

Supplementary Material: Evaluation of Changes to the Oral Microbiome Based on 16S rRNA Sequencing among Children Treated for Cancer

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Table S1. Detailed cancer status in the study group.

| ID | sex | diagnosis | treatment regimen | age at diagnosis (years) | age at the end of the therapy (years) | length of therapy (months) |
|----------|-----|-------------------------------------|-------------------|--------------------------|---------------------------------------|----------------------------|
| 18. S.N. | 0 | Hodgkin's lymphoma | OEPA | 13.91 | 14.33 | 4 |
| 20. W.K. | 0 | Hodgkin's lymphoma | OEPA | 18.25 | 18.91 | 8 |
| 1. B.B. | 1 | Hodgkin's lymphoma | OEPA | 13.50 | 16.16 | 32 |
| 11. K.N. | 0 | Hodgkin's lymphoma | OEPA | 15.25 | 17.66 | 29 |
| 5. D.M. | 0 | medulloblastoma | I prot CZD | 5.83 | 7.41 | 19 |
| 14. L.K. | 1 | Ependimoma | VI prot CZD | 8.00 | 9.25 | 15 |
| 3. D.B. | 1 | Germinoma | V prot CZD | 16.00 | 16.41 | 5 |
| 10. K.M. | 1 | Germinoma | V prot CZD | 12.50 | 12.91 | 4 |
| 19. T.K. | 1 | Rhabdomyosarcoma | CWS | 16.16 | 16.75 | 7 |
| 9. K.A. | 1 | Rhabdomyosarcoma | CWS | 6.75 | 7.83 | 13 |
| 8. K.D. | 1 | non-Hodgkin's lymphoma | B-NHL 13 | 17.91 | 18.16 | 3 |
| 16. S.M. | 1 | non-Hodgkin's lymphoma | B-NHL 13 | 7.25 | 9.33 | 24 |
| 4. D.D. | 1 | acute B-cell lymphoblastic leukemia | B-NHL 13 | 13.66 | 14.08 | 4 |
| 6.F.M | 1 | non-Hodgkin's lymphoma | T-NHL | 14.00 | 16.08 | 24 |
| 2. C.G. | 0 | neuroblastoma | COJEC/PACE | 6.58 | 9.33 | 32 |
| 13. K.N. | 0 | acute myeloid leukemia | ANLL 02 | 13.58 | 15.08 | 17 |
| 15. R.I. | 1 | acute lymphoblastic leukemia | ALLIC | 16.41 | 16.83 | 5 |
| 17. S.N. | 1 | chronic myelogenous leukemia | CML | 14.50 | 17.91 | 40 |
| 12. K.J. | 1 | tumour of testis | TGM 95 | 17.66 | 17.91 | 3 |
| 7.J.W | 0 | ovarian tumour | TGM 95 | 10.25 | 10.91 | 8 |

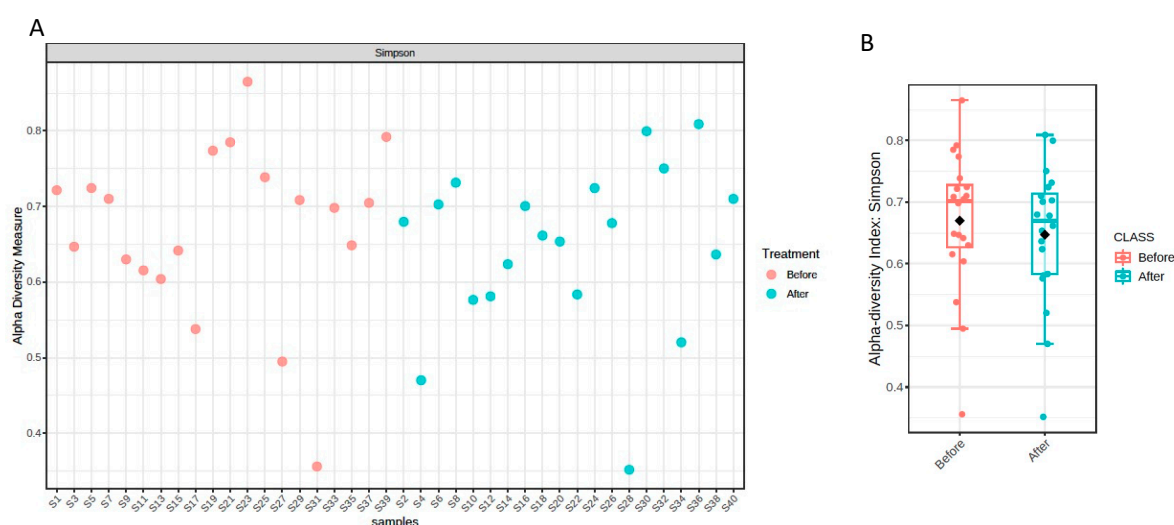
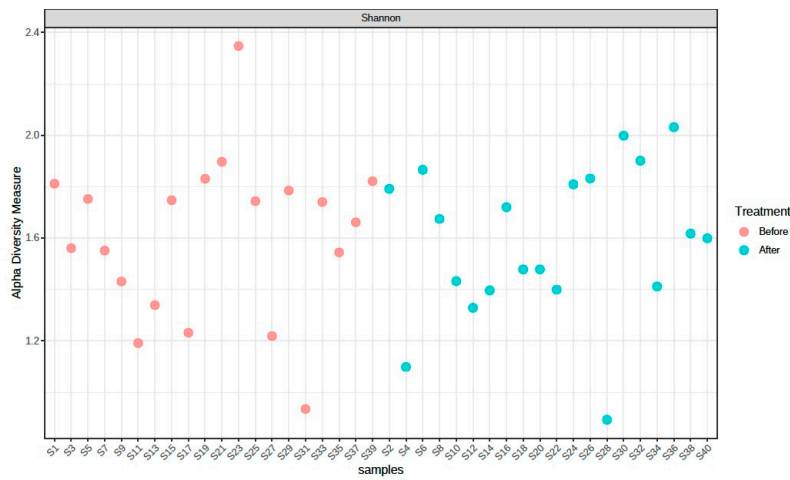


Figure S1. Alpha-diversity measure using Simpson at Genus level across all the samples. A - The samples are represented on X-axis and their estimated diversity on Y-axis, each sample is colored based on Treatment class; B - Box plot presentation, each boxplot represents the diversity distribution of a group present within Treatment class.

A



B

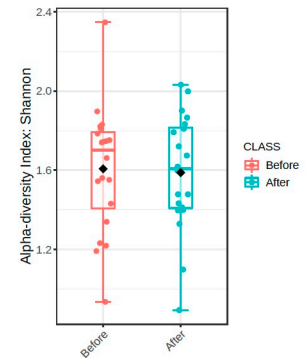


Figure S2. Alpha-diversity measure using Shannon at Genus level across all the samples. A - The samples are represented on X-axis and their estimated diversity on Y-axis, each sample is colored based on Treatment class; B - Box plot presentation, each boxplot represents the diversity distribution of a group present within Treatment class.