

Table S1. List of species accessions used to compile the Tree of Life.

Table S2. List of sequence read archive datasets.

Table S3. List of 64-mer probes. (A) Probes covering the microbial Tree of Life. (B) Housekeeping gene probes. (C) Probes for retroelements and endogenous retroviruses.

Table S4. List of human-associated species (PATHLIST).

Table S5. Matches between key viruses and the human genome.

Table S6. Stripped viral genomes. This Table is 350 pages in length and is supplied separately.

Table S7. Identification of liver- and brain (cortex)-specific signals.

Figure S1. Some brain microbiome profiles are suggestive of contamination.

Figure S2. Microbiome profiles of liver versus cortex.

Table S1. List of species accessions used to compile the Tree of Life.

Domain	Code	Kingdom/Phylum	Subtaxon	Species	Systematic name	Accession
Archaea	A	Halobacteria		<i>Halobacterium salinarum</i>	A_Hsalinarum_16S	NR_025555.1
		Methanococci		<i>Methanocaldococcus</i> SG1	A_MethanocaldococcusSG1_16S	MK602649.1
		Methanopyri		<i>Methanopyrus kandleri</i>	A_Mkandleri_16S	NR_074539.1
		Thermococci		Thermococci archaeon NE31B05cA	A_Tarchaeon_16S	DQ423947.1
		Korarchaeota	SRI-306	Korarchaeota SRI-306	A_KorarchaeotaSRI306_16S	AF255604.1
		Thermoplasmata		Thermoplasmata archaeon Kjm51a	A_ThermoplasmataKjm51a_16S	AB749767.1
		Thaumarchaeota		Thaumarchaeota archaeon NAOA2	A_ThaumarchaeotaNAOA2_16S	KT380501.1
		Archaeoglobi		Archaeon TE1-87-T7	A_ArchaeonTE187T7_16S	KX098446.1
		Methanoliparaceae		<i>Methanoliparum thermophilum</i>	A_Mthermophilum_16S	RXIF01000002.1
		Asgard		Archaeon 26ABF_S2	A_Archaeon26ABFS2_16S	MN444134.1
Bacteria	B0	Desulfobacteraceae		Desulfobacteraceae cLaKi	B0_DesulfobacteraceaecLaKi_16S	AJ582710.1
	B0	Coriobacteriia		<i>Coriobacterium</i> CCUG_33917	B0_CoriobacteriumCCUG33917_16S	AJ131149.1
	B0	Thermotogae		<i>Thermotoga maritima</i>	B0_Tmaritima_16S	NR_102775.2
	B0	Limnochordia		<i>Limnochorda pilosa</i>	B0_Lpilosa_16S	AP014924.1
	B0	EM3		<i>Marinobacter</i> EM3	B0_MarinobacterEM3_16S	HG004173.1
	B0	Aquificae		Aquificae SHNS732	B0_AquificaeSHNS732_16S	HM110206.1
	B0	Acetothermia		Acetothermia TuzSed3B	B0_AcetothermiaTuzSed3B_16S	MT523014.1

	B1	Spirochaetes	<i>Treponema pallidum</i> subsp. <i>pertenue</i>	B1_Tpallidum_16S	AF426102.1
	B2	Saccharibacteria	Candidatus Saccharibacteria HXBF1-28	B2_CsaccharibacteriaHXBF128_16S	KJ540650.1
	B2	Peregrinibacteria	Candidatus Peregrinibacteria GW2011	B2_CperegrinibacteriaGW2011_16S	KX123616.1
	B2	Parcubacteria	Parcubacteria GBS- 2	B2_ParcubacteriaGBS2_16S	KT033776.1
	B3	Acidobacteria	Acidobacteria KBS96	B3_AcidobacteriaKBS96_16S	FJ870384.1
	B3	Deltaproteobacteria	<i>Deltaproteobacteria</i> hwp6	B3_Deltaproteobacteriahwp6_16S	MT084045.1
	B4	Planctomycetes	<i>Planctomycetes</i> V144	B4_PlanctomycetesV144_16S	MK554519.1
	B5	Latescibacteria	Latescibacteria 134476n2	B5_Latescibacteria134476n2_16S	MK048603.1
	B5	Marinimicrobia	Candidatus <i>Marinimicrobia</i> 61467n6	B5_Cmarinimicrobia61467n6_16S	MK048793.1
	B6	Bacteriodes	<i>Thermonema</i> <i>rossianum</i>	B6_Trossianum_16S	NR_026367.1
	B6	Bacteriodes	<i>Prevotella intermedia</i>	B6_Pintermedia_16S	LT707625.1
Chloroplastida	C1	Euglenozoa	<i>Phacus</i> <i>brachykentron</i>	C1_Pbrachykentron_18S	AJ532481.1
		Euglenozoa	<i>Colacium</i> <i>mucronatum</i>	C1_Cmucronatum_18S	AJ532440.1
		Parabasalia	<i>Trichomonas</i> <i>vaginalis</i>	C1_Tvaginalis_18S	KM282377.1
		Jakobida	<i>Jakoba libera</i>	C1_Jlibera_18S	AF411288.1
		Preaxostyla	<i>Paratrimastix</i> <i>pyriformis</i>	C1_Ppyriformis_18S	KT388052.1
	C2	Glaucophyta	<i>Glaucocystis</i> ARP- 2014	C2_GlaucocystisARP2014_18S	KF631388.1
		Haptophyta	<i>Isochrysis galbana</i>	C2_Igalbana_18S	KX980524.1

	SAR/Ciliophora	<i>Spirostomum minus</i>	C2_Sminus_18S	MK929559.1
	SAR/Apicomplexa	<i>Plasmodium falciparum</i>	C2_Pfalciparum_18S	XR_002966654.1
	SAR/Apicomplexa	<i>Plasmodium gallinaceum</i>	C2_Pgallinaceum_18S	XR_003699198.1
	SAR/Stramenopiles	<i>Heteromita globosa</i>	C2_Hglobosa_18S	U42447.1
	SAR/Rhizaria	<i>Plasmodiophora brassicae</i>	C2_Pbrassicae_18S	AB094976.1
C3	Galdieria	<i>Galdieria sulphuraria</i>	C3_Gsulphuraria_18S	LC504058.1
	Cyanidioschyzon	<i>Cyanidioschyzon merolae</i>	C3_Cmerolae_18S	XR_002461616.1
	Cyanadinium	<i>Cyanadinium caldarium</i>	C3_Ccaldarium_18S	AB091231.1
	Compsopogonales	<i>Compsopogon caeruleus</i>	C3_Ccaeruleus_18S	KC596285.1
	Porphyridiophyceae	<i>Porphyridium aerugineum</i>	C3_Paerugineum_18S	AJ421145.1
	Floridophycidea	<i>Porphyridium purpureum</i>	C3_Ppurpureum_18S	KY054989.1
	Rhodellophyceae	<i>Rhodella violacea</i>	C3_Rviolacea_18S	AB045580.1
	Goniotrichopsis	<i>Goniotrichiopsis sublittoralis</i>	C3_Gsublittoralis_18S	AF168629.1
C4	Chlorophyta	<i>Atractomorpha echinata</i>	C4_Aechinata_18S	U73470.1
	Chlorophyta	<i>Golenkinia longispicula</i>	C4_Glongispicula_18S	AF499923.1
	Chlorophyta	<i>Pleuraestrosarcina brevispinosa</i>	C4_Pbrevispinosa_18S	KM020187.1
	Chlorophyta	<i>Elliptochloris bilobata</i>	C4_Ebilobata_18S	AM422984.1
	Streptophyta	<i>Chlorokybus atmophyticus</i>	C4_Catmophyticus_18S	AF408244.1
	Streptophyta	<i>Chara vulgaris</i>	C4_Cvulgaris_18S	AF032747.1
	Kathablepharidae	<i>Leucocryptos marina</i>	C4_Lmarina_18S	KY980342.1
	Cryptomodadales	<i>Guillardia theta</i>	C4_Gtheta_18S	X57162.1

		Goniomonas	<i>Goniomonas avonlea</i>	C4_Gavonlea_18S	JQ434475.1
Amoebozoa	D	Amoebozoa	<i>Diderma testaceum</i>	D_Dtestaceum_18S	HM101142.1
		Archamoebae	<i>Rhizomastix bicoronata</i>	D_Rbicoronata_18S	KP343638.1
		Ciliophryidea	<i>Ciliophora aOmb2</i>	D_CaOmb2_18S	LN869948.1
		Hemimastigida	<i>Hemimastix kukwesjijk</i>	D_Hkukwesjijk_18S	MF682191.1
		Centrohelida	<i>Raphidocystis contractilis</i>	D_Rcontractilis_18S	AB196984.1
		Nucleomyxa	<i>Fonticula alba</i>	D_Falba_18S	FJ816018.1
		Physarum	<i>Trichia varia</i>	D_Tvaria_18S	KM495055.1
Basal Eukaryota	E0	Rhodelphida	<i>Rhodelphis limneticus</i>	E0_Rlimneticus_18S	MK966713.1
		Micronuclearia	<i>Rigifila ramosa</i>	E0_Rramosa_18S	AB686266.1
		Diphyllia	<i>Diphyllia rotans</i>	E0_Drotans_18S	MF039354.1
		Apusomonadida	<i>Multimonas media</i>	E0_Mmedia_18S	KP996852.1
		Centrohelida	<i>Spiculophrys agregata</i>	E0_Sagregata_18S	KU178913.1
Fungi	F0	Paraphelidium	<i>Paraphelidium tribonemae</i>	F0_Ptribonemae_18S	KX576681.1
		Nucleariida	<i>Nuclearia thermophila</i>	F0_Nthermophila_18S	HG530253.1
		Rozellida	<i>Rozella allomyces</i>	F0_Rallomyces_18S	KX354828.1
		Amoeboaphelidium	<i>Amoeboaphelidium WZ01</i>	F0_AmoebaphelidiumWZ01_18S	KU983765.1
	F1	Antonosporea/Chytridiopsidae	<i>Enterocytozoon bieneusi</i>	F1_Ebieneusi_18S	ABGB01001533.1
		Glugea	<i>Glugea LM2016</i>	F1_GlugeaLM2016_18S	KU577431.1
		Chytridiopsida	<i>Enterocytozoon hepatopenaei</i>	F1_Ehepatopenaei_18S	KY643648.1
		Fibrillaspora	<i>Fibrillaspora daphniae</i>	F1_Fdaphniae_18S	MF278272.1
		Nosema	<i>Nosema BM201821</i>	F1_NosemaBM201821_18S	LC467329.1

	Culicosporidae	<i>Edhazardia aedis</i>	F1_Eaedis_18S	AF027684.1
	Anncaliia	<i>Anncaliia algerae</i>	F1_Aalgerae_18S	HM216911.1
	Metchnikovellida	<i>Metchnikovella spiralis</i>	F1_Mspiralis_18S	MW344837.1
	h2007-2/Diversisporales	<i>Entrophospora colombiana</i>	F2_Ecolombiana_18S	AB220170.1
	h2007-2/Glomerales	<i>Rhizophagus intraradices</i>	F2_Rintraradices_18S	MF401586.1
	h2007-2/Glomerales	<i>Glomus NBRPP1</i>	F2_GlomusNBRPP1_18S	EF136912.1
	Zoopagales	<i>Rhopalomyces elegans</i>	F2_Relegans_18S	AY635834.1
	Zoopagales	<i>Thamnocephalis sphaerospora</i>	F2_Tsphaerospora_18S	AB016013.1
F3	Monoblepharidales	<i>Gonapodya polymorpha</i>	F3_Gpolymorpha_18S	AY349028.1
	Neocallimastigales	<i>Orpinomyces CA34</i>	F3_OrpinomycesCA34_18S	KC922183.1
	Rhizophydiales	<i>Boothiomyces macroporosum</i>	F3_Bmacroporosum_18S	NG_017171.1
	Polychytrium	<i>Polychytrium aggregatum</i>	F3_Paggregatum_18S	MT409103.1
F4	Lobulomycetaceae	<i>Lobulomyces angularis</i>	F4_Langularis_18S	NG_061011.1
	Physoderma	<i>Physoderma lycopi</i>	F4_Plycopi_18S	HQ888716.1
F5	Coelomymycetaceae	<i>Coelomomyces lativittatus</i>	F5_Clativittatus_18S	HQ888713.1
	Allomyces	<i>Allomyces anomalus</i>	F5_Aanomalus_18S	JN941234.1
	Entomophthoromycota	<i>Basidiobolus meristosporus</i>	F5_Bmeristosporus_18S	JX242609.1
F6	Kickxellomycotina	<i>Furculomyces boomerangus</i>	F6_Fboomerangus_18S	AF277013.1
	Zoopageles	<i>Atractospora aquatica</i>	F6_Aaquatica_18S	NG_070122.1

		Mucoromycotina		<i>Cokeromyces recurvatus</i>	F6_Crecurvatus_18S	AF113416.1
		Cryptococcus		<i>Cryptococcus neoformans</i>	F6_Cneoformans_18S	NG_064879.1
		Eurotialis		<i>Talaromyces macrosporus</i>	F6_Tmacrosporus_18S	M83262.1
		Entorrhizaceae		<i>Entorrhiza aschersoniana</i>	F6_Easchersoniana_18S	DQ363318.1
Holozoa/Metazoa	H0	Filasterea		<i>Capsaspora owczarzaki</i>	H0_Cowczarzaki_18S	XR_889848.1
		Ichthyosporea		<i>Dermocystidium salmonis</i>	H0_Dsalmonis_18S	U21337.1
		Ichthyosporea		<i>Sphaerothecum destruens</i>	H0_Sdestruens_18S	FN996945.1
		Choanoflagellida		<i>Monosiga brevicollis</i>	H0_Mbrevicollis_18S	AF100940.1
		Choanoflagellida		<i>Choanoflagellida</i> SL163	H0_ChoanoflagellidaSL163_18S	EF432541.1
	H1	Ctenophora	Cydropida	<i>Pleurobrachia pileus</i>	H1_Ppileus_18S	MF599313.1
		Ctenophora	Lobata	<i>Mnemiopsis leidyi</i>	H1_Mleidyi_18S	KJ754158.1
	H2	Porifora	Hexactinellida	<i>Hexactinella carolinensis</i>	H2_Hcarolinensis_18S	AM886408.1
		Porifora	Desmospongiae	<i>Amphimedon compressa</i>	H2_Acompressa_18S	KC902400.1
		Porifora	Desmospongiae	<i>Halisarca dujardini</i>	H2_Hdujardini_18S	EU702418.1
		Porifora	Homoscleromorpha	<i>Plakinastrella onkodes</i>	H2_Ponkodes_18S	HM118548.1
		Porifora	Calcarea	<i>Plectroninia neocaledoniense</i>	H2_Pneocaledoniense_18S	AM180979.1
		Placozoa	Trichoplacidae	<i>Trichoplax</i> H8	H2_TrichoplaxH8_18S	AY652581.1
		Bilateria	Ecdysozoa	<i>Afrosteronophorus</i> sp. JM-2008	H2_AfrosteronophorusJM-2008_18S	EU559360.1

	Bilateria	Nematoda	<i>Leptonchus granulosus</i>	H2_Lgranulosus_18S	KR184128.1
	Cnidaria	Anthozoa	<i>Isarachnanthus maderensis</i>	H2_Imaderensis_18S	AB859825.1
	Cnidaria	Anthozoa	<i>Eudendrium californicum</i>	H2_Ecalifornicum_18S	EU305492.1
H3	Orthonectida	Rhopaluridae	<i>Rhopalura ophiocomae</i>	H3_Rophiocomae_18S	U58369.1
	Rhombozoa	Dicyema	<i>Dicyema acuticephalum</i>	H3_Dacuticephalum_18S	D26530.1

Table S2. List of sequence read archive datasets.

Sequence read archive	Dataset^b	Tissue
Brain (first series)		
SRX1250555	Rockfeller, USA	DLPFC
SRX1250556	Rockfeller, USA	DLPFC
SRX1250557	Rockfeller, USA	DLPFC
SRX1250558	Rockfeller, USA	DLPFC
SRX1250559	Rockfeller, USA	DLPFC
SRX1250560	Rockfeller, USA	DLPFC
SRX1250561	Rockfeller, USA	DLPFC
SRX1250562	Rockfeller, USA	DLPFC
SRX970051	Miami, USA	HPC
SRX970052	Miami, USA	HPC
SRX970053	Miami, USA	HPC
SRX970054	Miami, USA	HPC
Brain (second series)		
SRX10561059	University of Sydney, Australia	Cortex ^c
SRX11187945	Johns Hopkins, USA	DLPFC
SRX12960438	TRON Mainz, Germany	Brain
SRX9350010	Boston University, USA	PFC
SRX5541734	Skolkovo, Russia	Cortex (polyA+ selection) ^c
SRX5527594	CRI Seattle, USA	Cortex ^c
SRX10869684	University of Pittsburgh, USA	DLPFC
SRX10859671	University of California Irvine, USA	PFC
SRX2983651	NINS, Japan	DPFC
SRX3119985	Icahn School of Medicine, USA	DLPFC

SRX3098239	Lieber Institute, USA	DLPFC
SRX3009308	Columbia University, USA	DLPFC
SRX2497777	PICB, Shanghai, China	PFC
SRX834731	Boston University, USA	PFC
SRX390440	NIMH, NIH, USA	DLPFC
SRX272967	University of Pennsylvania, USA	DLPFC
SRX081982	University of Lausanne, Switzerland	Cortex (polyA+ selection) ^c
Liver		
SRX10498444	Changsha, China	Liver
SRX10498445	Changsha, China	Liver
SRX10498446	Changsha, China	Liver
SRX10498447	Changsha, China	Liver
SRX10498448	Changsha, China	Liver
SRX10498449	Changsha, China	Liver
SRX10498450	Changsha, China	Liver
SRX10498451	Changsha, China	Liver
Skin		
SRX6457388	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457389	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457390	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457391	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457392	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457393	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457394	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
SRX6457395	LSB, NIAMS, NIH, USA	Skin (diabetic foot)
Tapwater		

SRX831467	Peking University	Water ('pure')
SRX831468	Peking University	Tapwater 0.04 mg/l FC
SRX831470	Peking University	Tapwater 0.56 mg/l FC
SRX831472	Peking University	Tapwater 1.76 mg/l FC

^aAbbreviations: CRI, Cancer Research Institute (USA) DPFC, dorsal prefrontal cortex; DLPFC, dorsolateral prefrontal cortex; FC, free chlorine; HPC, hippocampus; LSB, Laboratory for Skin Biology (USA); NIAMS, National Institute of Arthritis and Musculoskeletal and Skin Diseases; NIH, National Institutes of Health (USA); NIMH, National Institute of Mental Health (USA); NINS, National Institutes of Natural Sciences (Japan); PFC, prefrontal cortex; PICB, Partner Institute for Computational Biology (China).

^bThe key RNA-seq data used in this work were from Magistri *et al.* (Magistri *et al.* 2015) (Miami), Scheckel *et al.* (Scheckel *et al.* 2016) (Rockefeller), Sawaya *et al.* [Sawaya Stone Brooks 2020] (LSB), Wu *et al.* (Wu *et al.* 2021) (Changsha, China), and Peking University Bioproject PRJNA267517; 'Dynamics of microbial communities in tap water networks'. Full details for all datasets may be accessed at <https://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?>.

^cDatasets used for polyA+ versus total RNA comparison.

Table S3 (A). List of 64-mer probes covering the Tree of Life.

>A_Hsalinarum_16S_1
GGCCATTGCTATCGGAGTCCGATTTAGCCATGCTAGTTGTGCGGGTTTAGACCCGCAGCGGAAA
>A_Hsalinarum_16S_2
TTGCTCCTGGAAGGGGCAAAGCCGGAACGCTCCGGCGCCACAGGATGCGGCTGCGGTGCGATTAA
>A_Hsalinarum_16S_3
TGAGACAAGATTCCGGGGCCCTACGGGGGCGCAGCAGGCGCGAAACCTTTACACTGTACGAAAGTG
>A_Hsalinarum_16S_4
GGGCAAGACCGGTGCCAGCCGCCGCGGTAATACCGGCAGTCCGAGTGATGGCCGATCTTATTGG
>A_Hsalinarum_16S_5
CTGTTTCAGCTTGGGACCGGAAGACCTGAGGGGTACGTCTGGGGTAGGAGTGAAATCCTGTAATC
>A_Hsalinarum_16S_6
CCGGATTAGATACCCGGGTAGTCCTAGCTGTAAACGATGTCCGCTAGGTGTGGCGCAGGCTACG
>A_Hsalinarum_16S_7
ATTGGCGGGGGAGCACTACAACCGGAGGAGCCTGCGGTTTAATTGGACTCAACGCCGGACATCT
>A_Hsalinarum_16S_8
CGTCAGCTCGTACCGTGAGGCGTCTGTAAAGTCAGGCAACGAGCGAGACCCGCACTCCTAATT
>A_Hsalinarum_16S_9
GTAGGTCAGTATGCCCCGAATGGGCTGGGCAACACGCGGGCTACAATGGTCGAGACAATGGGAA
>A_Hsalinarum_16S_10
GCTGGATTCCGTAGTAATCGCGTGTACGAGCGCGCGGTGAATACGTCCCTGCTCCTTGACAC
>A_MethanocaldococcusSG1_16S_1
GGGGCTCCCTTCGGGGAGCACCGGCGCACGGCTCAGTAACACGTGGCTAACCTACCCTCGGGTG
>A_MethanocaldococcusSG1_16S_2
GCGGCCGCCCCGAGGATGGGGCTGCGGCGGATTAGGTAGTTGGTGGGGTAACGGCCCCACCAAGCC
>A_MethanocaldococcusSG1_16S_3
GCAGGCGCGAAACCTCCGCAATGCGCGAAAGCGCGACGGGGGACCCCGAGTGCCCACGCTCCG
>A_MethanocaldococcusSG1_16S_4
CGGCGGCCCGAGTGGTGGCCACTGTTATTGGGCCTAAAGCGTCCGTAGCCGGCCCCGGTAAGTCT
>A_MethanocaldococcusSG1_16S_5
CCCCAGGGGTAGCGGTGAAATGCGTTGATCCCTGGGGGACCACCTGTGGCGAAGGCGCCCCGGCT
>A_MethanocaldococcusSG1_16S_6
CTCTGCGGACTAGGTGTGCGGTGCGCTTCGGGCCGGCGCGGTGCCGAAGGGAAGCCGTTAAGTC
>A_MethanocaldococcusSG1_16S_7
CGGTTTAATTGGATTCAACGCCGGGCATCTTACCAGGGGCGACGGCAGGATGAAGGCCAGGTTG
>A_MethanocaldococcusSG1_16S_8
GTAACGAGCGAGACCCGTGCCCCATGTTGCTATCCCCTCCTCCGGGAGGGGGGCACTCATGGGG
>A_MethanocaldococcusSG1_16S_9
GGCTACAATGGCCGGGACAATGGGATGCGACCCCGAAAGGGGGAGCAAATCCCCTAAACCCGGT
>A_MethanocaldococcusSG1_16S_10
TGAATGCGTCCCTGCTCCTTGACACACCGCCCCGTACGCCACCCGAGTTGGGCCCAAGTGAGG
>A_Mkandleri_16S_1
ACTCCGGTTGATCCTGCCGGAGGCCACCGCTATCGGGGTCCGACTAAGCCATGCAAGTCGAGGG
>A_Mkandleri_16S_2
CGGCGAAAGTGGGGCTAATCCCCGATAGGCGGGGCGGCCTGGAACGGTCTCCGCCGAAAGGGC
>A_Mkandleri_16S_3
AAGCCGATAATCGGTACGGGCGGTGAGAGCCGGAGCCCGGAGACGGGGACTGAGACAAGGCCCC
>A_Mkandleri_16S_4
GGGCAAAGCCCCGGCGGCTGTACGGGGGTGTAAAAAGCCCCGGGTAGAAAGCGGCGGGCAAGAC

>A_Mkandleri_16S_5
 TCCCGTGGGTCCCCGCCGAAAGCCCGCGGCTTAACCGCGGGAGTCGGCGGGGAAACTGCGGGAC
 >A_Mkandleri_16S_6
 AAGGCGTCCGGCTGGAACGGGTCCGACGGTGAGGGCCGAAAGCCGGGGGAGCAAACCGGATTAG
 >A_Mkandleri_16S_7
 AAGCCGTAAAGTCCGCCGCTGGGGAGTACGGCCGCAAGGCTGAACTTAAAGGAATTGGCGGG
 >A_Mkandleri_16S_8
 GAAGGCCAGGTTGACGACCTTGCCGGACGAGCTGAGAGGAGGTGCATGGCCGCCGTCAGCTCGT
 >A_Mkandleri_16S_9
 CCGGGCACTCTGCGGGGATCGCCGCCGTTAAGGCGGATGAAAGTGGGGGCGACGGCAGGTCCGT
 >A_Mkandleri_16S_10
 ATCCCTAAACCCCGTCGTAGTTCGGATTGCGGGCTGCAACTCGCCGCATGAAGGTGGAATCG
 >A_Mkandleri_16S_11
 CCCCCGGGGGCAAGCCCCCGTCCGCAAGGGCTGGGGGCGAGCCCCGGGGGGTGAGGGGGGC
 >A_Tarchaeon_16S_1
 GTAGCCGGTATGGTAAGTTCCTGGTAAAATTGGGCAGCTTAACTGTCCTTGTGCTAGGGATACT
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 GATGATCAGATACCGTCGTAGTCCTAACCATAAACTATGCCGACTAGGGATTGGTGGATGTTAA
 >H0_Sdestruens_18S_12
 TGCAATTTTCGATCTTAAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGC GTTGATTAC
 >H0_Sdestruens_18S_13
 ACCGCTGGCAACAGCAGTGAGGCTGCCGAAAAGTTGATCAAACCTTGATCATTTAGAGGAAGTAA
 >H0_Mbrevicollis_18S_2
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 >H0_Mbrevicollis_18S_3
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 >H0_Mbrevicollis_18S_4
 CAAATTACCCAATCCTGACACAGGGAGGTAGTGACAATAAATAACAATACAGAGCTCTTTGAGC
 >H0_Mbrevicollis_18S_7
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>H0_Mbrevicollis_18S_11
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 >H0_Mbrevicollis_18S_12
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 >H0_Mbrevicollis_18S_13
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 >H0_ChoanoflagellidaSL163_18S_2
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 >H0_ChoanoflagellidaSL163_18S_3
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 >H0_ChoanoflagellidaSL163_18S_4
 AATAAATAACAATACAGGGCCTTTTAGGTTTTGTAATTGGAATGAGTACAATTTAAATCTCTTA
 >H0_ChoanoflagellidaSL163_18S_5
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 >H0_ChoanoflagellidaSL163_18S_7
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 >H0_ChoanoflagellidaSL163_18S_8
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 >H0_ChoanoflagellidaSL163_18S_9
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 >H0_ChoanoflagellidaSL163_18S_10
 CCGTTAACGAACGAGACCTTAACCTGCTAAATAGTGACGCGATTCTCGAATCGCGGGTTACTTC
 >H0_ChoanoflagellidaSL163_18S_11
 CCGCACGCGCGCTACACTGACGAGGACAACGAGTTTATAACCTGCGCCGGAAGGTGTGGGTAAAT
 >H1_Ppileus_18S_2
 TAACCGTAGTAATTCTAGAGCTAATACATGCGAAAAGTCCCGACTTCTGGAAGGGATGTATTTA
 >H1_Ppileus_18S_3
 GGCGATGTTTCATTCGAGTTTCTGCCCTATCAACTTTCGATGGTAAGGTATTGGCTTACCATGG
 >H1_Ppileus_18S_4
 CAGCAGGCGCGCAAATTACCCAATCCCGATTGCGGGGAGGTAGTGACAATAAATAACGTTGCAGG
 >H1_Ppileus_18S_6
 ACTCCGTGTGCCCTTAACCTGGGTGGGCGAAGGATTGCGGACGTTTACTTTGAAAAAATTAGAGT
 >H1_Ppileus_18S_7
 CGAGACCGAAGTAATGATTAATAGGGACAGTTGGGGGCATTCTGATTTTCATTGTCAGAGGTGAA
 >H1_Ppileus_18S_8
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 >H1_Ppileus_18S_12
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 >H1_Ppileus_18S_13
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 >H1_Mleidy_18S_2
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 >H1_Mleidy_18S_3
 GTAAGGTATTGGCTTACCATGGTGACAACGGGTAACGGAGAATTAGGGTTCGATTCCGGAGAGG
 >H1_Mleidy_18S_4
 TGACAATAAATAACGTTGCAGGCGCCAACGGCTTCTGCAGTCGGAATGAGTACAATATAACACC
 >H1_Mleidy_18S_7
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 >H1_Mleidy_18S_8
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>H1_Mleidy_i_18S_9
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 >H1_Mleidy_i_18S_10
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 >H1_Mleidy_i_18S_11
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 >H2_Hcarolinensis_18S_3
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 >H2_Hcarolinensis_18S_6
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 >H2_Hcarolinensis_18S_8
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 >H2_Acompressa_18S_3
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 >H2_Acompressa_18S_4
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 >H2_Acompressa_18S_7
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 >H2_Acompressa_18S_8
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 >H2_Acompressa_18S_10
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 >H2_Acompressa_18S_11
 GCCCTTAGATGTCCTGGGCGCGACGCGGCTACACTGACGGAGCCAGCGAGCGTGTCTTCGCC
 >H2_Acompressa_18S_12
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 >H2_Hdujardini_18S_2
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 >H2_Hdujardini_18S_3
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 >H2_Hdujardini_18S_4
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 >H2_Hdujardini_18S_6
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 >H2_Hdujardini_18S_7
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 >H2_Hdujardini_18S_8
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 >H2_Hdujardini_18S_12
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 >H2_Hdujardini_18S_13
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 >H2_Ponkodes_18S_2
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 >H2_Ponkodes_18S_4
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>H2_Ponkodes_18S_5
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 >H2_Ponkodes_18S_6
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 >H2_Ponkodes_18S_7
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 >H2_Ponkodes_18S_8
 GAGGACGTTATATCAGACTCCTTCGGCACCTTTTCGAGAAATCAAAGTTTCTGGGTTCCGGGGG
 >H2_Ponkodes_18S_9
 GACTCAACACGGGAAAACTCACCAGGTCCGGACACAGTAAGGATTGACAGATCGAGAGCTCTTT
 >H2_Ponkodes_18S_10
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 >H2_Ponkodes_18S_11
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 >H2_Pneocaledoniense_18S_2
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 >H2_Pneocaledoniense_18S_3
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 >H2_Pneocaledoniense_18S_6
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 >H2_Pneocaledoniense_18S_7
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 >H2_Pneocaledoniense_18S_12
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 >H2_Pneocaledoniense_18S_13
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 >H2_TrichoplaxH8_18S_2
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 >H2_TrichoplaxH8_18S_3
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 >H2_TrichoplaxH8_18S_4
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 >H2_TrichoplaxH8_18S_6
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 >H2_TrichoplaxH8_18S_7
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 >H2_TrichoplaxH8_18S_12
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 >H2_TrichoplaxH8_18S_13
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 >H2_AfrosteronophorusJM-2008_18S_2
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 >H2_AfrosteronophorusJM-2008_18S_3
 TGGTAGGTTATGCGCCTACCATGGTTATTACGGGTAACGGGGAATCAGAGTTCGATTCCGGAGA
 >H2_AfrosteronophorusJM-2008_18S_4
 AGTGACGAAAAATAACAATACGGGACTTTTTTAAGGCTCGTAATTGGAATGAGTACACTCTAAA
 >H2_AfrosteronophorusJM-2008_18S_5
 AAAGTTGTTGCGGTTAAAAGCTCGTAGTTGGATCTCAGTCGCGCTCCAGCGATACGTTGCAA
 >H2_AfrosteronophorusJM-2008_18S_6
 TTTACTTTGAAAAAATTAGGGTGCTCAAAGCAGGCTTGTGCCTGGATATTGGTGCATGGAATAA

>H2_AfrosterphorusJM-2008_18S_7
 CGTATTGCGGCGTTAGAGGTGAAATCTTGATCGCTGCAAGACGAAGTACTGCGAAAGCATT
 >H2_AfrosterphorusJM-2008_18S_8
 TAAACGATGCCAACAGCGATCCGCCTGAGTTCCTCAAACGACTCTGCGGGCAGCCTCCGGGAA
 >H2_AfrosterphorusJM-2008_18S_11
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 >H2_Lgranulosus_18S_1
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 >H2_Lgranulosus_18S_2
 TTAGAATAAAAACCAATCGGGCCTCGGCCCCGTGATTTGGTGAATCTGAATAACTCCGCCGATCG
 >H2_Lgranulosus_18S_4
 AGTCCTCTTCGAGGTCTGTCATCGGAATGGGTACAATTTAAATCCTTTAACGAGGATCTATTGG
 >H2_Lgranulosus_18S_5
 TCGTAGTTGGATCTGCGGCCGAGCGGGGCGGTCCCCGAAAGGGCGGTACCCGTACCCGCTAGC
 >H2_Lgranulosus_18S_6
 GAGTGCTTAAAGCAGGCGAAATAGCCTGAATAAGGTGCATGGAATAATGGAATAGGACCTCGGT
 >H2_Lgranulosus_18S_8
 CGATTAGTCGGCGTTAATCTACGACCCGACTAGCAGCTTCCGGGAAACCAAAGTTTTTCGTTTC
 >H2_Lgranulosus_18S_9
 TAATTTGACTCAACACGGGAAACTCACCCGGCCCCGGACACCGTAAGGATTGACAGACTGAGAG
 >H2_Lgranulosus_18S_10
 ACGAACGAGACTCTGGCCTATTAAATAGACGGCGTATCGAAAAGTACGCCGAGCTTCTTAGAGG
 >H2_Lgranulosus_18S_11
 CGCTACACTGAAAGAATCAGCGTGCGCGATTGCGCTGGTCCGGAAGGATCGGGTAACCCGAGTA
 >H2_Imaderensis_18S_1
 TGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCCTTACTACTTGGATAACCGTAGTAAT
 >H2_Imaderensis_18S_2
 TAGCTTCGGCCAGCCGATCGTTGGTGATTCATAGTAACTGTTCAATCGCAGGGCCCTTTGCG
 >H2_Imaderensis_18S_5
 TTCGGGAGGGGTTCGGCCGTCCGCCGCAAGGTGTGCTACTGGTTCGGCCCGTCTTCTGCGCA
 >H2_Imaderensis_18S_6
 GCTCGCCGGCTTGATACATAAGCATGGAATAATGGAATAGGACTCTGGTTCTATTTTGTGGT
 >H2_Imaderensis_18S_9
 CGGGAAACTCACCAGGTCCGGACATGGTAAGGATTGAACAGATTGAGAGCTCTTCTTGATTC
 >H2_Imaderensis_18S_10
 GACCTGCTAAATAGTCACGCCGTTCCCGAACGGTGGCTGACTTCTTAGAGGGACTGTTGGTGTC
 >H2_Imaderensis_18S_11
 GTATCAGCGAGTCCCTCCTTGCCGTCAGGCATGGGTAATCTTGTGAAATATCATCGTGCTGGG
 >H2_Ecalifornicum_18S_2
 TTCTGGAAGGGATGTATTTATTAGATTAATAACCAATGCGGGTCCTCGTGGCTCGTCTTCTGG
 >H2_Ecalifornicum_18S_3
 CGATGGTAAGGTAGTGGCTTACCATGGTTGTAACGGGTGACGGAGAATTAGGGTTCGATTCCGG
 >H2_Ecalifornicum_18S_4
 GGTAGTGACAAGAAATAACGATACGGGGCTTAATAGGTCTCGCAATTGGAATGAGTACAATTT
 >H2_Ecalifornicum_18S_7
 ATCCGTATTTCTGTTGTCAGAGGTGAAATCTTGGATTACGAAAGACGAACAACTGCGAAAGCA
 >H2_Ecalifornicum_18S_8
 CCATAAACGATGTCGACTAGGGATCAGCGGGCGTTATTGTACGACCTCGTTGGCACCTTACGGG
 >H2_Ecalifornicum_18S_10
 TTGTCTGGTTAATCCGTTAACGAACGAGACCTTAACCGGCTAAATAGTCACACGATTCTCGAA

>H2_Ecalifornicum_18S_11
 AGATGTTCTGGGCCGCACGCGCTACACTGTCGGATTGAGCGAGTCTTAACCTTAACCGAAAG
 >H3_Rophiocomae_18S_2
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 >H3_Rophiocomae_18S_3
 TGCCGATCGTAGGGCCTAGAGCCGACGATAGATCCTTCAAGTGTCTGCCCTATCAACTTTCGAT
 >H3_Rophiocomae_18S_4
 ACAGCTCTACTTCCAAGGAGGGCAGCAGGCGCGCAAACTACCCAATCCCGGCTCGGGGAGGTG
 >H3_Rophiocomae_18S_6
 AATCCTTATGTTAGTCGNNTTTCAGTTCTCTTTATTGAGTGCTGTGAATGACTACAAATTTTACT
 >H3_Rophiocomae_18S_7
 TTCTATCTGTTGGTTGATGAACTTGAGGTAATGATTAAGAGGGACAGTCGGGGGCATTCACTACT
 >H3_Rophiocomae_18S_10
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 >H3_Rophiocomae_18S_11
 TCAGCGGTCATTTATCTTCTTAGAGGGACTGGTTGGTTCGGCTTAATATGTAGAAACACGAAA
 >H3_Rophiocomae_18S_12
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 >H3_Rophiocomae_18S_13
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 >H3_Dacuticephalum_18S_1
 GTATAAGTTCATGCTCTCTAATGAGCGAGACCGCAACGGCTCATTAAATCGGACATAACTTACT
 >H3_Dacuticephalum_18S_2
 TATTAGATTAGTTGACTCTGGATAAATTTGCTGATCACGGGCTGTGCTGTGACGTATCAATTAG
 >H3_Dacuticephalum_18S_3
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 >H3_Dacuticephalum_18S_5
 AAGTAGGCCTTTGCTGTAGTTGAGTGCTACGGCTTTACCTTGAACAAAATAGAGTGCTTAAGGC
 >H3_Dacuticephalum_18S_6
 GATTAACAGAGACAGACGGGGGCATTGCTATTGCACCGCTAGAGGTGAAATTCGTAGATCGGTG
 >H3_Dacuticephalum_18S_7
 TAGATCTCGTCGTAGTTCCAACATAAACGATGCCAACTAGCACTCCGCTAATAAGATTTTGAC
 >H3_Dacuticephalum_18S_8
 TTGACGGAAGGGCACCACAGGAGTGAGCCTGCGCTAATTTGACTCAACACAGAAAACTCACCC
 >H3_Dacuticephalum_18S_10
 TGCCTTAGACGTTTCGGGGCTGAACGCGCGCTACAATGGAGAAAGCAGTGGGTGTCTTGCTTGGC

Table S3 (B). List of 64-mer probes for housekeeping genes

>Housekeeping_hPGK1_p1
 AACTCAAATCTCTGCTGGGCAAGGATGTTCTGTTCTTGAAGGACTGTGTAGGCCCAGAAGTGGA
 >Housekeeping_hPGK1_p3
 GTACTTTCTGCCTTTTAGTTCTGTGCACAGCCCTAAGTCAACTTAGCATTTTCTGCATCTC
 >Housekeeping_hHMGCR_ex2
 TGGCCTCTTTGTGGCTCCCATCCCTGGGAAGTCATAGTGGGGACAGTGACACTGACCATCTGC
 >Housekeeping_hHMGCR_ex3
 ATAATTCTGACAATAACACGATGCATAGCCATCCTGTATATTTACTTCCAGTTCAGAAATTAC
 >Housekeeping_hNSE_ex2
 GAGAAGATCTGGGCCCCGGGAGATCCTGGACTCCCGCGGGAACCCACAGTGGAGGTGGATCTCT

>Housekeeping_hNSE_ex3
TGCCCACTGGAGCCTCTACGGGCATCTATGAGGCCCTGGAGCTGAGGGATGGAGACAAACAGCG

Table S3 (C). List of 64-mer probes for retroelements

>R1_LINE1_RT
TGGCAAACCAAATCCAGCAGCACATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCATCCC
>R1_LINE1md_RT
TCACATATAGTGTGGCAATGAACACTGTTGCTTGTTACATATACTTCAAGCATCCAGCAGCCAT
>R1_LINE1dr_RT
TGGAGTGGAATGTCAAGGAAGGACATCTGGACATTCAACCCCTGAGAATCAGGTTCTTGATCC
>R1_CONSENSUS_hLINE1
AATACATCCCATCAATACCTAATTTATTGAGAGTTTTAGCATGAAGGGTTGTTGAATTTTGTC
>R1_hLINE2_HUMAN_BRAIN
CACCACATAAACAGAATTAACAAAAACAAAAATCACATGATCATCTCACTAGATGCAGAAAAAGCAT
>R2_hALU_Konkel
GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAC
>R3_MLV_c19
AGGTCCCCATGGTTCACGACCCTGATATCCACCATTATGGGCCCTCTGATAGTACCTTAAAC
>R3_hsHERVW_gag1
CAACTCACAATTATGTAAAAAGTGTGGTTTATGCCCTACAGGAAGCCCTCAGAGTCCACCTCCC
>R3_hsHERVW_gag2
CAGCCAGAGTGCCTGTACCTTTTTCTCTCTCAGACTTAAAGCAAATTAATAGACCTAGGTAA
>R3_hsHERVK_gag1
CCCAGAAAGTCAGTATGGATATCCAGGAATGCCCCCAGCACACAGGGCAGGGCGCCATACCT
>R3_hsHERVK_gag2
GGCAATCCCAATAACGTTAGAACCGATGCCACCTGGAGAAGGAGCCCAAGAGGGAGAGCCTCC
>R3_hsHERVK_pol1
TCTCCGGCCATGATCCCAAAGACTGGCCTTTAATTATAATTGATCTGAAAGATCGCTTTTTTA
>R3_hsHERVK_pol2
GGATTGTGAAAAATTTGCCTTTACTATACCAGCCATAAATAGTAAAGAACTAGCCACCAGGTTG
>R3_hsRTVL_pol1
TTCTCACCTTATTCAATATATTGATGACCTTCGTCTTTGTAGCCCCCTCTTTGAATCTTCTCA
>R3_hsHERVP4_pol2
AAGAGGGACCTAATTTCCACAAGAGAAGTGGCCAGATAGGATGAAGCTAACGGAAAGGAGTGC
>R3_hsHERVHC2_pol1
ATGCACTCCTTATGGGGCTGGGTTTTACCTTTTGAATCATGTATGGAAGGGCTCCGCCTATC
>R3_hsHERVHC2_pol2
GTGCAGTCTCTCAACAGGTACAAGACATCATCCAGCCGCTTGTCTGGGGAGCTCATCCCAATC
>R3_hsERV9_pol1
TTCTGAAGTCCAGGCATTCTAGTCCTTCAGTATGTGGATGATTTACTTTTGGCTACCAGTTTGG
>R3_hsERV9_pol2
TATGCTGGCTTATCGGCACCCTAAGACATTAACAAATTGTGGGGGTTCTTGAATCACTGGC
>R3_hsHIV_gag1
CAATGTATAAAAGATACTATCAATGAGGAAGCTGCAGAATGGGACAGGGTACATCCAGTACATG
>R3_hsHIV_gag2
GATGAGAGAACCGAGGGGAAGTGACATAGCAGGAAGTACCAGTACCCTTCAGGAACAAATAGGA
>R3_hsHIV1_pol1
TGACAAAAATTTAGAGCCTTTTAGAAAAACAAACCCAGAAAGTGGTTATCTATCAATACATGGA

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>R3_hsHIV1_pol2
GTGCCCACACTAATGATGTAAAGCAATTAACAGAGGCAGTACAGAAAATAGCCACAGAAAGCAT
>R3_hsHTLV_gag1
TAGAAACGCCAGTCTGGATGTGTCCCATTAATACTCCCTCCTAGCTAGTCTACTCCCAAAGG
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Table S4. List of human-associated species (PATHLIST).

Class	Species	Accession
A	<i>Methanobrevibacter massiliensis</i>	NR_115169.1
A	<i>Methanobrevibacter oralis</i>	LR590665.1
A	<i>Methanomassiliicoccus luminyensis</i>	HQ896499.1
A	<i>Methanomethylophilus alvus</i>	KC412010.1
A	<i>Methanosphaera stadtmanae</i>	NR_028236.1
B	<i>Actinomyces israelii</i>	AF479270.1
B	<i>Bacillus anthracis</i>	AB592486.1
B	<i>Bacteroides fragilis</i>	LR999640.1
B	<i>Bartonella henselae</i>	NR_074335.2
B	<i>Bordetella pertussis</i>	NR_025951.1
B	<i>Borrelia burgdorferi</i>	NR_044732.2
B	<i>Brucella abortus</i>	NR_042460.1
B	<i>Campylobacter jejuni</i>	NR_041834.1
B	<i>Chlamydophila psittaci</i>	NR_036864.2
B	<i>Clostridium botulinum</i>	NR_029157.1
B	<i>Corynebacterium diphtheria</i>	Y09044.1
B	<i>Ehrlichia canis</i>	NR_118741.1
B	<i>Enterococcus faecalis</i>	NR_040789.1
B	<i>Escherichia coli</i>	NR_024570.1
B	<i>Francisella tularensis</i>	NR_029362.1
B	<i>Haemophilus influenza</i>	NR_044682.2
B	<i>Helicobacter pylori</i>	NR_044761.1
B	<i>Klebsiella pneumoniae</i>	NR_036794.1
B	<i>Legionella pneumophila</i>	NR_041742.1
B	<i>Leptospira interrogans</i>	NR_029361.1
B	<i>Listeria monocytogenes</i>	NR_044823.1
B	<i>Mycobacterium leprae</i>	X53999.1
B	<i>Mycobacterium tuberculosis</i>	NR_102810.2
B	<i>Mycoplasma pneumoniae</i>	NR_041751.1
B	<i>Neisseria gonorrhoeae</i>	NR_026079.2
B	<i>Neisseria meningitidis</i>	NR_104946.1
B	<i>Nocardia asteroides</i>	NR_041856.1
B	<i>Porphyromonas gingivalis</i>	NR_040838.1
B	<i>Pseudomonas aeruginosa</i>	NR_026078.1
B	<i>Rickettsia rickettsii</i>	NR_028018.1
B	<i>Salmonella typhi</i>	NR_074799.1
B	<i>Shigella dysenteriae</i>	NR_026332.1
B	<i>Shigella sonnei</i>	NR_104826.1
B	<i>Staphylococcus aureus</i>	NR_118997.2
B	<i>Streptococcus agalactiae</i>	NR_040821.1
B	<i>Streptococcus pyogenes</i>	NR_028598.1
B	<i>Treponema pallidum</i>	M88726.1
B	<i>Ureaplasma urealyticum</i>	NR_041710.1
B	<i>Vibrio cholerae</i>	NR_044050.1
B	<i>Yersinia pestis</i>	NR_025160.1
C/D	<i>Cryptosporidium muris</i>	AB089284.1
C/D	<i>Toxoplasma gondii</i>	L24381.1

C/D	<i>Cyclospora cayetanensis</i>	FJ009129.1
E	<i>Microsporidium spp.</i>	AF151529.1
E	<i>Plasmodium falciparum</i>	XR_002966654.1
E	<i>Toxoplasma gondii</i>	XR_001974253.1
E	<i>Giardia intestinalis</i>	XR_005248693.1
E	<i>Leishmania donovani</i>	XR_002966730.1
E	<i>Naegleria fowleri</i>	KY062165.1
E	<i>Chlorella vulgaris</i>	MF686487.1
E	<i>Mallomonas papillosa</i>	HF549062.1
E	<i>Dientamoeba fragilis</i>	JQ677148.1
F	<i>Candida albicans</i>	NG_070791.1
F	<i>Candida tropicalis</i>	HG798647.1
F	<i>Aspergillus fumigatus</i>	AB008401.1
F	<i>Aspergillus flavus</i>	D63696.1
F	<i>Cryptococcus neoformans</i>	NG_064879.1
F	<i>Histoplasma capsulatum</i>	AF320009.1
F	<i>Pneumocystis jirovecii</i>	AB266392.1
F	<i>Stachybotrys chartaru</i>	DQ680066.1
F	<i>Blastomyces dermatitidis</i>	M63096.1
F	<i>Coccidioides immitis</i>	XR_001099882.1
F	<i>Paracoccidioides brasiliensis</i>	XR_001551862.1
F	<i>Talaromyces marneffe</i>	NG_074941.1
H	<i>Ancylostoma caninum</i>	AJ920347.2
H	<i>Anisakis pegreffii</i>	EF180082.1
H	<i>Ascaris lumbricoides</i>	X06225.1
H	<i>Blastocystis hominis</i>	AM275395.1
H	<i>Brachionus plicatilis</i>	U49911.1
H	<i>Brugia malayi</i>	KP760121.1
H	<i>Clonorchis sinensis</i>	JF314770.1
H	<i>Diphylobothrium latum</i>	DQ925309.1
H	<i>Dipylidium caninum</i>	AB731643.1
H	<i>Dirofilaria immitis</i>	AF182647.1
H	<i>Echinococcus multilocularis</i>	AB731634.1
H	<i>Encentrum astridae</i>	DQ297695.1
H	<i>Endolimax nana</i>	LC230015.1
H	<i>Entamoeba histolytica</i>	KP233836.1
H	<i>Enterobius vermicularis</i>	JF934731.1
H	<i>Fasciola hepatica</i>	AJ004969.1
H	<i>Fasciolopsis buski</i>	L06668.1
H	<i>Giardia lamblia</i>	XR_005248690.1
H	<i>Leishmania braziliensis</i>	JX030192.1
H	<i>Loa loa</i>	XR_002251421.1
H	<i>Mansonella streptocerca</i>	KP760145.1
H	<i>Moniliformis moniliformis</i>	Z19562.1
H	<i>Necator americanus</i>	AY295811.1
H	<i>Onchocerca volvulus</i>	KT031393.1
H	<i>Paragonimus westermani</i>	AJ287556.1
H	<i>Plasmodium vivax</i>	XR_003001206.1
H	<i>Pneumocystis carinii</i>	AH001732.2
H	<i>Schistosoma japonicum</i>	AY157226.1

H	<i>Strongyloides stercoralis</i>	AB453316.1
H	<i>Taenia saginata</i>	AB731616.1
H	<i>Toxocara canis</i>	JN256977.1
H	<i>Trichinella spiralis</i>	MH289515.1
H	<i>Trichomonas vaginalis</i>	KX061409.1
H	<i>Wuchereria bancrofti</i>	AY843438.1

Table S5. Matches between key viruses and the human genome.

A Identities of human matches					
Virus	Isolate; sequence identifier	Major matches		Partial matches	
		Gene symbol	Gene name	Gene symbol	Gene name
Adeno-associated virus	Adeno-associated virus isolate MHH-05-2015; NC_040671.1	ND	NA	CCNA2	Cyclin A2
Adenovirus A	Human adenovirus A; NC_001460.1	ND	NA	Unknown	Chr.18
				IRF2BPL	Interferon regulatory factor 2 binding protein like
Adenovirus type C	Human mastadenovirus C K67-339; LC504573.1	Human integrated adenovirus 2 VA RNA	NA	YWHAB	Tyrosine/tryptophan monooxygenase activation protein beta
				TMEM9B	TMEM9 domain family member B
				NCBP3	Nuclear cap binding subunit 3
				PABPC1L2B	Poly(A) binding protein cytoplasmic 1 like 2B
Adenovirus 54	Human adenovirus 54; NC_012959.1	ND	NA	CHIC1	Cysteine rich hydrophobic domain 1
Coronavirus 229E	Human coronavirus 229E strain 229E/human/USA/933-40/1993; KF514433.1	ND	NA	SPARC	Secreted protein acidic and cysteine rich
				IL6ST	Interleukin 6 signal transducer
				PLC1B1	Phospholipase C beta1
				Unknown	Chr.11
HEPC2	Hepatitis C virus genotype 2; NC_009823.1	ND	NA	Unknown	Chr.11
HEPC4	Hepatitis C virus genotype; NC_009825.1	ND	NA		
HHV1/HSV1	Human herpesvirus 1 strain 17; LT576869.1	ND	NA	MAPK3	Mitogen-activated protein kinase 3

				<i>CYT2H</i>	Cytohesin 2
				<i>PLPPR3</i>	Phospholipid phosphatase-related 3
HHV2/HSV2	Human herpesvirus 2 strain HG52; NC_001798.2	ND	NA	<i>POLD1</i>	DNA polymerase delta1, catalytic subunit
				<i>TAOK1</i>	TAO kinase 1
				<i>SOBP</i>	Sine oculis binding protein homolog
				<i>RPS6KB2</i>	Ribosomal protein S6 kinase B2
				<i>PGAP1</i>	Inositol deacylase
				<i>FGFR4</i>	Fibroblast growth factor receptor 4
				<i>CDH15</i>	Cadherin 15
				<i>MLLT10</i>	Histone methyltransferase cofactor
				<i>TBXAS1</i>	Thromboxane A synthase 1
				<i>RRAGC</i>	Ras-related GTP binding C
				<i>FBLL1</i>	Fibrillarin-like 1
HHV3/VZV	Human alphaherpesvirus 3 strain VZVs/Pasadena.US A/48.12/Z{2}; KF811485.1	<i>TYMS/ENOSF 1</i>	Thymidylate synthase		
HHV4/EBV	Human herpesvirus 4 strain YCCEL1; AP015016.1	<i>IL10</i>	Interleukin-10 variant	PFAS	Phosphoribosylformylglycinamide synthase
				TAF4B	TATA-box binding protein-associated factor 4b
HHV5/CMV	Human herpesvirus 5 strain Merlin; NC_006273.2	ND	NA	ANKRD28	Ankyrin repeat domain 28
				SFPQ	Splicing factor factor proline and glutamine rich
				SMARCA2	SWI/SNF-related, matrix associated
				GNAO1	G protein subunit O1
				APP	Amyloid precursor protein
				RBFOX1	RNA-binding FOX1 homolog
				CDK16	Cyclin-dependent kinase 16
HHV6A	Human herpesvirus 6A isolate AJ; KP257584.1	Endogenous HHV6	NA	DCAF7	DDB1 and CUL4 associated factor 7
		*No matches to <i>Pan troglodytes</i>			
		* <i>Gorilla gorilla</i>	Unknown		

		Human telomeric DNA repeats			
HHV6B	Human herpesvirus 6B; NC_000898.1	Endogenous HHV6	NA		
		*No matches to <i>Pan troglodytes</i>			
		* <i>Gorilla gorilla</i> ribosomal RNA			
		Human telomeric DNA repeats			
HHV7	Human herpesvirus-7 (HHV7) JI; U43400.1	Endogenous HHV6	NA	DAPK1	
		*No matches to <i>Pan troglodytes</i>			
		*Five matches to <i>Gorilla gorilla</i>	Telomeric region and unknown		
		Human telomeric DNA repeats			
HHV8	Human herpesvirus 8 strain GK18; NC_009333.1	<i>TYMS/ENOSF 1</i>	Thymidylate synthase	GTF2A1	General transcription factor IIA subunit 1
				HMGB1	High mobility group box 1
				APLP2	Amyloid beta precursor like protein 2
				CENPB	Centromere protein B
				NCL	CLN8 transmembrane ER and ERGIC protein
				ARMH4	Armadillo like helical domain containing 4
HPV6	Human papillomavirus type 6 isolate HPV6-gw-0611; MK463909.1	ND	NA	Unknown	Chr.6
HPV16	Human papillomavirus type 16; K02718.1	NA	ND		
TTV	Torque teno virus; NC_015783.1	NA	ND	TRPM3	Transient receptor cation channel M3

VARIOLAV	Variola virus; NC_001611.1	<i>RRM1</i>	Ribonucleotide reductase		
		<i>RRM2B</i>	Ribonucleotide reductase		
		VACV		Unknown	Chr.1p32

Sequence matches were detected by two procedures with different cut-offs for similarity. (i) Direct BLASTn searching of human databases for matches with full-length viral genomes. (ii) BLASTn searching of SRA libraries with full-length viral genomes, retrieval of matches, and second-round searching of these human sequences in the human databases, then in virus databases, and then in the entire NCBI repository. In this second analysis a sequence was deemed to be of human origin if matches to the human database achieved higher scores (homology x coverage) than in any other search. *For HHV6A, HHV6B, and HHV7, searching was also performed against *Pan troglodytes* (chimpanzee) and *Gorilla gorilla* (gorilla) because their genomes/transcriptomes are similar to those of human but contain no integrated viruses of this class.

Abbreviations: NA, not applicable; ND, none detected

B Identity of viral genes and extent of homology					
Virus	Human gene	Virus gene name	Encoding	% Identity	Extent of homology
HHV3	<i>TYMS/ENOSF1</i>	<i>ORF13/PTZ00164</i>	Thymidylate synthase/bifunctional dihydrofolate reductase-thymidylate synthase	70%	797 nt
HHV4	<i>IL10</i>	<i>BCRF1</i>	Viral interleukin 10	77%	391 nt
HHV6A/6B	Telomeric repeats	Region 200–400 (HSV6A)	Left extremity of genome	81%	Multiple matches >100 nt
		Region 151500–151700 (HSV6A)	Close to DR1/US22, near to right extremity of genome	81%	Multiple matches >100 nt
HHV8	<i>TYMS/ENOSF1</i>	<i>ORF70/PTZ00164</i>	Bifunctional dihydrofolate reductase-thymidylate synthase	69%	650 nt
Variola virus	<i>RRM1</i>	<i>PLN02437</i>	Ribonucleoside-diphosphate reductase large subunit	69%	2268 nt
Variola virus	<i>RRM2</i>	<i>PLN02437</i>	Ribonucleoside-diphosphate reductase large subunit	71%	933 nt

Table S6. Stripped viral genomes. Supplied separately (350 pages)

Table S7. Identification of liver- and brain (cortex)-specific signals

Probe	Species detected	Sequence similarity	
		Contig length	% Identity
Liver-specific			
C3_Rviolacea_18S_10	<i>Staphylococcus aureus</i> ^a	251	99.6
D_CaOmb2_18S_1	<i>Staphylococcus aureus</i> ^a	151	99.3
F1_Mspiralis_18S_4	<i>Cryptosporidium</i> sp.	159	99.4
F5_Clativittatus_18S_3	<i>Staphylococcus aureus</i> ^a	232	99.6
F6_Fboomerangus_18S_6	<i>Aspergillus flavis</i>	251	99.6
Brain-specific			
B6_Pintermedia_16S_8 ^b	Uncultured Bacteriodes	129	98.4
	<i>Flavobacterium</i> sp. (Bacteriodes)	169	99.4
F2_GlomusNBRPP1_18S_6 ^b	<i>Malassezia restricta</i> ^c	145	100
	<i>Malassezia globosa</i> ^c	200	100
F6_Aaquatica_18S_6	<i>Malassezia globosa</i> ^c	187	100
F6_Cneoformans_18S_2	<i>Malassezia restricta</i> ^c	180	100
^a Insecure identification in view of similarities to human rRNA sequences.			
^b Two contigs of similar abundance were generated.			
^c The presence of <i>Malassezia</i> spp. in brain (but not liver) was also confirmed through mtDNA analysis.			

Figure S1.

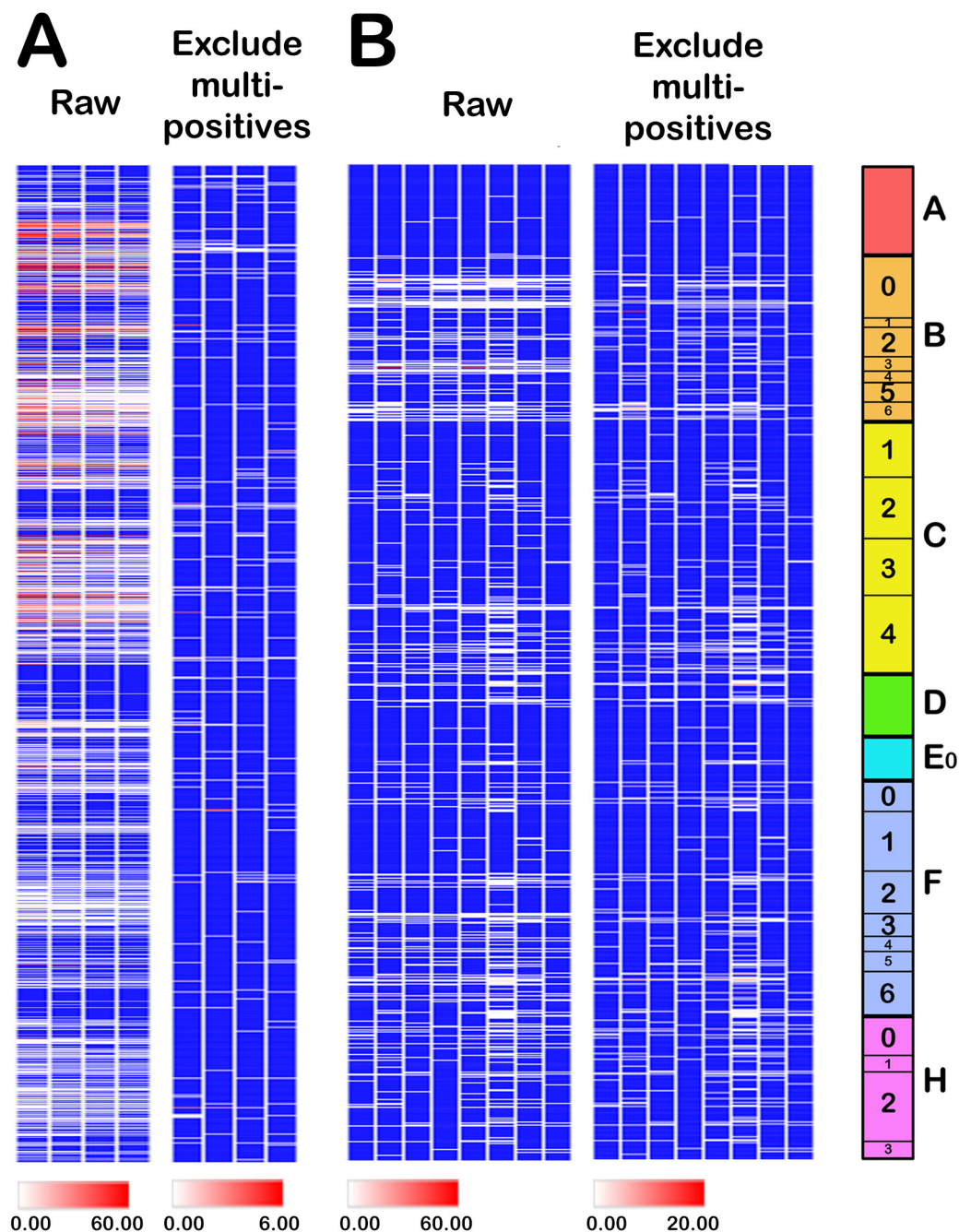


Figure S1. Profiles for four RNA-seq datasets from normal human hippocampus (Left, Miami dataset) and eight RNA-seq datasets from normal human dorsolateral prefrontal cortex (Right, Rockefeller dataset). (A) Exclusion of signals that were present in all samples led to a major reduction in the microbiome profile, suggestive of contamination, whereas in (B) the same exclusion technique led to minimal changes in the overall profile. Because (A) and (B) are RNA-seq from different brain regions, they are not directly comparable to each other.

Figure S2.

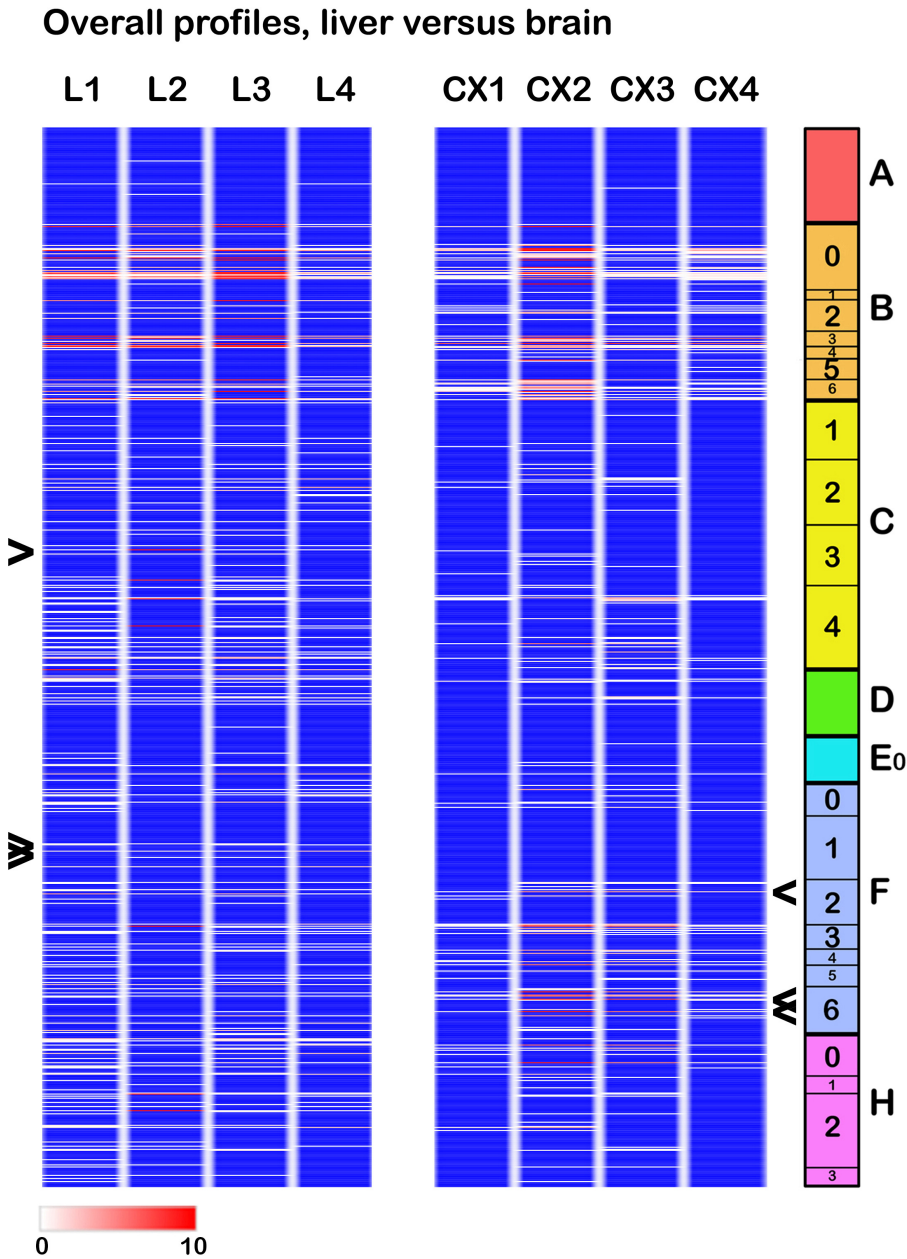


Figure S2. Similarities and differences between the overall microbiome profiles of liver (left) versus cortex (CX, right). Some differential signals are indicated (arrows).

Figure S3

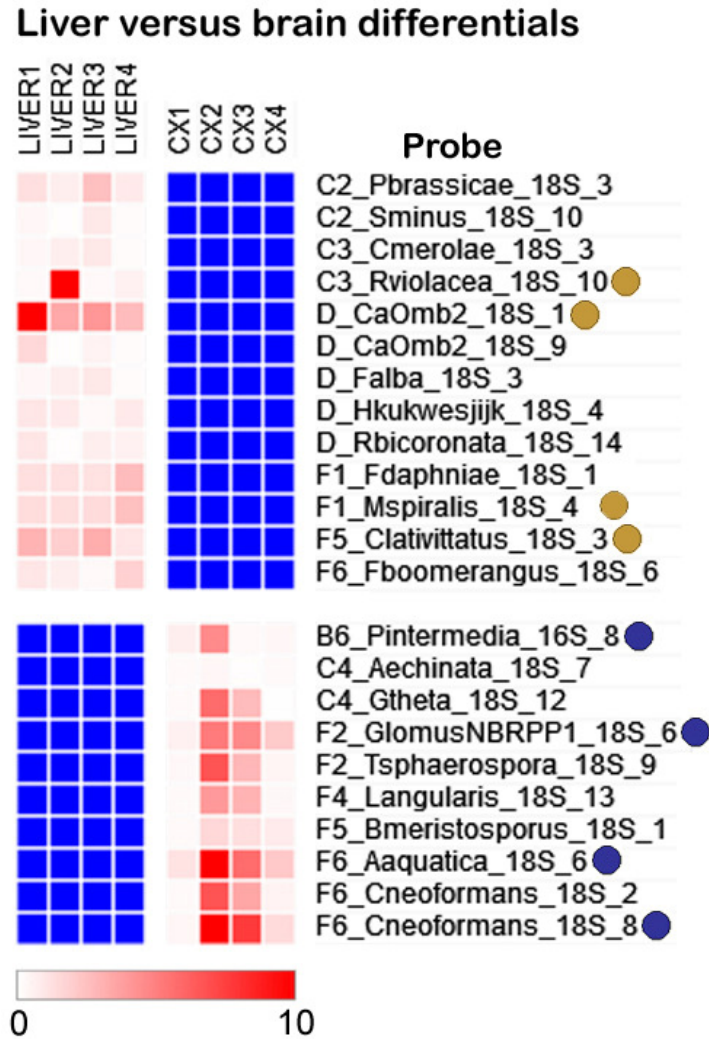


Figure S3. Microbiome signals that appear to be specific for liver (above) and brain (below). Differential signals were confirmed for the probes (marked in gold and blue) by retrieval of matching sequences from the original SRA datasets, contig assembly, and species identification (**Table S7**), as well as through 23S/28S analysis (not presented).

