

## Supplementary Data

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

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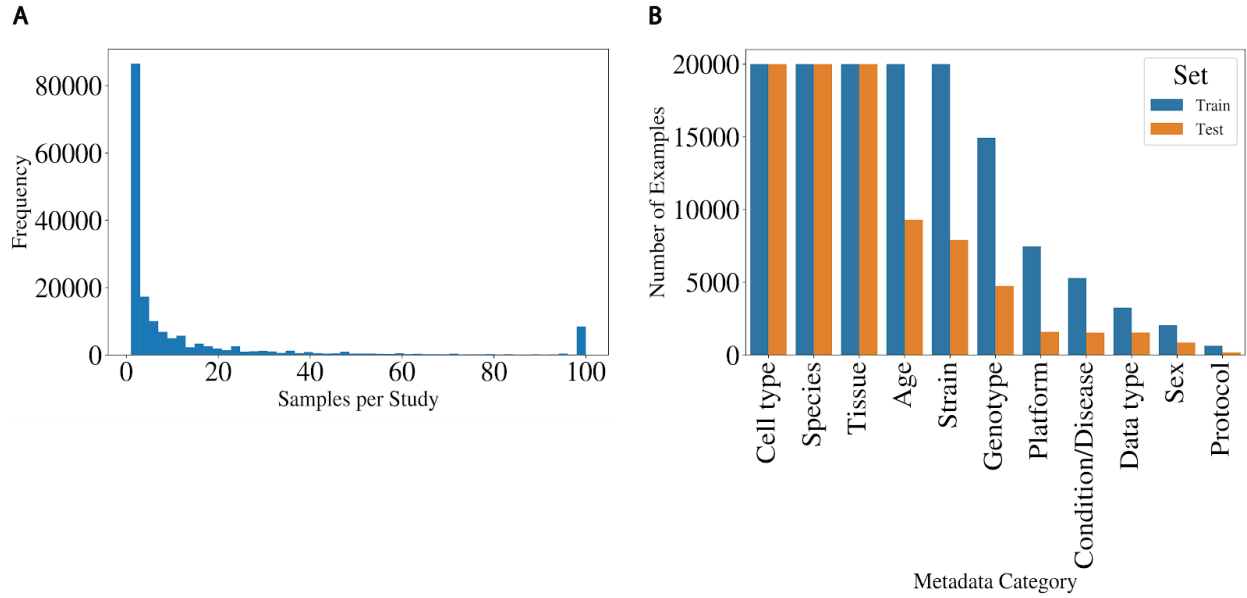
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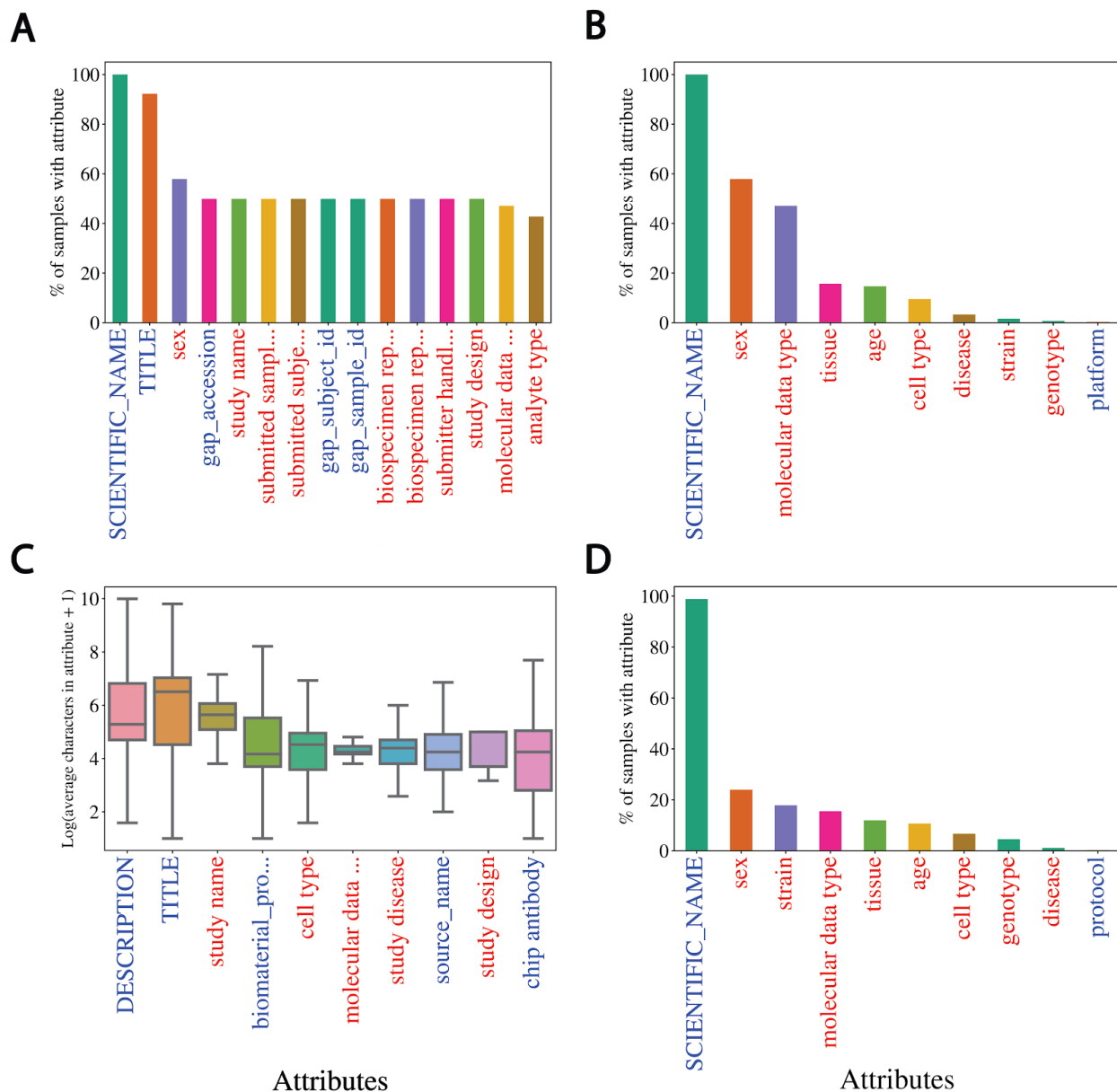
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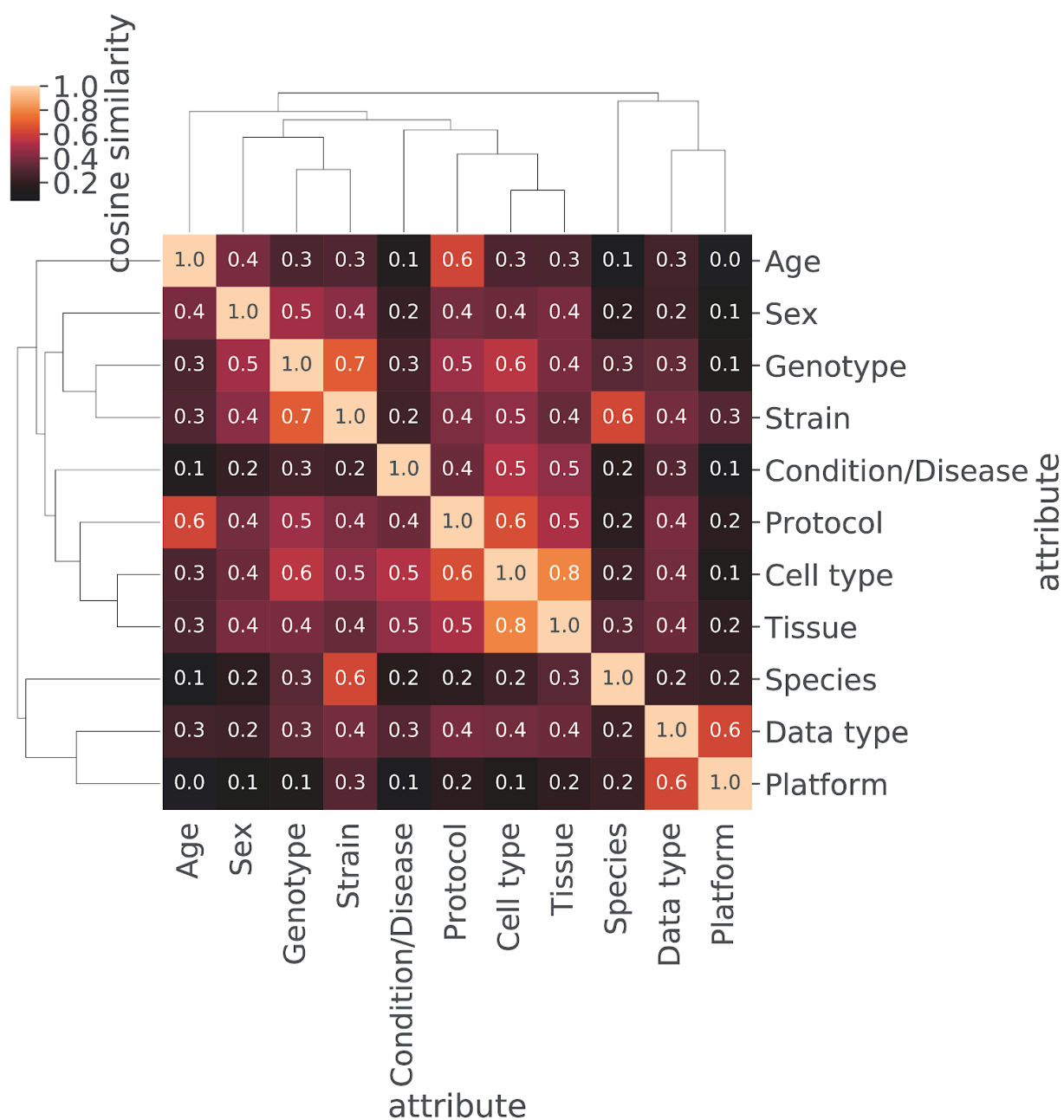
1. **Supplementary Figure 1** - Breakdown of training and testing data.
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**Supplementary Figure 1.** Breakdown of training and testing data. **(A)** Histogram showing the distribution of samples in each study (capped at 100) used to generate training 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  $\text{Log}_2(\text{average characters})$  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	Attribute	Cosine Similarity
Species	<b>SCIENTIFIC_NAME</b>	1.000
	Organism	0.917
	host scientific name	0.911
	organism	0.903
	host_scientific_name	0.886
	host	0.884
	nat-host	0.859
	specific host	0.853
	host organism	0.851
	host species	0.831
	specific_host	0.805
	HostSpecies	0.801
Strain	<b>strain</b>	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
	host strain	0.891
	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

	maternal strain	0.835
	paternal strain	0.812
Cell type	<b>cell type</b>	1.000
	cell_type	0.897
	source_name	0.886
	source cell type	0.885
	CellType	0.869
	progenitor cell type	0.866
	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
	<b>genotype</b>	1.000
	genotype/variation	0.940
	Genotype	0.895
Genotype	mutant	0.882
	mutation	0.847
	plant genotype	0.824
	genetic variation	0.812
	idh2.gene.mutation	0.801
	host genotype	0.801
	<b>disease</b>	1.000
	disease status	0.833
	tumor type	0.828
Condition/Disease	health state	0.828
	cancer type	0.826
	cell description	0.813
	<b>tissue</b>	1.000
	tissue_type	0.913
	organism part	0.848
Tissue	tissue-type	0.827
	source_name	0.800
	<b>sex</b>	1.000
	host_sex	0.997
	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	0.994
	;	0.987
	breeding direction	0.981
	Gender	0.939
	host sex	0.930
	SEX	0.900
	sex_def_prob	0.865
Age	<b>age</b>	1.000
	Age	0.832
Data type	<b>molecular data type</b>	1.000
Platform	<b>platform</b>	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
	labversion description	0.914
	illumina_technology	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	<b>protocol</b>	1.000
	technology	0.887
	extract_protocol	0.860
	experiment type	0.858
	assay	0.850
	protocol description	0.844
	application	0.843



	library_type	0.800
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**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	Transcriptomics potato tubers infected Streptomyces turgidiscabies	Streptomyces turgidiscabies	solanum tuberosum
Species	Uncultivated Candidatus UAP2 archaeon UBA543 genome recovered ERX552263	Candidatus UAP2	archaeon uba543
Species	Whole genome analysis Clostridium saccharogumia VE202-01	Clostridium saccharogumia	[clostridium] saccharogumia
Species	cecal microbiota sample Microtus brandti	Microtus brandti	lasiopodomys brandtii
Species	drifting hotspot microbial diversity	microbial diversity	caulerpa taxifolia
Species	foliar sample Castanea sativa	Castanea sativa	uncultured fungus
Species	foliar sample Vitis vinifera	Vitis vinifera	uncultured fungus
Species	foliar sample Vitis vinifera	Vitis vinifera	uncultured fungus
Species	hRSV RSV+PIV3 F insert C 03	hRSV RSV+PIV3	human orthopneumovirus
Species	live-1 pig low backfat thickness	live-1 pig	sus scrofa
Species	sativus contaminated Alternaria brassicicola Abra43	Alternaria brassicicola	raphanus sativus var. sativus
Species	treated plants polyethylene glycol PEG NaCl carried transcriptomic metabolomics measurements across time-course five days	polyethylene glycol	calotropis procera
Species	unspecified weed species yellowing mosaic-like symptoms	weed species	unidentified plant
Strain	1 New Tech Library sample 21095	New Tech	2.4.1
Strain	4 mM - R-1 (ncra)	R-1 (ncra)	fgsc 2489
Strain	A-1 rbs	A-1 rbs	tc1769
Strain	Aspergillus niger NRRL 3 delta araR Preculture Gene expression profiling - Pa	NRRL 3	nrrl3 delta arar
Strain	Aureus strain DSM799	strain DSM799	dsm 799
Strain	CR0044 serovar Typhi 13438	CR0044 serovar	13438
Strain	CRISPR 128 genomic zebrafish loci ,Äi sgRNAs ,Äi Pull-down expt ,Äi Canonical ,Äi Mutant pool1	expt ,Äi	tu
Strain	Candida glabrata genome-wide nucleosome data Jan2809	data Jan2809	clib 138
Strain	CgPho2 ChIP Pi media w/ CgPho4	w/ CgPho4	cg40
Strain	Escherichia coli serovar O101:H33 175562	serovar O101:H33	175562
Strain	Escherichia coli serovar O11:H25 204427	serovar O11:H25	204427
Strain	Fungi PEN-treated leaves SM2 rep	SM2 rep	49
Strain	Generic sample Enterococcus columbae DSM 7374 = ATCC 51263	ATCC 51263	dsm 7374
Strain	Khuskia oryzae ATCC28132 Annotated Standard Draft	ATCC28132 Annotated	atcc 28132
Strain	LES CF sputum CF03 isolate 14	CF03 isolate	liverpool epidemic strain
Strain	LPS 48h pf 13 Replicate 1	13 Replicate 1	c57bl/6babr
Strain	Louis clinical isolate (#12)	Louis clinical	68
Strain	Neurospora crassa FGSC2489 X	FGSC2489 X	2489x8790 370a
Strain	Neurospora crassa FGSC2489 X	FGSC2489 X	2489x8790 90a
Strain	Neurospora crassa FGSC2489 X	FGSC2489 X	2489x8790 305a
Strain	Neurospora crassa FGSC2489 X	FGSC2489 X	2489x8790 362a
Strain	Pyronema omphalodes CBS 100304	CBS 100304	cbs100304
Strain	RNA-seq data Paratyphi A 45157 grown stationary phase 42C	A 45157	paratyphi a
Strain	Resequencing evolved clone P4C7	clone P4C7	cc2937
Strain	Salmonella enterica enterica serovar Salmonella Monschaui 369918	Salmonella Monschaui	369918
Strain	Salmonella enterica serovar Agona SL483 uid59431 serovar Agona 9165	SL483 uid59431	9165
Strain	Salmonella enterica subsp I enterica serovar Ajiobo 63502	serovar Ajiobo	63502
Strain	Salmonella enterica subsp I enterica serovar Goelzau H120240584	serovar Goelzau	h120240584
Strain	Salmonella enterica subsp I enterica serovar	serovar Monschaui	63893

	Monschau 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	lvpi12
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) cells
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 ER $\alpha$ ± MCF-7 cells transfected LRH-1 siRNA Replicate 1	ER $\alpha$ ± 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 epithelial 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 naive 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	escs
Cell type	H3K4me1 sequencing non-treated (DMSO vehicle) MCF-7 cells	MCF-7 cells	breast cancer cells
Cell type	H3K4me3 HFFs H3K27ac HFFs input	HFFs H3K27ac	foreskin fibroblast
Cell type	H3K4me3 marks naive WIS2 ES stem cells	stem cells	escs
Cell type	H3K9me3 marks naive C1 induced stem cells	stem cells	ips cells
Cell type	H3K9me3 marks naive 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 <sup>6</sup> M 5-Aza	10 <sup>6</sup> M 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 PPAR $\alpha$ $\leq$ 10 <sup>-6</sup> M DMSO 24hr normoxia replicate 1	PPAR $\alpha$ $\leq$ 10 <sup>-6</sup> M 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	fac 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	analysis CEM cells upon treatment	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

Cell type	Strains used generate cells must carry Fv2 sensitive allele (Fv2s)	generate cells	leukemia stem cell
Cell type	SuRE K562 cDNA	SuRE K562	erythroleukemia
Cell type	Total RNA Pol2 ChIP-seq mES cells shSpt4 flavopiridol	cells shSpt4	v6.5 embryonic stem cells
Cell type	Treg CNS2-/- Foxp3 low rep1	CNS2-/- Foxp3	regulatory t (treg) cells
Cell type	bisulfite treated genomic DNA G1 fibroblasts A	DNA G1	primary dermal fibroblasts
Cell type	bisulfite treated genomic DNA arrested	DNA arrested	primary dermal fibroblasts
Cell type	human KRAS Q61H mutant form overexpressed HMEC cells [KRAS Q61H-5]	HMEC cells	human mammary epithelial (hmec) cells
Cell type	long term repopulating hematopoietic stem cells control 3	stem cells	bone marrow cells
Cell type	mESC m6A IP sample	mESC m6A	mouse embryonic stem cells
Cell type	nucARRB1 C4-2(high nuclear ARRB1)_H3K4me3 ChIP	ARRB1)_H3K4me3 ChIP	immortalised prostate epithelial cells
Cell type	overexpressed HMEC cells GFP18 control 10	cells GFP18 control 10	human mammary epithelial cells
Cell type	overexpressed HMEC cells GFP18 control 7	cells GFP18 control 7	human mammary epithelial cells
Cell type	overexpressed HMEC cells GFP30 control 4	cells GFP30 control 4	human mammary epithelial cells
Cell type	overexpressed HMEC cells GFP30 control 6	cells GFP30 control 6	human mammary epithelial cells
Cell type	overexpressed HMEC cells RAF1 overexpressed 5	cells RAF1 overexpressed 5	human mammary epithelial cells
Cell type	overexpressed HMEC cells 3	HMEC cells 3	mammary epithelial cells
Cell type	overexpressed HMEC cells 3	HMEC cells 3	mammary epithelial cells
Cell type	overexpressed HMEC cells 5	HMEC cells 5	mammary epithelial cells
Cell type	peripheral blood CD34+ cells pooled CD34pB	cells pooled CD34pB	peripheral blood cd34+ cells
Genotype	1 cKO rep2 LPS + IL-4	#NAME?	spi1 fl/fl cd23t/+
Genotype	14028s $\Delta$ ESTM14 3463 + pBAD24 -2	$\Delta$ ESTM14 3463 +	pbad24
Genotype	3 DMSO me3 rep2	me3 rep2	h3wt
Genotype	An WT No Carbon #1	WT No	wildtype
Genotype	BLESS control sample mouse bone marrow	BLESS control	ssb1 fl/flssb2 fl/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
Genotype	D2 Control no2	D2 Control	myoiats control
Genotype	Dietary emulsifiers directly alter human microbiota composition gene expression ex vivo potentiating intestinal inflammation	gene expression	c57bl6
Genotype	Drosophila melanogaster - Ovary stages 1-8 follicle cell nuclei - OR s8 - Wild type - MNase-Seq	Wild type	modencode
Genotype	Ezh2 +/- replicate1 batch2	Ezh2 +/-	scldre
Genotype	Ezh2 -/- replicate6	Ezh2 -/-	scldre 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
Genotype	Human set 4 36N H3K9Ac	36N H3K9Ac	gfi1 36n/36s
Genotype	Input ChIP Aly-HA w1118 rep1 (negative control	(negative control	w[1118]
Genotype	Knockout Rv0954 H37Rv	Knockout Rv0954	rv0954 ko
Genotype	M202 - control - rep 4	control - rep	m202
Genotype	Msx1-2 (f-f) WT - LCM RNA-Seq - Stroma	WT -	control (f/f)
Genotype	NPC Suv39h dn H3K9me3 ChIP-seq	Suv39h dn	suv39h double null
Genotype	P0testis mRNA seq: WT	P0testis mRNA seq:	wt, biological replicate 2,

		WT	read1
Genotype	P0testis mRNA seq: WT	P0testis_mRNA_seq: WT	wt, biological replicate 1, read1
Genotype	PET111GFP EZ 6DO rep 1	6DO rep	pet111:gfp
Genotype	PET111GFP MZ 6DO rep 1	6DO 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	VB18 allele	vb18 passenger mice
Genotype	Productive VB18 allele Splenic 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 atmorc4/7 rep 1	atmorc4/7 rep	atmorc6
Genotype	Ribosome protected fragments MZdicer 6hpf-2	MZdicer 6hpf-2	mzdicer mutant
Genotype	Whole testis RNA Dnmt3C IAP/WT 20 dpp 2	Dnmt3C IAP/WT	heterozygous control
Genotype	Wild Type 6 month Female Heart mRNA rep1	mRNA rep1	wild type
Genotype	Wt HSC treated IFN $\gamma$ +VN-4	treated IFN $\gamma$ +VN-4	wild type
Genotype	anti-H3 T11ph Wild type culture #1 4h	T11ph Wild	wild type (mata/matalpha, ho::lys2/", lys2/", leu2::hisg/", ura3/")
Genotype	col0 - H3K9ac flg treated	H3K9ac flg	wt
Genotype	hebibaAOC Mock Time 24 hpt	hebibaAOC Mock	mutant
Genotype	htz1,ΔÜHYG Rad5+ t2 batch 3	htz1,ΔÜHYG Rad5+	htz1 delta
Genotype	iPSC 7dupASD1-C2 (GDB-Cf G) GTF2I KD	GTF2I KD	7dupasd
Genotype	maize ear V12 rep 3	V12 rep	b73
Genotype	maize ear V14 drought rep 2	drought rep	b73
Genotype	maize leaf V14 drought rep 3	drought rep	b73
Genotype	maize leaf V14 drought rep 4	drought rep	b73
Genotype	maize tassel R1 rep 3	R1 rep	b73
Genotype	maize tassel V12 drought rep 2	drought rep	b73
Genotype	repeat 2 [Rlim KO]	[Rlim KO]	wt
Genotype	wild type retina sample 2 (WR2)	wild type	wildtype
Condition/Disease	inflamed region patient B1/non-stricturing	patient B1/non-stricturing	crohn's disease
Tissue	4-6h afer egg laying	egg laying	embryonic
Tissue	5 skin extract	skin extract	adult skin
Tissue	6127 sigmoid stroma phase 1	sigmoid stroma	colon
Tissue	Barin tissue sample - rep3	tissue sample	brain
Tissue	CD Female Macroscopic inflammation Deep Ulcer (CCFA Risk 143)	Deep Ulcer	ileal biopsy
Tissue	CD Female Macroscopic inflammation No Deep Ulcer (CCFA Risk 018)	Deep Ulcer	ileal biopsy
Tissue	CD Male Macroscopic inflammation Deep Ulcer (CCFA Risk 150)	Deep Ulcer	ileal biopsy
Tissue	CD Male Macroscopic inflammation Deep Ulcer (CCFA Risk 216)	Deep Ulcer	ileal biopsy
Tissue	CD Male Macroscopic inflammation No Deep Ulcer (CCFA Risk 134)	Deep Ulcer	ileal biopsy
Tissue	CD Male Microscopic inflammation No Deep Ulcer (CCFA Risk 060)	Deep Ulcer	ileal biopsy
Tissue	Chandelier cells deep layer WT brain (CHC2-3)	deep layer	frontal cortex layers 5 & 6
Tissue	DNA plasma patient P50_006 prostate cancer radical prostatectomy	P50_006 prostate	plasma before radical prostatectomy.
Tissue	DNA urine patient P50_008 prostate cancer radical prostatectomy	P50_008 prostate	urine after radical prostatectomy.
Tissue	DNA urine patient P50_010 prostate cancer radical prostatectomy	P50_010 prostate	urine before radical prostatectomy.
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	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 ENCBS04VDB: Esophagus mucosa tissue aliquot received Gingeras lab conduct RNA-Seq assays	mucosa tissue	esophagus squamous epithelium
Tissue	ENCODE biosample ENCBS765HGS: EnTEX: Colon - Transverse	biosample ENCBS765HGS:	transverse colon
Tissue	ENCODE biosample ENCBS802FTI: Midbrain 88 embryonic 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
Tissue	Generic sample Neohirasea fruhstorferi	sample Neohirasea	head and thorax
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	new moon	branch tip
Tissue	Kidney tumor tissue 1 RP	tumor tissue	kidney
Tissue	LD tissue sample Sus scrofa	tissue sample	longissimus dorsi
Tissue	Leaf tissue Brachypodium distachyon accession ABR6	Leaf tissue	fourth and fifth leaf
Tissue	Leaf 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 Dichorragia	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

	Hypolimnas bolina		
Tissue	RNAseq Ptychodera flava: head regeneration 0h-3	regeneration 0h-3	head amputation plane, anterior to collar
Tissue	RNAseq Ptychodera flava: head regeneration 96h-1	regeneration 96h-1	head amputation plane, anterior to collar
Tissue	Sample ABHDF1 RNASeq bacteria-HDFa co-culture experiments	Sample ABHDF1	adult skin
Tissue	Single-cell sequencing individual murine aortal smooth muscle cells [Harmandeep SMC run2 09]	smooth muscle	aorta
Tissue	Single-cell sequencing individual murine aortal smooth muscle cells [Harmandeep SMC run2 86]	smooth muscle	aorta
Tissue	Skin sample old subjects	Skin sample	skin (epidermal suction blister samples)
Tissue	Sunflower species whole genome shotgun sequencing	whole genome	leaves
Tissue	The blood sample KPGP-00336	sample KPGP-00336	blood
Tissue	The integument Dazao 16 h head capsule slippage fourth molt	head capsule	integument
Tissue	Thymus tissue sample male female Indian-origin rhesus macaque	tissue sample	thymus
Tissue	Transcriptome analysis table grape berry cv	grape berry	baya
Tissue	Triticum aestivum microspore embryogenesis sample	embryogenesis sample	anther in vitro culture
Tissue	Tumor DNA STAT1 +/- mouse model human breast cancer sample M CA-SSM3-SSM3	Tumor DNA	cl
Tissue	Tumor DNA sample human female participant Texas Cancer Research Biobank Open Access Data Sharing BioProject	Tumor DNA	pancreas
Tissue	WR1913 subject 10 oropharyngeal swab	WR1913 subject	oropharynx
Tissue	Whole genome bisulfite sequencing control CD1A dendritic cells	Whole genome	primary cells
Tissue	Whole genome sequence vervet Chlorocebus tantalus animal	Whole genome	blood cell pellet
Tissue	copper treatment control sample shoot 01	sample shoot	shoots
Tissue	copper treatment treated sample root 02	sample root	roots
Tissue	copper treatment treated sample shoot 02	sample shoot	shoots
Tissue	islet preparation 1 control condition	islet preparation	islets of langerhans
Tissue	islet preparation 3 cytokine treatment	islet preparation	islets of langerhans
Tissue	juvenile skin biopsy	skin biopsy	whole skin
Tissue	muscle tissue Tibetan 279	muscle tissue	longissimus dorsi muscle
Tissue	muscle tissue Wujin 48	muscle tissue	longissimus dorsi muscle
Tissue	non-injured ovaries ovarian surgery model	surgery model	ovary
Tissue	purified Tomato-positive PDAC cancer cells mouse 0758 LN metastasis - technical replicate1	LN metastasis	ln met (pdac)
Tissue	rosette plant cold treatment	plant cold	shoot apices
Tissue	sample ID 19	sample ID	hippocampus
Tissue	sample P53hom-22c	sample P53hom-22c	tail
Tissue	sample P53hom-39c	sample P53hom-39c	tail
Tissue	sample P53hom-48c	sample P53hom-48c	tail
Tissue	sample Rp048c	sample Rp048c	tail
Tissue	scion mature leaves removed	leaves removed	developing leaf, grafted
Tissue	scion mature leaves removed	leaves removed	shoot apex, grafted
Tissue	specimen D015	specimen D015	regenerating tail
Age	0 days old	days old	0
Age	10 dpf old	dpf old	10
Age	16S rDNA based microbial profile ileostoma effluent collected subject 1 morning day 1	morning day	79
Age	16S rRNA based microbial profile ileostoma	afternoon day	65

	effluent collected subject 2 afternoon day 1		
Age	2 hours post exposure	hours post	juvenile
Age	2 week dark-adapted	2 week	7 days old
Age	2 week dark-adapted	2 week	7 days old
Age	2014 Sum - mean (22101)	2014 Sum	3
Age	4 hr FGF + LY294002 Rep2	4 hr	e13.5
Age	4 hr FGF + PD325901 Rep1	4 hr	e13.5
Age	5 weeks old	weeks old	5
Age	7 week age	week age	7 weeks
Age	7 week age	week age	7 week
Age	8-oxoG challenge - 60 min	60 min	8 weeks
Age	Alamo Salt Experiment Control Rep 2 - 12 h	12 h	30d
Age	Alamo Salt Experiment Treatment Rep 1 - 24 h	24 h	30d
Age	Arabidopsis thaliana Cold Treatment 12 hours	12 hours	21 day
Age	DMD sample Replicate 2 myotube day 2	day 2	1 years old
Age	DMD sample Replicate 3 myotube day 1	day 1	2 years old
Age	Day 14 Of Antibiotic Treatment Human Gut Metagenome	Day 14	68
Age	Dental lamina Pre-initiation stage rep2	Pre-initiation stage	one year old
Age	ENCODE biosample ENCBS080PZG: Established 1987 peripheral blood patient T-cell acute lymphoblastic leukemia (T-ALL) obtained two months prior death	months prior	38 year
Age	ENCODE biosample ENCBS835VCD: Day 13 (T13)	Day 13	25 year
Age	Embryonic transcriptome domesticated turkey aflatoxin B1 1 day exposure liver sample 2	day exposure	day 18 embryo
Age	Embryonic transcriptome domesticated turkey aflatoxin B1 1 day exposure liver sample 6	day exposure	day 18 embryo
Age	Embryonic transcriptome domesticated turkey aflatoxin B1 1 day exposure liver sample 7	day exposure	day 18 embryo
Age	Flower inflorescence buds stage I	stage I	two years
Age	Hepatitis B booster immunisation study - 1066	booster immunisation	42
Age	Hepatitis B booster immunisation study - 1070	booster immunisation	57
Age	Hepatitis B booster immunisation study - 1070	booster immunisation	57
Age	Hepatitis B booster immunisation study - 1776	booster immunisation	28
Age	Injured spinal cord Trachemys scripta elegans 4 dpl N2	4 dpl	1 year
Age	Inoculated resistant cultivar 6hr post inoculation	6hr post	14 days
Age	Inoculated susceptible cultivar 24hr post inoculation	24hr post	14 days
Age	Late flowering PHYTOCHROME C mutant sample Brachypodium distachyon	Late flowering	few months
Age	Library 3 MiSeq Cre normal PCR 15 cycles	15 cycles	21 days
Age	May value evaluating role t(16	May value evaluating role t(16	38 year
Age	Methylome WT Root 21 -Pi r2	21 -Pi r2	2 weeks + 21 d
Age	Methylome dcl3a Root 21 -Pi r2	21 -Pi r2	2 weeks + 21 d
Age	Microbiota infant TB15 1 month age	month age	1 month
Age	Model organism animal sample Dermacentor andersoni 2 days	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	7 days	3
Age	Nuclear_RNA extract Differentiated Myotubes 7 days cell culture Healthy donors Caucasian origin Nuclear CTRL MT-7 10006 11	7 days	3
Age	Patient 2 Day 3	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
Age	T1 - horses intensive training stage (after slow 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
Age	Vaginal microbiota associated preterm delivery	preterm delivery	31
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	29
Age	Vaginal microbiota associated preterm delivery	preterm delivery	27
Age	Vaginal microbiota associated preterm delivery	preterm delivery	19
Age	Vaginal microbiota associated preterm delivery	preterm delivery	20
Age	Vaginal microbiota associated preterm delivery	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	preterm delivery	27
Age	Vaginal microbiota associated preterm delivery	preterm delivery	25
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	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 Sequencing	454 Sequencing	454 flx titanium
Platform	Mouse fecal sample VLP-purification 454 Sequencing	454 Sequencing	454 flx titanium
Platform	Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings	Pyrosequencing 16S rRNA amplicons	pyrosequencing
Platform	Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings	Pyrosequencing 16S rRNA amplicons	pyrosequencing
Platform	Pyrosequencing 16S rRNA amplicons pig gastrointestinal mucosal scrapings	Pyrosequencing 16S rRNA amplicons	pyrosequencing
Platform	SAG SCGC AB-704-M06 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-704-N13 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-C03 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-E02 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-E13 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-E22 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-F21 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-K06 partial SSU rRNA gene	SSU rRNA	sanger
Platform	SAG SCGC AB-706-M02 partial SSU rRNA gene	SSU rRNA	sanger

