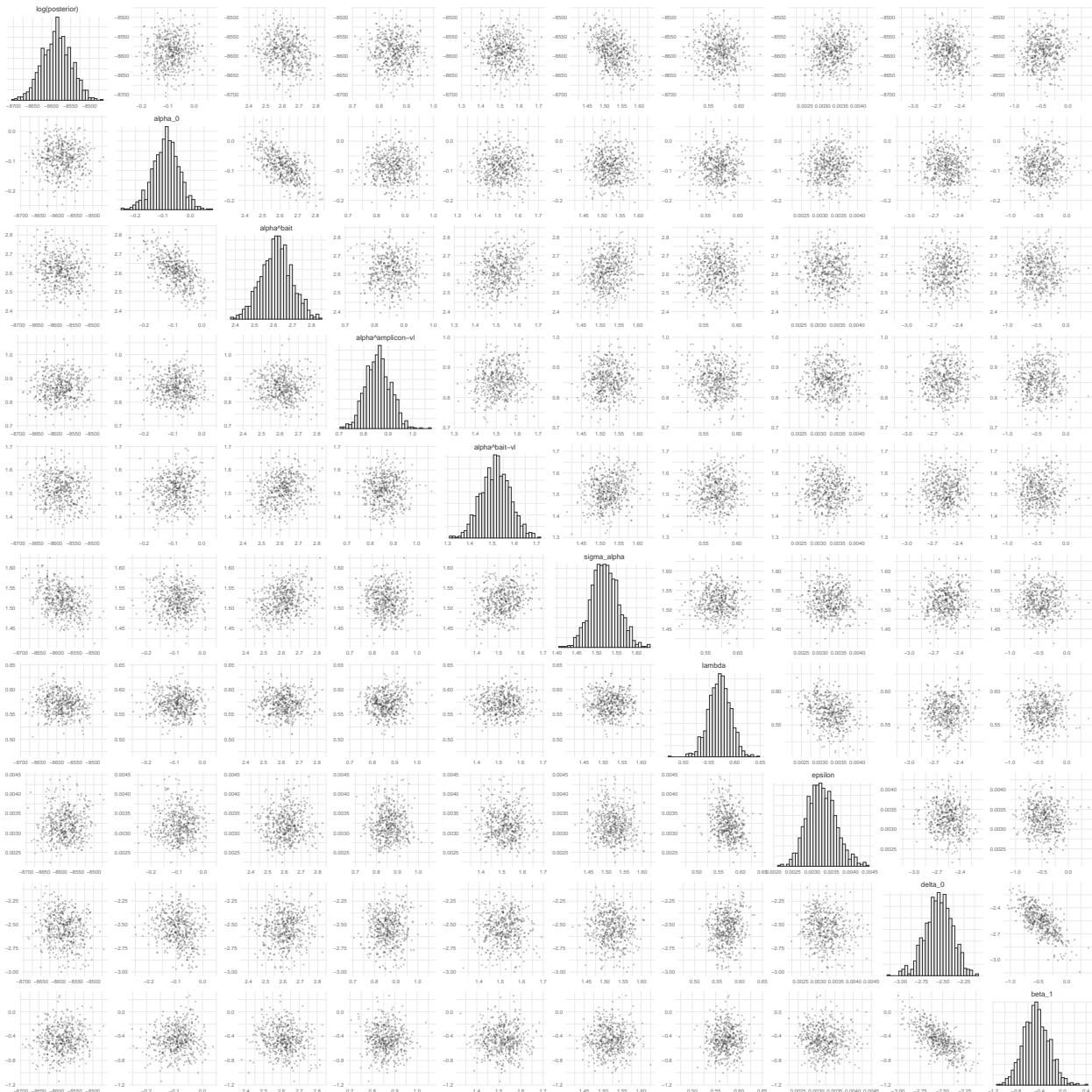
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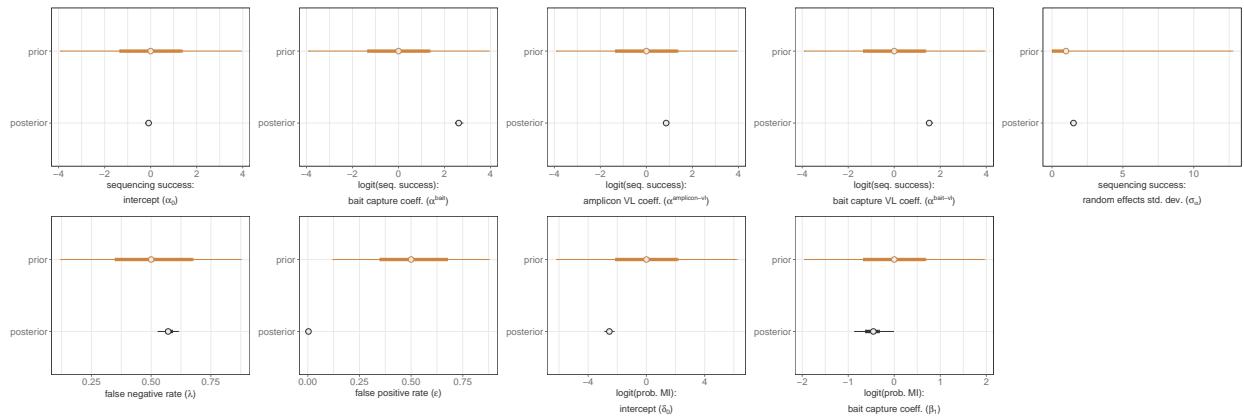
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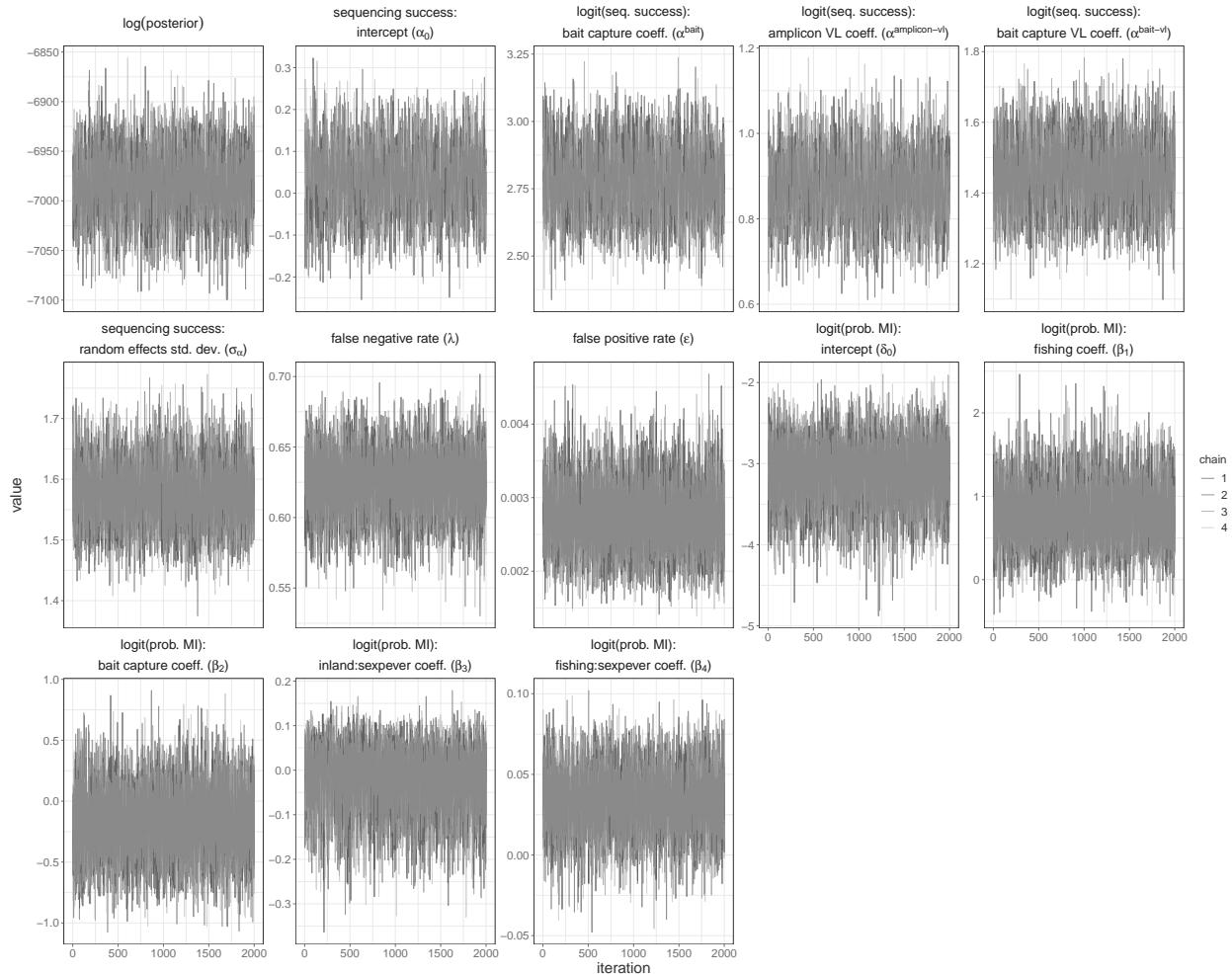
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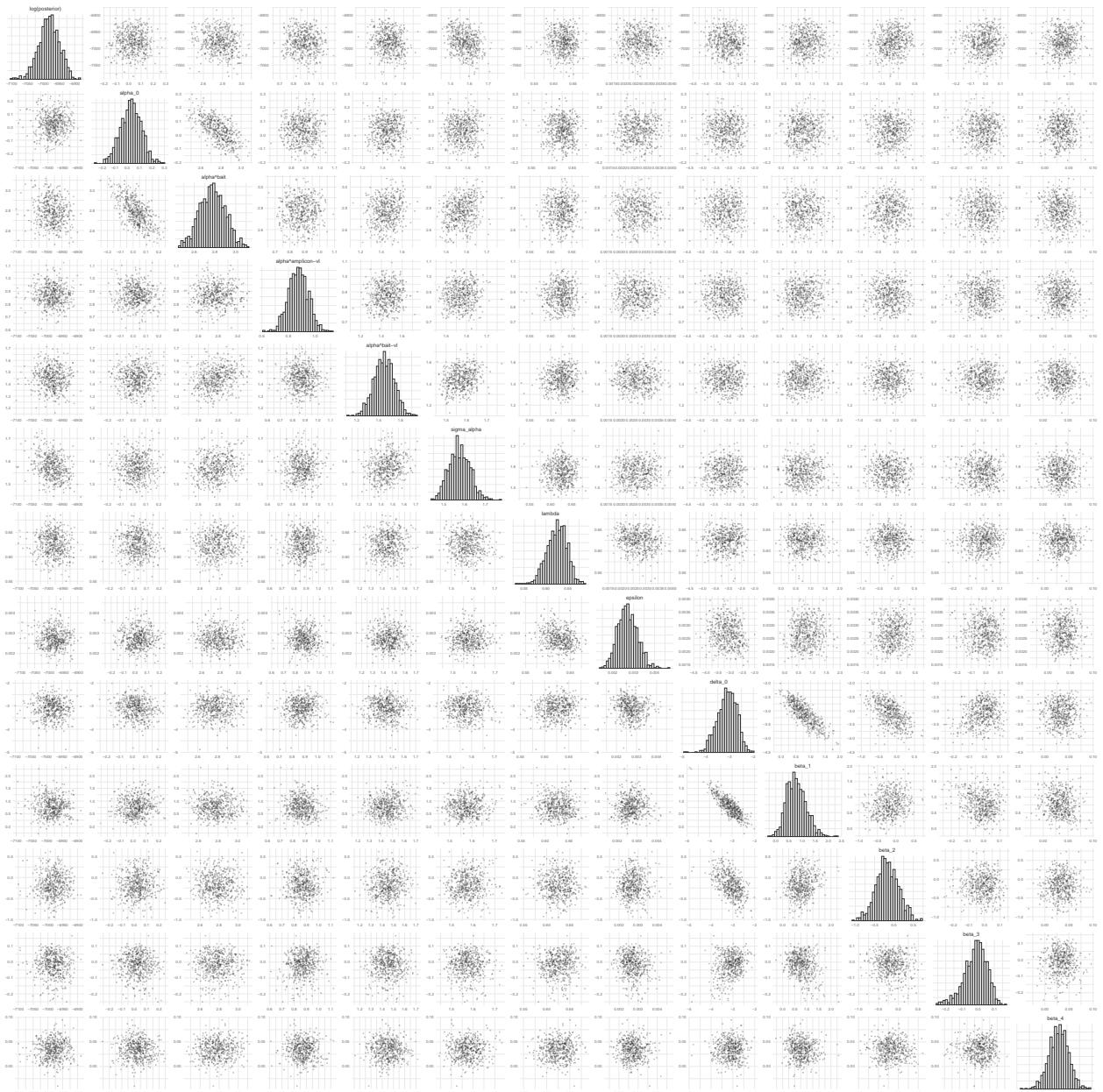
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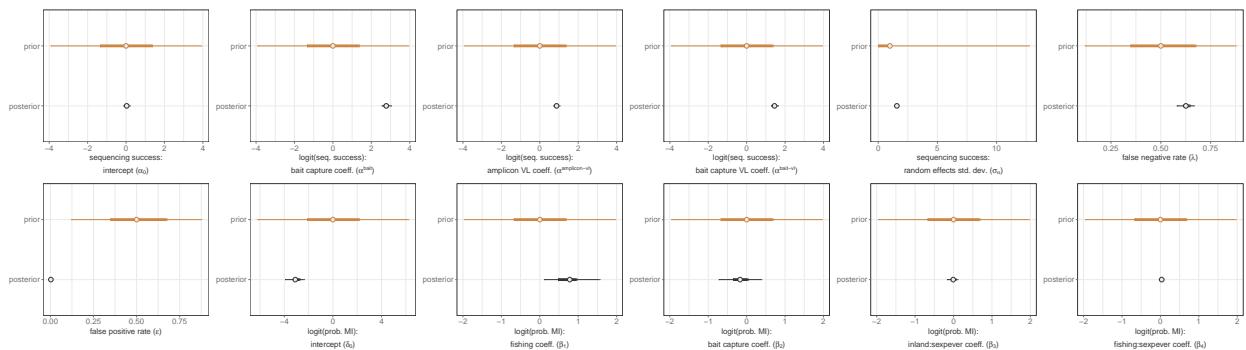
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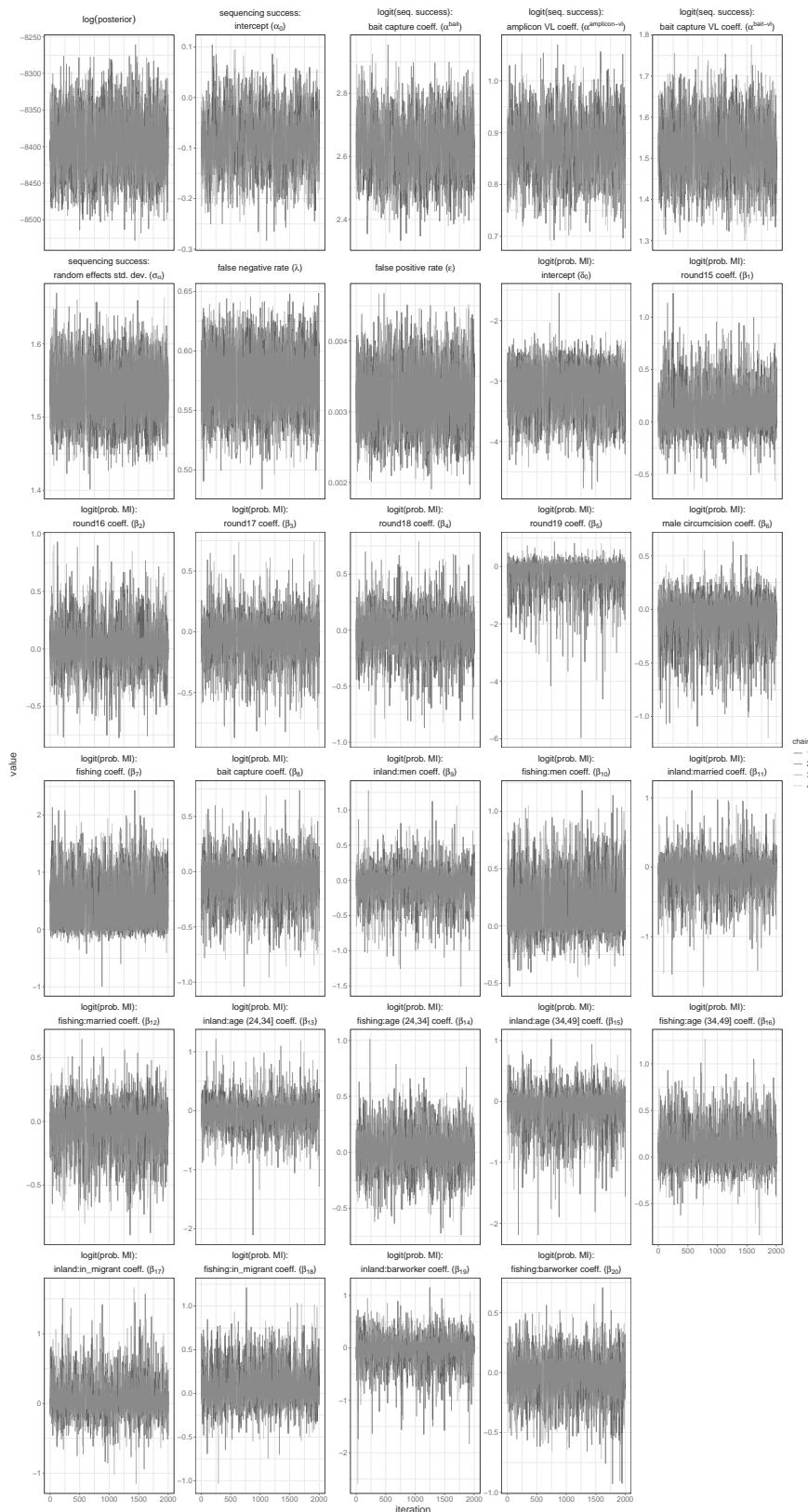
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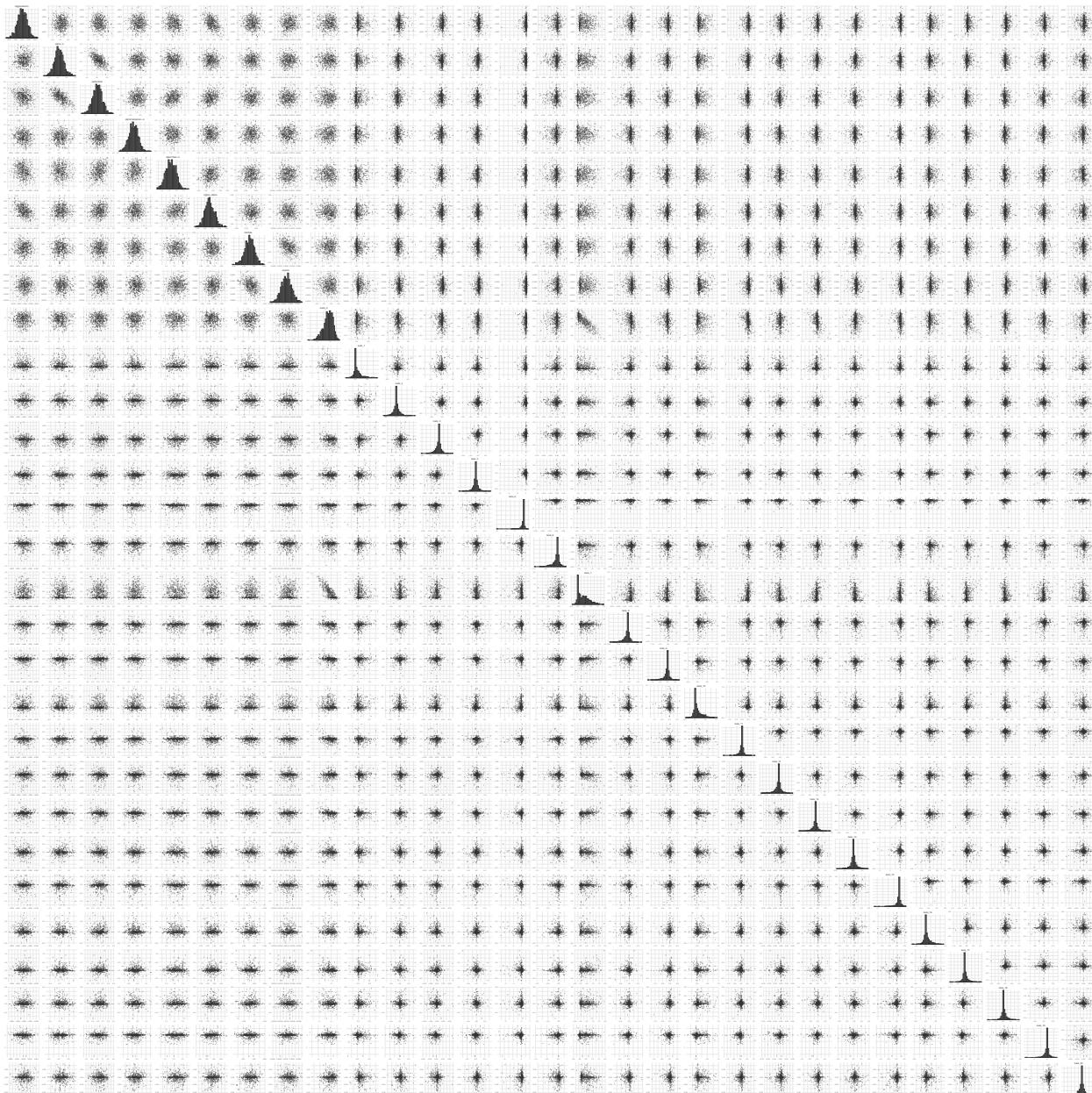
**Fig S.D. 23.** MCMC pairs plots for parameters in extended model with community type and lifetime sex partners as a risk factor for harboring multiple infections fit to deep sequence data generated from 997 men living with viremic HIV who participated in the Rakai Community Cohort Study. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.



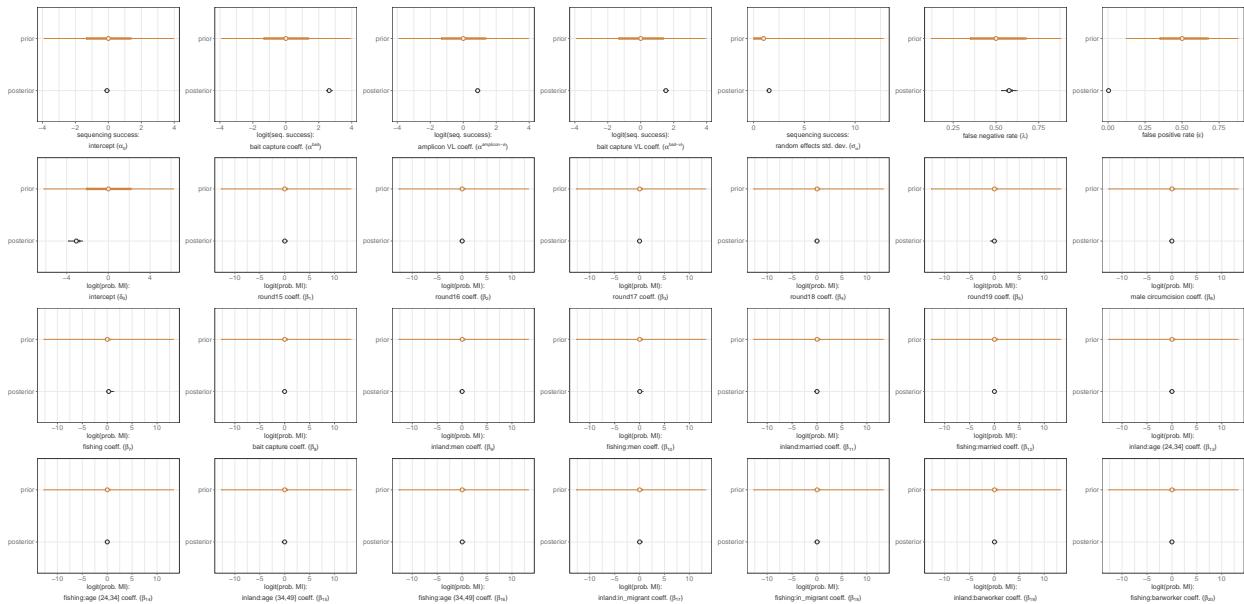
**Fig S.D. 24. Comparison of posterior and prior distributions of parameters in extended model with sequencing technology as a risk factor fit to deep sequence data generated from 997 Rakai Community Cohort Study participants living with viremic HIV.** Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. Some horizontal bars do not extend beyond the central point. Warm-up iterations are excluded. MI = multiple infection. VL = viral load ( $\log_{10}$  copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



**Fig S.D. 25. MCMC trace plots for parameters in extended model with variable selection to identify risk factor for harboring multiple infections fit to deep sequence data generated from 1,970 Rakai Community Cohort Study participants living with viremic HIV.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load ( $\log_{10}$  copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



**Fig S.D. 26.** MCMC pairs plots for parameters in extended model with variable selection to identify risk factor for harboring multiple infections fit to deep sequence data generated from 1,970 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.



**Fig S.D. 27. Comparison of posterior and prior distributions of parameters in extended model with variable selection to identify risk factor fit to deep sequence data generated from 1,970 Rakai Community Cohort Study participants living with viremic HIV.** Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. Some horizontal bars do not extend beyond the central point. Warm-up iterations are excluded. MI = multiple infection. VL = viral load ( $\log_{10}$  copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.