# Study links specific gut bacteria to increased risk of severe malaria

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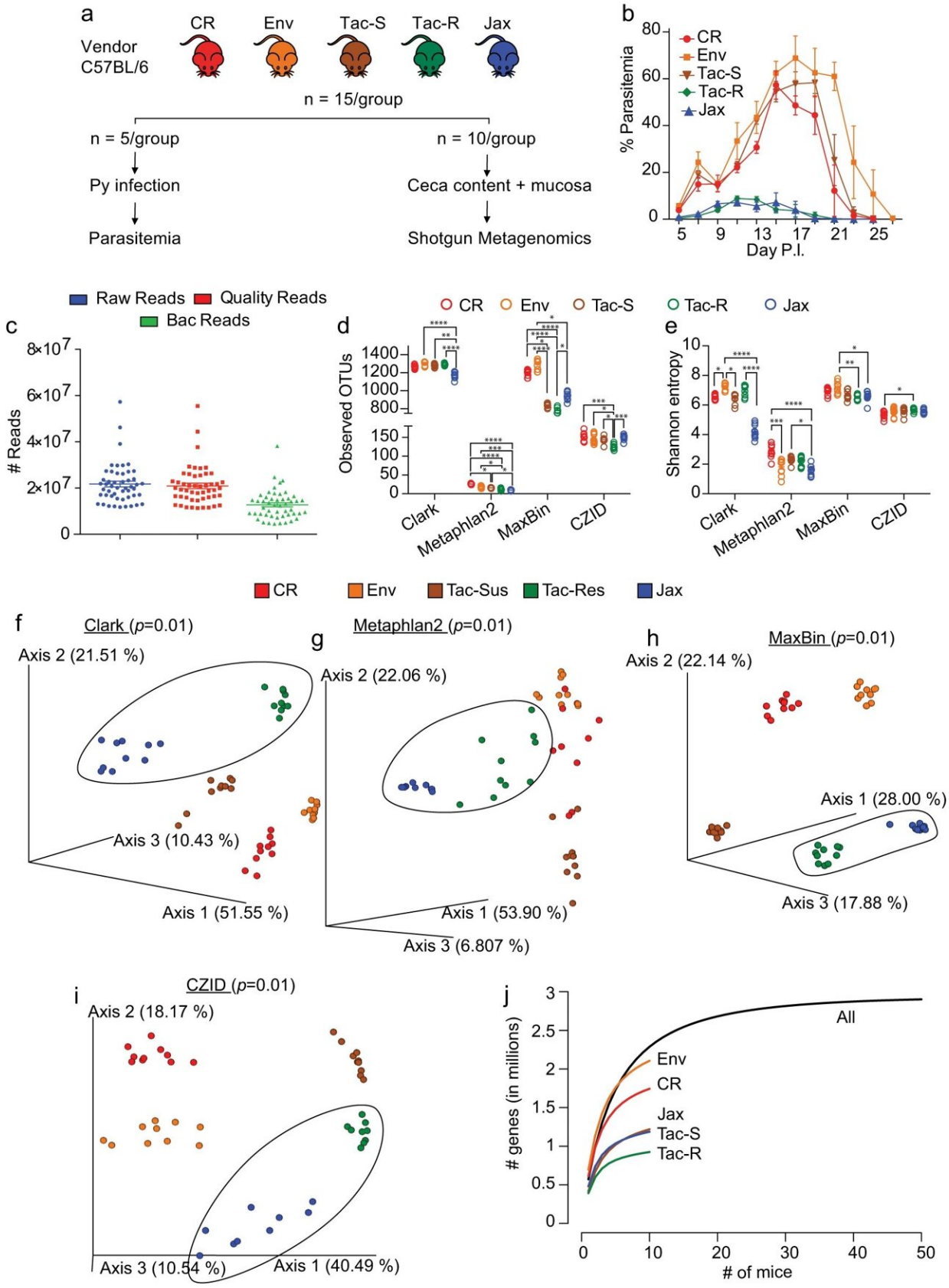
a
Vendor
C57BL/6
CR
Env
Tac-S
Tac-R
Jax
n = 15/group
n = 5/group
n = 10/group
Py infection
Ceca content + mucosa
Parasitemia
Shotgun Metagenomics
b
% Parasitemia
Day P.I.
c
Raw Reads
Quality Reads
Bac Reads
# Reads
d
Observed OTUs
Clark
Metaphlan2
MaxBin
CZID
e
Shannon entropy
Tac-Sus
Tac-Res
f
Clark (p=0.01)
Axis 2 (21.51 %)
Axis 3 (10.43 %)
Axis 1 (51.55 %)
g
Metaphlan2 (p=0.01)
Axis 2 (22.06 %)
Axis 1 (53.90 %)
Axis 3 (6.807 %)
h
MaxBin (p=0.01)
Axis 2 (22.14 %)
Axis 1 (28.00 %)
Axis 3 (17.88 %)
i
CZID (p=0.01)
Axis 2 (18.17 %)
Axis 3 (10.54 %)
Axis 1 (40.49 %)
j
# genes (in millions)
All
# of mice

Shotgun metagenomics revealed distinct gut microbiota composition and genetic potential within and between the hyperparasitemia resistant and susceptible mice. **a** C57BL/6 mice were acquired from four different vendors (*N* = 15/group): Charles River Laboratories (CR), Envigo (Env), Taconic Biosciences (Tac), and Jackson Laboratory (Jax). Mice from Taconic Biosciences were obtained from two different facilities with differential susceptibility to Py hyperparasitemia[12]. Five mice from each group were infected with Py while the remaining ten mice were sacrificed to collect ceca content along with mucosa scrapes for shotgun metagenomics. **b** Parasitemia curve of mice infected with Py. **c** Number of fastq reads after shotgun sequencing and quality control. **d** Alpha diversity measured using observed taxonomic units (OTUs) defined at species level. **e** Alpha diversity measure by Shannon entropy. **f** Beta diversity shown by Principal coordinate analysis (PCoA) plot using Clark output at species level with Bray-Curtis distance. **g** Beta diversity shown by PCoA plot using Metaphlan2 output at species level with Bray-Curtis distance. **h** Beta diversity shown by PCoA plot using MaxBin output at species level with Bray-Curtis distance. **i** Beta diversity shown by PCoA plot using CZID output at bin level with Bray-Curtis distance. **j** Number of unique genes detected at 95% sequence homology. All data are mean ± SE (standard error) unless explicitly stated. Bacterial diversity was performed on normalized data. Mice resistant to hyperparasitemia are encircled (**f–i**). Alpha diversity significance were calculated with Kruskal Wallis test and beta diversity significance by pairwise Permutational multivariate analysis of variance (PERMANOVA). *$p$