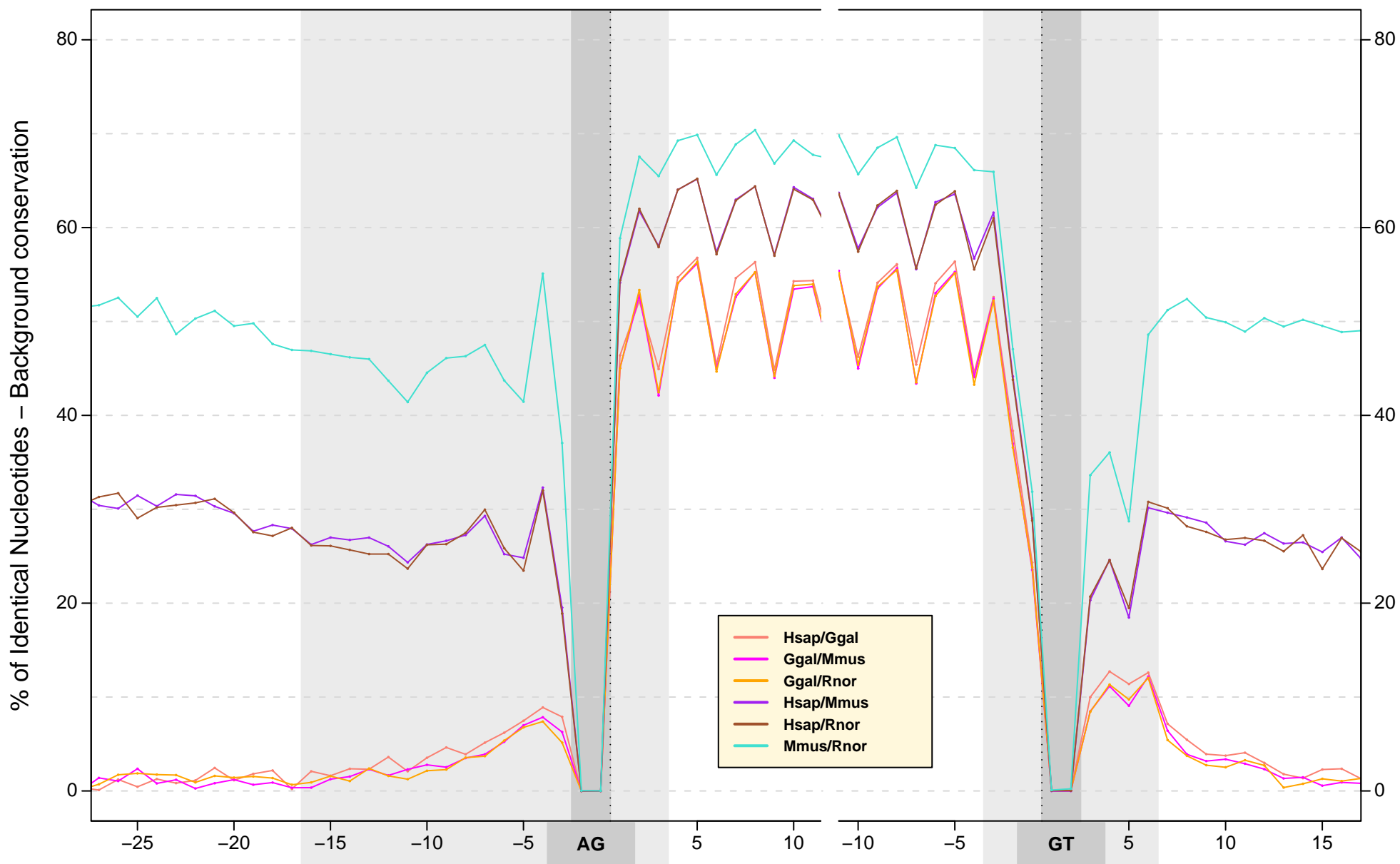
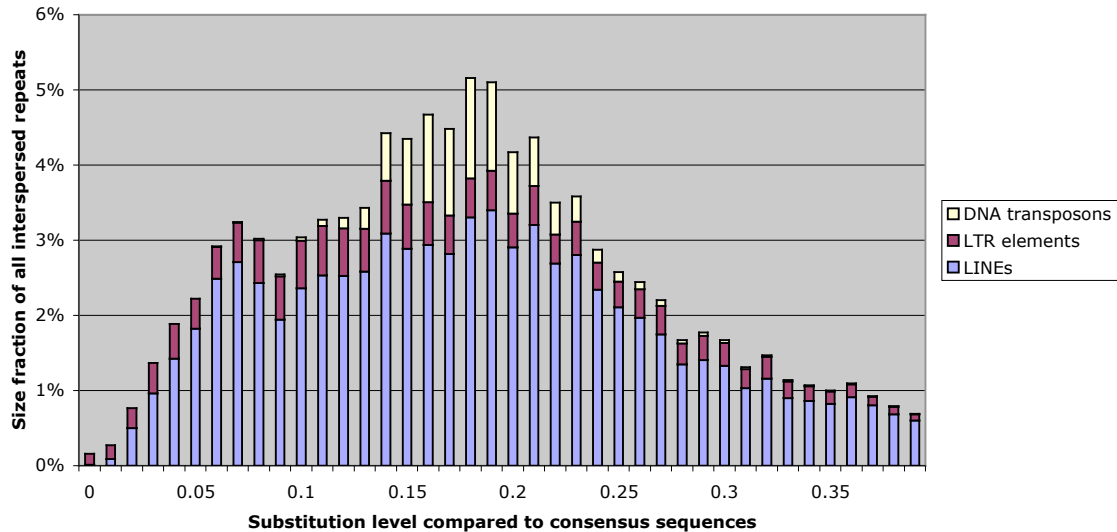


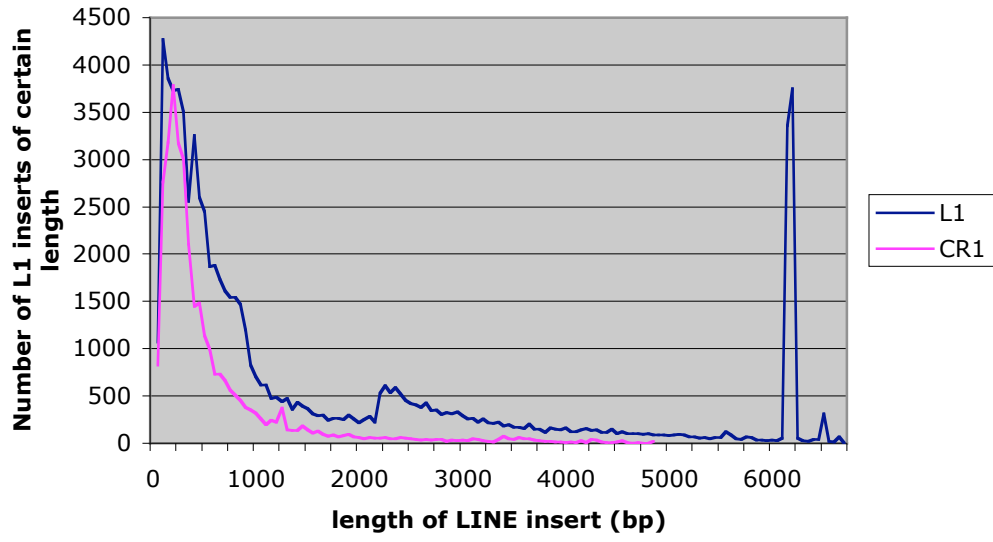
Sequence Conservation at 'U2' Splice Sites (aligned introns + unaligned background)

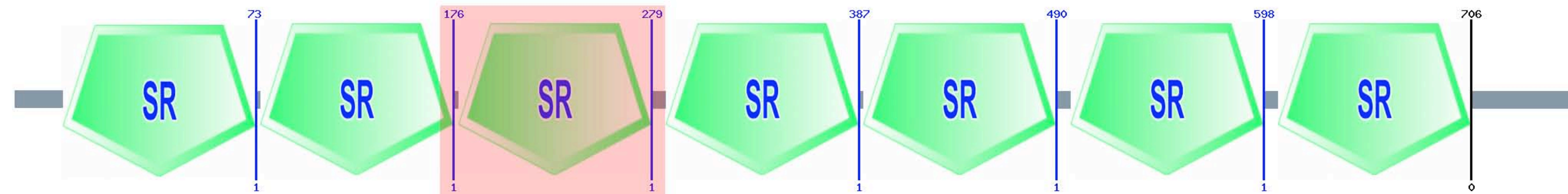


Nucleotide Position Relative to Acceptor and Donor Splice Sites (in bp)

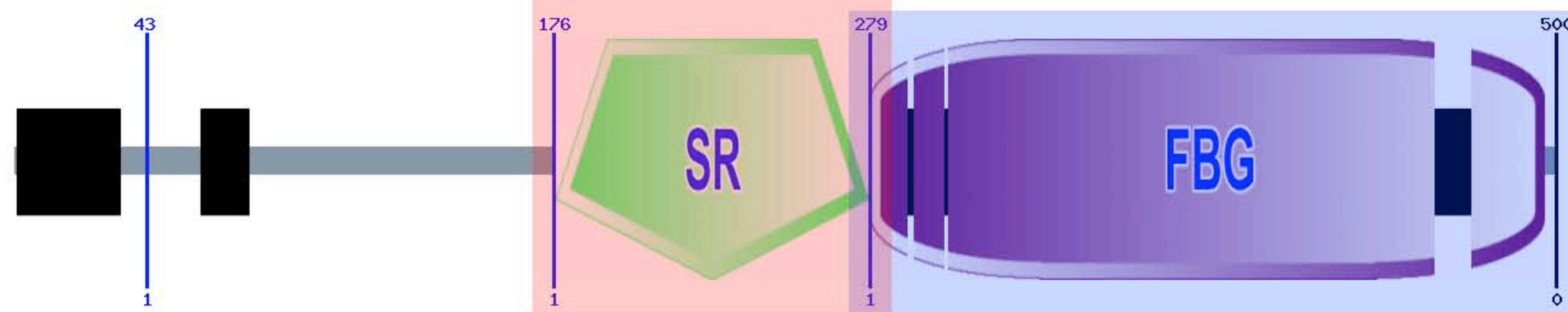


**Distribution of CR1 and L1 insertion sizes**

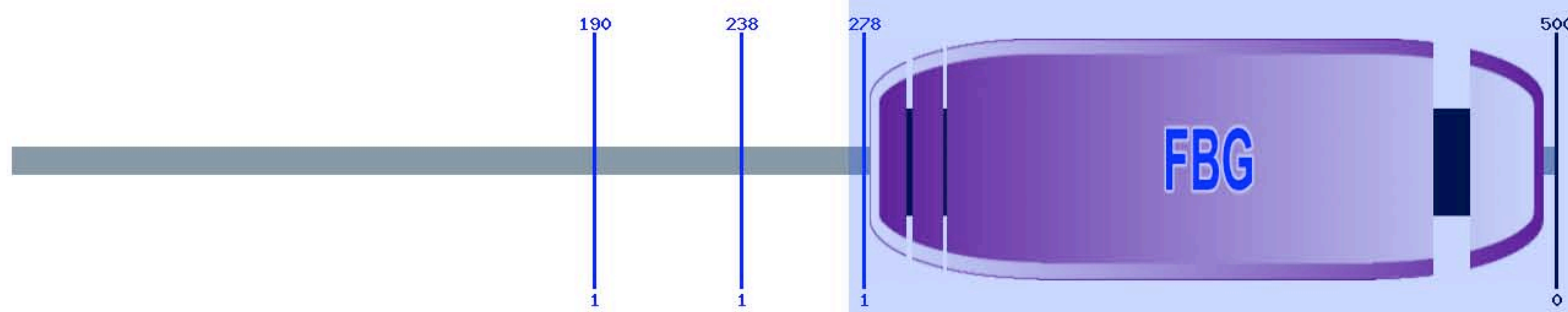




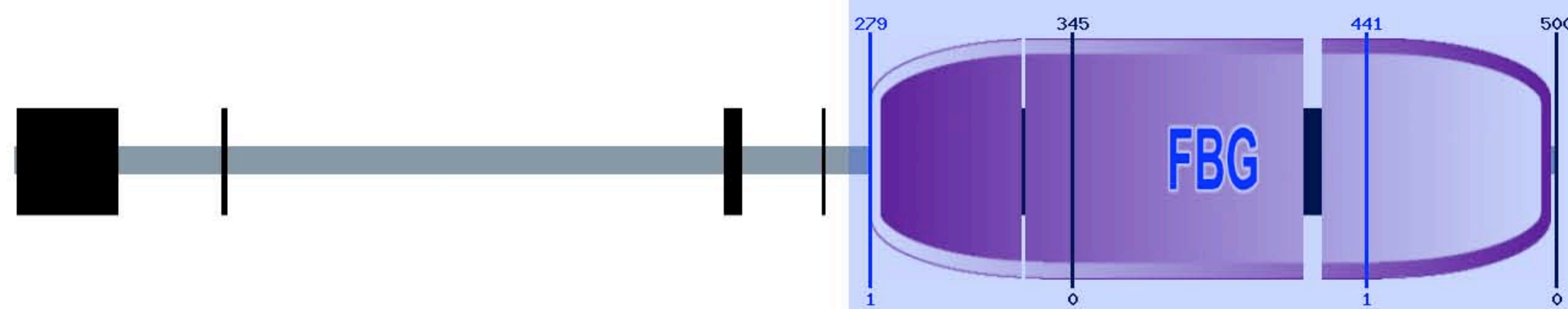
**ENSGALP00000014869**



**ENSGALP00000001164**

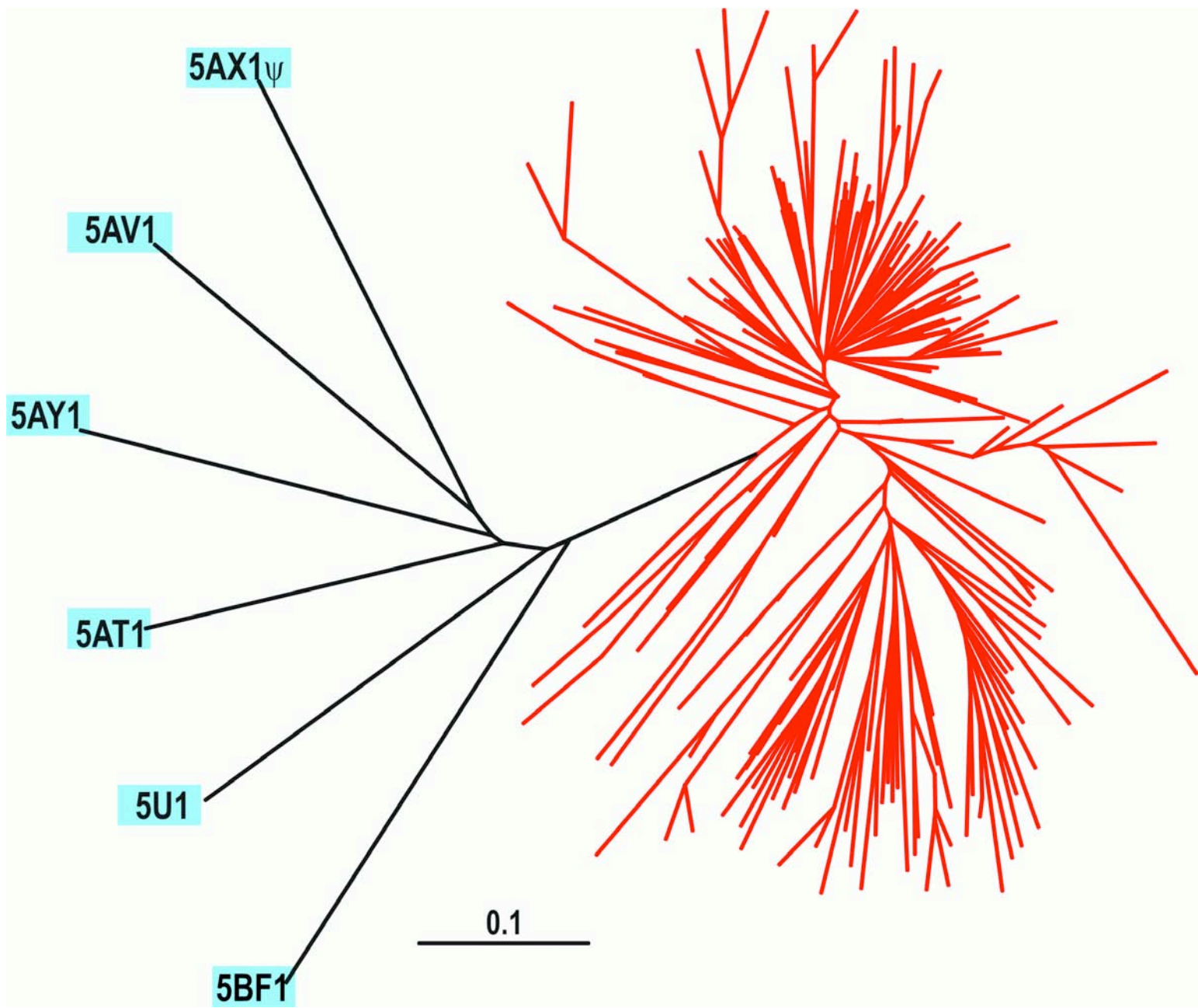


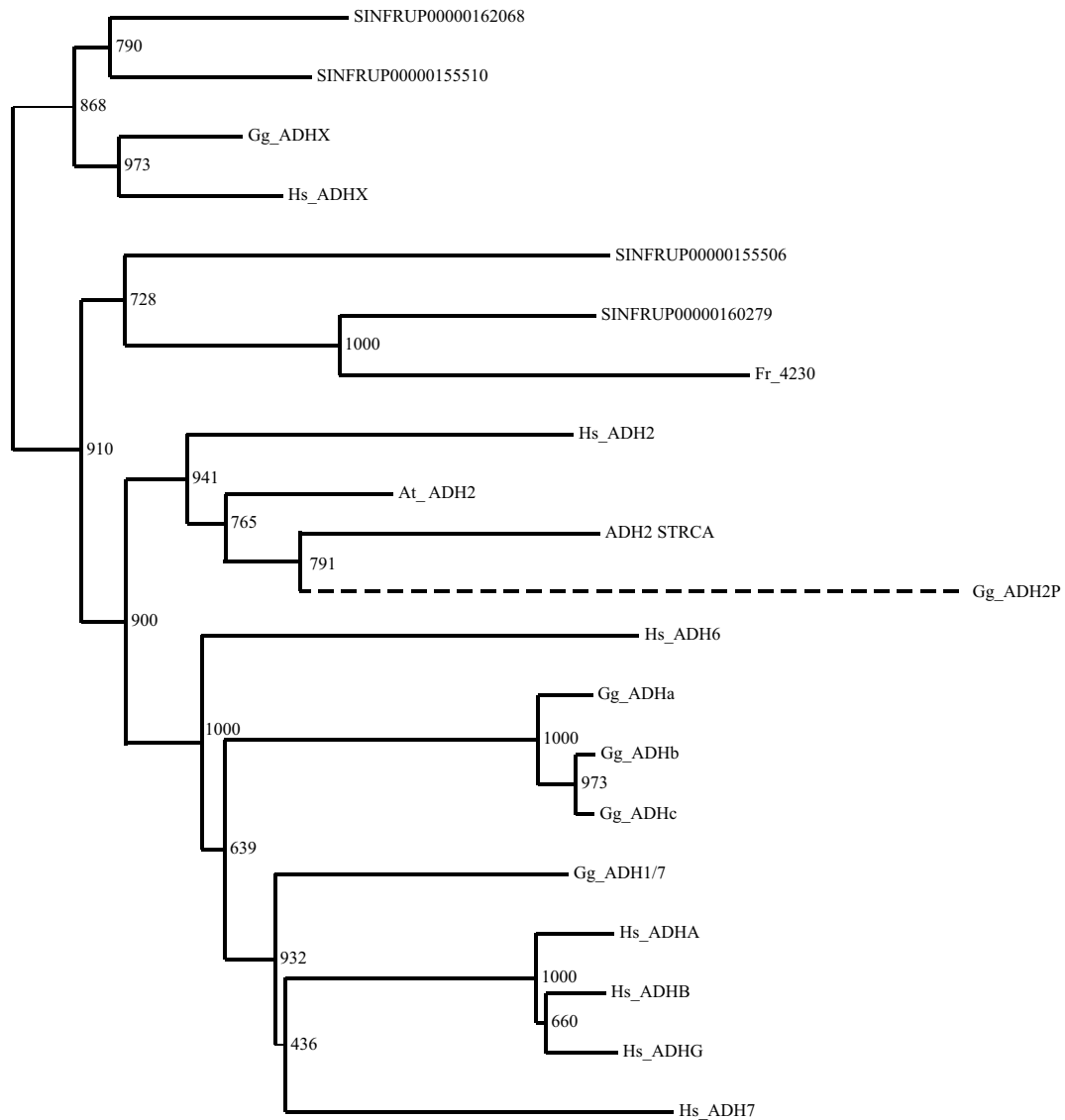
**ENSGALP00000001042**



**SINFRUP00000129054**







0.1

# A:

Human MTRILTAFKVVRITLKTGFGEINVTAHQKTKSRPGIRLLSVKAQTAHTVLEDGTKMKQYS  
Chick MTRILTACKMKITLGRLEICKVSA-DHSEWRSCTRLLSIIKAQTANVLEDGTKMKQYS

Human FGHPSVAGEVVFNTGLGSPEAITDPAIKGQILTMANPTIIGNGAPDITALDELGLSKY  
Chick FGYPSSTAGEVVFNTGISSEYTEAITDPSIKGQILTLANPVVGNCGVPDIAALDEIGRRF

Human LESNGIKVSGLLVLDYSKDNHWLATKSLGQMLQEEKVPAIYGVDRMTKIIIRDKGMML  
Chick LESDGIKVSGLLVLDYSNEISHWQAARSLGEWLQEEKVPAIYGVDRMTSKLIIRDKGTVL

Human GKIEFEGQPVDFVDPNKQNLIAEVSTKDVKVGKGNPTKVVAVDCGKIKNVIRLLVKRGA  
Chick GKIEFEGQPTFADPNKQNLIAEVSTKELRTAEGDYCFRMLMDCEVSLNIVLDTEGQGA

Human EVHLVPAWHDFTKMEYDGLIAGGPGNPALAEPLIQNVRKILESDRKEPLFCISTGNLIT  
Chick EVHLVPAWHDFTSMEYDGLISGGPGDEMKAEVLIQNVKVLLESNRKEPLFCIGMGNLIT

Human GLAAGAKTKKSMANRQNOQPVLNITNKQAFITAQNHGVALDN-TLPAEWKPLFVNVNDQ  
Chick GLAAGATSRQMANRQNOQPVNLTLSGQAVITAQNHAVALDSSTLPPWRPLFVNVNDQ

Human TNEGIMHESKPEFAVQPHPEVTPGPIDIEYLFDSFSLIKKQKATTITSVLPKPAIVASR  
Chick TNEGIMHETREIFETAQFYEDANPGPTDIEELFDSFISLVKRSKGTITIASVLPKAGATA SR

Human VEVSKVLILGSGCLSTICQAGEFDYSGSQAVKAMKEENVKTVLMNPNIASVQITNEVGLKQA  
Chick VEVSKVLILGSGCLSTICQAGEFDYSGSQAVKALKEENVKI VLMNPNIASVQITNETGLKQA

Human DTVYFLPITPQFVTEVIKAEQPDGLILEMGGQTALNCGVELFKRGVLKEYGVKVLGTSVE  
Chick DAVYFLPITPQFVTEVIKAEHPDGLILEMGGQTALNCGVELFKQGVLOQGVKVLGTSVE

Human SIMATEDRQLFSDKLNELNEKIAPSPFAVESIEDALKAA DTNGYPPVMIRSAVALGGLGSGT  
Chick SIMATEDRKLFSDKLMELNEKIAPSPFAVESIEDALEAAEKISYPPVMIRSAVALGGLGSGV

Human CPNRETLMDLSTKAFAMINQILVEKSVTEWKEIEYEVVRDADDNCVTVCNMENVDAMGVH  
Chick CTDKESLDLIGTKAFAVIKQILVEKSVVSWKEIEYEVVRDADDNCIACVNMENIDAMGVH

Human TGDVVVA PAQTLNAEFQMLRRTSINVVRLHGVIVGECNIQFALHPTSMEXCIIEVNARL  
Chick TGDVVVA PSQLTNEEFQMLRDRAIKVRYLDIVGECNIQFALHPTSLIYYTIEVNARL

Human SRSSALASKATCYPLAFIAAKIALGIPLEIKNVVSGKTSACEPESLD MVTKIPRNDLD  
Chick SRSSALASKATCYPLAFIAAKIALGIPLEIKNVVTGKTSAYFEPESLDVVTKIPRNDLD

Human RFHGTS SRIGSSMKSVGEVMAIGRTFEESEFQKALRMCHPSIEGFTPRLPNKKEWPSNLDL  
Chick RFQGTSNQIGSSMKSVGEVMAIGRTFEESEFQKALRMCHPSIDGFTSHLPNKKA WPAIADL

Human RKELSEPSSIRIYAIKAIADDNMSLDEIEKLYIDKWFLYKMRDILNMEKTLKGLNSESM  
Chick QKELSEPSSIRIYAMAKALENGVPVDVIEHKLTAIDKWFLCKMRSIVNMEKILKEVKHEEI

Human TEETLKRKEIGFSDKQISKCLGLTEAQTRELRKKNIH PWVKQIDTLAAEVPSVTNYLY  
Chick PEETIRKAKQMGFSDRQIGKCLGLTEVQCRQIRLRKNVVPWVKKIDTLAAEYPAVTNYLY

Human VTYNGQEHVNFDDHGMVVLGCGPYHIGSSVEFDWCAVSSIRTLRLQEGKKVVVVNCNPEI  
Chick VTYNGQEHDIKFDDCGVVVLGCGPYHIGSSVEFDWCAVSSIRTLRLQENKIVVVVNCNPEI

Human VSTDFDECDKLYFEELSLERILDIYHQEAGGSCIIISVGGQIPNNLAVPIYKNGVKIMCIS  
Chick VSTDFDECDRLYFEEMSLERILDIYQYEGGSCIIISVGGQIPNNLAVPIHQSGVKIFGTH

Human PLQIDRAEDRSIFSAVLDEIKVAQAPWKAVENTLNEALEYAKSVDYPCILRPSYVLSGSAM  
Chick PLQINRAEDRSIFSAVLDEIHLVAQAPWKAVENTLVDAVEFAGSVSYPCILRPSYVLSGSAM

Human NVVFSSEDEKKFLEEATRVSQEHPPVLTKEVEGAREVEMDAVGKDRVISHAISEHVEDA  
Chick NVVFTSEELKKFLVEATRVSQDHPVLTKEVEDAREVEMDAVAKAGRVIHAHAVSEHVEDA

Human GVHSGDATIMLPTQTISQGAIEKVKDAIRKIAKAFATISGPFNVQFLVKENDVLVIECNLR  
Chick GVHSGDATIMLPTQTISQGAIEKVKSAIKKIANAFATISGPFNVQFLVRENVLVIECNLR

Human ASRSFPFVSKTLGVDFLDVATKVMIGENVDEKHLPTLDHPITPADYVAIKAPMFSWPRVR  
Chick ASRSFPFVSKTLGVDFLDVATKVMIGKENESSLPTLEHPILPSKYIGIKAPVFSWSRVR

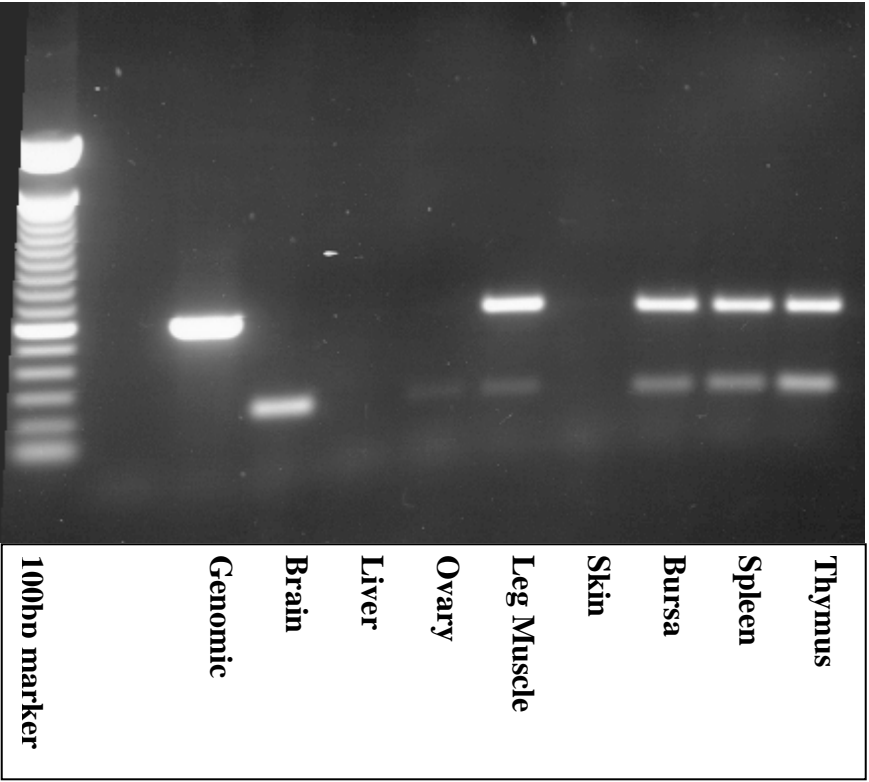
Human DADPILRCEMASTGEVACFGEGIHTAF LKAMLS TGFKLPQKGLILIGIQQSFRPRFLGVAE  
Chick DADPVLRCMASTGEVACFGEDEVYSAFQKAMLATGFTFPKQGLILIGIQQSFRPKFLGVAE

Human QLHNEGKLFATEATS DNLNANNVPATPVAWPSQEGQNPSSIRKLRDGSIDLVINLP  
Chick LLYGKGFKLYATEATS DNLNANGIPADPVAWPSQESLSPSLPPVRRLRDGGIDLVINLP

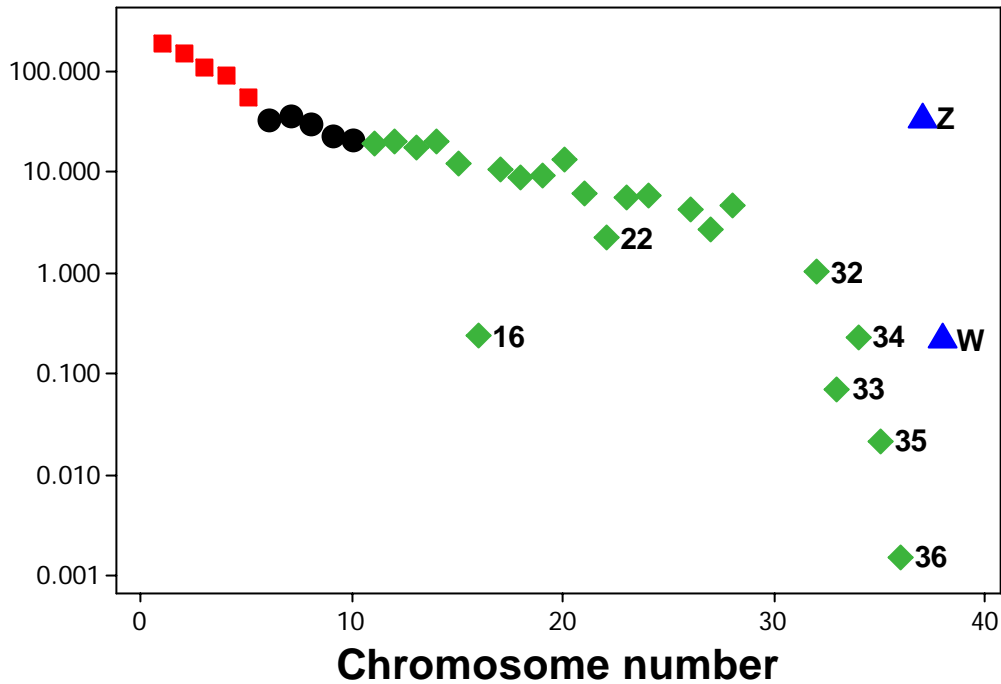
Human NNNTKFDHNVIRRTAVDSGIPLLTNFQVTKLFAEAVQKSRKVDKSLFHVROYSAGKAA  
Chick NSNTKFDHNVIRRMADSGIALLLTNFQVTKLFAEAIKYSGLKLDKSLFHVROFDKGDAA



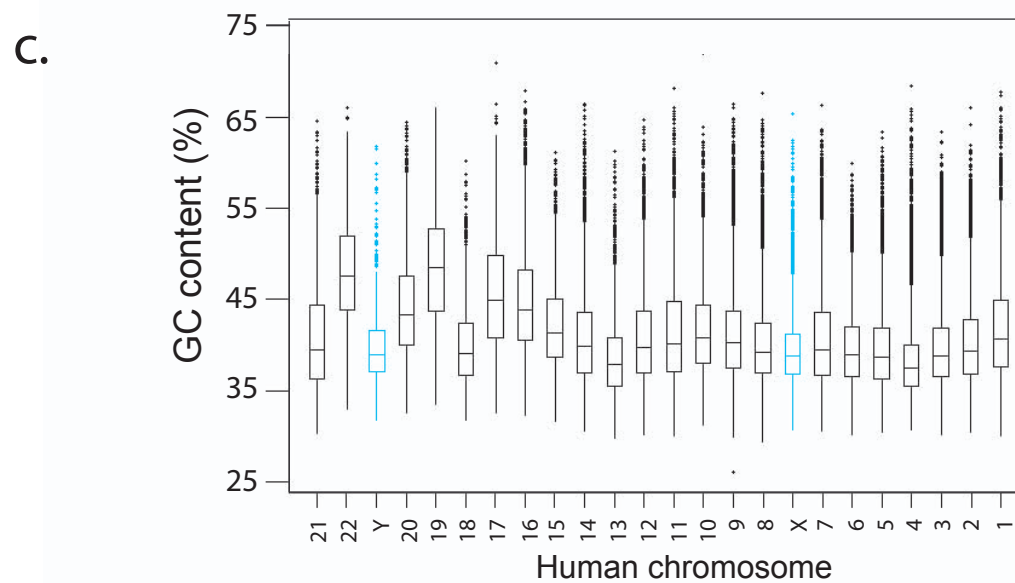
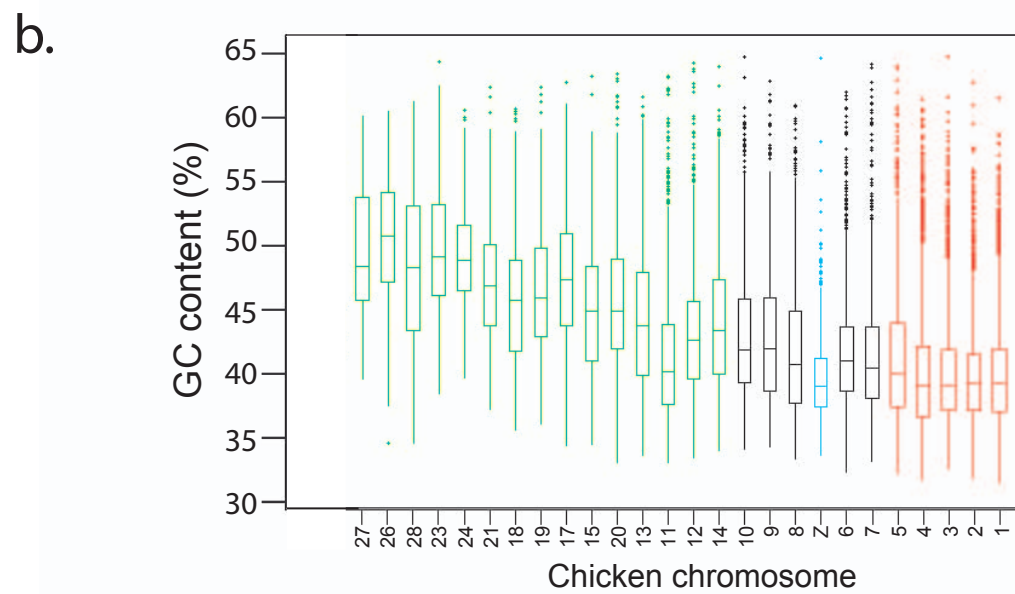
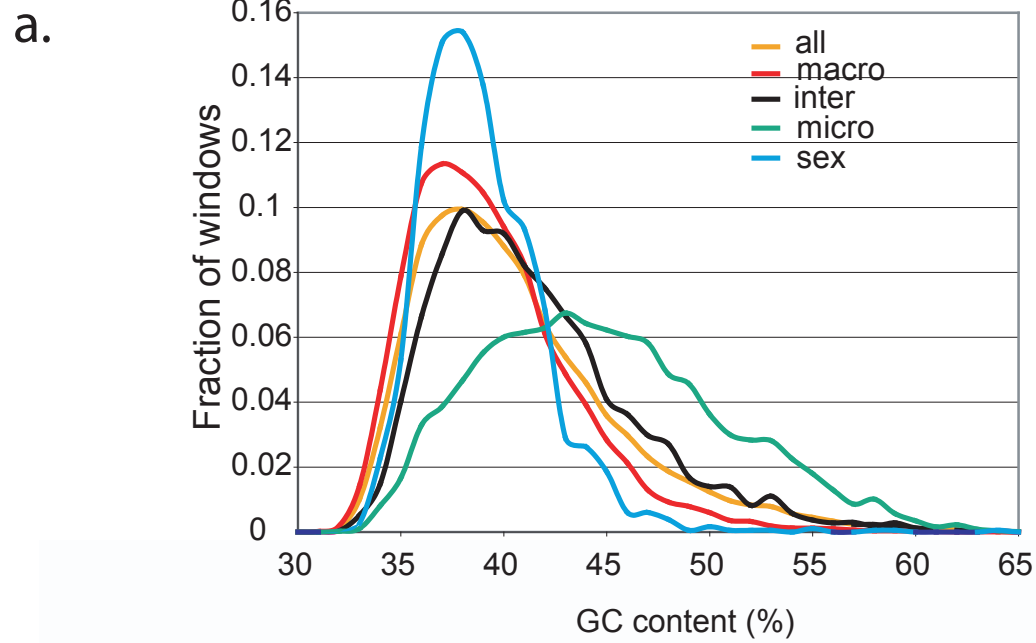
**B:**



**Chromosome length (Mb)**

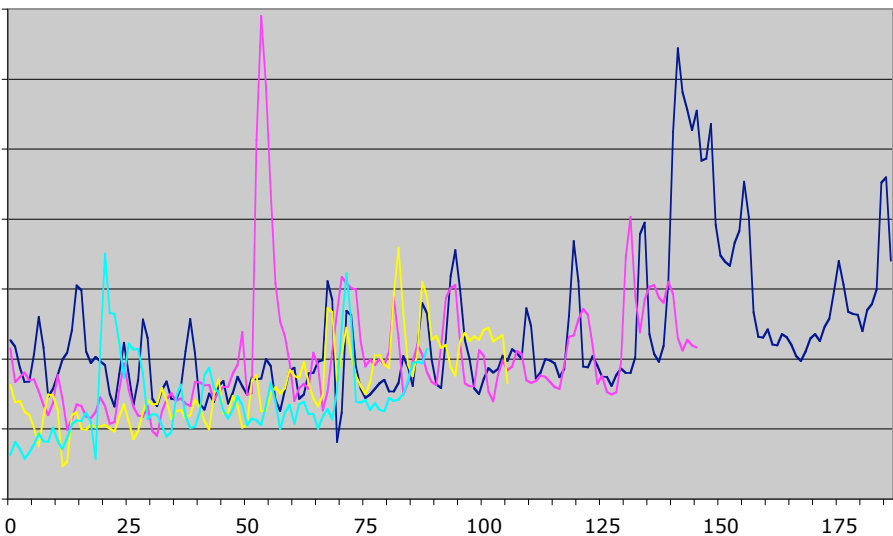




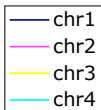


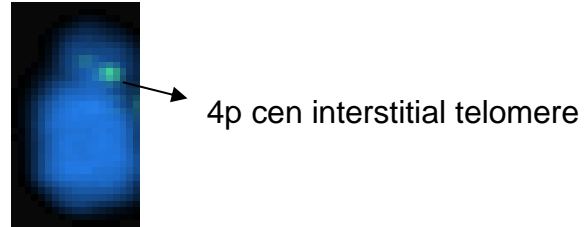
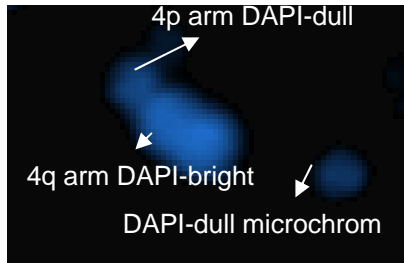
**Fraction of 2 Mbp window comprised by interspersed repeats**

0.35  
0.30  
0.25  
0.20  
0.15  
0.10  
0.05  
0.00

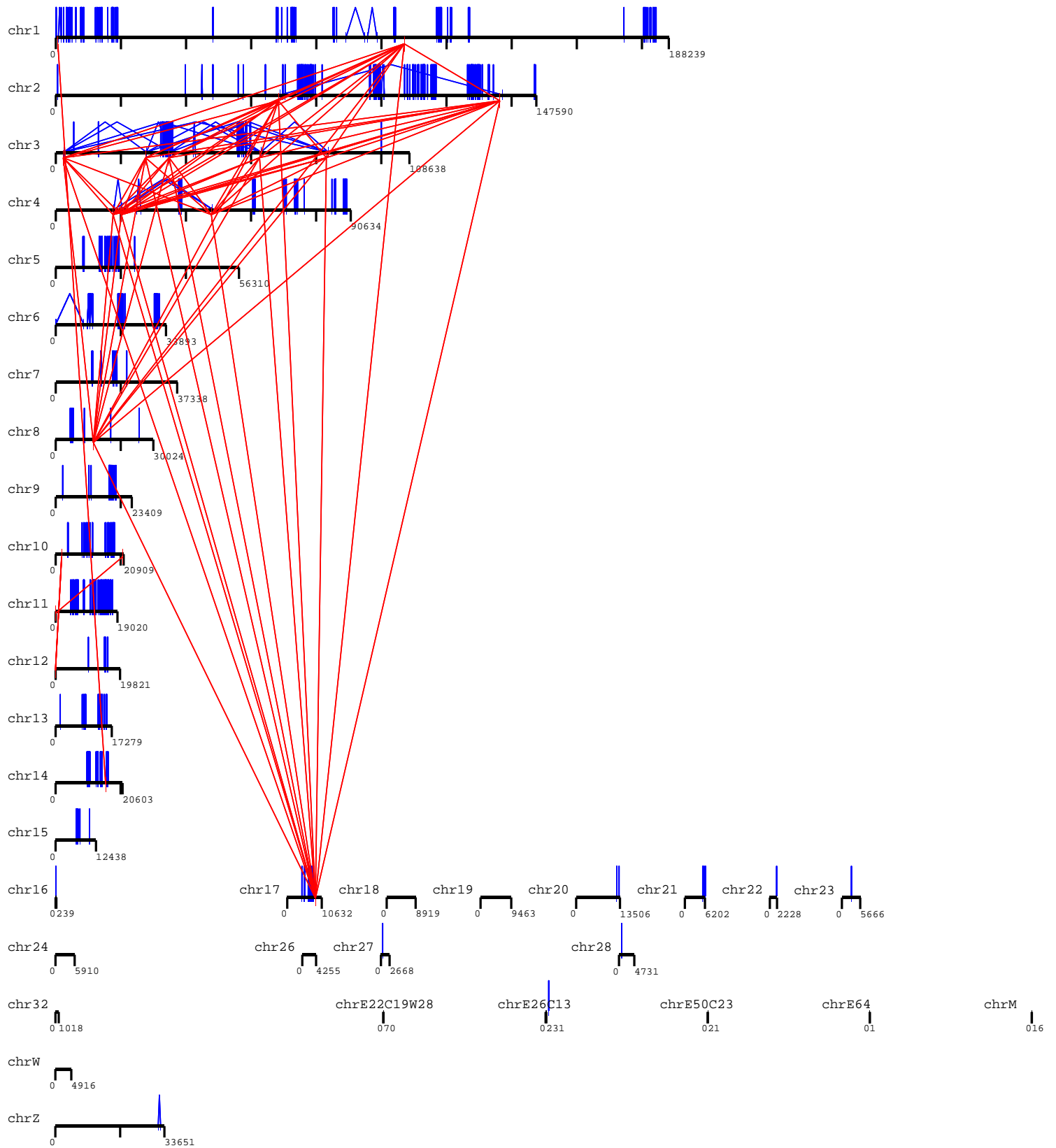


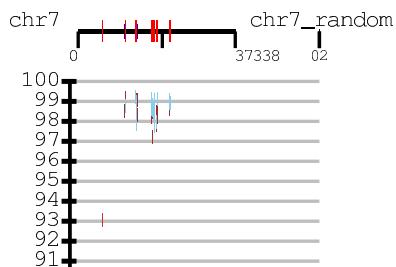
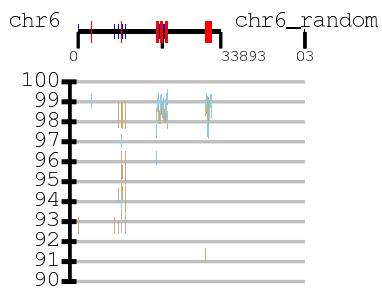
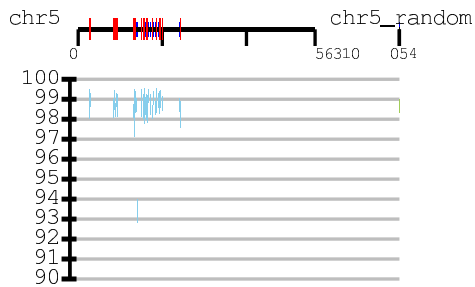
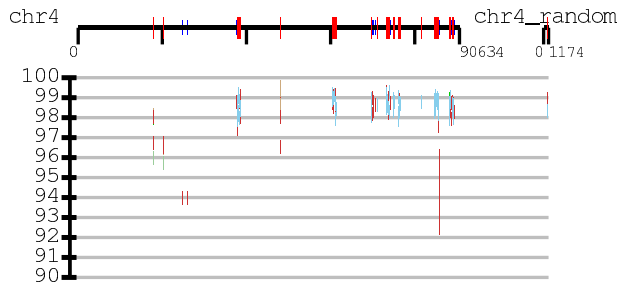
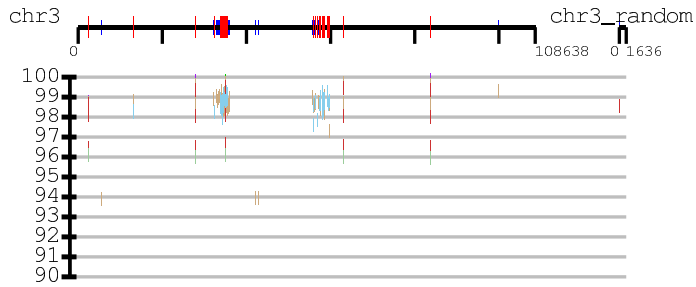
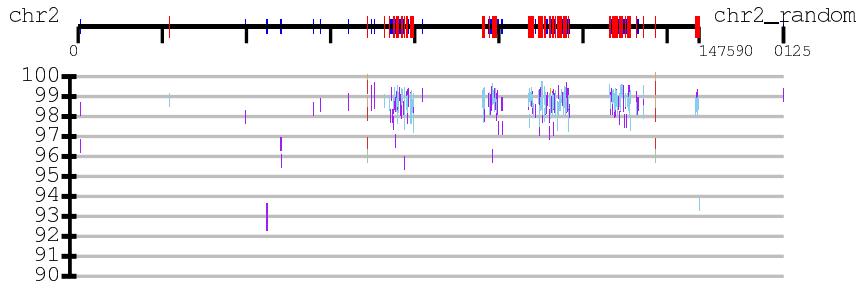
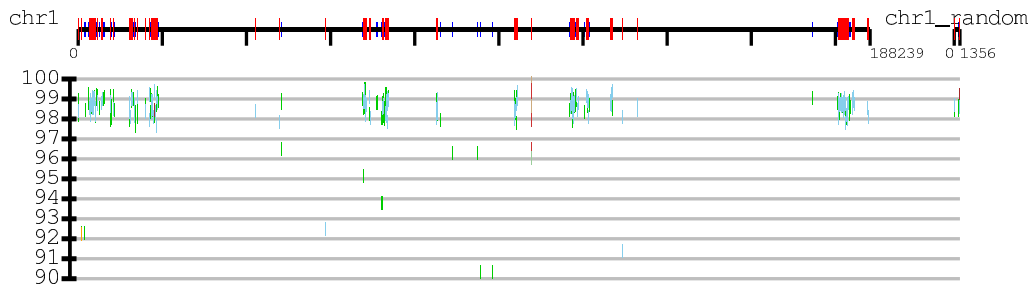
**Position along chromosome (Mbp)**

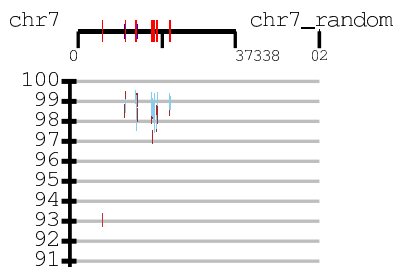
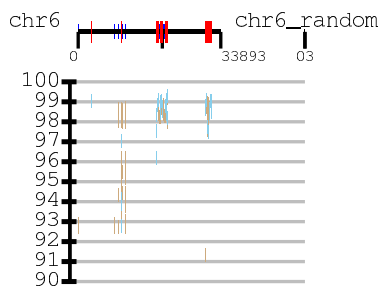
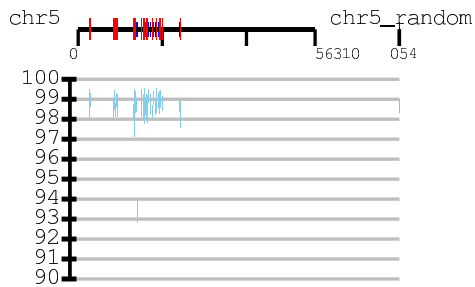
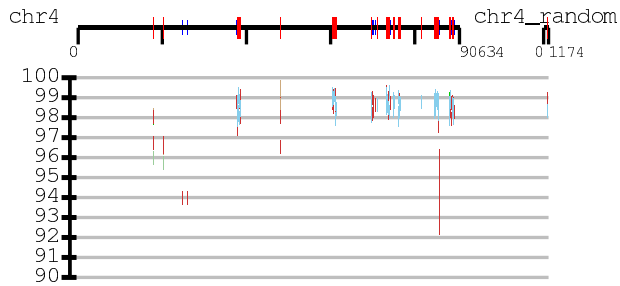
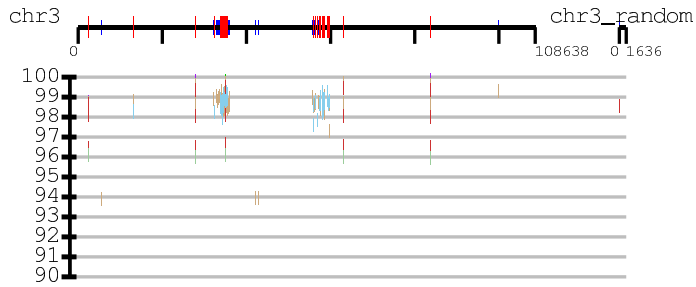
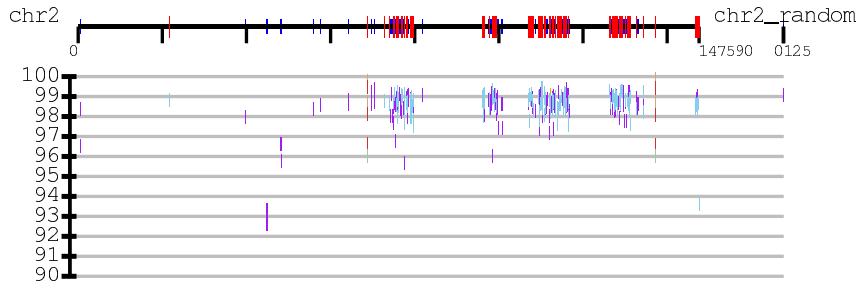
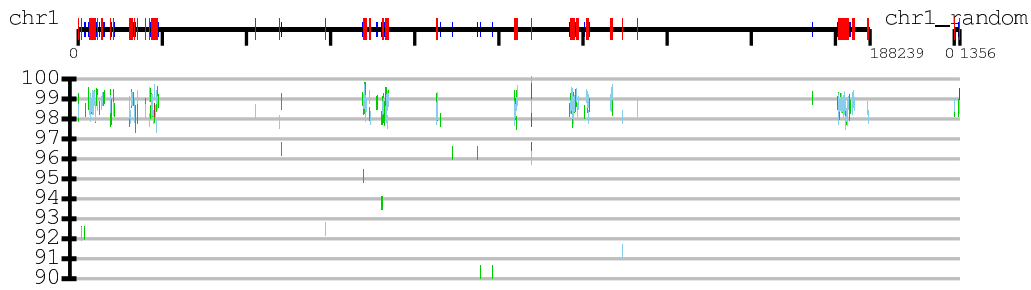


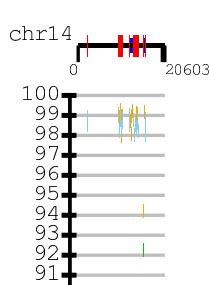
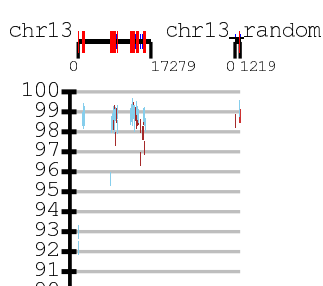
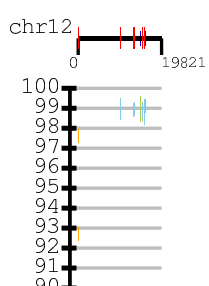
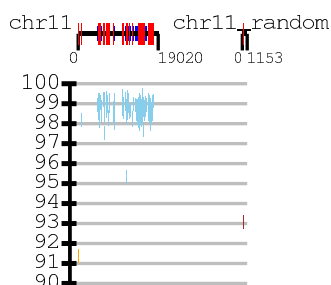
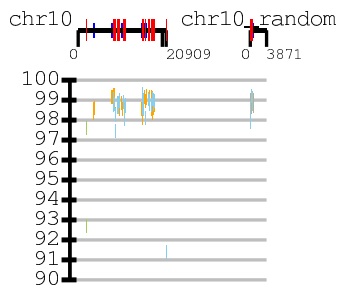
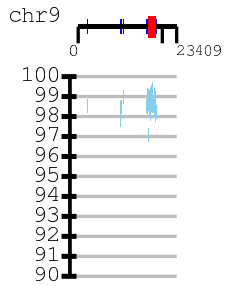
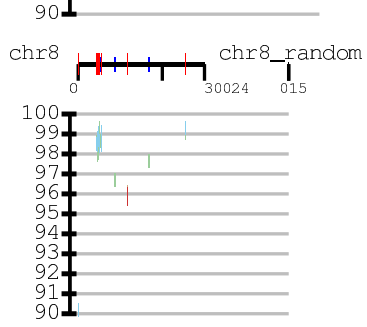




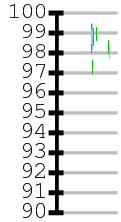




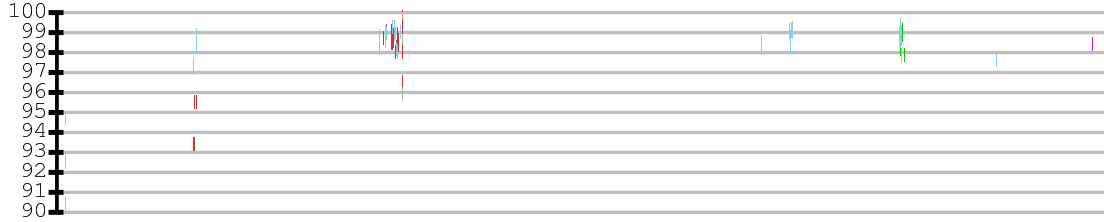




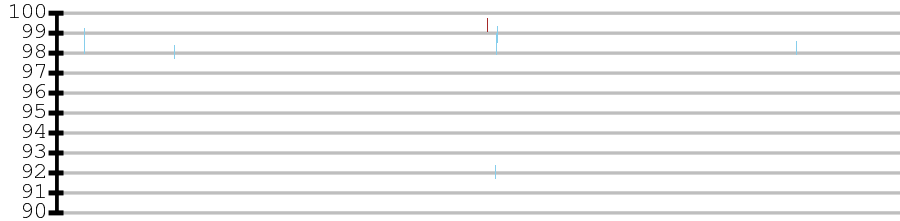
chr15  
0 12438



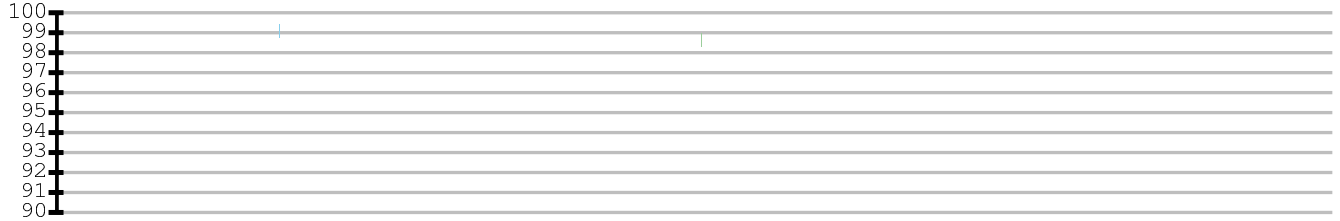
chr16 chr16\_random chr17 chr18 chr19 chr20 chr21 chr22 chr23  
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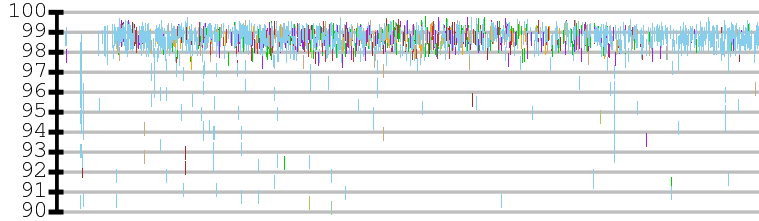
chr24 chr24\_random chr26 chr27 chr27\_random chr28 chr28\_random  
0 5910 0 149 0 4255 0 2668 0 721 0 4731 0 6



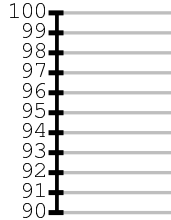
chr32 chr32\_random chrE22C19W28 chrE26C13 chrE50C23 chrE64 chrM  
0 1018 0 61 0 70 0 231 0 21 0 1 0 16



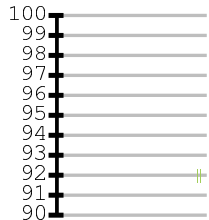
chrUn  
0 165033



chrW chrW\_random  
0 4916 0 455



chrZ  
0 33651







first line: shared orthologs (random expectation); second: number of synteny blocks (random expectation); color marks over-/under- representation of orthologs (p-value<1%)																									
Human	4 (849)	6 (1113)	10 (839)	14 (709)	1 (2165)	2 (1455)	15 (679)	20 (636)	12 (1088)	5 (1008)	9 (844)	3 (1138)	8 (788)	16 (946)	17 (1222)	19 (1377)	11 (1415)	13 (377)	X (869)	7 (1063)	22 (528)	18 (306)	21 (261)	DR51 (2)	Y (110)
4 (1178)	461 (31) 36 (2)					29 (49) 4 (4)		11 (20) 2 (2)					38 (25) 7 (1)						174 (19) 32 (2)						
3 (1267)		414 (39) 15 (2)			126 (73) 8 (7)	225 (53) 22 (4)		27 (21) 5 (2)					43 (27) 5 (2)				24 (35) 1 (3)								
6 (549)			349 (14) 38 (1)																						
5 (931)				334 (18) 11 (0)			63 (18) 6 (2)		2 (28) 1 (1)								223 (26) 24 (2)								
8 (561)				4 (10) 1 (0)	376 (32) 16 (3)																				
7 (561)						321 (23) 19 (2)		2 (16) 1 (1)			25 (22) 4 (2)												13 (3) 2 (0)		
10 (421)						2 (17) 1 (1)	273 (8) 31 (1)																		
20 (361)							2 (7) 1 (0)	226 (6) 20 (0)																	
1 (2080)		16 (54) 3 (6)		46 (120) 9 (12)	45 (87) 1 (7)	7 (41) 3 (5)		344 (62) 21 (4)			104 (83) 11 (9)						102 (58) 9 (6)	231 (27) 10 (1)	114 (33) 5 (4)	149 (56) 14 (5)	146 (28) 6 (2)		105 (14) 4 (0)		
13 (352)										221 (10) 24 (1)															
17 (313)											199 (7) 16 (0)														
9 (463)						89 (19) 11 (1)						220 (18) 22 (2)												6 (3) 2 (0)	
2 (1432)	79 (45) 7 (2)	75 (37) 2 (4)		9 (83) 1 (8)						46 (42) 7 (5)	16 (32) 4 (3)	146 (57) 15 (6)	230 (30) 11 (2)								204 (38) 15 (3)		120 (12) 12 (1)		
11 (304)														173 (6) 25 (1)			27 (2) 1 (0)								
19 (332)															179 (10) 21 (1)						48 (9) 8 (0)				
28 (181)																	111 (1) 21 (0)								
12 (369)											17 (8) 2 (1)	213 (14) 29 (1)													
14 (518)	3 (16) 1 (0)	9 (13) 2 (1)		4 (30) 1 (3)	6 (21) 3 (1)		34 (8) 4 (0)							163 (11) 25 (1)	30 (15) 3 (2)						77 (14) 8 (1)		11 (4) 1 (0)		
15 (374)								156 (11) 7 (0)															96 (5) 13 (0)		
18 (217)															146 (6) 17 (0)										
21 (231)					148 (13) 12 (1)																				
Z (369)	7 (9) 3 (0)										128 (10) 12 (1)	83 (8) 12 (1)		7 (7) 2 (0)										2 (3) 1 (0)	
24 (185)																		120 (5) 10 (0)							
23 (212)					128 (12) 20 (1)																				
26 (185)		43 (5) 5 (0)			84 (10) 6 (1)																				
27 (116)					2 (2) 1 (0)												60 (3) 13 (0)								
W (45)											28 (1) 2 (0)														
32 (60)		9 (1) 2 (0)			30 (3) 6 (0)																				
22 (49)						8 (2) 1 (0)		6 (0) 1 (0)					18 (1) 1 (0)												
E26C13 (14)					12 (0) 3 (0)																				
16 (22)		3 (0) 1 (0)																							
E22C19W28 (5)																									
Un (2870)	2 (76) 1 (6)	6 (90) 1 (5)	18 (75) 8 (8)	5 (55) 2 (2)	64 (166) 20 (16)	16 (120) 5 (10)	7 (57) 3 (7)	2 (49) 1 (5)	29 (86) 8 (6)	19 (84) 6 (10)	12 (65) 3 (7)	7 (115) 3 (13)	47 (62) 4 (4)	26 (63) 8 (10)	24 (88) 9 (11)	18 (25) 8 (4)	15 (80) 6 (8)				4 (78) 2 (7)	2 (39) 1 (3)	23 (25) 5 (3)		
E50C23 (2)																									

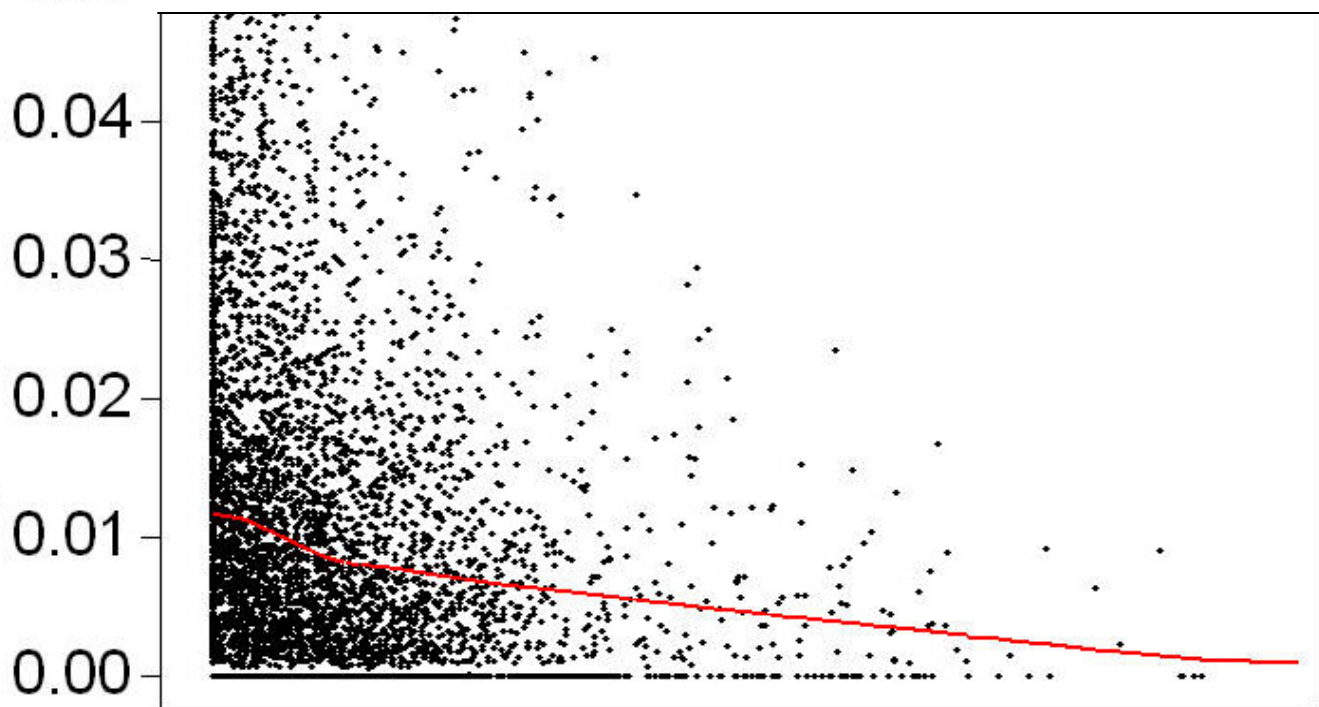
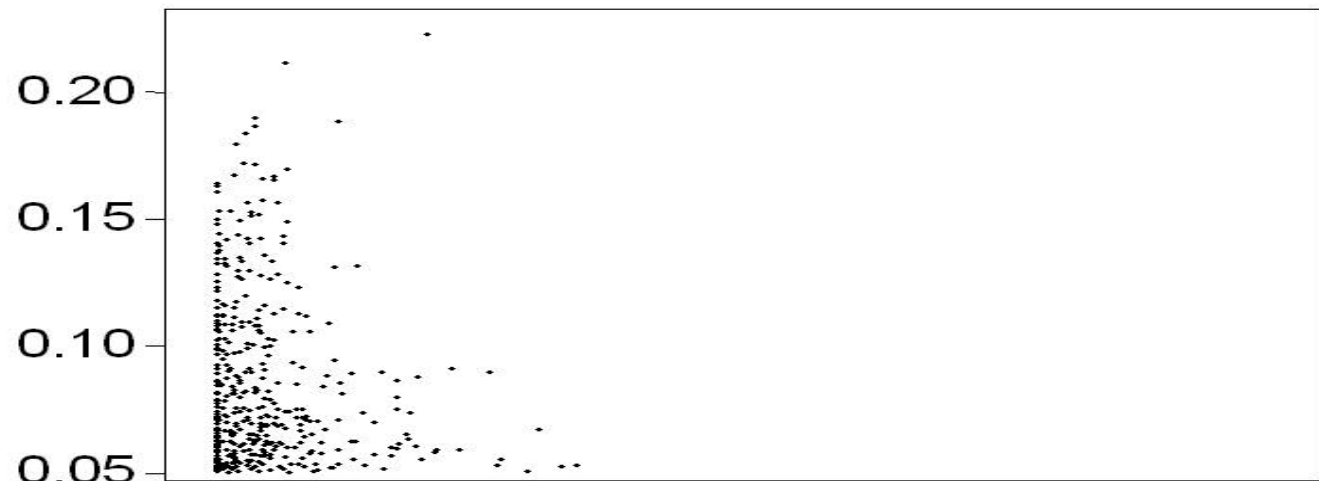
Number of inter-chromosomal relations: 84 (16 on diagonal)

first line: shared orthologs (random expectation); second: number of synteny blocks (random expectation); color marks over-/under- representation of orthologs (p-value<1%)

Human	1 (2165)	14 (709)	X (869)	20 (636)	17 (1222)	19 (1377)	2 (1455)	6 (1113)	16 (946)	4 (849)	5 (1008)	11 (1415)	3 (1138)	12 (1088)	18 (306)	8 (788)	13 (377)	7 (1063)	10 (839)	9 (844)	22 (528)	15 (679)	21 (261)	Y (110)	DR51 (2)	
Mouse																										
4 (1499)	596 (93) 16 (3)							40 (46) 2 (2)								53 (30) 3 (1)					236 (34) 15 (2)					
12 (852)		356 (17) 9 (0)				81 (32) 8 (1)												53 (23) 5 (1)								
X (1116)			483 (21) 42 (1)																							
2 (2058)				445 (36) 11 (0)		189 (77) 11 (4)			170 (84) 13 (3)											88 (48) 4 (2)	215 (47) 12 (3)		140 (36) 2 (1)			
11 (1877)	27 (117) 4 (3)				931 (70) 31 (2)	56 (71) 2 (3)		6 (49) 1 (1)	150 (51) 9 (2)									43 (50) 4 (2)				47 (24) 1 (1)				
7 (2003)				430 (68) 22 (3)	2 (75) 1 (3)		157 (52) 9 (2)		344 (81) 18 (3)										71 (46) 2 (2)			112 (35) 12 (1)				
1 (1504)	429 (93) 12 (3)					382 (56) 16 (2)	35 (46) 4 (2)			7 (41) 2 (2)			17 (12) 1 (0)	45 (30) 2 (1)	9 (15) 1 (1)											
17 (1157)				80 (39) 5 (1)	85 (43) 4 (2)	326 (35) 11 (1)	113 (30) 3 (1)			14 (31) 3 (1)		10 (40) 1 (1)			23 (9) 2 (0)									18 (6) 1 (0)		
8 (1189)	36 (74) 1 (2)			166 (40) 6 (1)			298 (31) 8 (1)	93 (27) 6 (1)							106 (24) 12 (1)	47 (12) 4 (0)			4 (27) 1 (1)			5 (15) 1 (0)				
5 (1478)	23 (92) 1 (3)		2 (28) 1 (2)			50 (55) 1 (2)		303 (33) 8 (1)			189 (48) 5 (1)					35 (15) 1 (1)	296 (40) 17 (2)					20 (19) 3 (1)				
13 (1012)	16 (63) 2 (2)					120 (31) 8 (1)				255 (27) 15 (1)						3 (20) 1 (1)		21 (27) 1 (1)	17 (23) 3 (1)	55 (23) 5 (1)						
19 (795)											252 (32) 4 (1)										207 (18) 5 (0)	64 (18) 5 (1)				
16 (811)	3 (50) 1 (1)							81 (21) 4 (0)				239 (28) 13 (1)	4 (26) 1 (0)		6 (16) 1 (1)							46 (10) 5 (0)	93 (4) 3 (0)			
10 (1205)				113 (41) 4 (1)	7 (45) 1 (2)	194 (37) 8 (1)						258 (39) 7 (1)							78 (28) 3 (1)		25 (15) 4 (0)		36 (7) 2 (0)			
18 (628)						11 (23) 1 (1)					185 (17) 5 (0)				165 (5) 8 (0)				21 (14) 4 (0)							
15 (953)											77 (26) 5 (1)			157 (31) 3 (0)		187 (19) 6 (1)						175 (12) 5 (0)				
14 (898)	2 (56) 1 (1)	151 (18) 6 (0)						3 (27) 1 (1)				84 (31) 7 (1)				77 (18) 3 (1)	146 (9) 12 (0)		82 (21) 5 (1)							
3 (1237)	422 (77) 12 (2)								153 (28) 9 (1)			118 (42) 7 (2)				28 (25) 3 (1)	20 (12) 1 (0)									
6 (1282)	5 (80) 1 (2)					81 (48) 4 (2)		18 (29) 3 (1)				134 (44) 7 (2)	204 (41) 10 (1)						253 (34) 7 (1)	17 (30) 2 (1)		13 (17) 1 (1)				
9 (1394)					60 (47) 4 (2)		53 (43) 2 (2)					255 (57) 7 (2)	280 (48) 8 (2)							10 (37) 3 (2)			196 (25) 7 (1)			

Number of inter-chromosomal relations: 113 (17 on diagonal)

non-coding fraction conserved



0.00

0.05

0.10

coding fraction

