Supplementary Data

Increasing metadata coverage of SRA BioSample entries using deep learning based Named Entity Recognition

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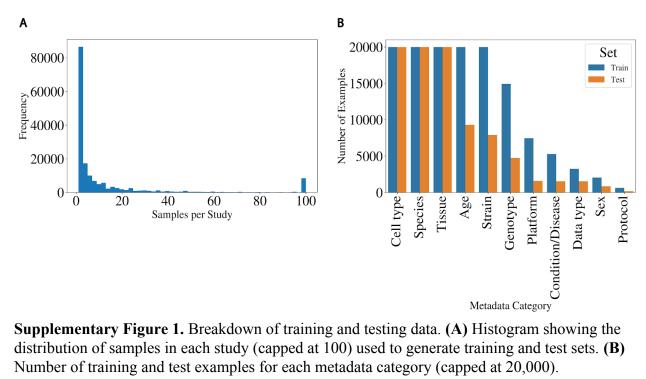
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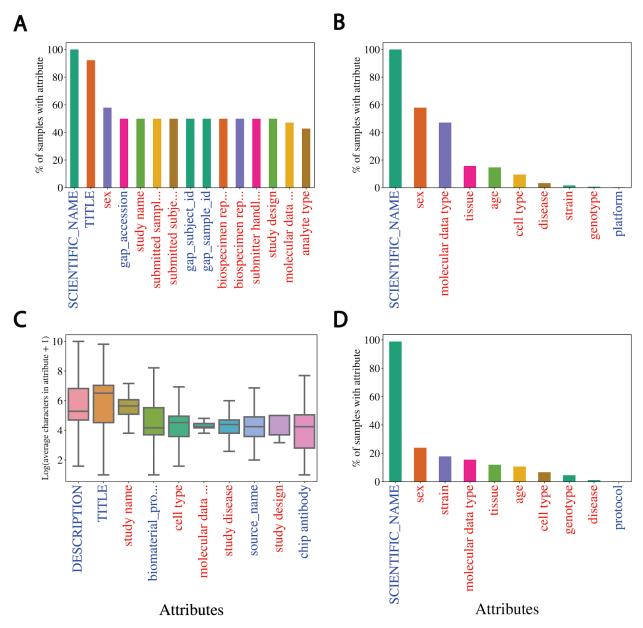
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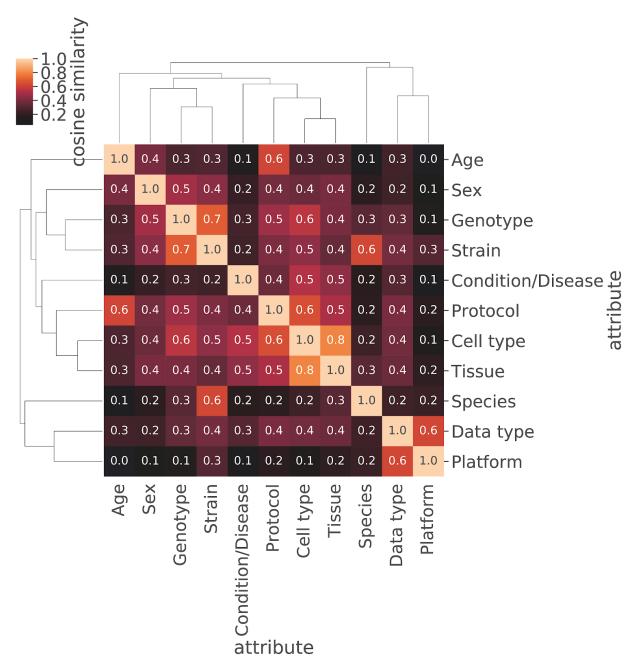
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Supplementary Figure 1. Breakdown of training and testing data. (A) Histogram showing the distribution of samples in each study (capped at 100) used to generate training and test sets. (B) Number of training and test examples for each metadata category (capped at 20,000).



Supplementary Figure 2. *Homo sapien* and TITLE sample metadata coverage. **(A)** Top 15 attribute coverage, **(B)** 11 selected attribute coverage, and **(C)** top 10 distributions (by mean) of Log₂(average characters) for *Homo sapien* samples only. Samples annotated with "Homo sapien" show relatively low coverage for most attributes, but contain longer TITLEs for NER. **(D)** Selected attribute coverage for samples with a TITLE attribute only. This shows that samples with TITLEs are missing metadata in all attributes besides SCIENTIFIC NAME.



Supplementary Figure 3. Training set metadata categories show a large degree of similarity in the embedding space. Cosine similarity heatmap of mean vectors for the 11 categories in the training set with hierarchical clustering shown. Many categories in the training data show a high degree of semantic similarity in the embedding space.

Supplementary Table 1. Selected attributes from BioSample and their corresponding category name for model training. The category names represent multiple attributes that were merged with the selected attribute based on cosine similarity in the word embedding space.

Selected Attribute	Category Name
age	Age
cell type	Cell Type
disease	Condition/Disease
molecular data type	Data type
genotype	Genotype
platform	Platform
protocol	Protocol
sex	Sex
SCIENTIFIC_NAME	Species
strain	Strain
tissue	Tissue

Supplementary Table 2. Cosine similarity between attributes used in merging. Cosine similarities of mean embedding vectors for each attribute compared to selected attributes. The selected attributes used are bolded. All those attributes with a cosine similarity to the bolded attribute of greater than 0.8 were selected for merging and are shown here.

Category Name		
	SCIENTIFIC_NAME	Similarity 1.000
	Organism	0.917
	host scientific name	0.911
	organism	0.903
	host_scientific_name	0.886
C	host	0.884
Species	nat-host	0.859
	specific host	0.853
	host organism	0.851
	host species	0.831
	specific_host	0.805
	HostSpecies	0.801
	strain	1.000
	strain background	0.932
	host_genotype	0.931
	background strain	0.927
	strain/background	0.925
	genetic background	0.912
	mouse strain	0.906
	Mouse_Strain	0.899
	StrainOrLine	0.894
Strain	host strain	0.891
Suam	stain	0.891
	host_strain	0.881
	strain or line	0.880
	strain name	0.879
	host infra-specific name	0.870
	host genotype	0.865
	background	0.864
	host_breed	0.849
	Strain	0.836

	. 1	0.025
	maternal strain	0.835
	paternal strain	0.812
	cell type	1.000
	cell_type	0.897
	source_name	0.886
	source cell type	0.885
	CellType	0.869
Cell type	progenitor cell type	0.866
Cen type	cell types	0.865
	cell-type	0.853
	cell description	0.849
	CELL_TYPE	0.845
	biomaterial_type	0.841
	tissue/cell type	0.827
	genotype	1.000
	genotype/variation	0.940
	Genotype	0.895
	mutant	0.882
Genotype	mutation	0.847
	plant genotype	0.824
	genetic variation	0.812
	idh2.gene.mutation	0.801
	host genotype	0.801
	disease	1.000
	disease status	0.833
C1:t:/D:	tumor type	0.828
Condition/Disease	health state	0.828
	cancer type	0.826
	cell description	0.813
	tissue	1.000
	tissue_type	0.913
Tissue	organism part	0.848
	tissue-type	0.827
	source_name	0.800
	sex	1.000
	host_sex	0.997
Sov	Sex	0.996
Sex	host ex	0.995
	sex infant 1	0.995

	sex / reassigned sex	0.995
	Host Gender	0.995
	babygender_m_f	0.994
	gender gender	0.994
	·	0.987
	breeding direction	0.981
	Gender	0.939
	host sex	0.930
	SEX	0.900
	sex def prob	0.865
	age	1.000
Age	Age	0.832
Data type	molecular data type	1.000
	platform	1.000
	Platform	0.942
	instrument model	0.935
	Sequencing_method	0.934
	sequencing method	0.932
	INSTRUMENT MODEL	0.930
	SequencingTechnology	0.926
	sequencer	0.916
	illumina_technology	0.914
Platform	labversion description	0.914
	illumina_technlogy	0.910
	Sequencer	0.910
	seq meth	0.903
	sequencing platform	0.892
	seq_methods	0.891
	sequencing_machine	0.890
	sequencing_method	0.874
	runchemistry	0.850
	seq_method	0.802
	protocol	1.000
	technology	0.887
	extract_protocol	0.860
Protocol	experiment type	0.858
11010001	assay	0.850
	protocol description	0.844
	application	0.843

library_type	0.800

Supplementary Table 3. Coverage increase for merged metadata categories

Category Name	Selected Attribute	Selected Attribute Count	Category Name Count	Fold Increase
Age	age	363161	370206	1.02
Cell type	cell type	150652	685002	4.55
Condition/Disease	disease	36349	40315	1.11
Data type	molecular data type	544515	544515	1.00
Genotype	genotype	117332	154376	1.32
Platform	platform	3476	147827	42.53
Protocol	protocol	5851	9290	1.59
Sex	sex	643290	808204	1.26
Species	SCIENTIFIC_NAME	2773124	3635784	1.31
Strain	strain	598496	730595	1.22
Tissue	tissue	446429	499537	1.12

Supplementary Table 4. Incorrect metadata predictions across all 11 categories

Category Name	TITLE Sentence	Predicted	Actual
Species	32% Streptococcus mutans UA159 69	Streptococcus mutans	mixed sample
Species	68% Lactobacillus casei 4646	Lactobacillus casei	mixed sample
Species	A cucumber genomic variation map reveals impact human selection	A cucumber	cucumis sativus
Species	Bulk soils compared rhizosphere communities plant Saxifraga oppositifolia along glacier chronosequence	Saxifraga oppositifolia	unidentified bacterium
Species	CBo1 isolated gut Bactrocera oleae	Bactrocera oleae	chryseobacterium sp. 113(2015)
Species	Endophytic isolate branches Citrus sinensis	Citrus sinensis	curtobacterium sp. er1/6
Species	Environmental/Metagenome sample subarctic root fungi	subarctic root	fungi
Species	Generic sample Fusobacterium nucleatum	Fusobacterium nucleatum	fusobacterium phage funu1
Species	Generic sample Homo sapiens respiratory syncytial virus	Homo sapiens	human orthopneumovirus
Species	Generic sample Mimulus guttatus	Mimulus guttatus	erythranthe guttata
Species	Human respiratory syncytial virus	syncytial virus	human orthopneumovirus
Species	Hyphomicrobium facile subsp	facile subsp	hyphomicrobium facile
Species	Ip394 Japanese crested ibis (founder E)	Ip394_Japanese crested ibis	nipponia nippon
Species	Lathyrus pratensis clone 275 reared Lathyrus pratensis	Lathyrus pratensis	acyrthosiphon pisum
Species	MIMARKS Survey related sample Borrelia burgdorferi species complex	Borrelia burgdorferi	borrelia sp. s07cg098
Species	MIMARKS Survey related sample Borrelia burgdorferi species complex	Borrelia burgdorferi	borrelia sp. s07as020
Species	MIMARKS Survey related sample Borrelia burgdorferi species complex	Borrelia burgdorferi	borrelia sp. s10cg023
Species	MIMARKS Survey related sample Borrelia burgdorferi species complex	Borrelia burgdorferi	borrelia sp. s08cg103
Species	Medicago truncatula	Medicago truncatula	mixed culture
Species	Mycobacterium lepromatosis red squirrel M1960/270411	squirrel M1960/270411	mycobacterium lepromatosis
Species	Phylogenomic characterization causative strain one largest worldwide outbreaks Legionnaires' disease occurred Portugal 2014	characterization causative	legionella pneumophila
Species	Picea engelmannii cultivated The Arboretum Horsholm University Copenhagen Denmark	Picea engelmannii	populus tremula
Species	Plant DNA metabarcoding data uncleaned surface cleaned wood subfossil tree trunks	subfossil tree	pinus sylvestris
Species	Plant DNA metabarcoding data uncleaned surface cleaned wood subfossil tree trunks	subfossil tree	pinus sylvestris
Species	Plant DNA metabarcoding data uncleaned surface cleaned wood subfossil tree trunks	subfossil tree	pinus sylvestris
Species	Root tissue samples Caladium hortulanum (MissMuffet)	Caladium hortulanum	caladium bicolor
Species	SYNE2/ESR2A CALM1 loci Clupea pallisii PH3	Clupea pallisii	clupea pallasii
Species	SYNE2/ESR2A CALM1 loci Clupea pallisii PH5	Clupea pallisii	clupea pallasii
Species	Small RNAs Miscanthus rhizomes	Miscanthus rhizomes	miscanthus x giganteus
Species	Stable isotope probing targeting methane-utilizing bacteria arctic lake sediment	arctic lake	bacteria
Species	Streptococcus agalactiae	Streptococcus agalactiae	mixed culture

Species Whole genome analysis Clostridium saccharogumia VE202-01 Species ceeal microbiota sample Microtus brandti Microtus brandti Institution Species foliar sample Castanea sativa Castanea	Species	Transcriptomics potato tubers infected Streptomyces turgidiscabies	Streptomyces turgidiscabies	solanum tuberosum
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Species drifting hotspot microbial diversity Catanea sativa Catanea sativa Uncultured fingus	Species			[clostridium] saccharogumia
Species foliar sample Castanea sativa Castanea sativa Uncultured Imngus	Species	cecal microbiota sample Microtus brandti		lasiopodomys brandtii
Species foliar sample Vitis vinifera Vitis vinifera uncultured fungus	Species	drifting hotspot microbial diversity	microbial diversity	caulerpa taxifolia
Species foliar sample Vitis vinifera Vitis vinifera uncultured fungues	Species	foliar sample Castanea sativa	Castanea sativa	uncultured fungus
Species hRSV RSV+PlV3 F insert C 03 hRSV RSV+PlV3 human orthopneumovinus	Species	foliar sample Vitis vinifera	Vitis vinifera	uncultured fungus
Species Spec	Species	foliar sample Vitis vinifera	Vitis vinifera	uncultured fungus
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Species sativus contaminated Alternaria brassicicola treated plants polyethylene glycol PEG NaCl carried transcriptomic metabolomics measurements across time-course five days symptomic metabolomics measurements across time-course five days symptomics symptomic	Species	live-1 pig low backfat thickness	live-1 pig	sus scrofa
Species				raphanus sativus var. sativus
Strain		treated plants polyethylene glycol PEG NaCl carried transcriptomic metabolomics measurements across	polyethylene glycol	
Strain	Species	symptoms	weed species	unidentified plant
Strain	Strain	1 New Tech Library sample 21095		
Strain	Strain		R-1 (ncra)	fgsc 2489
Strain	Strain	A-1 rbs	A-1 rbs	tc1769
Strain	Strain		NRRL 3	nrrl3 delta arar
Strain	Strain		strain DSM799	dsm 799
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StrainNeurospora crassa FGSC2489 XFGSC2489 X2489x8790 305aStrainNeurospora crassa FGSC2489 XFGSC2489 X2489x8790 362aStrainPyronema omphalodes CBS 100304CBS 100304cbs100304StrainRNA-seq data Paratyphi A 45157 grown stationary phase 42CA 45157paratyphi aStrainResequencing evolved clone P4C7clone P4C7cc2937StrainSalmonella enterica enterica serovar Salmonella MonschauiSalmonella Monschaui369918StrainSalmonella enterica serovar Agona SL483 uid59431SL483 uid594319165StrainSalmonella enterica subsp I enterica serovar Ajioboserovar Ajiobo63502StrainSalmonella enterica subsp I enterica serovarserovar Ajiobo63502	Strain	Neurospora crassa FGSC2489 X	FGSC2489 X	2489x8790 370a
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	Monschaui 63893		
Strain	Salmonella enterica subsp I enterica serovar Stanley 32479	serovar Stanley	32479
Strain	Salmonella enterica subsp I enterica serovar Stanley 78659	serovar Stanley	78659
Strain	Sample UHHS A	UHHS A	abuh434
Strain	Use samples cell lines derived common laboratory model organisms	laboratory model	lvpib12
Strain	VC1639 mutant polymyxin B replicate 2	polymyxin B	vc1639
Strain	Wildtype head X1 single cell 33	X1 single	asexual ciw4
Strain	aeruginosa PASGNDM strains isolated Singapore	PASGNDM strains	pasgndm593
Strain	hot springs Yunnan Tibet	Yunnan Tibet	a12b
Strain	military healthcare system	military healthcare	mrsn7485
Strain	military healthcare system	military healthcare	mrsn7087
Strain	military healthcare system	military healthcare	mrsn15047
Strain	military healthcare system	military healthcare	mrsn7132
Strain	military healthcare system	military healthcare	mrsn7376
Strain	military healthcare system	military healthcare	mrsn11693
Strain	military healthcare system	military healthcare	mrsn11754
Strain	military healthcare system	military healthcare	mrsn7237
Strain	military healthcare system	military healthcare	mrsn7498
Strain	military healthcare system	military healthcare	mrsn908
Strain	military healthcare system	military healthcare	mrsn7730
Strain	military healthcare system	military healthcare	mrsn953
Strain	military healthcare system	military healthcare	mrsn7188
Strain	military healthcare system	military healthcare	mrsn3384
Strain	military healthcare system	military healthcare	mrsn7140
Strain	viewpoint 155	viewpoint 155	c57bl/6j & 129s5svevbrd
Cell type	14SA cells	14SA cells	fetal muscle myoblast
Cell type	3-HA ChIP-seq ES cells 4dRA 1hr DOX	4dRA 1hr	mesc 4dra
Cell type	34516 mESC 1h chase Rep 1	34516 mESC	mouse embryonic stem (mes) cells
Cell type	34521 mESC 3h chase Rep 3	34521 mESC	mouse embryonic stem (mes)
Cell type	37054 mESC wt 12h pulse	37054 mESC	mouse embryonic stem (mes) cells
Cell type	37061 mESC Mettl3KO #2 3h pulse	mESC Mettl3KO	mouse embryonic stem (mes) cells
Cell type	AR ChIP sequencing 2hr 100nM DHT treated VCaP cells	VCaP cells	prostate cancer cells
Cell type	Activated Erk1/2 Promotes Formation Chromatin Features Inherent Developmental Promoters Mouse Embryonic Stem Cells	Stem Cells	es cells
Cell type	Aorta smooth muscle cells AoSMC2	cells AoSMC2	aorta smooth muscle cells
Cell type	ChIP-Seq Med1 mES cells	mES cells	v6.5 embryonic stem cells
Cell type	ChIP-Seq Smc3 mES cells	mES cells	v6.5 embryonic stem cells
Cell type	ChIP-Seq analysis H3K79me2 mouse ESCs shControl knockdown treatment replicate 2	analysis H3K79me2	mouse embryonic stem cells
Cell type	ChIP-Seq analysis HA-Phf5a mouse ESCs doxycycline treatment replicate 1	mouse ESCs doxycycline treatment	mouse embryonic stem cells
Cell type	ChIP-Seq analysis Leo1 mouse ESCs shControl knockdown treatment replicate 1	mouse ESCs shControl knockdown treatment	mouse embryonic stem cells
Cell type	Chromatin IP ERα MCF-7 cells transfected LRH-1 siRNA Replicate 1	ERα MCF-7	breast cancer
Cell type	Chromatin IP HA MCF-7 cells transfected HA-LRH1 vector Replicate 2	MCF-7 cells	breast cancer
Cell type	DDX5-/- mESCs Line #1 (miRNA-seq)	DDX5-/- mESCs	mus musculus
Cell type	DDX5-/- mESCs Line #2 (miRNA-seq)	DDX5-/- mESCs	mus musculus

Cell type	DKO1 H3K27ac replicate 1 ChIP-seq	DKO1 H3K27ac	human colorectal cancer cell line
Cell type	DS20201 SE DNaseI-seq seed coat cell 4DPA	cell 4DPA	seed coat cell (4 days past anthesis)
Cell type	ENCODE biosample ENCBS478HYO: Differentiated 3T3-L1 (Day 8)	Differentiated 3T3-L1	adipocyte
Cell type	ENCODE biosample ENCBS513ENC: neurons derived H1 embryonic stem cells	stem cells	neural cell
Cell type	Embryonic Stem cells Jarid2 -/- rescue Jarid2K116A BAC H3K27me3 IP	Stem cells	esc serum + lif grown
Cell type	Enteroendocrine Cells RNA-seq biological rep1	Enteroendocrine Cells	adult epitheial cells; proximal 1/3 of intestine
Cell type	GRO-Seq analysis mouse ESCs flavopiridol treatment replicate 2	analysis mouse ESCs flavopiridol treatment	mouse embryonic stem cells
Cell type	Gm6871-HA ChIP-seq mES cells	mES cells	embryonic stem cells
Cell type	H3K27ac marks naïve LIS2 ES stem cells	stem cells	escs
Cell type	H3K27ac marks primed LIS2 ES stem cells	stem cells	escs
Cell type	H3K27ac marks primed WIS2 ES stem cells	stem cells	escs
Cell type	H3K27me3 ChIP	H3K27me3 ChIP	fibroblasts
Cell type	H3K27me3 marks primed WIS2 ES stem cells	stem cells	
Cell type	H3K4me1 sequencing non-treated (DMSO vehicle) MCF-7 cells	MCF-7 cells	escs breast cancer cells
Cell type	H3K4me3 HFFs H3K27ac HFFs input	HFFs H3K27ac	foreskin fibroblast
Cell type	H3K4me3 marks naïve WIS2 ES stem cells	stem cells	
Cell type	H3K9me3 marks naïve C1 induced stem cells	stem cells	escs ips cells
Cell type	H3K9me3 marks naïve WIBR3 embryonic stem cells	stem cells	hes cells
Cell type	H3K9me3 marks primed WIBR3 embryonic stem cells	stem cells	hes cells
Cell type	H929 cells expressing FAM46CWTGFP 72 hrs rep3 total RNA	H929 cells	multiple myeloma cell line
Cell type	HSC cd41low cd9low Gfi1 KO	HSC cd41low cd9low	hematopoietic stem cells cd41low cd9low
Cell type	HT29 10 ΡM 5-Aza	μM 5-Aza	colon cancer
Cell type	HUVEC AX15839 treated cells replicate 2	HUVEC AX15839	huvec cells
Cell type	HUVEC AX15839 treated cells replicate 3	HUVEC AX15839	huvec cells
Cell type	HUVEC PPARβ/δ DMSO 24hr normoxia replicate 1	PPARβ/δ DMSO	human umbilical vein cells
Cell type	Input PolII Activin 1h ChipSeq biological replicate 2	PolII Activin	embryonic teratoma
Cell type	LNCaP GIPZ EtOH AR ChIP m77	ChIP m77	prostate tumor
Cell type	LNCaP shGATA2 R1881 (10nM	LNCaP shGATA2	prostate tumor
Cell type	Luciferase knockdown PC3 cells using shRNa replicate 2	PC3 cells	prostate cancer cells
Cell type	MC1-ZE7 cells (Em+ high fraction) Hpa II	MC1-ZE7 cells	facs sorted emerald+ es cells
Cell type	Mettl3-KO EBs 0h Actinomycin treatment	Mettl3-KO EBs	embroid bodies
Cell type	Mettl3-KO ESCs 0h Actinomycin treatment	Mettl3-KO ESCs	embryonic stem cells
Cell type	Mmu bRG H3K27me3 replicate 1	bRG H3K27me3	basal radial glia
Cell type	PR1 - Pol2 mES cells + DMSO 18 hr ChipSeq	mES cells	v6.5 embryonic stem cells
Cell type	RNA-Seq analysis CEM cells upon treatment short hairpin UTX replicate 2		human t cell leukemia cells
Cell type	RNA-Seq analysis HCT116 FBXW7 KO cells recovery heat shock treatment replicate 1	analysis HCT116	human colon cancer cells
Cell type	RNA-seq sample timecourse siRNA knock-down Tcf7l2: siRNA - Scrambled	timecourse siRNA	hepatocytes
Cell type	S2 T1 H3K27ac ChIP rep1	T1 H3K27ac	s2 cell
Cell type	Sample 9 P14 effector CTLs IL-2 #1	CTLs IL-2	in vitro generated ctls
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Cell type SuRE K562 cDNA SuRE K562 ery Cell type Total RNA Pol2 ChIP-seq mES cells shSpt4 cells shSpt4 v6.5 em	xemia stem cell ythroleukemia
Cell type SuRE K562 cDNA SuRE K562 ery Cell type Total RNA Pol2 ChIP-seq mES cells shSpt4 flavopiridol cells shSpt4 v6.5 em	throleukemia
Cell type Total RNA Pol2 ChIP-seq mES cells shSpt4 cells shSpt4 v6.5 em	
	nbryonic stem cells
The contract to the contract t	tory t (treg) cells
	dermal fibroblasts
Cell type bisfulfite treated genomic DNA arrested DNA arrested primary	dermal fibroblasts
HMEC cells [KRAS Q61H-5]	nammary epithelial (hmec) cells
control 3	e marrow cells
	mbryonic stem cells
ChIP ChIP ep	ortalised prostate oithelial cells
Cell type overexpressed HMEC cells GFP18 control 10 cells GFP18 control 10	nammary epithelial cells
Cen type overexpressed finale cens GFF16 control /	nammary epithelial cells
Cen type	nammary epithelial cells
Cell type	nammary epithelial cells
RAF1 overexpressed 5	nammary epithelial cells
	ary epithelial cells
	ary epithelial cells
	ary epithelial cells
	al blood cd34+ cells
	i1fl/fl cd23t/+
Genotype 14028s ΔSTM14 3463 + pBAD24 -2 ΔSTM14 3463 +	pbad24
Genotype 3 DMSO me3 rep2 me3 rep2	h3wt
Genotype An WT No Carbon #1 WT No	wildtype
	o1fl/flssb2fl/fl
Genotype ChIP Kmg wild-type rep1 Kmg wild-type	w[1118]
Genotype Chlamydomonas reinhardtii 2137 - Copper sufficient - TAP - 4 sufficient -	wt
Genotype Chlamydomonas reinhardtii 2137 - Copper sufficient - TAP - 5 sufficient -	wt
	yoiats control
Genotype Dietary emulsifiers directly alter human microbiota composition gene expression ex vivo potentiating intestinal inflammation gene expression	c57bl6
cell nuclei - OR s8 - Wild type - MNase-Seq	modencode
Genotype Ezh2 +/- replicate1 batch2 Ezh2 +/-	sclcre
	cre jak2v617f
Genotype Gp 3 WT L 3 WT L	sc5314
Genotype H4K8ac OR Head Nuclei D H4K8ac OR	wild type
Genotype HWT Start-seq females NextSeq rep2 NextSeq rep2	hwt
Genotype HWT Start-seq mixed NextSeq rep2 NextSeq rep2	hwt
	gfi1 36n/36s
Genotype Input ChIP Aly-HA w1118 rep1 (negative control (negative control	w[1118]
	rv0954 ko
Genotype M202 - control - rep 4 control - rep	m202
Construe May 1 2 (f.f.) WT I CM DNA Can Change	control (f/f)
	101 1 11 11
Genotype NPC Suv39h dn H3K9me3 ChIP-seq Suv39h dn suv3	39h double null logical replicate 2,

Genotype Whole testis RNA Dunita ClaPW12 Gd pp. Genotype Genotype Genotype Genotype Genotype Whole testis RNA Dunita ClaPW12 Gd pp. Genotype AbblasAOC Mock Time 24 hpt Genotype Genotype Genotype Male tested Genotype Male Genotype Male tested Genotyp			WT	read1
Genotype PET111GFP EZ 6DO rep 1 6DO rep pet111:gfp Genotype PET111GFP MZ 7DO rep 1 7DO rep pet111:gfp Genotype PET111GFP MZ 7DO rep 1 7DO rep pet111:gfp Genotype PET111GFP MZ 7DO rep 1 7DO rep pet111:gfp Genotype PET111GFP MZ 7DO rep 1 7DO rep pet111:gfp Genotype PET111GFP MZ 7DO rep 1 7DO rep pet111:gfp Genotype Productive VB18 allele PP PNA low B cells VB18 passenger mice Genotype RNA pol II ChIP-seq WT Rep2 Genotype RNA pol II ChIP-seq WT Rep2 Genotype RNA seq round 2 atmore47 rep 1 atmore47 rep Genotype RNA seq round 2 atmore47 rep 1 atmore47 rep Genotype Whole testis RNA Dmmt2 (1AP/WT 20 dpp 2 atmore47 rep Genotype WH HSC reated IFNG≥+VN-4 treated IFNG≥+VN-4 wild type Genotype WH HSC reated IFNG≥+VN-4 treated IFNG≥+VN-4 wild type Genotype wild Type of month Female Heart mRNA rep1 wild lype Genotype colo - 118/Sua flu treated HSCs≥+VN-4 Genotype bebbaAOC Mock Time 24 hpt hebbaAOC Mock mic trime 24 hpt hebbaAOC M	Genotyne	POtestis mRNA sea: WT		wt, biological replicate 1,
Genotype Whole testis RNA Dnmt3C IAP/WT 20 dpp 2 Genotype Genotype Genotype Whole testis RNA Dnmt3C IAP/WT 20 dpp 2 Genotype Genotype Whit SC reacted BrNE=YNA-A Genotype Whit SC reacted BrNE=YNA-A Genotype Julia Gilly Grads-12 battch 3 Genotype Julia Genotype Julia Gilly Grads-12 battch 3 Genotype Julia Genotype Julia Gilly Grads-12 battch 3 Genotype Julia Gilly Grads-12 battch 3 Genotype Manaze car V12 rep 3 Genotype Manaze car V14 drought rep 2 Genotype Manaze car V14 drought rep 3 Genotype Manaze lassel V14 drought rep 4 Genotype Manaze lassel V14 drought rep 3 Genotype Manaze lassel V14 drought rep 4 Genotype Manaze lassel V14 drought rep 3 Genotype Manaze lassel V14 drought rep 3 Genotype Manaze lassel V14 Grought rep 4 Genotype Manaze lassel V14 Grought rep 3 Genotype Manaze lassel V14 Grought rep 3 Genotype Manaze lassel V14 Grought rep 4 Genotype Manaze lassel V14 Grought rep 5 Genotype Manaze lassel V14 Grought rep 5 Genotype Manaze lassel V14 Grought rep 5 Genotype Manaze lassel V14 Grought rep 6 Genotype Manaze lassel V14 Grought rep 7 Genotype Manaze lassel V14 Grought rep 7 Genotype Manaze lassel V14 Grought rep 8 Genotype Manaze lassel V14 Grought rep 9 Genotype Manaze lassel V14 Grought rep 9 Genotype Genotype Manaze lassel V14 Grought rep 9 Genotype Genotype Genotype Manaze lassel V14 Grought rep 9 Genotype Genotype Genotype Genotype Genotype Ge		·		
Genotype Mill Tyre Mi				
Genotype Mill Yope Mill Yope Mild Type				
Genotype Ge	Genotype		7DO rep	pet111:gfp
Genotype Productive VB18 allele splenies GC B cells bglobin passenger mice VB18 allele bglobin mice Genotype RNA pol II ChIP-seq WT Rep2 WT Rep2 wildtype Genotype RNAseq round 2 atmore/4/ rep1 atmore/4/ rep atmore/4/ rep Genotype Whole testis RNA Dmm3C IAP/WT 20 dpp 2 Dmm3C IAP/WT before Genotype Will SU treated IFNE≥+VN-4 treated IFNE≥+VN-4 beteroxygous control Genotype will type 6 month Female Heart mRNA rep1 mRNA rep1 wild type wild type wild type Genotype will SU treated IFNE≥+VN-4 treated IFNE≥+VN-4 treated IFNE≥+VN-4 Genotype anti-H3 T11ph Wild type culture #1 4h T11ph Wild wild type (mata/matalpha, hc:sy2-7, lys2/", leu2:-hisge", ura3/") Genotype anti-H3 T11ph Wild type culture #1 4h hbsbaAOC Mock mutant Genotype hebibaAOC Mock Time 24 hpt hebibaAOC Mock mutant Genotype hbz1 all HYG rad5+ 2 batch 3 hbz1 all HYG rad5+ 2 batch 3 hbz1 delta Genotype mize car V12 (drught rep 3 V12 rep b73 Genotype mize car V14 drought rep 2 dro	Genotype		VB18 allele	vb18 passenger mice
Genotype RNA pol II ChIP-seq WT Rep2 atmore4/7 rep atmore6/7 rep Genotype Ribsosome protected fragments MZdicer 6hpf-2 MZdicer 6hpf-2 mZdicer mutant Genotype Wild Type 6 month Female Heart mRNA rep1 wild type Genotype Wild Type 6 month Female Heart mRNA rep1 wild type Genotype Wt HSC treated IFN€≥+VN-4 treated IFN€≥+VN-4 wild type Genotype wild Type 6 month Female Heart mRNA rep1 wild type wild type wild type control mRNA rep1 wild type Genotype wild Type 6 month Female Heart mRNA rep1 wild type wild type make type 6 month Female Heart mRNA rep1 wild type wild type wild type wild type control mRNA rep1 wild type control mRNA rep1 wild type wild type rep3 wild type rep3 drought rep b73	Genotype	Productive VB18 allele Splenic GC B cells bglobin	VB18 allele	bglobin mice
Genotype RNAscq round 2 atmore47 rep 1 atmore6 Genotype Ribosome protected fragments MZdicer 6hpf-2 MZdicer 6hpf-2 mzdicer mutant Genotype Whole testis RNA Dmmt3C IAPWT 20 dpp 2 Dmmt3C IAPWT betrozygous control Genotype Wild Type 6 month Female Heart mRNA rep1 mRNA rep1 wild type wild type Genotype Wt HSC treated IFNGE≠VN-4 treated IFNGE≠VN-4 wild type wild type Genotype anti-H3 T11ph Wild type culture #1 4h T11ph Wild type (mata/matalpha, ho::)ys2²², lys2²², leu2::hsg²², ura3²²) wild type mutant Genotype hebibaAOC Mock Time 24 hpt hebibaAOC Mock Time 24	Genotype		WT Ren2	wildtype
Genotype Whole testis RNA Dimit3C IAPWT 20 dpp 2 Genotype Whole testis RNA Dimit3C IAPWT 20 dpp 2 Genotype Wild Type 6 month Female Heart mRNA rep1 Genotype Wild Type 6 month Female Heart mRNA rep1 Genotype Wild Type 6 month Female Heart mRNA rep1 Genotype Wild Type 6 month Female Heart mRNA rep1 Genotype wild type 6 month Female Heart mRNA rep1 Genotype anti-H3 T11ph Wild type culture #1 4h Genotype col0 - H3K9ac fig treated H3K9ac fig Genotype hebbaAOC Mock Time 24 hpt hebbaAOC Mock Genotype hebbaAOC Mock Time 24 hpt hebbaAOC Mock Genotype hebbaAOC Mock Time 24 hpt hebbaAOC Mock Genotype iPSC 7dupASD1-C2 (GDB-CF G) GTF21 KD Genotype maize ear V12 rep3 Genotype maize ear V14 drought rep2 drought rep b73 Genotype maize leaf V14 drought rep3 drought rep b73 Genotype maize leaf V14 drought rep4 drought rep b73 Genotype maize tassel R1 rep3 R1 rep b73 Genotype wild type retina sample 2 (WR2) wild type w				
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Tissue Diet: High Fat High Fat pancreatic islets	Tissue	DNA urine patient P50_010 prostate cancer radical	P50 010 prostate	urine before radical
	Tissue		High Fat	
	Tissue	Diet: High Fat	High Fat	pancreatic islets

Tissue	Diet: High Fat	High Fat	pancreatic islets
Tissue	Diet: High Fat	High Fat	pancreatic islets
Tissue	Does timing matter pesticide resistance? One splice form variant MDR49 provides early	Does timing matter	whole body
Tissue	Drosophila simulans male body small RNA	body small	abdomen and thorax
Tissue	ENCODE biosample ENCBS046IMM: Heart embryonic 11	biosample ENCBS046IMM:	heart
Tissue	ENCODE biosample ENCBS504VDB: Esophagus mucosa tissue aliquot received Gingeras lab conduct RNA-Seq assays ENCODE biosample ENCBS765HGS: EnTEX:		esophagus squamous epithelium
Tissue	ENCODE biosample ENCBS765HGS: EnTEX: biosample Colon - Transverse ENCBS765HGS:		transverse colon
Tissue	ENCODE biosample ENCBS802FTI: Midbrain 88 embyronic 11	biosample ENCBS802FTI:	midbrain
Tissue	ENCODE biosample ENCBS836VES: Skin lower leg aliquot received Gingeras lab conduct RNA-Seq assays	ENCBS836VES: Skin	lower leg skin
Tissue	ENCODE biosample ENCBS926XRV: Skin - Sun Exposed (Lower leg)	ENCBS926XRV: Skin	lower leg skin
Tissue	Enteropathy-associated T-cell Lymphoma tumor tissue	tumor tissue	eatl
Tissue	Fall'12 Day 42 Control Ross Heart Fat 1210	Heart Fat	cardiac adipose
Tissue	Flag Leaf Tissue Biological Rep 2	Leaf Tissue	flag leaf
Tissue	Generic sample Ctenopharynodon idellus	sample Ctenopharynodon	gill
Tissue	Generic sample Ctenopharynodon idellus Sample Ctenopharynodon		gill head and thorax
Tissue	Generic sample Neohirasea fruhstorferi		
Tissue	Generic sample Oreophoetes peruana	sample Oreophoetes	head and thorax
Tissue	Genetic variations rectal cancer	variations rectal	primary tumor
Tissue	H3K27ac Chimpanzee Brain OccipitalPole PT1	Brain OccipitalPole	occipital pole
Tissue	Hosui leaf defoliation research	leaf defoliation	flower buds
Tissue	Human sample Homo sapiens UUS2 tumor tissue	UUS2 tumor	uterus
Tissue	Invertebrate sample Acropora humilis: Tank - biological replicate 1 -noon- new moon	noon- new moon	
Tissue	Kidney tumor tissue 1 RP tumor tissue		kidney
Tissue Tissue	LD tissue sample Sus scrofa Leaf tissue Brachypodium distachyon accession ABR6	tissue sample Leaf tissue	longissimus dorsi fourth and fifth leaf
Tissue	eaf transcriptome Euphorbia pekinensis (replicate = biological replicate 2) Leaf transcriptome		leaf (replicate = biological replicate 2)
Tissue	Leave segment region 4 (photosynthetic) collected 10pm Leave segment		leaf segment region 4
Tissue	Leave segment region 5 (photosynthetic) collected 10pm Leave segment		leaf segment region 5
Tissue	MCF-10A digested nuclei biological replicate 1 nuclei biological		breast
Tissue	Model organism animal sample Dichorragia nesimachus sample Dichor		thoracic muscle tissue or legs
Tissue	Model organism animal sample litopenaeus vannamei sample litopenaeus		gill
Tissue	Multispecies transcriptome raw reads Solanum lycopersicum style tissue pollinated Solanum pennellii pollen +1 days flower opening (individual L2+P1)	style tissue	style+pollen
Tissue	Multispecies transcriptome raw reads Solanum pennellii style tissue pollinated Solanum lycopersicum pollen +1 days flower opening (individual P3+L3) style tissue		style+pollen
Tissue	Partial transcriptome abdominal tissue female	abdominal tissue	abdomen

Tissue RNAseq Ptychodera flava: head regeneration 0h-3 regeneration 0h-3 marterior to collar bead amputation plane, anterior to collar bead amputation bead anterior to collar		Hypolimnas bolina		
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Age andersoni 2 days 2 days adults	Age		2 days	adults
Age Nuclear_RNA extract Differentiated Myotubes 7 days cell culture Duchenne Muscular Dystrophy (DMD) donors Caucasian origin Nuclear DMD MT-7 9813 21	Age	Nuclear_RNA extract Differentiated Myotubes 7 days cell culture Duchenne Muscular Dystrophy (DMD) donors Caucasian origin Nuclear DMD MT-7 9813 21	7 days	3
Age Nuclear_RNA extract Differentiated Myotubes 7 days cell culture Healthy donors Caucasian 7 days origin Nuclear CTRL MT-7 10006 11	Age	days cell culture Healthy donors Caucasian	7 days	3
Age Patient 2 Day 3 Day 3 21	Age		Day 3	21

Age	RESA-Seq - WT 8h pA r3 B1	8h pA	8
Age	RRGD Timepoint VI - recovery 15 min	15 min	23 days
Age	Retina Aipl1 knockout mouse postnatal day 50	postnatal day	50 days
Age	Single cell 4 month old LMPP 10	month old	4 months
Age	Skeletal muscle 8-week old mouse	8-week old	8 weeks
	T1 - horses intensive training stage (after slow		
Age	canter phase) (March) 3	stage (after	3 year old
Age	Vaginal microbiota associated preterm delivery	preterm delivery	35
Age	Vaginal microbiota associated preterm delivery	preterm delivery	42
Age	Vaginal microbiota associated preterm delivery	preterm delivery	30
Age	Vaginal microbiota associated preterm delivery	preterm delivery	26
Age	Vaginal microbiota associated preterm delivery	preterm delivery	19
Age	Vaginal microbiota associated preterm delivery	preterm delivery	37
Age	Vaginal microbiota associated preterm delivery	preterm delivery	35
Age	Vaginal microbiota associated preterm delivery	preterm delivery	33
Age	Vaginal microbiota associated preterm delivery	preterm delivery	33
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	35 31
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	27 19
Age	Vaginal microbiota associated preterm delivery Vaginal microbiota associated preterm delivery	preterm delivery	20
Age		preterm delivery	23
Age	Vaginal microbiota associated preterm delivery	preterm delivery	32
Age	Vaginal microbiota associated preterm delivery	preterm delivery	22
Age	Vaginal microbiota associated preterm delivery	preterm delivery	27
Age	Vaginal microbiota associated preterm delivery	preterm delivery	37
Age	Vaginal microbiota associated preterm delivery Vaginal microbiota associated preterm delivery	preterm delivery preterm delivery	27
Age Age	Vaginal microbiota associated preterm delivery	preterm delivery	25
Age	Vaginal microbiota associated preterm delivery	preterm delivery	33
Age	Vaginal microbiota associated preterm derivery Vaginal microbiota associated preterm delivery	preterm delivery	38
Age	Vaginal microbiota associated preterm derivery Vaginal microbiota associated preterm delivery	preterm delivery	28
Age	Vaginal microbiota associated preterm delivery	preterm delivery	33
Age	Vaginal microbiota associated preterm delivery	preterm delivery	24
Age	Vaginal microbiota associated preterm delivery	preterm delivery	33
Age	Vaginal microbiota associated preterm delivery	preterm delivery	17
Age	Vaginal microbiota associated preterm delivery	preterm delivery	20
Age	Vaginal microbiota associated preterm delivery	preterm delivery	21
Age	Vaginal microbiota associated preterm delivery	preterm delivery	36
Age	Vaginal microbiota associated preterm delivery	preterm delivery	24
Age	Vaginal microbiota associated preterm delivery	preterm delivery	28
Age	Vaginal microbiota associated preterm delivery	preterm delivery	22
Age	Vaginal microbiota associated preterm delivery	preterm delivery	23
Age	Vaginal microbiota associated preterm delivery	preterm delivery	33
Age	Vaginal microbiota associated preterm delivery	preterm delivery	38
Age	Vaginal microbiota associated preterm delivery	preterm delivery	26
Age	Vaginal microbiota associated preterm delivery	preterm delivery	34
Age	Vaginal microbiota associated preterm delivery	preterm delivery	35
Age	Vaginal microbiota associated preterm delivery	preterm delivery	37
Age	Vaginal microbiota associated preterm delivery	preterm delivery	27
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	24
Age	Vaginal microbiota associated preterm delivery	preterm delivery	31
Age	Vaginal microbiota associated preterm delivery	preterm delivery	37
Age	Vaginal microbiota associated preterm delivery	preterm delivery	25

Age	Vaginal microbiota associated preterm delivery	preterm delivery	25
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	22
Age	Vaginal microbiota associated preterm delivery	preterm delivery	22
Age	Vaginal microbiota associated preterm delivery	preterm delivery	22
Age	Vaginal microbiota associated preterm delivery	preterm delivery	38
Age	Vaginal microbiota associated preterm delivery	preterm delivery	42
Age	Vaginal microbiota associated preterm delivery	preterm delivery	35
Age	Vaginal microbiota associated preterm delivery	preterm delivery	24
Age	Vaginal microbiota associated preterm delivery	preterm delivery	31
Age	Vaginal microbiota associated preterm delivery	preterm delivery	21
Age	Zeitgeber Time 00	Zeitgeber Time	3 weeks
Age	Zeitgeber Time 18	Zeitgeber Time	5 weeks
Age	bisulfite treated genomic DNA old sun exposed epidermis 3	old sun	83
Age	cinerea B9 different inoculation time treatments	time treatments	1 year
Age	five 5w old individuals (male)	5w old	5 week
Age	time point 2	time point	65.397
Age	zebrafish normal developmental age 72hpf control rep2	developmental age	72 hpf£¨hour post fertilization£©
Data type	Non-tumor DNA sample human male participant dbGaP study "Whole Exome Sequencing Chronic Lymphocytic Leukemia"	Exome Sequencing Chronic	snv aggregate (.maf)
Data type	Tumor DNA sample human male participant dbGaP study "Whole Exome Sequencing Chronic Lymphocytic Leukemia"	Exome Sequencing Chronic	snv aggregate (.maf)
Platform	16S rDNA amplicon patient 11	16S rDNA amplicon	454
Platform	16S rDNA amplicon patient 5	16S rDNA amplicon	454
Platform	16S rRNA control root 3	16S rRNA	ion torrent
Platform	16S rRNA mycorrhiza leaf 1	16S rRNA	ion torrent
Platform	16S rRNA sequences fecal bacterial community Chicken	16S rRNA	454 gs flx
Platform	Mouse fecal sample VLP-purification 454	454 Sequencing	
	Sequencing	434 Sequencing	454 flx titanium
Platform	Sequencing Mouse fecal sample VLP-purification 454 Sequencing	454 Sequencing	454 flx titanium 454 flx titanium
Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings	454 Sequencing Pyrosequencing 16S rRNA amplicons	
	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig	454 Sequencing Pyrosequencing 16S	454 flx titanium
Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings	Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons	454 flx titanium pyrosequncing
Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig	Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S	454 flx titanium pyrosequncing pyrosequncing
Platform Platform Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene SAG SCGC AB-704-N13 partial SSU rRNA gene	Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons	454 flx titanium pyrosequncing pyrosequncing pyrosequncing
Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene	454 Sequencing Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons SSU rRNA	454 flx titanium pyrosequncing pyrosequncing pyrosequncing sanger
Platform Platform Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene SAG SCGC AB-704-N13 partial SSU rRNA gene	454 Sequencing Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons SSU rRNA SSU rRNA	454 flx titanium pyrosequncing pyrosequncing pyrosequncing sanger sanger
Platform Platform Platform Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene SAG SCGC AB-704-N13 partial SSU rRNA gene SAG SCGC AB-706-C03 partial SSU rRNA gene	454 Sequencing Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons SSU rRNA SSU rRNA SSU rRNA	pyrosequncing pyrosequncing pyrosequncing pyrosequncing sanger sanger sanger
Platform Platform Platform Platform Platform Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene SAG SCGC AB-706-C03 partial SSU rRNA gene SAG SCGC AB-706-E02 partial SSU rRNA gene	454 Sequencing Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons SSU rRNA SSU rRNA SSU rRNA SSU rRNA SSU rRNA	pyrosequncing pyrosequncing pyrosequncing sanger sanger sanger sanger sanger
Platform Platform Platform Platform Platform Platform Platform Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene SAG SCGC AB-704-N13 partial SSU rRNA gene SAG SCGC AB-706-E02 partial SSU rRNA gene SAG SCGC AB-706-E13 partial SSU rRNA gene	Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons SSU rRNA	pyrosequncing pyrosequncing pyrosequncing sanger sanger sanger sanger sanger sanger sanger
Platform Platform	Mouse fecal sample VLP-purification 454 Sequencing Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings SAG SCGC AB-704-M06 partial SSU rRNA gene SAG SCGC AB-706-C03 partial SSU rRNA gene SAG SCGC AB-706-E02 partial SSU rRNA gene SAG SCGC AB-706-E13 partial SSU rRNA gene SAG SCGC AB-706-E22 partial SSU rRNA gene	Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons Pyrosequencing 16S rRNA amplicons SSU rRNA SSU rRNA SSU rRNA SSU rRNA SSU rRNA SSU rRNA	pyrosequncing pyrosequncing pyrosequncing sanger sanger sanger sanger sanger sanger sanger sanger sanger