



ZYMO RESEARCH

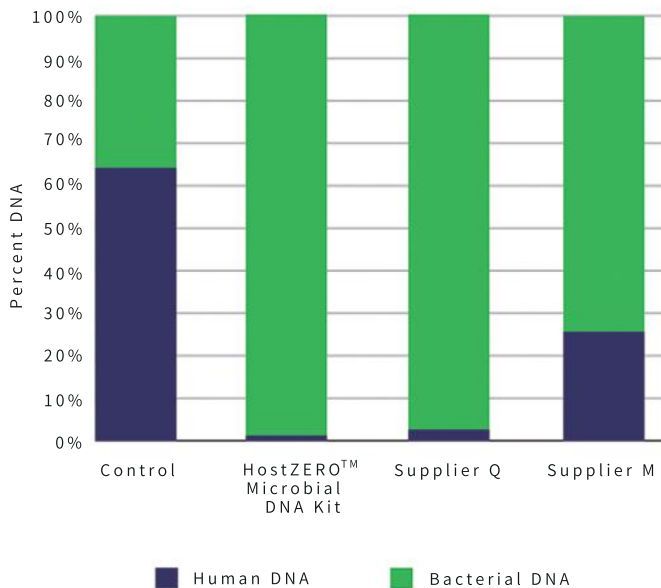
The Beauty of Science is to Make Things Simple®

最简单的宿主DNA去除方法

HostZERO™ Microbial DNA Kit

- 去除宿主DNA：在适用样品类型中宿主DNA去除率高达90%以上。
- 微生物DNA完整度：可有效回收85%的微生物DNA并且最低程度的对微生物群落造成影响。
- 简单快速：操作时间只有30分钟。

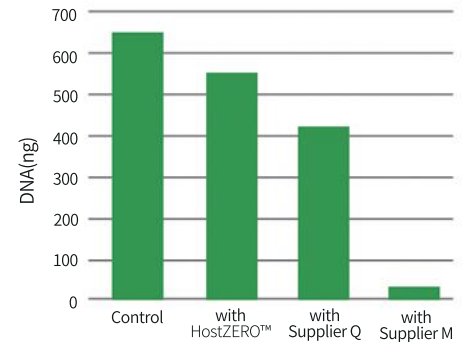
宿主DNA的去除效率



HostZERO™ Microbial DNA Kit去除了宿主DNA。相同的人类唾液样本是使用HostZERO™ Microbial DNA Kit或供应商Q和M的试剂盒进行处理。纯化的DNA样品通过RT-PCR进行评估。DNA的组成是以相对细菌和人类DNA的丰度显示。对照样品是用ZymoBIOMICS® DNA Microprep Kit处理后，从试剂盒中提取总DNA中没有去除宿主DNA。

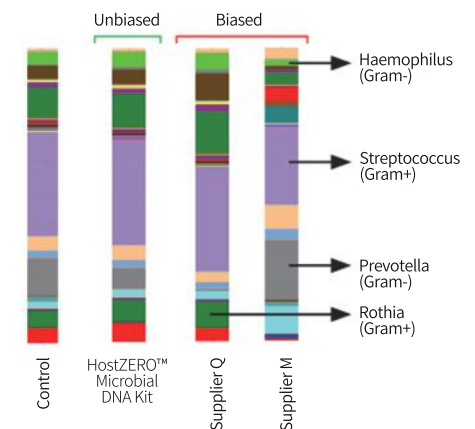
可与 Zymo Research 的纯化产品配合使用。

细菌DNA的回收效率



HostZERO™ 技术可以有效回收细菌DNA。使用HostZERO Microbial DNA Kit或供应商Q和M的试剂盒处理同一个人唾液样品。一式三份的DNA样品通过RT-PCR评估。对照样品用DNA Microprep Kit处理，该试剂盒可从样品中提取细菌总DNA。

保留微生物完整性



使用HostZERO™ Microbial DNA Kit处理样品中的微生物成分保持不变。

使用HostZERO™ Microbial DNA Kit或供应商的试剂盒Q和M。一式三份的纯化DNA样品进行了分析使用16S rRNA基因靶向测序，使用引物定位到V3-V4区域。得到的扩增子是在IlluminaMiSeq® (2x300bp)上测序。对照样品是用DNA Microprep Kit处理。

产品	货号	规格
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HostZERO™ Microbial DNA Kit	D4310	50 preps
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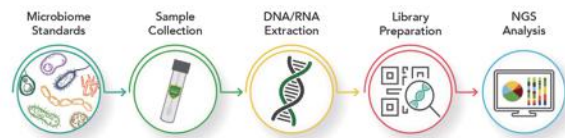
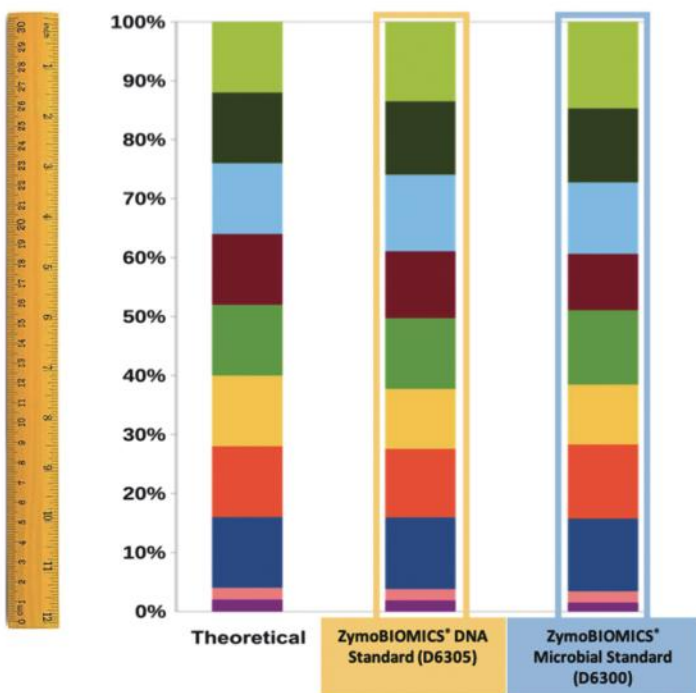
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ZymoBIOMICS Microbiome Standards 微生物标准品



准确的表征微生物组成部分

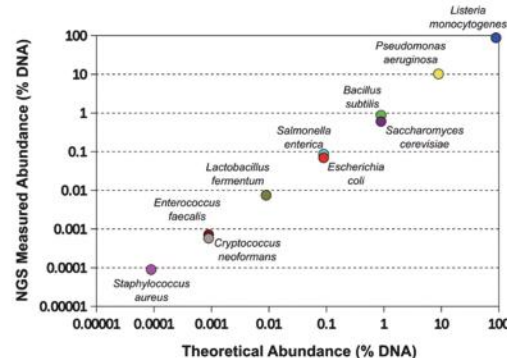


低杂质，微生物组QC
的理想选择

Species	mOTU counts	Abund. (%)
<i>Bacillus subtilis</i>	9048	11.86
<i>Enterococcus faecalis</i>	11322	14.84
<i>Escherichia coli</i>	6994	9.17
<i>Lactobacillus fermentum</i>	17081	22.39
<i>Listeria monocytogenes</i>	11454	15.01
<i>Pseudomonas aeruginosa</i>	4484	5.88
<i>Salmonella enterica</i>	7939	10.41
<i>Staphylococcus aureus</i>	7960	10.43
<i>Propionibacterium acnes</i>	1	0.0013

< 0.01% foreign microbial DNA

评估微生物组度量中的偏差
可以评估操作流程的准确性，
误报率和检测限。



ZymoBIOMICS® Standards	Microbial Community Standard		Microbial Community Standard II		Spike-in Control		HMW DNA Standard
	Cat #	D6300	D6305, D6306	D6310	D6311	D6320, D6320-10	D6321, D6321-10
Formats	Microbial Cell	Isolated DNA	Microbial Cell	Isolated DNA	High Microbial Load	Low Microbial Load	Isolated DNA
Number of Organisms	10	10	10	10	2	3	8
Composition	Even	Even	Staggered (Log)	Staggered (Log)	Even	Staggered (Log)	Even
Detect Bias In:	Complete Workflow & DNA Extraction	Library Prep & Sequencing	Complete Workflow & DNA Extraction	Library Prep & Sequencing	Complete Workflow & DNA Extraction	Complete Workflow & DNA Extraction	Long-read Library Prep & Sequencing
Recommended Use	General benchmarking and microbiome profiling control		Assess detection limit and sensitivity		Absolute quantification of high bacterial-load samples (i.e., feces)	Absolute quantification of low bacterial-load samples (i.e., sputum)	General benchmarking and microbiome profiling control for long-read sequencing