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                                                 	Symmetric	
                                                 	Okazaki	
                                                 	Chromatin	
    	Splice	
                                                 	unknown	no cluster
                                                 	multiexon, cluster	multiexon, cluster
                                                 	monoexon, cluster	monoexon, cluster
                                                 	no evidence	
                                                 	broken assembly, no expression	broken assembly, partial expression
                                                 	broken assembly, complete expression	broken assembly, complete expression
               		

Acetyltransf_1.HG1.29:like:NAT14:like...
 Acetyltransf_1.HG1.38:NAT8/NAT8L
 Acetyltransf_1.HG2.0:KAT14
 Acetyltransf_1.HG30.0:NA
 Acetyltransf_1.HG4.1:SAT1/SAT2/SATL1
 Acetyltransf_1.HG5.1:KAT2A/KAT2B

Coka
 Chabra
 Ernie
 Morvir
 Auraur
 Skow

unknown
 multiexon, no cluster
 multiexon, cluster
 monoexon, no cluster
 monoexon, cluster

no evidence
 broken assembly, no expression
 broken assembly, partial expression
 contiguous assembly, complete expression
 contiguous assembly, no expression
 contiguous assembly, partial expression
 contiguous assembly, complete expression

RVT_1
 Ipe
 Padr_2
 Integrase_H2C2
 HT_24
 FUR_3
 DDE_1

Unknown
 RTGypsy-ERV
 DNA Tc2-group

Acetyltransf_1 TEs

Hist_deacetyl.HG1.12:like:HDAC4/HDAC5...
Hist_deacetyl.HG1.19:HDAC4/HDAC5/HDAC...
Hist_deacetyl.HG1.6:like:HDAC4/HDAC5/...

0	1	Coka
0	1	Emue
0	0	unknown
0	0	multexon, no cluster
0	0	multexon, cluster
0	0	monoxon, no cluster
0	0	monoxon, cluster
0	0	no evidence
1	0	broken assembly, no expression
0	0	broken assembly, partial expression
0	0	broken assembly, complete expression
0	0	contiguous assembly, no expression
0	0	contiguous assembly, partial expression
0	0	contiguous assembly, complete expression
0	1	Trans_reg_C
0	0	Marr_2
1	0	gag-asp-proteas
0	0	DDE_inp_4
0	0	Unknown
0	0	DNA_Pif-Harbinger

SIR2.HG1.14.SIRT2
SIR2.HG3.1.SIRT6

0 0 Chabira
1 0 Notgen

0 0 unknown, no cluster
0 0 multiexon, cluster
0 0 monoexon, no cluster
0 0 monoexon, cluster

0 0 no evidence
0 0 broken assembly, no expression
0 0 broken assembly, partial expression
0 0 broken assembly, complete expression
0 0 contiguous assembly, no expression
0 1 contiguous assembly, partial expression
0 0 contiguous assembly, complete expression

0 0 Integrase_H2C2
1 0 DDE_np_4

0 0 RT_Gypsy-ERV
1 0 DNA_PIF-Harbinger

SIR2 TEs

SET TEs

	SET_HG1.19.SMYD1/SMYD2/SMYD3	Symmetric
✓	SET_HG1.50.like.SMYD1/SMYD2/SMYD3/SMY...	Germ
✓	SET_HG12.0.NA	Euro
✓	SET_HG2.19.like.SETD3/SETD4:likeclu:1...	Afro
✓	SET_HG2.8.SETD6	Sas
✓	SET_HG5.3.SETMAR	Hvayul
✓	SET_HG5.7.SETDB1/SETDB2	Csau
✓	SET_HG6.0.like.KMT5A:likeclu:6	Pvtia
✓	SET_HG7.1.like.PRDM1/PRDM2/PRDM6/PRDM...	Hsap
		unknown
		multiplex, no cluster
		monoxon, no cluster
		monoxon, cluster
		no evidence
		broken assembly, no expression
		broken assembly, partial expression
		complete assembly, complete expression
		contiguous assembly, no expression
		contiguous assembly, partial expression
		complete assembly, complete expression
		Transposase_21
		THAP
		RVT-2
		RNase_H
		DDE_Tnp_4
		DDE_Tnp_1_7
		Unknown
		RTE_group
		Long_terminal_Repeat_Element
		RT_CR-group
		RT_CRI
		DNA_Ic1-Marinex
		DNA_PolyBac_Group
		DNA_PI-Harbinger
		DNA CMC

SWIRM.HG2.1:TADA2A
SWIRM.HG3.0:KDM1A

0 0 Chabira
1 1 Scf

0 0 unknown
1 1 multiexon, no cluster
0 0 multiexon, cluster
0 0 monoexon, no cluster
0 0 monoexon, cluster

0 0 no evidence
0 0 broken assembly, no expression
0 0 broken assembly, partial expression
0 0 broken assembly, complete expression
1 0 contiguous assembly, no expression
1 0 contiguous assembly, partial expression
0 0 contiguous assembly, complete expression

0 0 THAP
1 0 RVT_1

0 0 Unknown
1 0 RT Gypsy-ERV

SWIRM TEs

CupinJmjC TEs

	0	0	0	0	0	Symicm
	0	0	0	0	0	Btremn
	0	0	0	0	0	P erkma
	0	0	0	0	0	Mbre
	0	0	0	0	0	Emue
	0	0	0	0	0	Morvir
	0	0	0	0	0	
	0	0	0	0	0	unknown
	0	0	0	0	0	no cluster
	0	0	0	0	0	mulexon
	0	0	0	0	0	monoxon
	0	0	0	0	0	cluster
	0	0	0	0	0	
	0	0	0	0	0	no evidence
	0	0	0	0	0	broken assembly
	0	0	0	0	0	partial expression
	0	0	0	0	0	broken assembly
	0	0	0	0	0	complete expression
	0	0	0	0	0	continuous assembly
	0	0	0	0	0	partial expression
	0	0	0	0	0	continuous assembly
	0	0	0	0	0	complete expression
	0	0	0	0	0	
	0	0	0	0	0	RVT_2
	0	0	0	0	0	RVT_1
	0	0	0	0	0	Nase_H
	0	0	0	0	0	integrase_HQC2
	0	0	0	0	0	DDE_trp_1_7
	0	0	0	0	0	
	0	0	0	0	0	
	0	0	0	0	0	Utpyosn
	0	0	0	0	0	Recombinase_Elements
	0	0	0	0	0	RTT_group
	0	0	0	0	0	RTT_R4-like
	0	0	0	0	0	Long_Terminal_Repeat_Element
	0	0	0	0	0	Gypsy-ERV

CupinJmjC.HG1.15:like:KDM8:likeclu:45
CupinJmjC.HG1.47:like:HIF1AN:likeclu:31
CupinJmjC.HG1.5:like:KDM8:likeclu:45
CupinJmjC.HG1.58:like:KDM8:likeclu:45
CupinJmjC.HG3.0:RIOX2
CupinJmjC.HG5.1:NA

BIR.HG1.0:BIRC5

BIR TEs

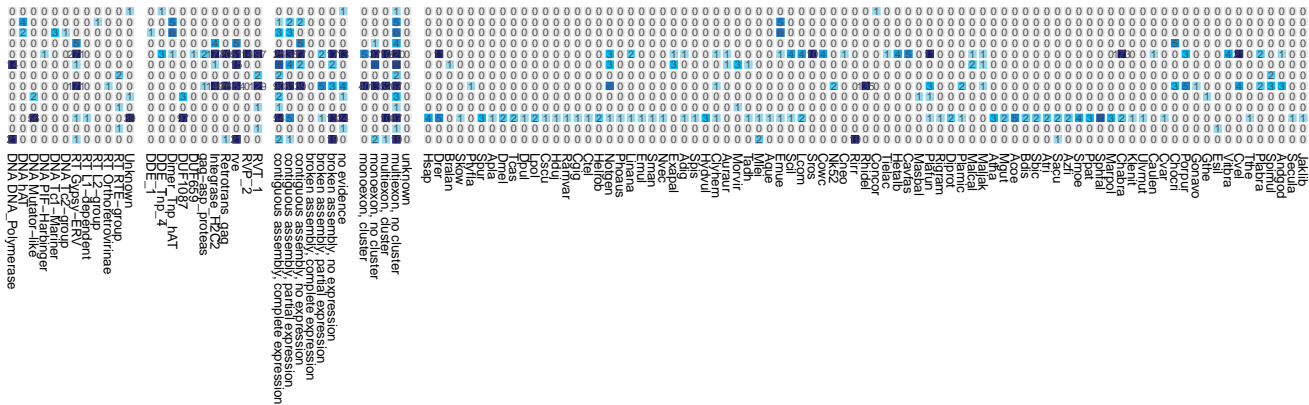
1	Noigen
0	unknown
1	multexon, no cluster
0	multexon, cluster
0	monoxon, no cluster
0	monoxon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
0	contiguous assembly, no expression
1	contiguous assembly, partial expression
1	contiguous assembly, complete expression
1	RV/T_1
1	RT CR1-group

Bromodomain TEs

[illegible]

Bromodomain.HG1.16:like:BRD2/BRD3/BRD...
Bromodomain.HG2.3:BRD7/BRD9
Bromodomain.HG3.10:KAT2A/KAT2B
Bromodomain.HG3.7:CECR2
Bromodomain.HG5.2:BAZ1A/BAZ1B/BAZ2A/B...
Bromodomain.HG7.1:BRWD1/BRWD3/PHIP

Chromo TEs



Chromo.HG.23.1like:CBX1/CBX3/CBX5like;
Chromo.HG.128.1like:CBX2/CBX6/CBX8/CBX9;
Chromo.HG.146.CDY1/CDY1B/CDY2A/CDY2B...
Chromo.HG2.0:NA
Chromo.HG2.1:NA
Chromo.HG3.0:NA
Chromo.HG3.4:NA
Chromo.HG3.m2/3.5:NA
Chromo.HG4.0.1like:AC006064.6/CHD1/CHD...
Chromo.HG4.0.2like:CHD1/CHD2
Chromo.HG4.2like:AC006064.6/CHD3/CHD4/CHD5
Chromo.HG5.2.1like:CHD6/CHD7/CHD8/CHD9...
Chromo.HG6.0:NA

MBT.HG1.1:PHF20L1
MBT.HG1.2:AL031681.3/L3MBTL1/L3MBTL2/...

MBT TEs	
<div><div></div><div></div></div>	Tcas
<div><div></div><div></div></div>	Dier
<div><div></div><div></div></div>	unknown, no cluster
<div><div></div><div></div></div>	multiexon, cluster
<div><div></div><div></div></div>	monoexon, no cluster
<div><div></div><div></div></div>	monoexon, cluster
<div><div></div><div></div></div>	no evidence
<div><div></div><div></div></div>	broken assembly, no expression
<div><div></div><div></div></div>	broken assembly, partial expression
<div><div></div><div></div></div>	broken assembly, complete expression
<div><div></div><div></div></div>	contiguous assembly, no expression
<div><div></div><div></div></div>	contiguous assembly, partial expression
<div><div></div><div></div></div>	contiguous assembly, complete expression
<div><div></div><div></div></div>	THAP
<div><div></div><div></div></div>	Unknown
<div><div></div><div></div></div>	DNA hat

MRG.HG1.1:MORF4L1/MORF4L2/MSL3

1	Chabra
0	unknown
0	multiexon, no cluster
0	multiexon, cluster
0	monoexon, no cluster
0	monoexon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
0	contiguous assembly, no expression
0	contiguous assembly, partial expression
0	contiguous assembly, complete expression
1	DDE_Tnp_4
1	DNA PIF-Harbinger

MRG TEs

PHD TEs

[illegible]

PWWP.HG1.8:AC098650.1/GLYR1/HDGFL1/HD...

1	Morvir
0	unknown
1	multiexon, no cluster
0	multiexon, cluster
0	monoexon, no cluster
0	monoexon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
0	contiguous assembly, no expression
0	contiguous assembly, partial expression
0	contiguous assembly, complete expression
1	RT RTE-group
1	RT_1

PWWP TEs

SAWADEE.HG1.1:NA

SAWADEE TEs

2	Chabra
0	unknown
2	multiexon, no cluster
0	multiexon, cluster
0	monoxon, no cluster
0	monoxon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
2	contiguous assembly, no expression
0	contiguous assembly, partial expression
0	contiguous assembly, complete expression
1	RVT_1
1	Integrase_H2C2
2	RT Gypsy-ERV

TUDOR TEs

[illegible]

zf-CW.HG1.14:AC098650.1/ZCWPW2
 zf-CW.HG1.16:MORC1/MORC2/MORC3/MORC4
 zf-CW.HG1.3:like:AC098650.1/KDM1B/MOR...

zf-CW TEs

0	1	0	Morvir
0	0	0	Bralan
0	0	0	unknown
1	1	0	multiexon, no cluster
0	0	0	multiexon, cluster
0	0	0	monoexon, no cluster
0	0	0	monoexon, cluster
0	0	0	no evidence
0	0	0	broken assembly, no expression
0	0	0	broken assembly, partial expression
0	0	0	broken assembly, complete expression
0	0	0	contiguous assembly, no expression
0	0	0	contiguous assembly, partial expression
0	0	0	contiguous assembly, complete expression
1	1	1	RV/T_1
0	0	1	lve
0	0	2	Integrase_H2C2
1	1	0	RT RTE-group
0	0	0	RT Gypsy-ERV

YEATS.HG1.6:YEATS2

YEATS TEs

1	Morvir
0	unknown
1	multexon, no cluster
0	multexon, cluster
0	monoxon, no cluster
0	monoxon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
1	broken assembly, complete expression
0	contiguous assembly, no expression
0	contiguous assembly, partial expression
0	contiguous assembly, complete expression
0	RVT_1
1	Integrase_H2C2
1	RT Gypsy-ERV

SNF2_N TEs

[illegible]

Daxx.HG1.0:DAXX

Daxx TEs

■	Cscu
■	unknown
■	multiexon, no cluster
■	multiexon, cluster
■	monoexon, no cluster
■	monoexon, cluster
■	no evidence
■	broken assembly, no expression
■	broken assembly, partial expression
■	broken assembly, complete expression
■	contiguous assembly, no expression
■	contiguous assembly, partial expression
■	contiguous assembly, complete expression
■	Transposase_1
■	RT Gypsy—ERV

Hira.HG1.0:HIRA

1	Skow
0	unknown
0	multiexon, no cluster
0	multiexon, cluster
0	monoexon, no cluster
0	monoexon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	contiguous assembly, complete expression
0	contiguous assembly, no expression
1	Integrase_H2C2
1	RT Long_Terminal_Repeat_Element

Hira TEs

NAP.HG1.1:like:NAP1L1/NAP1L2/NAP1L3/N...

NAP.HG1.5:like:NAP1L1/NAP1L2/NAP1L3/N...

NAP TEs

<div><div></div><div></div></div>	Chabra
<div><div></div><div></div></div>	unknown, no cluster
<div><div></div><div></div></div>	multiexon, cluster
<div><div></div><div></div></div>	monoexon, no cluster
<div><div></div><div></div></div>	no evidence
<div><div></div><div></div></div>	broken assembly, no expression
<div><div></div><div></div></div>	broken assembly, partial expression
<div><div></div><div></div></div>	broken assembly, complete expression
<div><div></div><div></div></div>	contiguous assembly, no expression
<div><div></div><div></div></div>	contiguous assembly, partial expression
<div><div></div><div></div></div>	contiguous assembly, complete expression
<div><div></div><div></div></div>	Ive
<div><div></div><div></div></div>	Integrase_H2C2
<div><div></div><div></div></div>	RT Gypsy-ERV

zf-CCHH.HG1.16:like:APLF:likeclu:6

zf-CCHH TEs

1	Symtic
0	unknown
0	multiexon, no cluster
1	multiexon, cluster
0	monoexon, no cluster
0	monoexon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
1	contiguous assembly, no expression
0	contiguous assembly, partial expression
0	contiguous assembly, complete expression
1	R/T_2
1	RT Long_Terminal_Repeat_Element

Dpy-30.HG1.6:like:NME5:likeclu:7

Dpy-30 TEs

1	Chabra	
0	unknown	
1	multiexon, no cluster	
0	multiexon, cluster	
0	monoexon, no cluster	
0	monoexon, cluster	
0	no evidence	
1	broken assembly, no expression	
0	broken assembly, partial expression	
0	broken assembly, complete expression	
0	broken assembly, no expression	
0	contiguous assembly, partial expression	
0	contiguous assembly, complete expression	
1	Me	
1	Integrase_H2C2	
1	RT Gypsy-ERV	

PTIP TEs

00000	Chka	
00000	Marvir	
00000	Hydvali	
00000	Spur	
00000	Pvita	
00000	unknown	
00000	multiexon	no cluster
00000	multiexon	cluster
00000	monoexon	no cluster
00000	monoexon	cluster
00000	no evidence	
00000	broken assembly	no expression
00000	broken assembly	partial expression
00000	coniguous assembly	no expression
00000	coniguous assembly	partial expression
00000	coniguous assembly	complete expression
00000	Trans_reg_C	
00000	Kv1.1	
00000	Helitron_like_N	
00000	Unknown	
00000	RT_LTE-group	
00000	RT_L2-group	
00000	RT_CRT	
00000	DNA Helicase	

PTIP.HG1.15:like:BRCA1/ECT2/MCPH1/PAX...
PTIP.HG1.25:MCPH1
PTIP.HG1.33:BRCA1
PTIP.HG1.9:ECT2
PTIP.HG3.0:like:RFC1:likeclu:4

PCRing.HG0.1:BMI1/COMMD3-BMI1/PCGF1/P...

PCRing TEs

- 1 Loom
- 2 Nitrogen
- 3 Ciel
- 4 unknown
- 5 unknown, no cluster
- 6 multixen, cluster
- 7 monoxen, no cluster
- 8 monoxen, cluster
- 9 no evidence
- 10 broken assembly, no expression
- 11 broken assembly, partial expression
- 12 broken assembly, complete expression
- 13 contiguous assembly, no expression
- 14 contiguous assembly, partial expression
- 15 contiguous assembly, complete expression
- 16 THAP
- 17 RVT_1
- 18 Unknown
- 19 R1 OR1-group

CAF1C.HG1.1:RBBP4/RBBP7

CAF1C TEs

1	Cscu
1	unknown
0	multexon, no cluster
1	multexon, cluster
0	monoxon, no cluster
0	monoxon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
0	contiguous assembly, no expression
1	contiguous assembly, partial expression
1	contiguous assembly, complete expression
1	THAP
1	Unknown

Kelch.HG0.1:like:FBXQ42/KLHDC1/KLHDC3...
Kelch.HG0.14:KLHDC3

Chabra

no evidence
broken assembly, no expression
broken assembly, partial expression
contiguous assembly, no expression
contiguous assembly, partial expression
contiguous assembly, complete expression

Kelch TEs

RVT_1
Integrase_H2C2
DUF659
RT_Gypsy-ERV
DNAI1A1

NA

2	Morvir
1	Gscu
1	Skow
0	unknown
0	multexon, no cluster
0	multexon, cluster
0	monoxon, no cluster
0	monoxon, cluster
0	no evidence
0	broken assembly, no expression
0	broken assembly, partial expression
0	broken assembly, complete expression
1	contiguous assembly, no expression
1	contiguous assembly, partial expression
1	contiguous assembly, complete expression
1	THAP
2	RT_1
1	Integrase_H2C2
2	Unknown
1	RT_RTE-group
1	RT_Long_Terminal_Repeat_Element

WD40 TEs