## **Supplementary information**

## Regulatory genomic circuitry of human disease loci by integrative epigenomics

In the format provided by the authors and unedited

	Group	BSSID	Extended Info	Group	BSSID	Extended Info	Group	BSSID	Extended Info
1	Adipose	BSS00038	ADIPOCYTE 288	Digestive	BSS01654	STOMACH 57		BSS01533	RENAL PELVIS
2	Adipose	BSS00043	ADIPOSE TISSUE 289	Digestive	BSS01651	STOMACH 57		BSS01497	RENAL PELVIS
3	Adipose	BSS01671	ADIPOSE TISSUE 290 ADIPOSE TISSUE 291	Digestive	BSS01639 BSS01284	STOMACH 57 STOMACH MUCOSA 57	Kidney	BSS01498	RENAL PELVIS RENAL PELVIS
5	Adipose Adipose	BSS01665 BSS01666	ADIPOSE TISSUE 291 ADIPOSE TISSUE 292	Digestive Digestive	BSS01284 BSS01848	TRANSVERSE COLON 57		BSS01153 BSS01534	RENAL PELVIS
6	Adipose	BSS01668	ADIPOSE TISSUE 293	Digestive	BSS01851	TRANSVERSE COLON 58		BSS01499	RENAL PELVIS
7	Adipose	BSS01669	ADIPOSE TISSUE 294	Digestive	BSS01849	TRANSVERSE COLON 58		BSS00553	HEPATIC STELLATE CELL
8	Adipose	BSS01667	ADIPOSE TISSUE 295	Digestive	BSS01850	TRANSVERSE COLON 58		BSS00554	HEPATOCYTE
9	Adipose	BSS01394	OMENTAL FAT PAD 296	Endocrine	BSS00282	ENDOCRINE PANCREAS 58	Liver	BSS00511	LIVER
10	Adipose	BSS01393	OMENTAL FAT PAD 297	Endocrine	BSS00283	ENDOCRINE PANCREAS 58	4 Liver	BSS01164	LIVER
11	Blood & T-cell	BSS00188	CD4 T CELL 298	Endocrine	BSS00284	ENDOCRINE PANCREAS 58		BSS01170	LIVER
12	Blood & T-cell	BSS00185	CD4 T CELL 299	Endocrine	BSS00281	ENDOCRINE PANCREAS 58		BSS01169	LIVER
13	Blood & T-cell Blood & T-cell	BSS00189	CD4 T CELL 300 CD4 T CELL 301	Endocrine	BSS01403	OVARY 58		BSS01159 BSS01168	LIVER
14 15	Blood & T-cell	BSS00190 BSS00183	CD4 T CELL 301 CD4 T CELL 302	Endocrine	BSS01401 BSS01402	OVARY         58           OVARY         58		BSS01519	LIVER LIVER
	Blood & T-cell	BSS00186	CD4 T CELL 303	Endocrine	BSS01399	OVARY 59		BSS01158	LIVER
17	Blood & T-cell	BSS00191	CD4 T CELL 304	Endocrine	BSS01719	TESTIS 59		BSS01195	LUNG
18	Blood & T-cell	BSS00192	CD4 T CELL 305	Endocrine	BSS01718	TESTIS 59	2 Lung	BSS01142	LUNG
19	Blood & T-cell	BSS00274	CD4 T CELL 306	Endocrine	BSS01715	TESTIS 59	Lung	BSS01525	LUNG
20	Blood & T-cell	BSS00195	CD8 T CELL 307	Endocrine	BSS00052	ADRENAL GLAND 59		BSS01143	LUNG
21	Blood & T-cell	BSS00196	CD8 T CELL 308		BSS00050	ADRENAL GLAND 59		BSS01526	LUNG
22	Blood & T-cell	BSS00198	CD8 T CELL 309		BSS00051	ADRENAL GLAND 59		BSS01137	LUNG
23	Blood & T-cell Blood & T-cell	BSS00200 BSS00193	CD8 T CELL 310 CD8 T CELL 311	Endocrine Endocrine	BSS00059 BSS00057	ADRENAL GLAND         59           ADRENAL GLAND         59		BSS01520 BSS01138	LUNG LUNG
25	Blood & T-cell	BSS00193	CD8 T CELL 311		BSS00057 BSS00058	ADRENAL GLAND 59		BSS01521	LUNG
26	Blood & T-cell	BSS00197	CD8 T CELL 313		BSS00045	ADRENAL GLAND 60		BSS01139	LUNG
27	Blood & T-cell	BSS01420	MONONUCLEAR CELL 314	Endocrine	BSS00046	ADRENAL GLAND 60		BSS01192	LUNG
28	Blood & T-cell	BSS01421	MONONUCLEAR CELL 315		BSS00047	ADRENAL GLAND 60		BSS01522	LUNG
29	Blood & T-cell	BSS01279	MONONUCLEAR CELL 316	Endocrine	BSS00048	ADRENAL GLAND 60	Lung	BSS01140	LUNG
30	Blood & T-cell	BSS01419	MONONUCLEAR CELL 317		BSS00054	ADRENAL GLAND 60		BSS01523	LUNG
31	Blood & T-cell	BSS01423	MONONUCLEAR CELL 318		BSS00060	ADRENAL GLAND 60		BSS01141	LUNG
32 33	Blood & T-cell	BSS01424	MONONUCLEAR CELL 319		BSS00055	ADRENAL CLAND		BSS01524	LUNG LUNG
34	Blood & T-cell Blood & T-cell	BSS01347 BSS01348	NAIVE T CELL 320 NAIVE T CELL 321	Endocrine Endocrine	BSS00056 BSS01831	ADRENAL GLAND 66 THYROID GLAND 66		BSS01205 BSS01147	LUNG
35	Blood & T-cell	BSS01346	NAIVE T CELL 322		BSS01834	THYROID GLAND 60		BSS01529	LUNG
36	Blood & T-cell		T CELL 323		BSS01832	THYROID GLAND 61		BSS01148	LUNG
37	Blood & T-cell		T CELL 324		BSS01835	THYROID GLAND 61		BSS01149	LUNG
38	Blood & T-cell	BSS01689	T CELL 325	Endothelial	BSS00143	BRAIN MICROVASCULAR ENDOTHELIAL CELL 61	2 Lung	BSS01530	LUNG
39	Blood & T-cell	BSS01684	T CELL 326	Endothelial	BSS00387	GLOMERULUS ENDOTHELIAL CELL 61	Lung	BSS01202	LUNG
40	Blood & T-cell		T1 CELL 327		BSS01077	KIDNEY CAPILLARY ENDOTHELIAL CELL 61		BSS01144	LUNG
41	Blood & T-cell		T1 CELL 328		BSS01206	LUNG MICROVASCULAR ENDOTHELIAL CELL 61		BSS01527	LUNG
42 43	Blood & T-cell Blood & T-cell		T1 CELL 329		BSS01465	PULMONARY ARTERY ENDOTHELIAL CELL 61 UMBILICAL VEIN ENDOTHELIAL CELL 61		BSS01203	LUNG LUNG
43	Blood & T-cell		T17 CELL 330 T17 CELL 331		BSS00298 BSS00296	UMBILICAL VEIN ENDOTHELIAL CELL 61 UMBILICAL VEIN ENDOTHELIAL CELL 61		BSS01145 BSS01146	LUNG
45	Blood & T-cell		T17 CELL 332		BSS00250	DERMIS BLOOD VESSEL ENDOTHELIAL CELL 61		BSS01528	LUNG
46	Blood & T-cell		T2 CELL 333		BSS00260	DERMIS BLOOD VESSEL ENDOTHELIAL CELL 62		BSS01204	LUNG
47	Blood & T-cell	BSS01698	T2 CELL 334	Endothelial	BSS00262	DERMIS LYMPHATIC VESSEL ENDOTHELIAL CELL 62		BSS01189	LUNG
48	Blood & T-cell	BSS01696	T2 CELL 335	Endothelial	BSS00264	DERMIS LYMPHATIC VESSEL ENDOTHELIAL CELL 62	2 Lung	BSS01188	LUNG
49	Blood & T-cell	BSS01478	TREG CELL 336		BSS00704	BONE MARROW EPITHELIAL CELL 62		BSS01187	LUNG
50	Blood & T-cell	BSS01479	TREG CELL 337	Epithelial	BSS00218	CHOROID PLEXUS EPITHELIAL CELL 62		BSS01198	LUNG
51	Blood & T-cell	BSS01480	TREG CELL 338		BSS00223	COLON EPITHELIAL CELL 62		BSS01186	LUNG
52 53	Bone Bone	BSS00084 BSS00330	BONE ARM 339 BONE FEMUR 340	Epithelial Epithelial	BSS00307 BSS00743	ESOPHAGUS EPITHELIAL CELL 62 IRIS PIGMENT EPITHELIAL CELL 62	-	BSS01869 BSS01196	LUNG LUNG
54	Bone	BSS01154	BONE LEG 341	Epithelial	BSS01385	NON-PIGMENTED CILIARY EPITHELIAL CELL 62		BSS01190	LUNG
55	Bone	BSS00705	BONE MARROW STROMA 342		BSS01092	GLOMERULUS EPITHELIAL CELL 62		BSS01871	LUNG
56	Bone	BSS01397	OSTEOBLAST 343		BSS00389	GLOMERULUS VISCERAL EPITHELIAL CELL 63		BSS01201	LUNG
57	Brain	BSS00071	AMMONS HORN 344		BSS01080	KIDNEY EPITHELIAL CELL 63		BSS01190	LUNG
58	Brain	BSS00077	ANGULAR GYRUS 345	Epithelial	BSS00310	PROXIMAL TUBULE EPITHELIAL CELL 63	2 Lung	BSS01870	LUNG
59	Brain	BSS00078	ANGULAR GYRUS 346		BSS00701		Lung	BSS01193	LUNG
	Brain	BSS00089	ASTROCYTE SEPERALLIM 347		BSS01491	RENAL CORTICAL EPITHELIAL CELL 63		BSS00403	LYMPHOBLASTOID CELL LINE
61 62	Brain Brain	BSS00090 BSS00091	ASTROCYTE CEREBELLUM 348 ASTROCYTE HIPPOCAMPUS 349		BSS01505 BSS01103		Lymphoblastoid Lymphoblastoid	BSS00462 BSS00456	LYMPHOBLASTOID CELL LINE LYMPHOBLASTOID CELL LINE
63		BSS00091		Epithelial Epithelial	BSS01103 BSS01102		Lymphoblastoid	BSS00456 BSS00457	LYMPHOBLASTOID CELL LINE LYMPHOBLASTOID CELL LINE
	Brain	BSS00135		Epithelial	BSS00153		B Lymphoblastoid	BSS00437	LYMPHOBLASTOID CELL LINE
	Brain	BSS00136		Epithelial	BSS00150		Lymphoblastoid	BSS00473	LYMPHOBLASTOID CELL LINE
66	Brain	BSS00129	BRAIN 353	Epithelial	BSS00703	PANCREATIC DUCT EPITHELIAL CELL 64	Lymphoblastoid	BSS00471	LYMPHOBLASTOID CELL LINE
67		BSS00130	BRAIN 354		BSS00075	AMNION EPITHELIAL CELL 64	-5	BSS00474	LYMPHOBLASTOID CELL LINE
	Brain	BSS00131		Epithelial	BSS00308		Lymphoblastoid	BSS00404	LYMPHOBLASTOID CELL LINE
	Brain	BSS00133	BRAIN 356		BSS00309	PROSTATE EPITHELIAL CELL 64		BSS00405	LYMPHOBLASTOID CELL LINE
70 71	Brain Brain	BSS00138	BRAIN 357 BRAIN 358		BSS01539	PROSTATE EPITHELIAL CELL 64 PROSTATE EPITHELIAL CELL 64		BSS00472	LYMPHOBLASTOID CELL LINE
	Brain Brain	BSS00139		Epithelial Epithelial	BSS01538 BSS01217		Lymphoblastoid Lymphoblastoid	BSS00428 BSS00454	LYMPHOBLASTOID CELL LINE
	Brain Brain	BSS00140 BSS00142	BRAIN 369		BSS01217 BSS01224		Lymphoblastoid	BSS00454 BSS00427	LYMPHOBLASTOID CELL LINE LYMPHOBLASTOID CELL LINE
	Brain	BSS00142 BSS00126	BRAIN 361		BSS01224 BSS01225		B Lymphoblastoid	BSS00427	LYMPHOBLASTOID CELL LINE
75		BSS00127	BRAIN 362		BSS00356	FORESKIN KERATINOCYTE 64		BSS00395	LYMPHOBLASTOID CELL LINE
76	Brain	BSS00125	BRAIN 363	Epithelial	BSS00357	FORESKIN KERATINOCYTE 65	Lymphoblastoid	BSS00439	LYMPHOBLASTOID CELL LINE
	Brain	BSS00132	BRAIN 364		BSS00358	FORESKIN KERATINOCYTE 65	Mesench	BSS00039	ADIPOCYTE FROM MSC
	Brain	BSS00134	BRAIN 365		BSS00359	FORESKIN KERATINOCYTE 65		BSS00250	AMNIOTIC FLUID FROM MSC
	Brain	BSS00141	BRAIN 366		BSS00360	FORESKIN KERATINOCYTE 65		BSS00279	EMBRYONIC FACIAL PROMINENCE
80	Brain	BSS00174	CAUDATE NUCLEUS 367		BSS00362	FORESKIN KERATINOCYTE 65		BSS01260	MESENCHYMAL STEM CELL
	Brain Brain	BSS00175 BSS00173		Epithelial Epithelial	BSS00363 BSS00364	FORESKIN KERATINOCYTE 65 FORESKIN KERATINOCYTE 65		BSS01293 BSS01294	ARM MUSCLE ARM MUSCLE
	Brain	BSS00201		Epithelial	BSS00365	FORESKIN KERATINOCYTE 65		BSS01294 BSS01290	ARM MUSCLE
	Brain	BSS00205		Epithelial	BSS00366		Muscle	BSS00352	ARM MUSCLE
	Brain	BSS00207		Epithelial	BSS00355		Muscle	BSS01291	ARM MUSCLE
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**Figure S1:** Sample list with tissue group, unique identifier, and short name for 859 observed/imputed samples (full metadata in Table S1, page 1 of 4).

_	Group	BSSID	Extended Info	Group	BSSID	Extended Info	Group	BSSID	Extended Info
86		BSS00206	CEREBELLUM 373	Epithelial	BSS00361	FORESKIN KERATINOCYTE 660	Muscle	BSS01292	ARM MUSCLE
87		BSS00219	CINGULATE GYRUS 374		BSS00367	FORESKIN KERATINOCYTE 661	Muscle	BSS01303	ARM MUSCLE
88		BSS00220	CINGULATE GYRUS 375		BSS00354	FORESKIN KERATINOCYTE 662	Muscle	BSS01304	ARM MUSCLE
89 90	Brain Brain	BSS00369	FRONTAL CORTEX 376 FRONTAL CORTEX 377	Epithelial Epithelial	BSS01071	KERATINOCYTE 663 KERATINOCYTE 664	Muscle Muscle	BSS01295 BSS01296	ARM MUSCLE ARM MUSCLE
91	Brain	BSS00371 BSS00385	GERMINAL MATRIX 378	Epithelial	BSS01068 BSS01209	MAMMARY EPITHELIAL CELL 665		BSS01290 BSS01297	ARM MUSCLE
92	Brain	BSS00386	GLOBUS PALLIDUS 379	Epithelial	BSS01211	MAMMARY EPITHELIAL CELL 666		BSS01298	ARM MUSCLE
93	Brain	BSS01125	HIPPOCAMPUS 380	Epithelial	BSS01213	MAMMARY EPITHELIAL CELL 667	Muscle	BSS01299	ARM MUSCLE
94		BSS01126	HIPPOCAMPUS 381	Epithelial	BSS01185	MAMMARY LUMINAL EPITHELIAL CELL 668	Muscle	BSS01300	ARM MUSCLE
95		BSS01124	HIPPOCAMPUS 382	Epithelial	BSS01340	MAMMARY MYOEPITHELIAL CELL 669	Muscle	BSS01301	ARM MUSCLE
96		BSS00729	INFERIOR PARIETAL CORTEX 383	Epithelial	BSS01341	MAMMARY MYOEPITHELIAL CELL 670	Muscle	BSS01289	ARM MUSCLE
97		BSS01250	MEDULLA OBLONGATA 384	Epithelial	BSS01181	SKIN LEG 671	Muscle	BSS01308	BACK MUSCLE
98		BSS01270	MIDBRAIN 385	Epithelial	BSS01182	SKIN LEG 672		BSS01309	BACK MUSCLE
99		BSS01271	MIDDLE FRONTAL AREA 386	Epithelial	BSS01587	SKIN OF BODY 673		BSS01305	BACK MUSCLE
100	Brain Brain	BSS01272 BSS01273	MIDDLE FRONTAL AREA 387 MIDDLE FRONTAL GYRUS 388	ES-deriv ES-deriv	BSS00112 BSS01366	BIPOLAR NEURON DERIV 674 NEURAL DERIV 675		BSS01306 BSS01307	BACK MUSCLE BACK MUSCLE
102		BSS01388	OCCIPITAL LOBE 389	ES-deriv	BSS00272	NEURAL PROGENITOR DERIV 676		BSS01307	BACK MUSCLE
103		BSS01451	PONS 390	ES-deriv	BSS01372	NEURAL PROGENITOR DERIV 677	Muscle		BACK MUSCLE
104		BSS01452	POSTERIOR CINGULATE CORTEX 391	ES-deriv	BSS01370	NEURAL PROGENITOR DERIV 678	Muscle		BACK MUSCLE
105		BSS01469	PUTAMEN 392	ES-deriv	BSS01371	NEURAL PROGENITOR DERIV 679	Muscle	BSS01310	BACK MUSCLE
106		BSS01675	SUBSTANTIA NIGRA 393	ES-deriv	BSS01375	NEURON DERIV 680	Muscle	BSS01311	BACK MUSCLE
107		BSS01676	SUBSTANTIA NIGRA 394	ES-deriv	BSS00169	CARDIAC MESODERM DERIV 681	Muscle	BSS01312	BACK MUSCLE
108		BSS01677	SUPERIOR TEMPORAL GYRUS 395	ES-deriv	BSS00171	CARDIAC MUSCLE DERIV 682	Muscle	BSS01313	BACK MUSCLE
109		BSS01714	TEMPORAL LOBE 396	ES-deriv	BSS00556	HEPATOCYTE DERIV 683	Muscle	BSS01314	BACK MUSCLE
110	Brain	BSS01712	TEMPORAL LOBE 397	ES-deriv	BSS01261	MESENCHYMAL STEM DERIV 684	Muscle	BSS00170	CARDIAC MYOCYTE
111 112	Cancer	BSS01105 BSS00267	ACUTE LYMPHOBLASTIC LEUKEMIA 398 ACUTE LYMPHOBLASTIC LEUKEMIA 399	ES-deriv ES-deriv	BSS01857 BSS01612	TROPHOBLAST DERIV 685 SMOOTH MUSCLE DERIV 686	Muscle Muscle	BSS00376 BSS00378	GASTROCNEMIUS MEDIALIS GASTROCNEMIUS MEDIALIS
112	Cancer Cancer	BSS00267 BSS01178	ACUTE LYMPHOBLASTIC LEUKEMIA 399 ACUTE LYMPHOBLASTIC LEUKEMIA 400	ES-deriv ES-deriv	BSS00273	ECTODERMAL DERIV 687	Muscle Muscle	BSS00378 BSS00377	GASTROCNEMIUS MEDIALIS GASTROCNEMIUS MEDIALIS
114	Cancer	BSS01267	OSTEOSARCOMA 401	ES-deriv	BSS00273	ENDODERMAL CELL 688	Muscle	BSS00377	GASTROCNEMIUS MEDIALIS
115	Cancer	BSS01550	OSTEOSARCOMA 402	ES-deriv	BSS00287	ENDODERMAL DERIV 689	Muscle	BSS00373	LEG MUSCLE
116	Cancer	BSS00246	DESMOPLASTIC MEDULLOBLASTOMA 403	ES-deriv	BSS01263	MESENDODERM DERIV 690	Muscle	BSS01318	LEG MUSCLE
117	Cancer	BSS01208	GLIOBLASTOMA 404	ES-deriv	BSS01264	MESODERMAL DERIV 691	Muscle	BSS01320	LEG MUSCLE
118	Cancer	BSS00004	GLIOBLASTOMA 405	ESC	BSS00277	ESC 692	Muscle	BSS01321	LEG MUSCLE
119	Cancer	BSS00482	GLIOBLASTOMA 406	ESC	BSS00315	ESC 693		BSS01329	LEG MUSCLE
120	Cancer	BSS01251	MEDULLOBLASTOMA 407 NEUROBLASTOMA 408	ESC ESC	BSS01866	ESC 694 ESC 695	Muscle Muscle		LEG MUSCLE
121 122	Cancer Cancer	BSS01554 BSS01558	NEUROBLASTOMA 408 NEUROBLASTOMA 409	ESC	BSS00483 BSS00715	ESC 695			LEG MUSCLE LEG MUSCLE
123	Cancer	BSS00103	NEUROBLASTOMA 410	ESC	BSS00715	ESC 697	Muscle	BSS01324 BSS01325	LEG MUSCLE
124	Cancer	BSS01571	NEUROBLASTOMA 411	ESC	BSS00717	ESC 698	Muscle		LEG MUSCLE
125	Cancer	BSS01562	NEUROBLASTOMA 412	ESC	BSS00484	ESC 699	Muscle	BSS00700	LEG MUSCLE
126	Cancer	BSS01559	NEUROEPITHELIOMA 413	ESC	BSS00478	ESC 700	Muscle		LEG MUSCLE
127	Cancer	BSS00481	NEUROGLIOMA 414	Eye	BSS00329	EYE 701	Muscle		LEG MUSCLE
128 129	Cancer	BSS01535 BSS01682	COLON CARCINOMA 415 COLORECTAL ADENOCARCINOMA 416	Eye	BSS00328 BSS01504	EYE 702 EYE RETINA 703		BSS01460 BSS01461	PSOAS MUSCLE PSOAS MUSCLE
130	Cancer Cancer	BSS00708	COLORECTAL ADENOCARCINOMA 416 COLORECTAL ADENOCARCINOMA 417	Eye	BSS01504 BSS01503	EYE RETINA 704		BSS01461	PSOAS MUSCLE
131	Cancer	BSS01179	COLORECTAL ADENOCARCINOMA 418	Eve	BSS01502	EYE RETINA 705		BSS01463	PSOAS MUSCLE
132	Cancer	BSS00159	COLORECTAL ADENOCARCINOMA 419	Heart	BSS00079	AORTA 706	Muscle	BSS01581	SKELETAL MUSCLE
133	Cancer	BSS00492	COLORECTAL ADENOCARCINOMA 420	Heart	BSS00080	AORTA 707	Muscle	BSS01577	SKELETAL MUSCLE
134	Cancer	BSS01412	PARATHYROID ADENOMA 421	Heart	BSS00088	ASCENDING AORTA 708	Muscle	BSS01578	SKELETAL MUSCLE
135	Cancer	BSS01411	PARATHYROID ADENOMA 422	Heart	BSS00087	ASCENDING AORTA 709		BSS01572	SKELETAL MUSCLE CELL
136 137	Cancer Cancer	BSS01386 BSS01536	TESTICULAR EMBRYONAL CARCINOMA 423 MELANOMA 424	Heart Heart	BSS00242 BSS00243	CORONARY ARTERY 710 CORONARY ARTERY 711	Muscle Muscle	BSS01845 BSS01846	TONGUE TONGUE
138	Cancer	BSS01551	MELANOMA 425	Heart	BSS00505	HEART 712		BSS01331	TRUNK MUSCLE
139	Cancer	BSS00222	MELANOMA 426	Heart	BSS00498	HEART 713		BSS01333	TRUNK MUSCLE
140	Cancer	BSS01365	MYELOMA 427	Heart	BSS00499	HEART 714	Muscle	BSS01334	TRUNK MUSCLE
141	Cancer	BSS01890	EYE RETINOBLASTOMA 428	Heart	BSS00500	HEART 715	Muscle	BSS01332	TRUNK MUSCLE
142	Cancer	BSS00702	ACUTE PROMYELOCYTIC LEUKEMIA 429	Heart	BSS00502	HEART 716		BSS01338	MYOCYTE
143	Cancer	BSS01356	ACUTE PROMYELOCYTIC LEUKEMIA 430	Heart	BSS00503	HEART 717			MYOTUBE
144 145	Cancer Cancer	BSS01391 BSS01300	B CELL LYMPHOMA 431 B CELL LYMPHOMA 432	Heart Heart	BSS00501 BSS00516	HEART 718 HEART 719		BSS01155 BSS01573	SKELETAL MUSCLE MYOBLAST SKELETAL MUSCLE MYOBLAST
145	Cancer	BSS01065	B CELL LYMPHOMA 433		BSS00516	HEART 720		BSS01573	SKELETAL MUSCLE MYOBLAST
147	Cancer	BSS00268	B CELL LYMPHOMA 434		BSS00518	HEART 721		BSS01571	SKELETAL MUSCLE SATELLITE CELL
148	Cancer	BSS01664	B CELL LYMPHOMA 435	Heart	BSS00519	HEART 722	Neurosph	BSS01378	NEUROSPHERE
149	Cancer	BSS01389	B CELL LYMPHOMA 436	Heart	BSS00514	HEART 723	Neurosph	BSS01379	NEUROSPHERE
150	Cancer	BSS01350	BURKITT LYMPHOMA 437	Heart	BSS00520	HEART 724		BSS01377	NEUROSPHERE
151	Cancer	BSS01351	BURKITT LYMPHOMA 438		BSS00495	HEART 725		BSS01392 BSS00148	OLFACTORY NEUROSPHERE
152 153	Cancer Cancer	BSS00491 BSS01038	HAPLOID MYELOGENOUS LEUKEMIA 439 MYELOGENOUS LEUKEMIA 440	Heart Heart	BSS00496 BSS00494	HEART 726 HEART 727		BSS00148 BSS00145	BREAST EPITHELIUM BREAST EPITHELIUM
154	Cancer	BSS01039	MYELOGENOUS LEUKEMIA 441	Heart	BSS00521	HEART 728		BSS00145	BREAST EPITHELIUM
155	Cancer	BSS01056	MYELOGENOUS LEUKEMIA 442	Heart	BSS00517	HEART 729		BSS00304	EPIDERMAL MELANOCYTE
156	Cancer	BSS01057	MYELOGENOUS LEUKEMIA 443	Heart	BSS00493	HEART 730	Other	BSS00368	FORESKIN MELANOCYTE
157	Cancer	BSS01059	MYELOGENOUS LEUKEMIA 444	Heart	BSS01127	HEART LEFT ATRIUM 731	Other	BSS01156	LIMB EMBRYO
158	Cancer	BSS00221	MYELOGENOUS LEUKEMIA 445		BSS00509	HEART LEFT VENTRICLE 732			LIMB EMBRYO
159	Cancer	BSS01066	MYELOGENOUS LEUKEMIA 446	Heart	BSS00508	HEART LEFT VENTRICLE 733		BSS01216	MAMMARY STEM CELL
160	Cancer	BSS00762	MYELOGENOUS LEUKEMIA 447	Heart	BSS00506	HEART LEFT VENTRICLE 734		BSS00121	BODY OF PANCREAS
161	Cancer	BSS01104	MYELOMA 448 MYELOMA 449	Heart	BSS00513	HEART LEFT VENTRICLE 735 HEART LEFT VENTRICLE 736		BSS00122 BSS00123	BODY OF PANCREAS
162 163	Cancer Cancer	BSS01274 BSS01537	PLASMA CELL MYELOMA 450	Heart Heart	BSS00512 BSS00507	HEART LEFT VENTRICLE 736 HEART LEFT VENTRICLE 737		BSS00123 BSS00124	BODY OF PANCREAS BODY OF PANCREAS
164	Cancer	BSS00160	KIDNEY CLEAR CELL CARCINOMA 451	Heart	BSS01506	HEART RIGHT ATRIUM 738		BSS00758	ISLET PRECURSOR CELL
165	Cancer	BSS00372	KIDNEY RHABOID TUMOR 452	Heart	BSS01508	HEART RIGHT ATRIUM 739		BSS01406	PANCREAS
166	Cancer	BSS00037	RENAL CELL ADENOCARCINOMA 453	Heart	BSS01507	HEART RIGHT ATRIUM 740	Pancreas	BSS01407	PANCREAS
167	Cancer	BSS01474	RENAL CELL ADENOCARCINOMA 454		BSS00523	HEART RIGHT VENTRICLE 741		BSS00074	AMNION
168	Cancer	BSS01481	RENAL CELL CARCINOMA 455		BSS00524	HEART RIGHT VENTRICLE 742		BSS00076	AMNION STEM CELL CHORION
169	Cancer	BSS00718	HEPATOCELLULAR CARCINOMA 456	Heart	BSS00525	HEART RIGHT VENTRICLE 743	Placenta & EEM	BSS00209	CHONTON

Figure S1: (continued, 2 of 4)

	Group	BSSID	Extended Info	Group	BSSID	Extended Info	G	iroup	BSSID	Extended Info
170	Cancer	BSS00719	HEPATOCELLULAR CARCINOMA 457	Heart	BSS01815	THORACIC AORTA 74	44 P	Placenta & EEM	BSS00211	CHORION
171	Cancer	BSS00558	HEPATOCELLULAR CARCINOMA 458	Heart	BSS01814	THORACIC AORTA 74	45 P	Placenta & EEM	BSS00212	CHORION
172	Cancer	BSS01360	LARGE CELL LUNG CANCER 459		BSS01839				BSS00215	CHORIONIC VILLUS
173	Cancer	BSS01415	LUNG ADENOCARCINOMA 460		BSS01838	TIBIAL ARTERY 74			BSS00216	CHORIONIC VILLUS
174 175	Cancer Cancer	BSS00017 BSS00019	LUNG EPITHELIAL CARCINOMA 461 LUNG EPITHELIAL CARCINOMA 462	Heart HSC & B-cell	BSS01837 BSS00097	TIBIAL ARTERY 74 B CELL 74		Placenta & EEM	BSS00217 BSS00214	CHORIONIC VILLUS CHORIONIC VILLUS
176	Cancer	BSS00011	LUNG EPITHELIAL CARCINOMA 463		BSS01345	B CELL 75			BSS01440	PLACENTA
177	Cancer	BSS00022	LUNG EPITHELIAL CARCINOMA 464	HSC & B-cell	BSS00098	B CELL 75	51 P	Placenta & EEM	BSS01436	PLACENTA
178	Cancer	BSS00027	LUNG EPITHELIAL CARCINOMA 465	HSC & B-cell	BSS00093	B CELL 75	52 P	Placenta & EEM	BSS01437	PLACENTA
179	Cancer	BSS00016	LUNG EPITHELIAL CARCINOMA 466		BSS00096	B CELL 75			BSS01435	PLACENTA
180	Cancer	BSS00020	LUNG EPITHELIAL CARCINOMA 467	HSC & B-cell	BSS00100	B CELL 75				PLACENTA
181 182	Cancer Cancer	BSS00023 BSS00024	LUNG EPITHELIAL CARCINOMA 468 LUNG EPITHELIAL CARCINOMA 469	HSC & B-cell HSC & B-cell	BSS00101 BSS00095	B CELL 75 B CELL 75				PLACENTA PLACENTA
183	Cancer	BSS00024	LUNG EPITHELIAL CARCINOMA 470	HSC & B-cell	BSS00179	CD14 MONOCYTE 75				PLACENTA
184	Cancer	BSS00028	LUNG EPITHELIAL CARCINOMA 471	HSC & B-cell	BSS00181	CD14 MONOCYTE 75				PLACENTA
185	Cancer	BSS00029	LUNG EPITHELIAL CARCINOMA 472	HSC & B-cell	BSS00180	CD14 MONOCYTE 75	59 P	Placenta & EEM	BSS01448	PLACENTA
186	Cancer	BSS00018	LUNG EPITHELIAL CARCINOMA 473		BSS00178	CD14 MONOCYTE 76	50 P	Placenta & EEM	BSS01446	PLACENTA
187	Cancer	BSS00025	LUNG EPITHELIAL CARCINOMA 474		BSS00182	CD1C MYELOID DENDRITIC CELL 76			BSS01441	PLACENTA
188 189	Cancer Cancer	BSS00030 BSS00007	LUNG EPITHELIAL CARCINOMA 475 LUNG EPITHELIAL CARCINOMA 476	HSC & B-cell HSC & B-cell	BSS00233 BSS00230	CD34 CMP 76 CD34 CMP 76				PLACENTA PLACENTA
199	Cancer	BSS00007	LUNG EPITHELIAL CARCINOMA 477	HSC & B-cell	BSS00236	CD34 CMP 76			BSS00714	TROPHOBLAST
191	Cancer	BSS00015	LUNG EPITHELIAL CARCINOMA 478		BSS00238	CD34 CMP 76	55 P		BSS01856	TROPHOBLAST
192	Cancer	BSS01359	SQUAMOUS CELL CARCINOMA 479	HSC & B-cell	BSS00240	CD34 CMP 76	56 P	Placenta & EEM	BSS01853	TROPHOBLAST
193	Cancer	BSS00035	MUSCLE EWING SARCOMA 480		BSS00241				BSS01855	TROPHOBLAST
194	Cancer	BSS01549	RHABDOMYOSARCOMA 481	HSC & B-cell	BSS00234	CD34 CMP 76			BSS01852	TROPHOBLAST
195 196	Cancer Cancer	BSS00036 BSS01240	ADENOID CYSTIC CARCINOMA 482 MAMMARY GLAND ADENOCARCINOMA 483	HSC & B-cell HSC & B-cell	BSS00235 BSS00229	CD34 CMP 76 CD34 CMP 77			BSS01859 BSS01860	TROPHOBLAST TROPHOBLAST
197	Cancer	BSS01240	MAMMARY GLAND ADENOCARCINOMA 484	HSC & B-cell	BSS00223	CD34 CMP 77			BSS01867	UMBILICAL CORD
198	Cancer	BSS01244	MAMMARY GLAND ADENOCARCINOMA 485	HSC & B-cell	BSS00239	CD34 CMP 77	_		BSS01618	SPINAL CORD
199	Cancer	BSS01235	MAMMARY GLAND ADENOCARCINOMA 486	HSC & B-cell	BSS00231	CD34 CMP 77			BSS01619	SPINAL CORD
200	Cancer	BSS01226	MAMMARY GLAND ADENOCARCINOMA 487	HSC & B-cell	BSS00232	CD34 CMP 77	74		BSS01617	SPINAL CORD
201	Cancer	BSS01699	MAMMARY GLAND DUCTAL CARCINOMA 488	HSC & B-cell	BSS00384	GERMINAL CENTER 77			BSS01621	SPINAL CORD
202 203	Cancer	BSS01705	MAMMARY GLAND DUCTAL CARCINOMA 489 PANCREAS ADENOCARCINOMA 490	HSC & B-cell HSC & B-cell	BSS00760	LYMPHOCYTE 77 MPP 77			BSS01620	SPINAL CORD SPINAL CORD
203	Cancer Cancer	BSS00003 BSS01405	PANCREAS ADENOCARCINOMA 490 PANCREAS DUCT EPITHELIAL CARCINOMA 491	HSC & B-cell	BSS00544 BSS00545	MPP 77 MPP 77			BSS01614 BSS01613	SPINAL CORD
205	Cancer	BSS00541	CERVIX ADENOCARCINOMA 492		BSS00546	MPP 77				TIBIAL NERVE
206	Cancer	BSS00531	CERVIX ADENOCARCINOMA 493		BSS00547	MPP 78	80		BSS01840	TIBIAL NERVE
207	Cancer	BSS00529	CERVIX ADENOCARCINOMA 494	HSC & B-cell	BSS00548	MPP 78	81	PNS	BSS01841	TIBIAL NERVE
208	Cancer	BSS00748	ENDOMETRIAL ADENOCARCINOMA 495	HSC & B-cell	BSS00549	MPP 78			BSS01456	PROSTATE GLAND
209	Cancer	BSS00756	ENDOMETRIAL ADENOCARCINOMA 496	HSC & B-cell	BSS00550	MPP 78			BSS01457	PROSTATE GLAND
210 211	Cancer Cancer	BSS00745 BSS01174	ENDOMETRIAL ADENOCARCINOMA 497 PROSTATE ADENOCARCINOMA 498	HSC & B-cell HSC & B-cell	BSS00551 BSS00552	MPP 78		Reproductive Reproductive	BSS01459 BSS01884	PROSTATE GLAND UTERUS
211	Cancer	BSS01174 BSS01173	PROSTATE ADENOCARCINOMA 499  PROSTATE ADENOCARCINOMA 499	HSC & B-cell	BSS00543	MPP 78			BSS01886	VAGINA
213	Cancer	BSS01414	PROSTATE ADENOCARCINOMA 500	HSC & B-cell	BSS01381	NEUTROPHIL 78			BSS01887	VAGINA
214	Cancer	BSS00157	PROSTATE CANCER 501	HSC & B-cell	BSS01380	NEUTROPHIL 78	88	Sm. Muscle	BSS01606	BRAIN VASCULATURE SMOOTH MUSCLE CELL
215	Cancer	BSS01888	PROSTATE EPITHELIAL CARCINOMA 502		BSS01353	NK CELL 78			BSS01285	COLON MUSCLE
216	Cancer	BSS00001	PROSTATE EPITHELIAL CARCINOMA 503		BSS01355	NK CELL 79			BSS01286	COLON MUSCLE
217 218	Cancer	BSS00002 BSS00709	PROSTATE EPITHELIAL CARCINOMA 504 FIBROSARCOMA 505	HSC & B-cell iPSC	BSS01354 BSS00742	NK CELL 79 iPSC 79			BSS01288 BSS01287	DUODENUM MUSCLE DUODENUM MUSCLE
219	Digestive	BSS00227	COLON MUCOSA 506	iPSC	BSS00742	iPSC 79			BSS01475	RECTUM MUSCLE
220	Digestive	BSS00228	COLON MUCOSA 507	iPSC	BSS00741	iPSC 79		Sm. Muscle	BSS01660	STOMACH MUSCLE
221	Digestive	BSS00271	DUODENUM MUCOSA 508	iPSC	BSS00732	iPSC 79	95	Sm. Muscle	BSS01659	STOMACH MUSCLE
222	Digestive	BSS00270	DUODENUM MUCOSA 509	iPSC	BSS00733	iPSC 79			BSS01625	SPLEEN
223	Digestive	BSS00316	ESOPHAGUS 510	iPSC	BSS00244	iPSC 79			BSS01628	SPLEEN
224 225	Digestive Digestive	BSS00318 BSS00323	ESOPHAGUS 511 ESOPHAGUS MUSCULARIS MUCOSA 512	iPSC iPSC	BSS01107 BSS01108	iPSC 79 iPSC 79			BSS01629 BSS01633	SPLEEN SPLEEN
226	Digestive	BSS00322	ESOPHAGUS MUSCULARIS MUCOSA 513	iPSC	BSS00738	iPSC 80			BSS01634	SPLEEN
227	Digestive	BSS00321	ESOPHAGUS MUSCULARIS MUCOSA 514	iPSC	BSS00736	iPSC 80	91 S		BSS01631	SPLEEN
228	Digestive	BSS00324	ESOPHAGUS SQUAMOUS EPITHELIUM 515	iPSC	BSS00737	iPSC 80		Spleen	BSS01630	SPLEEN
229	Digestive	BSS00326	ESOPHAGUS SQUAMOUS EPITHELIUM 516			iPSC 80				BONE MARROW STROMAL CELL
230 231	Digestive Digestive	BSS00325 BSS00380	ESOPHAGUS SQUAMOUS EPITHELIUM 517 GASTROESOPHAGEAL SPHINCTER 518		BSS00731 BSS00734					PERICYTE CONJUNCTIVA FIBROBLAST
232	Digestive	BSS00380	GASTROESOPHAGEAL SPHINCTER 519						BSS00347	AORTA FIBROBLAST
233	Digestive	BSS01116	LARGE INTESTINE 520		BSS01091				BSS00168	CARDIAC FIBROBLAST
234	Digestive	BSS01117	LARGE INTESTINE 521	Kidney	BSS01132	KIDNEY 80	98 S	Stromal	BSS00166	CARDIAC FIBROBLAST
235		BSS01109	LARGE INTESTINE 522							CARDIAC FIBROBLAST
236 237	Digestive Digestive		LARGE INTESTINE 523							LUNG FIBROBLAST
237	Digestive		LARGE INTESTINE 524  LARGE INTESTINE 525							LUNG FIBROBLAST LUNG FIBROBLAST
239	Digestive		LARGE INTESTINE 526							LUNG FIBROBLAST
240	Digestive		LARGE INTESTINE 527		BSS01509					LUNG FIBROBLAST
241	Digestive		LARGE INTESTINE 528							LUNG FIBROBLAST
242	Digestive		LARGE INTESTINE 529							LUNG FIBROBLAST
243	Digestive		LARGE INTESTINE 530  LARGE INTESTINE 531							PULMONARY ARTERY FIBROBLAST GINGLYAL FIBROBLAST
244 245	Digestive Digestive	BSS01121 BSS01119	LARGE INTESTINE 531  LARGE INTESTINE 532	Kidney Kidney	BSS01510 BSS01089				BSS00338 BSS00067	GINGIVAL FIBROBLAST GINGIVAL FIBROBLAST
245	Digestive	BSS01427	PEYERS PATCH 533						BSS00344	PERIDONTAL LIGAMENT FIBROBLAST
247	Digestive	BSS01428	PEYERS PATCH 534						BSS00350	VILLOUS MESENCHYME FIBROBLAST
248	Digestive	BSS01426	PEYERS PATCH 535		BSS01090					BREAST FIBROBLAST
249	Digestive	BSS01282	RECTUM MUCOSA 536							BREAST FIBROBLAST
250 251	Digestive Digestive	BSS01283 BSS01542	RECTUM MUCOSA 537 SIGMOID COLON 538		BSS01100 BSS01101					DERMIS FIBROBLAST DERMIS FIBROBLAST
251	Digestive Digestive	BSS01542 BSS01546		Kidney						DERMIS FIBROBLAST DERMIS FIBROBLAST
253	Digestive			Kidney	BSS01516					FORESKIN FIBROBLAST

Figure S1: (continued, 3 of 4)

	Group	BSSID	Extended Info	Group	BSSID	Extended Info	G	Group	BSSID	Extended Info
254	Digestive	BSS01548	SIGMOID COLON 54	Kidney	BSS01517	KIDNEY 82	28	Stromal	BSS00353	FORESKIN FIBROBLAST
255		BSS01545	SIGMOID COLON 54	Kidney	BSS01136	KIDNEY 82	29		BSS00343	MAMMARY FIBROBLAST
256		BSS01543	SIGMOID COLON 54	Kidney	BSS01518	KIDNEY 83	30		BSS00275	SKIN FIBROBLAST
257		BSS01595	SMALL INTESTINE 54	Kidney	BSS01099	KIDNEY 83	31 5		BSS00276	SKIN FIBROBLAST
258		BSS01596	SMALL INTESTINE 54	Kidney	BSS01514	KIDNEY 83	32		BSS00393	SKIN FIBROBLAST
259		BSS01590	SMALL INTESTINE 540	Kidney	BSS01134	KIDNEY 83	33		BSS00394	SKIN FIBROBLAST
260		BSS01591	SMALL INTESTINE 54	Kidney	BSS01515	KIDNEY 83	34		BSS00063	SKIN FIBROBLAST
261		BSS01592	SMALL INTESTINE 548	Kidney	BSS01131	KIDNEY 83	35		BSS00069	SKIN FIBROBLAST
262		BSS01593	SMALL INTESTINE 549	Kidney	BSS01079	KIDNEY 83	36		BSS00346	SKIN FIBROBLAST
263		BSS01594	SMALL INTESTINE 550	Kidney	BSS01096	KIDNEY 83	37		BSS01583	SKIN FIBROBLAST
264		BSS01603	SMALL INTESTINE 55	Kidney	BSS01097	KIDNEY 83	38		BSS00278	SKIN FIBROBLAST
265		BSS01604	SMALL INTESTINE 553	Kidney	BSS01088	KIDNEY 83	39		BSS00390	SKIN FIBROBLAST
266		BSS01600	SMALL INTESTINE 55:	Kidney	BSS00528	KIDNEY CELL 84	10		BSS00066	SKIN FIBROBLAST
267		BSS01602	SMALL INTESTINE 554	Kidney	BSS00526	KIDNEY CELL 84	<b>1</b> 1 S		BSS00061	SKIN FIBROBLAST
268		BSS01597	SMALL INTESTINE 555	Kidney	BSS01484	RENAL CORTEX INTERSTITIUM 84	12		BSS00068	SKIN FIBROBLAST
269		BSS01599	SMALL INTESTINE 550	Kidney	BSS01485	RENAL CORTEX INTERSTITIUM 84	13		BSS00476	SKIN FIBROBLAST
270		BSS01588	SMALL INTESTINE 55	Kidney	BSS01482	RENAL CORTEX INTERSTITIUM 84	14	Stromal	BSS00113	SKIN FIBROBLAST
271		BSS01601	SMALL INTESTINE 558	Kidney	BSS01483	RENAL CORTEX INTERSTITIUM 84	15		BSS01824	THYMUS
272		BSS01637	STOMACH 559	Kidney	BSS01489	RENAL CORTEX INTERSTITIUM 84	16		BSS01819	THYMUS
273		BSS01642	STOMACH 560	Kidney	BSS01490	RENAL CORTEX INTERSTITIUM 84	17		BSS01821	THYMUS
274		BSS01643	STOMACH 56	Kidney	BSS01150	RENAL CORTEX INTERSTITIUM 84	18		BSS01823	THYMUS
275		BSS01644	STOMACH 563	Kidney	BSS01531	RENAL CORTEX INTERSTITIUM 84	19		BSS01818	THYMUS
276		BSS01646	STOMACH 56:	Kidney	BSS01486	RENAL CORTEX INTERSTITIUM 85	50		BSS01826	THYMUS
277		BSS01647	STOMACH 564	Kidney	BSS01487	RENAL CORTEX INTERSTITIUM 85	51		BSS01827	THYMUS
278		BSS01641	STOMACH 569	Kidney	BSS01151	RENAL CORTEX INTERSTITIUM 85	52		BSS01828	THYMUS
279		BSS01658	STOMACH 566	Kidney	BSS01532	RENAL CORTEX INTERSTITIUM 85	53		BSS01829	THYMUS
280		BSS01655	STOMACH 56	Kidney	BSS01488	RENAL CORTEX INTERSTITIUM 85	54		BSS01820	THYMUS
281		BSS01656	STOMACH 568	Kidney	BSS01495	RENAL PELVIS 85	55	Thymus	BSS01825	THYMUS
282		BSS01657	STOMACH 569	Kidney	BSS01496	RENAL PELVIS 85			BSS01878	URINARY BLADDER
283		BSS01636	STOMACH 570		BSS01493	RENAL PELVIS 85			BSS01876	URINARY BLADDER
284		BSS01638	STOMACH 57	Kidney	BSS01494	RENAL PELVIS 85	58 L		BSS01879	UROTHELIUM CELL
285		BSS01650	STOMACH 572	Kidney	BSS01500	RENAL PELVIS 85	59 L	Urinary	BSS01880	UROTHELIUM CELL
286		BSS01653	STOMACH 573	Kidney	BSS01501	RENAL PELVIS	П			
287	Digestive	BSS01649	STOMACH 574	Kidney	BSS01152	RENAL PELVIS				

Figure S1: (continued, 4 of 4)

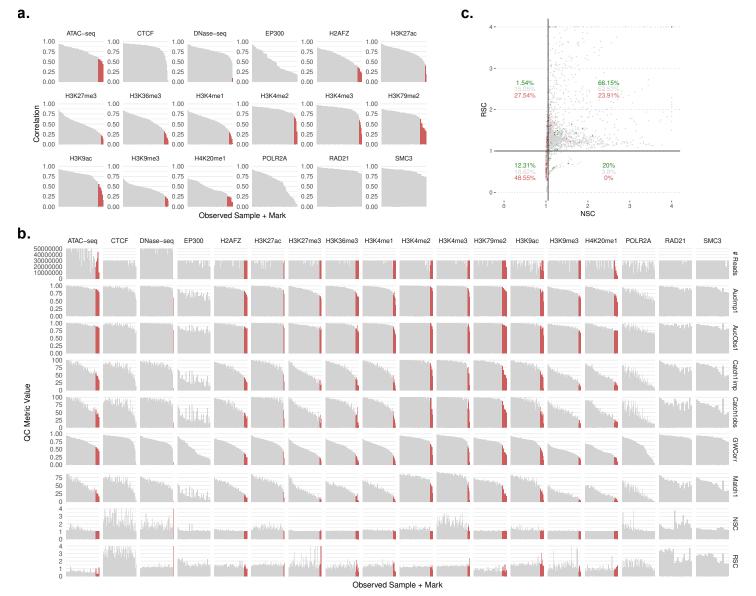


Figure S2: a. Track agreement between observed and imputed in the Tier 1 marks, where both are available, by genome wide correlation. Top (green) and bottom (red) tracks are labeled according to automated elbow discovery in the ranked list. b. All imputation metrics (from original ChromImpute paper: correlation, AUC, and peak recovery) and QC metrics (reads, NSC, RSC) across all 18 imputed Tier 1,2, and 3 assays, ordered according to correlation between imputed and observed within each assay. Bottom tracks for Tier 1 and 2 assays are labeled in red, as above. c. Imputation QC metrics reflect external ChIP-seq quality metrics (NSC and RSC). Normalized Strand Cross-correlation coefficient (NSC) against Relative Strand Cross-correlation coefficient (RSC) for observed tracks. Top (green) and bottom (red) tracks are labeled according to automated elbow discovery in imputed vs. observed correlation ranked list. Poor agreement tracks are strongly clustered in lower left quadrant of tracks failing QC. Critical values subdivide the plot for NSC (1.05) and RSC (1).

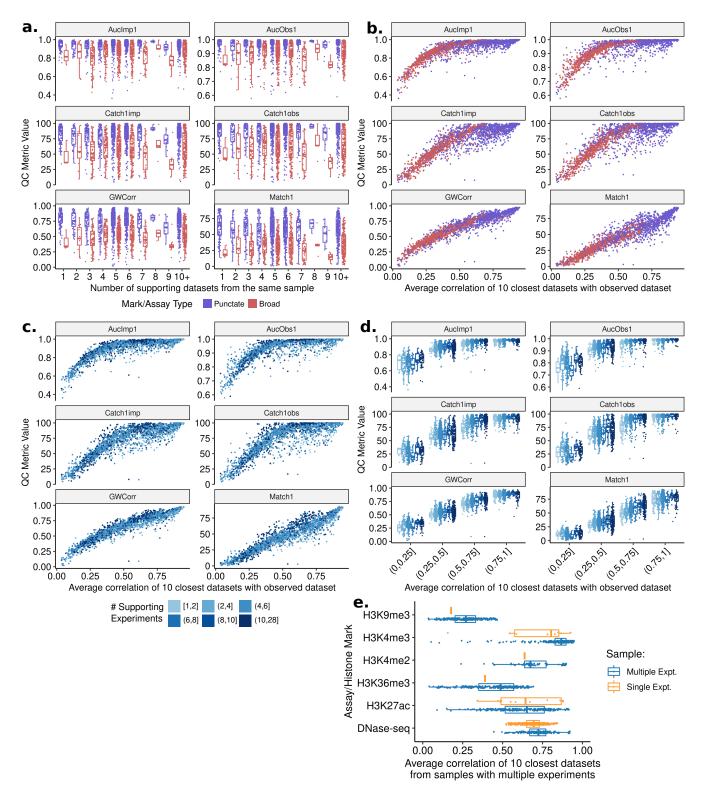
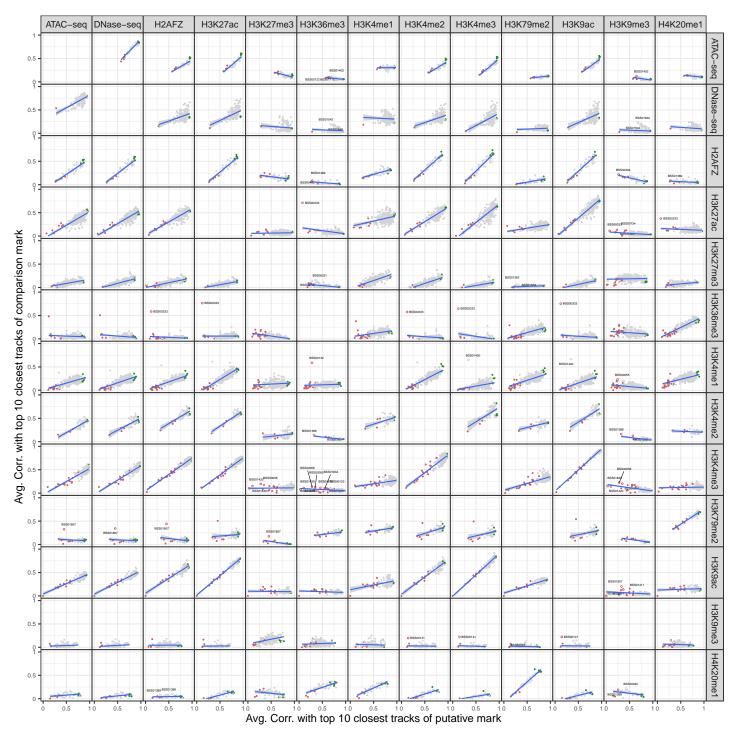


Figure S3: Imputation quality by level of sample-internal and sample-external support. a.

Imputation QC metrics in punctate (blue) and broad (red) marks by number of other supporting datasets from the same sample (sample-internal support). b. Imputation QC metrics for punctate and broad marks against the average correlation of the 10 closest datasets with the observed dataset. (sample-external support). c-d. Metrics against continuous (c) and quartiles of (d) sample-external support, colored by level of sample-internal support, showing that imputation metrics are dominated by the level of sample-external support. e. Level of sample-external support from samples with multiple experiments for samples with only one experiment (orange) or samples with multiple experiments (blue), by available mark or assay. Almost all samples with only DNase-seq have strong cross-sample support from other samples with multiple experiments (average correlation of nearest samples above 50



**Figure S4:** Imputed-observed agreement can be used to systematically flag antibody swaps. Each panel shows the average correlation with closest 10 tracks within the putative mark (each row) for each observed dataset against all other Tier 1 and 2 marks and assays. We used the overall mark-mark trend to flag outliers for visual inspection.

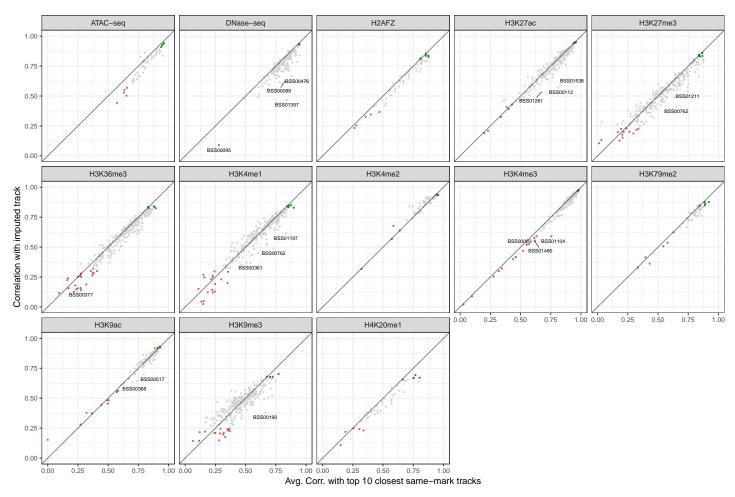


Figure S5: Imputed-observed agreement can be used to flag sample swaps. We compare the imputed-observed correlation to the average imputed-observed correlation within the top 10 closest samples for the putative mark and flagged outliers for visual inspection (after removing antibody swaps).

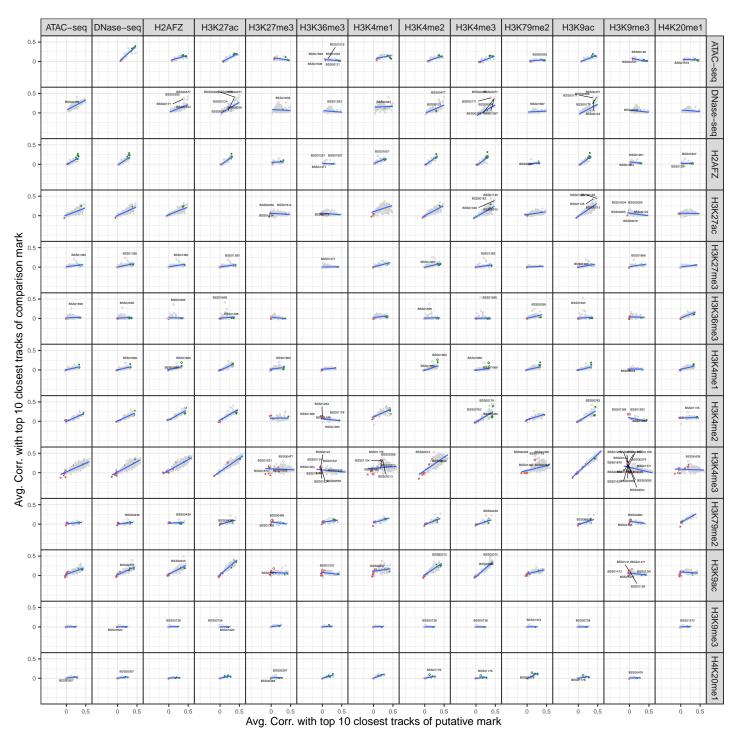


Figure S6: Imputed-observed agreement can be used to systematically flag secondary reactivities of antibodies. Each panel shows the average correlation of the difference between a pair of observed and imputed datasets with closest 10 tracks within the putative mark (each row) for each dataset against all other Tier 1 and 2 marks and assays. As with antibody swaps, we used the overall mark-mark trend to flag outliers for visual inspection.

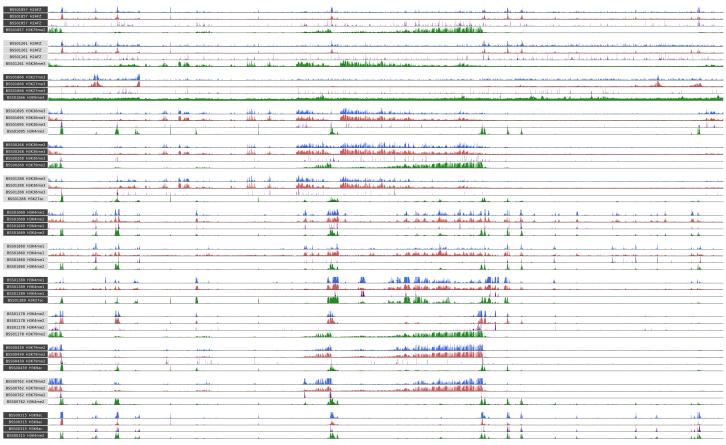


Figure S7: We can use imputation to identify antibodies with secondary reactivities. Track sets for 13 flagged samples highlight a disagreement from secondary reactivity (or sample swapping of one experiment out of multiple replicates), where the difference between observed and imputed best correlate with an external histone mark or assay. Each track set shows the Difference (purple) from Observed (blue) to Imputed (red) and the best Match (green) to the difference (a mark in the same sample) in chromosome 1 from 1.5Mb to 2Mb (chosen to show a range of diverse elements and marks).

	id	mark	(low	quality	tracks)					id	mark	potential.abswap
1	BSS01365	H3K4me2	47	BSS01857	H3K9ac	93	BSS00734	H3K27ac	1	BSS00333	H3K36me3	H3K27ac
2	BSS01104	H3K4me2	48	BSS01832	H3K36me3	94	BSS01715	H3K9me3	2	BSS00333	H3K27ac	H3K36me3
3	BSS01365	H3K79me2	49	BSS01841	H3K36me3	95	BSS00325	H3K9me3	3	BSS01857	H3K9ac	H3K79me2
4	BSS00556	H3K4me3	50	BSS01424	H3K4me3	96	BSS01850	H3K27me3	4	BSS01857	H3K79me2	H3K9ac
5	BSS01104	H3K4me3	51	BSS00055	H3K4me1	97	BSS01407	H3K27me3	5	BSS00141	H3K9me3	H3K9ac
6	BSS01263	H3K4me3	52	BSS00087	H3K4me1	98	BSS00381	H3K4me1	6	BSS00132	H3K4me1	H3K36me3
7	BSS01815	ATAC-seq	53	BSS00080	H3K4me1	99	BSS00395	H3K27me3	7	BSS01420	H3K4me1	H3K4me3
8	BSS01263	H3K4me2	54	BSS00325	H3K36me3	100	BSS00381	H3K9me3				
9	BSS01475	H3K9ac	55	BSS00556	H3K36me3	101	BSS00321	H3K4me1		id	mark	potential.sampswap
10	BSS01196	H3K9ac	56	BSS01340	H3K9ac	102	BSS01424	H3K27ac	1	BSS00089	DNase-seq	BSS00339
11	BSS00093	H3K4me3	57	BSS00284	H3K36me3	103	BSS00124	H3K36me3	2	BSS00095	DNase-seq	BSS01452
12	BSS01506	ATAC-seq	58	BSS00055	H3K36me3	104	BSS01507	H3K27me3	3	BSS00476	DNase-seq	BSS01397
13	BSS01667	H3K9ac	59	BSS00281	H3K4me1	105	BSS01715	H3K36me3	4	BSS01397	DNase-seq	BSS00334
14	BSS01480	H3K4me3	60	BSS01543	H3K36me3	106	BSS01209	H3K27me3	5	BSS00112	H3K27ac	BSS01366
15	BSS00484	H3K79me2	61	BSS01835	H3K4me1	107	BSS01832	H3K9me3	6	BSS01261	H3K27ac	BSS00387
16	BSS01715	ATAC-seq	62	BSS01080	H3K36me3	108	BSS01850	H3K36me3	7	BSS01538	H3K27ac	BSS00703
17	BSS00123	H3K4me3	63	BSS00056	H3K4me3	109	BSS01411	H3K36me3	8	BSS00762	H3K27me3	BSS00547
18	BSS01834	H3K4me3	64	BSS01389	H2AFZ	110	BSS01370	H3K36me3	9	BSS01211	H3K27me3	BSS01224
19	BSS01835	H3K4me3	65	BSS00493	H3K36me3	111	BSS01366	H3K9ac	10	BSS00377	H3K36me3	BSS01715
20	BSS01366	H3K79me2	66	BSS01835	H3K36me3	112	BSS01870	H3K27me3	11	BSS00361	H3K4me1	BSS00365
21	BSS01402	ATAC-seq	67	BSS00284	H3K4me1	113	BSS01834	H3K4me1	12	BSS00762	H3K4me1	BSS01038
22	BSS01371	H3K9ac	68	BSS01389	H4K20me1	114	BSS01887	H3K36me3	13	BSS01197	H3K4me1	BSS01144
23	BSS01370	H3K9ac	69	BSS00054	H3K4me1	115	BSS01831	H3K9me3	14	BSS00093	H3K4me3	BSS00702
24	BSS00284	H3K4me3	70	BSS00122	H3K9me3	116	BSS01630	H3K4me1	15	BSS01104	H3K4me3	BSS01365
25	BSS00197	H3K9ac	71	BSS00123	H3K9me3	117	BSS01459	H3K9me3	16	BSS01480	H3K4me3	BSS00702
26	BSS01341	H3K9ac	72	BSS01850	H3K9me3	118	BSS01424	H3K9me3	17	BSS00368	H3K9ac	BSS00207
27	BSS00122	ATAC-seq	73	BSS01213	H4K20me1	119	BSS00377	H3K36me3	18	BSS00517	H3K9ac	BSS00502
28	BSS00055	H3K27ac	74	BSS00093	H3K36me3	120	BSS00159	H3K27me3	19	BSS00190	H3K9me3	BSS00196
29	BSS01870	H3K4me3	75	BSS00132	H3K4me1	121	BSS01507	H3K4me1				
30	BSS01412	H3K79me2	76	BSS00492	H2AFZ	122	BSS01837	H3K27me3	_	id	mark	potential.secondary
31	BSS00141	H3K4me3	77	BSS01876	H3K4me1	123	BSS01426	H3K36me3	1	BSS01857	H2AFZ	H3K79me2
32	BSS00074	H3K27ac	78	BSS01370	H3K9me3	124	BSS01837	H3K4me1		BSS01261		H3K36me3
	BSS00521		79	BSS00439	H4K20me1	125	BSS01426	H3K4me1		BSS01866		H3K9me3
34	BSS01857	H3K79me2	80	BSS00325	H3K4me1	126	BSS01459	H3K36me3	4	BSS01695	H3K36me3	H3K4me3
35	BSS01866	H3K27ac	81	BSS01178	H3K27me3	127	BSS00484	H4K20me1		BSS00268		H3K79me2
36	BSS01412	H3K9ac	82	BSS00141	H3K9me3			H3K27me3	6	BSS01288	H3K36me3	H3K27ac
	BSS01411				H3K27me3			H3K36me3	7	BSS01669	H3K4me1	H3K4me2
	BSS00478			BSS01543			BSS00093			BSS01860		H3K4me2
	BSS00556				H3K27me3		BSS01562	DNase-seq		BSS01389		H3K27ac
	BSS00558				H3K36me3		BSS00095	DNase-seq		BSS01178		H3K79me2
	BSS01411			BSS00493			BSS01420	H3K4me3		BSS00439		H3K9ac
	BSS00477				H4K20me1		BSS00333	H3K27ac		BSS00762		H3K4me2
	BSS00281				H3K27me3			H3K4me1	13	BSS00315	H3K9ac	H3K4me2
	BSS00055			BSS00074			BSS01519					
	BSS00378			BSS01426			BSS01543					
46	BSS01366	H3K4me2	92	BSS00483	H3K9me3	138	BSS01849	H3K4me3				

Figure S8: Table of flagged samples. (left) low agreement tracks, (right, top) potential antibody swaps, (right, middle) potential sample swaps, (right, bottom) potential secondary antibody reactivities or single replicate or experiment swaps.

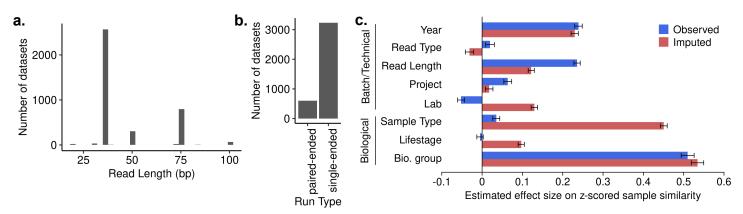


Figure S9: a. Read length distribution in observed datasets before processing. Over two-thirds of observed datasets have read-length of 36bp or lower. b. Distribution of sequencing run type in observed datasets. c. Estimated effect sizes of technical and biological covariates on the genome-wide correlation between two imputed or two observed datasets in the same mark. We regressed indicator variables for each covariate against per-mark z-scored correlations of all pair-wise combinations of either observed or imputed datasets in each mark. Imputed datasets show lower effect sizes from all technical covariates except for lab or origin and higher effect sizes for all biological covariates than observed datasets. Error bars represent two standard errors.

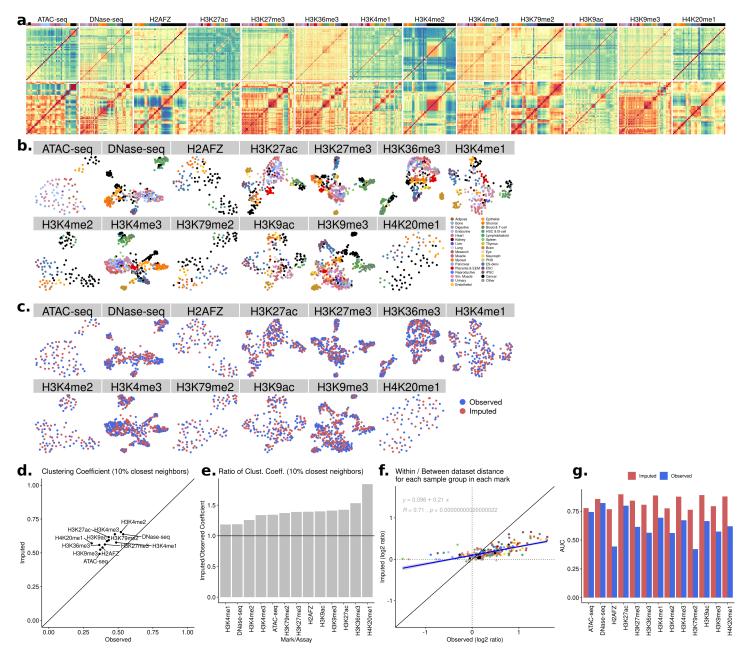


Figure S10: Data clustering and homogeneity in samples with both observed and imputed data. a. Per-mark heatmap of Spearman correlation for observed (top) and imputed (bottom) data in samples with both observed and imputed data in the mark or assay. b,c. Joint imputed and observed per-mark dimensionality reduction (UMAP) from Spearman correlation between all imputed and observed tracks in the subset of samples with both datatypes, colored by b. sample group and c. datatype. d. Per-mark observed versus imputed clustering coefficients. Clustering coefficients were computed on per-mark networks for either observed or imputed datasets constructed by connecting each dataset with its top decile of closest neighbors. e. Ratio of imputed to observed clustering coefficients. f. Ratio of within-group to between-group distance in observed versus imputed data for each sample group (colors) and each mark. Imputed and observed data show concordant ratios (Pearson R = 0.72, Spearman  $\rho = 0.71$ ) g. AUC for predicting whether a pair of marks is in the same sample group from their pairwise distance. Imputed data outperforms observed data across all marks and assays and achieves AUC > 0.75 for most marks.

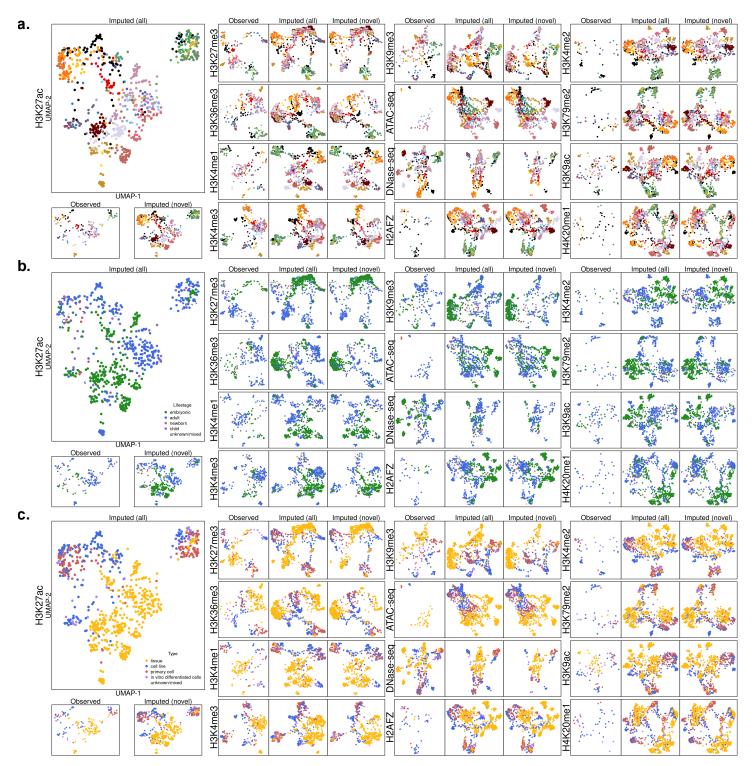


Figure S11: a-c. Joint UMAP embeddings of observed and imputed data within each Tier 1 and 2 mark/assay. Separately, observed, imputed samples, and all novel imputed tracks are plotted for each mark/assay and colored according to a. tissue group, b. biological lifestage, or d. sample type. Imputed UMAP highlights differences in cell types: H3K27ac clusters hematopoietic cells and tissues (green in panel a) closely, reflecting lineage, whereas H3K27me3 clusters iPSC, ESCs, and derived cells (purple/blue in panel a), reflecting differentiation stage. UMAP embedding was calculated from spearman correlation of tracks within regions marked by mark or assay relevant states within the Roadmap compendium.

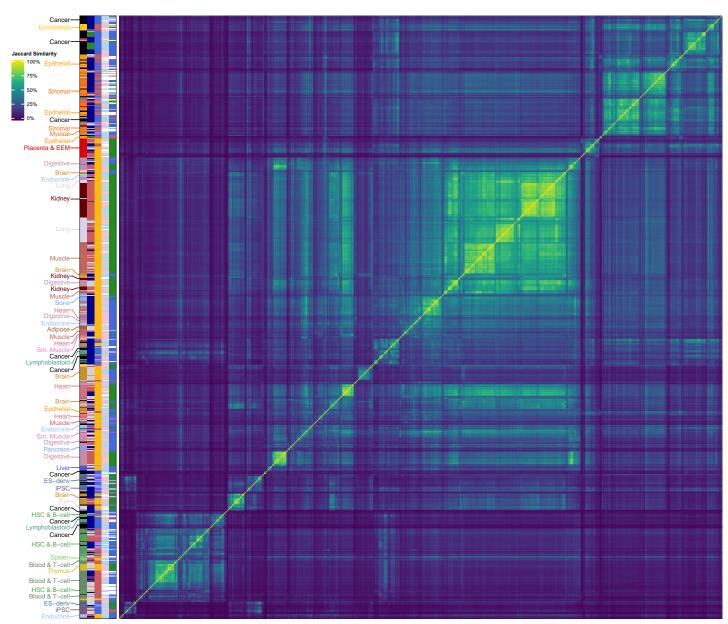


Figure S12: Jaccard similarity matrix (heatmap) across 833 epigenomes (metadata on left) from binarized enhancer activity matrix (2.1M enhancers by 833 epigenomes). Similarity matrix clustered by complete-linkage clustering. Consecutive blocks of at least six samples from the same group are labeled on the left.

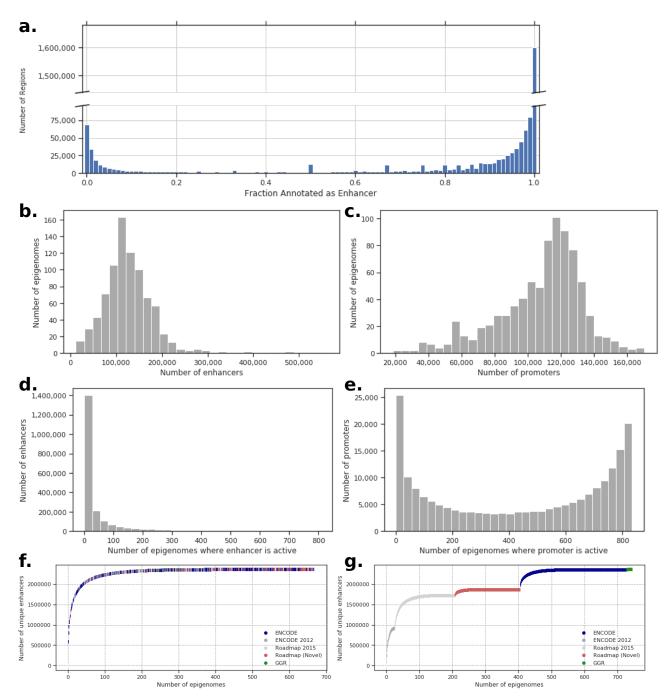


Figure S13: a. Number of DHS sites annotated as enhancers instead of promoters across 833 epigenomes. Most regions are either labeled enhancer (at least 75% of occurrences are enhancers) or promoter (at least 75% of occurrences are promoters) across all of their active occurrences. Using these cutoffs, we labeled 2,069,090 enhancers, 204,104 promoters, and 122,358 dyadic elements (neither specifically promoter or enhancer). b,c. Histogram of number of active enhancers (b) and promoters (c) per sample (row-margins of binary activity matrix). d,e. Histogram of the number of samples for which each enhancer (d) or promoter (e) is an active enhancer (column-margins of binary activity matrix) f. Rarefaction curve for enhancer recovery for all enhancer and dyadic elements (2.3M total) across 833 samples (points, colored by project of origin). Curve was created by iteratively adding the sample contributing the most novel active elements until all 2.3M elements were accounted for. g. Rarefaction curve for enhancer recovery, shown in order of project completion, for all enhancer and dyadic elements (2.3M total) across 833 samples (points, colored by project of origin). Curve was created by iteratively adding the sample contributing the most novel active elements until all 2.3M elements were accounted for. Samples were considered in order of project publication/completion, only taking samples from the next project when the current project did not contribute any more enhancers.

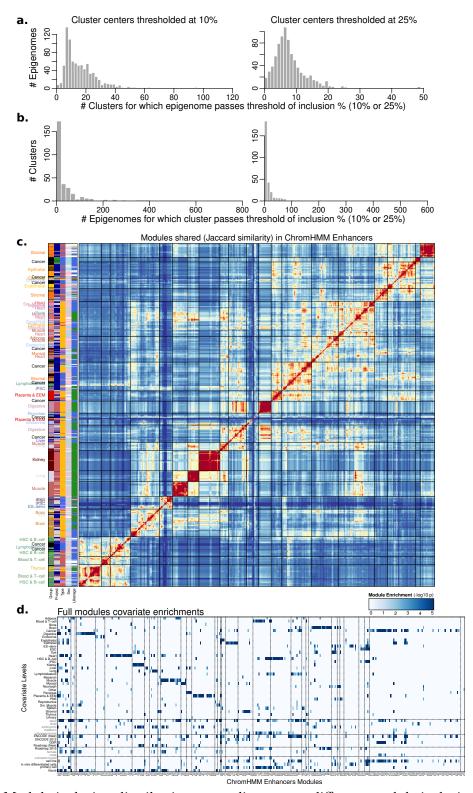


Figure S14: a,b. Module inclusion distributions according to two different module inclusion cutoffs of 10% and 25% (columns). a. Number of modules (N=300) for each of 833 epigenomes with module inclusion of at least 10% or 25% (top). b. Number of epigenomes (N=833) for each of 300 modules at the same inclusion cutoffs. c. Sample similarity (heatmap) across 833 epigenomes by their number of shared modules.(jaccard similarity, intersection over union of modules of each pair of epigenomes). Similarity matrix clustered by Ward's method. Consecutive blocks of at least six samples from the same group are labeled on the left. d. Full module enrichments across main metadata facets of group, project, type, sex, and lifestage, for which the reduced version is shown as a panel in Figure 2a. Significance assessed according to hypergeometric test on the module centers matrix with module inclusion of at least 25%.

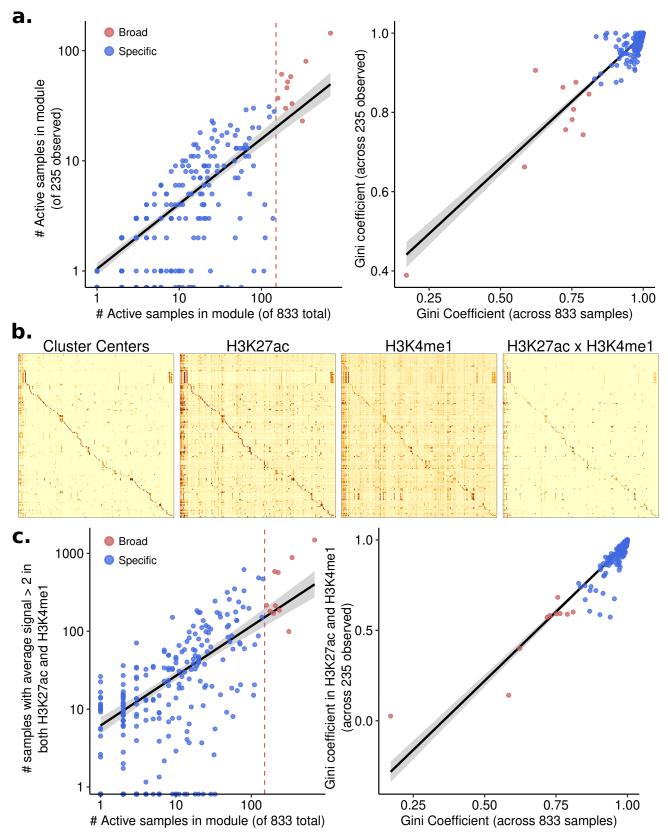


Figure S15: Observed data validation of broad and specific modules. a. Validation with 235 observed H3K27ac datasets. Number of samples (left) and Gini coefficient (right) per module in the full data versus the observed-only H3K27ac data. Broad modules are defined as modules with over 150 actie samples in the full data (dashed line) and labeled in red. Despite the sample composition differences in observed vs. full data, the fraction of active samples is quite consistent between the datasets (left, R<sup>2</sup>=0.802, right R<sup>2</sup>=0.82). For the 10 broad modules (red) from the full data, all were active in at least 9.7

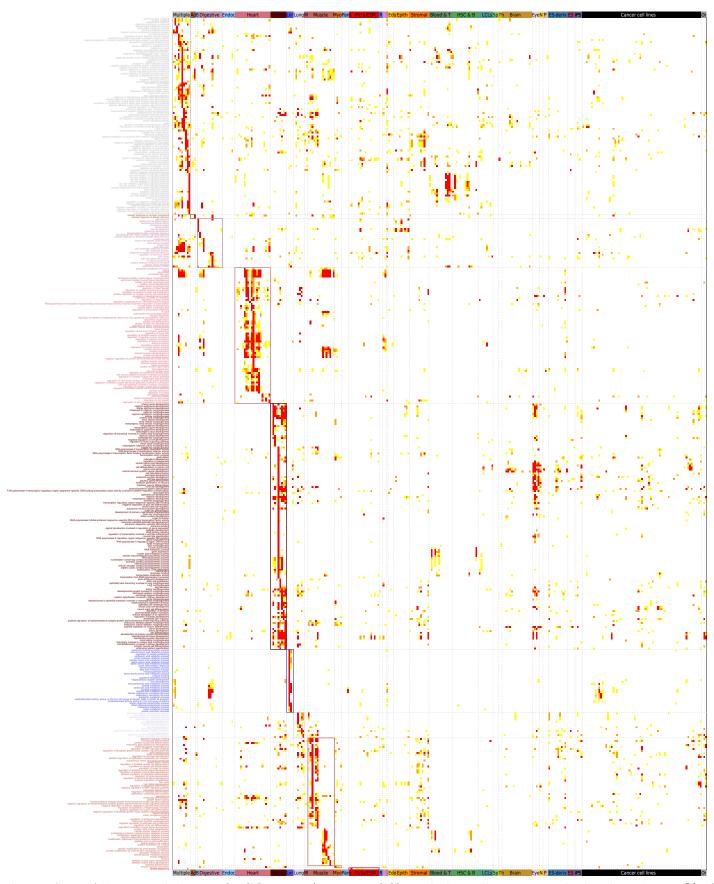
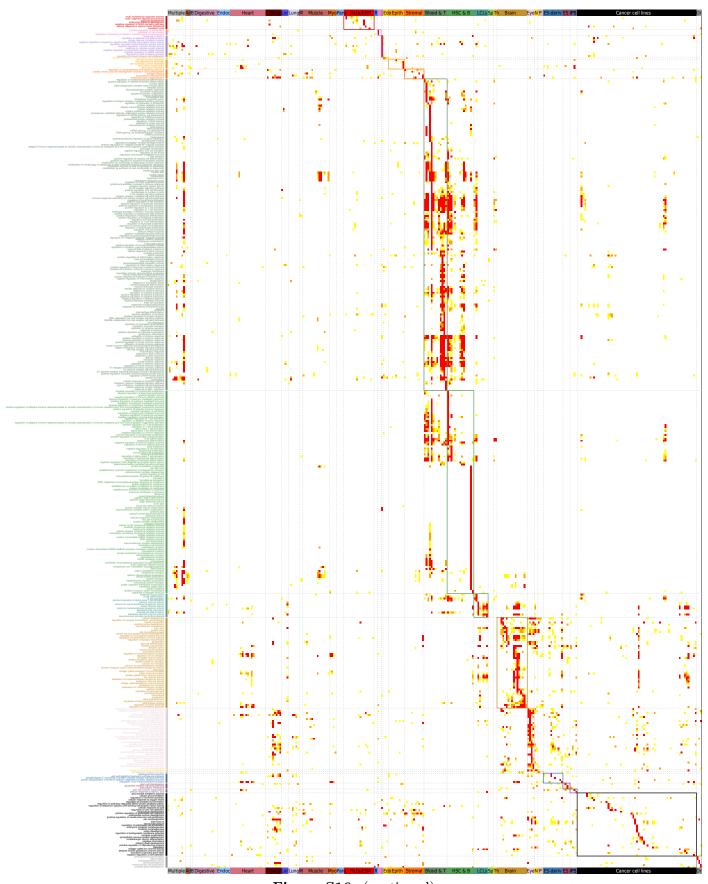


Figure S16: All 865 module-specific GO terms (BP, MF, CC), including all terms enriched in less than 10% of modules and with a maximum enrichment of at least  $-\log_{10}p > 4$ . Full version of Figure 2b.



 $\textbf{Figure S16:} \ (\text{continued}) \\$ 

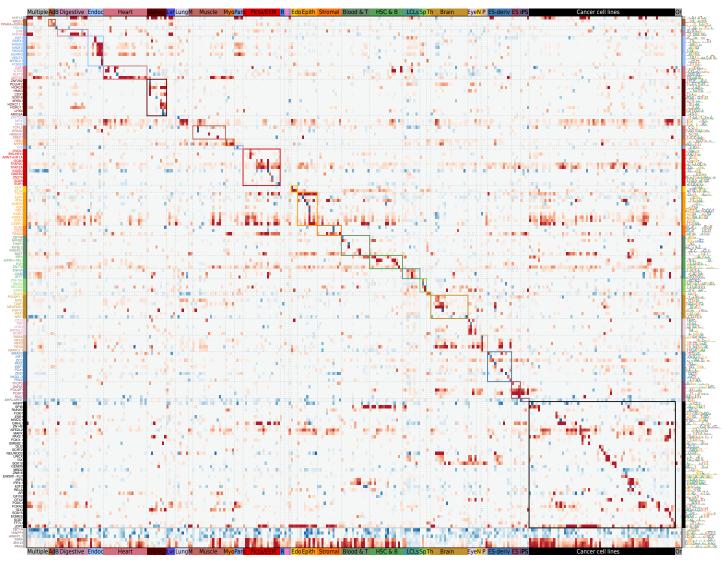
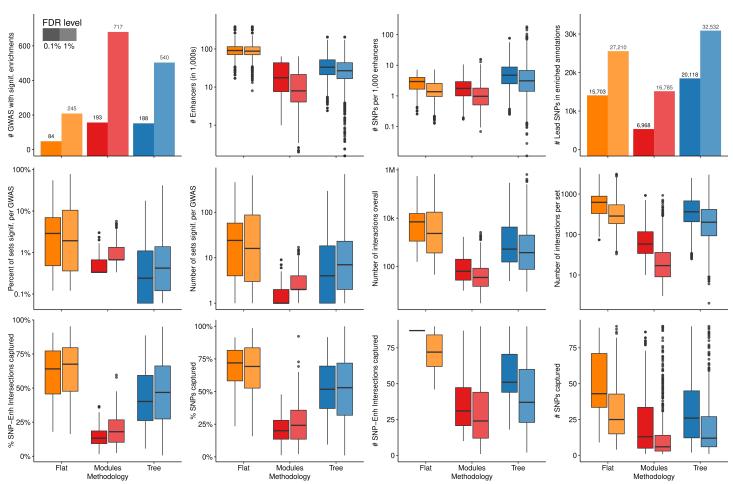


Figure S17: Full motif enrichments for 160 motif families with enrichments with log 2FC >= 1 on modules (Figure 2c).



**Figure S18:** Extended method validation figures comparing epigenomic GWAS enrichments using different methodologies (x-axis) for three FDR cutoffs (shades). First and last figures from top row are shown as Extended Data Fig. 7e.

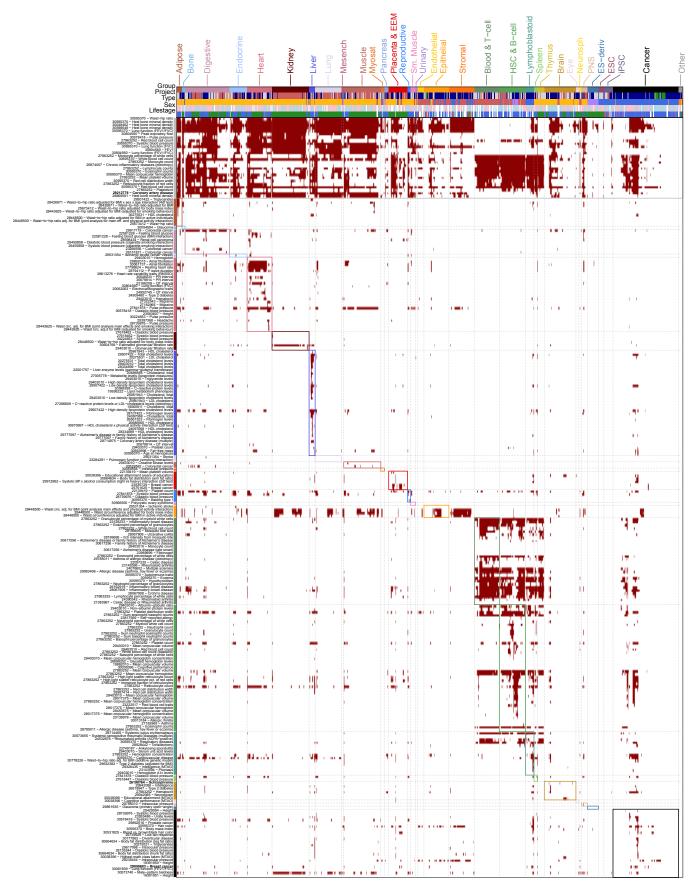


Figure S19: All epigenome trait enrichments at FDR < 1%, for 245 traits (rows) and 833 epigenomes (columns)

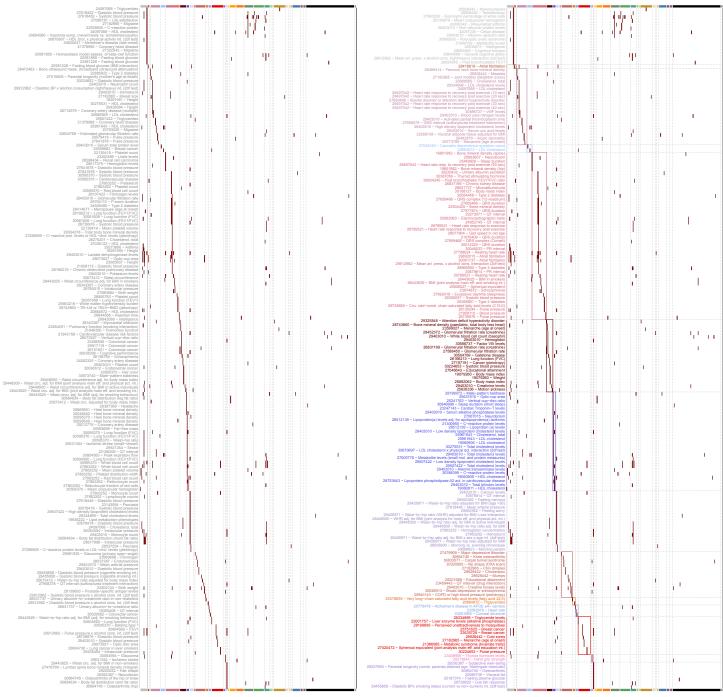


Figure S20: All module trait enrichments at FDR < 1%, for 717 traits (rows) and 300 modules (columns). Modules are ordered as in Figure 2a.

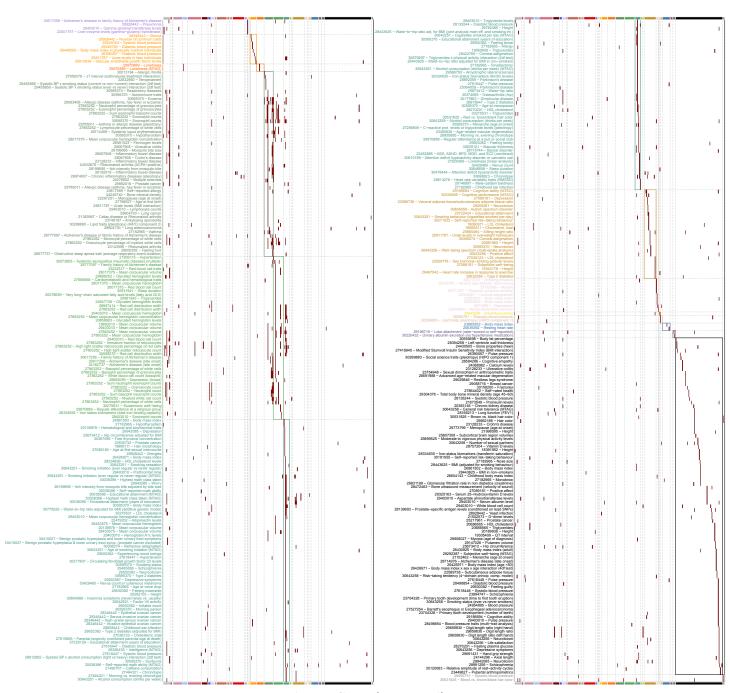


Figure S20: (continued)

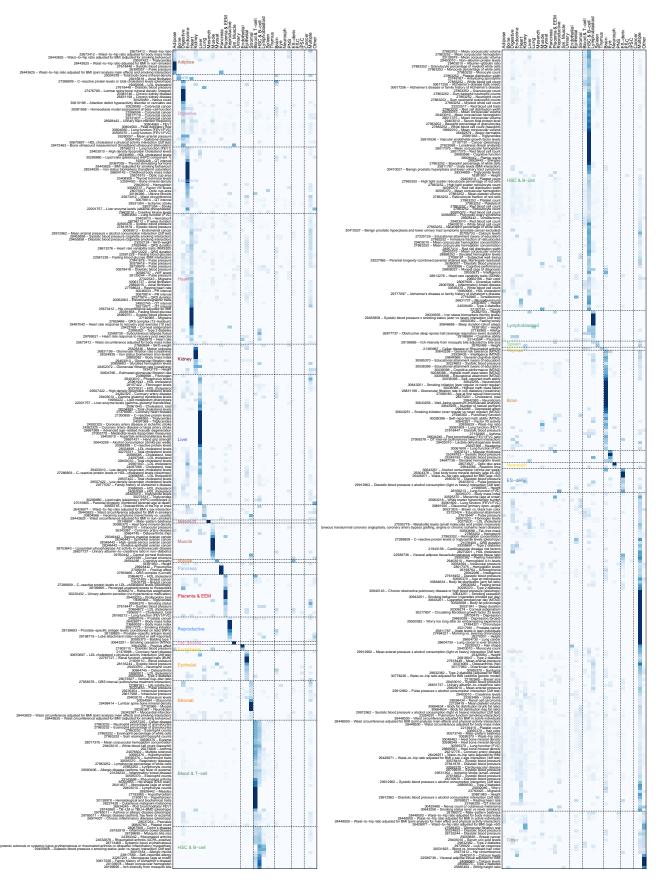


Figure S21: Overall tissue-level prioritization of 540 traits at FDR < 1%. Heatmap represents trait (rows) vs. tissue matrix and is split for visibility. Traits are diagonalized according to their top tissue enrichment, and values are the trait-normalized and tissue aggregated  $-\log_{10}$ p-values.

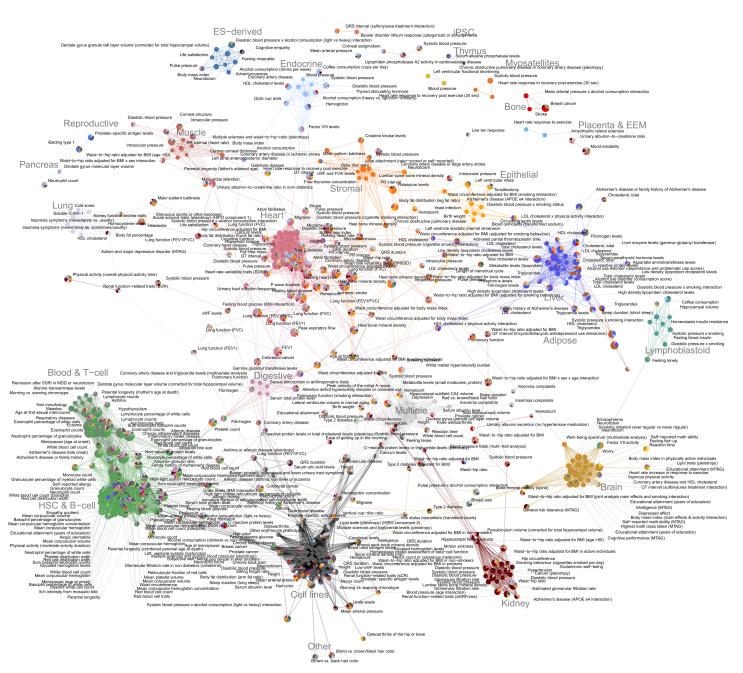


Figure S22: Trait-trait network (as Figure 5) across 511 traits by similarity of epigenetic enrichments (cosine sim.  $\geq 0.75$ ), laid out using the Fruchterman-Reingold algorithm. Traits (nodes) are colored by contributing groups (pie chart by fraction of -log10p, size by maximal -log10p) and interactions (edges) by the group with maximal dot product of enrichments between two traits. All 511 traits labeled.

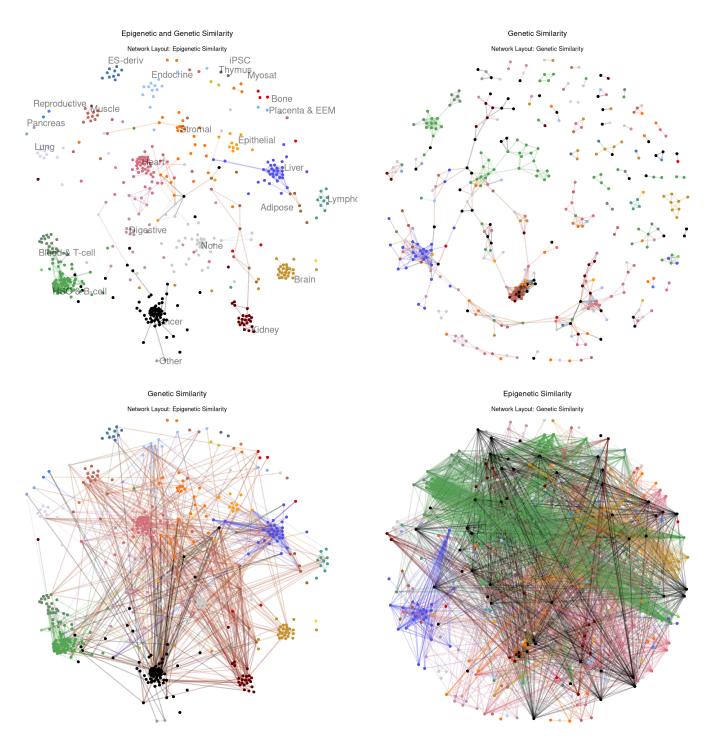


Figure S23: Comparison networks with genetics and epigenetics. (top left) Edges with both high epigenetic similarity and any genetic overlap on epigenetic similarity layout. (bottom left) All trait pairs with genetic overlap (> 5% jaccard similarity of lead SNPs overlapping when binned into 10k bp bins starting from the start of each chromosome, network using epigenetic layout. (top right) Network of trait pairs with any genetic overlap laid out by genetics. (bottom right) All trait pairs with high epigenetic similarity on the genetic layout network

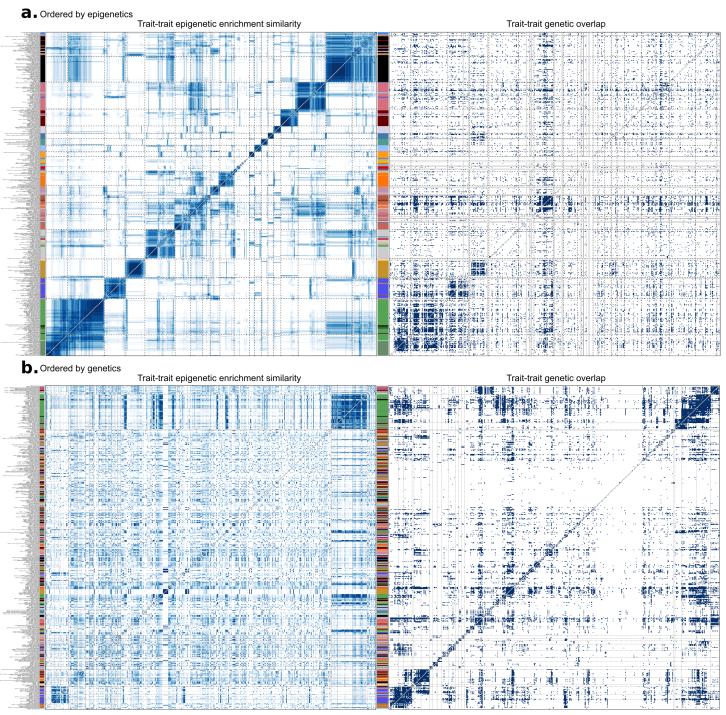
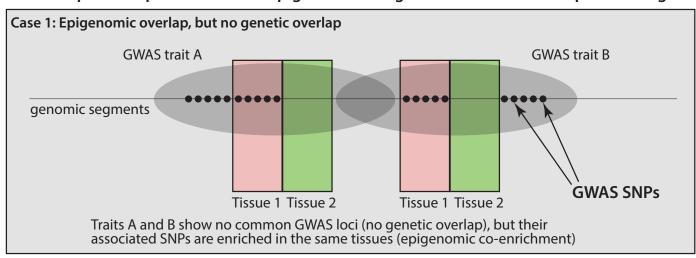


Figure S24: a. Trait-trait similarity matrix by cosine similarity of epigenetic enrichments (left) and by 0/1 genetic similarity (defined as > 5% jaccard similarity of lead SNPs overlapping when binned into 10k bp bins starting from the start of each chromosome). Matrices are ordered by hierarchical clustering according to Ward's method on the epigenetic matrix. b. Epigenetic similarity (left) and genetic similarity (right) matrices, as above. Matrices ordered by hierarchical clustering according to Ward's method on the genetic similarity matrix.

## Two simple example cases where epigenomic and genetic trait-trait overlaps can disagree



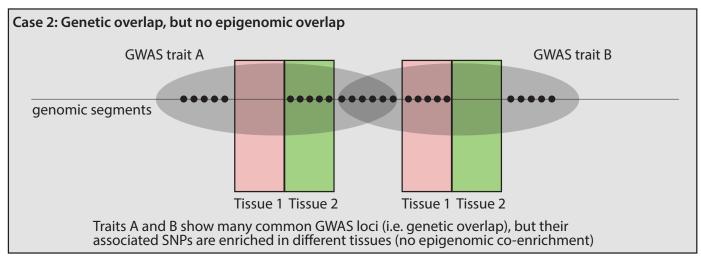
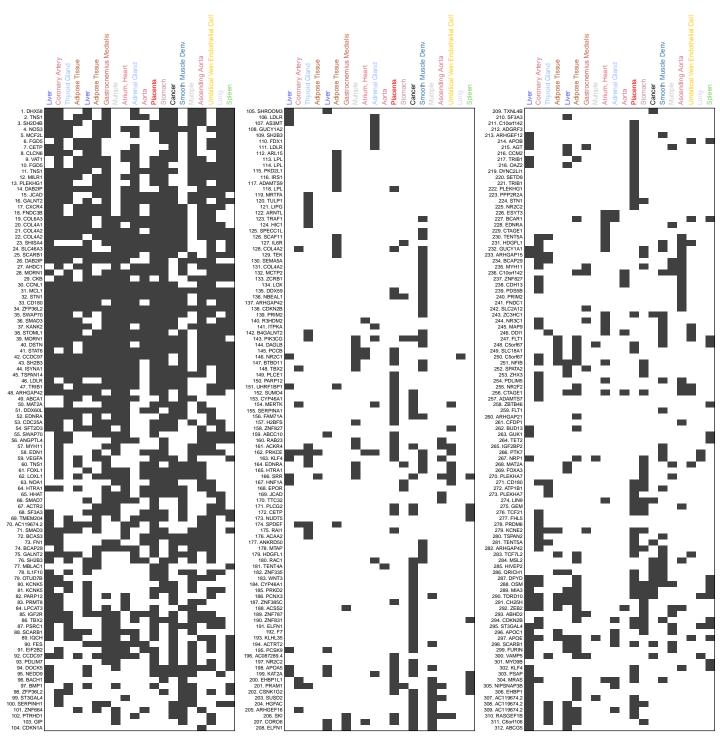
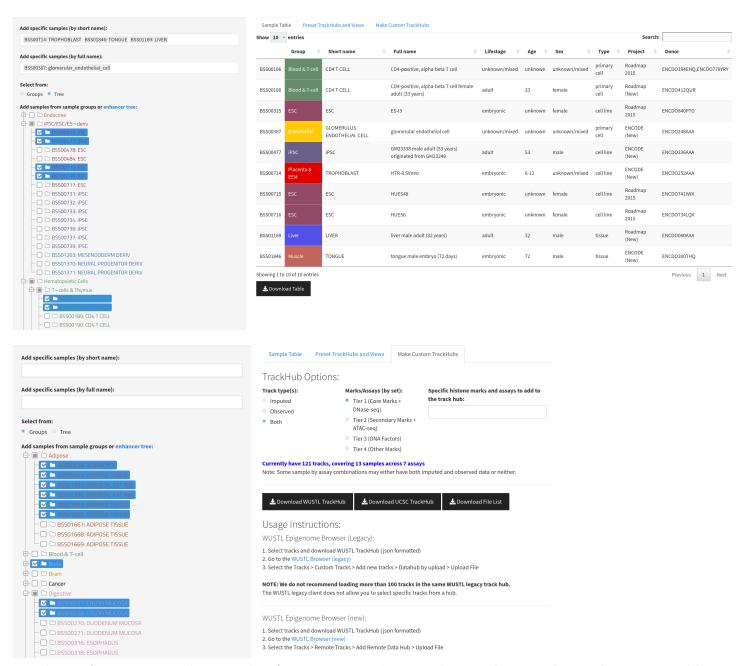


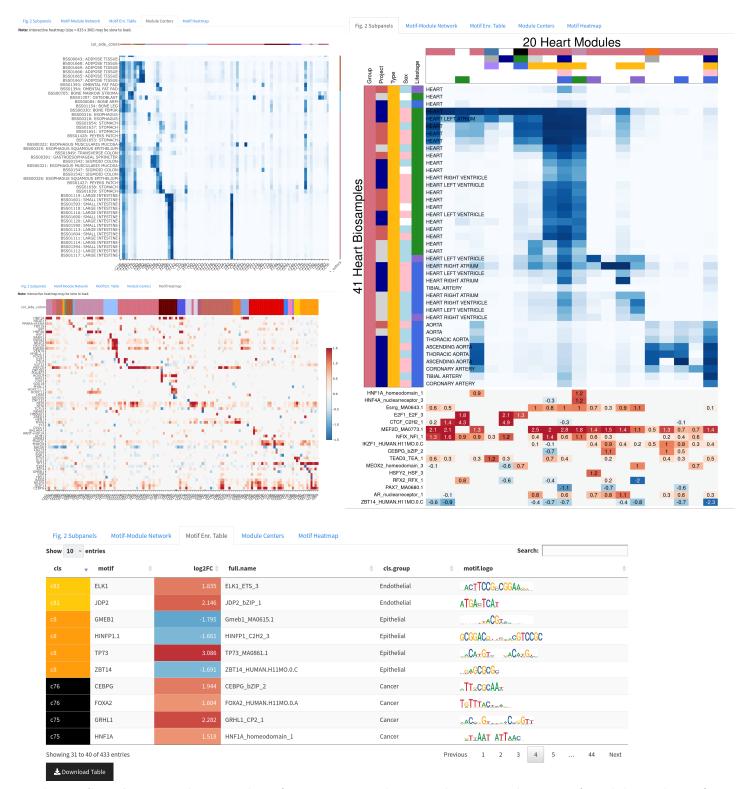
Figure S25: Two example cases where the epigenetic and the genetic trait-trait links may not agree.



**Figure S26:** Loci of lead SNPs for CAD in top 20 significantly enriched nodes. Matrix is split in three and shows 312 SNPs against 20 nodes, by presence (black) or absence (white) in the node's enhancers. Loci are ordered by clustering their jaccard similarity across nodes using the Ward method. Each SNP is annotated with its nearest protein-coding gene.



**Figure S27: a.** Example screenshot from interactive browser showing dataset selection by groups and by enhancer tree, metadata, and custom trackhub creation.



**Figure S27: b.** Example screenshots from interactive browser showing exploration of modules and motifs, subpanels of Figure 2 for heart, and motif enrichments as a table.

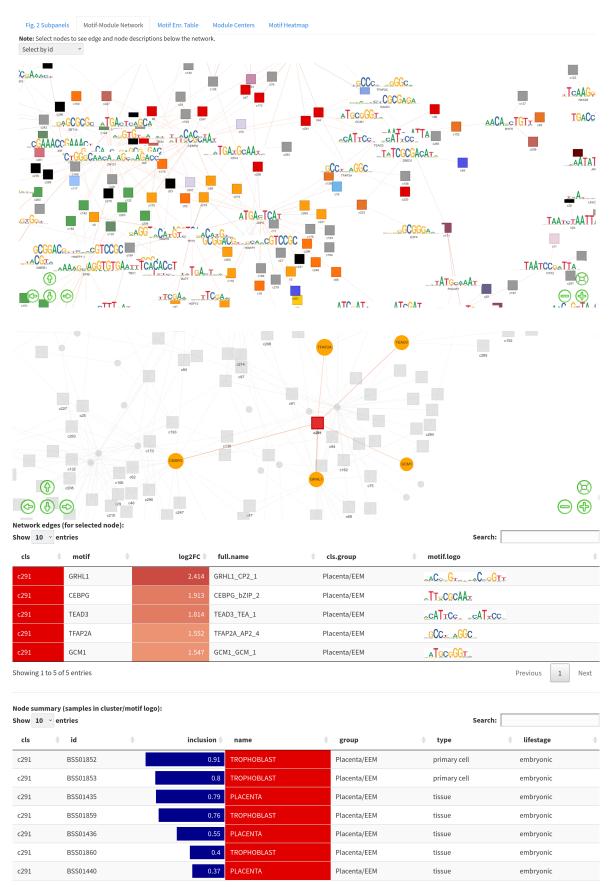
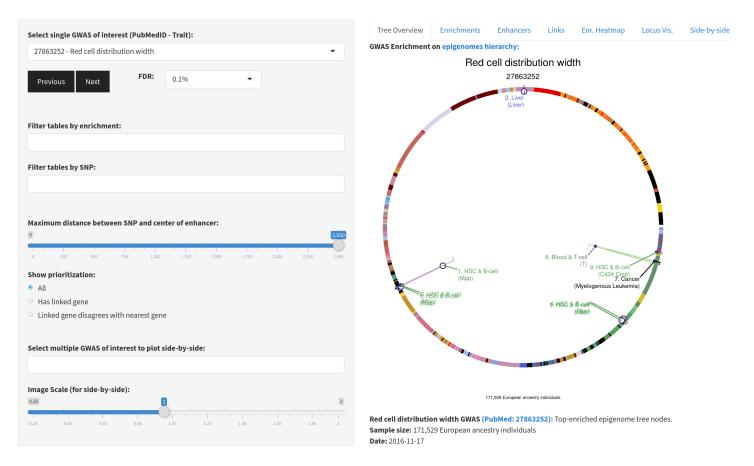


Figure S27: c. Example screenshots from interactive browser showing motif-module network and selection of specific module nodes to show enriched motifs and all included samples in the module.



Red cell distribution width GWAS (PubMed: 27863252): Top-enriched epigenome tree nodes and nominal enrichment p-values.

Sample size: 171,529 European ancestry individuals

Date: 2016-11-17

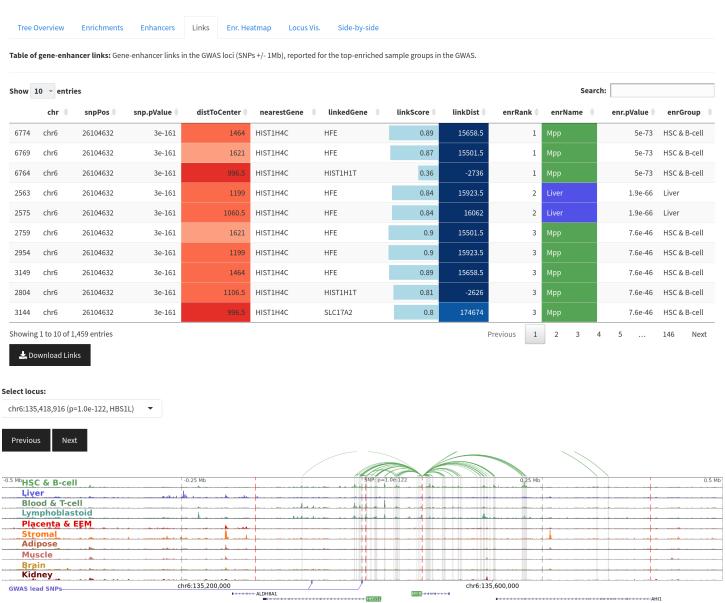
Show 10	entries					Search:
	enrRank 🏺	enrName \$	enr.pValue 🌲	pubMedID		enrGroup
1	1	Мрр	5e-73	27863252	Red cell distribution wid	th HSC & B-cell
2	2	Liver	1.9e-66	27863252	Red cell distribution wid	th Liver
3	3	Мрр	7.6e-46	27863252	Red cell distribution wid	th HSC & B-cell
4	4	Мрр	1.2e-41	27863252	Red cell distribution wid	th HSC & B-cell
5	5	Мрр	6.2e-39	27863252	Red cell distribution wid	th HSC & B-cell
6	6	Мрр	1.4e-36	27863252	Red cell distribution wid	th HSC & B-cell
7	7	Myelogenous Leukemia	1.5e-31	27863252	Red cell distribution wid	th Cancer
8	8	Т	1e-29	27863252	Red cell distribution wid	th Blood & T-cell
9	9	Cd34 Cmp	4.3e-28	27863252	Red cell distribution wid	th HSC & B-cell
howing 1	to 9 of 9 entries					Previous 1 Nex

Figure S27: d. Example screenshots from interactive browser showing GWAS browsing and enrichments in figure and table view.

Tissue-specific enhancers near GWAS lead SNPs: All enhancers within 2.5kb of a GWAS lead SNP that are also active in one of the top-enriched tree nodes in the GWAS.

	snpPos	snp.pValue	♦ enhStart ♦	enhEnd 🔷	distToCenter $\phi$	nearestGene	enrRank 🖣	enrName	♦ enr	.pValue 🌲	enrGroup
chr1	4342875	7 1e-16	343429771	43430151	1204.5	SLC2A1	9	Cd34 Cmp		4.3e-28	HSC & B-ce
chr2	6072545	i 8e-21	60727115	60727295	1754.5	BCL11A	9	Cd34 Cmp		4.3e-28	HSC & B-co
chr8	2624313	6 9e-19	26243356	26243576	330.5	BNIP3L	9	Cd34 Cmp		4.3e-28	HSC & B-c
chr1	4342875	7 1e-16	43429051	43429407	472.5	SLC2A1	9	Cd34 Cmp		4.3e-28	HSC & B-c
chr11	20519	8 4e-24	202620	202880	2447.5	BET1L	9	Cd34 Cmp		4.3e-28	HSC & B-co
chr1	369199	8 1e-17	3691784	3692024	93.5	SMIM1	9	Cd34 Cmp		4.3e-28	HSC & B-ce
chr11	4459461	1 1e-21	44595064	44595290	566.5	CD82	9	Cd34 Cmp		4.3e-28	HSC & B-ce
chr8	2624313	6 9e-19	26244376	26244596	1350.5	BNIP3L	9	Cd34 Cmp		4.3e-28	HSC & B-co
chr19	101453	8 1e-12	1016279	1016819	2011.5	TMEM259	9	Cd34 Cmp		4.3e-28	HSC & B-co
chr1	20328117	5 6e-14	203279688	203279808	1426.5	BTG2	9	Cd34 Cmp		4.3e-28	HSC & B-c
Downloa	ad Enhancers										
17_80480 3_2434; 2_16931; 1_20328;	8_98655 16_218 20_5599 3_18250 17_76181 14_7035 9_18833	19.17252 22.29151252 12.38918 11.6852 12.48022 12.48022 10.11351 10.11351 10.11351	1, 2558, 14 2531, 14	17_4233 17_4233 19_4422 9_13965 12_5468 11_4459 5_1068 5_1068 1_1367 1_368 2_50722	6_4999 6_4999 6_49999 5_105996 9_318696 19_118382 19_12896 19_12896 19_12896 19_12896 19_12896	15_7633 15_76635 1_07675 11_16305 11_61565 6_41925 6_109685 6_109685 5_10969 6_109685	18. 4383 22. 374ap 14. 2249a 22. 37865 17. 27171 10. 24858 7. 33080 7. 33080 2. 237465 2. 237465	22, 37885 6, 2607 6, 28100 15, 91000 6, 13541 5, 1100			
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Figure S27: e. Example screenshots from interactive browser showing enhancer predictions nearby GWAS SNPs and enhancer versus subtree intersection, showing the closest enhancer to the SNP in each tissue.



Locus overview for 1Mb around selected lead SNP: Tracks show average H3K27ac signal of enhancers in locus, and red dashed lines indicate the TSSes of nearby genes. Two types of correlation-based links are plotted: (1) Links from one of the enhancers near a lead SNP in the enriched epigenomes. (2) Any links in the locus present in at least half of the samples in one of the top sample groups (HSC & B-cell). Genes linked to an enhancer within 2.5kb of a GWAS lead SNP are highlighted and colored according to the sample group with the highest link score. Link data and images for this GWAS are also available from our data repository. Click to enable/disable zoom on locus, scroll to change zoom size.

**Figure S27: f.** Example screenshots from interactive browser showing linking predictions on GWAS SNPs and locus visualization with links, enhancers, and prioritized genes.