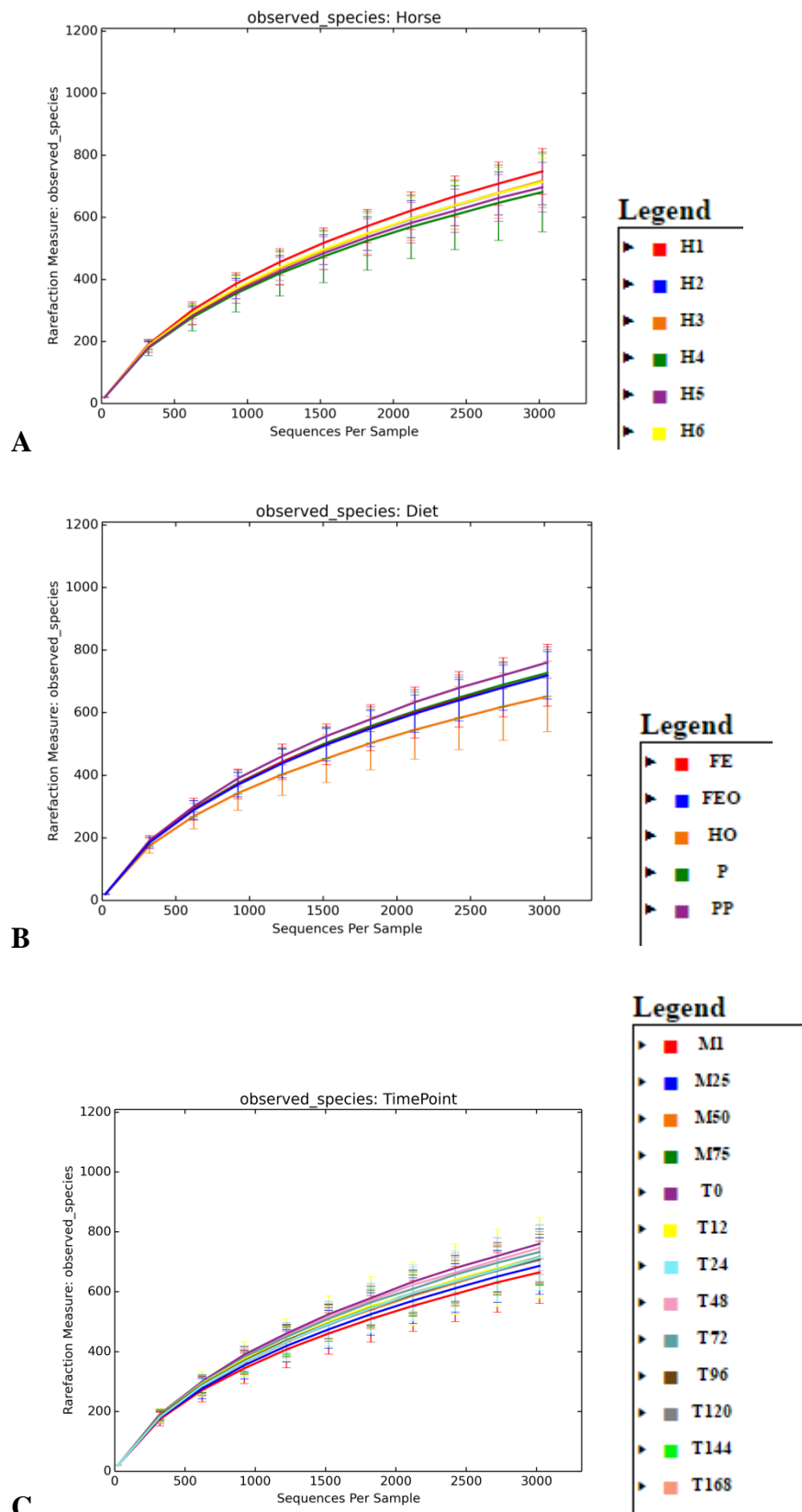**Figure S1. Rarefaction curves of the number of observed species presented by horse, diet and time points.**



A



B



C

Panel A shows the rarefaction curves for the six horses (labelled H1-H6). Panel B shows the rarefaction curves presented by diets. The diets were labelled as PP (grazing on pasture in paddocks on day 0), P (cut pasture fed in stables, representing diet periods P1, P2 and P3 together), FE (chopped ensiled Lucerne and Timothy fed in stables), FE+O (chopped ensiled Lucerne and Timothy fed with whole oats in stables), and H+O (hay fed with whole oats in stables). Panel C shows the rarefaction curves for the time points, labelled as M1 (recovery of 1st marker in the faeces), M25, M50 and M75 (represent timepoints when 25%, 50% and 75% of markers were recoverd in the faeces), T0 (day 0 samples at the beginning of the trail), and T12-168 (represent the timepoints in hours following dietary transition).

**Figure S2. UPGMA dendrogram of bacterial communities (genus-level) in the faecal samples of horses fed pasture (P1, P2, P3) and three conserved forage diets (FE, FE+O, H+O) on days 5, 6 and 7 of the study period.**
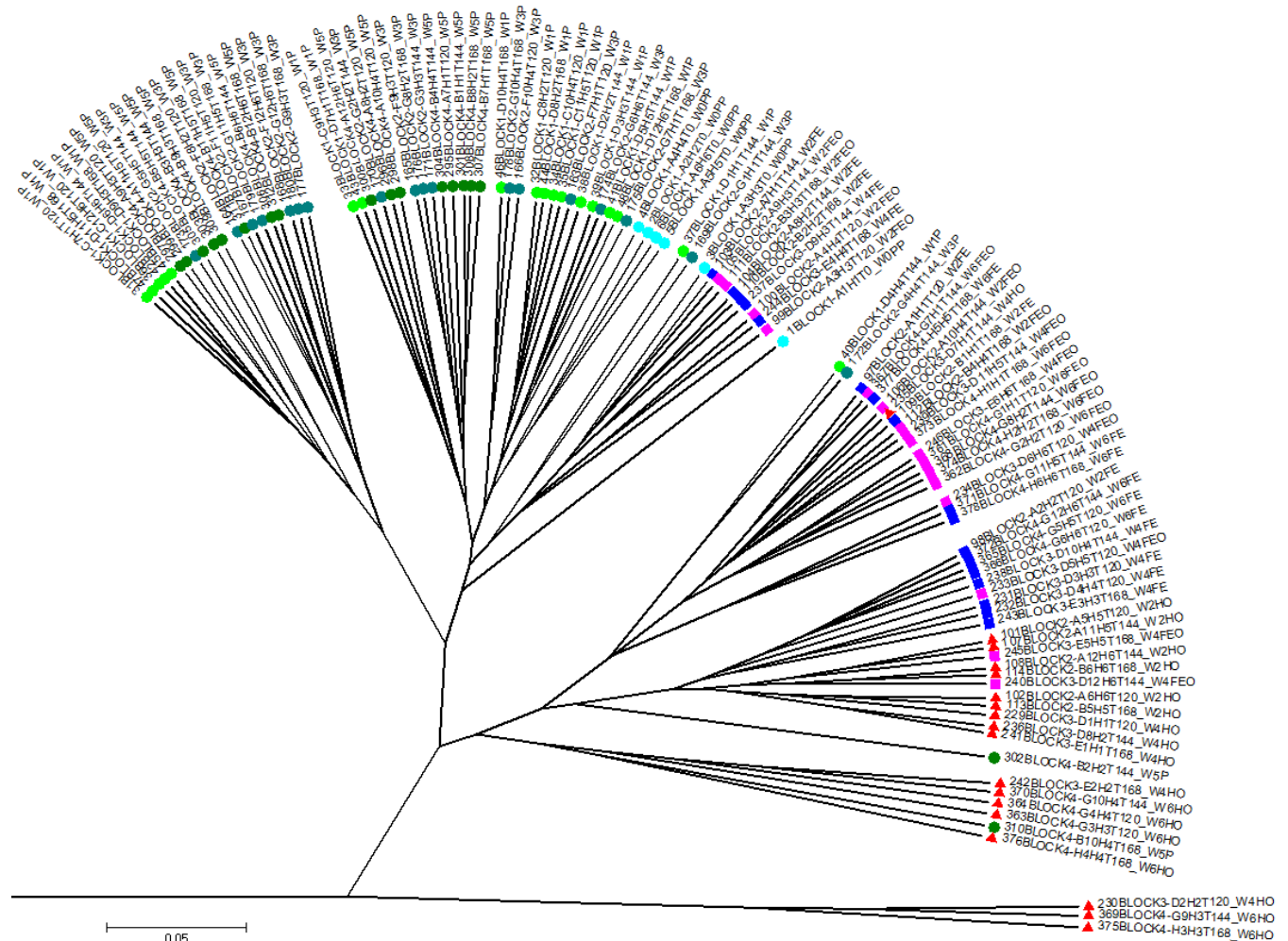


Unweighted pair group method with arithmetic mean (UPGMA) generated using the Bray Curtis dissimilarity metric of bacterial genera in all faecal samples included in the study. Samples collected on days 5, 6 and 7 of each treatment block were included in the analysis (see methods). Samples are colour-coded to visualise clustering by diet. Each sample is labelled using the prototype: Sample-Block-Well-Horse-Timepoint-Week-Diet (e.g. 31BLOCK1-C7H1T120_W1P reads as sample 31, on block 1, well C7, from horse 1, at time point 120 h, in week 1, on pasture diet), with blocks 1-4, wells A-H; horse numbers H1-6; time points T144-168; weeks 1-6. Diets are represented as PP (teal circles; grazing pasture in

paddock), P (light or dark green circles; cut pasture fed in stable), FE (Blue square; chopped ensiled Lucerne and Timothy fed in stable), FEO (Pink square; chopped ensiled Lucerne and Timothy fed with whole oats in stable), HO (red triangle; hay fed with whole oats in stable). The scale bar indicates 0.05 dissimilarity between samples.

**Figure S3. Comparison of the relative abundances of the six dominant faecal bacterial genera from 0 to 168 hours following dietary change.**
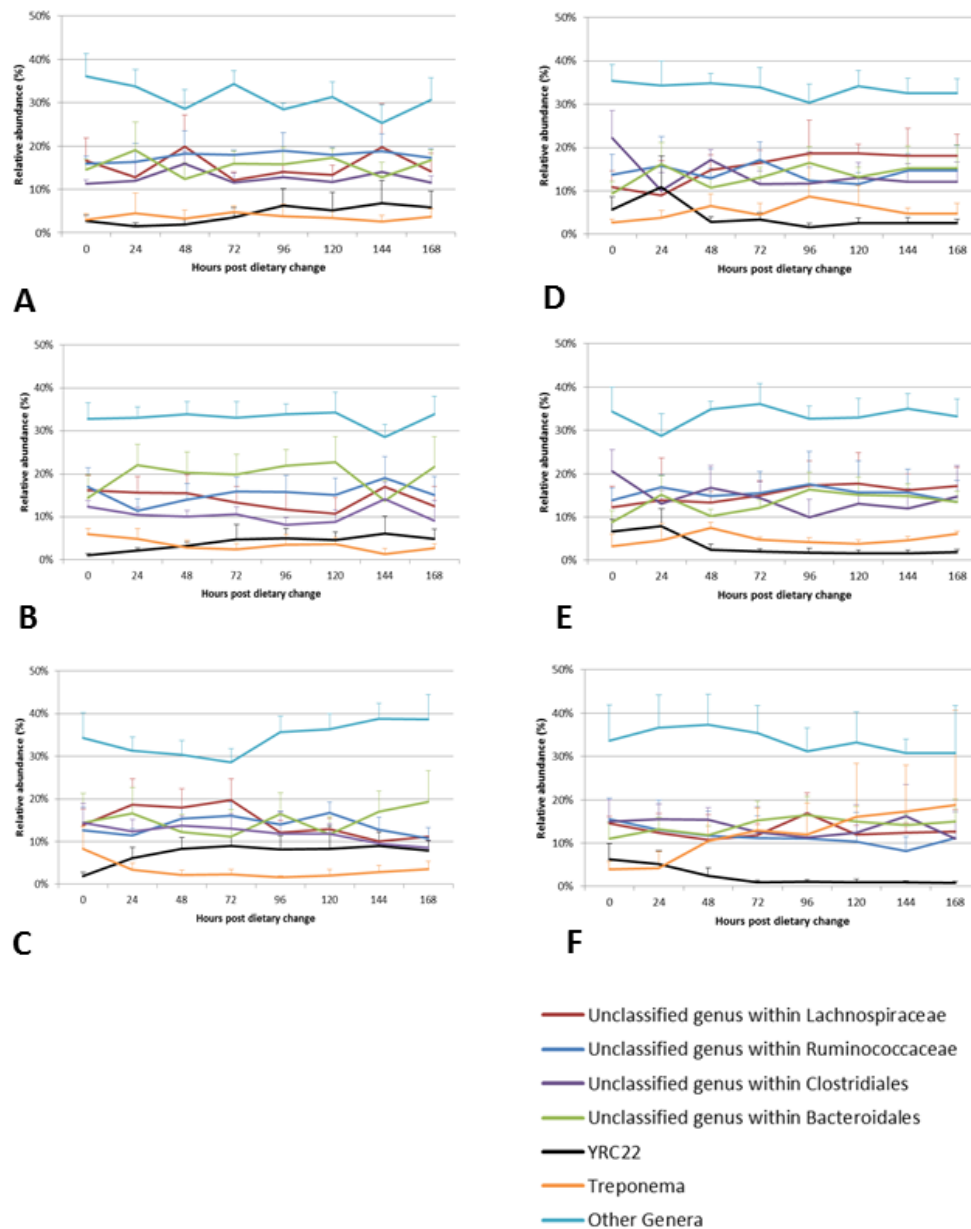


Mean relative abundances of the six most dominant genera that comprise the faecal bacterial community of horses included in the study are shown in the line graphs. Each panel represents a dietary treatment block. Panel A) Diet P1- cut pasture; Panel B) Diet P2 – cut pasture; Panel C) Diet P3 – cut pasture; Panel D) Diet FE - chopped ensiled Lucerne and Timothy; Panel E) Diet FE+O - chopped ensiled Lucerne and Timothy fed with whole oats; Panel F) Diet H+O - hay fed with whole oats. The time points in hours following dietary change are shown on the x-axis of the primary graph in each panel. Error bars represent the standard deviation (only positive shown).

**Figure S4. Comparison of the six most dominant genera with transit time of digesta (T0, M1, M25, M50 and M75) in horses (n=6) across the forage-based diets included in the study.**
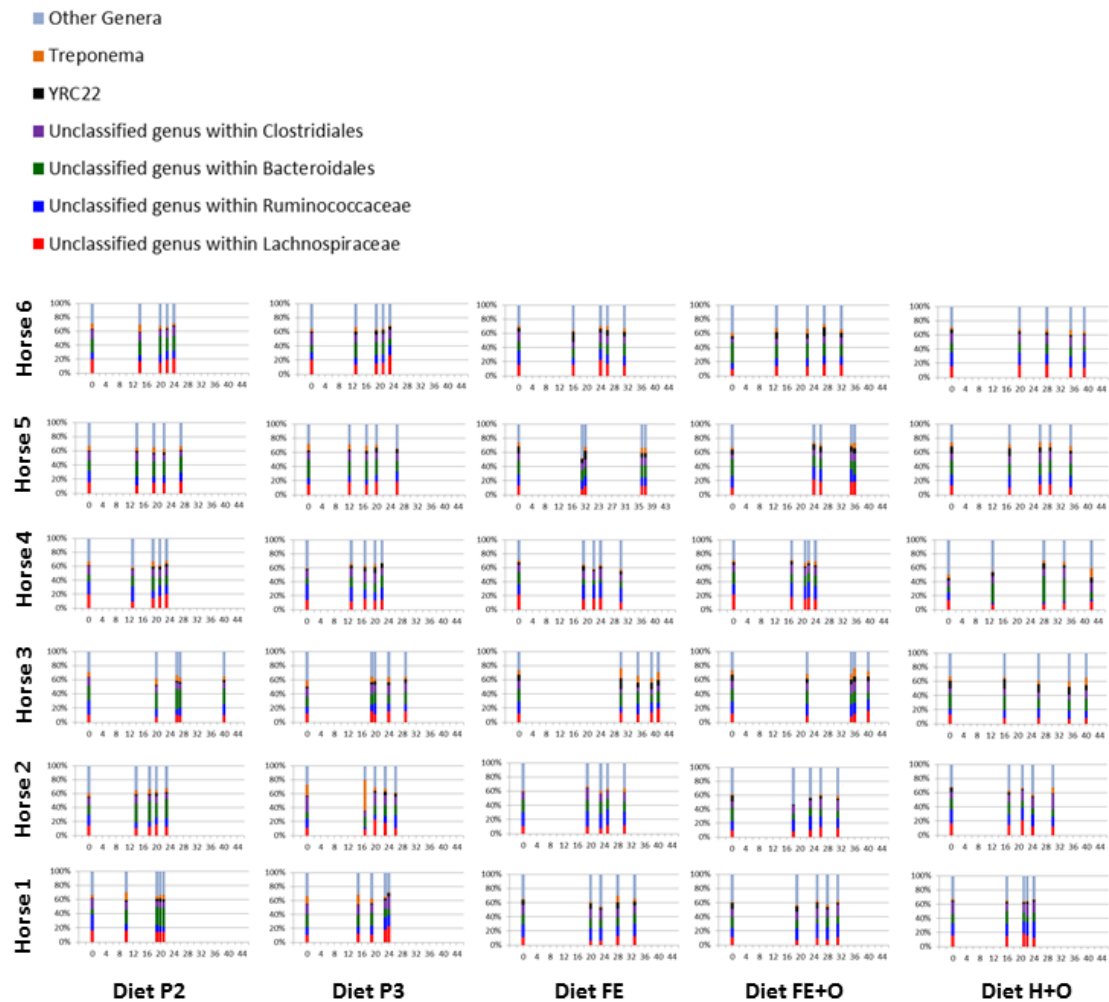


**Legend:** Relative abundances of the six most dominant genera and the remaining genera (Other Genera) that comprise the faecal bacterial community of horses included in the study are shown in the stacked bar graphs. The sequence of the stacked bars along the x-axis in each panel is: T0 (time 0 when the diet was changed); M1 (time when the first intestinal marker was retrieved in the faeces); M25 (time when 25% of the intestinal markers were retrieved in the faeces); M50 (time when 50% of the intestinal markers were retrieved in the faeces); and M75 (time when 75% of the intestinal markers were retrieved in the faeces). The time points in hours following dietary change are shown on the x-axis of each graph panel and the relative abundance of the phyla as percentage are shown on the y-axis. The diets are labelled as Diet P2 – cut pasture fed during washout period 2; Diet P3 – cut pasture fed during washout period 3; Diet FE- ensiled chopped forage; Diet FE+O - ensiled chopped forage fed with whole oats; and Diet H+O - hay fed with whole oats.

**Table S1. Metrics of sequencing and quality screening.**

| Details | Bacterial sequences |
|---|:---:|
| **Initial processed reads §** | |
| Total number of reads | 181,673,688 |
| Mean number of reads per sample | 345,288 |
| (range) | (87,312 – 748,408) |
| | |
| **High quality reads used in downstream analysis †** | |
| Total number of reads | 5,531,552 |
| Mean number of reads per sample | 14,673 |
| (range) | (3,022 – 43,275) |
| Mean length of reads (bp) | 283 |
| (range) | (250 – 301) |
| Total OTUs detected at 97% similarity | 14,889 |

§ After using SolexaQA++, fastaQC, fastQscreen, BWA PhiX, fastq-mcf
† After using DynamicTrim, LengthShort, Chimera check

**Table S2. Metadata on the faecal samples (n=377) included in the study on the population dynamics of faecal microbiota of forage-fed horses (n=6).**

| SampleID | Barcode1 | Barcode2 | MiSeqRun | SampleDescription | Horse | TimePoint | Week | Diet | Age |
|---|---|---|---|---|---|---|---|---|---|
| 1BLOCK1-A1H1T0_W0PP | CGAGAGTT | ATCGTACG | 1 | H1T0_W0PP | H1 | T0 | W0 | PP | 9 |
| 2BLOCK1-A2H2T0_W0PP | GACATAGT | ATCGTACG | 1 | H2T0_W0PP | H2 | T0 | W0 | PP | 16 |
| 3BLOCK1-A3H3T0_W0PP | ACGCTACT | ATCGTACG | 1 | H3T0_W0PP | H3 | T0 | W0 | PP | 16 |
| 4BLOCK1-A4H4T0_W0PP | ACTCACTG | ATCGTACG | 1 | H4T0_W0PP | H4 | T0 | W0 | PP | 16 |
| 5BLOCK1-A5H5T0_W0PP | TGAGTACG | ATCGTACG | 1 | H5T0_W0PP | H5 | T0 | W0 | PP | 16 |
| 6BLOCK1-A6H6T0_W0PP | CTGCGTAG | ATCGTACG | 1 | H6T0_W0PP | H6 | T0 | W0 | PP | 9 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 7BLOCK1-A7H1T24_W1P | TAGTCTCC | ATCGTACG | 1 | H1T24_W1P | H1 | T24 | W1 | P1 | 9 |
| 8BLOCK1-A8H2T24_W1P | CGAGCGAC | ATCGTACG | 1 | H2T24_W1P | H2 | T24 | W1 | P1 | 16 |
| 9BLOCK1-A9H3T24_W1P | ACTACGAC | ATCGTACG | 1 | H3T24_W1P | H3 | T24 | W1 | P1 | 16 |
| 10BLOCK1-A10H4T24_W1P | GTCTGCTA | ATCGTACG | 1 | H4T24_W1P | H4 | T24 | W1 | P1 | 16 |
| 11BLOCK1-A11H5T24_W1P | GTCTATGA | ATCGTACG | 1 | H5T24_W1P | H5 | T24 | W1 | P1 | 16 |
| 12BLOCK1-A12H6T24_W1P | TATAGCGA | ATCGTACG | 1 | H6T24_W1P | H6 | T24 | W1 | P1 | 9 |
| 13BLOCK1-B1H1T48_W1P | CGAGAGTT | ACTATCTG | 1 | H1T48_W1P | H1 | T48 | W1 | P1 | 9 |
| 14BLOCK1-B2H2T48_W1P | GACATAGT | ACTATCTG | 1 | H2T48_W1P | H2 | T48 | W1 | P1 | 16 |
| 15BLOCK1-B3H3T48_W1P | ACGCTACT | ACTATCTG | 1 | H3T48_W1P | H3 | T48 | W1 | P1 | 16 |
| 16BLOCK1-B4H4T48_W1P | ACTCACTG | ACTATCTG | 1 | H4T48_W1P | H4 | T48 | W1 | P1 | 16 |
| 17BLOCK1-B5H5T48_W1P | TGAGTACG | ACTATCTG | 1 | H5T48_W1P | H5 | T48 | W1 | P1 | 16 |
| 18BLOCK1-B6H6T48_W1P | CTGCGTAG | ACTATCTG | 1 | H6T48_W1P | H6 | T48 | W1 | P1 | 9 |
| 19BLOCK1-B7H1T72_W1P | TAGTCTCC | ACTATCTG | 1 | H1T72_W1P | H1 | T72 | W1 | P1 | 9 |
| 20BLOCK1-B8H2T72_W1P | CGAGCGAC | ACTATCTG | 1 | H2T72_W1P | H2 | T72 | W1 | P1 | 16 |
| 21BLOCK1-B9H3T72_W1P | ACTACGAC | ACTATCTG | 1 | H3T72_W1P | H3 | T72 | W1 | P1 | 16 |
| 22BLOCK1-B10H4T72_W1P | GTCTGCTA | ACTATCTG | 1 | H4T72_W1P | H4 | T72 | W1 | P1 | 16 |
| 23BLOCK1-B11H5T72_W1P | GTCTATGA | ACTATCTG | 1 | H5T72_W1P | H5 | T72 | W1 | P1 | 16 |
| 24BLOCK1-B12H6T72_W1P | TATAGCGA | ACTATCTG | 1 | H6T72_W1P | H6 | T72 | W1 | P1 | 9 |
| 25BLOCK1-C1H1T96_W1P | CGAGAGTT | TAGCGAGT | 1 | H1T96_W1P | H1 | T96 | W1 | P1 | 9 |
| 26BLOCK1-C2H2T96_W1P | GACATAGT | TAGCGAGT | 1 | H2T96_W1P | H2 | T96 | W1 | P1 | 16 |
| 27BLOCK1-C3H3T96_W1P | ACGCTACT | TAGCGAGT | 1 | H3T96_W1P | H3 | T96 | W1 | P1 | 16 |
| 28BLOCK1-C4H4T96_W1P | ACTCACTG | TAGCGAGT | 1 | H4T96_W1P | H4 | T96 | W1 | P1 | 16 |
| 29BLOCK1-C5H5T96_W1P | TGAGTACG | TAGCGAGT | 1 | H5T96_W1P | H5 | T96 | W1 | P1 | 16 |
| 30BLOCK1-C6H6T96_W1P | CTGCGTAG | TAGCGAGT | 1 | H6T96_W1P | H6 | T96 | W1 | P1 | 9 |
| 31BLOCK1-C7H1T120_W1P | TAGTCTCC | TAGCGAGT | 1 | H1T120_W1P | H1 | T120 | W1 | P1 | 9 |
| 32BLOCK1-C8H2T120_W1P | CGAGCGAC | TAGCGAGT | 1 | H2T120_W1P | H2 | T120 | W1 | P1 | 16 |
| 33BLOCK1-C9H3T120_W1P | ACTACGAC | TAGCGAGT | 1 | H3T120_W1P | H3 | T120 | W1 | P1 | 16 |
| 34BLOCK1-C10H4T120_W1P | GTCTGCTA | TAGCGAGT | 1 | H4T120_W1P | H4 | T120 | W1 | P1 | 16 |
| 35BLOCK1-C11H5T120_W1P | GTCTATGA | TAGCGAGT | 1 | H5T120_W1P | H5 | T120 | W1 | P1 | 16 |
| 36BLOCK1-C12H6T120_W1P | TATAGCGA | TAGCGAGT | 1 | H6T120_W1P | H6 | T120 | W1 | P1 | 9 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 37BLOCK1-D1H1T144_W1P | CGAGAGTT | CTGCGTGT | 1 | H1T144_W1P | H1 | T144 | W1 | P1 | 9 |
| 38BLOCK1-D2H2T144_W1P | GACATAGT | CTGCGTGT | 1 | H2T144_W1P | H2 | T144 | W1 | P1 | 16 |
| 39BLOCK1-D3H3T144_W1P | ACGCTACT | CTGCGTGT | 1 | H3T144_W1P | H3 | T144 | W1 | P1 | 16 |
| 40BLOCK1-D4H4T144_W1P | ACTCACTG | CTGCGTGT | 1 | H4T144_W1P | H4 | T144 | W1 | P1 | 16 |
| 41BLOCK1-D5H5T144_W1P | TGAGTACG | CTGCGTGT | 1 | H5T144_W1P | H5 | T144 | W1 | P1 | 16 |
| 42BLOCK1-D6H6T144_W1P | CTGCGTAG | CTGCGTGT | 1 | H6T144_W1P | H6 | T144 | W1 | P1 | 9 |
| 43BLOCK1-D7H1T168_W1P | TAGTCTCC | CTGCGTGT | 1 | H1T168_W1P | H1 | T168 | W1 | P1 | 9 |
| 44BLOCK1-D8H2T168_W1P | CGAGCGAC | CTGCGTGT | 1 | H2T168_W1P | H2 | T168 | W1 | P1 | 16 |
| 45BLOCK1-D9H3T168_W1P | ACTACGAC | CTGCGTGT | 1 | H3T168_W1P | H3 | T168 | W1 | P1 | 16 |
| 46BLOCK1-D10H4T168_W1P | GTCTGCTA | CTGCGTGT | 1 | H4T168_W1P | H4 | T168 | W1 | P1 | 16 |
| 47BLOCK1-D11H5T168_W1P | GTCTATGA | CTGCGTGT | 1 | H5T168_W1P | H5 | T168 | W1 | P1 | 16 |
| 48BLOCK1-D12H6T168_W1P | TATAGCGA | CTGCGTGT | 1 | H6T168_W1P | H6 | T168 | W1 | P1 | 9 |
| 49BLOCK1-E1H1M1_W2FE | CGAGAGTT | TCATCGAG | 1 | H1M1_W2FE | H1 | M1 | W2 | FE | 9 |
| 50BLOCK1-E2H2M1_W2FE | GACATAGT | TCATCGAG | 1 | H2M1_W2FE | H2 | M1 | W2 | FE | 16 |
| 51BLOCK1-E3H3M1_W2FEO | ACGCTACT | TCATCGAG | 1 | H3M1_W2FEO | H3 | M1 | W2 | FEO | 16 |
| 52BLOCK1-E4H4M1_W2FEO | ACTCACTG | TCATCGAG | 1 | H4M1_W2FEO | H4 | M1 | W2 | FEO | 16 |
| 53BLOCK1-E5H5M1_W2HO | TGAGTACG | TCATCGAG | 1 | H5M1_W2HO | H5 | M1 | W2 | HO | 16 |
| 54BLOCK1-E6H6M1_W2HO | CTGCGTAG | TCATCGAG | 1 | H6M1_W2HO | H6 | M1 | W2 | HO | 9 |
| 55BLOCK1-E7H1M25_W2FE | TAGTCTCC | TCATCGAG | 1 | H1M25_W2FE | H1 | M25 | W2 | FE | 9 |
| 56BLOCK1-E8H2M25_W2FE | CGAGCGAC | TCATCGAG | 1 | H2M25_W2FE | H2 | M25 | W2 | FE | 16 |
| 57BLOCK1-E9H3M25_W2FEO | ACTACGAC | TCATCGAG | 1 | H3M25_W2FEO | H3 | M25 | W2 | FEO | 16 |
| 58BLOCK1-E10H4M25_W2FEO | GTCTGCTA | TCATCGAG | 1 | H4M25_W2FEO | H4 | M25 | W2 | FEO | 16 |
| 59BLOCK1-E11H5M25_W2HO | GTCTATGA | TCATCGAG | 1 | H5M25_W2HO | H5 | M25 | W2 | HO | 16 |
| 60BLOCK1-E12H6M25_W2HO | TATAGCGA | TCATCGAG | 1 | H6M25_W2HO | H6 | M25 | W2 | HO | 9 |
| 61BLOCK1-F1H1M50_W2FE | CGAGAGTT | CGTGAGTG | 1 | H1M50_W2FE | H1 | M50 | W2 | FE | 9 |
| 62BLOCK1-F2H2M50_W2FE | GACATAGT | CGTGAGTG | 1 | H2M50_W2FE | H2 | M50 | W2 | FE | 16 |
| 63BLOCK1-F3H3M50_W2FEO | ACGCTACT | CGTGAGTG | 1 | H3M50_W2FEO | H3 | M50 | W2 | FEO | 16 |
| 64BLOCK1-F4H4M50_W2FEO | ACTCACTG | CGTGAGTG | 1 | H4M50_W2FEO | H4 | M50 | W2 | FEO | 16 |
| 65BLOCK1-F5H5M50_W2HO | TGAGTACG | CGTGAGTG | 1 | H5M50_W2HO | H5 | M50 | W2 | HO | 16 |
| 66BLOCK1-F6H6M50_W2HO | CTGCGTAG | CGTGAGTG | 1 | H6M50_W2HO | H6 | M50 | W2 | HO | 9 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 67BLOCK1-F7H1M75_W2FE | TAGTCTCC | CGTGAGTG | 1 | H1M75_W2FE | H1 | M75 | W2 | FE | 9 |
| 68BLOCK1-F8H2M75_W2FE | CGAGCGAC | CGTGAGTG | 1 | H2M75_W2FE | H2 | M75 | W2 | FE | 16 |
| 69BLOCK1-F9H3M75_W2FEO | ACTACGAC | CGTGAGTG | 1 | H3M75_W2FEO | H3 | M75 | W2 | FEO | 16 |
| 70BLOCK1-F10H4M75_W2FEO | GTCTGCTA | CGTGAGTG | 1 | H4M75_W2FEO | H4 | M75 | W2 | FEO | 16 |
| 71BLOCK1-F11H5M75_W2HO | GTCTATGA | CGTGAGTG | 1 | H5M75_W2HO | H5 | M75 | W2 | HO | 16 |
| 72BLOCK1-F12H6M75_W2HO | TATAGCGA | CGTGAGTG | 1 | H6M75_W2HO | H6 | M75 | W2 | HO | 9 |
| BLANK SAMPLE | | | | | | | | | |
| 74BLOCK1-G2H2T24_W2FE | GACATAGT | GGATATCT | 1 | H2T24_W2FE | H2 | T24 | W2 | FE | 16 |
| 75BLOCK1-G3H3T24_W2FEO | ACGCTACT | GGATATCT | 1 | H3T24_W2FEO | H3 | T24 | W2 | FEO | 16 |
| 76BLOCK1-G4H4T24_W2FEO | ACTCACTG | GGATATCT | 1 | H4T24_W2FEO | H4 | T24 | W2 | FEO | 16 |
| 77BLOCK1-G5H5T24_W2HO | TGAGTACG | GGATATCT | 1 | H5T24_W2HO | H5 | T24 | W2 | HO | 16 |
| 78BLOCK1-G6H6T24_W2HO | CTGCGTAG | GGATATCT | 1 | H6T24_W2HO | H6 | T24 | W2 | HO | 9 |
| 79BLOCK1-G7H1T48_W2FE | TAGTCTCC | GGATATCT | 1 | H1T48_W2FE | H1 | T48 | W2 | FE | 9 |
| 80BLOCK1-G8H2T48_W2FE | CGAGCGAC | GGATATCT | 1 | H2T48_W2FE | H2 | T48 | W2 | FE | 16 |
| 81BLOCK1-G9H3T48_W2FEO | ACTACGAC | GGATATCT | 1 | H3T48_W2FEO | H3 | T48 | W2 | FEO | 16 |
| 82BLOCK1-G10H4T48_W2FEO | GTCTGCTA | GGATATCT | 1 | H4T48_W2FEO | H4 | T48 | W2 | FEO | 16 |
| 83BLOCK1-G11H5T48_W2HO | GTCTATGA | GGATATCT | 1 | H5T48_W2HO | H5 | T48 | W2 | HO | 16 |
| 84BLOCK1-G12H6T48_W2HO | TATAGCGA | GGATATCT | 1 | H6T48_W2HO | H6 | T48 | W2 | HO | 9 |
| 85BLOCK1-H1H1T72_W2FE | CGAGAGTT | GACACCGT | 1 | H1T72_W2FE | H1 | T72 | W2 | FE | 9 |
| 86BLOCK1-H2H2T72_W2FE | GACATAGT | GACACCGT | 1 | H2T72_W2FE | H2 | T72 | W2 | FE | 16 |
| 87BLOCK1-H3H3T72_W2FEO | ACGCTACT | GACACCGT | 1 | H3T72_W2FEO | H3 | T72 | W2 | FEO | 16 |
| 88BLOCK1-H4H4T72_W2FEO | ACTCACTG | GACACCGT | 1 | H4T72_W2FEO | H4 | T72 | W2 | FEO | 16 |
| 89BLOCK1-H5H5T72_W2HO | TGAGTACG | GACACCGT | 1 | H5T72_W2HO | H5 | T72 | W2 | HO | 16 |
| 90BLOCK1-H6H6T72_W2HO | CTGCGTAG | GACACCGT | 1 | H6T72_W2HO | H6 | T72 | W2 | HO | 9 |
| 91BLOCK1-H7H1T96_W2FE | TAGTCTCC | GACACCGT | 1 | H1T96_W2FE | H1 | T96 | W2 | FE | 9 |
| 92BLOCK1-H8H2T96_W2FE | CGAGCGAC | GACACCGT | 1 | H2T96_W2FE | H2 | T96 | W2 | FE | 16 |
| 93BLOCK1-H9H3T96_W2FEO | ACTACGAC | GACACCGT | 1 | H3T96_W2FEO | H3 | T96 | W2 | FEO | 16 |
| 94BLOCK1-H10H4T96_W2FEO | GTCTGCTA | GACACCGT | 1 | H4T96_W2FEO | H4 | T96 | W2 | FEO | 16 |
| 95BLOCK1-H11H5T96_W2HO | GTCTATGA | GACACCGT | 1 | H5T96_W2HO | H5 | T96 | W2 | HO | 16 |
| 96BLOCK1-H12H6T96_W2HO | TATAGCGA | GACACCGT | 1 | H6T96_W2HO | H6 | T96 | W2 | HO | 9 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 97BLOCK2-A1H1T120_W2FE | CGAGAGTT | CTACTATA | 1 | H1T120_W2FE | H1 | T120 | W2 | FE | 9 |
| 98BLOCK2-A2H2T120_W2FE | GACATAGT | CTACTATA | 1 | H2T120_W2FE | H2 | T120 | W2 | FE | 16 |
| 99BLOCK2-A3H3T120_W2FEO | ACGCTACT | CTACTATA | 1 | H3T120_W2FEO | H3 | T120 | W2 | FEO | 16 |
| 100BLOCK2-A4H4T120_W2FEO | ACTCACTG | CTACTATA | 1 | H4T120_W2FEO | H4 | T120 | W2 | FEO | 16 |
| 101BLOCK2-A5H5T120_W2HO | TGAGTACG | CTACTATA | 1 | H5T120_W2HO | H5 | T120 | W2 | HO | 16 |
| 102BLOCK2-A6H6T120_W2HO | CTGCGTAG | CTACTATA | 1 | H6T120_W2HO | H6 | T120 | W2 | HO | 9 |
| 103BLOCK2-A7H1T144_W2FE | TAGTCTCC | CTACTATA | 1 | H1T144_W2FE | H1 | T144 | W2 | FE | 9 |
| 104BLOCK2-A8H2T144_W2FE | CGAGCGAC | CTACTATA | 1 | H2T144_W2FE | H2 | T144 | W2 | FE | 16 |
| 105BLOCK2-A9H3T144_W2FEO | ACTACGAC | CTACTATA | 1 | H3T144_W2FEO | H3 | T144 | W2 | FEO | 16 |
| 106BLOCK2-A10H4T144_W2FEO | GTCTGCTA | CTACTATA | 1 | H4T144_W2FEO | H4 | T144 | W2 | FEO | 16 |
| 107BLOCK2-A11H5T144_W2HO | GTCTATGA | CTACTATA | 1 | H5T144_W2HO | H5 | T144 | W2 | HO | 16 |
| 108BLOCK2-A12H6T144_W2HO | TATAGCGA | CTACTATA | 1 | H6T144_W2HO | H6 | T144 | W2 | HO | 9 |
| 109BLOCK2-B1H1T168_W2FE | CGAGAGTT | CGTTACTA | 1 | H1T168_W2FE | H1 | T168 | W2 | FE | 9 |
| 110BLOCK2-B2H2T168_W2FE | GACATAGT | CGTTACTA | 1 | H2T168_W2FE | H2 | T168 | W2 | FE | 16 |
| 111BLOCK2-B3H3T168_W2FEO | ACGCTACT | CGTTACTA | 1 | H3T168_W2FEO | H3 | T168 | W2 | FEO | 16 |
| 112BLOCK2-B4H4T168_W2FEO | ACTCACTG | CGTTACTA | 1 | H4T168_W2FEO | H4 | T168 | W2 | FEO | 16 |
| 113BLOCK2-B5H5T168_W2HO | TGAGTACG | CGTTACTA | 1 | H5T168_W2HO | H5 | T168 | W2 | HO | 16 |
| 114BLOCK2-B6H6T168_W2HO | CTGCGTAG | CGTTACTA | 1 | H6T168_W2HO | H6 | T168 | W2 | HO | 9 |
| 115BLOCK2-B7H1M1_W3P | TAGTCTCC | CGTTACTA | 1 | H1M1_W3P | H1 | M1 | W3 | P2 | 9 |
| 116BLOCK2-B8H2M1_W3P | CGAGCGAC | CGTTACTA | 1 | H2M1_W3P | H2 | M1 | W3 | P2 | 16 |
| 117BLOCK2-B9H3M1_W3P | ACTACGAC | CGTTACTA | 1 | H3M1_W3P | H3 | M1 | W3 | P2 | 16 |
| 118BLOCK2-B10H4M1_W3P | GTCTGCTA | CGTTACTA | 1 | H4M1_W3P | H4 | M1 | W3 | P2 | 16 |
| 119BLOCK2-B11H5M1_W3P | GTCTATGA | CGTTACTA | 1 | H5M1_W3P | H5 | M1 | W3 | P2 | 16 |
| 120BLOCK2-B12H6M1_W3P | TATAGCGA | CGTTACTA | 1 | H6M1_W3P | H6 | M1 | W3 | P2 | 9 |
| 121BLOCK2-C1H1M25_W3P | CGAGAGTT | AGAGTCAC | 1 | H1M25_W3P | H1 | M25 | W3 | P2 | 9 |
| 122BLOCK2-C2H2M25_W3P | GACATAGT | AGAGTCAC | 1 | H2M25_W3P | H2 | M25 | W3 | P2 | 16 |
| 123BLOCK2-C3H3M25_W3P | ACGCTACT | AGAGTCAC | 1 | H3M25_W3P | H3 | M25 | W3 | P2 | 16 |
| 124BLOCK2-C4H4M25_W3P | ACTCACTG | AGAGTCAC | 1 | H4M25_W3P | H4 | M25 | W3 | P2 | 16 |
| 125BLOCK2-C5H5M25_W3P | TGAGTACG | AGAGTCAC | 1 | H5M25_W3P | H5 | M25 | W3 | P2 | 16 |
| 126BLOCK2-C6H6M25_W3P | CTGCGTAG | AGAGTCAC | 1 | H6M25_W3P | H6 | M25 | W3 | P2 | 9 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 127BLOCK2-C7H1M50_W3P | TAGTCTCC | AGAGTCAC | 1 | H1M50_W3P | H1 | M50 | W3 | P2 | 9 |
| 128BLOCK2-C8H2M50_W3P | CGAGCGAC | AGAGTCAC | 1 | H2M50_W3P | H2 | M50 | W3 | P2 | 16 |
| 129BLOCK2-C9H3M50_W3P | ACTACGAC | AGAGTCAC | 1 | H3M50_W3P | H3 | M50 | W3 | P2 | 16 |
| 130BLOCK2-C10H4M50_W3P | GTCTGCTA | AGAGTCAC | 1 | H4M50_W3P | H4 | M50 | W3 | P2 | 16 |
| 131BLOCK2-C11H5M50_W3P | GTCTATGA | AGAGTCAC | 1 | H5M50_W3P | H5 | M50 | W3 | P2 | 16 |
| 132BLOCK2-C12H6M50_W3P | TATAGCGA | AGAGTCAC | 1 | H6M50_W3P | H6 | M50 | W3 | P2 | 9 |
| 133BLOCK2-D1H1M75_W3P | CGAGAGTT | TACGAGAC | 1 | H1M75_W3P | H1 | M75 | W3 | P2 | 9 |
| 134BLOCK2-D2H2M75_W3P | GACATAGT | TACGAGAC | 1 | H2M75_W3P | H2 | M75 | W3 | P2 | 16 |
| 135BLOCK2-D3H3M75_W3P | ACGCTACT | TACGAGAC | 1 | H3M75_W3P | H3 | M75 | W3 | P2 | 16 |
| 136BLOCK2-D4H4M75_W3P | ACTCACTG | TACGAGAC | 1 | H4M75_W3P | H4 | M75 | W3 | P2 | 16 |
| 137BLOCK2-D5H5M75_W3P | TGAGTACG | TACGAGAC | 1 | H5M75_W3P | H5 | M75 | W3 | P2 | 16 |
| 138BLOCK2-D6H6M75_W3P | CTGCGTAG | TACGAGAC | 1 | H6M75_W3P | H6 | M75 | W3 | P2 | 9 |
| 139BLOCK2-D7H1T24_W3P | TAGTCTCC | TACGAGAC | 1 | H1T24_W3P | H1 | T24 | W3 | P2 | 9 |
| 140BLOCK2-D8H2T24_W3P | CGAGCGAC | TACGAGAC | 1 | H2T24_W3P | H2 | T24 | W3 | P2 | 16 |
| 141BLOCK2-D9H3T24_W3P | ACTACGAC | TACGAGAC | 1 | H3T24_W3P | H3 | T24 | W3 | P2 | 16 |
| 142BLOCK2-D10H4T24_W3P | GTCTGCTA | TACGAGAC | 1 | H4T24_W3P | H4 | T24 | W3 | P2 | 16 |
| 143BLOCK2-D11H5T24_W3P | GTCTATGA | TACGAGAC | 1 | H5T24_W3P | H5 | T24 | W3 | P2 | 16 |
| BLANK SAMPLE | | | | | | | | | |
| 145BLOCK2-E1H1T48_W3P | CGAGAGTT | ACGTCTCG | 1 | H1T48_W3P | H1 | T48 | W3 | P2 | 9 |
| 146BLOCK2-E2H2T48_W3P | GACATAGT | ACGTCTCG | 1 | H2T48_W3P | H2 | T48 | W3 | P2 | 16 |
| 147BLOCK2-E3H3T48_W3P | ACGCTACT | ACGTCTCG | 1 | H3T48_W3P | H3 | T48 | W3 | P2 | 16 |
| 148BLOCK2-E4H4T48_W3P | ACTCACTG | ACGTCTCG | 1 | H4T48_W3P | H4 | T48 | W3 | P2 | 16 |
| 149BLOCK2-E5H5T48_W3P | TGAGTACG | ACGTCTCG | 1 | H5T48_W3P | H5 | T48 | W3 | P2 | 16 |
| 150BLOCK2-E6H6T48_W3P | CTGCGTAG | ACGTCTCG | 1 | H6T48_W3P | H6 | T48 | W3 | P2 | 9 |
| 151BLOCK2-E7H1T72_W3P | TAGTCTCC | ACGTCTCG | 1 | H1T72_W3P | H1 | T72 | W3 | P2 | 9 |
| 152BLOCK2-E8H2T72_W3P | CGAGCGAC | ACGTCTCG | 1 | H2T72_W3P | H2 | T72 | W3 | P2 | 16 |
| 153BLOCK2-E9H3T72_W3P | ACTACGAC | ACGTCTCG | 1 | H3T72_W3P | H3 | T72 | W3 | P2 | 16 |
| 154BLOCK2-E10H4T72_W3P | GTCTGCTA | ACGTCTCG | 1 | H4T72_W3P | H4 | T72 | W3 | P2 | 16 |
| 155BLOCK2-E11H5T72_W3P | GTCTATGA | ACGTCTCG | 1 | H5T72_W3P | H5 | T72 | W3 | P2 | 16 |
| 156BLOCK2-E12H6T72_W3P | TATAGCGA | ACGTCTCG | 1 | H6T72_W3P | H6 | T72 | W3 | P2 | 9 |

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|---|---|---|---|---|---|---|---|---|---|
| 157BLOCK2-F1H1T96_W3P | CGAGAGTT | TCGACGAG | 1 | H1T96_W3P | H1 | T96 | W3 | P2 | 9 |
| 158BLOCK2-F2H2T96_W3P | GACATAGT | TCGACGAG | 1 | H2T96_W3P | H2 | T96 | W3 | P2 | 16 |
| 159BLOCK2-F3H3T96_W3P | ACGCTACT | TCGACGAG | 1 | H3T96_W3P | H3 | T96 | W3 | P2 | 16 |
| 160BLOCK2-F4H4T96_W3P | ACTCACTG | TCGACGAG | 1 | H4T96_W3P | H4 | T96 | W3 | P2 | 16 |
| 161BLOCK2-F5H5T96_W3P | TGAGTACG | TCGACGAG | 1 | H5T96_W3P | H5 | T96 | W3 | P2 | 16 |
| 162BLOCK2-F6H6T96_W3P | CTGCGTAG | TCGACGAG | 1 | H6T96_W3P | H6 | T96 | W3 | P2 | 9 |
| 163BLOCK2-F7H1T120_W3P | TAGTCTCC | TCGACGAG | 1 | H1T120_W3P | H1 | T120 | W3 | P2 | 9 |
| 164BLOCK2-F8H2T120_W3P | CGAGCGAC | TCGACGAG | 1 | H2T120_W3P | H2 | T120 | W3 | P2 | 16 |
| 165BLOCK2-F9H3T120_W3P | ACTACGAC | TCGACGAG | 1 | H3T120_W3P | H3 | T120 | W3 | P2 | 16 |
| 166BLOCK2-F10H4T120_W3P | GTCTGCTA | TCGACGAG | 1 | H4T120_W3P | H4 | T120 | W3 | P2 | 16 |
| 167BLOCK2-F11H5T120_W3P | GTCTATGA | TCGACGAG | 1 | H5T120_W3P | H5 | T120 | W3 | P2 | 16 |
| 168BLOCK2-F12H6T120_W3P | TATAGCGA | TCGACGAG | 1 | H6T120_W3P | H6 | T120 | W3 | P2 | 9 |
| 169BLOCK2-G1H1T144_W3P | CGAGAGTT | GATCGTGT | 1 | H1T144_W3P | H1 | T144 | W3 | P2 | 9 |
| 170BLOCK2-G2H2T144_W3P | GACATAGT | GATCGTGT | 1 | H2T144_W3P | H2 | T144 | W3 | P2 | 16 |
| 171BLOCK2-G3H3T144_W3P | ACGCTACT | GATCGTGT | 1 | H3T144_W3P | H3 | T144 | W3 | P2 | 16 |
| 172BLOCK2-G4H4T144_W3P | ACTCACTG | GATCGTGT | 1 | H4T144_W3P | H4 | T144 | W3 | P2 | 16 |
| 173BLOCK2-G5H5T144_W3P | TGAGTACG | GATCGTGT | 1 | H5T144_W3P | H5 | T144 | W3 | P2 | 16 |
| 174BLOCK2-G6H6T144_W3P | CTGCGTAG | GATCGTGT | 1 | H6T144_W3P | H6 | T144 | W3 | P2 | 9 |
| 175BLOCK2-G7H1T168_W3P | TAGTCTCC | GATCGTGT | 1 | H1T168_W3P | H1 | T168 | W3 | P2 | 9 |
| 176BLOCK2-G8H2T168_W3P | CGAGCGAC | GATCGTGT | 1 | H2T168_W3P | H2 | T168 | W3 | P2 | 16 |
| 177BLOCK2-G9H3T168_W3P | ACTACGAC | GATCGTGT | 1 | H3T168_W3P | H3 | T168 | W3 | P2 | 16 |
| 178BLOCK2-G10H4T168_W3P | GTCTGCTA | GATCGTGT | 1 | H4T168_W3P | H4 | T168 | W3 | P2 | 16 |
| 179BLOCK2-G11H5T168_W3P | GTCTATGA | GATCGTGT | 1 | H5T168_W3P | H5 | T168 | W3 | P2 | 16 |
| 180BLOCK2-G12H6T168_W3P | TATAGCGA | GATCGTGT | 1 | H6T168_W3P | H6 | T168 | W3 | P2 | 9 |
| 181BLOCK2-H1H1M1_W4HO | CGAGAGTT | GTCAGATA | 1 | H1M1_W4HO | H1 | M1 | W4 | HO | 9 |
| 182BLOCK2-H2H2M1_W4HO | GACATAGT | GTCAGATA | 1 | H2M1_W4HO | H2 | M1 | W4 | HO | 16 |
| 183BLOCK2-H3H3M1_W4FE | ACGCTACT | GTCAGATA | 1 | H3M1_W4FE | H3 | M1 | W4 | FE | 16 |
| 184BLOCK2-H4H4M1_W4FE | ACTCACTG | GTCAGATA | 1 | H4M1_W4FE | H4 | M1 | W4 | FE | 16 |
| 185BLOCK2-H5H5M1_W4FEO | TGAGTACG | GTCAGATA | 1 | H5M1_W4FEO | H5 | M1 | W4 | FEO | 16 |
| 186BLOCK2-H6H6M1_W4FEO | CTGCGTAG | GTCAGATA | 1 | H6M1_W4FEO | H6 | M1 | W4 | FEO | 9 |

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|---|---|---|---|---|---|---|---|---|---|
| 187BLOCK2-H7H1M25_W4HO | TAGTCTCC | GTCAGATA | 1 | H1M25_W4HO | H1 | M25 | W4 | HO | 9 |
| 188BLOCK2-H8H2M25_W4HO | CGAGCGAC | GTCAGATA | 1 | H2M25_W4HO | H2 | M25 | W4 | HO | 16 |
| 189BLOCK2-H9H3M25_W4FE | ACTACGAC | GTCAGATA | 1 | H3M25_W4FE | H3 | M25 | W4 | FE | 16 |
| 190BLOCK2-H10H4M25_W4FE | GTCTGCTA | GTCAGATA | 1 | H4M25_W4FE | H4 | M25 | W4 | FE | 16 |
| 191BLOCK2-H11H5M25_W4FEO | GTCTATGA | GTCAGATA | 1 | H5M25_W4FEO | H5 | M25 | W4 | FEO | 16 |
| 192BLOCK2-H12H6M25_W4FEO | TATAGCGA | GTCAGATA | 1 | H6M25_W4FEO | H6 | M25 | W4 | FEO | 9 |
| 193BLOCK3-A1H1M50_W4HO | CTCGACTT | ATCGTACG | 2 | H1M50_W4HO | H1 | M50 | W4 | HO | 9 |
| 194BLOCK3-A2H2M50_W4HO | CGAAGTAT | ATCGTACG | 2 | H2M50_W4HO | H2 | M50 | W4 | HO | 16 |
| 195BLOCK3-A3H3M50_W4FE | TAGCAGCT | ATCGTACG | 2 | H3M50_W4FE | H3 | M50 | W4 | FE | 16 |
| 196BLOCK3-A4H4M50_W4FE | TCTCTATG | ATCGTACG | 2 | H4M50_W4FE | H4 | M50 | W4 | FE | 16 |
| 197BLOCK3-A5H5M50_W4FEO | GATCTACG | ATCGTACG | 2 | H5M50_W4FEO | H5 | M50 | W4 | FEO | 16 |
| 198BLOCK3-A6H6M50_W4FEO | GTAACGAG | ATCGTACG | 2 | H6M50_W4FEO | H6 | M50 | W4 | FEO | 9 |
| 199BLOCK3-A7H1M75_W4HO | ACGTGCGC | ATCGTACG | 2 | H1M75_W4HO | H1 | M75 | W4 | HO | 9 |
| 200BLOCK3-A8H2M75_W4HO | ATAGTACC | ATCGTACG | 2 | H2M75_W4HO | H2 | M75 | W4 | HO | 16 |
| 201BLOCK3-A9H3M75_W4FE | GCGTATAC | ATCGTACG | 2 | H3M75_W4FE | H3 | M75 | W4 | FE | 16 |
| 202BLOCK3-A10H4M75_W4FE | TGCTCGTA | ATCGTACG | 2 | H4M75_W4FE | H4 | M75 | W4 | FE | 16 |
| 203BLOCK3-A11H5M75_W4FEO | AACGCTGA | ATCGTACG | 2 | H5M75_W4FEO | H5 | M75 | W4 | FEO | 16 |
| 204BLOCK3-A12H6M75_W4FEO | CGTAGCGA | ATCGTACG | 2 | H6M75_W4FEO | H6 | M75 | W4 | FEO | 9 |
| 205BLOCK3-B1H1T24_W4HO | CTCGACTT | ACTATCTG | 2 | H1T24_W4HO | H1 | T24 | W4 | HO | 9 |
| BLANK SAMPLE | | | | | | | | | |
| 207BLOCK3-B3H3T24_W4FE | TAGCAGCT | ACTATCTG | 2 | H3T24_W4FE | H3 | T24 | W4 | FE | 16 |
| BLANK SAMPLE | | | | | | | | | |
| 209BLOCK3-B5H5T24_W4FEO | GATCTACG | ACTATCTG | 2 | H5T24_W4FEO | H5 | T24 | W4 | FEO | 16 |
| 210BLOCK3-B6H6T24_W4FEO | GTAACGAG | ACTATCTG | 2 | H6T24_W4FEO | H6 | T24 | W4 | FEO | 9 |
| 211BLOCK3-B7H1T48_W4HO | ACGTGCGC | ACTATCTG | 2 | H1T48_W4HO | H1 | T48 | W4 | HO | 9 |
| 212BLOCK3-B8H2T48_W4HO | ATAGTACC | ACTATCTG | 2 | H2T48_W4HO | H2 | T48 | W4 | HO | 16 |
| 213BLOCK3-B9H3T48_W4FE | GCGTATAC | ACTATCTG | 2 | H3T48_W4FE | H3 | T48 | W4 | FE | 16 |
| 214BLOCK3-B10H4T48_W4FE | TGCTCGTA | ACTATCTG | 2 | H4T48_W4FE | H4 | T48 | W4 | FE | 16 |
| 215BLOCK3-B11H5T48_W4FEO | AACGCTGA | ACTATCTG | 2 | H5T48_W4FEO | H5 | T48 | W4 | FEO | 16 |
| 216BLOCK3-B12H6T48_W4FEO | CGTAGCGA | ACTATCTG | 2 | H6T48_W4FEO | H6 | T48 | W4 | FEO | 9 |

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|---|---|---|---|---|---|---|---|---|---|
| 217BLOCK3-C1H1T72_W4HO | CTCGACTT | TAGCGAGT | 2 | H1T72_W4HO | H1 | T72 | W4 | HO | 9 |
| 218BLOCK3-C2H2T72_W4HO | CGAAGTAT | TAGCGAGT | 2 | H2T72_W4HO | H2 | T72 | W4 | HO | 16 |
| 219BLOCK3-C3H3T72_W4FE | TAGCAGCT | TAGCGAGT | 2 | H3T72_W4FE | H3 | T72 | W4 | FE | 16 |
| 220BLOCK3-C4H4T72_W4FE | TCTCTATG | TAGCGAGT | 2 | H4T72_W4FE | H4 | T72 | W4 | FE | 16 |
| 221BLOCK3-C5H5T72_W4FEO | GATCTACG | TAGCGAGT | 2 | H5T72_W4FEO | H5 | T72 | W4 | FEO | 16 |
| 222BLOCK3-C6H6T72_W4FEO | GTAACGAG | TAGCGAGT | 2 | H6T72_W4FEO | H6 | T72 | W4 | FEO | 9 |
| 223BLOCK3-C7H1T96_W4HO | ACGTGCGC | TAGCGAGT | 2 | H1T96_W4HO | H1 | T96 | W4 | HO | 9 |
| 224BLOCK3-C8H2T96_W4HO | ATAGTACC | TAGCGAGT | 2 | H2T96_W4HO | H2 | T96 | W4 | HO | 16 |
| 225BLOCK3-C9H3T96_W4FE | GCGTATAC | TAGCGAGT | 2 | H3T96_W4FE | H3 | T96 | W4 | FE | 16 |
| 226BLOCK3-C10H4T96_W4FE | TGCTCGTA | TAGCGAGT | 2 | H4T96_W4FE | H4 | T96 | W4 | FE | 16 |
| 227BLOCK3-C11H5T96_W4FEO | AACGCTGA | TAGCGAGT | 2 | H5T96_W4FEO | H5 | T96 | W4 | FEO | 16 |
| 228BLOCK3-C12H6T96_W4FEO | CGTAGCGA | TAGCGAGT | 2 | H6T96_W4FEO | H6 | T96 | W4 | FEO | 9 |
| 229BLOCK3-D1H1T120_W4HO | CTCGACTT | CTGCGTGT | 2 | H1T120_W4HO | H1 | T120 | W4 | HO | 9 |
| 230BLOCK3-D2H2T120_W4HO | CGAAGTAT | CTGCGTGT | 2 | H2T120_W4HO | H2 | T120 | W4 | HO | 16 |
| 231BLOCK3-D3H3T120_W4FE | TAGCAGCT | CTGCGTGT | 2 | H3T120_W4FE | H3 | T120 | W4 | FE | 16 |
| 232BLOCK3-D4H4T120_W4FE | TCTCTATG | CTGCGTGT | 2 | H4T120_W4FE | H4 | T120 | W4 | FE | 16 |
| 233BLOCK3-D5H5T120_W4FEO | GATCTACG | CTGCGTGT | 2 | H5T120_W4FEO | H5 | T120 | W4 | FEO | 16 |
| 234BLOCK3-D6H6T120_W4FEO | GTAACGAG | CTGCGTGT | 2 | H6T120_W4FEO | H6 | T120 | W4 | FEO | 9 |
| 235BLOCK3-D7H1T144_W4HO | ACGTGCGC | CTGCGTGT | 2 | H1T144_W4HO | H1 | T144 | W4 | HO | 9 |
| 236BLOCK3-D8H2T144_W4HO | ATAGTACC | CTGCGTGT | 2 | H2T144_W4HO | H2 | T144 | W4 | HO | 16 |
| 237BLOCK3-D9H3T144_W4FE | GCGTATAC | CTGCGTGT | 2 | H3T144_W4FE | H3 | T144 | W4 | FE | 16 |
| 238BLOCK3-D10H4T144_W4FE | TGCTCGTA | CTGCGTGT | 2 | H4T144_W4FE | H4 | T144 | W4 | FE | 16 |
| 239BLOCK3-D11H5T144_W4FEO | AACGCTGA | CTGCGTGT | 2 | H5T144_W4FEO | H5 | T144 | W4 | FEO | 16 |
| 240BLOCK3-D12H6T144_W4FEO | CGTAGCGA | CTGCGTGT | 2 | H6T144_W4FEO | H6 | T144 | W4 | FEO | 9 |
| 241BLOCK3-E1H1T168_W4HO | CTCGACTT | TCATCGAG | 2 | H1T168_W4HO | H1 | T168 | W4 | HO | 9 |
| 242BLOCK3-E2H2T168_W4HO | CGAAGTAT | TCATCGAG | 2 | H2T168_W4HO | H2 | T168 | W4 | HO | 16 |
| 243BLOCK3-E3H3T168_W4FE | TAGCAGCT | TCATCGAG | 2 | H3T168_W4FE | H3 | T168 | W4 | FE | 16 |
| 244BLOCK3-E4H4T168_W4FE | TCTCTATG | TCATCGAG | 2 | H4T168_W4FE | H4 | T168 | W4 | FE | 16 |
| 245BLOCK3-E5H5T168_W4FEO | GATCTACG | TCATCGAG | 2 | H5T168_W4FEO | H5 | T168 | W4 | FEO | 16 |
| 246BLOCK3-E6H6T168_W4FEO | GTAACGAG | TCATCGAG | 2 | H6T168_W4FEO | H6 | T168 | W4 | FEO | 9 |

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|---|---|---|---|---|---|---|---|---|---|
| 247BLOCK3-E7H1M1_W5P | ACGTGCGC | TCATCGAG | 2 | H1M1_W5P | H1 | M1 | W5 | P3 | 9 |
| 248BLOCK3-E8H2M1_W5P | ATAGTACC | TCATCGAG | 2 | H2M1_W5P | H2 | M1 | W5 | P3 | 16 |
| 249BLOCK3-E9H3M1_W5P | GCGTATAC | TCATCGAG | 2 | H3M1_W5P | H3 | M1 | W5 | P3 | 16 |
| 250BLOCK3-E10H4M1_W5P | TGCTCGTA | TCATCGAG | 2 | H4M1_W5P | H4 | M1 | W5 | P3 | 16 |
| 251BLOCK3-E11H5M1_W5P | AACGCTGA | TCATCGAG | 2 | H5M1_W5P | H5 | M1 | W5 | P3 | 16 |
| 252BLOCK3-E12H6M1_W5P | CGTAGCGA | TCATCGAG | 2 | H6M1_W5P | H6 | M1 | W5 | P3 | 9 |
| 253BLOCK3-F1H1M25_W5P | CTCGACTT | CGTGAGTG | 2 | H1M25_W5P | H1 | M25 | W5 | P3 | 9 |
| 254BLOCK3-F2H2M25_W5P | CGAAGTAT | CGTGAGTG | 2 | H2M25_W5P | H2 | M25 | W5 | P3 | 16 |
| 255BLOCK3-F3H3M25_W5P | TAGCAGCT | CGTGAGTG | 2 | H3M25_W5P | H3 | M25 | W5 | P3 | 16 |
| 256BLOCK3-F4H4M25_W5P | TCTCTATG | CGTGAGTG | 2 | H4M25_W5P | H4 | M25 | W5 | P3 | 16 |
| 257BLOCK3-F5H5M25_W5P | GATCTACG | CGTGAGTG | 2 | H5M25_W5P | H5 | M25 | W5 | P3 | 16 |
| 258BLOCK3-F6H6M25_W5P | GTAACGAG | CGTGAGTG | 2 | H6M25_W5P | H6 | M25 | W5 | P3 | 9 |
| 259BLOCK3-F7H1M50_W5P | ACGTGCGC | CGTGAGTG | 2 | H1M50_W5P | H1 | M50 | W5 | P3 | 9 |
| 260BLOCK3-F8H2M50_W5P | ATAGTACC | CGTGAGTG | 2 | H2M50_W5P | H2 | M50 | W5 | P3 | 16 |
| 261BLOCK3-F9H3M50_W5P | GCGTATAC | CGTGAGTG | 2 | H3M50_W5P | H3 | M50 | W5 | P3 | 16 |
| 262BLOCK3-F10H4M50_W5P | TGCTCGTA | CGTGAGTG | 2 | H4M50_W5P | H4 | M50 | W5 | P3 | 16 |
| 263BLOCK3-F11H5M50_W5P | AACGCTGA | CGTGAGTG | 2 | H5M50_W5P | H5 | M50 | W5 | P3 | 16 |
| 264BLOCK3-F12H6M50_W5P | CGTAGCGA | CGTGAGTG | 2 | H6M50_W5P | H6 | M50 | W5 | P3 | 9 |
| BLANK SAMPLE | | | | | | | | | |
| 266BLOCK3-G2H2M75_W5P | CGAAGTAT | GGATATCT | 2 | H2M75_W5P | H2 | M75 | W5 | P3 | 16 |
| 267BLOCK3-G3H3M75_W5P | TAGCAGCT | GGATATCT | 2 | H3M75_W5P | H3 | M75 | W5 | P3 | 16 |
| 268BLOCK3-G4H4M75_W5P | TCTCTATG | GGATATCT | 2 | H4M75_W5P | H4 | M75 | W5 | P3 | 16 |
| 269BLOCK3-G5H5M75_W5P | GATCTACG | GGATATCT | 2 | H5M75_W5P | H5 | M75 | W5 | P3 | 16 |
| 270BLOCK3-G6H6M75_W5P | GTAACGAG | GGATATCT | 2 | H6M75_W5P | H6 | M75 | W5 | P3 | 9 |
| 271BLOCK3-G7H1T24_W5P | ACGTGCGC | GGATATCT | 2 | H1T24_W5P | H1 | T24 | W5 | P3 | 9 |
| 272BLOCK3-G8H2T24_W5P | ATAGTACC | GGATATCT | 2 | H2T24_W5P | H2 | T24 | W5 | P3 | 16 |
| BLANK SAMPLE | | | | | | | | | |
| 274BLOCK3-G10H4T24_W5P | TGCTCGTA | GGATATCT | 2 | H4T24_W5P | H4 | T24 | W5 | P3 | 16 |
| 275BLOCK3-G11H5T24_W5P | AACGCTGA | GGATATCT | 2 | H5T24_W5P | H5 | T24 | W5 | P3 | 16 |
| 276BLOCK3-G12H6T24_W5P | CGTAGCGA | GGATATCT | 2 | H6T24_W5P | H6 | T24 | W5 | P3 | 9 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 277BLOCK3-H1H1T48_W5P | CTCGACTT | GACACCGT | 2 | H1T48_W5P | H1 | T48 | W5 | P3 | 9 |
| 278BLOCK3-H2H2T48_W5P | CGAAGTAT | GACACCGT | 2 | H2T48_W5P | H2 | T48 | W5 | P3 | 16 |
| 279BLOCK3-H3H3T48_W5P | TAGCAGCT | GACACCGT | 2 | H3T48_W5P | H3 | T48 | W5 | P3 | 16 |
| 280BLOCK3-H4H4T48_W5P | TCTCTATG | GACACCGT | 2 | H4T48_W5P | H4 | T48 | W5 | P3 | 16 |
| 281BLOCK3-H5H5T48_W5P | GATCTACG | GACACCGT | 2 | H5T48_W5P | H5 | T48 | W5 | P3 | 16 |
| 282BLOCK3-H6H6T48_W5P | GTAACGAG | GACACCGT | 2 | H6T48_W5P | H6 | T48 | W5 | P3 | 9 |
| 283BLOCK3-H7H1T72_W5P | ACGTGCGC | GACACCGT | 2 | H1T72_W5P | H1 | T72 | W5 | P3 | 9 |
| 284BLOCK3-H8H2T72_W5P | ATAGTACC | GACACCGT | 2 | H2T72_W5P | H2 | T72 | W5 | P3 | 16 |
| 285BLOCK3-H9H3T72_W5P | GCGTATAC | GACACCGT | 2 | H3T72_W5P | H3 | T72 | W5 | P3 | 16 |
| 286BLOCK3-H10H4T72_W5P | TGCTCGTA | GACACCGT | 2 | H4T72_W5P | H4 | T72 | W5 | P3 | 16 |
| 287BLOCK3-H11H5T72_W5P | AACGCTGA | GACACCGT | 2 | H5T72_W5P | H5 | T72 | W5 | P3 | 16 |
| 288BLOCK3-H12H6T72_W5P | CGTAGCGA | GACACCGT | 2 | H6T72_W5P | H6 | T72 | W5 | P3 | 9 |
| 289BLOCK4-A1H1T96_W5P | CTCGACTT | CTACTATA | 2 | H1T96_W5P | H1 | T96 | W5 | P3 | 9 |
| 290BLOCK4-A2H2T96_W5P | CGAAGTAT | CTACTATA | 2 | H2T96_W5P | H2 | T96 | W5 | P3 | 16 |
| 291BLOCK4-A3H3T96_W5P | TAGCAGCT | CTACTATA | 2 | H3T96_W5P | H3 | T96 | W5 | P3 | 16 |
| 292BLOCK4-A4H4T96_W5P | TCTCTATG | CTACTATA | 2 | H4T96_W5P | H4 | T96 | W5 | P3 | 16 |
| 293BLOCK4-A5H5T96_W5P | GATCTACG | CTACTATA | 2 | H5T96_W5P | H5 | T96 | W5 | P3 | 16 |
| 294BLOCK4-A6H6T96_W5P | GTAACGAG | CTACTATA | 2 | H6T96_W5P | H6 | T96 | W5 | P3 | 9 |
| 295BLOCK4-A7H1T120_W5P | ACGTGCGC | CTACTATA | 2 | H1T120_W5P | H1 | T120 | W5 | P3 | 9 |
| 296BLOCK4-A8H2T120_W5P | ATAGTACC | CTACTATA | 2 | H2T120_W5P | H2 | T120 | W5 | P3 | 16 |
| 297BLOCK4-A9H3T120_W5P | GCGTATAC | CTACTATA | 2 | H3T120_W5P | H3 | T120 | W5 | P3 | 16 |
| 298BLOCK4-A10H4T120_W5P | TGCTCGTA | CTACTATA | 2 | H4T120_W5P | H4 | T120 | W5 | P3 | 16 |
| 299BLOCK4-A11H5T120_W5P | AACGCTGA | CTACTATA | 2 | H5T120_W5P | H5 | T120 | W5 | P3 | 16 |
| 300BLOCK4-A12H6T120_W5P | CGTAGCGA | CTACTATA | 2 | H6T120_W5P | H6 | T120 | W5 | P3 | 9 |
| 301BLOCK4-B1H1T144_W5P | CTCGACTT | CGTTACTA | 2 | H1T144_W5P | H1 | T144 | W5 | P3 | 9 |
| 302BLOCK4-B2H2T144_W5P | CGAAGTAT | CGTTACTA | 2 | H2T144_W5P | H2 | T144 | W5 | P3 | 16 |
| 303BLOCK4-B3H3T144_W5P | TAGCAGCT | CGTTACTA | 2 | H3T144_W5P | H3 | T144 | W5 | P3 | 16 |
| 304BLOCK4-B4H4T144_W5P | TCTCTATG | CGTTACTA | 2 | H4T144_W5P | H4 | T144 | W5 | P3 | 16 |
| 305BLOCK4-B5H5T144_W5P | GATCTACG | CGTTACTA | 2 | H5T144_W5P | H5 | T144 | W5 | P3 | 16 |
| 306BLOCK4-B6H6T144_W5P | GTAACGAG | CGTTACTA | 2 | H6T144_W5P | H6 | T144 | W5 | P3 | 9 |

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|---|---|---|---|---|---|---|---|---|---|
| 307BLOCK4-B7H1T168_W5P | ACGTGCGC | CGTTACTA | 2 | H1T168_W5P | H1 | T168 | W5 | P3 | 9 |
| 308BLOCK4-B8H2T168_W5P | ATAGTACC | CGTTACTA | 2 | H2T168_W5P | H2 | T168 | W5 | P3 | 16 |
| 309BLOCK4-B9H3T168_W5P | GCGTATAC | CGTTACTA | 2 | H3T168_W5P | H3 | T168 | W5 | P3 | 16 |
| 310BLOCK4-B10H4T168_W5P | TGCTCGTA | CGTTACTA | 2 | H4T168_W5P | H4 | T168 | W5 | P3 | 16 |
| 311BLOCK4-B11H5T168_W5P | AACGCTGA | CGTTACTA | 2 | H5T168_W5P | H5 | T168 | W5 | P3 | 16 |
| 312BLOCK4-B12H6T168_W5P | CGTAGCGA | CGTTACTA | 2 | H6T168_W5P | H6 | T168 | W5 | P3 | 9 |
| 313BLOCK4-C1H1M1_W6FEO | CTCGACTT | AGAGTCAC | 2 | H1M1_W6FEO | H1 | M1 | W6 | FEO | 9 |
| 314BLOCK4-C2H2M1_W6FEO | CGAAGTAT | AGAGTCAC | 2 | H2M1_W6FEO | H2 | M1 | W6 | FEO | 16 |
| 315BLOCK4-C3H3M1_W6HO | TAGCAGCT | AGAGTCAC | 2 | H3M1_W6HO | H3 | M1 | W6 | HO | 16 |
| 316BLOCK4-C4H4M1_W6HO | TCTCTATG | AGAGTCAC | 2 | H4M1_W6HO | H4 | M1 | W6 | HO | 16 |
| 317BLOCK4-C5H5M1_W6FE | GATCTACG | AGAGTCAC | 2 | H5M1_W6FE | H5 | M1 | W6 | FE | 16 |
| 318BLOCK4-C6H6M1_W6FE | GTAACGAG | AGAGTCAC | 2 | H6M1_W6FE | H6 | M1 | W6 | FE | 9 |
| 319BLOCK4-C7H1M25_W6FEO | ACGTGCGC | AGAGTCAC | 2 | H1M25_W6FEO | H1 | M25 | W6 | FEO | 9 |
| 320BLOCK4-C8H2M25_W6FEO | ATAGTACC | AGAGTCAC | 2 | H2M25_W6FEO | H2 | M25 | W6 | FEO | 16 |
| 321BLOCK4-C9H3M25_W6HO | GCGTATAC | AGAGTCAC | 2 | H3M25_W6HO | H3 | M25 | W6 | HO | 16 |
| 322BLOCK4-C10H4M25_W6HO | TGCTCGTA | AGAGTCAC | 2 | H4M25_W6HO | H4 | M25 | W6 | HO | 16 |
| 323BLOCK4-C11H5M25_W6FE | AACGCTGA | AGAGTCAC | 2 | H5M25_W6FE | H5 | M25 | W6 | FE | 16 |
| 324BLOCK4-C12H6M25_W6FE | CGTAGCGA | AGAGTCAC | 2 | H6M25_W6FE | H6 | M25 | W6 | FE | 9 |
| 325BLOCK4-D1H1M50_W6FEO | CTCGACTT | TACGAGAC | 2 | H1M50_W6FEO | H1 | M50 | W6 | FEO | 9 |
| 326BLOCK4-D2H2M50_W6FEO | CGAAGTAT | TACGAGAC | 2 | H2M50_W6FEO | H2 | M50 | W6 | FEO | 16 |
| 327BLOCK4-D3H3M50_W6HO | TAGCAGCT | TACGAGAC | 2 | H3M50_W6HO | H3 | M50 | W6 | HO | 16 |
| 328BLOCK4-D4H4M50_W6HO | TCTCTATG | TACGAGAC | 2 | H4M50_W6HO | H4 | M50 | W6 | HO | 16 |
| 329BLOCK4-D5H5M50_W6FE | GATCTACG | TACGAGAC | 2 | H5M50_W6FE | H5 | M50 | W6 | FE | 16 |
| 330BLOCK4-D6H6M50_W6FE | GTAACGAG | TACGAGAC | 2 | H6M50_W6FE | H6 | M50 | W6 | FE | 9 |
| 331BLOCK4-D7H1M75_W6FEO | ACGTGCGC | TACGAGAC | 2 | H1M75_W6FEO | H1 | M75 | W6 | FEO | 9 |
| 332BLOCK4-D8H2M75_W6FEO | ATAGTACC | TACGAGAC | 2 | H2M75_W6FEO | H2 | M75 | W6 | FEO | 16 |
| 333BLOCK4-D9H3M75_W6HO | GCGTATAC | TACGAGAC | 2 | H3M75_W6HO | H3 | M75 | W6 | HO | 16 |
| 334BLOCK4-D10H4M75_W6HO | TGCTCGTA | TACGAGAC | 2 | H4M75_W6HO | H4 | M75 | W6 | HO | 16 |
| 335BLOCK4-D11H4T12_W5P | AACGCTGA | TACGAGAC | 2 | H4T12_W5P | H4 | T12 | W5 | P3 | 16 |
| 336BLOCK4-D12H6M75_W6FE | CGTAGCGA | TACGAGAC | 2 | H6M75_W6FE | H6 | M75 | W6 | FE | 9 |

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|---|---|---|---|---|---|---|---|---|---|
| 337BLOCK4-E1H1T12_W5P | CTCGACTT | ACGTCTCG | 2 | H1T12_W5P | H1 | T12 | W5 | P3 | 9 |
| 338BLOCK4-E2H2T12_W5P | CGAAGTAT | ACGTCTCG | 2 | H2T12_W5P | H2 | T12 | W5 | P3 | 16 |
| 339BLOCK4-E3H3T12_W5P | TAGCAGCT | ACGTCTCG | 2 | H3T12_W5P | H3 | T12 | W5 | P3 | 16 |
| 340BLOCK4-E4H4T24_W6HO | TCTCTATG | ACGTCTCG | 2 | H4T24_W6HO | H4 | T24 | W6 | HO | 16 |
| 341BLOCK4-E5H5T24_W6FE | GATCTACG | ACGTCTCG | 2 | H5T24_W6FE | H5 | T24 | W6 | FE | 16 |
| 342BLOCK4-E6H6T12_W5P | GTAACGAG | ACGTCTCG | 2 | H6T12_W5P | H6 | T12 | W5 | P3 | 9 |
| 343BLOCK4-E7H1T48_W6FEO | ACGTGCGC | ACGTCTCG | 2 | H1T48_W6FEO | H1 | T48 | W6 | FEO | 9 |
| 344BLOCK4-E8H2T48_W6FEO | ATAGTACC | ACGTCTCG | 2 | H2T48_W6FEO | H2 | T48 | W6 | FEO | 16 |
| 345BLOCK4-E9H3T48_W6HO | GCGTATAC | ACGTCTCG | 2 | H3T48_W6HO | H3 | T48 | W6 | HO | 16 |
| 346BLOCK4-E10H4T48_W6HO | TGCTCGTA | ACGTCTCG | 2 | H4T48_W6HO | H4 | T48 | W6 | HO | 16 |
| 347BLOCK4-E11H5T48_W6FE | AACGCTGA | ACGTCTCG | 2 | H5T48_W6FE | H5 | T48 | W6 | FE | 16 |
| 348BLOCK4-E12H6T48_W6FE | CGTAGCGA | ACGTCTCG | 2 | H6T48_W6FE | H6 | T48 | W6 | FE | 9 |
| 349BLOCK4-F1H1T72_W6FEO | CTCGACTT | TCGACGAG | 2 | H1T72_W6FEO | H1 | T72 | W6 | FEO | 9 |
| 350BLOCK4-F2H2T72_W6FEO | CGAAGTAT | TCGACGAG | 2 | H2T72_W6FEO | H2 | T72 | W6 | FEO | 16 |
| 351BLOCK4-F3H3T72_W6HO | TAGCAGCT | TCGACGAG | 2 | H3T72_W6HO | H3 | T72 | W6 | HO | 16 |
| 352BLOCK4-F4H4T72_W6HO | TCTCTATG | TCGACGAG | 2 | H4T72_W6HO | H4 | T72 | W6 | HO | 16 |
| 353BLOCK4-F5H5T72_W6FE | GATCTACG | TCGACGAG | 2 | H5T72_W6FE | H5 | T72 | W6 | FE | 16 |
| 354BLOCK4-F6H6T72_W6FE | GTAACGAG | TCGACGAG | 2 | H6T72_W6FE | H6 | T72 | W6 | FE | 9 |
| 355BLOCK4-F7H1T96_W6FEO | ACGTGCGC | TCGACGAG | 2 | H1T96_W6FEO | H1 | T96 | W6 | FEO | 9 |
| 356BLOCK4-F8H2T96_W6FEO | ATAGTACC | TCGACGAG | 2 | H2T96_W6FEO | H2 | T96 | W6 | FEO | 16 |
| 357BLOCK4-F9H3T96_W6HO | GCGTATAC | TCGACGAG | 2 | H3T96_W6HO | H3 | T96 | W6 | HO | 16 |
| 358BLOCK4-F10H4T96_W6HO | TGCTCGTA | TCGACGAG | 2 | H4T96_W6HO | H4 | T96 | W6 | HO | 16 |
| 359BLOCK4-F11H5T96_W6FE | AACGCTGA | TCGACGAG | 2 | H5T96_W6FE | H5 | T96 | W6 | FE | 16 |
| 360BLOCK4-F12H6T96_W6FE | CGTAGCGA | TCGACGAG | 2 | H6T96_W6FE | H6 | T96 | W6 | FE | 9 |
| 361BLOCK4-G1H1T120_W6FEO | CTCGACTT | GATCGTGT | 2 | H1T120_W6FEO | H1 | T120 | W6 | FEO | 9 |
| 362BLOCK4-G2H2T120_W6FEO | CGAAGTAT | GATCGTGT | 2 | H2T120_W6FEO | H2 | T120 | W6 | FEO | 16 |
| 363BLOCK4-G3H3T120_W6HO | TAGCAGCT | GATCGTGT | 2 | H3T120_W6HO | H3 | T120 | W6 | HO | 16 |
| 364BLOCK4-G4H4T120_W6HO | TCTCTATG | GATCGTGT | 2 | H4T120_W6HO | H4 | T120 | W6 | HO | 16 |
| 365BLOCK4-G5H5T120_W6FE | GATCTACG | GATCGTGT | 2 | H5T120_W6FE | H5 | T120 | W6 | FE | 16 |
| 366BLOCK4-G6H6T120_W6FE | GTAACGAG | GATCGTGT | 2 | H6T120_W6FE | H6 | T120 | W6 | FE | 9 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 367BLOCK4-G7H1T144_W6FEO | ACGTGCGC | GATCGTGT | 2 | H1T144_W6FEO | H1 | T144 | W6 | FEO | 9 |
| 368BLOCK4-G8H2T144_W6FEO | ATAGTACC | GATCGTGT | 2 | H2T144_W6FEO | H2 | T144 | W6 | FEO | 16 |
| 369BLOCK4-G9H3T144_W6HO | GCGTATAC | GATCGTGT | 2 | H3T144_W6HO | H3 | T144 | W6 | HO | 16 |
| 370BLOCK4-G10H4T144_W6HO | TGCTCGTA | GATCGTGT | 2 | H4T144_W6HO | H4 | T144 | W6 | HO | 16 |
| 371BLOCK4-G11H5T144_W6FE | AACGCTGA | GATCGTGT | 2 | H5T144_W6FE | H5 | T144 | W6 | FE | 16 |
| 372BLOCK4-G12H6T144_W6FE | CGTAGCGA | GATCGTGT | 2 | H6T144_W6FE | H6 | T144 | W6 | FE | 9 |
| 373BLOCK4-H1H1T168_W6FEO | CTCGACTT | GTCAGATA | 2 | H1T168_W6FEO | H1 | T168 | W6 | FEO | 9 |
| 374BLOCK4-H2H2T168_W6FEO | CGAAGTAT | GTCAGATA | 2 | H2T168_W6FEO | H2 | T168 | W6 | FEO | 16 |
| 375BLOCK4-H3H3T168_W6HO | TAGCAGCT | GTCAGATA | 2 | H3T168_W6HO | H3 | T168 | W6 | HO | 16 |
| 376BLOCK4-H4H4T168_W6HO | TCTCTATG | GTCAGATA | 2 | H4T168_W6HO | H4 | T168 | W6 | HO | 16 |
| 377BLOCK4-H5H5T168_W6FE | GATCTACG | GTCAGATA | 2 | H5T168_W6FE | H5 | T168 | W6 | FE | 16 |
| 378BLOCK4-H6H6T168_W6FE | GTAACGAG | GTCAGATA | 2 | H6T168_W6FE | H6 | T168 | W6 | FE | 9 |
| 379BLOCK4-H7H1T12_W3P | ACGTGCGC | GTCAGATA | 2 | H1T12_W3P | H1 | T12 | W3 | P2 | 9 |
| 380BLOCK4-H8H2T12_W3P | ATAGTACC | GTCAGATA | 2 | H2T12_W3P | H2 | T12 | W3 | P2 | 16 |
| 381BLOCK4-H9H3T12_W3P | GCGTATAC | GTCAGATA | 2 | H3T12_W3P | H3 | T12 | W3 | P2 | 16 |
| BLANK SAMPLE | | | | | | | | | |
| 383BLOCK4-H11H5T12_W3P | AACGCTGA | GTCAGATA | 2 | H5T12_W3P | H5 | T12 | W3 | P2 | 16 |
| 384BLOCK4-H12H6T12_W3P | CGTAGCGA | GTCAGATA | 2 | H6T12_W3P | H6 | T12 | W3 | P2 | 9 |

The linker primer sequence used for the samples was 5'- GTGCCAGCMGCCGCGGTAA-3'. Horses – H1-6; Time points in hours – T0-T168; Time points for % of markers retrieved – M1-M75; Weeks W0-6; Diets – PP (grazing pasture in paddocks); P1, P2 and P3 (cut pasture fed in stables in diet periods 1, 2 and 3, during weeks 1, 3 and 5 respectively); FE (ensiled chopped forage diet); FEO (ensiled chopped forage fed with whole oats); HO (hay fed with whole oats).

**Table S3. Diet-wise comparison of the alpha diversity indices of faecal bacterial genera across the three time points on days 5 (120h), 6 (144h) and 7 (168h) of the study period.**

| Alpha diversity index | Time points | | | P value* |
|---|---|---|---|---|
| | **120h** | **144h** | **168h** | |
| **Diet P1** | | | | |
| Simpson's (diversity) | 0.895 | 0.879 | 0.895 | 0.349 |
| Shannon-Weiner (entropy) | 2.756 | 2.612 | 2.769 | 0.132 |
| Chao 1 (richness) | 60 | 60 | 65 | 0.177 |
| | | | | |
| **Diet P2** | | | | |
| Simpson's (diversity) | 0.887 | 0.881 | 0.887 | 0.667 |
| Shannon-Weiner (entropy) | 2.774 | 2.663 | 2.768 | 0.155 |
| Chao 1 (richness) | 65 | 65 | 65 | 0.802 |
| | | | | |
| **Diet P3** | | | | |
| Simpson's (diversity) | 0.909 | 0.915 | 0.907 | 0.567 |
| Shannon-Weiner (entropy) | 2.912 | 2.944 | 2.884 | 0.155 |
| Chao 1 (richness) | 70 | 67 | 68 | 0.989 |
| | | | | |
| **Diet FE** | | | | |
| Simpson's (diversity) | 0.899 | 0.899 | 0.893 | 0.667 |
| Shannon-Weiner (entropy) | 2.786 | 2.798 | 2.853 | 0.567 |
| Chao 1 (richness) | 61 | 58 | 65 | 0.349 |
| | | | | |
| **Diet FE+O** | | | | |
| Simpson's (diversity) | 0.879 | 0.895 | 0.897 | 0.349 |
| Shannon-Weiner (entropy) | 2.725 | 2.817 | 2.831 | 0.081 |
| Chao 1 (richness) | 60 | 62 | 61 | 0.349 |
| | | | | |
| **Diet H+O** | | | | |
| Simpson's (diversity) | 0.898 | 0.886 | 0.891 | 0.922 |
| Shannon-Weiner (entropy) | 2.783 | 2.677 | 2.726 | 0.922 |
| Chao 1 (richness) | 64 | 61 | 62 | 0.959 |

*Friedman's test; level of significance was P≤0.016 after Bonferroni correction for multiple comparisons. The median values for alpha diversity indices are presented. Diets are represented as P1, P2, P3 - cut pasture fed during weeks 1, 3 and 5, respectively; FE - ensiled chopped forage; FE+O - ensiled chopped forage fed with whole oats; and H+O - hay fed with whole oats.

**Table S4. Relative abundance of the bacterial phyla in the faeces compared across diets.**

| Phyla | Mean relative abundance | | | | | | P value* |
|-------|------|------|------|------|------|------|----------|
|       | **P1** | **P2** | **P3** | **FE** | **FE+O** | **H+O** | |
| Firmicutes | 0.556 | 0.508 | 0.467 | 0.637 | 0.621 | 0.489 | <0.001* |
| Bacteroidetes | 0.319 | 0.365 | 0.376 | 0.227 | 0.239 | 0.214 | <0.001* |
| Spirochaetes | 0.032 | 0.027 | 0.029 | 0.052 | 0.048 | 0.168 | <0.001* |
| Verrucomicrobia | 0.026 | 0.022 | 0.043 | 0.013 | 0.016 | 0.032 | <0.001* |
| TM7 | 0.014 | 0.007 | 0.012 | 0.012 | 0.015 | 0.004 | <0.001* |
| Actinobacteria | 0.012 | 0.009 | 0.015 | 0.022 | 0.021 | 0.027 | <0.001* |
| Unassigned Phyla | 0.012 | 0.012 | 0.015 | 0.014 | 0.011 | 0.020 | 0.003* |
| WPS-2 | 0.007 | 0.005 | 0.005 | 0.003 | 0.002 | <0.001 | <0.001* |
| Fibrobacteres | 0.006 | 0.022 | 0.015 | 0.008 | 0.012 | 0.035 | <0.001* |
| Cyanobacteria | 0.004 | 0.010 | 0.009 | 0.002 | 0.003 | 0.003 | <0.001* |
| Proteobacteria | 0.004 | 0.004 | 0.004 | 0.003 | 0.003 | 0.002 | 0.002* |
| Synergistetes | 0.003 | 0.004 | 0.005 | 0.002 | 0.003 | 0.001 | 0.002* |
| Other Phyla <1% | 0.003 | 0.003 | 0.003 | 0.001 | 0.001 | <0.001 | <0.001* |
| Euryarchaeota | 0.002 | <0.001 | <0.001 | <0.001 | 0.001 | <0.001 | 0.274 |

*Kruskal-Wallis test; level of significance was P≤0.003 after Bonferroni correction for multiple comparisons. Samples collected on days 5, 6 and 7 of each treatment block were included in the analysis (see methods). Diets are represented as P1, P2, P3 - cut pasture fed during weeks 1, 3 and 5, respectively; FE - ensiled chopped forage; FE+O - ensiled chopped forage fed with whole oats; and H+O - hay fed with whole oats.

**Table S5. Relative abundance of the bacterial genera in the faeces compared across diets.**

| Genera | Mean relative abundance | | | | | | P value* |
|---|---|---|---|---|---|---|---|
| | P1 | P2 | P3 | FE | FE+O | H+O | |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Ruminococcaceae>unclassified genus | 0.180 | 0.164 | 0.135 | 0.143 | 0.150 | 0.100 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>unclassified genus | 0.158 | 0.135 | 0.114 | 0.181 | 0.171 | 0.125 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>unclassified family>unclassified genus | 0.157 | 0.195 | 0.16 | 0.113 | 0.133 | 0.134 | 0.004 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>unclassified family>unclassified genus | 0.125 | 0.108 | 0.100 | 0.145 | 0.145 | 0.150 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>YRC22 | 0.060 | 0.053 | 0.084 | 0.022 | 0.017 | 0.009 | <0.001* |
| Bacteria>Spirochaetes>Spirochaetes>Spirochaetales>Spirochaetaceae>Treponema | 0.032 | 0.026 | 0.029 | 0.053 | 0.049 | 0.169 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>Bacteroidaceae>BF311 | 0.025 | 0.020 | 0.018 | 0.007 | 0.010 | 0.011 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>BS11>unclassified genus | 0.020 | 0.020 | 0.033 | 0.017 | 0.017 | 0.011 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>unclassified genus | 0.018 | 0.014 | 0.014 | 0.011 | 0.013 | 0.012 | 0.031 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>CF231 | 0.018 | 0.020 | 0.023 | 0.031 | 0.024 | 0.019 | 0.032 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>[Mogibacteriaceae]>unclassified genus | 0.018 | 0.014 | 0.017 | 0.022 | 0.022 | 0.013 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Ruminococcaceae>Ruminococcus | 0.015 | 0.028 | 0.027 | 0.024 | 0.024 | 0.026 | 0.009 |
| Bacteria>TM7>TM7-3>CW040>F16>unclassified genus | 0.014 | 0.007 | 0.011 | 0.012 | 0.016 | 0.005 | <0.001* |
| Bacteria>Verrucomicrobia>Verruco-5>WCHB1-41>RFP12>unclassified genus | 0.013 | 0.017 | 0.030 | 0.008 | 0.008 | 0.010 | <0.001* |
| Bacteria>Verrucomicrobia>Verrucomicrobiae>Verrucomicrobiales>Verrucomicrobiaceae>Akkermansia | 0.013 | 0.006 | 0.015 | 0.007 | 0.010 | 0.023 | 0.009 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>Prevotellaceae>Prevotella | 0.010 | 0.013 | 0.019 | 0.017 | 0.013 | 0.011 | 0.004 |
| Bacteria>Actinobacteria>Coriobacteriia>Coriobacteriales>Coriobacteriaceae>unclassified genus | 0.009 | 0.005 | 0.009 | 0.012 | 0.011 | 0.010 | 0.066 |
| Bacteria>WPS-2>unclassified class>unclassified order >unclassified family>unclassified genus | 0.008 | 0.006 | 0.006 | 0.003 | 0.002 | 0.001 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>Clostridium | 0.007 | 0.005 | 0.008 | 0.027 | 0.027 | 0.011 | <0.001* |
| Bacteria>Fibrobacteres>Fibrobacteria>Fibrobacterales>Fibrobacteraceae>Fibrobacter | 0.007 | 0.023 | 0.016 | 0.009 | 0.013 | 0.035 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Ruminococcaceae>Oscillospira | 0.006 | 0.006 | 0.004 | 0.008 | 0.007 | 0.006 | 0.250 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Veillonellaceae>Phascolarctobacterium | 0.006 | 0.007 | 0.011 | 0.021 | 0.011 | 0.008 | 0.009 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Eubacteriaceae>Pseudoramibacter_Eubacterium | 0.006 | 0.005 | 0.007 | 0.003 | 0.003 | 0.002 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>unclassified genus | 0.006 | 0.004 | 0.006 | 0.006 | 0.007 | 0.007 | 0.081 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>Coprococcus | 0.006 | 0.006 | 0.007 | 0.023 | 0.021 | 0.014 | <0.001* |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>Porphyromonadaceae>Paludibacter | 0.006 | 0.014 | 0.014 | 0.003 | 0.005 | 0.002 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Christensenellaceae>unclassified genus | 0.005 | 0.004 | 0.005 | 0.006 | 0.007 | 0.005 | 0.002 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>[Mogibacteriaceae]>Mogibacterium | 0.004 | 0.003 | 0.006 | 0.004 | 0.004 | 0.002 | 0.015 |
| Bacteria>Cyanobacteria>4C0d-2>YS2>unclassified family>unclassified genus | 0.004 | 0.011 | 0.009 | 0.003 | 0.003 | 0.003 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>RF16>unclassified genus | 0.004 | 0.013 | 0.006 | 0.002 | 0.002 | 0.003 | <0.001* |
| Bacteria>Actinobacteria>Coriobacteriia>Coriobacteriales>Coriobacteriaceae>Adlercreutzia | 0.004 | 0.003 | 0.005 | 0.009 | 0.010 | 0.014 | <0.001* |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>S24-7>unclassified genus | 0.004 | 0.002 | 0.005 | 0.005 | 0.006 | 0.002 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Veillonellaceae>unclassified genus | 0.004 | 0.002 | 0.003 | 0.005 | 0.004 | 0.002 | <0.001* |
| Bacteria>Firmicutes>Erysipelotrichi>Erysipelotrichales>Erysipelotrichaceae>p-75-a5 | 0.004 | 0.002 | 0.004 | 0.002 | 0.002 | 0.001 | <0.001* |
| Bacteria>Synergistetes>Synergistia>Synergistales>Synergistaceae>unclassified genus | 0.003 | 0.004 | 0.005 | 0.002 | 0.003 | 0.002 | 0.003 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>unclassified genus | 0.003 | 0.006 | 0.004 | 0.005 | 0.005 | 0.004 | 0.002 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>[Prevotella] | 0.003 | 0.006 | 0.005 | 0.007 | 0.004 | 0.006 | 0.108 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>unclassified genus | 0.003 | 0.001 | 0.001 | <0.001 | <0.001 | 0.001 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>unclassified family>unclassified genus | 0.002 | 0.005 | 0.005 | 0.005 | 0.005 | 0.006 | 0.003 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>Pseudobutyrivibrio | 0.002 | 0.005 | 0.003 | 0.004 | 0.002 | 0.007 | <0.001* |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>Blautia | 0.002 | 0.002 | 0.002 | 0.008 | 0.007 | 0.004 | <0.001* |
| Bacteria>Firmicutes>Bacilli>Lactobacillales>Lactobacillaceae>Lactobacillus | 0.001 | 0.002 | 0.002 | <0.001 | 0.001 | 0.002 | <0.001* |
| Bacteria>Firmicutes>Erysipelotrichi>Erysipelotrichales>Erysipelotrichaceae>RFN20 | 0.001 | 0.002 | 0.003 | 0.001 | 0.001 | 0.001 | <0.001* |
| Bacteria>Spirochaetes>MVP-15>PL-11B10>unclassified family>unclassified genus | 0.001 | 0.002 | 0.001 | 0.001 | 0.001 | 0.001 | <0.001* |
| Bacteria>Actinobacteria>Actinobacteria>Actinomycetales>Corynebacteriaceae>Corynebacterium | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.009 |
| Bacteria>Firmicutes>Erysipelotrichi>Erysipelotrichales>Erysipelotrichaceae>[Eubacterium] | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.002 | 0.009 |
| Bacteria>Actinobacteria>Coriobacteriia>Coriobacteriales>Coriobacteriaceae>Collinsella | 0.001 | 0.001 | 0.001 | 0.002 | 0.002 | 0.003 | <0.001* |
| Bacteria>Proteobacteria>Gammaproteobacteria>Pseudomonadales>Moraxellaceae>Acinetobacter | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.165 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>SMB53 | 0.001 | 0.001 | 0.001 | <0.001 | <0.001 | <0.001 | <0.001* |
| Bacteria>Proteobacteria>Alphaproteobacteria>Rhizobiales>Hyphomicrobiaceae>Devosia | <0.001 | 0.001 | 0.001 | 0.001 | <0.001 | 0.001 | 0.517 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Veillonellaceae>Megasphaera | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | - |
| Other Genera <1% | 0.013 | 0.014 | 0.016 | 0.012 | 0.014 | 0.010 | 0.024 |
| Unassigned Genera | 0.012 | 0.012 | 0.015 | 0.014 | 0.012 | 0.021 | 0.004 |

*Kruskal-Wallis test; level of significance was P≤0.001 after Bonferroni correction for multiple comparisons. Samples collected on days 5, 6 and 7 of each treatment block were included in the analysis (see methods). Diets are represented as P1, P2, P3 - cut pasture fed during weeks 1, 3 and 5, respectively; FE - ensiled chopped forage; FE+O - ensiled chopped forage fed with whole oats; and H+O - hay fed with whole oats.

**Table S6. Relative abundance of faecal bacterial phyla across three time points on day 5 (T120), day6 (T144) and day 7 (T168) of the study period.**

| Phyla | Mean relative abundance | | | P value* |
|---|---|---|---|---|
| | **T120** | **T144** | **T168** | |
| Firmicutes | 0.574 | 0.541 | 0.527 | 0.343 |
| Bacteroidetes | 0.280 | 0.293 | 0.301 | 0.835 |
| Spirochaetes | 0.055 | 0.062 | 0.064 | 0.081 |
| Verrucomicrobia | 0.019 | 0.029 | 0.031 | 0.253 |
| Fibrobacteres | 0.017 | 0.017 | 0.017 | 0.462 |
| Actinobacteria | 0.017 | 0.019 | 0.018 | 0.817 |
| Unassigned Phyla | 0.013 | 0.014 | 0.016 | 0.644 |
| TM7 | 0.010 | 0.011 | 0.012 | 0.986 |
| Cyanobacteria | 0.005 | 0.006 | 0.006 | 0.317 |
| WPS-2 | 0.005 | 0.004 | 0.004 | 0.760 |
| Proteobacteria | 0.004 | 0.004 | 0.004 | 0.271 |
| Synergistetes | 0.004 | 0.003 | 0.004 | 0.199 |
| Other Phyla <1% | 0.002 | 0.003 | 0.003 | 0.695 |
| Euryarchaeota | <0.001 | 0.002 | 0.002 | 0.137 |

*Friedman's test; level of significance was $P \leq 0.003$ after Bonferroni correction for multiple comparisons.

**Table S7. Relative abundance of faecal bacterial genera across three time points on day 5 (T120), day6 (T144) and day 7 (T168) of the study period.**

| Genera | Mean relative abundance | | | P value* |
|---|---|---|---|---|
| | **T120** | **T144** | **T168** | |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>unclassified genus | 0.157 | 0.143 | 0.142 | 0.907 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Ruminococcaceae>unclassified genus | 0.152 | 0.143 | 0.141 | 0.507 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>unclassified family>unclassified genus | 0.138 | 0.152 | 0.156 | 0.576 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>unclassified family>unclassified genus | 0.137 | 0.128 | 0.121 | 0.707 |
| Bacteria>Spirochaetes>Spirochaetes>Spirochaetales>Spirochaetaceae>Treponema | 0.055 | 0.061 | 0.063 | 0.679 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>YRC22 | 0.046 | 0.039 | 0.038 | 0.907 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Ruminococcaceae>Ruminococcus | 0.027 | 0.022 | 0.023 | 0.105 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>CF231 | 0.023 | 0.022 | 0.023 | 0.888 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>[Mogibacteriaceae]>unclassified genus | 0.017 | 0.018 | 0.018 | 0.635 |
| Bacteria>Fibrobacteres>Fibrobacteria>Fibrobacterales>Fibrobacteraceae>Fibrobacter | 0.017 | 0.017 | 0.017 | 0.833 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>BS11>unclassified genus | 0.016 | 0.022 | 0.021 | 0.126 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>Bacteroidaceae>BF311 | 0.014 | 0.017 | 0.015 | 0.268 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>Clostridium | 0.014 | 0.016 | 0.013 | 0.904 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>Prevotellaceae>Prevotella | 0.014 | 0.013 | 0.014 | 0.720 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>unclassified genus | 0.014 | 0.013 | 0.013 | 0.653 |
| Bacteria>Verrucomicrobia>Verruco-5>WCHB1-41>RFP12>unclassified genus | 0.012 | 0.016 | 0.016 | 0.119 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Veillonellaceae>Phascolarctobacterium | 0.012 | 0.009 | 0.011 | 0.473 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>Coprococcus | 0.012 | 0.013 | 0.013 | 0.986 |
| Bacteria>TM7>TM7-3>CW040>F16>unclassified genus | 0.010 | 0.011 | 0.012 | 0.307 |
| Bacteria>Actinobacteria>Coriobacteriia>Coriobacteriales>Coriobacteriaceae>unclassified genus | 0.009 | 0.010 | 0.009 | 0.218 |
| Bacteria>Verrucomicrobia>Verrucomicrobiae>Verrucomicrobiales>Verrucomicrobiaceae>Akkermansia | 0.008 | 0.013 | 0.016 | 0.166 |
| Bacteria>Actinobacteria>Coriobacteriia>Coriobacteriales>Coriobacteriaceae>Adlercreutzia | 0.007 | 0.007 | 0.008 | 0.768 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Ruminococcaceae>Oscillospira | 0.006 | 0.006 | 0.006 | 0.201 |

| | | | | |
|---|---|---|---|---|
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>Porphyromonadaceae>Paludibacter | 0.006 | 0.007 | 0.008 | 0.167 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Christensenellaceae>unclassified genus | 0.006 | 0.006 | 0.005 | 0.573 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>unclassified family>unclassified genus | 0.005 | 0.004 | 0.004 | 0.048 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>[Paraprevotellaceae]>[Prevotella] | 0.005 | 0.004 | 0.006 | 0.703 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>Blautia | 0.005 | 0.004 | 0.004 | 0.748 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>RF16>unclassified genus | 0.005 | 0.005 | 0.005 | 0.461 |
| Bacteria>WPS-2>unclassified class>unclassified order>unclassified family>unclassified genus | 0.005 | 0.004 | 0.004 | 0.449 |
| Bacteria>Cyanobacteria>4C0d-2>YS2>unclassified family>unclassified genus | 0.005 | 0.006 | 0.006 | 0.925 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>unclassified genus | 0.005 | 0.004 | 0.004 | 1.000 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>unclassified genus | 0.005 | 0.007 | 0.006 | 0.677 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Eubacteriaceae>Pseudoramibacter_Eubacterium | 0.004 | 0.005 | 0.004 | 0.309 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Lachnospiraceae>Pseudobutyrivibrio | 0.004 | 0.004 | 0.004 | 0.922 |
| Bacteria>Bacteroidetes>Bacteroidia>Bacteroidales>S24-7>unclassified genus | 0.004 | 0.004 | 0.004 | 0.965 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>[Mogibacteriaceae]>Mogibacterium | 0.003 | 0.005 | 0.003 | 0.076 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Veillonellaceae>unclassified genus | 0.003 | 0.003 | 0.003 | 0.508 |
| Bacteria>Synergistetes>Synergistia>Synergistales>Synergistaceae>unclassified genus | 0.003 | 0.003 | 0.004 | 0.281 |
| Bacteria>Firmicutes>Erysipelotrichi>Erysipelotrichales>Erysipelotrichaceae>p-75-a5 | 0.002 | 0.003 | 0.003 | 0.924 |
| Bacteria>Proteobacteria>Alphaproteobacteria>Rhizobiales>Hyphomicrobiaceae>Devosia | <0.001 | <0.001 | <0.001 | - |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>SMB53 | <0.001 | <0.001 | <0.001 | 0.453 |
| Bacteria>Actinobacteria>Coriobacteriia>Coriobacteriales>Coriobacteriaceae>Collinsella | <0.001 | 0.002 | <0.001 | 0.602 |
| Bacteria>Firmicutes>Bacilli>Lactobacillales>Lactobacillaceae>Lactobacillus | <0.001 | <0.001 | <0.001 | 0.729 |
| Bacteria>Proteobacteria>Gammaproteobacteria>Pseudomonadales>Moraxellaceae>Acinetobacter | <0.001 | 0.001 | 0.001 | 0.541 |
| Bacteria>Firmicutes>Erysipelotrichi>Erysipelotrichales>Erysipelotrichaceae>RFN20 | <0.001 | <0.001 | <0.001 | 0.958 |
| Bacteria>Actinobacteria>Actinobacteria>Actinomycetales>Corynebacteriaceae>Corynebacterium | <0.001 | <0.001 | <0.001 | 0.833 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Clostridiaceae>unclassified genus | <0.001 | <0.001 | <0.001 | 0.989 |
| Bacteria>Firmicutes>Erysipelotrichi>Erysipelotrichales>Erysipelotrichaceae>[Eubacterium] | <0.001 | <0.001 | <0.001 | 1.000 |
| Bacteria>Spirochaetes>MVP-15>PL-11B10>unclassified family>unclassified genus | <0.001 | <0.001 | <0.001 | 0.921 |
| Bacteria>Firmicutes>Clostridia>Clostridiales>Veillonellaceae>Megasphaera | <0.001 | <0.001 | <0.001 | - |

| | | | | |
|---|---|---|---|---|
| Other Genera <1% | 0.012 | 0.013 | 0.014 | 0.115 |
| Unassigned Genera | 0.013 | 0.014 | 0.016 | 0.232 |

*Friedman's test; level of significance was P≤0.001 after Bonferroni correction for multiple comparisons.