

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

Michael A. Martin^{1,†}, Andrea Brizzi², Xiaoyue Xi^{2,3}, Ronald Moses Galiwango⁴, Sikhulile Moyo^{5,6}, Deogratius Ssemwanga^{7,8} Alexandra Blenkinsop², Andrew D. Redd^{9,10,11}, Lucie Abeler-Dörner¹², Christophe Fraser¹², Steven J. Reynolds^{4,9,10}, Thomas C. Quinn^{4,9,10}, Joseph Kagaayi^{4,13}, David Bonsall¹⁴, David Serwadda⁴, Gertrude Nakigozi⁴, Godfrey Kigozi⁴, M. Kate Grabowski^{1,4,15,†}, Oliver Ratmann^{2,†}, with the PANGEA-HIV Consortium and the Rakai Health Sciences Program

1 Department of Pathology, Johns Hopkins School of Medicine, Baltimore, MD, USA

2 Department of Mathematics, Imperial College London, London, United Kingdom

3 Medical Research Council Biostatistics Unit, University of Cambridge, Cambridge, UK

4 Rakai Health Sciences Program, Kalisizo, Uganda

5 Botswana Harvard AIDS Institute Partnership, Botswana Harvard HIV Reference Laboratory, Gaborone, Botswana

6 Harvard T.H. Chan School of Public Health, Boston, MA, USA

7 Medical Research Council/Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine Uganda Research Unit, Entebbe, Uganda

8 Uganda Virus Research Institute, Entebbe, Uganda

9 Department of Medicine, Johns Hopkins School of Medicine, Baltimore, MD, USA

10 Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, USA

11 Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa

12 Pandemic Sciences Institute, Nuffield Department of Medicine, University of Oxford, Oxford, UK

13 Makerere University School of Public Health, Kampala, Uganda

14 Wellcome Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, Oxford, UK

15 Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA

† Corresponding authors mmart108@jhmi.edu, mgrabow2@jhu.edu, oliver.ratmann@imperial.ac.uk

List of Figures

| | | |
|----|--|----|
| 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. 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. | 5 |
| 2 | MCMC pairs plots for parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection. | 6 |
| 3 | Comparison of posterior and prior distributions of parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows. 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. | 7 |
| 4 | MCMC trace plots for parameters in base model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows. 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. | 7 |
| 5 | MCMC pairs plots for parameters in base model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows trace. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection. | 8 |
| 6 | Comparison of posterior and prior distributions of parameters in base model fit to simulated data with partial sequencing success and false positive or false negative multiple subgraph windows. 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. | 9 |
| 7 | MCMC trace plots for parameters in full model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows. 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. | 9 |
| 8 | MCMC pairs plots for parameters in full model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows trace. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. | 10 |
| 9 | Comparison of posterior and prior distributions of parameters in full model fit to simulated data with partial sequencing success and false positive or false negative multiple subgraph windows. 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. | 11 |
| 10 | MCMC trace plots for parameters in extended model fit to simulated data with partial sequencing success, false positive and false negative multiple subgraph windows, and a binary risk factor for harboring multiple infection. 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. | 12 |

- 11 MCMC pairs plots for parameters in extended model fit to simulated data with
partial sequencing success, false positive and false negative multiple subgraph
windows, and a binary risk factor for harboring multiple infection. Independent
chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250
iterations per chain. MI = multiple infection. 13
- 12 Comparison of posterior and prior distributions of parameters in full model fit
to simulated data with partial sequencing success, false positive or false negative
multiple subgraph windows, and a binary risk factor for harboring multiple
infection. 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. 14
- 13 MCMC trace plots for parameters in full model fit to deep sequence data generated
from 2,029 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. 15
- 14 MCMC pairs plots for parameters in full model fit to deep sequence data generated
from 2,029 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. 16
- 15 Comparison of posterior and prior distributions of parameters in full model fit
to deep sequence data generated from 2,029 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. 17
- 16 MCMC trace plots for parameters in extended model with community type
and sequencing technology as a risk factor fit to deep sequence data generated
from 2,029 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. 18
- 17 MCMC pairs plots for parameters in extended model with community type and
sequencing technology as a risk factor fit to deep sequence data generated from
2,029 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. 19
- 18 Comparison of posterior and prior distributions of parameters in extended model
with community type and sequencing technology as a risk factor fit to deep
sequence data generated from 2,029 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. 20
- 19 MCMC trace plots for parameters in extended model with deep-sequencing
protocol as a risk factor fit to deep sequence data generated from 2,029 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. 21

| | | |
|----|---|----|
| 20 | MCMC pairs plots for parameters in extended model with deep-sequencing protocol as a risk factor fit to deep sequence data generated from 2,029 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. | 22 |
| 21 | 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 2,029 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. | 23 |
| 22 | MCMC trace 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. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation. | 24 |
| 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. | 25 |
| 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. | 26 |
| 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. | 27 |
| 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. | 28 |
| 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. | 29 |

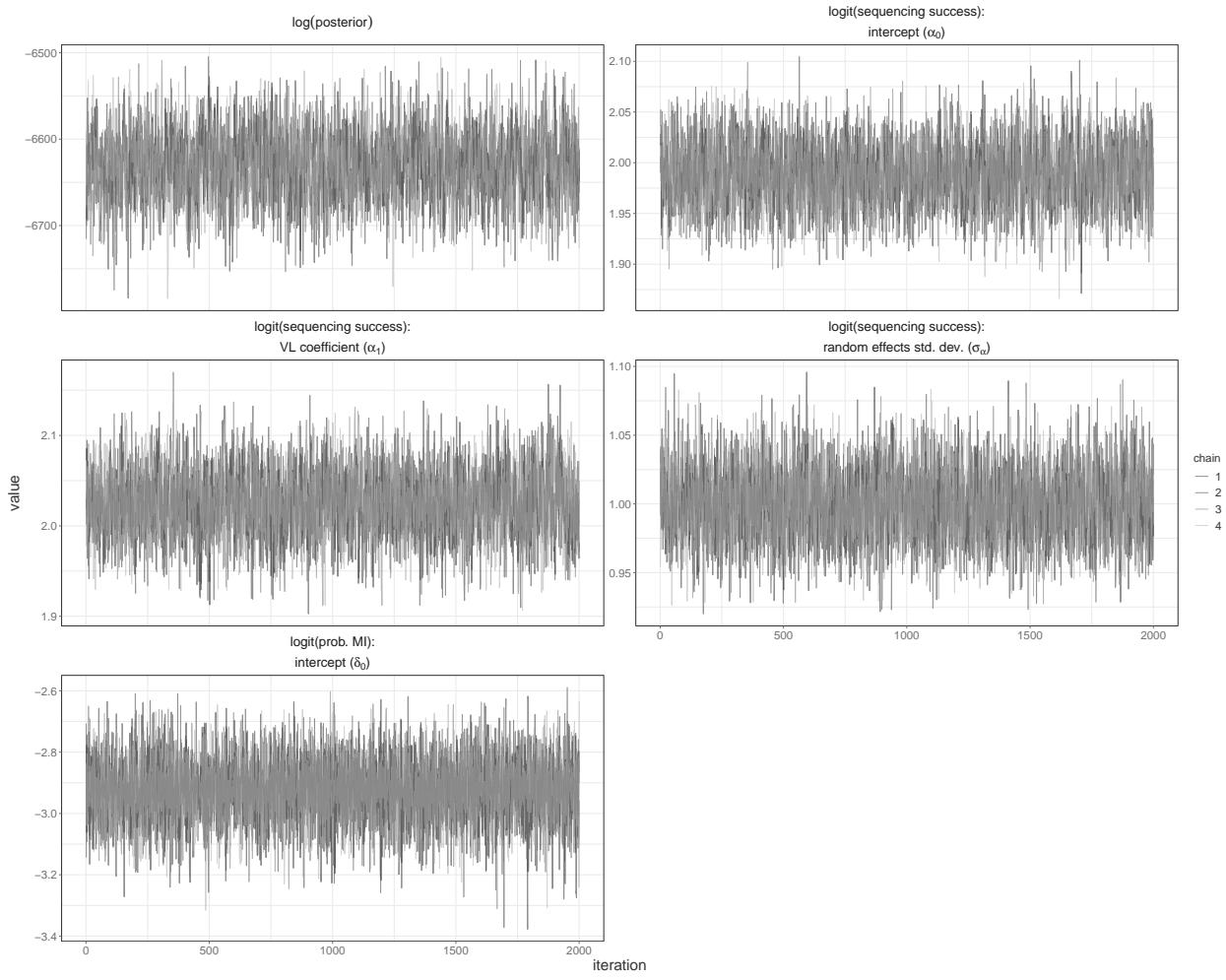


Fig S.D. 1. MCMC trace plots for parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows.

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.

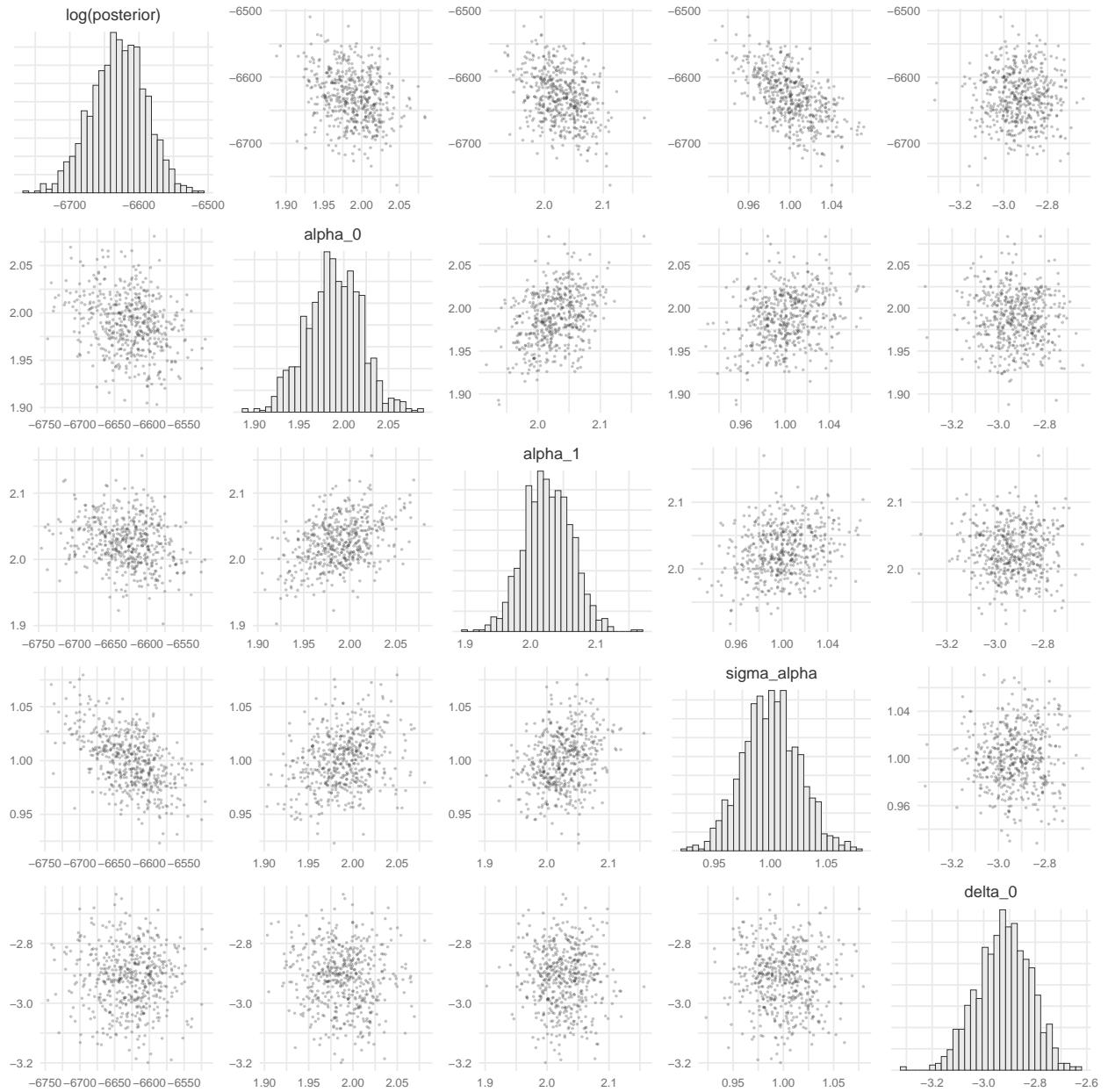


Fig S.D. 2. MCMC pairs plots for parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows.
 Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.

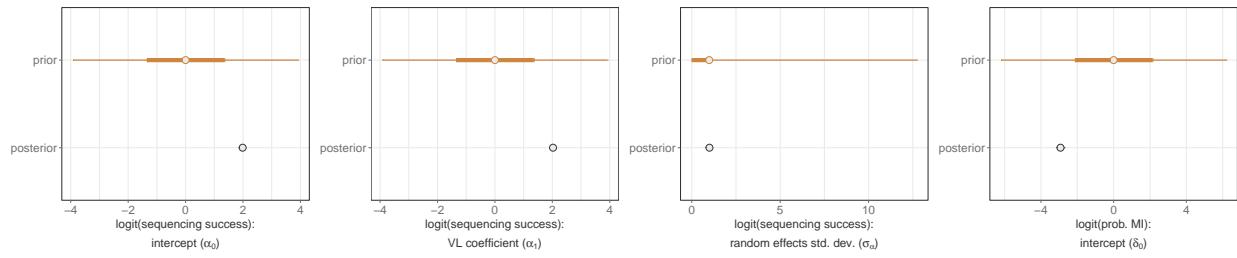


Fig S.D. 3. Comparison of posterior and prior distributions of parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows. Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. 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.

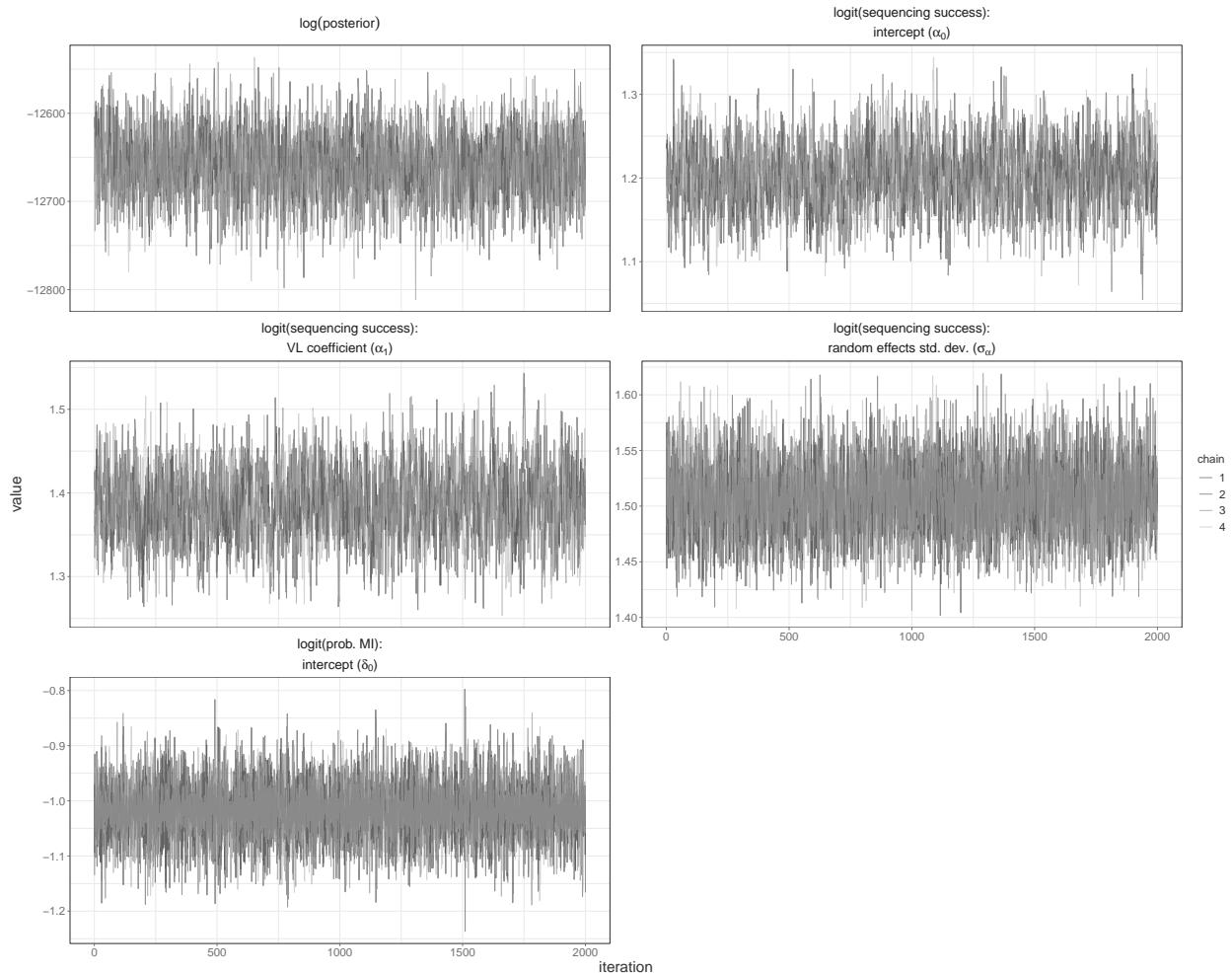


Fig S.D. 4. MCMC trace plots for parameters in base model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

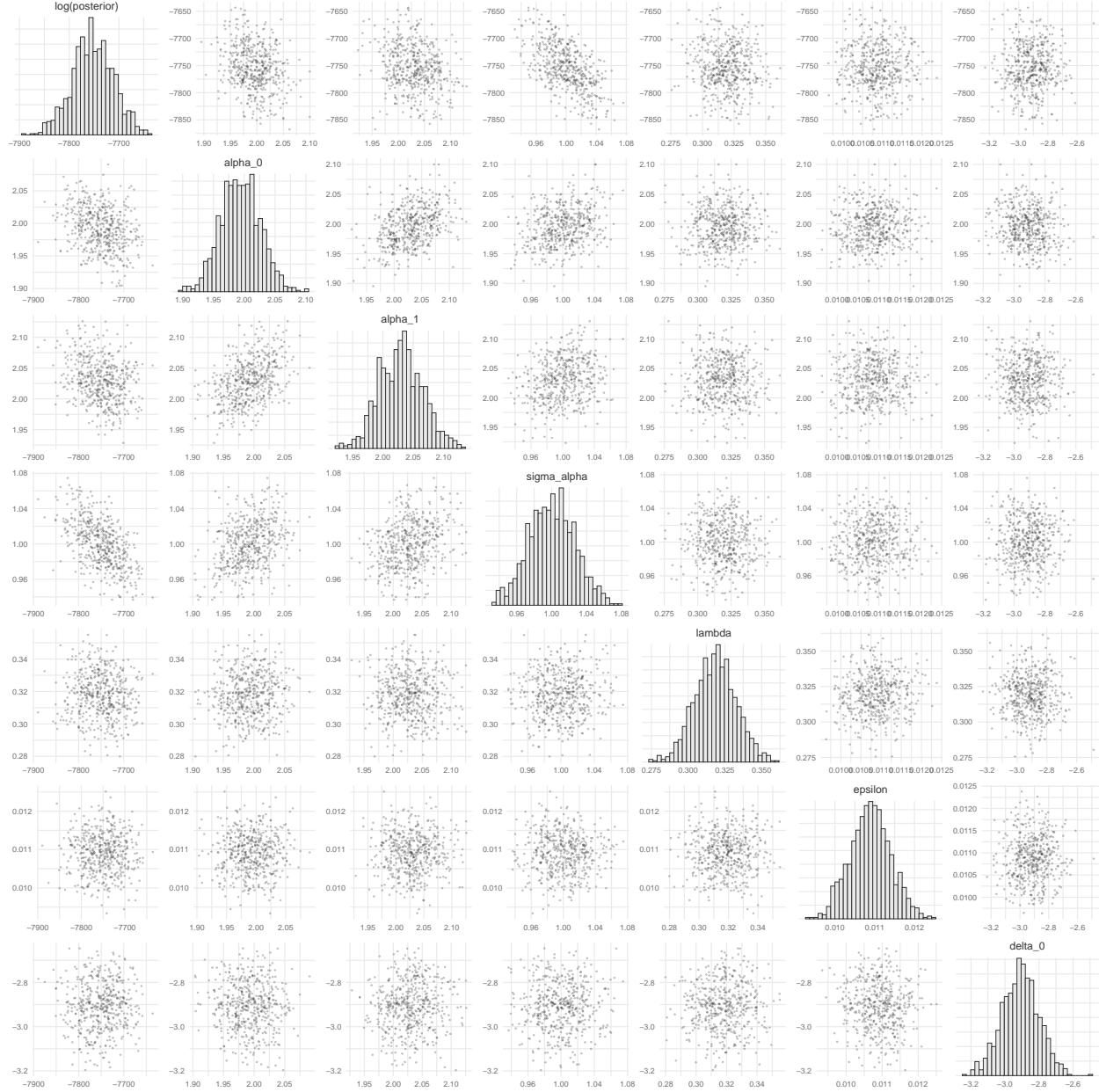


Fig S.D. 5. MCMC pairs plots for parameters in base model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows trace.
 Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.

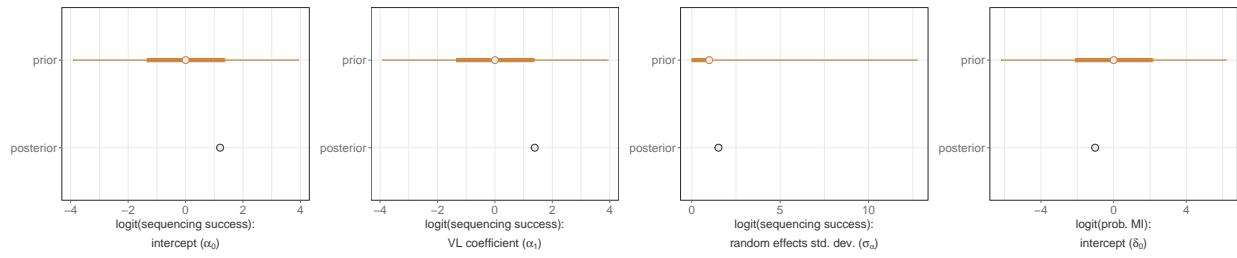


Fig S.D. 6. Comparison of posterior and prior distributions of parameters in base model fit to simulated data with partial sequencing success and false positive or false negative multiple subgraph windows. Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. Some 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.

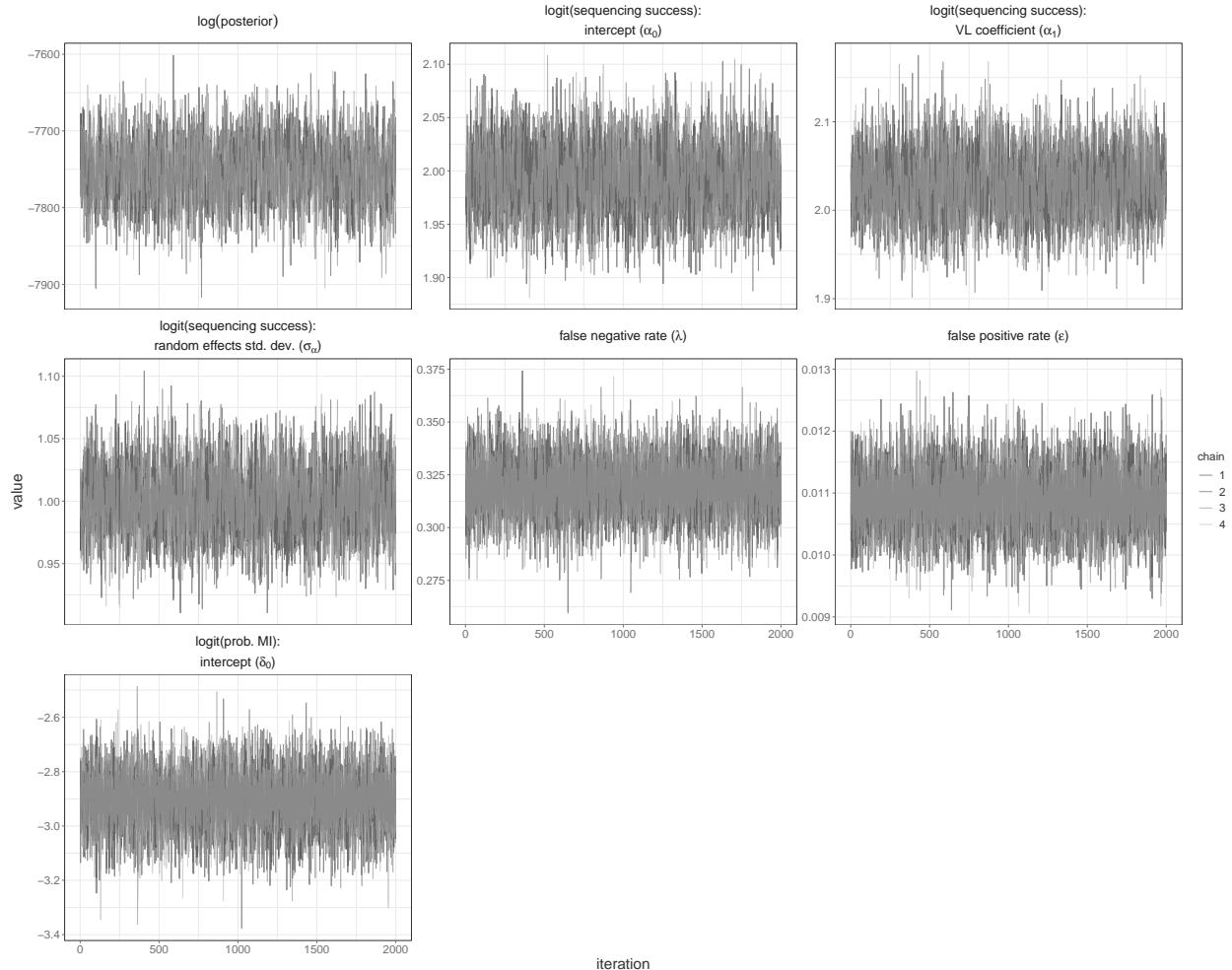


Fig S.D. 7. MCMC trace plots for parameters in full model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

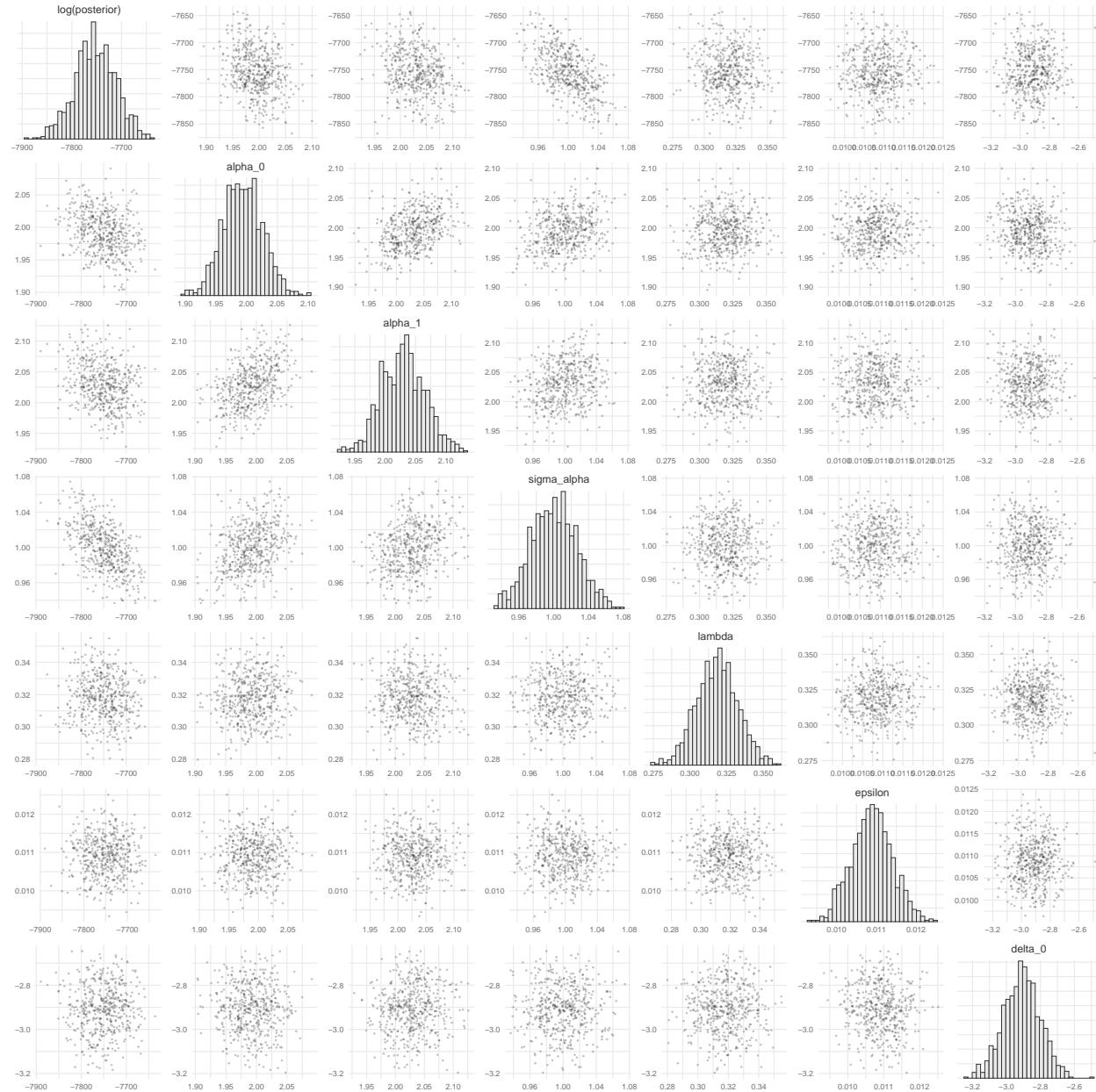


Fig S.D. 8. MCMC pairs plots for parameters in full model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows trace.
Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection.

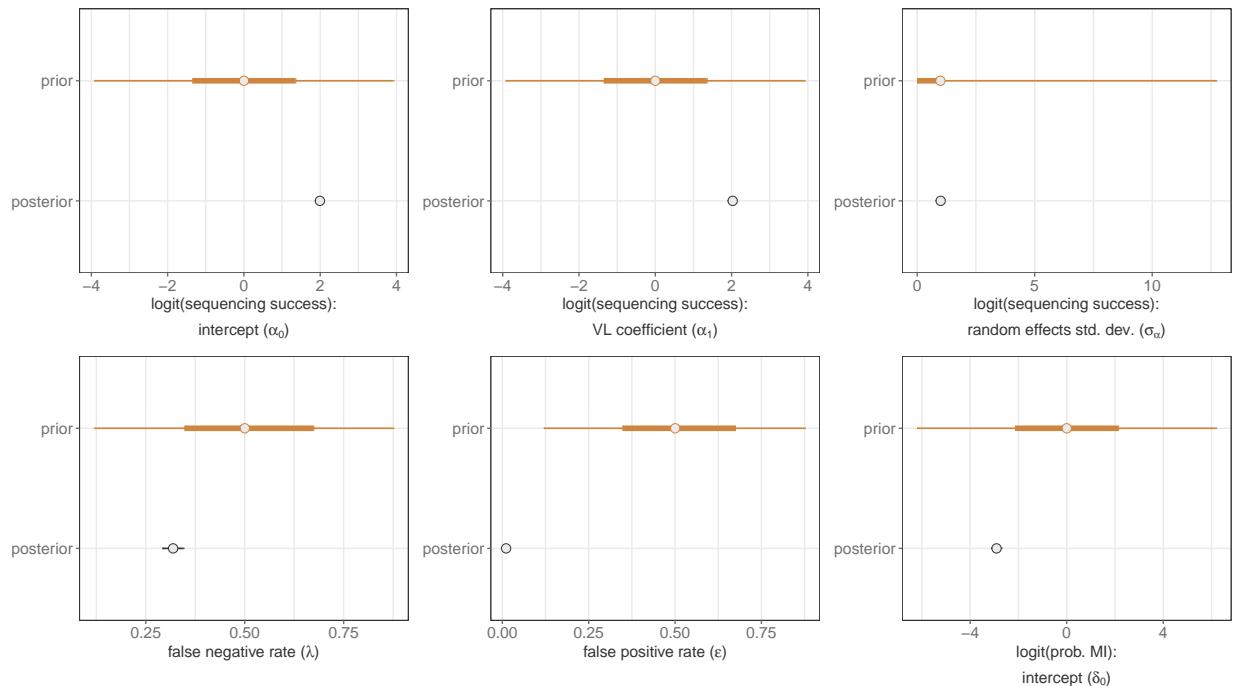


Fig S.D. 9. Comparison of posterior and prior distributions of parameters in full model fit to simulated data with partial sequencing success and false positive or false negative multiple subgraph windows. Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. Some 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.

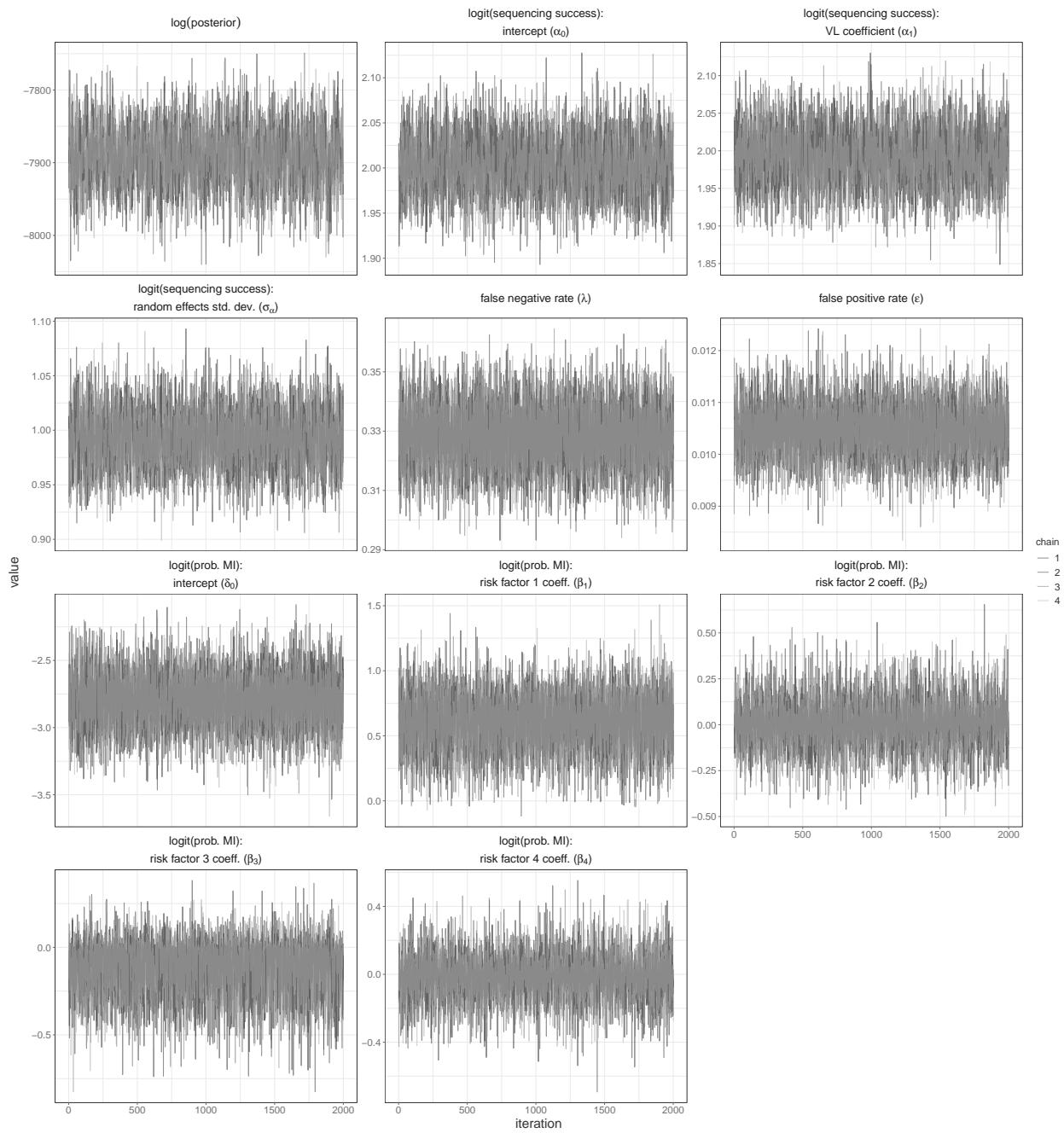


Fig S.D. 10. MCMC trace plots for parameters in extended model fit to simulated data with partial sequencing success, false positive and false negative multiple subgraph windows, and a binary risk factor for harboring multiple infection. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

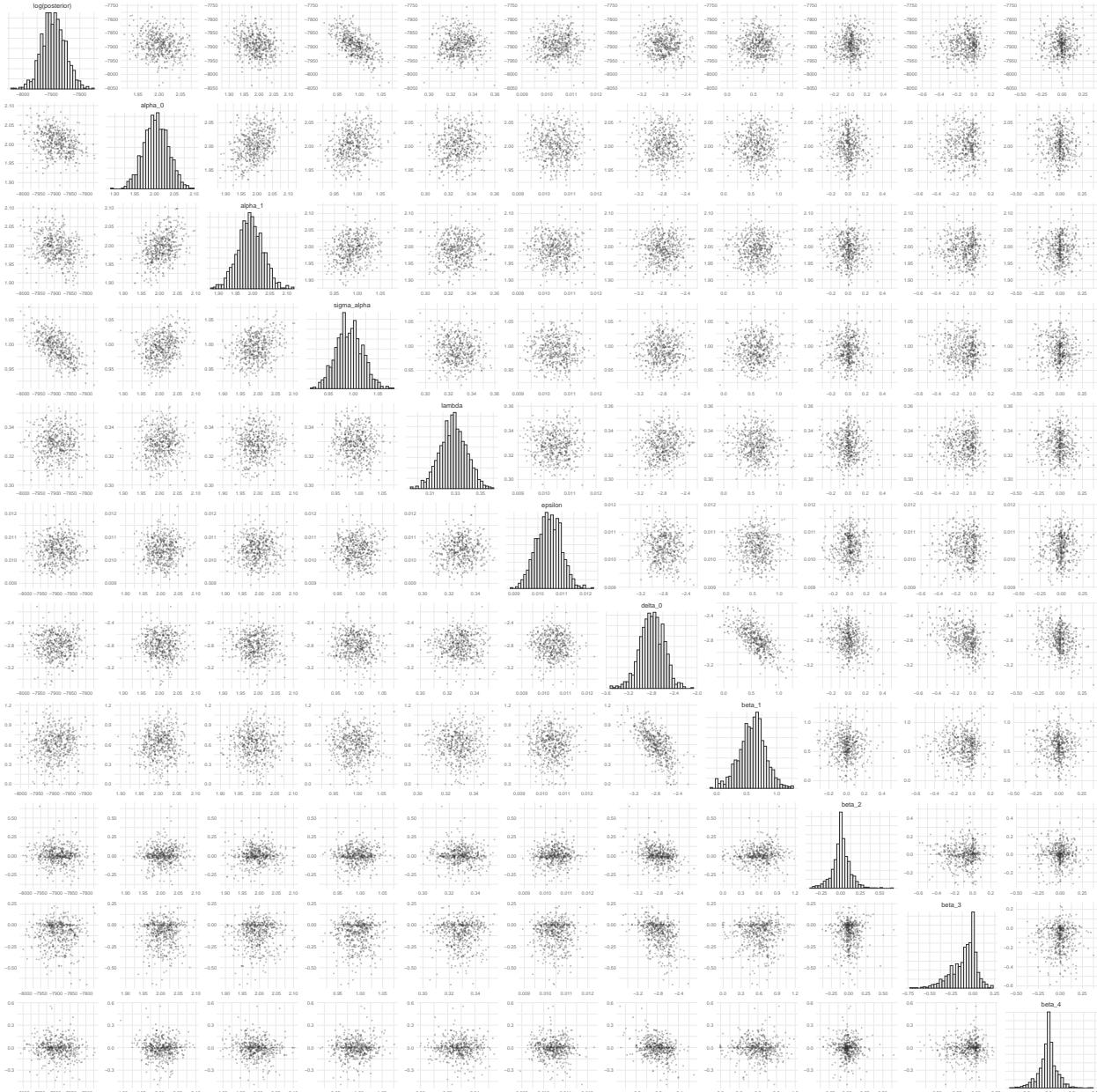


Fig S.D. 11. MCMC pairs plots for parameters in extended model fit to simulated data with partial sequencing success, false positive and false negative multiple subgraph windows, and a binary risk factor for harboring multiple infection. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.

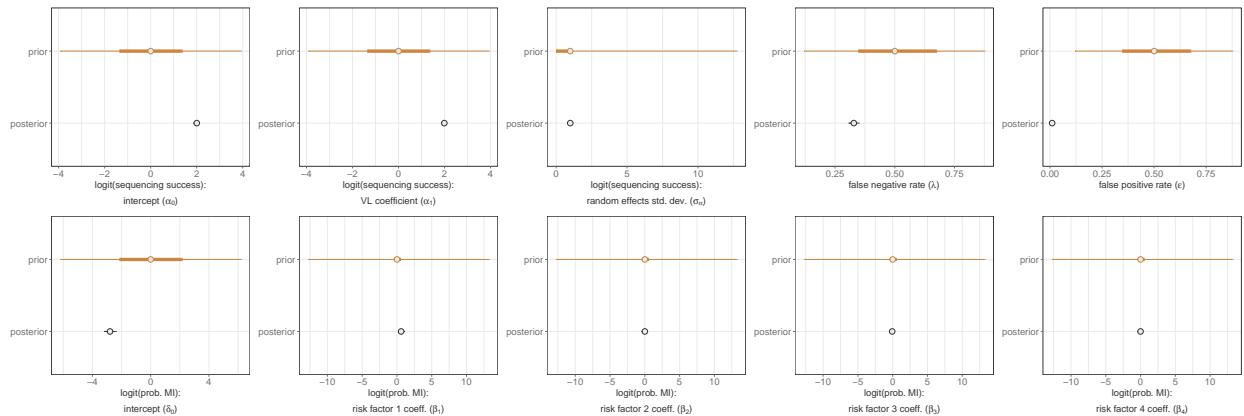


Fig S.D. 12. Comparison of posterior and prior distributions of parameters in full model fit to simulated data with partial sequencing success, false positive or false negative multiple subgraph windows, and a binary risk factor for harboring multiple infection. Median is plotted as the central estimate 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.

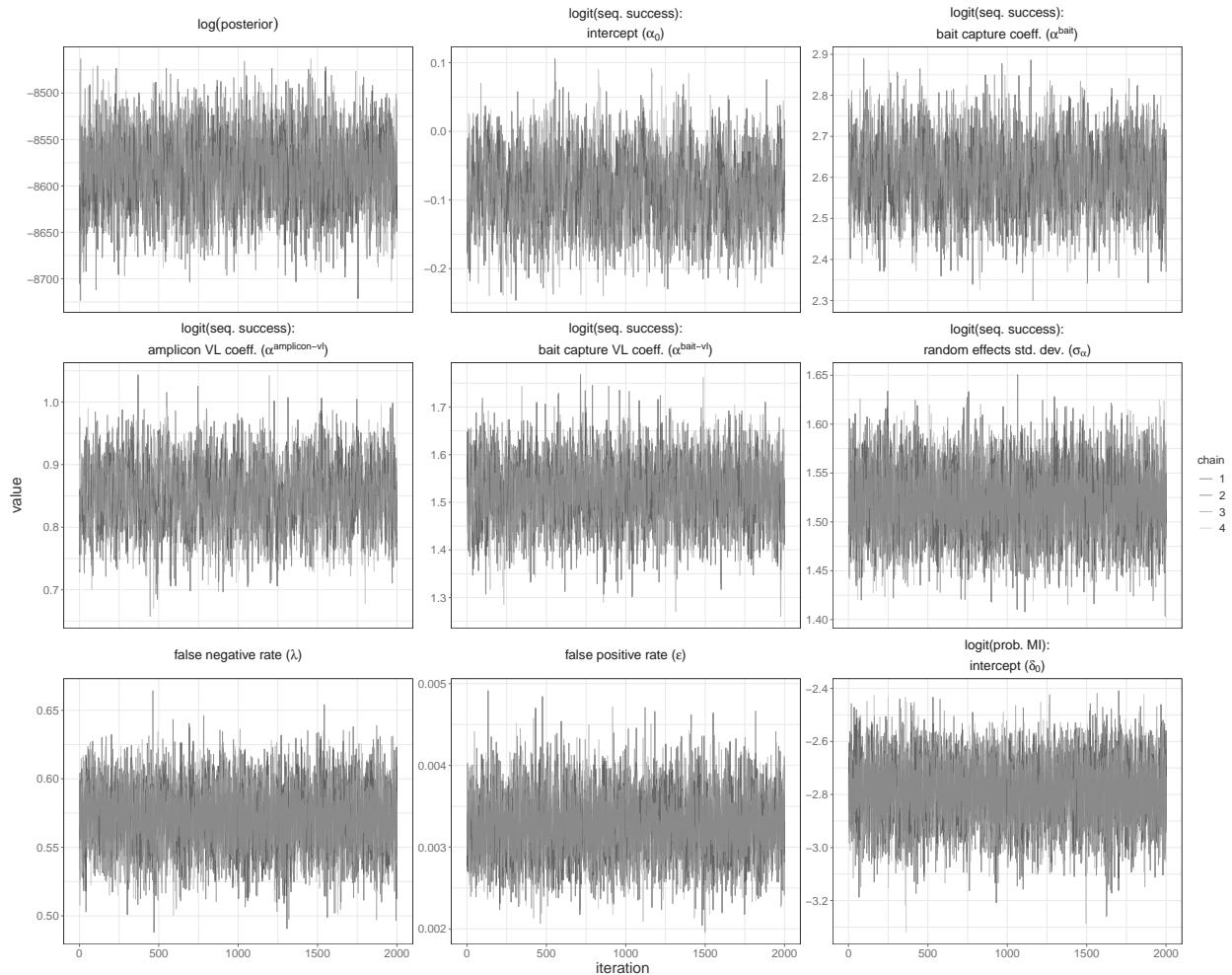


Fig S.D. 13. MCMC trace plots for parameters in full model fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

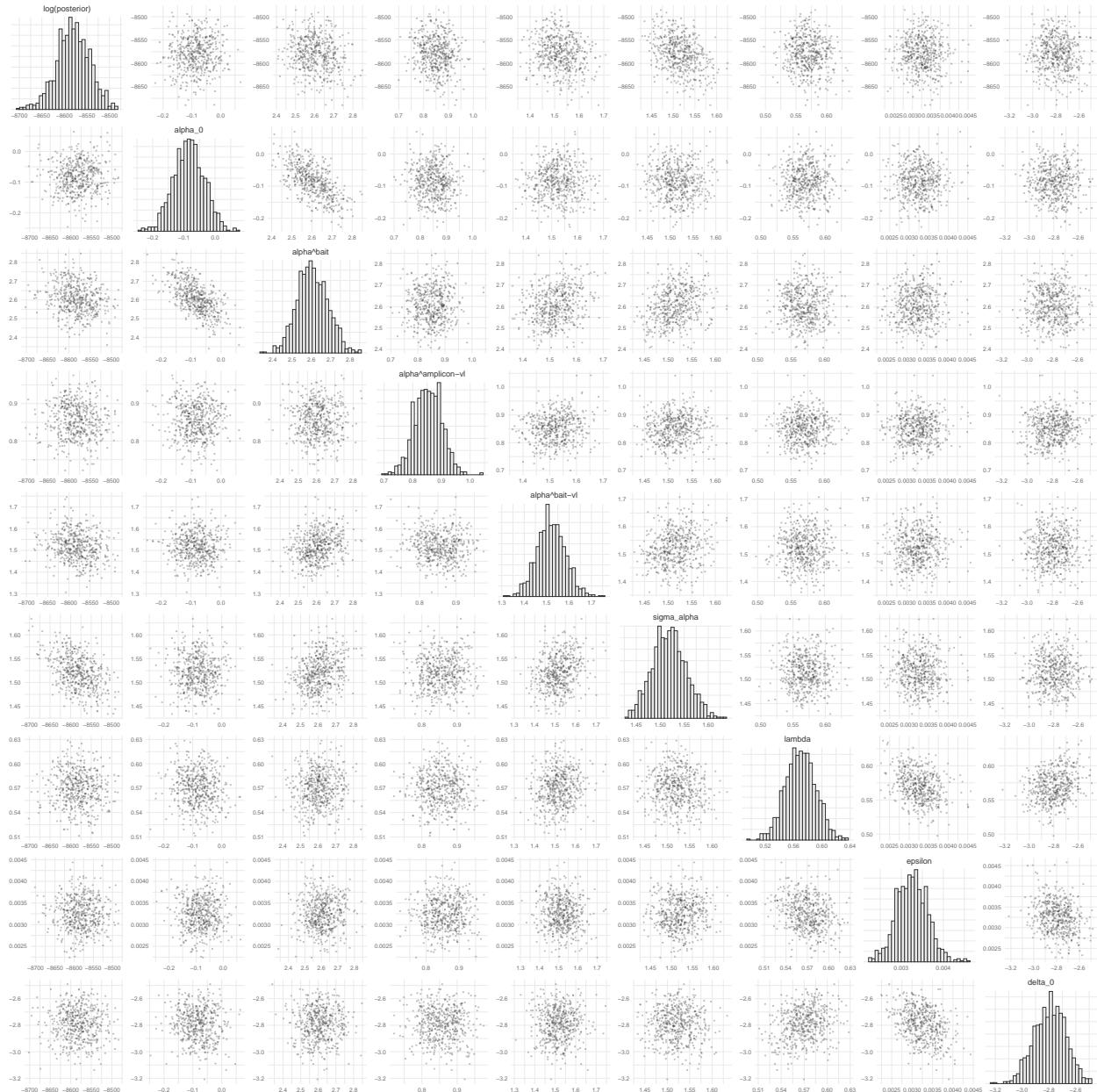


Fig S.D. 14. MCMC pairs plots for parameters in full model fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.

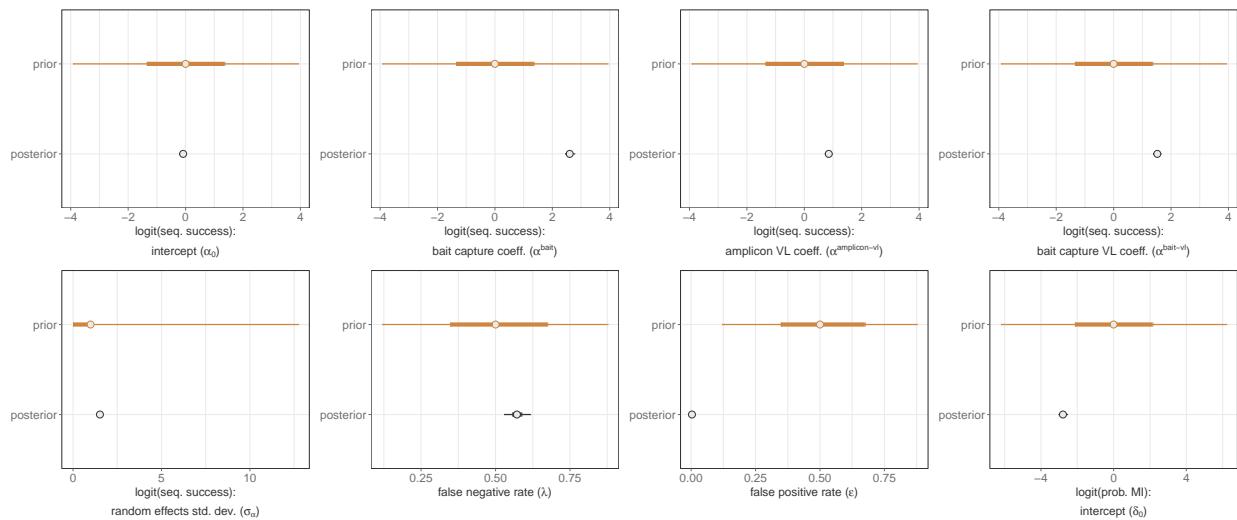


Fig S.D. 15. Comparison of posterior and prior distributions of parameters in full model fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. Some 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.

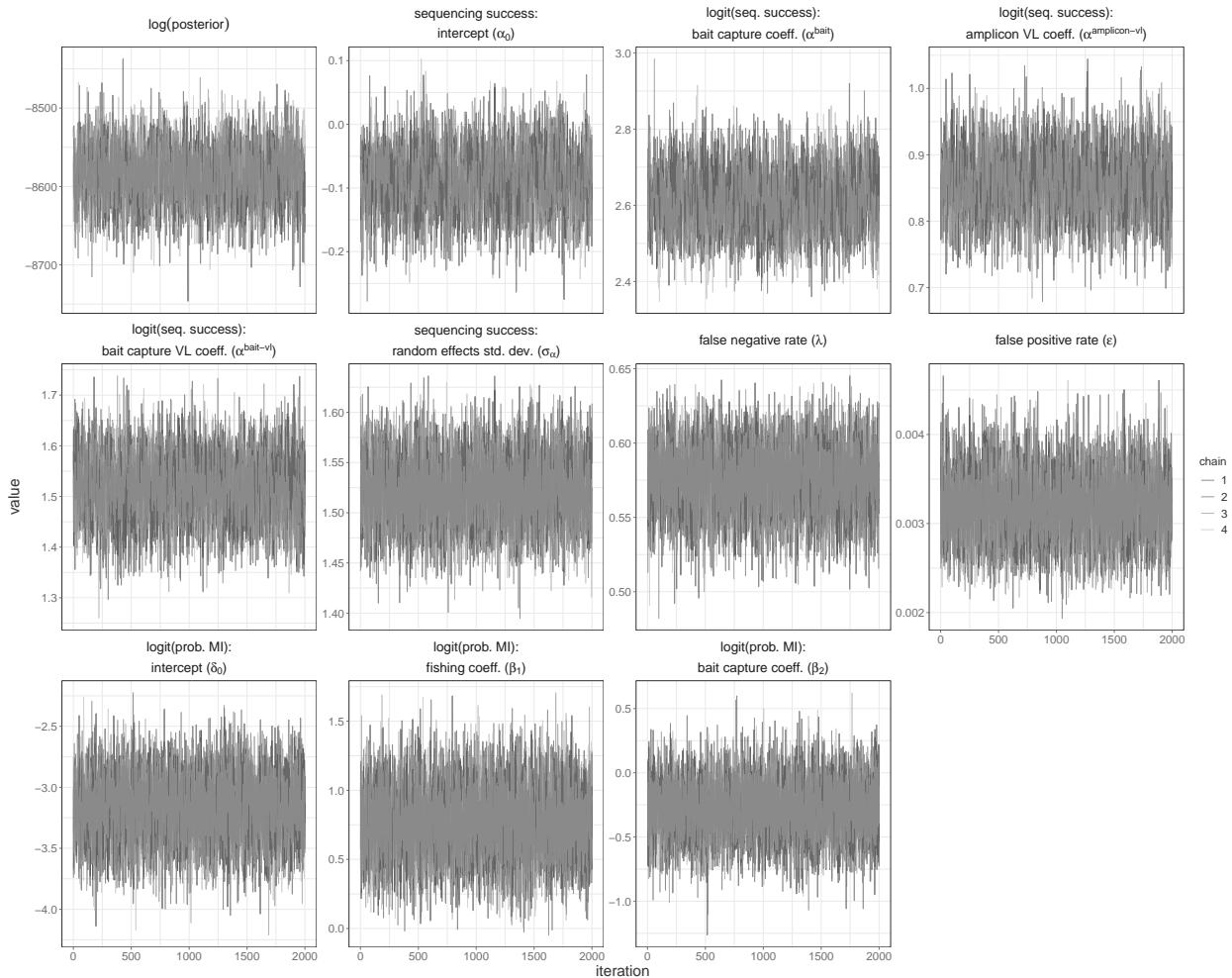


Fig S.D. 16. MCMC trace plots for parameters in extended model with community type and sequencing technology as a risk factor fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

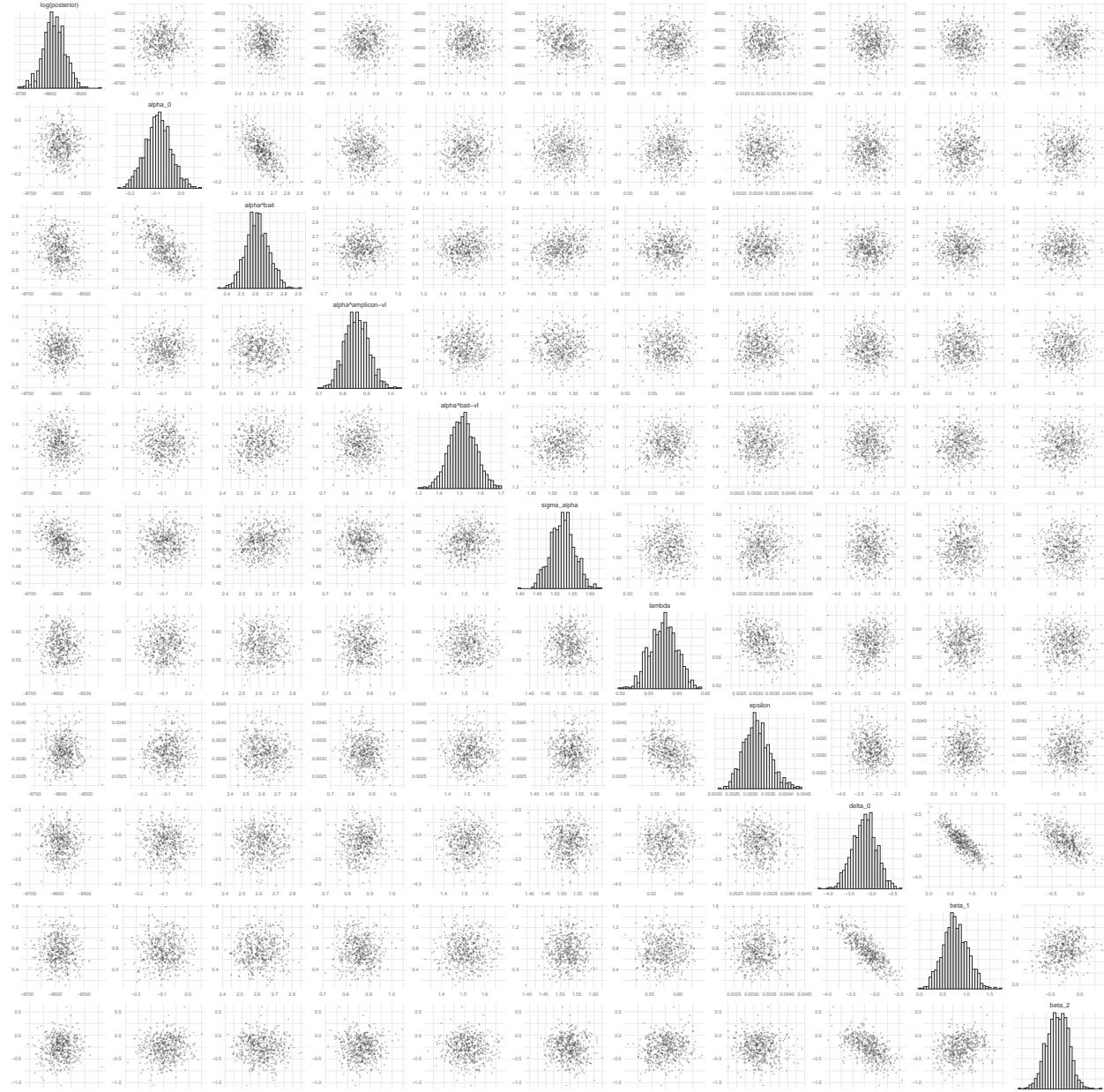


Fig S.D. 17. MCMC pairs plots for parameters in extended model with community type and sequencing technology as a risk factor fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.

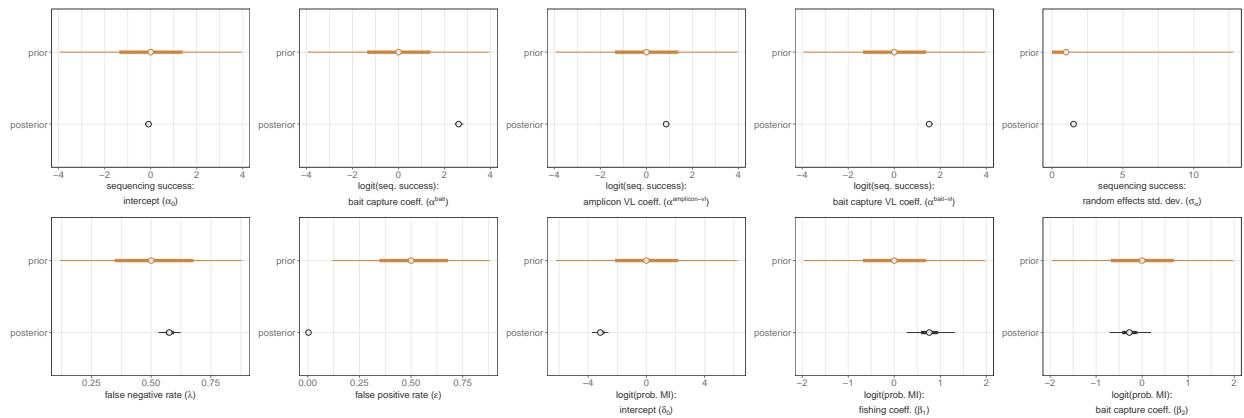


Fig S.D. 18. Comparison of posterior and prior distributions of parameters in extended model with community type and sequencing technology as a risk factor fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Median is plotted as the central 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.

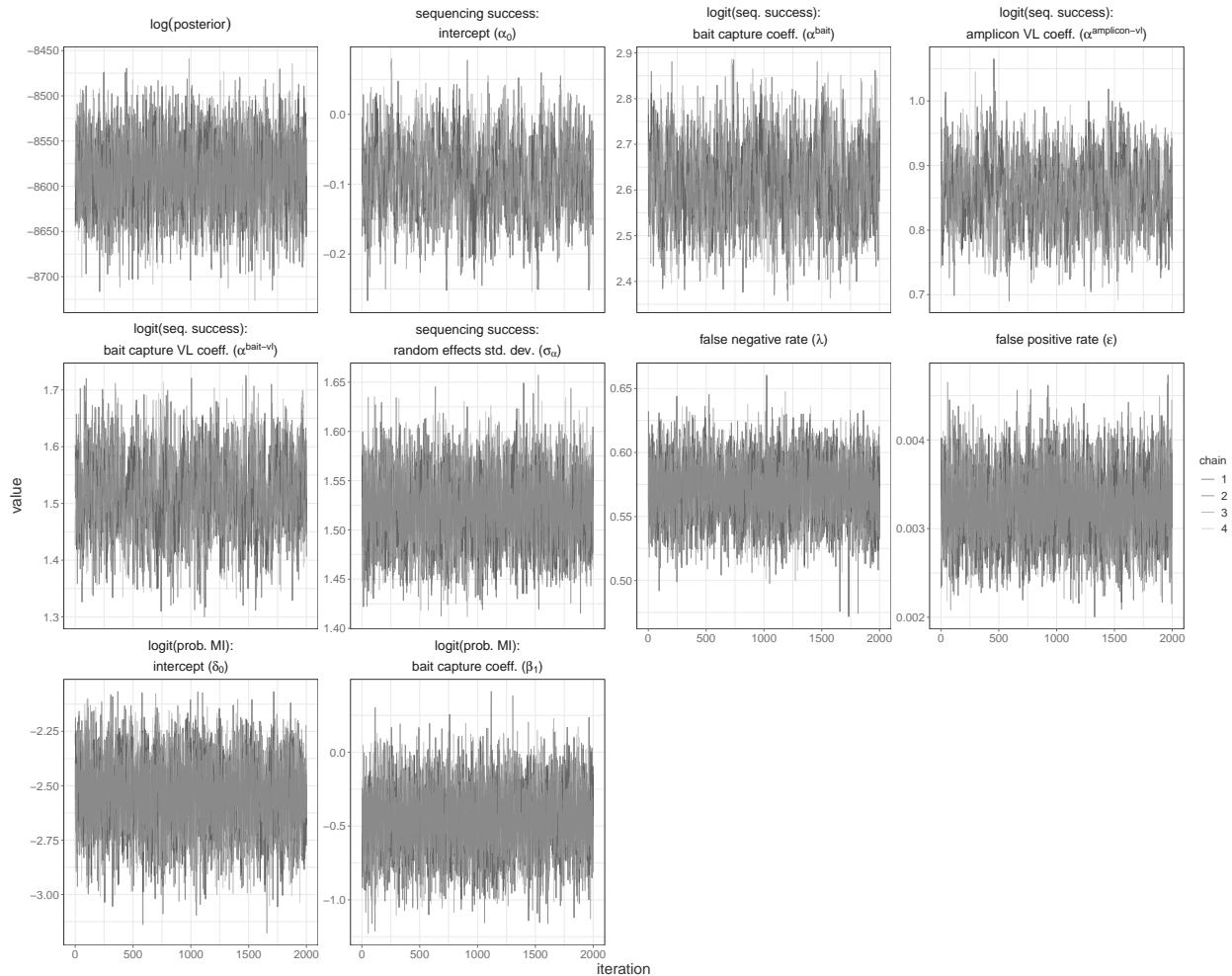


Fig S.D. 19. MCMC trace plots for parameters in extended model with deep-sequencing protocol as a risk factor fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

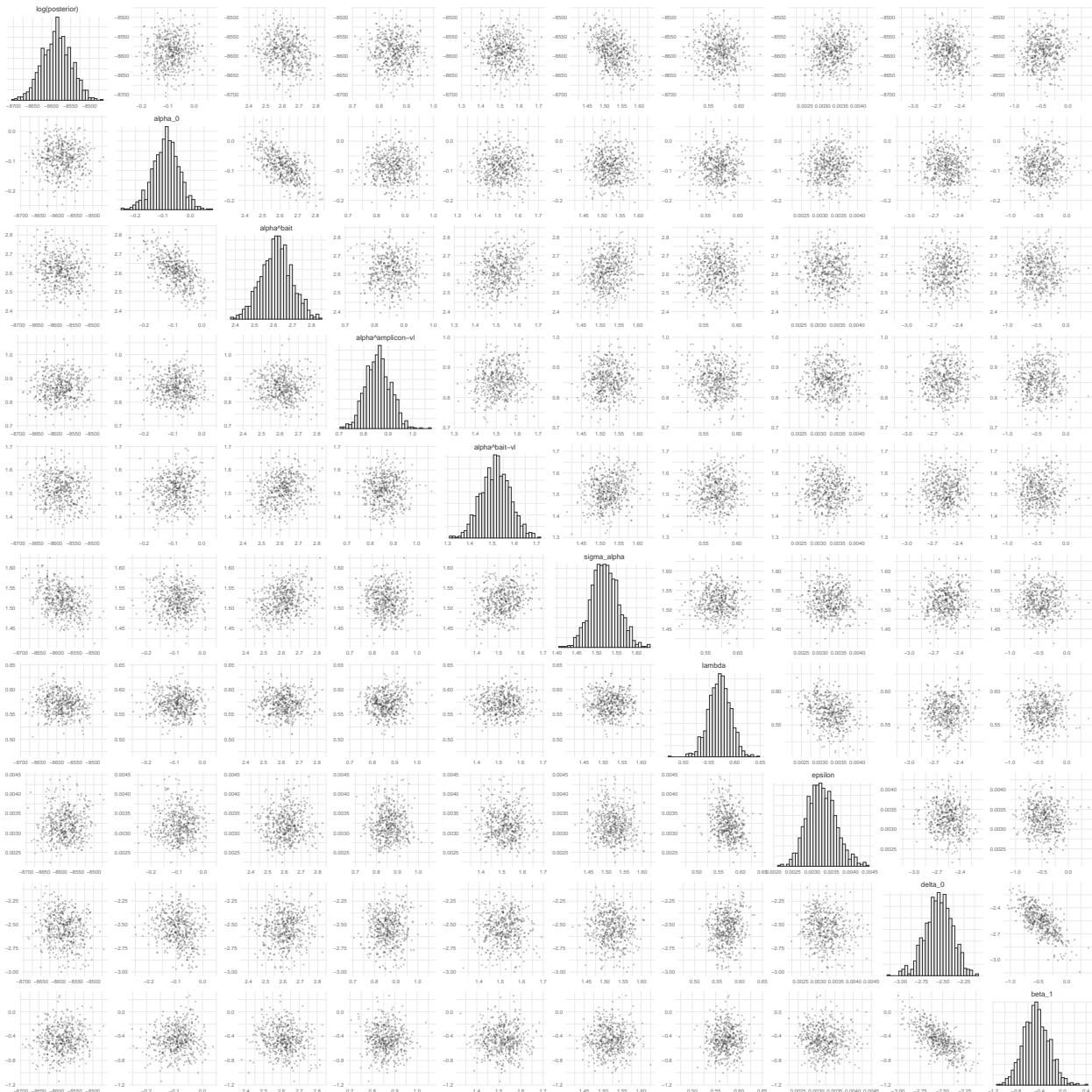


Fig S.D. 20. MCMC pairs plots for parameters in extended model with deep-sequencing protocol as a risk factor fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.

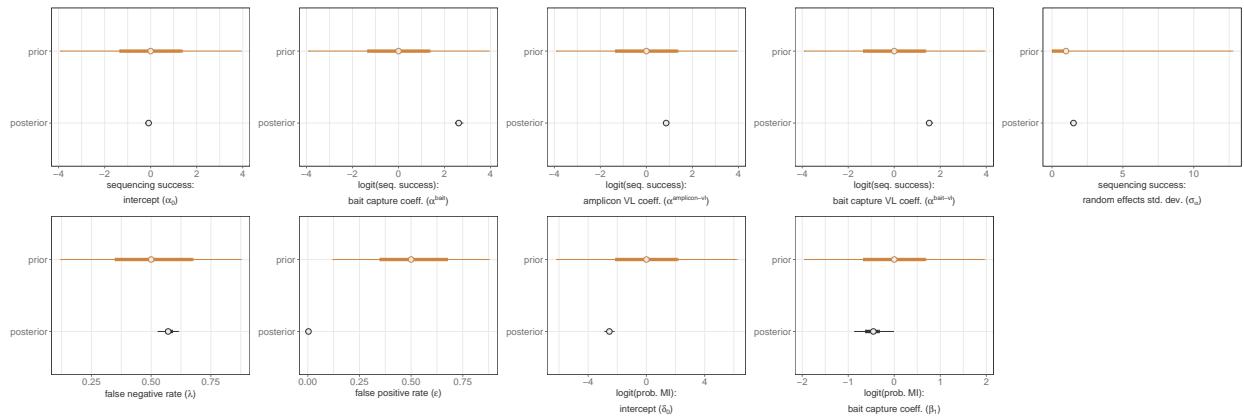


Fig S.D. 21. Comparison of posterior and prior distributions of parameters in extended model with sequencing technology as a risk factor fit to deep sequence data generated from 2,029 Rakai Community Cohort Study participants living with viremic HIV. Median is plotted as the central estimate and horizontal 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.

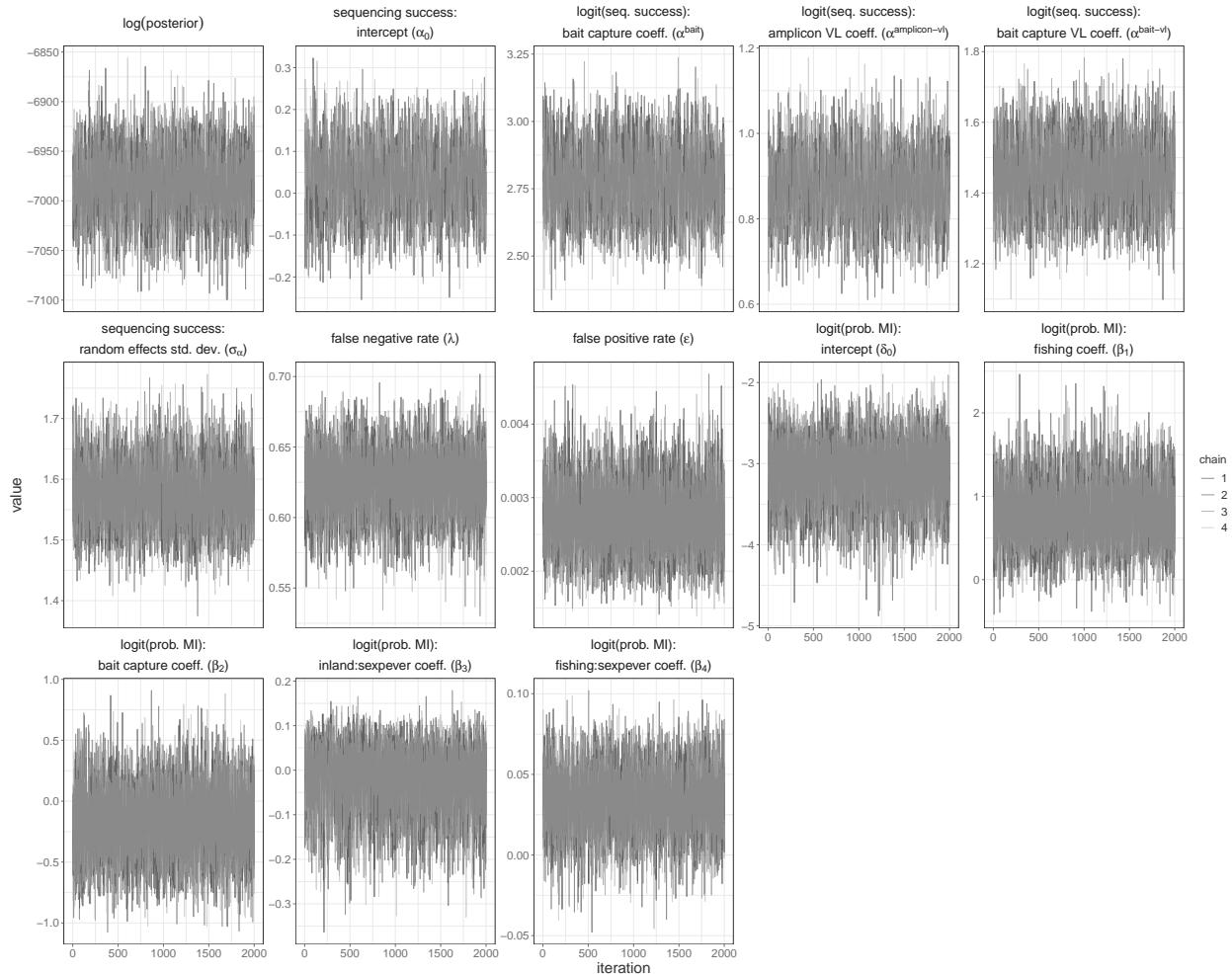


Fig S.D. 22. MCMC trace plots for parameters in extended model with community type and lifetime sex partners as a risk factor for harboring multiple infections fit to deep sequence data generated from 997 men living with viremic HIV who participated in the Rakai Community Cohort Study. Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (\log_{10} copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.

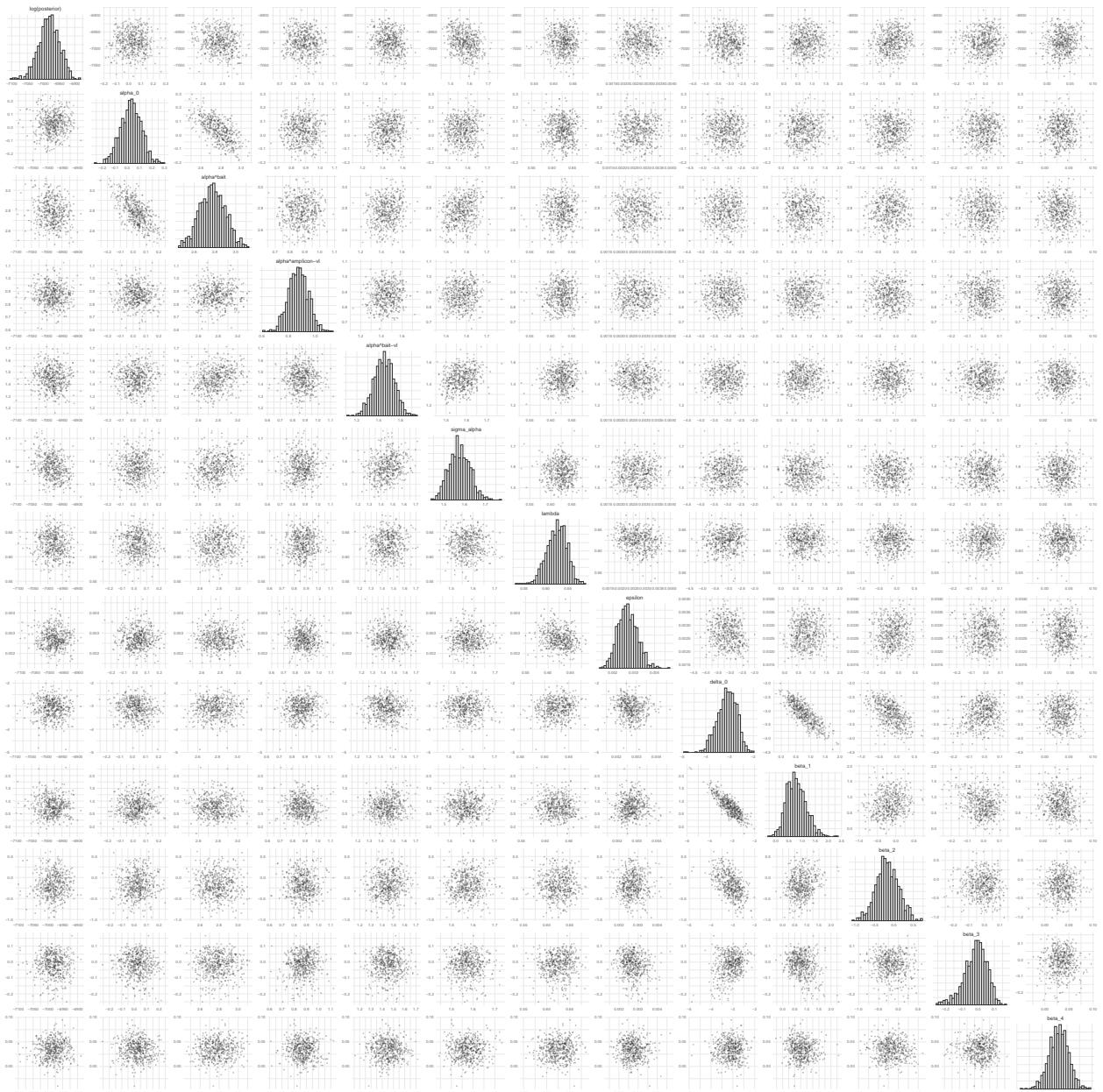


Fig S.D. 23. MCMC pairs plots for parameters in extended model with community type and lifetime sex partners as a risk factor for harboring multiple infections fit to deep sequence data generated from 997 men living with viremic HIV who participated in the Rakai Community Cohort Study. Independent chains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

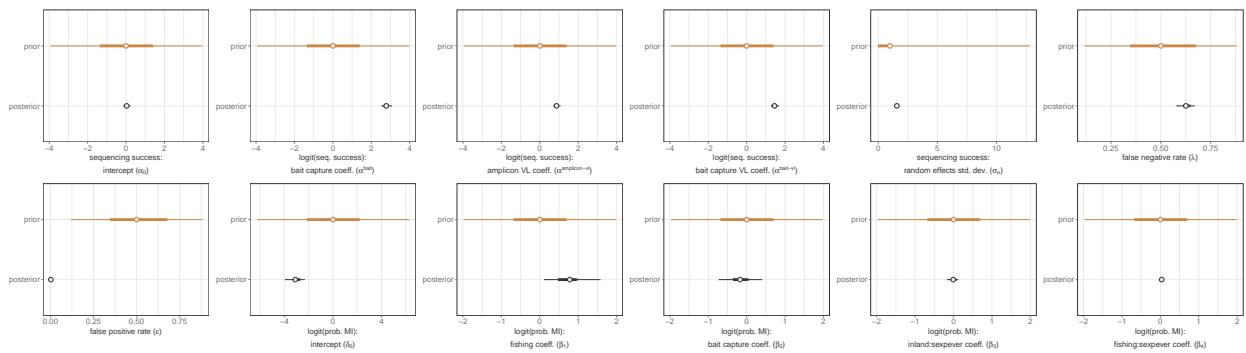


Fig S.D. 24. Comparison of posterior and prior distributions of parameters in extended model with sequencing technology as a risk factor fit to deep sequence data generated from 997 Rakai Community Cohort Study participants living with viremic HIV. Median is plotted as the central estimate and horizontal 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.

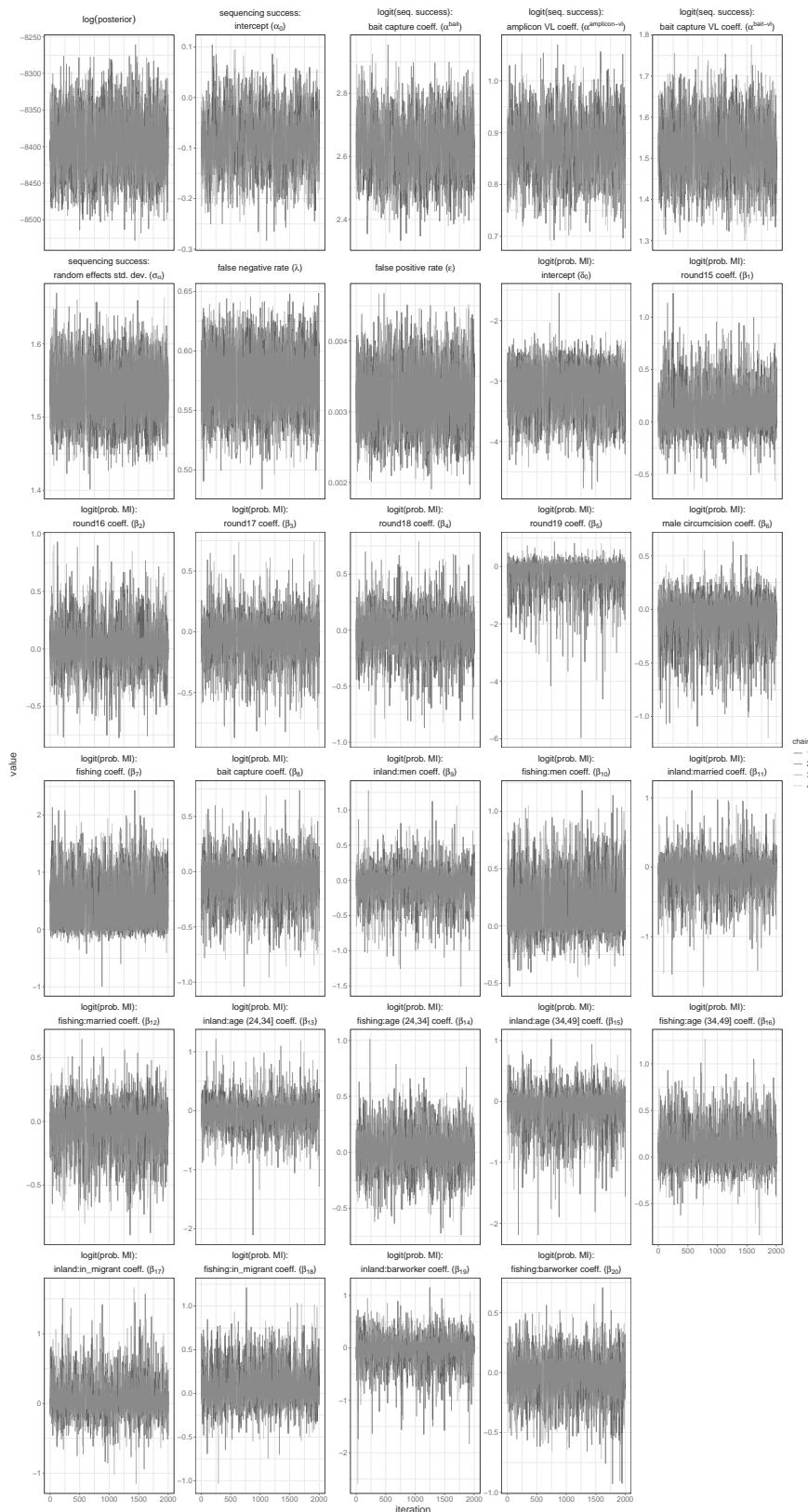


Fig S.D. 25. MCMC trace plots for parameters in extended model with variable selection to identify risk factor for harboring multiple infections fit to deep sequence data generated from 1,970 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of 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.

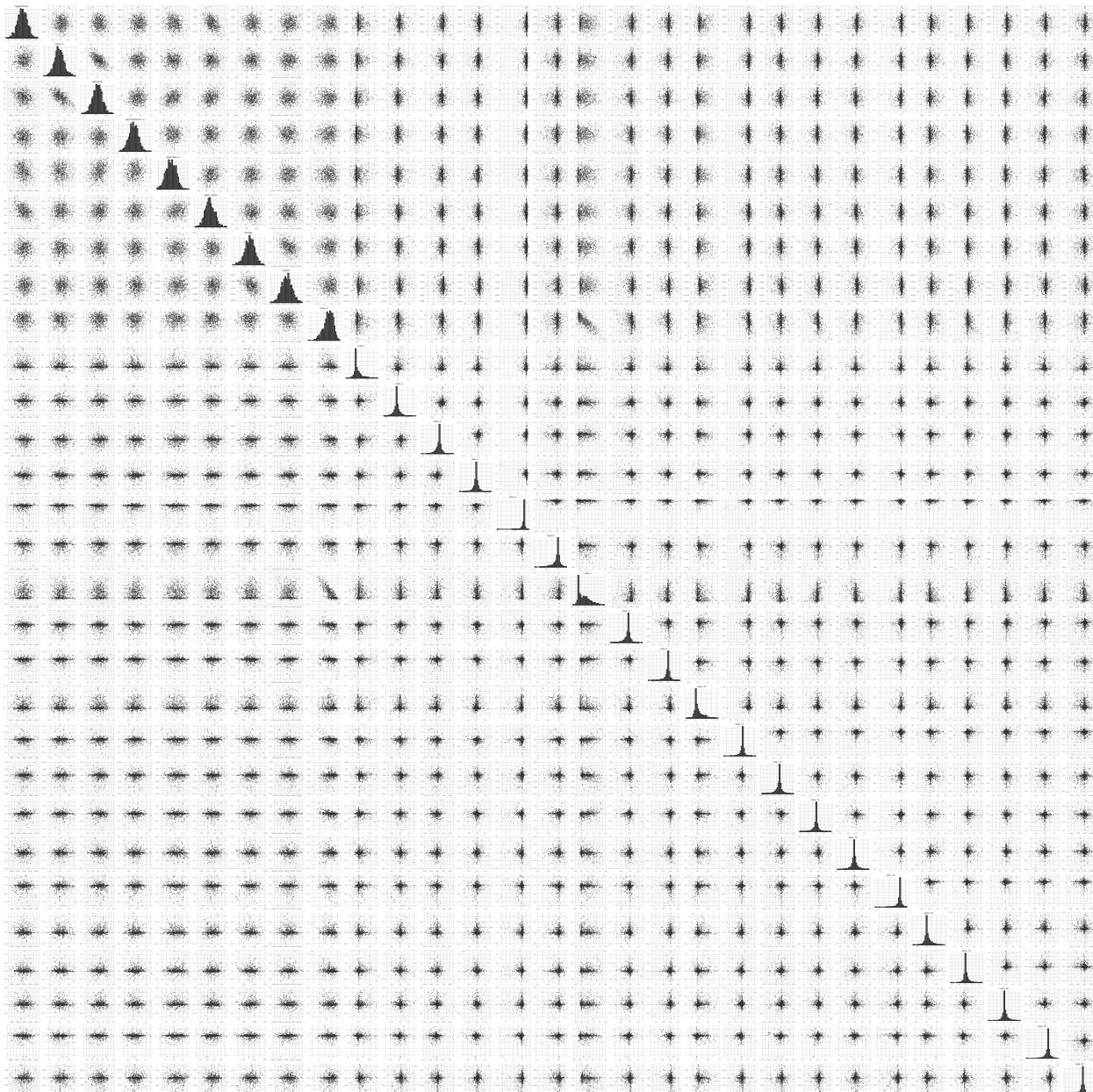


Fig S.D. 26. MCMC pairs plots for parameters in extended model with variable selection to identify risk factor for harboring multiple infections fit to deep sequence data generated from 1,970 Rakai Community Cohort Study participants living with viremic HIV. Independent chains are shown in shades of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

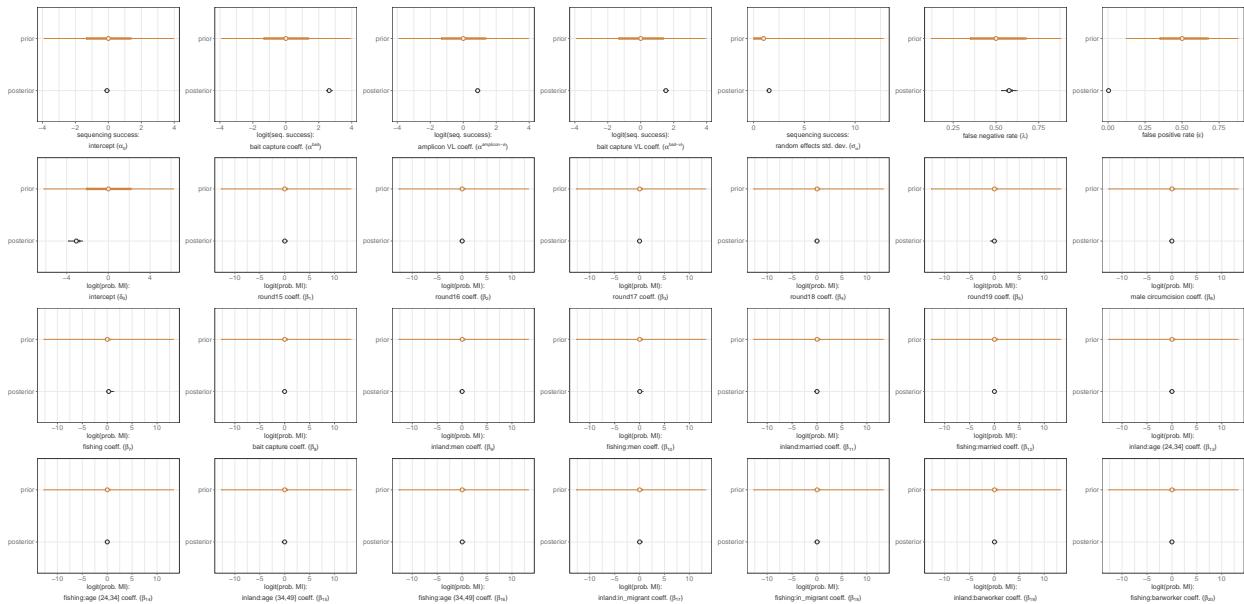


Fig S.D. 27. Comparison of posterior and prior distributions of parameters in extended model with variable selection to identify risk factor fit to deep sequence data generated from 1,970 Rakai Community Cohort Study participants living with viremic HIV. Median is plotted as the central estimate and 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.