Table S1. Haplotype analysis of SF1 monomers

Monomers with box A

	Haplotype positions																	
Sequence name	**4**	**15**	**20**	**21**	**36**	**42**	**60**	**61**	**79**	**94**	**110**	**127**	**140**	**153**	**164**	**171**	**Simtc[1]**	**Simcc[2]**
cons A-type	C	C	G	G	T	G	A	C	G	T	A	G	G	T	T	G		
cons J1m master modern	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A		
cons_D2_AJ130752	C	C	G	G	T	G	C	C	G	T	A	G	G	T	T	G	15	0
cons_R2v2	C	T	G	G	T	G	A	C	G	T	A	G	G	T	T	G	15	0
cons_W4_AJ130761	C	C	G	G	T	G	A	C	G	A	A	G	G	G	T	G	14	2
cons_W5_AJ130762	C	G	G	G	T	A	A	T	G	T	G	G	G	C	T	G	11	4
Archaic monomers																		
S1C3H1L.9	T	T	T	G	T	T	A	T	T	A	A	G	T	T	C	G	7	4
S1C3H1L.10	T	T	A	G	T	A	C	C	G	G	A	C	A	T	T	G	8	2
S1C3H3d.1_cons	T	T	A	G	T	A	A	C	G	A	A	G	G	T	T	G	11	3
S1C3H3d.3_cons	T	T	A	G	T	A	A	T	T	A	G	T	G	T	T	G	7	7
S1C3H3d.5_cons	T	T	A	G	T	A	A	T	T	A	A	T	G	T	T	G	8	6
S1C3H2.1	T	T	A	G	T	A	A	C	G	A	C	G	G	T	T	G	10	3
S1C3H2.3	T	T	A	G	T	G	A	T	T	A	C	T	G	T	T	G	8	5
S1C3H2.5	T	T	A	C	T	A	A	C	T	G	A	T	G	G	T	G	7	5
S1C3H2.6	T	T	A	G	T	A	A	C	G	T	A	G	G	T	T	G	12	2
S1C3H2.8	T	T	A	G	T	A	G	T	T	A	G	T	G	T	T	G	6	8
S1C3H2.10	T	T	A	G	T	A	A	C	T	A	A	T	C	T	T	G	8	6
S1C6H1L.1	T	T	A	G	T	A	A	T	T	G	G	T	G	T	T	G	7	6
S1C6H1L.3	T	T	A	T	T	A	C	T	T	G	G	A	G	T	T	G	5	5
S1C6H1L.4	T	T	A	G	C	A	A	C	G	A	A	G	T	T	T	G	9	3
S1C6H1L.6	T	T	A	G	T	A	A	T	T	A	G	T	G	T	C	A	5	8
S1C6H1L.8	T	T	A	G	T	A	C	C	G	C	A	G	G	G	T	G	9	3
S1C6H1L.10	T	C	A	G	T	A	C	C	G	A	A	C	G	G	T	G	9	4
S1C6H1L.12	T	T	G	G	T	A	C	C	C	A	A	G	G	T	T	G	10	3
S1C6H1L.14	T	T	A	G	T	A	C	C	G	A	A	G	G	T	T	G	10	3
S1C6H1L.17	T	T	A	G	T	A	C	C	G	A	A	G	G	T	T	G	10	3
S1C12H3d.1_cons	T	T	A	G	T	A	A	C	G	A	A	C	G	G	T	G	9	4
S1C12H3d.3_cons	T	T	G	A	T	A	A	C	T	A	G	T	G	T	G/T	A	6	8
S1C12H3d.5_cons	T	T	G	G	G	A	A	T	T	A	C/G /A	T	G	T	G	A	5	8
S1C12H3d.6_cons	T	T	A	A	T	A	A	T	G	A	G	G	G	T	G	A	6	8
S1C12H3d.8_cons	T	T	A	G	T	A	A	T	T	A	A/G	T	G	T	T	G	7	6
S1CMH1d.1_cons	T	T	A	G	T	A	A	C	G	A	A	G	G	T	T	G	11	3
S1CMH1d.3_cons	T	T	A	G	T	A	A	T	T	A	G	T	G	T	G	A	5	9
Modern monomers																		
cons_J1_AJ130753	T	G	C	A	A	A	G	T	T	A/G	G	T	C	G	G	A	0	15
S1C1/5/19H1L.1	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	15
S1C1/5/19H1L.3	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	C	0	14
S1C1/5/19H1L.5	T	G	C	A	A	A	G	T	T	T	G	T	C	G	G	A	1	15
S1C3H1L.1	T	G	C	A	A	A	G	T	T	G	A	T	C	G	G	A	1	14
S1C3H1L.3	T	G	C	A	A	G	G	T	T	A	A	T	C	G	G	A	2	14

Table S1. Haplotype analysis of SF1 monomers

Monomers with box A

	Haplotype positions																	
Sequence name	**4**	**15**	**20**	**21**	**36**	**42**	**60**	**61**	**79**	**94**	**110**	**127**	**140**	**153**	**164**	**171**	**Simtc[1]**	**Simcc[2]**
cons A-type	C	C	G	G	T	G	A	C	G	T	A	G	G	T	T	G		
cons J1m master modern	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A		
S1C3H1L.5	T	A	C	T	A	A	G	T	T	G	A	G	C	G	G	C	2	10
S1C3H1L.7	T	G	C	T	A	A	G	T	T	A	G	T	C	G	G	A	0	15
S1C3H1L.12	T	G	C	A	A	A	G	T	T	G	G	T	C	C	T	G	2	12
S1C3H1L.14	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A	0	16
S1C3H1L.16	T	G	C	A	A	A	G	T	T	A	G	T	C	G	T	G	2	14
S1C5pH2.2	T	A	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	14
S1C5pH2.4	T	G	C	A	A	A	G	T	T	G	G	C	C	G	G	A	0	14
S1C5pH2.6	T	G	C	A	A	A	A	C	T	G	G	T	C	G	G	A	2	13
S1C5pH2.8	T	G	C	A	A	A	G	A	T	G	G	T	C	G	G	A	0	14
S1C5pH2.10	T	G	C	A	A	A	G	C	T	G	A	T	C	G	G	A	2	13
S1C5pH2.12	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A	0	16
S1C5pH2.14	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	15
S1C5pH2.16	T	G	C	A	A	A	T	T	T	G	G	T	C	G	G	C	0	13
S1C7H1L.1	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	15
S1C7H1L.3	T	G	C	T	A	A	A	A	T	T	G	T	C	G	G	A	2	12
S1C7H1L.5	T	G	C	A	A	A	A	A	T	A	C	T	C	A	G	A	1	12
S1C10/12H1d.1_cons	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A	0	16
S1C10H1-B.1	T	G	C	G	T	A	G	T	T	A	C	T	C	G	G	A	2	13
S1C10H1-B.3	T	G	C	A	A	A	A	T	T	A	G	T	A	G	T	A	2	13
S1C10H1-B.5	T	G	C	A	T	A	G	T	T	A	G	T	C	G	G	A	1	15
S1C10H1-B.7	T	G	C	A	A	T	G	T	T	A	G	T	C	G	G	A	0	15
S1C10H1-B.3.2	T	G	C	A	A	A	G	T	T	A	G	T	A	G	C	A	0	14
S1C10H1-B.5.2	T	G	C	A	T	A	G	T	T	A	G	T	C	G	G	A	1	15
S1C10H1-B.7.2	T	G	C	A	A	T	G	T	T	G	G	T	T	G	G	A	0	13
S1C10H1-C.1	T	G	C	A	A	A	G	T	T	A	C	T	A	G	A	A	0	13
S1C10H1-C.3	T	G	C	A	A	A	G	T	T	A	G	T	A	G	C	A	0	14
S1C10H1-C.5	T	G	C	A	T	A	G	T	T	A	G	T	A	G	G	A	1	14
S1C10H1-C.7	T	G	C	A	A	T	G	T	T	A	G	T	C	G	G	A	0	15
S1C10H1L.1	T	G	C	A	A	A	A	T	T	A	C	T	C	G	A	A	1	13
S1C10H1L.3	T	G	C	A	A	A	G	T	T	A	G	T	A	G	C	A	0	14
S1C10H1L.5	T	G	C	A	T	A	G	T	T	A	G	T	C	G	G	A	1	15
S1C10H1L.7	T	G	C	A	A	T	G	T	T	G	G	C	C	G	G	A	0	13
S1C10H2.1	T	G	C	A	A	A	G	T	T	A	G	T	A	G	C	A	0	14
S1C10H2.3	T	G	C	T	A	A	G	T	T	A	G	T	C	G	A	A	0	14
S1C10H2.5	T	G	C	A	A	A	G	T	T	A	G	T	A	G	T	A	1	14
S1C10H2.7	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A	0	16
S1C10H2.9	T	G	C	A	A	A	G	A	T	A	G	T	C	G	C	A	0	14
S1C10H2.11	T	G	C	A	A	A	G	T	T	T	G	T	C	G	C	A	1	14
S1C10H2.13	T	G	C	A	A	A	G	T	C	G	G	T	C	G	T	A	1	13
S1C10H2.15	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A	0	16

Table S1. Haplotype analysis of SF1 monomers

Monomers with box A

	Haplotype positions																	
Sequence name	**4**	**15**	**20**	**21**	**36**	**42**	**60**	**61**	**79**	**94**	**110**	**127**	**140**	**153**	**164**	**171**	**Simtc[1]**	**Simcc[2]**
cons A-type	C	C	G	G	T	G	A	C	G	T	A	G	G	T	T	G		
cons J1m master modern	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A		
S1C10H2.17	T	G	C	A	A	A	G	A	T	A	G	T	C	G	C	A	0	14
S1C12H1L.1	T	G	C	A	A	A	G	T	T	A	G	T	G	G	G	A	1	15
S1C12H1L.3	T	G	C	A	T	A	T	T	T	T	G	T	G	G	G	A	3	12
S1C12H1L.5	T	G	C	A	A	A	G	T	T	A	G	T	C	G	G	A	0	16
S1C12H1L.7	T	G	C	A	A	A	G	T	T	A	G	T	G	G	C	A	1	14
S1C12H2.1	T	G	C	A	A	A	G	T	T	A	G	T	C	G	-	A	0	15
S1C12H2.3	T	A	C	A	A	A	A	T	T	A	G	T	C	G	G	A	1	14
S1C12H2.5	T	G	G	T	A	A	G	T	T	A	G	T	C	G	G	A	1	14
S1C12H2.7	T	G	C	A	A	A	G	T	T	A	G	T	C	A	C	A	0	14
S1C12H2.9	T	G	C	G	A	A	G	T	T	A	G	T	G	G	C	A	2	13
S1C12H2.11	T	A	C	A	A	A	G	T	T	A	G	T	C	G	G	T	0	14
S1C12H2.13	T	G	C	A	A	A	G	T	T	A	G	T	C	A	C	A	0	14
S1C12H2.15	T	G	T	A	A	A	G	T	T	A	G	T	G	G	C	A	1	13
S1C12H2.17	T	G	C	A	A	A	G	T	T	A	G	T	C	G	C	A	0	15
S1C16H1L.1	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	15
S1C16H1L.3	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	15
S1C16H1L.5	T	G	C	A	A	A	G	T	T	C	G	T	C	G	G	A	0	15
S1C16H1L.7	T	G	C	A	A	A	G	T	T	G	G	T	C	G	G	A	0	15
S1C16H1L.9	T	G	C	A	A	A	C	T	T	G	G	T	C	G	G	A	0	14

Table S1. Haplotype analysis of SF1 monomers

Monomers with box B

	Haplotype positions																
Sequence name	**2**	**52**	**54**	**61**	**66**	**67**	**68**	**80**	**89**	**102**	**109**	**139**	**142**	**150**	**170**	**Simtc[1]**	**Simcc[2]**
cons B-type	A	A	A	C	A	A	A	C	A	A	C	T	T	G/T	A		
cons J2m master modern	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G		
cons_D1_AJ130751	A	A	A	T	A	A	T	C	A	A	C	T	T	G	A	13	1
cons_R1_AJ130756	A	A	A	C	A	A	A	C	A	A	C	T	T	T	A	15	0
cons_W1_AJ130758	A	T	A	C	-	-	-	C	A	A	C	-	T	G	A	10	1
cons_W2_AJ130759	A	A	A	C	A	A	C	C	A	A	C	T	T	T	G	13	1
cons_W3_AJ130760	A	T	A	C	A	A	A	C	A	A	T	T	C/T	C	A	11	1
Archaic monomers																	
S1C3H1L.8	G	-	T	T	A	C	-	A	A	A	C	G	A	T	A	6	6
S1C3H3d.2_cons	A	-	T	T	A	A	-	A	A	A	C	C	T	T	A	9	5
S1C3H3d.4_cons	A	-	T	T	A	A	-	A	A	A	C	C	T	T	A	9	5
S1C3H2.2	A	-	T	T	A	A	-	A	A	A	C	C	T	T	A	9	5
S1C3H2.4	A	-	T	T	A	A	-	A	A	A	C	C	T	C	A	8	5
S1C3H2.7	G	-	T	T	A	A	-	A	A	A	C	C	T	T	A	8	6
S1C3H2.9	A	-	T	T	A	C	-	A	A	A	C	T	T	G	A	9	5
S1C6H1L.2	A	-	T	T	C	T	-	A	A	A	C	T	C	T	A	7	6
S1C6H1L.5	A	-	T	T	C	C	-	A	A	A	C	T	T	T	A	8	5
S1C6H1L.7	G	A	G	C	A	A	G	T	A	A	T	T	G	T	A	9	2
S1C6H1L.9	A	-	T	T	A	C	-	A	A	A	C	T	T	T	A	9	5
S1C6H1L.11	A	-	T	T	A	C	-	A	A	A	A	T	T	T	A	8	5
S1C6H1L.13	A	-	T	T	A	T	-	A	A	T	C	G	T	-	A	6	6
S1C6H1L.15	A	-	T	T	C	T	-	A	A	A	C	T	T	T	A	8	5
S1C6H1L.16	A	-	T	T	A	T	-	A	A	A	C	G	T	T	A	8	5
S1C6H1L.18	A	-	T	T	A	C	-	A	T	A	C	T	T	T	A	8	6
S1C12H3d.2_cons	A	-	T	T	A	A	-	A	A	A	T	C	T	T	A	8	6
S1C12H3d.4_cons	G	-	T	T	A	A	-	A	A	A	C	T	T	T	T	8	6
S1C12H3d.7_cons	G	-	T	T	A	A	-	A	A	A	T	C	T	T	A	7	7
S1CMH1d.2_cons	A	-	T	T	A	A	-	A	A	A	C	T	T	A/T	A	9	5
S1CMH1d.4_cons	G	A	A	C	A	A	A	T	A	A	T	T	T	T	A	12	2
Modern monomers																	
cons J2	G	-	T	T	T	G	-	A	T	T	T	A	C/T	A	G	0	14
S1C1/5/19H1L.2	G	-	T	T	G	C	-	A	T	T	C	A	C	A	G	1	12
S1C1/5/19H1L.4	T	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	14
S1C1/5/19H1L.6	C	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	13
S1C3H1L.2	G	-	T	T	T	G	-	A	G	G	T	A	C	A	G	0	13
S1C3H1L.4	T	-	T	C	T	G	-	A	T	A	T	A	C	A	G	2	12
S1C3H1L.6	G	-	T	T	T	T	T	A	T	-	T	A	C	A	G	0	12
S1C3H1L.11	A	-	T	T	T	G	-	A	G	G	T	A	C	A	G	1	12
S1C3H1L.13	A	-	T	T	T	G	-	A	T	T	T	A	A	A	G	1	13
S1C3H1L.15	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C3H1L.17	A	-	T	T	T	G	-	A	T	T	T	A	C	A	G	1	14
S1C5pH2.1	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15

Table S1. Haplotype analysis of SF1 monomers

Monomers with box B

	Haplotype positions																
Sequence name	**2**	**52**	**54**	**61**	**66**	**67**	**68**	**80**	**89**	**102**	**109**	**139**	**142**	**150**	**170**	**Simtc[1]**	**Simcc[2]**
cons B-type	A	A	A	C	A	A	A	C	A	A	C	T	T	G/T	A		
cons J2m master modern	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G		
S1C5pH2.3	G	-	T	T	G	G	-	A	T	T	T	A	T	A	G	1	13
S1C5pH2.5	G	-	T	T	T	G	-	A	T	T	T	A	T	A	G	1	14
S1C5pH2.7	G	-	T	T	G	G	-	A	T	T	T	A	T	A	G	1	13
S1C5pH2.9	G	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	14
S1C5pH2.11	A	-	T	T	T	G	-	A	T	T	T	A	T	A	G	2	13
S1C5pH2.13	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C5pH2.15	G	-	T	T	G	G	-	A	T	T	T	A	C	A	G	0	14
S1C7H1L.2	G	-	T	T	T	G	-	A	T	T	C	A	C	A	G	1	14
S1C7H1L.4	G	-	T	T	T	G	-	A	T	C	T	A	C	A	G	0	14
S1C7H1L.6	G	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	14
S1C10/12H1d.2_cons	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C10H1-B.2	G	-	T	T	C	G	-	A	T	T	C	A	G	A	G	1	12
S1C10H1-B.4	G	-	T	T	T	G	-	A	T	T	T	G	G	A	G	0	13
S1C10H1-B.6	G	-	T	T	T	G	-	A	T	T	T	A	C	T	G	1	14
S1C10H1-B.8	G	-	T	T	T	G	-	A	T	T	A	A	C	C	G	0	13
S1C10H1-B.2.2	G	-	T	T	C	G	-	A	T	T	C	A	G	A	G	1	12
S1C10H1-B.4.2	G	-	T	T	T	T	-	A	T	T	T	A	G	A	G	0	13
S1C10H1-B.6.2	G	-	T	T	T	G	-	A	T	T	T	A	C	T	G	1	14
S1C10H1-C.2	G	-	T	T	C	G	-	A	T	T	T	A	G	A	G	0	13
S1C10H1-C.4	G	-	T	C	T	G	-	A	T	T	T	A	G	A	G	1	13
S1C10H1-C.6	G	-	T	T	C	G	-	A	T	T	T	A	C	T	G	1	13
S1C10H1-C.8	G	-	T	T	T	G	-	A	T	C	T	A	C	T	G	1	13
S1C10H1L.2	G	-	T	T	C	G	-	A	T	T	T	A	G	A	G	0	13
S1C10H1L.4	G	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	14
S1C10H1L.6	G	-	T	T	T	G	-	A	T	T	T	A	C	T	G	1	14
S1C10H1L.8	G	-	T	T	T	G	-	A	T	T	T	A	C	T	G	1	14
S1C10H2.2	G	-	T	T	T	G	-	A	T	T	T	A	A	T	G	1	13
S1C10H2.4	G	-	T	T	T	G	-	T	T	T	T	A	G	A	G	0	13
S1C10H2.6	G	-	T	T	T	G	-	C	T	T	T	A	C	A	G	1	14
S1C10H2.8	G	-	T	T	T	C	-	A	T	T	C	A	C	T	G	2	12
S1C10H2.10	G	-	T	T	T	G	-	A	T	C	T	A	C	A	G	0	14
S1C10H2.12	G	-	T	T	T	G	-	A	T	T	T	A	C	A	T	0	14
S1C10H2.14	G	-	T	T	T	G	-	C	T	T	T	A	C	A	G	1	14
S1C10H2.16	G	-	T	T	T	G	-	A	T	T	C	A	C	T	G	2	13
S1C10H2.18	G	-	T	T	T	G	-	A	T	T	C	A	G	A	G	1	13
S1C12H1L.2	G	-	T	T	T	G	-	A	T	C	T	A	-	A	G	0	13
S1C12H1L.4	G	-	T	A	T	G	-	A	T	G	T	A	C	A	G	0	13
S1C12H1L.6	G	-	T	T	C	G	-	A	T	T	T	A	C	A	G	0	14
S1C12H1L.8	G	-	T	T	T	G	-	A	T	G	T	A	A	A	G	0	13
S1C12H2.2	G	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	14

Table S1. Haplotype analysis of SF1 monomers

Monomers with box B

	Haplotype positions																
Sequence name	**2**	**52**	**54**	**61**	**66**	**67**	**68**	**80**	**89**	**102**	**109**	**139**	**142**	**150**	**170**	**Simtc[1]**	**Simcc[2]**
cons B-type	A	A	A	C	A	A	A	C	A	A	C	T	T	G/T	A		
cons J2m master modern	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G		
S1C12H2.4	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C12H2.6	G	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	14
S1C12H2.8	A	-	T	T	T	G	-	A	T	T	T	A	A	A	G	1	13
S1C12H2.10	T	-	T	T	T	G	-	A	T	T	C	A	C	A	G	1	13
S1C12H2.12	G	-	T	T	T	G	-	A	T	T	T	A	G	A	G	0	14
S1C12H2.14	A	-	T	T	T	G	-	A	T	T	T	A	T	A	G	2	13
S1C12H2.16	G	-	T	T	T	G	-	A	A	T	T	T	C	A	G	2	13
S1C12H2.18	G	-	T	T	T	G	-	A	T	G	T	A	C	A	T	0	13
S1C16H1L.2	G	-	T	T	G	G	-	A	T	T	C	A	C	A	G	1	13
S1C16H1L.4	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C16H1L.6	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C16H1L.8	G	-	T	T	T	G	-	A	T	T	T	A	C	A	G	0	15
S1C16H1L.10	G	-	T	T	G	G	-	A	T	T	T	A	C	A	G	0	14

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[1] A number of positions coinciding with type consensus. [2] A number of positions coinciding with class consensus.

Note to table S1.

Haplotype analysis was performed as described in [1] (see Supplementary note 1 there) and briefly summarized in section 2.2 of the main text in this paper. Slight changes in consensus monomers used are described in section 2.10 of the main text in this paper and are shown in Table S3. Table S1 is divided in two sections (J1 and J2 haplotypes) with archaic monomers shown in the upper part of each section and modern monomers at the bottom. Type-specific A or B monomers and class-specific consensus monomers from which the type-specific monomers were derived are shown at the top of each section. J1m or J2m shared positions are marked pink, ancestral positions are marked grey, and non-informative positions are white. One can see that monomers of archaic HORs have only partial SF1 haplotypes and the monomers of modern HORs have complete or almost complete haplotypes.

Table S2. Divergence values for each monomer of 8 selected HORs

HOR name	Number of monomers	Min (%)	Max (%)	Mean (%)	Median (%)
S1C3H3d.1	150	0	22.75	13.38	13.45
S1C3H3d.2	148	0	22.49	13.49	13.61
S1C3H3d.3	156	0	24.26	14.21	14.12
S1C3H3d.4	160	2.37	25.6	14.68	14.79
S1C3H3d.5	144	1.18	25.15	14.91	14.79
S1C6H1L.1	302	0	5.26	1.04	1.17
S1C6H1L.2	303	0	6.06	1.05	0.6
S1C6H1L.3	304	0	14.37	1.71	1.76
S1C6H1L.4	302	0	8.77	0.89	0.58
S1C6H1L.5	301	0	11.98	0.72	0.59
S1C6H1L.6	302	0	5.26	0.64	0.58
S1C6H1L.7	303	0	7.83	0.74	0.58
S1C6H1L.8	303	0	9.04	0.51	0.58
S1C6H1L.9	303	0	16.36	0.43	0
S1C6H1L.10	303	0	11.7	1.24	1.17
S1C6H1L.11	303	0	6.55	1.52	1.78
S1C6H1L.12	303	0	5.92	0.93	0.58
S1C6H1L.13	302	0	6.63	1.07	0.61
S1C6H1L.14	301	0	4.71	0.75	0.59
S1C6H1L.15	302	0	6.51	1.2	1.18
S1C6H1L.16	301	0	10.65	0.62	0
S1C6H1L.17	301	0	5.26	0.34	0
S1C6H1L.18	303	0	16.07	1.18	1.19
S1C7H1L.1	297	0	5.52	1.34	1.1
S1C7H1L.2	316	0	10.17	1.64	1.67
S1C7H1L.3	319	0	13.41	1.25	0.55
S1C7H1L.4	301	0	11.73	1.92	1.67
S1C7H1L.5	292	0	10.86	1.41	1.1
S1C7H1L.6	293	0	12.14	0.99	0.55
S1C10H1L.1	695	0	11.98	3.03	2.92
S1C10H1L.2	465	0	11.52	2.93	2.96
S1C10H1L.3	234	0	7.06	1.46	1.18
S1C10H1L.4	179	0	15.06	4.53	4.19
S1C10H1L.5	428	0	15.66	2.27	1.75
S1C10H1L.6	517	0	11.24	3.21	2.99
S1C10H1L.7	702	0	11.11	2.73	2.92
S1C10H1L.8	698	0	13.17	2.77	2.41
S1C10/12H1d.1	27	2.34	21.76	14.14	14.2
S1C10/12H1d.2	29	2.98	22.02	13.22	13.02
S1C12H1L.1	307	0	11.67	2.43	1.66
S1C12H1L.2	296	0	16.29	2.48	1.69
S1C12H1L.3	296	0	11.17	2.26	1.73

Table S2. Divergence values for each monomer of 8 selected HORs

HOR name	Number of monomers	Min (%)	Max (%)	Mean (%)	Median (%)
S1C12H1L.4	296	0	10.67	2.74	2.25
S1C12H1L.5	299	0	13.33	2.77	1.67
S1C12H1L.6	313	0	11.73	2.42	2.22
S1C12H1L.7	311	0	9.44	1.45	1.1
S1C12H1L.8	311	0	11.17	1.94	1.67
S1C12H3d.1	5	2.94	12.43	7.89	6.82
S1C12H3d.2	6	5.33	13.02	8.64	8.28
S1C12H3d.3	6	4.19	12.28	8.97	8.98
S1C12H3d.4	15	5.39	17.86	11.42	11.31
S1C12H3d.5	15	4.19	14.04	10.26	9.94
S1C12H3d.6	5	2.92	12.35	9.32	9.94
S1C12H3d.7	4	5.33	11.98	8.15	7.44
S1C12H3d.8	5	4.73	14.62	8.98	9.06
S1CMH1d.1	44	3.51	21.69	13.09	12.94
S1CMH1d.2	26	8.28	21.43	14.09	14.2
S1CMH1d.3	24	6.47	25.15	14.63	14.62
S1CMH1d.4	24	4.09	21.64	13.47	13.61

Note to Table S2.

This Table presents the data used for the boxplot in Fig. 1, but separately for each monomer in a HOR. For divergent HORs, we used aligned monomers from the master regions utilized for MSA profiles (see Alignment file 1 and Legend to Fig. 1). We chose to use these relatively short but hand-picked and well studied regions to avoid possible problems with false recognition, rearranged monomers, etc., which would arise if we collected monomers genome-wide through the Table Browser. Such problems could exaggerate the divergence. The number of monomers in the master regions varied greatly because for some HORs longer continuous and relatively pure arrays were not available in the assembly. As very large arrays of homogeneous HORs were available in the RMs, we sought to obtain statistically robust estimates which would not be affected by possible more homogenous domains within arrays. As the divergence for polymorphic S1C10H1L appeared to be somewhat higher than for non-polymorphic homogenous HORs, we tested for possible effects of domain structure within the RM. We first determined the divergence in one more sample region, then mixed both samples and determined the divergence again. The results were similar. In conclusion, one can see that there is a large gap in divergence between homogenous and divergent HORs and S1C10H1L is somewhat more divergent than non-polymorphic homogenous HORs.

Table S3. Modifications to consensus monomers shown in Alignment files made for haplotype analysis

Sequence name (Alignment file 2 and 3)	Position	Base unmodified	Base modified
cons_A_type_AJ131207|modified|12-G|44-A_deleted	15	N	C
	153	N	T
cons_J1_AJ130753	94	N	A/G
	152	N	T/A
S1C10/12H1d.1_cons_th_0.50	26	N	C/A
S1C12H3d.3_cons_th_0.50	68	N	A/C
	131	N	A/C
	163	N	C/T
	164	N	G/T
S1C12H3d.5_cons_th_0.50	110	N	C/G/A
S1C12H3d.6_cons_th_0.50	95	N	C/G
S1C12H3d.8_cons_th_0.50	29	N	C/G
	110	N	A/G
cons_B_type_AJ131208	25	N	T
	68	N	A
	106	N	G
	131	N	C
	150	N	G/T
cons_J2_AJ130754|modified|19C-T|20A-G|63N-T|64N-A|65T-A|66G-T|67A-G|79A-G|80C-A|88T-G|89A-T|101T-G|102A-T|108T-G|109C-T|130N-C|138A-T|139TA|141C-A|142T-C|149A-G|150T-A|169G-T|170A-G	142	C	C/T
cons_D1_AJ130751	106	N	T
cons_W3_AJ130760	142	N	C/T
cons_R1_AJ130756	25	N	G
S1C12H3d.2_cons_th_0.50	158	N	A/C
S1C12H3d.7_cons_th_0.50	39	N	G/A/T
	47	N	C/T
	140	N	A/G
S1CMH1d.2_cons_th_0.50	150	N	A/T
S1CMH1d.4_cons_th_0.50	35	N	C/T

Note to Table S3.

Modifications made to consensus sequences for haplotype analysis are described in detail in section 2.10 of the main text. Unmodified consensus monomers are shown in Alignment files 2 and 3. Type and class consensus monomers there are the same that have been published in [1]. Modifications listed in the names of type A and J2 consensus monomers refer to the differences between consensus monomers published in [1] and the sequences deposited in GenBank previously (acession numbers are included in the name).

Table S4. HOR assignments of SF1/SF5 mixed AS regions in hg38 assembly (modified Table 4 from [1])

SF	Location	Position in hg38	Contig	Size (bp)[1]	HORs on dot-matrix	HORs identified in this paper
1/5	3p11.1	chr3:90482385-90722299	ABBA01004652.1, AEKP01209350.1, ABBA01004653.1, AEKP01209353.1, ABBA01004654.1, ABBA01004655.1, ABBA01004656.1	229,441	No HOR	Mainly S1C3H3d plus large piece of pure S1CMH1d.
1/5	3p11.1	chr3:90772554-91233510	GJ211866.1	460,956	HOR 1.7 kb	Pure S1C3H2.
1/5	3q11.1	chr3:91233782-91247547	GJ211867.1	13,765	No HOR other than AB dimer identity ~93%	S1C3H2-related made of hybrids. Misprocessed RM?
1/5	3q11.1	chr3:91247775-91286183	ABBA01000927.1, ABBA01000928.1, ABBA01000929.1, ABBA01000930.1, ABBA01000931.1	17,430	HOR 1.7 kb	Pure S1C3H2.
1/5	3q11.1	chr3:93716246-93725946	ABBA01026974.1	9700	No HOR	Pure S1CMH1d.
1/5	6q11.1	chr6:60230028-60241613	AC244258.2	11,401	No HOR	Small piece of S1C3H3 and larger S1CMH1d interspersed with pieces of S1C3H3.
1/5	6q11.1	chr6:61371445-61427364	AEKP01189806.1, AEKP01189805.1, AEKP01189804.1, AEKP01189803.1, AEKP01189802.1, FP325349.3	55,519	No HOR	Poorly covered[2] S1CMH1d interspersed with single S1C3H3 monomers.
1/5	8p11.1	chr8:43940231-43965733	AC127507.4, AC144576.3	22,886	No HOR	Poorly covered[2] S1CMH1d.
1/5	8q11.1	chr8:45946092-45971262	AC118650.5	22,549	No HOR	Poorly covered[2] S1CMH1d. SD of the above.
1/5	10p11.1	chr10:39548571-39555979	ABBA01020707.1	7408	No HOR	Pure S1CMH1d.
1/5	10q	chr10:41830204-41842397	BX322613.6	12,194	No HOR	S1CMH1d interspersed with S1C12H3.8 and S1C10/12H1 with a small piece of pure S1C10/12H1 at the end.
1/5	12p11.1	chr12:34686342-34715037	AC144535.4, AUXG01000432.1	28,658	No HOR	Large pure S1CMH1d and smaller pure S1C12H3d.
1/5	12q	chr12:37268020-37276031	ABBA01049496.1, AEKP01211346.1	8012	No HOR	Pure S1C12H3d.

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[1] Size has been corrected to exclude L1-repeats and gaps.

[2] Monomers which are not covered with SF1 HOR monomers mainly identify with SF5 class monomers and are invisible in the HOR-track.