Supplemental Table 1. Sample characteristics and sequencing metadata.

RNA-Seq

GEO Accession	Patient ID/cell line	Sample type	Sample ID	Gender	Age	Input cell number	RIN	Total mapped reads (2x76bp)
GSM3290917	HIM13	Human_kidney_tubule	DS33394	F	80	2,000,000	10	244,151,932
GSM3290918	HIM13	Human_renal_cell_carcinoma	DS33395	F	80	500,000	9.9	257,438,823
GSM3290919	HIM15	Human_kidney_tubule	DS37923	M	62	2,000,000	9.9	124,435,785
GSM3290920	HIM15	Human_kidney_tubule	DS37924	M	62	2,000,000	9.9	104,505,925
GSM3290921	HIM15	Human_renal_cell_carcinoma	DS37925	M	62	125,000	9.9	99,037,346
GSM3290922	HIM15	Human_renal_cell_carcinoma	DS37926	M	62	125,000	9.8	147,534,033
GSM3290923	HIM23	Human_kidney_tubule	DS40494	M	63	500,000	7.2	246,217,904
GSM3290924	HIM23	Human_renal_cell_carcinoma	DS40496	M	63	500,000	9.1	113,565,853
GSM3290925	786-O	Human_renal_cell_carcinoma	DS34766	M	58	4,750,000	9.8	187,589,844
GSM3290926	ACHN	Human_renal_cell_carcinoma	DS37193	M	22	2,250,000	7.4	85,933,914

DNase-seq

GEO Accession	Patient ID/cell line	Sample type	Sample ID	Gender	Age	Input cell number	SPOT	Total mapped reads (2x36bp)
GSM3291010	HIM13	Human_kidney_tubule	DS26689	F	80	9,000,000	0.5650	201,833,536
GSM3291012	HIM13	Human_kidney_tubule	DS27824	F	80	9,000,000	0.4462	211,342,862
GSM3291022	HIM13	Human_renal_cell_carcinoma	DS26693A	F	80	5,000,000	0.5721	295,184,545
GSM3291023	HIM13	Human_renal_cell_carcinoma	DS26692B	F	80	5,000,000	0.4865	39,174,471
GSM3291014	HIM15	Human_kidney_tubule	DS37969	M	62	2,000,000	0.3638	53,455,680
GSM3291015	HIM15	Human_kidney_tubule	DS37971	M	62	2,000,000	0.4493	350,791,957
GSM3291016	HIM15	Human_renal_cell_carcinoma	DS37973	M	62	300,000	0.4951	260,802,880
GSM3291017	HIM15	Human_renal_cell_carcinoma	DS37974	M	62	300,000	0.5024	55,333,228
GSM3291020	HIM23	Human_kidney_tubule	DS41160	M	63	80,000	0.3944	221,916,751
GSM3291021	HIM23	Human_kidney_tubule	DS41396	M	63	80,000	0.5052	34,333,942
GSM3291018	HIM23	Human_renal_cell_carcinoma	DS40508	M	63	80,000	0.2764	201,007,725
GSM3291019	HIM23	Human_renal_cell_carcinoma	DS40509	M	62	80,000	0.2179	55,078,250
GSM3291011	786-O	Human_renal_cell_carcinoma	DS27192	M	58	9,000,000	0.3238	214,308,625
GSM3291013	786-O	Human_renal_cell_carcinoma	DS37199	M	58	100,000	0.3742	360,466,731
GSM3291024	ACHN	Human_renal_cell_carcinoma	DS24547A	M	22	13,100,000	0.4583	261,250,750
GSM3291025	ACHN	Human_renal_cell_carcinoma	DS24471A	M	22	3,000,000	0.4256	224,800,319

Supplemental Table 2. Transcriptional activity at HIF-bound LTRs.

Repeat Element								RNA-seq read counts 1kb downstream of LTR element												log2 RCC/TUB of read counts						Nearest gene up-reg in RCC		log2 RCC/TUB FPKM			
seqnames	elementStart	elementEnd	family	rep	strand	dDHS	At_least_1_sample_20cts	Pt1-TUB.neg	Pt1-RCC.neg	Pt1-TUB.pos	Pt1-RCC-pos	Pt2-TUB.neg	Pt2-RCC.neg	Pt2-TUB.pos	Pt2-RCC-pos	Pt3-TUB.neg	Pt3-RCC.neg	Pt3-TUB.pos	Pt3-RCC-pos	Pt1.neg	Pt2.neg	Pt3.neg	Pt1.pos	Pt2.pos	Pt3.pos	dGene	dGene.dist	Pt1.log2FC	Pt2.log2FC	Pt3.log2FC	TCGA-KIRC.log2FC
chr10	99320198	99321082	ERV1	Harlequin-int	-	FALSE	11	46	112	41	33	45	121	23	9	26	28	59	31	1.11	1.65	1.07	-0.37	-0.83	0.21	MORN4	54,112	0.63	1.80	1.44	-1.16
chr10	46951323	46951472	ERVL	LTR41B	+	FALSE	9	14	48	37	99	19	15	45	73	74	77	75	278	1.41	-0.04	1.15	1.22	0.99	2.94	RP11-38I	-	1.54	2.47	3.26	NA
chr6	89371917	89372311	ERV1	LTR2C	+	FALSE	9	88	67	3	108	92	48	5	208	189	29	3	26	-0.46	-0.62	-1.45	3.83	4.98	2.68	PNRC1	417,158	1.21	1.03	2.63	0.59
chr1	1549545	1550009	ERV1	MER65D	+	TRUE	9	68	72	12	43	42	44	14	17	123	26	26	23	-0.02	0.34	-0.99	1.42	0.54	0.82	MIB2	-	1.67	1.10	0.38	0.35
chr19	53401777	53402250	ERV1	LTR2B	-	TRUE	7	119	134	7	14	62	95	2	4	155	234	18	24	0.07	0.88	1.71	0.60	0.64	1.26	ZNF320	-	0.53	0.95	2.10	0.79
chr6	31153183	31154067	ERV1	Harlequin-int	-	FALSE	6	259	674	0	0	499	444	0	1	48	107	0	0	1.27	0.13	2.16	0.00	0.49	0.00	POU5F1	3,674	1.02	1.09	0.54	2.94
chr6	31154067	31154546	ERV1	LTR2B	-	TRUE	6	354	863	4	0	561	690	2	4	343	586	1	1	1.17	0.59	1.91	-0.93	0.64	0.24	POU5F1	4,558	1.02	1.09	0.54	2.94
chr2	34902259	34902729	ERV1	LTR2B	+	TRUE	6	0	4	53	272	0	14	23	66	2	0	35	119	0.85	2.63	-0.38	2.16	1.73	2.70	AC07321	-	3.75	3.77	1.75	NA
chr2	34902729	34903107	ERV1	Harlequin-int	+	TRUE	6	0	2	36	232	0	13	30	55	2	0	23	92	0.49	2.56	-0.38	2.44	1.13	2.80	AC07321	-	3.75	3.77	1.75	NA
chr7	134856015	134856493	ERV1	LTR2B	+	FALSE	6	2	3	225	202	8	3	97	92	3	6	136	205	0.19	-0.70	1.10	-0.25	0.26	1.70	RP11-134	2,194	-0.28	0.00	6.71	NA
chr7	134856494	134856835	ERV1	Harlequin-int	+	FALSE	6	4	1	259	222	10	4	119	112	3	6	130	169	-0.66	-0.68	1.10	-0.32	0.25	1.49	RP11-134	2,536	-0.28	0.00	6.71	NA
chr1	46791219	46791711	ERV1	LTR2B	-	TRUE	6	30	161	2	2	21	161	0	0	128	96	2	0	2.17	3.05	0.72	0.00	0.00	-0.38	LRRC41	20,938	0.76	0.43	0.43	0.59
chr1	46797740	46798229	ERV1	LTR2B	-	FALSE	6	111	733	3	0	76	533	2	1	292	501	2	0	2.58	3.06	1.92	-0.68	-0.19	-0.38	LRRC41	27,459	0.76	0.43	0.43	0.59
chr10	46983558	46983841	ERVL-MaLR	MLT1M	+	TRUE	6	14	47	4	10	19	15	11	21	74	71	40	51	1.38	-0.04	1.04	0.66	1.05	1.36	RP11-38I	17,006	1.54	2.47	3.26	NA
chr7	150004328	150004792	ERV1	LTR7C	+	FALSE	6	34	31	0	0	31	54	4	2	84	86	5	0	-0.20	1.03	1.14	0.00	-0.29	-0.77	ZBED6CL	21,145	-1.30	0.55	1.40	NA
chr12	125423035	125423517	ERV1	LTR10E	+	TRUE	6	103	66	4	8	50	63	4	6	80	66	8	9	-0.70	0.60	0.83	0.45	0.58	0.86	MIR5188	23,312	0.00	0.00	12.88	NA
chr16	4702909	4703477	ERVL	MER21C	-	TRUE	6	0	2	198	187	0	0	216	224	2	0	1086	269	0.49	0.00	-0.38	-0.18	0.39	-0.84	UBALD1	36,880	-0.06	0.78	0.36	NA
chr10	101666198	101666666	ERVL-MaLR	MLT1F	+	FALSE	6	29	20	0	0	65	32	2	0	167	38	0	0	-0.54	-0.68	-0.92	0.00	-0.68	0.00	ABCC2	54,717	1.30	4.24	1.38	0.72
chr10	47057033	47057779	ERV1	LTR8	-	TRUE	6	16	49	4	10	19	15	11	21	74	71	36	51	1.30	-0.04	1.04	0.66	1.05	1.48	RP11-29	513,480	1.67	0.00	0.00	NA
chr15	80447864	80448809	ERVK	LTR13A	-	FALSE	6	0	0	83	148	0	0	55	51	0	0	128	103	0.00	0.00	0.00	0.70	0.22	0.81	MEX3B	1,886,255	-0.36	1.33	0.75	0.96
chr5	138905450	138905931	ERV1	LTR2B	+	TRUE	6	2	4	70	1247	0	2	81	462	1	2	237	2569	0.36	0.77	0.63	3.96	2.80	4.56	UBE2D2	-	0.82	0.17	1.18	0.42
chr5	138910671	138911149	ERV1	LTR2B	+	TRUE	6	0	2	37	459	0	0	32	268	0	0	134	789	0.49	0.00	0.00	3.37	3.27	3.65	UBE2D2	-	0.82	0.17	1.18	0.42
chr7	139367993	139368415	ERVL-MaLR	MLT1F	-	FALSE	6	62	58	0	2	99	65	0	2	255	129	1	0	-0.18	-0.30	0.17	0.49	0.85	-0.14	KLRG2	198,534	-1.84	2.74	1.38	-11.57
chr10	85931742	85932221	ERV1	LTR2B	-	FALSE	6	242	864	0	2	236	436	0	0	281	632	0	0	1.72	1.17	2.30	0.49	0.00	0.00	GLUD1	2,878,501	0.79	0.43	1.67	-0.57
chr10	85931365	85931742	ERV1	Harlequin-int	-	TRUE	6	165	813	0	4	192	358	0	0	114	400	0	0	2.17	1.18	2.90	0.85	0.00	0.00	GLUD1	2,878,878	0.79	0.43	1.67	-0.57
chr5	171702051	171702389	ERVL-MaLR	THE1C	-	TRUE	6	98	121	0	0	50	77	0	0	148	84	0	0	0.20	0.88	0.33	0.00	0.00	0.00	SNORA5	21,568	1.17	0.16	-1.13	0.00
chr7	101705188	101705485	ERVL-MaLR	MLT1I	-	FALSE	6	0	0	49	130	2	0	58	89	0	0	227	210	0.00	-0.68	0.00	1.22	0.92	1.03	SNORA4	132,168	0.98	0.23	0.17	0.00
chr19	53238533	53238999	ERV1	LTR2B	+	FALSE	6	30	32	0	6	60	40	0	2	201	120	2	3	0.00	-0.27	0.41	1.14	0.85	0.55	ZNF808	171,282	0.61	-0.37	0.52	-0.37
chr8	53607916	53608589	ERVL	MER77	+	TRUE	6	60	111	0	0	53	70	0	0	130	100	1	0	0.75	0.67	0.75	0.00	0.00	-0.14	NPBWR1	241,401	2.14	-5.64	5.55	0.00
chr3	58147296	58147738	ERVL-MaLR	MLT1L	-	FALSE	6	0	0	482	331	0	0	454	288	0	0	852	391	0.00	0.00	0.00	-0.64	-0.31	0.04	PDHB	266,061	-0.88	-0.54	0.66	-1.40
chr8	95452838	95453062	ERVL	MER21B	-	FALSE	5	85	31	0	0	76	20	0	0	92	14	0	0	-1.42	-1.50	-1.37	0.00	0.00	0.00	FSBP	2,657	0.75	0.94	0.72	NA
chr19	41873837	41874012	ERV1	LTR24	-	FALSE	5	0	1	39	38	0	2	11	33	0	2	83	31	0.26	0.77	0.77	-0.13	1.64	-0.24	B9D2	2,758	1.00	0.43	1.68	0.81
chr6	107187430	107187739	Gypsy	MamGypLTR2c	+	FALSE	5	82	164	1	0	55	58	1	0	2	175	2	2	0.87	0.36	5.51	-0.26	-0.38	0.30	MIR587	43,260	14.16	0.00	0.00	NA
chr17	41400485	41401528	ERVK	LTR13	-	TRUE	5	5	9	10	17	7	12	111	75	24	5	1440	22	0.47	0.83	-0.77	0.46	-0.22	-4.67	RNU6-11	72,876	13.81	0.00	0.00	NA
chr8	95453062	95453542	ERV1	LTR2B	+	FALSE	5	97	26	0	2	91	26	0	0	135	13	0	0	-1.81	-1.42	-1.99	0.49	0.00	0.00	DPY19L4	277,388	0.47	-0.45	1.23	-0.60
chr1	16279309	16279464	ERVL-MaLR	MLT1H	+	TRUE	5	21	36	4	2	22	20	2	1	80	19	7	0	0.58	0.14	-0.82	-0.44	-0.19	-1.00	SCARNA	410,665	3.10	0.66	3.42	0.00
chr2	232092933	232093411	ERVL-MaLR	MLT1G3	-	FALSE	5	0	0	46	37	0	0	40	18	0	0	100	31	0.00	0.00	0.00	-0.38	-0.71	-0.50	PDE6D	504,202	0.10	0.99	0.06	0.01
chr4	169304464	169304906	ERV1	LTR56	-	TRUE	5	56	55	0	0	58	45	0	0	29	7	0	0	-0.12	-0.07	-0.68	0.00	0.00	0.00	NEK1	1,009,962	0.61	-0.14	0.37	-0.53
chr8	95453542	95454141	ERVL	MER21B	-	FALSE	4	82	34	0	2	85	19	0	0	128	18	0	0	-1.26	-1.73	-1.52	0.49	0.00	0.00	FSBP	3,361	0.75	0.94	0.72	NA
chr12	123574544	123574916	ERVL-MaLR	MLT1F	-	TRUE	4	20	9	0	0	21	10	0	0	84	20	0	0	-0.90	-0.65	-0.81	0.00	0.00	0.00	Y_RNA	259,002	0.92	1.32	-0.18	NA
chr20	15966412	15966891	ERV1	LTR2B	-	FALSE	4	38	22	4	12	30	17	1	1	94	17	6	3	-0.77	-0.45	-1.16	0.84	0.11	0.08	Y_RNA	684,874	0.92	1.32	-0.18	NA
chr17	41381806	41382224	ERVL	RV3-16A3_I-int	+	TRUE	4	0	2	20	9	0	2	22	28	1	0	124	17	0.49	0.77	-0.14	-0.92	0.62	-1.55	TMEM10	10,163	0.01	1.48	-0.13	0.06
chr12	13529953	13530144	ERV1	LTR7C	-	FALSE	4	60	4	0	0	28	21	0	0	21	2	0	0	-2.98	-0.09	-1.27	0.00	0.00	0.00	LOH12CR	1,018,951	2.21	0.41	0.06	-1.50
chr4	68592776	68593363	ERV1	LTR26	+	TRUE	3	0	0	19	55	0	0	15	17	0	0	22	45	0.00	0.00	0.00	1.23	0.45	1.90	UBA6-AS	-	1.44	0.79	0.67	NA
chrX	10008214	10009016	ERVL	MER21C	-	TRUE	3	0	14	12	32	0	2	15	18	0	12	49	31	1.96	0.77	2.32	1.04	0.53	0.45	Y_RNA	164,472	0.92	1.32	-0.18	NA
chr13	49165573	49166054	ERV1	LTR2B	-	FALSE	2	0	91	0	6	3	15	0	0	1	20	0	0	4.31	1.80	2.81	1.14	0.00	0.00	LINC0046	12,348	12.18	10.40	5.25	NA
chr12	32463175	32463663	ERV1	PrimLTR79	-	FALSE	2	0	3	17	8	0	0	23	15	0	0	68	18	0.68	0.00	0.00	-0.85	-0.24	-0.68	Y_RNA	85,809	0.92	1.32	-0.18	NA
chr12	101026882	101027281	ERV1	LTR2	-	TRUE	2	5	84	2	9	6	5	11	3	0	18	23	3	3.12	0.05	2.81	1.00	-1.03	-1.14	Y_RNA	374,313	0.92	1.32	-0.18	NA
chr3	36716249	36716729	ERV1	LTR2B	+	TRUE	2	3	0	25	12	2	1	14	30	5	0	10	0	-0.77	-0.19	-0.77	-0.91	1.27	-1.26	RNU6-13	464,088	13.29	0.00	0.00	NA
chr20	44410052	44410585	ERVL	MER68	-	TRUE	2	16	21	0	1	4	9	0	0	28	6	0	0	0.24	1.00	-0.79	0.26	0.00	0.00	WFDC3	-	1.72	2.21	-0.59	-0.27
chr22	25404193	25404302	ERV1	MER66B	+	FALSE	2	2	0	5	10	0	0	10	15	0	0	54	34	-0.49	0.00	0.00	0.51	0.72	0.45	KIAA167	-	0.60	0.44	1.25	0.18
chr7	17422222	17422705	ERV1	LTR2B	-	FALSE	2	0	7	4	99	0	0	0	35	4	0	0	0	1.26	0.00	-0.68	3.46	3.82	0.00	SNORA6	8,271	1.07	-0.12	0.28	0.53
chr10	80876631	80877087	ERVL-MaLR	MLT1H	-	FALSE	2	0	0	10	27	0	0	11	8	0	0	108	16	0.00	0.00	0.00	1.00	-0.10	-1.43	ZCCHC24	265,450	1.55	1.02	0.73	-0.04
chr2	88356296	88356499	ERV1	PrimLTR79	-	TRUE	2	20	15	4	12	16	21	2	2	14	8	6	3	-0.40	0.59	0.26	0.84	0.17	0.08	EIF2AK3	499,963	1.07	0.41	0.34	0.01
chr12	46495273	46495613	ERV1	LTR38	+	TRUE	2	0	0	22	22	0	0	0	6	0	0	2	4	0.00	0.00	0.00	-0.08	1.72	0.76	ANO6	661,426	0.84	0.17	0.90	0.35
chr12	13530157	13530283	ERV1	LTR7C	-	FALSE	2	57	2	0	0	27	15	0	0	19	2	0	0	-3.28	-0.48	-1.16	0.00	0.00	0.00	LOH12CR	1,019,155	2.21	0.41	0.06	-1.50
chr1	95193635	95194067	ERVL	LTR33	-	TRUE	1	9	21	0	0	5	5	0	0	14	11	0	0	0.82	0.21	0.60	0.00	0.00	0.00	LINC0105	-	1.07	0.34	1.12	NA
chr17	78382751	78386864	ERV1	Harlequin-int	+	TRUE	1	1	12	0	4	1	12	2	3	13	32	0	2	1.54	2.08	2.01	0.85	0.39	0.68	ENDOV	1,100	0.72	0.55	1.16	NA
chr5	1567506	1568461	ERVK	LTR5B	-	TRUE	1	2	20	0	12	4	4	0	0	11	13	0	0	1.87	0.18	1.03	1.77	0.00	0.00	SDHAP3	1,131	1.98	1.31	1.55	1.84
chr5	43058236	43059213	ERVK	LTR5B	+	FALSE	1	9	10	7	4	3	3	8	13	8	4	22	18	0.05	0.14	0.06	-0.47	0.80	0.70	AC02517	13,721	0.96	0.62	0.28	NA
chr8	107099257	107099738	ERV1	LTR2B	-	TRUE	1	0	34	0	0	8	18	0	0	4	9	0	0	3.00	1.18	1.32	0.00	0.00	0.00	RP11-15	25,504	-0.60	2.35	3.67	NA
chr2	101850616	101851017	ERV1	LTR2	-	TRUE	1	3	15	0	0	1	29	0	0	11	8	0	0	1.27	3.18	0.51	0.00	0.00	0.00	RNF149	37,065	0.72	0.00	1.43	1.22
chr1	1440345	1441337	ERVK	LTR13	-	TRUE	1	2	0	12	0	0	0	1	2	0	0	45	4	-0.49	0.00	0.00	-1.85	0.47	-1.71	C1orf233	93,047	-2.33	1.56	-0.60	NA
chr5	80317522	80318038	ERV1	LTR26B	-	TRUE	1	0	0	11	1	0	0	9	7	0	0	29	0	0.00	0.00	0.00	-1.50	-0.04	-2.32	CKMT2-A	182,381	0.62	-1.07	1.11	NA
chr17	62916888	62917160	ERVL	MER21B	-	FALSE	1	6	8	15	16	6	21	10	9	11	10	15	7	0.18	1.67	0.73	0.00	0.14	0.05	LRRC37A	289	0.85	0.98	1.92	-0.39
chr7	158656846	158656944	ERV1	LTR56	-	TRUE	1	4	0	12	18	0	0	11	13	2	2	13	28	-0.93	0.00	0.39	0.35	0.46	1.78	ESYT2	32,901	1.11	0.16	0.78	0.16
chr13	37363147	37363518	ERVL-MaLR	MSTD	-	FALSE	1	3	23	0	0	0	2	0	0	5	0	0	0	1.75	0.77	-0.77	0.00	0.00	0.00	SMAD9	55,821	3.45	0.38	2.16	0.27
chr11	73664371	73664838	ERV1	LTR2B	-	TRUE	1	0	3	2	5	2	19	0	20	4	2	4	11	0.68	2.34	0.09	0.51	3.09	1.46	C2CD3	59,392	0.27	0.68	-0.04	-0.33
chr2	208259418	208259893	ERV1	LTR44	-	FALSE	1	10	18	0	0	8	3	0	3	22	0	0	0	0.55	-0.70	-2.10	0.00	1.07	0.00	PLEKHM3	433,609	0.62	-0.26	0.33	-0.14
chr13	23463517	23463986	ERV1	LTR2B	+	TRUE	1	0	2	16	13	0	0	1	3	2	0	55	1	0.49	0.00	-0.38	-0.29	0.69	-2.73	TNFRSF1	679,522	0.97	-0.35	-0.18	-0.39
chr15	98890215	98890710	ERVL-MaLR	MLT1G1	-	TRUE	1	4	155	0	0	1	0	0	0	12	0	0	0	4.11	-0.38	-1.49	0.00	0.00	0.00	TTC23	786,313	0.85	0.26	-0.10	-0.31
chr2	123464830	123465354	ERV1	PABL_B	-	TRUE	1	2	43	0	4	0	3	0	0	0	10	0	0	2.82	1.07	2.10	0.85	0.00	0.00	CLASP1	1,056,666	0.57	-0.10	0.74	-0.25
chr2	69961384	69961870	ERV1	MER87	+	TRUE	0	0	0	0	3	0	0	0	2	0	1	2	2	0.00	0.00	0.38	0.68	0.85	0.30	ANXA4	-	2.51	2.22	2.98	1.77
chr6	131956569	131956765	ERV1	PABL_B	+	TRUE	0	0	0	0	13	0	2	0	3	0	0	1	4	0.00	0.77	0.00	1.85	1.07	1.00	ENPP3	-	4.95	6.94	6.93	5.28
chr6	131956772	131957135	ERV1	PABL_A-int	+	TRUE	0	0	0	2	10	0	0	0	6	0	0	1	4	0.00	0.00	0.00	1.10	1.72	1.00	ENPP3	-	4.95	6.94	6.93	5.28
chr6	167371768	167372246	ERV1	LTR2B	-	FALSE	0	5	6	0	1	2	5	0	1	7	1	2	2	0.07	0.86	-0.62	0.26	0.49	0.30	RNASET2	88	1.76	1.68	1.58	3.02
chr22	36646281	36646764	ERV1	LTR2B	+	FALSE	0	3	1	0	0	1	0	0	2	7	0	1	0	-0.50	-0.38	-1.00	0.00	0.85	-0.14	APOL1	1,291	1.27	2.90	0.98	1.22
chr3	177531021	177531526	ERVL-MaLR	MLT1D	+	TRUE	0	0	0	0	2	0	0	0	0	0	0	0	1	0.00	0.00	0.00	0.49	0.00	0.38	RP11-91	2,126	3.94	3.59	4.06	NA
chr19	6609162	6609306	ERVL-MaLR	MLT1I	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	CD70	4,047	1.04	1.26	1.84	8.51
chr5	159408890	159409229	ERVL-MaLR	MLT1G3	+	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	ADRA1B	9,678	-0.12	1.37	0.17	1.47
chr12	52512654	52512748	ERV1	PABL_A	+	FALSE	0	0	0	2	4	2	0	2	0	0	2	0	0	0.00	-0.68	0.77	0.36	-0.68	0.00	OR7E47P	10,703	2.00	0.00	-4.64	NA
chr7	1215463	1215997	ERVL	RV3-16A3_I-int	-	FALSE	0	4	3	0	0	7	8	0	0	9	4	0	0	-0.25	0.37	0.00	0.00	0.00	0.00	ZFAND2A	14,067	0.49	0.33	0.64	0.70
chr7	1216151	1216592	ERVL	RV3-16A3_I-int	-	FALSE	0	4	0	0	0	4	9	0	0	9	2	0	0	-0.93	1.00	-0.44	0.00	0.00	0.00	ZFAND2A	14,755	0.49	0.33	0.64	0.70
chr16	47092501	47092912	ERVL	MER21C	-	TRUE	0	0	0	0	0	0	1	0	2	0	0	0	9	0.00	0.49	0.00	0.00	0.85	1.93	NETO2	19,113	-0.49	-0.10	0.71	3.49
chr5	10467449	10467912	ERV1	MER4C	-	TRUE	0	0	0	0	3	0	2	0	0	0	0	0	2	0.00	0.77	0.00	0.68	0.00	0.68	RP11-1C	25,954	5.31	8.37	2.93	NA
chr3	44564099	44564570	ERV1	LTR7C	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	ZKSCAN7	31,114	-0.08	0.17	1.28	NA
chr6	107268368	107268920	ERV1	LTR35A	+	FALSE	0	0	0	0	2	0	0	0	2	0	0	0	0	0.00	0.00	-0.38	0.49	0.00	0.00	MIR587	36,825	14.16	0.00	0.00	NA
chr5	10513813	10514187	ERVL	MER68B	+	FALSE	0	0	0	0	4	0	2	0	0	0	0	0	0	0.00	0.77	0.00	0.85	0.00	0.00	ROPN1L	42,046	3.61	1.73	3.29	1.18
chrX	18865819	18866478	ERV1	PABL_A	-	TRUE	0	0	2	0	0	0	1	0	1	0	0	0	0	0.49	0.49	-0.14	0.00	0.00	0.00	PHKA2	44,599	1.25	0.76	1.48	2.27
chr8	23278652	23279629	ERVK	HERVK3-int	+	FALSE	0	4	5	0	4	12	9	0	2	13	1	2	2	0.07	-0.10	-1.16	0.85	0.85	0.30	RP11-17	55,991	1.82	0.95	-0.34	NA
chr20	61506752	61507619	ERVL	ERVL-E-int	+	TRUE	0	5	4	0	2	1	0	0	0	3	2	0	0	-0.22	-0.38	0.28	0.49	0.00	0.00	OGFR	62,267	0.15	0.04	0.89	0.89
chr19	6601796	6602013	ERV1	LTR2	+	TRUE	0	0	7	0	0	0	4	0	9	6	2	0	1	1.26	1.32	-0.16	0.00	2.14	0.38	TNFSF9	66,082	0.16	0.98	0.41	4.23
chr8	68736127	68736970	ERVK	MER11C	-	FALSE	0	10	1	0	0	0	1	0	0	2	0	0	0	-1.42	0.49	-0.38	0.00	0.00	0.00	CPA6	76,506	0.53	-1.77	3.54	3.09
chr11	74760435	74760904	ERV1	LTR2B	-	TRUE	0	11	1	0	0	2	1	0	0	7	0	1	0	-1.50	-0.19	-1.00	0.00	0.00	-0.14	RNU6-21	80,097	13.29	0.00	0.00	NA
chr6	27020095	27020577	ERV1	LTR2B	-	TRUE	0	2	0	0	0	0	4	0	0	0	0	0	0	-0.49	1.32	0.00	0.00	0.00	0.00	GUSBP2	94,761	1.06	-0.11	0.91	NA
chr17	72631673	72632017	ERV1	LTR56	+	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	MIR3615	111,734	0.55	6.67	2.50	NA
chr9	126905181	126905307	ERVL-MaLR	MLT1J	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	NEK6	113,577	1.34	0.58	1.96	1.91
chr7	54947938	54948398	ERV1	LTR2	-	FALSE	0	0	0	2	8	0	0	0	3	0	0	0	0	0.00	0.00	0.00	0.89	1.07	0.00	SEC61G	119,270	0.36	0.04	1.74	0.91
chr15	73215657	73216056	ERV1	LTR38B	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	ADPGK-A	125,516	0.39	-0.38	0.95	NA
chr8	68736970	68737438	ERV1	LTR2B	+	FALSE	0	0	2	4	5	1	0	6	0	2	0	1	2	0.49	-0.38	-0.38	0.07	-1.49	0.54	PREX2	125,914	0.01	-0.52	2.75	1.66
chr1	230702558	230703181	ERV1	PABL_A	-	TRUE	0	2	15	0	0	0	0	0	0	0	3	0	0	1.55	0.00	1.00	0.00	0.00	0.00	AGT	135,711	2.54	3.03	4.75	0.96
chr8	94885846	94886476	ERV1	MER41B	-	TRUE	0	0	0	2	1	0	0	0	0	0	0	0	0	0.00	0.00	0.00	-0.22	0.00	0.00	CTD-2006	156,504	0.82	-0.01	1.92	NA
chr11	1803920	1804379	ERVL-MaLR	MLT1D	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	KRTAP5-	183,965	0.21	1.82	-0.03	NA
chr3	187225521	187226027	ERV1	PrimLTR79	-	TRUE	0	0	3	0	0	0	0	0	2	0	0	0	0	0.68	0.00	0.00	0.00	0.85	0.00	BCL6	213,644	0.64	0.63	2.01	0.78
chr8	94948223	94948890	ERVL	LTR62	-	TRUE	0	0	0	2	4	0	0	3	2	2	0	6	0	0.00	0.00	-0.38	0.36	-0.08	-0.85	CTD-2006	218,881	0.82	-0.01	1.92	NA
chr6	26296079	26296494	ERVK	LTR3	-	TRUE	0	0	0	0	0	0	0	2	1	1	0	2	0	0.00	0.00	-0.14	0.00	-0.19	-0.38	U91328.	295,683	0.72	0.00	0.00	NA
chr5	172882083	172882506	ERVL-MaLR	MLT1F1	+	FALSE	0	0	0	0	2	0	0	0	1	0	0	0	0	0.00	0.00	0.00	0.49	0.49	0.00	CREBRF	316,215	1.45	0.96	1.82	NA
chr10	134133760	134134266	ERV1	MER67A	-	FALSE	0	3	5	0	0	2	0	0	0	2	3	0	0	0.23	-0.68	0.62	0.00	0.00	0.00	BNIP3	337,324	0.79	-0.20	0.71	1.46
chr2	235100584	235100953	ERVL	LTR75	+	TRUE	0	0	0	0	0	0	0	1	0	0	0	1	0	0.00	0.00	0.00	0.00	-0.38	-0.14	UGT1A1	418,997	-3.53	2.69	1.82	3.08
chr1	15682661	15683084	ERV1	LTR24	-	TRUE	0	0	0	0	0	0	2	0	0	0	0	1	1	0.00	0.77	0.00	0.00	0.00	0.24	RP11-16	477,899	0.05	1.16	0.07	NA
chr10	3771703	3771793	ERVL	LTR67B	+	TRUE	0	0	0	0	0	0	0	0	0	0	0	1	1	0.00	0.00	0.00	0.00	0.00	0.00	PFKP	591,889	1.10	0.26	0.78	2.24
chr2	238136286	238136730	ERVL	LTR16E2	+	FALSE	0	0	0	0	2	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.49	0.00	0.00	ACKR3	645,729	5.32	5.16	4.51	NA
chr10	29649363	29649835	ERV1	LTR2B	-	FALSE	0	4	16	4	0	19	7	4	0	10	2	2	2	1.18	-0.92	-0.56	-0.93	-1.14	0.30	KIAA146	652,366	-0.64	3.50	2.37	0.82
chr2	30329218	30329691	ERV1	LTR46	-	TRUE	0	1	0	0	0	0	0	0	2	0	0	0	0	-0.26	0.00	-0.38	0.00	0.00	0.00	GALNT14	804,115	2.01	1.46	2.53	1.10
chr9	81836144	81836506	ERV1	LTR78	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	RP11-39	807,987	3.96	-0.63	1.82	NA
chr14	93631465	93631933	ERV1	LTR2B	+	FALSE	0	0	0	0	3	0	0	0	2	0	0	1	4	0.00	0.00	0.00	0.68	0.85	1.00	IFI27	938,248	3.83	5.82	5.65	1.20
chr10	2154038	2154441	ERVL	LTR40A1	-	FALSE	0	0	2	0	0	0	0	0	0	0	0	0	0	0.49	0.00	0.00	0.00	0.00	0.00	RP11-11	953,578	1.09	0.36	1.74	NA
chr2	123464041	123464830	ERV1	LTR8A	+	TRUE	0	2	13	0	2	0	2	0	0	0	5	0	0	1.40	0.77	1.43	0.49	0.00	0.00	AC01873	979,046	0.12	0.15	1.47	NA
chr16	10352525	10353491	ERVK	LTR13A	+	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	Y_RNA	1,054,432	0.92	1.32	-0.18	NA
chr13	102392091	102392608	ERV1	LTR2B	+	TRUE	0	0	0	0	0	0	2	0	0	2	0	0	0	0.00	0.00	0.77	0.00	-0.68	0.00	BIVM	1,057,790	1.02	0.62	2.28	0.59
chr6	166105104	166105152	ERVL	MLT2B4	+	TRUE	0	0	0	0	0	0	3	0	2	0	0	0	0	0.00	1.07	0.00	0.00	0.85	0.00	FGFR1OP	1,306,517	0.73	-0.05	-0.07	0.72
chr6	166104414	166104550	ERVL	MLT2B4	+	TRUE	0	0	0	0	0	0	5	0	0	0	0	0	0	0.00	1.54	0.00	0.00	0.00	0.00	FGFR1OP	1,307,119	0.73	-0.05	-0.07	0.72
chr3	95075681	95076154	ERV1	LTR2B	+	FALSE	0	0	0	4	4	0	0	0	0	1	0	0	0	0.00	0.00	0.38	-0.08	0.00	0.00	Y_RNA	1,389,290	0.92	1.32	-0.18	NA
chr16	63736905	63737059	ERV1	LTR24	+	TRUE	0	0	0	0	4	0	0	0	4	0	2	0	0	0.00	0.00	0.77	0.85	1.32	0.00	BEAN1	2,723,140	-1.91	1.71	-1.42	NA
chr1	67680425	67680907	ERV1	LTR2B	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	IL23R	-	1.13	0.00	0.00	0.56
chr4	24925950	24926533	ERVL-MaLR	MLT1G	-	FALSE	0	0	0	0	2	0	0	2	0	0	0	0	0	0.00	0.00	0.00	0.49	-0.68	0.00	CCDC149	-	0.65	0.14	0.56	-0.28
chr9	139690984	139691906	ERVK	LTR5B	+	TRUE	0	0	6	3	11	0	0	0	8	0	6	2	6	1.14	0.00	1.58	1.00	2.00	1.11	TMEM14	4,197	0.56	0.13	1.06	-0.57
chr1	28913418	28913900	ERV1	LTR2B	-	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	SNORD9	7,083	-18.95	20.64	0.00	0.00
chr7	76052543	76052956	ERV1	LTR35A	-	FALSE	0	0	6	3	13	0	1	2	7	1	2	12	16	1.14	0.49	0.63	1.17	1.17	1.13	SRCRB4D	12,530	0.66	0.92	-0.36	-2.36
chr8	143781241	143781576	ERV1	LTR43	-	FALSE	0	0	0	0	0	0	2	0	0	0	0	0	0	0.00	0.77	0.00	0.00	0.00	0.00	JRK	16,854	0.45	0.28	0.67	-0.16
chr11	70998281	70998711	LTR	MamRep1527	-	TRUE	0	0	2	0	0	0	0	0	0	0	0	0	0	0.49	0.00	0.00	0.00	0.00	0.00	SHANK2	33,657	2.60	0.90	2.03	-0.50
chr6	11430186	11430586	ERVL-MaLR	MSTD	-	TRUE	0	2	5	2	10	0	0	2	0	2	0	2	0	0.51	0.00	-0.38	1.10	-0.68	-0.38	NEDD9	46,604	-0.81	0.87	-1.11	-0.25
chr21	45669174	45669889	ERV1	MER49	+	FALSE	0	2	0	1	10	0	1	0	9	0	0	0	6	-0.49	0.49	0.00	1.32	2.14	1.49	PFKL	49,044	0.87	0.50	1.17	0.20
chr22	44946592	44947077	ERVL	LTR33C	-	TRUE	0	0	1	0	0	0	1	0	0	0	0	0	0	0.26	0.49	0.00	0.00	0.00	0.00	LDOC1L	51,413	0.24	0.26	0.79	-0.52
chr7	93686224	93686617	ERVL-MaLR	MLT1G3	-	FALSE	0	0	0	6	0	2	0	2	2	0	0	10	0	0.00	-0.68	0.00	-1.20	0.17	-1.26	BET1	51,529	0.52	-0.12	0.80	0.08
chr2	171730936	171731243	ERVL-MaLR	MLT1E2	+	TRUE	0	0	8	0	0	0	2	0	0	0	0	0	0	1.38	0.77	0.00	0.00	0.00	0.00	GORASP	52,730	-0.05	0.70	0.51	0.05
chr21	45822105	45822629	ERVL	MER77	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	C21orf2	61,819	1.10	0.58	1.34	-0.26
chr19	35620256	35621251	ERVK	LTR5B	+	FALSE	0	0	0	0	0	0	0	0	2	0	0	0	0	0.00	0.00	0.77	0.00	0.00	0.00	HPN	63,776	-1.33	4.19	0.50	0.09
chr1	31917401	31917880	ERV1	LTR44	-	TRUE	0	0	0	0	0	1	0	0	0	4	0	0	0	0.00	-0.38	-0.68	0.00	0.00	0.00	FABP3	66,703	-0.12	1.24	-5.41	-0.83
chr15	54123155	54123619	ERV1	LTR2	-	FALSE	0	0	0	0	0	7	2	0	0	0	0	0	0	0.00	-0.87	0.00	0.00	0.00	0.00	WDR72	67,079	1.70	1.11	2.46	-2.04
chr3	54080907	54081333	ERVL-MaLR	MLT1J1	+	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	CACNA2D	74,240	-1.25	-1.39	1.41	-3.29
chr21	43203703	43204124	ERVK	LTR3B	+	FALSE	0	2	0	0	0	0	2	0	0	2	0	0	0	-0.49	0.77	-0.38	0.00	0.00	0.00	SNORA3	97,189	1.24	0.64	-1.29	0.00
chr17	60973123	60973536	ERVL	LTR16C	+	TRUE	0	0	0	0	2	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.49	0.00	0.00	TANC2	112,380	1.45	0.39	-0.47	-0.15
chr7	75738247	75738590	ERV1	MER61A	-	FALSE	0	0	3	1	0	0	4	0	0	1	0	0	0	0.68	1.32	-0.14	-0.26	0.00	0.00	TMEM12	113,269	0.74	0.76	0.66	-0.09
chr9	139683249	139684228	ERVK	LTR5B	-	TRUE	0	0	2	0	0	0	0	0	0	0	0	0	0	0.49	0.00	0.00	0.00	0.00	0.00	FBXW5	151,638	-0.16	-0.17	0.67	0.27
chr9	139679465	139680614	ERVK	LTR13A	-	FALSE	0	0	6	0	0	2	0	0	0	0	0	0	0	1.14	-0.68	0.00	0.00	0.00	0.00	FBXW5	155,422	-0.16	-0.17	0.67	0.27
chr8	107072701	107073035	ERVL	LTR18A	+	TRUE	0	0	2	0	5	0	0	1	8	0	0	2	0	0.49	0.00	0.00	1.00	1.62	-0.38	OXR1	208,437	1.60	-0.02	1.67	-0.14
chr4	7962518	7962941	ERVL	LTR47B	+	TRUE	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	-0.49	0.00	0.00	SH3TC1	219,857	1.77	-0.16	0.11	0.29
chr9	93698339	93698672	ERVL	LTR16C	-	TRUE	0	0	0	0	1	0	0	2	0	0	0	0	0	0.00	-0.38	0.00	0.00	0.85	0.00	AUH	277,758	1.10	-0.11	1.36	-1.42
chr11	8405587	8406526	ERVK	LTR13A	+	FALSE	0	0	1	0	0	0	2	0	0	2	0	0	0	0.26	0.77	-0.38	0.00	0.00	0.00	TUB	278,867	1.33	0.98	-8.71	-0.94
chr6	110888055	110888612	ERV1	LTR26B	+	TRUE	0	0	6	0	0	0	2	0	0	0	0	0	0	1.14	0.77	0.00	0.00	0.00	0.00	SNORA4	280,136	3.31	14.77	14.35	0.00
chr20	10337798	10338174	ERVL-MaLR	THE1D	-	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	JAG1	280,534	-1.77	0.92	2.09	0.54
chr1	238027544	238027825	Gypsy?	LTR88a	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	SNORA2	308,072	1.75	-0.66	0.51	0.00
chr22	41062522	41062915	ERV1	LTR56	+	TRUE	0	0	1	0	0	0	1	0	2	0	0	0	0	0.26	0.00	-0.38	0.00	-0.38	0.00	TNRC6B	331,103	0.50	0.82	0.75	-0.24
chr16	88275922	88276240	ERVL-MaLR	MLT1B	-	FALSE	0	0	6	0	6	0	0	0	5	5	0	14	0	1.14	0.00	-0.77	1.14	1.54	-1.54	SLC7A5	371,827	1.40	0.59	-0.78	-0.18
chr5	41527447	41527871	ERV1	MER41B	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	C5orf51	375,418	-0.27	-0.18	0.62	-0.01
chr5	41527202	41527447	ERVL-MaLR	MLT1H	+	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	C5orf51	375,842	-0.27	-0.18	0.62	-0.01
chr12	122682011	122682164	ERV1	LTR71A	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	3	0	0.00	0.00	0.00	0.00	0.00	-0.49	HPD	379,508	1.01	-1.64	-4.52	-6.93
chr5	112689898	112690054	ERVL-MaLR	MLT1I	-	TRUE	0	1	11	0	0	0	6	0	0	1	3	0	0	1.46	1.68	0.86	0.00	0.00	0.00	REEP5	430,661	0.14	0.50	0.82	-0.46
chr8	127133463	127133765	ERVL-MaLR	THE1C	-	FALSE	0	0	2	0	0	0	0	0	0	0	0	0	0	0.49	0.00	0.00	0.00	0.00	0.00	FAM84B	431,224	0.11	0.50	0.59	-1.12
chr1	223617596	223617991	ERVL-MaLR	MLT1H	+	FALSE	0	0	4	0	0	0	0	0	0	0	0	0	0	0.85	0.00	0.00	0.00	0.00	0.00	DISP1	438,654	1.16	1.45	2.10	-0.36
chr21	38905458	38905727	ERVL	LTR41	-	TRUE	0	0	0	1	0	0	0	2	1	0	0	0	0	0.00	0.00	0.00	-0.26	-0.19	0.00	PIGP	458,987	0.69	0.80	2.45	0.18
chr1	224087179	224087624	ERV1	LTR37B	-	FALSE	0	0	0	2	1	0	3	0	2	0	0	2	0	0.00	1.07	0.00	-0.22	0.85	-0.38	SUSD4	548,634	4.45	2.44	2.37	-5.45
chr6	154936819	154937164	ERVL	LTR16A1	+	FALSE	0	0	0	0	0	0	0	2	0	0	0	0	0	0.00	0.00	0.00	0.00	-0.68	0.00	CLDN20	646,982	0.22	0.73	-1.59	-1.14
chr5	125264411	125264868	ERV1	LTR71A	+	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	2	0.00	0.00	0.00	0.00	0.00	0.68	PHAX	670,091	0.33	-0.15	0.86	-0.04
chr7	121170350	121170749	ERVL-MaLR	MLT1I	-	TRUE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	TSPAN12	670,893	2.59	2.00	3.42	0.01
chrX	35461069	35461538	ERV1	LTR2B	-	FALSE	0	2	0	0	0	0	0	0	0	0	0	0	0	-0.49	0.00	0.00	0.00	0.00	0.00	TMEM47	784,663	-0.37	-0.44	1.27	-0.10
chr20	53599867	53600109	ERVL	LTR79	-	FALSE	0	2	3	0	0	2	0	0	0	0	0	0	0	0.19	-0.68	0.00	0.00	0.00	0.00	CYP24A1	808,354	-1.18	0.61	-2.26	-4.10
chr20	53600193	53600652	ERV1	LTR2B	-	FALSE	0	4	4	0	0	2	0	0	0	0	0	0	0	-0.08	-0.68	0.00	0.00	0.00	0.00	CYP24A1	808,680	-1.18	0.61	-2.26	-4.10
chr9	31443703	31444185	ERV1	LTR2B	+	FALSE	0	0	0	2	0	0	0	2	0	0	0	0	0	0.00	0.00	0.00	-0.49	-0.68	0.00	ACO1	939,432	0.74	-0.01	0.56	-1.08
chr20	53734016	53734506	ERV1	LTR2B	-	TRUE	0	0	0	2	0	1	0	0	0	0	0	0	0	0.00	-0.38	0.00	-0.49	0.00	0.00	CYP24A1	942,503	-1.18	0.61	-2.26	-4.10
chr3	41724857	41725302	ERV1	HERV35I-int	+	TRUE	0	5	10	0	2	6	4	2	4	18	5	4	2	0.56	-0.16	-0.45	0.49	0.64	0.00	ZBTB47	968,873	0.22	1.18	-1.59	-0.59
chr2	47951581	47952019	ERVL-MaLR	MLT1K	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	PIGF	1,106,322	0.37	-0.03	0.72	-0.18
chr3	162426706	162427178	ERV1	LTR2B	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	SCARNA	2,192,681	1.17	0.40	1.70	0.00
chr10	66491529	66491834	ERV1	LTR2	-	FALSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	DNAJC12	3,064,898	2.71	1.03	2.43	-2.21
chr16	34974127	34979670	ERV1	HERVH-int	-	TRUE	0	3	0	0	0	0	0	0	0	0	0	0	0	-0.77	0.00	0.00	0.00	0.00	0.00	C16orf58	3,452,496	0.33	0.57	0.95	0.04
chr16	34979671	34980137	ERV1	LTR7C	-	FALSE	0	0	0	1	5	0	0	0	3	2	0	3	0	0.00	0.00	-0.38	0.74	1.07	-0.49	C16orf58	3,458,040	0.33	0.57	0.95	0.04
chr4	134787434	134788184	ERVL	MER76-int	+	FALSE	0	0	4	0	0	0	0	0	0	0	0	0	0	0.85	0.00	0.00	0.00	0.00	0.00	C4orf33	4,750,389	0.29	0.02	0.83	-0.50

Supplemental Figure 1. Characterization of primary RCC cultures and overview of DHS landscape

(a) *Karyotypes of primary RCC cultures.* Primary RCC cultures were submitted for G-band karyotyping at the University of Washington Cytogenetics Laboratory. Inferred karyotypes from 20 metaphase spreads are shown. All three patient tumors showed characteristic loss of chromosome 3p and gain of chromosome 5q.

(b) VHL *mutation status in primary tubule and RCC cultures.* Sanger sequencing of the coding regions identified an inactivating mutation in the single copy of the *VHL* gene in all three primary RCC cultures.

(c) *Chromosome arm level gains and losses are identified by DNase-seq tags.* Windowed aggregation (5Mb windows) of tags from DNase-seq datasets from the primary tubule and RCC cultures revealed arm level gains and losses, including the canonical loss of chromosome 3p and gain of chromosome 5q.

(d) *DNase I-hypersensitive sites identify predominantly distal regulatory elements.* A minority of the master list DHS derived from tubule and RCC datasets localized to promoter elements (1.9%) or lie within 5 kb of a known transcription start site (20.3%). The majority (77.8%) lay >5 kb from known transcription start sites, characteristic of distal regulatory elements such as enhancers.

(e) *Overlap of differential DHS identifies the shared regulatory landscape of RCC.* DHSs with differential accessibility in tumors vs. their matched tubule controls define the differentially accessible regulatory landscape of RCC. Pairwise comparisons of these differential DHS across patients revealed that ~35% of all differential DHS are shared among at least two patient samples.

Supplemental Figure 2. Individual renal cell carcinomas exhibit highly concordant RNA landscapes

(a) *Consistent patterns of gene expression among patients.* Comparison of expression fold change of genes (translucent blue dots) revealed largely consistent patterns of gene expression among patient tumor samples. Genes that typify the HIF transcriptional response (e.g. *CA9*, *VEGFA*, *EGLN3*) were upregulated and some genes associated with normal tubular function (e.g. *CDH1*, *ANPEP*) were downregulated in all three tumor samples compared to their normal tubule controls. Hatched lines represent 1.5x fold change on the log-scale axis.

(b) *Gene ontology enrichment.* Ranked list GOrilla enrichment analysis (rank in boldface) identified both canonical (e.g. hypoxia response, lipid metabolic process, chromatin organization) and unexpected gene ontologies (e.g. complement activation) that were differentially regulated in renal cell carcinoma compared to tubules.

Supplemental Figure 3. Expression of *PSORS1C3* in various TCGA tumors and matched normal tissues. The mRNA expression levels of the *PSORS1C3* gene in several non-germ cell tumors was compared to their matched normal tissue controls. The ends of the bar plots represent the 25th and 75th quartiles with whiskers representing 1.5x inter-quartile range (10% outlier trim applied for clarity).

Supplemental Figure 4. An adult kidney-specific DHS encodes an alternate promoter for *POU5F1*

The alternate promoter for *POU5F1* in RCC maps to a DHS that is only present in adult kidney derived tubules (RPTEC, renal proximal tubule epithelial cells), primary cultures (HRCE, human renal cortical epithelial cells; HRE, human renal epithelial cells) or tumors (786-O, ACHN). This DHS is not present in fetal kidney, embryonic stem cells, non-epithelial kidney cells (e.g. glomerular endothelial cells, HRGEC) or a variety of ontologically diverse cells. All tracks are shown at same scale/settings as those shown in Fig. 5.

Supplemental Figure 5. Numerous expressed sequence tags (ESTs) in the *POU5F1-PSORS1C3* genomic locus (hg19 chr6:31,125,253-31,156,354)

Known transcript isoforms for *POU5F1, PSORS1C3 and TCF19* are shown at the top in blue gene models. Annotated ESTs in GenBank are shown below in black gene models.

Supplemental Figure 6. Overview of the *POU5F1B* genomic locus (hg19 chr8:128,420,724-128,436,573)

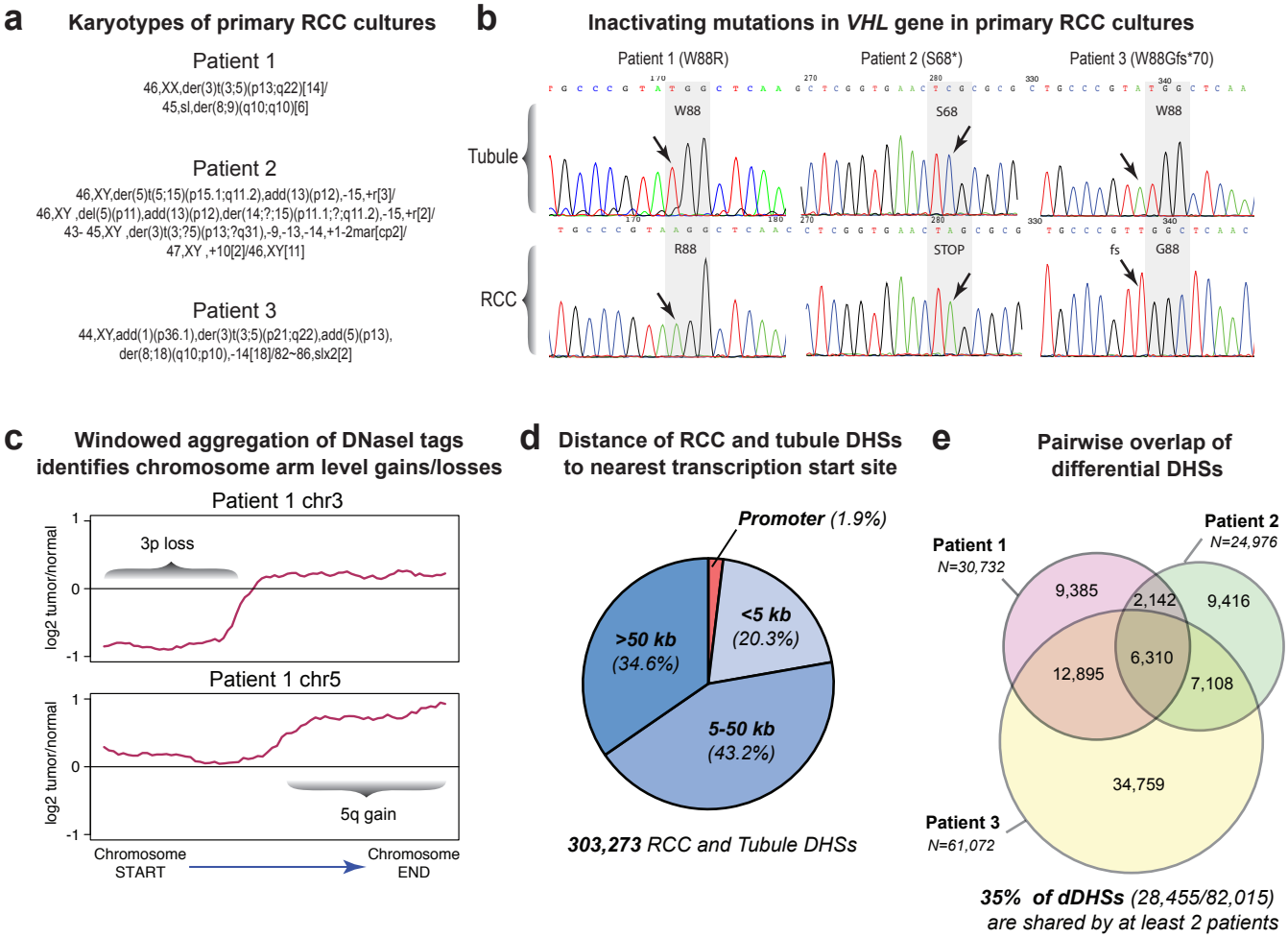
POU5F1B was expressed in human ESCs, but not in the primary tubule and RCC cultures described in this study. There were no DHSs in this genomic interval, and there is negligible binding of HIF components. Histone modifications typical of active transcription were also not present. All tracks are shown at same scale/settings as those shown in Fig. 5.

Supplemental Figure 7. Expression of *POU5F1* in RCC as a function of known metastasis status and pathologic stage. Each point represents the expression value of a single patient's tumor in the indicated subgroup. Black diamond indicates mean value for the indicated subgroup in both panels.

(a) Expression of *POU5F1* as a function of known metastasis status.

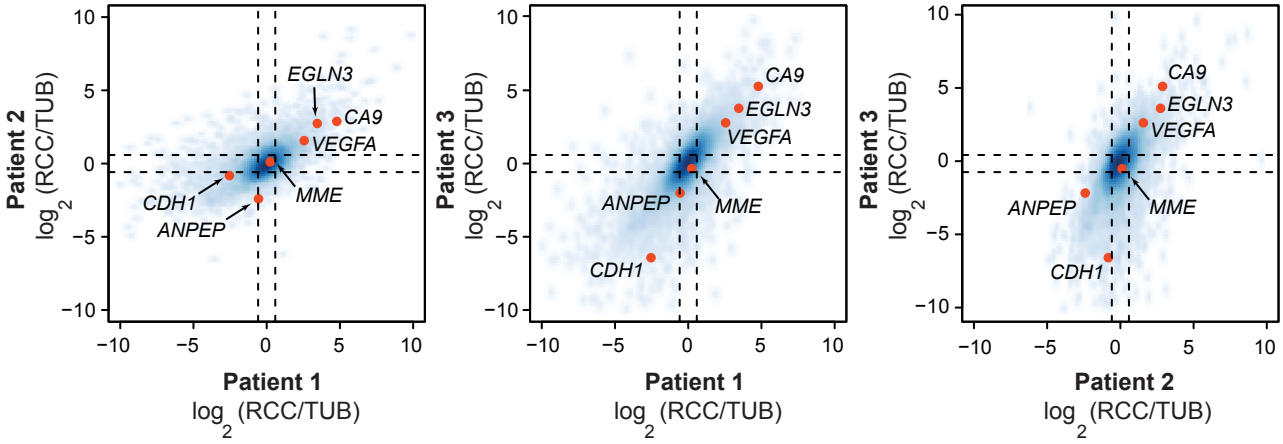
(b) Expression of *POU5F1* as a function of pathologic stage at the time of diagnosis. P-value = 0.037 by 1-factor ANOVA.

Supplemental Figure 1



Supplemental Figure 2

a **Pairwise comparison of differential RNA expression**



b **Gene ontology enrichment of genes changing >1.5x in all 3 patients**

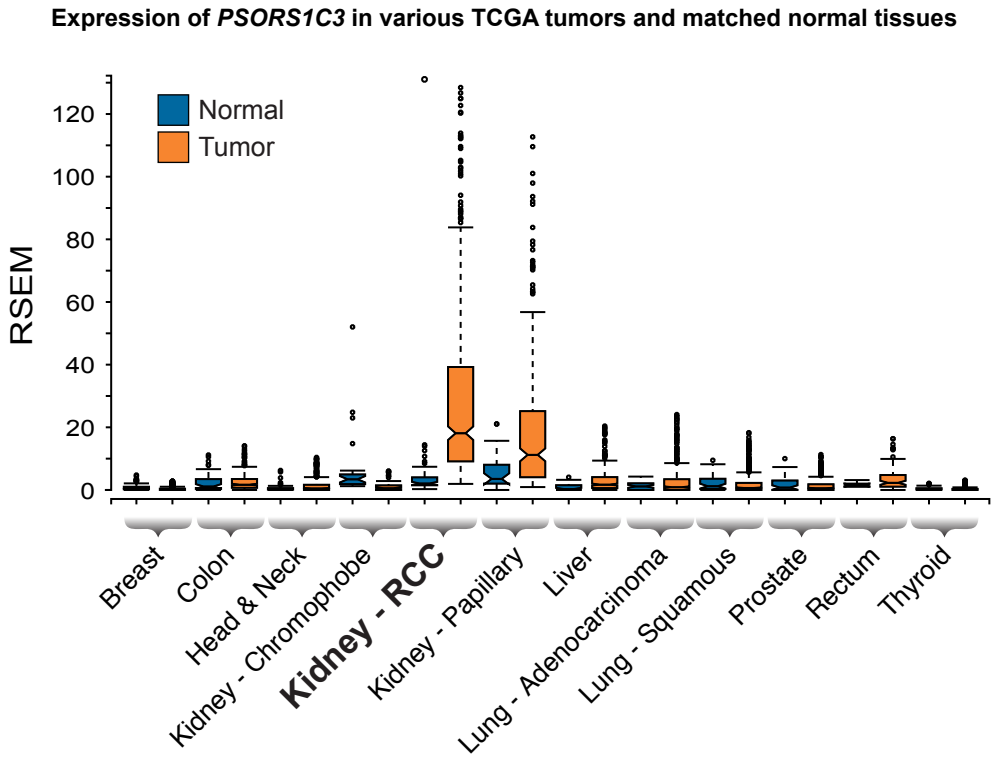
Upregulated = **1,072**

1. Biological adhesion – e.g. *VCAM1*
3. Anion transport – e.g. *CA9*
25. Complement activation – e.g. *C3*
45. Lipid metabolic process – e.g. *FABP6*
54. Response to hypoxia – e.g. *VEGFA*

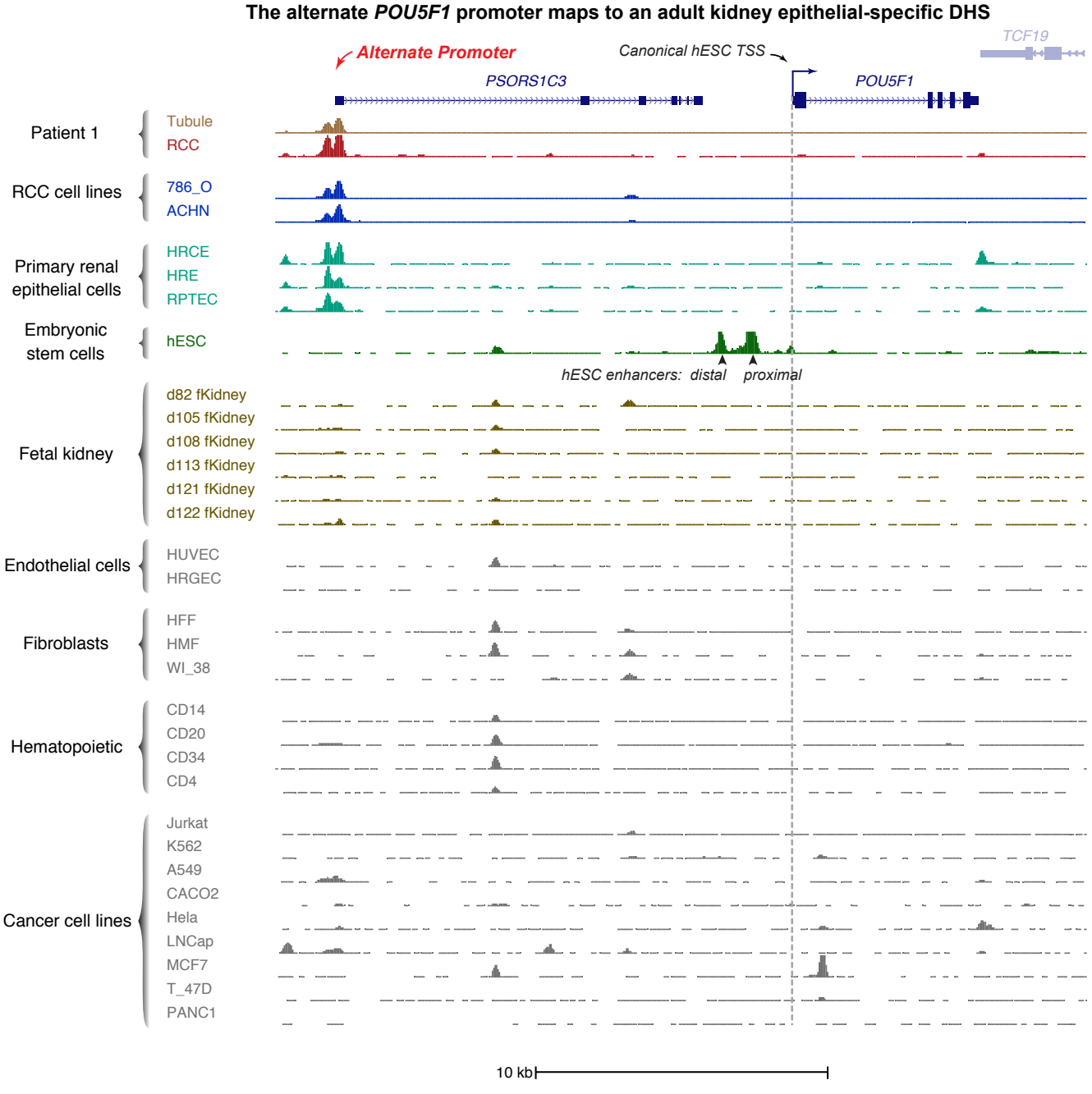
Downregulated = **1,207**

1. Cell cycle process – e.g. *AURKA*
2. Chromosome organization – e.g. *HMGA1*
3. Mitotic cell cycle process – e.g. *TOP2B*
16. Cellular component organization or biogenesis – e.g. *CDH1*
34. Negative regulation of gene expression, epigenetic – e.g. *EZH2*

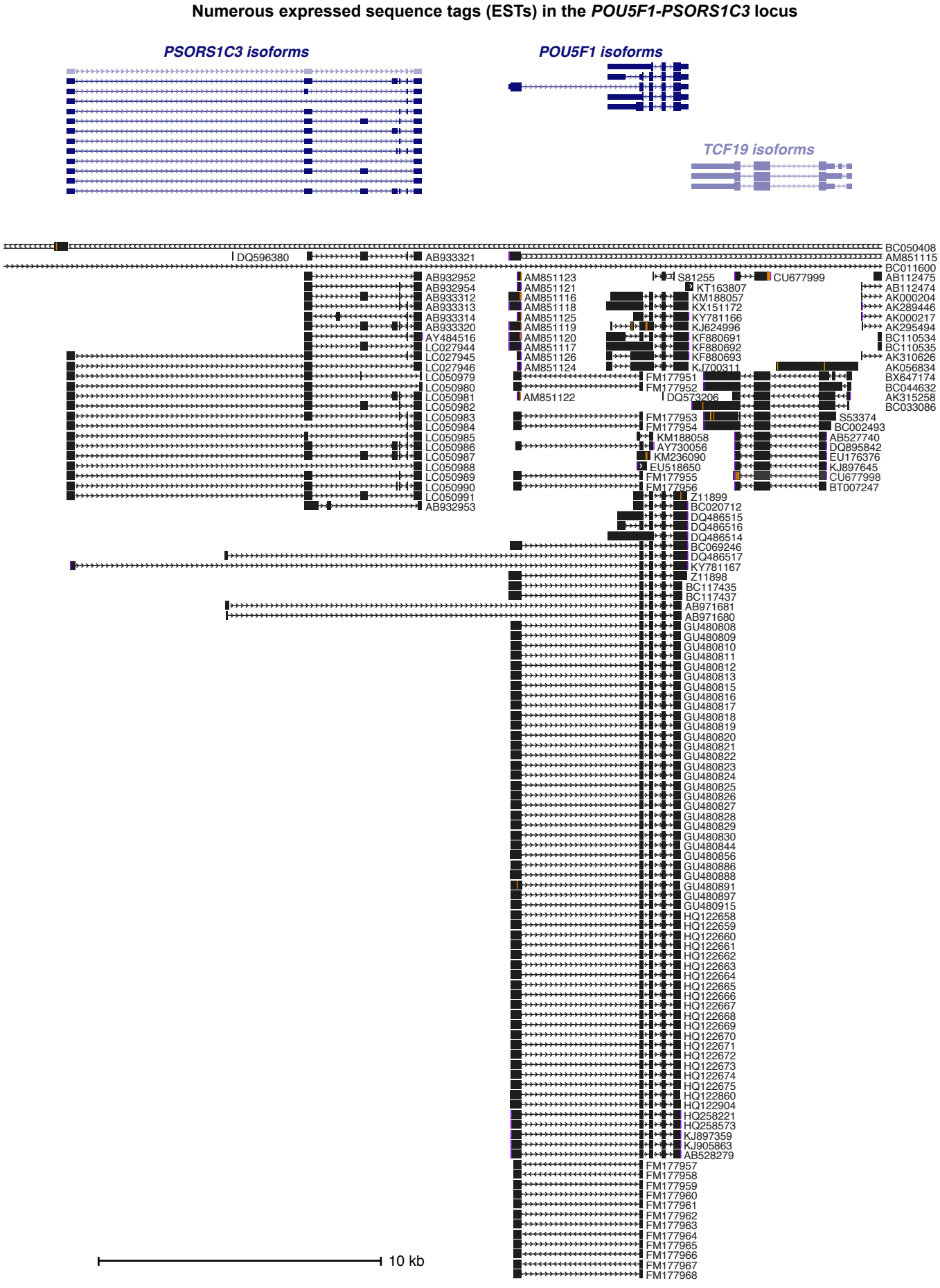
Supplemental Figure 3



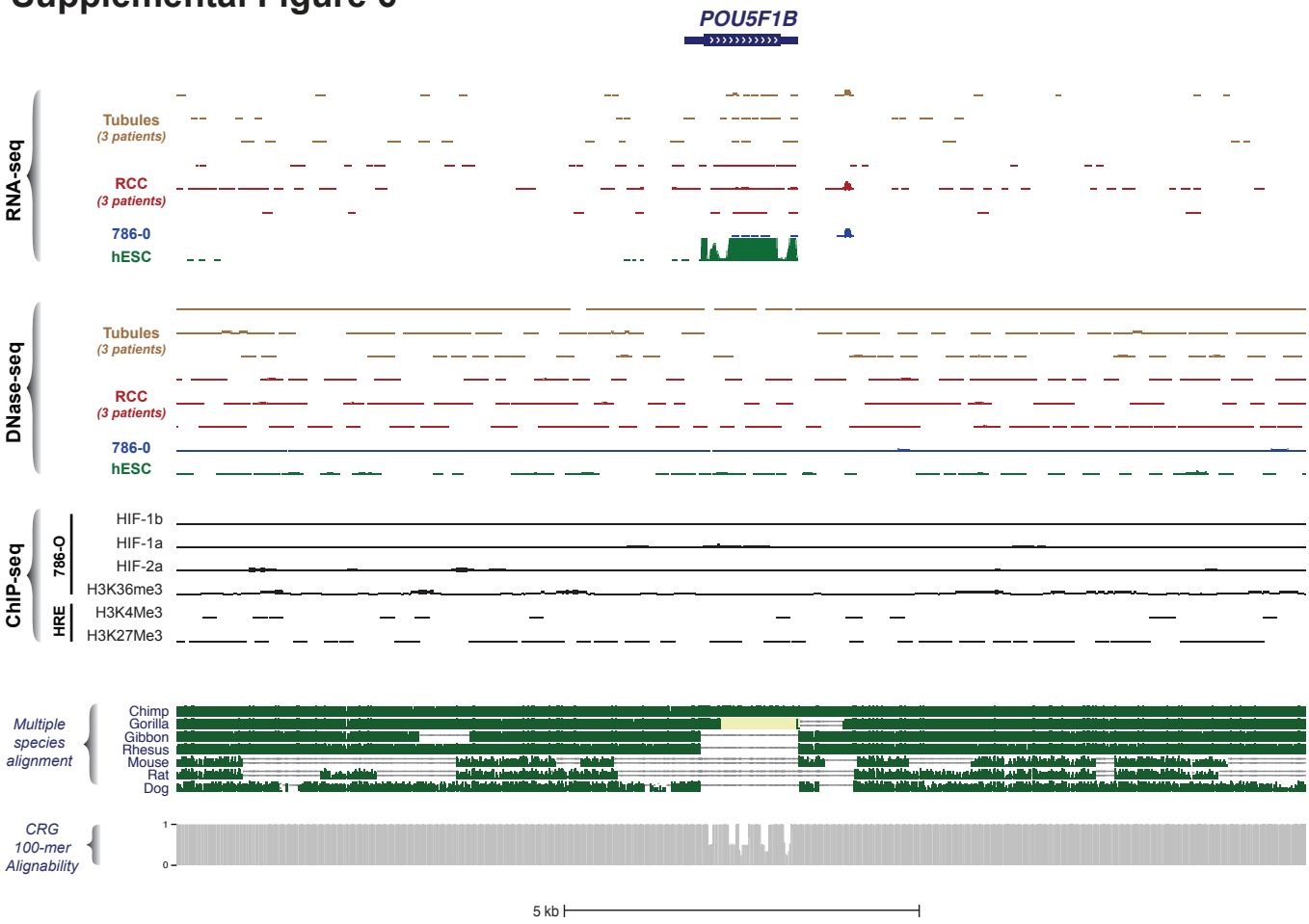
Supplemental Figure 4



Supplemental Figure 5



Supplemental Figure 6



Supplemental Figure 7