Homo_sapien GRCH38.82 Analysis

```r
Homo_sapien_exon <- read.csv("Homo_sapiens.GRCh38.82.abinitio.exon.gtf", sep = "", header = FALSE)
Homo_sapien_transcript <- read.csv("Homo_sapiens.GRCh38.82.abinitio.transcript.gtf", sep = "", header =
```

```r
colnames(Homo_sapien_exon)[1] <- "chromosome"
colnames(Homo_sapien_exon)[2] <- "type"
colnames(Homo_sapien_exon)[3] <- "start"
colnames(Homo_sapien_exon)[4] <- "end"
colnames(Homo_sapien_transcript)[1] <- "chromosome"
colnames(Homo_sapien_transcript)[2] <- "type"
colnames(Homo_sapien_transcript)[3] <- "start"
colnames(Homo_sapien_transcript)[4] <- "end"
```

```r
Homo_sapien_exon$length <- Homo_sapien_exon$end - Homo_sapien_exon$start
Homo_sapien_transcript$length <- Homo_sapien_transcript$end - Homo_sapien_transcript$start
```

```r
averageE <- aggregate(Homo_sapien_exon$length, list(Homo_sapien_exon$chromosome), mean)
averageTran <- aggregate(Homo_sapien_transcript$length, list(Homo_sapien_transcript$chromosome), mean)
stdE <- aggregate(Homo_sapien_exon$length, list(Homo_sapien_exon$chromosome), sd)
stdTran <- aggregate(Homo_sapien_transcript$length, list(Homo_sapien_transcript$chromosome), sd)
sumE <- aggregate(Homo_sapien_exon$length, list(Homo_sapien_exon$chromosome), sum)
sumTran <- aggregate(Homo_sapien_transcript$length, list(Homo_sapien_transcript$chromosome), sum)
averageE$sterr <- stdE$x/sqrt(sumE$x)
averageTran$sterr <- stdE$x/sqrt(sumE$x)
```

```r
library(knitr)
kable(averageE, caption = "Table for Exons")
```

Table 1: Table for Exons

Group.1	x	sterr
1	171.80680	0.0890678
10	172.48426	0.1309287
11	178.04851	0.1531558
12	166.45340	0.1167730
13	176.76896	0.2704681
14	177.29287	0.2005417
15	172.85302	0.1618782
16	172.86205	0.1420884
17	171.87736	0.1239308
18	174.17810	0.1859457
19	196.75402	0.1852717
2	170.23505	0.1264784
20	168.64316	0.1720108
21	175.68529	0.2347330
22	176.24921	0.2203012
3	167.44428	0.1224967
4	180.71032	0.1544545
5	179.45278	0.1603773
6	175.64212	0.1325706
7	175.29798	0.1452231
8	172.35652	0.1666879

Group.1	x	sterr
9	174.12196	0.1525327
CHR_HG126_PATCH	133.22000	1.2609910
CHR_HG1342_HG2282_PATCH	377.08036	1.2801938
CHR_HG1362_PATCH	206.09877	1.3446788
CHR_HG142_HG150_NOVEL_TEST	498.38462	4.1601133
CHR_HG151_NOVEL_TEST	472.69231	4.6069763
CHR_HG1651_PATCH	287.09302	2.6161453
CHR_HG1832_PATCH	189.27059	1.4789496
CHR_HG2021_PATCH	314.71698	2.0048459
CHR_HG2022_PATCH	231.61765	3.0077764
CHR_HG2030_PATCH	156.66272	1.4878894
CHR_HG2058_PATCH	99.71429	0.7936157
CHR_HG2062_PATCH	184.00000	2.3537727
CHR_HG2066_PATCH	249.54412	1.8165903
CHR_HG2095_PATCH	129.06731	0.6019315
CHR_HG2104_PATCH	374.37500	5.9891144
CHR_HG2128_PATCH	198.00000	2.9746153
CHR_HG2191_PATCH	223.13462	3.3442979
CHR_HG2216_PATCH	186.00000	3.6057998
CHR_HG2217_PATCH	138.77027	0.6408871
CHR_HG2232_PATCH	132.69767	1.1412708
CHR_HG2233_PATCH	155.30000	1.9865984
CHR_HG2235_PATCH	186.09836	1.3594978
CHR_HG2237_PATCH	219.68966	3.6373814
CHR_HG2239_PATCH	160.55556	1.6750706
CHR_HG2241_PATCH	339.80000	6.4683637
CHR_HG2242_HG2243_PATCH	171.50000	1.7184407
CHR_HG2244_HG2245_PATCH	215.57778	2.2451151
CHR_HG2247_PATCH	148.67857	2.2342034
CHR_HG2249_PATCH	185.26667	2.2358403
CHR_HG2288_HG2289_PATCH	238.44086	2.5561682
CHR_HG2290_PATCH	207.15702	0.8664480
CHR_HG2291_PATCH	244.91667	1.9397176
CHR_HG23_PATCH	416.00000	2.4562541
CHR_HG986_PATCH	154.16667	2.7959642
CHR_HSCHR1_1_CTG11	118.60000	1.7833889
CHR_HSCHR1_1_CTG3	121.19799	0.6244773
CHR_HSCHR1_1_CTG31	147.11111	1.0787844
CHR_HSCHR1_1_CTG32_1	226.38636	4.9995983
CHR_HSCHR1_2_CTG3	373.62500	1.5047100
CHR_HSCHR1_2_CTG31	149.33333	0.8247018
CHR_HSCHR1_2_CTG32_1	712.10000	4.6445549
CHR_HSCHR1_3_CTG31	152.16667	1.1457613
CHR_HSCHR1_3_CTG32_1	180.37349	1.7505480
CHR_HSCHR1_4_CTG31	189.47826	2.0408439
CHR_HSCHR1_4_CTG32_1	125.00000	1.6099689
CHR_HSCHR1_ALT2_1_CTG32_1	712.10000	4.6445549
CHR_HSCHR10_1_CTG1	191.64000	3.0792199
CHR_HSCHR10_1_CTG2	212.97059	2.3557246
CHR_HSCHR10_1_CTG3	326.00000	2.8759339
CHR_HSCHR10_1_CTG4	385.80645	2.9705035
CHR_HSCHR11_1_CTG1_2	522.47059	3.5459766

Group.1	x	sterr
CHR_HSCHR11_1_CTG2	227.57143	4.6801316
CHR_HSCHR11_1_CTG3	210.30000	4.0938565
CHR_HSCHR11_1_CTG5	590.60000	6.2138345
CHR_HSCHR11_1_CTG6	233.05556	2.0348707
CHR_HSCHR11_1_CTG7	151.54369	1.2285520
CHR_HSCHR11_1_CTG8	180.89600	1.6392124
CHR_HSCHR11_2_CTG1	272.04478	4.5203163
CHR_HSCHR11_2_CTG1_1	231.68000	2.0760149
CHR_HSCHR11_3_CTG1	203.42553	2.1269730
CHR_HSCHR12_1_CTG1	157.46809	1.9022725
CHR_HSCHR12_1_CTG2	129.20000	3.1055229
CHR_HSCHR12_1_CTG2_1	161.84615	2.1642190
CHR_HSCHR12_2_CTG2	161.00000	2.0153147
CHR_HSCHR12_2_CTG2_1	119.20000	2.3568763
CHR_HSCHR12_3_CTG2	196.55882	2.4490495
CHR_HSCHR12_3_CTG2_1	133.52941	1.5184823
CHR_HSCHR12_4_CTG2	152.03846	0.9379597
CHR_HSCHR12_4_CTG2_1	172.53333	1.6340666
CHR_HSCHR12_5_CTG2	493.00000	18.2157827
CHR_HSCHR12_5_CTG2_1	101.07692	0.9882577
CHR_HSCHR12_6_CTG2_1	183.42857	0.9307741
CHR_HSCHR12_7_CTG2_1	121.40000	2.0161893
CHR_HSCHR13_1_CTG1	158.61702	1.6697046
CHR_HSCHR13_1_CTG2	154.31818	1.4802853
CHR_HSCHR13_1_CTG3	181.70000	1.8598235
CHR_HSCHR13_1_CTG4	194.00000	2.3356640
CHR_HSCHR13_1_CTG5	466.00000	6.7708630
CHR_HSCHR14_1_CTG1	161.40000	1.8263448
CHR_HSCHR14_2_CTG1	146.75926	1.0391880
CHR_HSCHR14_3_CTG1	206.01603	0.7378461
CHR_HSCHR14_7_CTG1	173.42009	0.8592562
CHR_HSCHR15_1_CTG1	247.74390	1.4655537
CHR_HSCHR15_1_CTG3	131.70526	1.1999474
CHR_HSCHR15_1_CTG8	186.12903	1.8957592
CHR_HSCHR15_2_CTG3	138.54902	2.1142493
CHR_HSCHR15_2_CTG8	108.09434	0.6705249
CHR_HSCHR15_3_CTG3	142.76842	1.2284435
CHR_HSCHR15_3_CTG8	141.14706	1.5782223
CHR_HSCHR15_4_CTG8	167.56159	0.4830508
CHR_HSCHR15_5_CTG8	181.52846	1.4546385
CHR_HSCHR15_6_CTG8	195.55660	0.9309749
CHR_HSCHR16_1_CTG1	156.02299	0.5776564
CHR_HSCHR16_1_CTG3_1	118.72727	0.5545525
CHR_HSCHR16_2_CTG3_1	166.91667	3.0354037
CHR_HSCHR16_3_CTG1	159.46053	2.1790948
CHR_HSCHR16_3_CTG3_1	196.78571	6.7847592
CHR_HSCHR16_4_CTG1	239.36364	3.8083032
CHR_HSCHR16_CTG2	218.31429	4.7690003
CHR_HSCHR17_1_CTG1	231.76056	5.0564213
CHR_HSCHR17_1_CTG2	218.43636	2.2871383
CHR_HSCHR17_1_CTG4	183.50000	1.2192646
CHR_HSCHR17_1_CTG5	239.84783	1.5781003

Group.1	x	sterr
CHR_HSCHR17_1_CTG9	151.36471	1.2577959
CHR_HSCHR17_10_CTG4	108.30556	0.5323237
CHR_HSCHR17_2_CTG1	137.37500	1.0258749
CHR_HSCHR17_2_CTG2	155.69136	0.9513372
CHR_HSCHR17_2_CTG4	85.40000	1.5736908
CHR_HSCHR17_2_CTG5	216.71721	1.3579685
CHR_HSCHR17_3_CTG2	144.89130	1.0794966
CHR_HSCHR17_3_CTG4	131.05263	1.4296608
CHR_HSCHR17_4_CTG4	230.89062	1.4965122
CHR_HSCHR17_5_CTG4	232.07143	2.5583464
CHR_HSCHR17_6_CTG4	268.21429	2.9982560
CHR_HSCHR17_7_CTG4	151.17565	0.7151356
CHR_HSCHR17_8_CTG4	154.35714	2.6231611
CHR_HSCHR17_9_CTG4	126.20000	2.9753877
CHR_HSCHR18_1_CTG1_1	158.00000	1.7010106
CHR_HSCHR18_1_CTG2	98.00000	1.4652436
CHR_HSCHR18_1_CTG2_1	184.88462	2.6960073
CHR_HSCHR18_2_CTG1_1	149.75000	1.9785247
CHR_HSCHR18_2_CTG2	3638.00000	NA
CHR_HSCHR18_2_CTG2_1	302.71429	8.9545688
CHR_HSCHR18_3_CTG2_1	225.78261	2.3326610
CHR_HSCHR18_4_CTG1_1	137.00000	9.1416269
CHR_HSCHR18_ALT2_CTG2_1	300.63636	8.5938290
CHR_HSCHR18_ALT21_CTG2_1	177.63636	3.0611211
CHR_HSCHR19_1_CTG2	326.32353	3.3049057
CHR_HSCHR19_1_CTG3_1	181.27778	1.7603822
CHR_HSCHR19_2_CTG2	358.25000	5.1219656
CHR_HSCHR19_2_CTG3_1	166.85714	5.0078433
CHR_HSCHR19_3_CTG2	330.25000	6.6279706
CHR_HSCHR19_3_CTG3_1	185.33333	2.8853706
CHR_HSCHR19_4_CTG2	142.74419	1.1425466
CHR_HSCHR19_4_CTG3_1	170.09140	0.6322291
CHR_HSCHR19_5_CTG2	141.94286	0.8915110
CHR_HSCHR19KIR_ABC08_A1_HAP_CTG3_1	163.69231	0.9857000
CHR_HSCHR19KIR_ABC08_AB_HAP_C_P_CTG3_1	174.41860	1.2116923
CHR_HSCHR19KIR_ABC08_AB_HAP_T_P_CTG3_1	160.90769	0.9819331
CHR_HSCHR19KIR_FH05_A_HAP_CTG3_1	163.65152	0.9942905
CHR_HSCHR19KIR_FH05_B_HAP_CTG3_1	167.52000	0.8539655
CHR_HSCHR19KIR_FH06_A_HAP_CTG3_1	162.58462	0.9788975
CHR_HSCHR19KIR_FH06_BA1_HAP_CTG3_1	169.21538	0.9759887
CHR_HSCHR19KIR_FH08_A_HAP_CTG3_1	165.66154	0.9909528
CHR_HSCHR19KIR_FH08_BAX_HAP_CTG3_1	163.32500	0.9112464
CHR_HSCHR19KIR_FH13_A_HAP_CTG3_1	164.42188	0.9885677
CHR_HSCHR19KIR_FH13_BA2_HAP_CTG3_1	160.43529	0.8865199
CHR_HSCHR19KIR_FH15_A_HAP_CTG3_1	160.90909	0.9909393
CHR_HSCHR19KIR_FH15_B_HAP_CTG3_1	162.31250	0.8865956
CHR_HSCHR19KIR_G085_A_HAP_CTG3_1	162.90909	0.9736920
CHR_HSCHR19KIR_G085_BA1_HAP_CTG3_1	161.20339	1.0356558
CHR_HSCHR19KIR_G248_A_HAP_CTG3_1	164.42188	0.9885677
CHR_HSCHR19KIR_G248_BA2_HAP_CTG3_1	161.33333	0.9314794
CHR_HSCHR19KIR_GRC212_AB_HAP_CTG3_1	165.37838	0.9796373
CHR_HSCHR19KIR_GRC212_BA1_HAP_CTG3_1	164.60000	1.0333112

Group.1	x	sterr
CHR_HSCHR19KIR_LUCE_A_HAP_CTG3_1	162.38095	0.9974922
CHR_HSCHR19KIR_LUCE_BDEL_HAP_CTG3_1	173.76119	1.0156974
CHR_HSCHR19KIR_RP5_B_HAP_CTG3_1	172.86567	1.0197624
CHR_HSCHR19KIR_RSH_A_HAP_CTG3_1	164.42188	0.9885677
CHR_HSCHR19KIR_RSH_BA2_HAP_CTG3_1	164.25610	0.9058354
CHR_HSCHR19KIR_T7526_A_HAP_CTG3_1	164.42188	0.9885677
CHR_HSCHR19KIR_T7526_BDEL_HAP_CTG3_1	167.00000	1.0069399
CHR_HSCHR19LRC_COX1_CTG3_1	174.34528	0.7186160
CHR_HSCHR19LRC_COX2_CTG3_1	166.61111	0.8079783
CHR_HSCHR19LRC_LRC_I_CTG3_1	165.04520	1.0067153
CHR_HSCHR19LRC_LRC_J_CTG3_1	167.04908	1.0737376
CHR_HSCHR19LRC_LRC_S_CTG3_1	164.62264	1.0977374
CHR_HSCHR19LRC_LRC_T_CTG3_1	164.79096	1.0061067
CHR_HSCHR19LRC_PGF1_CTG3_1	168.09677	0.6785677
CHR_HSCHR19LRC_PGF2_CTG3_1	169.34008	0.7794657
CHR_HSCHR2_1_CTG1	139.58621	1.2326543
CHR_HSCHR2_1_CTG15	808.95000	12.3858078
CHR_HSCHR2_1_CTG5	163.57143	5.3258005
CHR_HSCHR2_1_CTG7	325.01852	1.9166843
CHR_HSCHR2_1_CTG7_2	158.11538	1.2755152
CHR_HSCHR2_2_CTG1	174.47368	3.6128570
CHR_HSCHR2_2_CTG15	343.03448	3.6593030
CHR_HSCHR2_2_CTG7	335.18182	2.0897610
CHR_HSCHR2_2_CTG7_2	117.58333	0.9865817
CHR_HSCHR2_3_CTG1	114.87500	1.6009904
CHR_HSCHR2_3_CTG15	254.20000	3.0147705
CHR_HSCHR2_3_CTG7_2	214.56522	2.1811396
CHR_HSCHR2_4_CTG1	193.12195	3.6775769
CHR_HSCHR2_4_CTG7_2	122.75000	2.9375429
CHR_HSCHR2_5_CTG7_2	123.00000	2.0607311
CHR_HSCHR20_1_CTG1	148.00000	1.7258691
CHR_HSCHR20_1_CTG2	175.23077	1.7751137
CHR_HSCHR20_1_CTG3	230.06667	2.0281799
CHR_HSCHR20_1_CTG4	145.06667	1.4868365
CHR_HSCHR21_1_CTG1_1	132.00000	NA
CHR_HSCHR21_2_CTG1_1	93.50000	0.3619614
CHR_HSCHR21_3_CTG1_1	396.50000	7.4827671
CHR_HSCHR21_4_CTG1_1	222.78947	4.0016913
CHR_HSCHR21_5_CTG2	136.03125	1.0214240
CHR_HSCHR21_6_CTG1_1	133.88889	1.2440268
CHR_HSCHR21_8_CTG1_1	241.00000	8.0889762
CHR_HSCHR22_1_CTG1	288.95000	8.1862859
CHR_HSCHR22_1_CTG2	141.90909	2.0895535
CHR_HSCHR22_1_CTG3	285.58824	3.3396839
CHR_HSCHR22_1_CTG4	164.86842	2.5522713
CHR_HSCHR22_1_CTG5	99.26087	1.5691778
CHR_HSCHR22_1_CTG6	129.20833	1.4650635
CHR_HSCHR22_1_CTG7	140.53279	0.5505302
CHR_HSCHR22_2_CTG1	159.05000	1.2000369
CHR_HSCHR22_3_CTG1	271.75000	7.0326537
CHR_HSCHR22_4_CTG1	300.28571	9.1940288
CHR_HSCHR22_5_CTG1	235.20000	6.0608425

Group.1	x	sterr
CHR_HSCHR3_1_CTG1	127.47826	0.9854748
CHR_HSCHR3_1_CTG2_1	178.00000	4.1340672
CHR_HSCHR3_1_CTG3	301.29787	5.5926411
CHR_HSCHR3_2_CTG2_1	161.54545	3.5358304
CHR_HSCHR3_2_CTG3	123.94118	2.3715515
CHR_HSCHR3_3_CTG1	110.66667	3.1462032
CHR_HSCHR3_3_CTG2_1	126.75000	1.4700047
CHR_HSCHR3_3_CTG3	243.98701	3.4083319
CHR_HSCHR3_4_CTG2_1	235.88000	2.7868332
CHR_HSCHR3_4_CTG3	271.50000	3.5710365
CHR_HSCHR3_5_CTG2_1	154.50000	2.7518071
CHR_HSCHR3_5_CTG3	244.06494	3.4077088
CHR_HSCHR3_6_CTG3	218.35294	2.7116802
CHR_HSCHR3_7_CTG3	243.98701	3.4068212
CHR_HSCHR3_8_CTG3	243.32468	3.4276817
CHR_HSCHR3_9_CTG3	197.31818	2.5783938
CHR_HSCHR4_1_CTG12	129.77273	1.1494297
CHR_HSCHR4_1_CTG4	116.70000	1.4760167
CHR_HSCHR4_1_CTG6	115.00000	2.2250224
CHR_HSCHR4_1_CTG8_1	136.00000	2.6114513
CHR_HSCHR4_1_CTG9	191.78333	1.4346415
CHR_HSCHR4_2_CTG12	136.54545	1.7517867
CHR_HSCHR4_3_CTG12	263.42857	4.8160959
CHR_HSCHR4_4_CTG12	99.50000	1.7414544
CHR_HSCHR4_5_CTG12	154.41304	1.4943060
CHR_HSCHR4_6_CTG12	256.87500	2.5461544
CHR_HSCHR4_7_CTG12	380.73973	7.1118571
CHR_HSCHR5_1_CTG1_1	310.45038	3.2800786
CHR_HSCHR5_1_CTG5	108.00000	2.1034217
CHR_HSCHR5_2_CTG1	182.00000	4.2251211
CHR_HSCHR5_2_CTG1_1	272.66667	2.6166715
CHR_HSCHR5_2_CTG5	203.95000	3.3024801
CHR_HSCHR5_3_CTG1	142.29762	1.3853938
CHR_HSCHR5_3_CTG1_1	117.00000	2.0339007
CHR_HSCHR5_3_CTG5	219.10714	2.8646030
CHR_HSCHR5_4_CTG1	174.36082	0.9677000
CHR_HSCHR5_4_CTG1_1	120.50000	1.3099863
CHR_HSCHR5_5_CTG1	197.16667	2.5570824
CHR_HSCHR5_6_CTG1	253.29412	4.7518782
CHR_HSCHR5_7_CTG1	586.29412	9.5186530
CHR_HSCHR6_1_CTG2	188.33333	1.8568616
CHR_HSCHR6_1_CTG3	1322.40741	18.9192827
CHR_HSCHR6_1_CTG4	304.38095	5.8432931
CHR_HSCHR6_1_CTG5	226.12727	2.3802366
CHR_HSCHR6_1_CTG7	713.00000	14.8303165
CHR_HSCHR6_1_CTG8	180.77551	2.1728625
CHR_HSCHR6_1_CTG9	113.00000	1.6874674
CHR_HSCHR6_8_CTG1	180.31250	2.0353743
CHR_HSCHR6_MHC_APD_CTG1	200.22294	0.8409252
CHR_HSCHR6_MHC_COX_CTG1	183.30876	0.4966280
CHR_HSCHR6_MHC_DBB_CTG1	179.52252	0.5049966
CHR_HSCHR6_MHC_MANN_CTG1	180.87227	0.5202857

Group.1	x	sterr
CHR_HSCHR6_MHC_MCF_CTG1	174.61728	0.4485155
CHR_HSCHR6_MHC_QBL_CTG1	179.02178	0.5036147
CHR_HSCHR6_MHC_SSTO_CTG1	170.27967	0.4389742
CHR_HSCHR7_1_CTG1	191.28571	2.5473211
CHR_HSCHR7_1_CTG4_4	313.76000	7.4917721
CHR_HSCHR7_1_CTG6	133.56250	1.0031720
CHR_HSCHR7_1_CTG7	296.11111	2.7871034
CHR_HSCHR7_2_CTG1	156.68750	1.6704492
CHR_HSCHR7_2_CTG4_4	137.97561	1.0493543
CHR_HSCHR7_2_CTG6	180.31805	0.6718175
CHR_HSCHR7_2_CTG7	219.23684	4.8167154
CHR_HSCHR7_3_CTG6	196.42857	2.2374090
CHR_HSCHR8_1_CTG1	229.00000	2.3027657
CHR_HSCHR8_1_CTG6	215.85714	1.3851596
CHR_HSCHR8_1_CTG7	135.66667	1.3888607
CHR_HSCHR8_2_CTG1	359.05882	3.3987307
CHR_HSCHR8_2_CTG7	253.64706	3.5300769
CHR_HSCHR8_3_CTG1	232.50000	2.1082672
CHR_HSCHR8_3_CTG7	211.47692	1.5539042
CHR_HSCHR8_4_CTG1	347.00000	5.6059970
CHR_HSCHR8_4_CTG7	289.51163	3.2710861
CHR_HSCHR8_5_CTG1	215.57143	2.3645613
CHR_HSCHR8_5_CTG7	174.80769	2.1716530
CHR_HSCHR8_6_CTG1	207.33333	1.9508802
CHR_HSCHR8_6_CTG7	179.00000	5.8190434
CHR_HSCHR8_7_CTG1	229.91429	3.3864559
CHR_HSCHR8_8_CTG1	179.05769	1.5244919
CHR_HSCHR8_9_CTG1	124.93023	0.9075555
CHR_HSCHR9_1_CTG1	302.85714	9.3548698
CHR_HSCHR9_1_CTG2	152.55556	1.7110620
CHR_HSCHR9_1_CTG3	177.57895	2.3138766
CHR_HSCHR9_1_CTG4	249.60000	7.5095719
CHR_HSCHR9_1_CTG5	197.17647	1.5447815
CHR_HSCHRX_1_CTG3	224.13235	2.0505401
CHR_HSCHRX_2_CTG12	155.42857	1.3926955
CHR_HSCHRX_2_CTG3	214.81538	2.1628191
GL000008.2	170.88235	1.9175550
GL000009.2	136.52632	1.5564201
GL000194.1	197.94737	1.7479385
GL000195.1	164.85185	1.5990353
GL000205.2	184.04348	1.7468081
GL000213.1	285.10345	2.7780378
GL000214.1	208.83333	2.6417544
GL000216.2	361.41304	1.2519264
GL000218.1	160.55000	1.6572159
GL000219.1	209.33333	2.5358994
GL000220.1	268.10526	4.1584722
GL000221.1	197.42857	1.8118949
GL000224.1	192.60000	1.8625018
GL000225.1	244.55556	2.5672001
KI270330.1	192.00000	NA
KI270435.1	428.00000	NA

Group.1	x	sterr
KI270438.1	339.20000	0.8492870
KI270442.1	194.23077	3.4372081
KI270519.1	185.00000	NA
KI270528.1	272.00000	3.2135970
KI270706.1	161.09524	1.3193450
KI270708.1	345.42857	5.7168369
KI270709.1	501.50000	1.9208307
KI270711.1	136.85000	1.4063224
KI270712.1	551.21053	7.1060688
KI270713.1	163.31579	1.3592794
KI270714.1	195.90476	1.7218315
KI270716.1	287.30000	1.6308141
KI270717.1	348.00000	11.7396323
KI270718.1	198.66667	2.2957991
KI270719.1	209.17647	1.6263810
KI270720.1	97.40000	1.5894286
KI270721.1	138.35185	1.3840790
KI270722.1	279.50000	3.5464678
KI270723.1	181.37500	2.8669398
KI270724.1	202.80000	4.1142169
KI270725.1	244.33333	4.4729189
KI270726.1	237.28571	2.1769372
KI270727.1	250.70000	1.4874710
KI270728.1	189.06481	1.0228750
KI270729.1	332.80282	0.6726096
KI270730.1	355.69231	0.8974439
KI270731.1	226.53488	3.0478640
KI270732.1	445.00000	NA
KI270733.1	262.96154	3.9444475
KI270734.1	167.66667	2.2461385
KI270735.1	576.50000	6.1848162
KI270736.1	440.00000	NA
KI270737.1	307.68000	0.8092471
KI270738.1	270.18310	0.5895912
KI270741.1	248.33333	4.2056742
KI270742.1	162.06250	1.9327752
KI270743.1	194.30000	1.7074009
KI270744.1	210.54286	2.0282471
KI270745.1	157.60000	3.0571544
KI270746.1	296.00000	7.4585567
KI270747.1	262.93617	0.8031156
KI270748.1	116.75000	1.4478195
KI270749.1	276.33333	4.3157798
KI270750.1	226.81250	3.9478050
KI270751.1	219.12500	5.2180775
KI270752.1	121.82353	1.1919079
KI270753.1	423.33333	9.5109358
KI270754.1	128.50000	4.3667028
KI270755.1	138.50000	3.0165009
KI270756.1	348.54545	0.9775761
X	193.39237	0.1869751
Y	191.06172	0.3239418

```r
kable(averageTran, caption = "Table for Transcript")
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Table 2: Table for Transcript

Group.1	x	sterr
1	38640.7541	0.0890678
10	37649.0076	0.1309287
11	37019.3280	0.1531558
12	44291.2077	0.1167730
13	46892.9970	0.2704681
14	43523.4184	0.2005417
15	40051.7286	0.1618782
16	29383.6975	0.1420884
17	30397.3793	0.1239308
18	44128.2194	0.1859457
19	22339.4047	0.1852717
2	45415.9958	0.1264784
20	36547.0123	0.1720108
21	39109.1294	0.2347330
22	26710.0540	0.2203012
3	50669.6469	0.1224967
4	51478.5129	0.1544545
5	48089.7041	0.1603773
6	43271.9013	0.1325706
7	39159.9787	0.1452231
8	44538.8063	0.1666879
9	42599.1699	0.1525327
CHR_HG126_PATCH	21164.6667	1.2609910
CHR_HG1342_HG2282_PATCH	5496.8529	1.2801938
CHR_HG1362_PATCH	18283.2500	1.3446788
CHR_HG142_HG150_NOVEL_TEST	8467.8750	4.1601133
CHR_HG151_NOVEL_TEST	10087.3333	4.6069763
CHR_HG1651_PATCH	11656.5000	2.6161453
CHR_HG1832_PATCH	18955.2941	1.4789496
CHR_HG2021_PATCH	29181.0000	2.0048459
CHR_HG2022_PATCH	16851.6364	3.0077764
CHR_HG2030_PATCH	7481.4800	1.4878894
CHR_HG2058_PATCH	43690.0000	0.7936157
CHR_HG2062_PATCH	8907.3333	2.3537727
CHR_HG2066_PATCH	10149.4815	1.8165903
CHR_HG2095_PATCH	41652.8333	0.6019315
CHR_HG2104_PATCH	10735.7500	5.9891144
CHR_HG2128_PATCH	11825.1250	2.9746153
CHR_HG2191_PATCH	29878.7143	3.3442979
CHR_HG2216_PATCH	5566.0000	3.6057998
CHR_HG2217_PATCH	12317.0000	0.6408871
CHR_HG2232_PATCH	26357.2727	1.1412708
CHR_HG2233_PATCH	24849.8000	1.9865984
CHR_HG2235_PATCH	13171.4375	1.3594978
CHR_HG2237_PATCH	29943.2500	3.6373814
CHR_HG2239_PATCH	16135.4286	1.6750706
CHR_HG2241_PATCH	3115.0000	6.4683637
CHR_HG2242_HG2243_PATCH	22935.6667	1.7184407

Group.1	x	sterr
CHR_HG2244_HG2245_PATCH	14492.4615	2.2451151
CHR_HG2247_PATCH	19787.3333	2.2342034
CHR_HG2249_PATCH	14557.8571	2.2358403
CHR_HG2288_HG2289_PATCH	9870.6667	2.5561682
CHR_HG2290_PATCH	3837.6939	0.8664480
CHR_HG2291_PATCH	12828.1579	1.9397176
CHR_HG23_PATCH	3863.4375	2.4562541
CHR_HG986_PATCH	38741.5000	2.7959642
CHR_HSCHR1_1_CTG11	38103.5000	1.7833889
CHR_HSCHR1_1_CTG3	35887.3333	0.6244773
CHR_HSCHR1_1_CTG31	26151.0000	1.0787844
CHR_HSCHR1_1_CTG32_1	34656.3750	4.9995983
CHR_HSCHR1_2_CTG3	5049.2143	1.5047100
CHR_HSCHR1_2_CTG31	9061.0000	0.8247018
CHR_HSCHR1_2_CTG32_1	15785.0000	4.6445549
CHR_HSCHR1_3_CTG31	42206.8000	1.1457613
CHR_HSCHR1_3_CTG32_1	117322.2857	1.7505480
CHR_HSCHR1_4_CTG31	14550.0000	2.0408439
CHR_HSCHR1_4_CTG32_1	25285.0000	1.6099689
CHR_HSCHR1_ALT2_1_CTG32_1	15827.4000	4.6445549
CHR_HSCHR10_1_CTG1	33740.7500	3.0792199
CHR_HSCHR10_1_CTG2	17519.8571	2.3557246
CHR_HSCHR10_1_CTG3	5330.0588	2.8759339
CHR_HSCHR10_1_CTG4	20413.8571	2.9705035
CHR_HSCHR11_1_CTG1_2	3878.8000	3.5459766
CHR_HSCHR11_1_CTG2	49087.0000	4.6801316
CHR_HSCHR11_1_CTG3	15934.6667	4.0938565
CHR_HSCHR11_1_CTG5	16938.7500	6.2138345
CHR_HSCHR11_1_CTG6	7680.2500	2.0348707
CHR_HSCHR11_1_CTG7	20707.2727	1.2285520
CHR_HSCHR11_1_CTG8	15834.8182	1.6392124
CHR_HSCHR11_2_CTG1	48890.5000	4.5203163
CHR_HSCHR11_2_CTG1_1	6026.5385	2.0760149
CHR_HSCHR11_3_CTG1	19185.7778	2.1269730
CHR_HSCHR12_1_CTG1	28064.8000	1.9022725
CHR_HSCHR12_1_CTG2	34830.0000	3.1055229
CHR_HSCHR12_1_CTG2_1	6926.2000	2.1642190
CHR_HSCHR12_2_CTG2	40373.8333	2.0153147
CHR_HSCHR12_2_CTG2_1	42808.0000	2.3568763
CHR_HSCHR12_3_CTG2	34100.6000	2.4490495
CHR_HSCHR12_3_CTG2_1	31480.0000	1.5184823
CHR_HSCHR12_4_CTG2	66546.3333	0.9379597
CHR_HSCHR12_4_CTG2_1	30296.2500	1.6340666
CHR_HSCHR12_5_CTG2	14548.0000	18.2157827
CHR_HSCHR12_5_CTG2_1	67828.0000	0.9882577
CHR_HSCHR12_6_CTG2_1	57640.5000	0.9307741
CHR_HSCHR12_7_CTG2_1	21404.0000	2.0161893
CHR_HSCHR13_1_CTG1	25567.2500	1.6697046
CHR_HSCHR13_1_CTG2	47615.3333	1.4802853
CHR_HSCHR13_1_CTG3	31581.4000	1.8598235
CHR_HSCHR13_1_CTG4	82773.0000	2.3356640
CHR_HSCHR13_1_CTG5	4528.6000	6.7708630

Group.1	x	sterr
CHR_HSCHR14_1_CTG1	94021.0000	1.8263448
CHR_HSCHR14_2_CTG1	10758.9000	1.0391880
CHR_HSCHR14_3_CTG1	14766.4211	0.7378461
CHR_HSCHR14_7_CTG1	44730.4074	0.8592562
CHR_HSCHR15_1_CTG1	12785.3333	1.4655537
CHR_HSCHR15_1_CTG3	42727.1667	1.1999474
CHR_HSCHR15_1_CTG8	15282.7000	1.8957592
CHR_HSCHR15_2_CTG3	20429.3333	2.1142493
CHR_HSCHR15_2_CTG8	65025.4000	0.6705249
CHR_HSCHR15_3_CTG3	18181.4444	1.2284435
CHR_HSCHR15_3_CTG8	40151.2500	1.5782223
CHR_HSCHR15_4_CTG8	39228.9663	0.4830508
CHR_HSCHR15_5_CTG8	27121.0000	1.4546385
CHR_HSCHR15_6_CTG8	48074.5814	0.9309749
CHR_HSCHR16_1_CTG1	60000.3143	0.5776564
CHR_HSCHR16_1_CTG3_1	38623.5000	0.5545525
CHR_HSCHR16_2_CTG3_1	22436.0000	3.0354037
CHR_HSCHR16_3_CTG1	16588.0000	2.1790948
CHR_HSCHR16_3_CTG3_1	25154.5000	6.7847592
CHR_HSCHR16_4_CTG1	12128.6667	3.8083032
CHR_HSCHR16_CTG2	20435.0000	4.7690003
CHR_HSCHR17_1_CTG1	32875.4444	5.0564213
CHR_HSCHR17_1_CTG2	15705.4444	2.2871383
CHR_HSCHR17_1_CTG4	124103.0000	1.2192646
CHR_HSCHR17_1_CTG5	40370.8182	1.5781003
CHR_HSCHR17_1_CTG9	18996.5000	1.2577959
CHR_HSCHR17_10_CTG4	18577.1818	0.5323237
CHR_HSCHR17_2_CTG1	39386.3333	1.0258749
CHR_HSCHR17_2_CTG2	26763.3000	0.9513372
CHR_HSCHR17_2_CTG4	98748.5000	1.5736908
CHR_HSCHR17_2_CTG5	36640.3793	1.3579685
CHR_HSCHR17_3_CTG2	20820.2000	1.0794966
CHR_HSCHR17_3_CTG4	37077.5000	1.4296608
CHR_HSCHR17_4_CTG4	10828.2000	1.4965122
CHR_HSCHR17_5_CTG4	7301.2500	2.5583464
CHR_HSCHR17_6_CTG4	8925.2000	2.9982560
CHR_HSCHR17_7_CTG4	38468.2679	0.7151356
CHR_HSCHR17_8_CTG4	33948.7500	2.6231611
CHR_HSCHR17_9_CTG4	83516.0000	2.9753877
CHR_HSCHR18_1_CTG1_1	34055.3333	1.7010106
CHR_HSCHR18_1_CTG2	25172.0000	1.4652436
CHR_HSCHR18_1_CTG2_1	22567.0000	2.6960073
CHR_HSCHR18_2_CTG1_1	60479.0000	1.9785247
CHR_HSCHR18_2_CTG2	3638.0000	NA
CHR_HSCHR18_2_CTG2_1	6020.8571	8.9545688
CHR_HSCHR18_3_CTG2_1	16119.4286	2.3326610
CHR_HSCHR18_4_CTG1_1	37814.0000	9.1416269
CHR_HSCHR18_ALT2_CTG2_1	6122.5714	8.5938290
CHR_HSCHR18_ALT21_CTG2_1	31667.5000	3.0611211
CHR_HSCHR19_1_CTG2	14253.7500	3.3049057
CHR_HSCHR19_1_CTG3_1	65396.0000	1.7603822
CHR_HSCHR19_2_CTG2	9443.2857	5.1219656

Group.1	x	sterr
CHR_HSCHR19_2_CTG3_1	15786.5000	5.0078433
CHR_HSCHR19_3_CTG2	8247.0000	6.6279706
CHR_HSCHR19_3_CTG3_1	8980.0000	2.8853706
CHR_HSCHR19_4_CTG2	51700.0000	1.1425466
CHR_HSCHR19_4_CTG3_1	20461.8611	0.6322291
CHR_HSCHR19_5_CTG2	5554.3333	0.8915110
CHR_HSCHR19KIR_ABC08_A1_HAP_CTG3_1	32151.2000	0.9857000
CHR_HSCHR19KIR_ABC08_AB_HAP_C_P_CTG3_1	38857.6667	1.2116923
CHR_HSCHR19KIR_ABC08_AB_HAP_T_P_CTG3_1	31609.8000	0.9819331
CHR_HSCHR19KIR_FH05_A_HAP_CTG3_1	31989.4000	0.9942905
CHR_HSCHR19KIR_FH05_B_HAP_CTG3_1	34722.1429	0.8539655
CHR_HSCHR19KIR_FH06_A_HAP_CTG3_1	32149.2000	0.9788975
CHR_HSCHR19KIR_FH06_BA1_HAP_CTG3_1	32612.2000	0.9759887
CHR_HSCHR19KIR_FH08_A_HAP_CTG3_1	31851.8000	0.9909528
CHR_HSCHR19KIR_FH08_BAX_HAP_CTG3_1	30944.8333	0.9112464
CHR_HSCHR19KIR_FH13_A_HAP_CTG3_1	39882.5000	0.9885677
CHR_HSCHR19KIR_FH13_BA2_HAP_CTG3_1	33381.0000	0.8865199
CHR_HSCHR19KIR_FH15_A_HAP_CTG3_1	31577.2000	0.9909393
CHR_HSCHR19KIR_FH15_B_HAP_CTG3_1	37856.6667	0.8865956
CHR_HSCHR19KIR_G085_A_HAP_CTG3_1	31602.8000	0.9736920
CHR_HSCHR19KIR_G085_BA1_HAP_CTG3_1	49834.3333	1.0356558
CHR_HSCHR19KIR_G248_A_HAP_CTG3_1	40114.2500	0.9885677
CHR_HSCHR19KIR_G248_BA2_HAP_CTG3_1	38281.4000	0.9314794
CHR_HSCHR19KIR_GRC212_AB_HAP_CTG3_1	36844.4000	0.9796373
CHR_HSCHR19KIR_GRC212_BA1_HAP_CTG3_1	49430.6667	1.0333112
CHR_HSCHR19KIR_LUCE_A_HAP_CTG3_1	40109.2500	0.9974922
CHR_HSCHR19KIR_LUCE_BDEL_HAP_CTG3_1	43459.0000	1.0156974
CHR_HSCHR19KIR_RP5_B_HAP_CTG3_1	41547.2500	1.0197624
CHR_HSCHR19KIR_RSH_A_HAP_CTG3_1	40104.5000	0.9885677
CHR_HSCHR19KIR_RSH_BA2_HAP_CTG3_1	31581.0000	0.9058354
CHR_HSCHR19KIR_T7526_A_HAP_CTG3_1	40101.0000	0.9885677
CHR_HSCHR19KIR_T7526_BDEL_HAP_CTG3_1	43502.0000	1.0069399
CHR_HSCHR19LRC_COX1_CTG3_1	26863.0000	0.7186160
CHR_HSCHR19LRC_COX2_CTG3_1	27119.4762	0.8079783
CHR_HSCHR19LRC_LRC_I_CTG3_1	24767.5294	1.0067153
CHR_HSCHR19LRC_LRC_J_CTG3_1	22444.0625	1.0737376
CHR_HSCHR19LRC_LRC_S_CTG3_1	20343.2500	1.0977374
CHR_HSCHR19LRC_LRC_T_CTG3_1	21938.8235	1.0061067
CHR_HSCHR19LRC_PGF1_CTG3_1	25135.0333	0.6785677
CHR_HSCHR19LRC_PGF2_CTG3_1	29400.8095	0.7794657
CHR_HSCHR2_1_CTG1	29077.3333	1.2326543
CHR_HSCHR2_1_CTG15	25590.7500	12.3858078
CHR_HSCHR2_1_CTG5	6073.0000	5.3258005
CHR_HSCHR2_1_CTG7	1729.3929	1.9166843
CHR_HSCHR2_1_CTG7_2	22059.0000	1.2755152
CHR_HSCHR2_2_CTG1	29274.3333	3.6128570
CHR_HSCHR2_2_CTG15	26728.2500	3.6593030
CHR_HSCHR2_2_CTG7	3888.7419	2.0897610
CHR_HSCHR2_2_CTG7_2	40346.0000	0.9865817
CHR_HSCHR2_3_CTG1	60566.0000	1.6009904
CHR_HSCHR2_3_CTG15	8989.5000	3.0147705
CHR_HSCHR2_3_CTG7_2	15568.7500	2.1811396

Group.1	x	sterr
CHR_HSCHR2_4_CTG1	18081.8571	3.6775769
CHR_HSCHR2_4_CTG7_2	6948.0000	2.9375429
CHR_HSCHR2_5_CTG7_2	8029.0000	2.0607311
CHR_HSCHR20_1_CTG1	118155.0000	1.7258691
CHR_HSCHR20_1_CTG2	28522.3333	1.7751137
CHR_HSCHR20_1_CTG3	22621.7143	2.0281799
CHR_HSCHR20_1_CTG4	16528.6667	1.4868365
CHR_HSCHR21_1_CTG1_1	132.0000	NA
CHR_HSCHR21_2_CTG1_1	53715.0000	0.3619614
CHR_HSCHR21_3_CTG1_1	663.6667	7.4827671
CHR_HSCHR21_4_CTG1_1	10125.0000	4.0016913
CHR_HSCHR21_5_CTG2	34936.0000	1.0214240
CHR_HSCHR21_6_CTG1_1	120432.0000	1.2440268
CHR_HSCHR21_8_CTG1_1	109046.0000	8.0889762
CHR_HSCHR22_1_CTG1	10829.4286	8.1862859
CHR_HSCHR22_1_CTG2	8866.0000	2.0895535
CHR_HSCHR22_1_CTG3	17481.5714	3.3396839
CHR_HSCHR22_1_CTG4	22610.8750	2.5522713
CHR_HSCHR22_1_CTG5	24414.0000	1.5691778
CHR_HSCHR22_1_CTG6	21911.0000	1.4650635
CHR_HSCHR22_1_CTG7	10612.0000	0.5505302
CHR_HSCHR22_2_CTG1	4535.5714	1.2000369
CHR_HSCHR22_3_CTG1	9883.8750	7.0326537
CHR_HSCHR22_4_CTG1	15014.8333	9.1940288
CHR_HSCHR22_5_CTG1	9656.9000	6.0608425
CHR_HSCHR3_1_CTG1	31927.3333	0.9854748
CHR_HSCHR3_1_CTG2_1	45296.5000	4.1340672
CHR_HSCHR3_1_CTG3	24679.1667	5.5926411
CHR_HSCHR3_2_CTG2_1	46592.3333	3.5358304
CHR_HSCHR3_2_CTG3	37048.6667	2.3715515
CHR_HSCHR3_3_CTG1	8832.0000	3.1462032
CHR_HSCHR3_3_CTG2_1	43790.5000	1.4700047
CHR_HSCHR3_3_CTG3	17273.0000	3.4083319
CHR_HSCHR3_4_CTG2_1	19113.3333	2.7868332
CHR_HSCHR3_4_CTG3	13016.1250	3.5710365
CHR_HSCHR3_5_CTG2_1	17468.3333	2.7518071
CHR_HSCHR3_5_CTG3	17366.6667	3.4077088
CHR_HSCHR3_6_CTG3	17090.0000	2.7116802
CHR_HSCHR3_7_CTG3	17484.1667	3.4068212
CHR_HSCHR3_8_CTG3	17699.6667	3.4276817
CHR_HSCHR3_9_CTG3	20294.5000	2.5783938
CHR_HSCHR4_1_CTG12	22401.0000	1.1494297
CHR_HSCHR4_1_CTG4	70095.0000	1.4760167
CHR_HSCHR4_1_CTG6	269460.0000	2.2250224
CHR_HSCHR4_1_CTG8_1	21532.3333	2.6114513
CHR_HSCHR4_1_CTG9	27322.5455	1.4346415
CHR_HSCHR4_2_CTG12	17284.5000	1.7517867
CHR_HSCHR4_3_CTG12	21351.3750	4.8160959
CHR_HSCHR4_4_CTG12	55207.0000	1.7414544
CHR_HSCHR4_5_CTG12	22165.2000	1.4943060
CHR_HSCHR4_6_CTG12	17952.4615	2.5461544
CHR_HSCHR4_7_CTG12	23732.3750	7.1118571

Group.1	x	sterr
CHR_HSCHR5_1_CTG1_1	51548.0588	3.2800786
CHR_HSCHR5_1_CTG5	50286.0000	2.1034217
CHR_HSCHR5_2_CTG1	44480.0000	4.2251211
CHR_HSCHR5_2_CTG1_1	47000.7692	2.6166715
CHR_HSCHR5_2_CTG5	15768.4000	3.3024801
CHR_HSCHR5_3_CTG1	21019.7500	1.3853938
CHR_HSCHR5_3_CTG1_1	10515.0000	2.0339007
CHR_HSCHR5_3_CTG5	14388.5000	2.8646030
CHR_HSCHR5_4_CTG1	12999.5000	0.9677000
CHR_HSCHR5_4_CTG1_1	54653.5000	1.3099863
CHR_HSCHR5_5_CTG1	9884.6250	2.5570824
CHR_HSCHR5_6_CTG1	16872.0000	4.7518782
CHR_HSCHR5_7_CTG1	15788.8333	9.5186530
CHR_HSCHR6_1_CTG2	13222.3333	1.8568616
CHR_HSCHR6_1_CTG3	16675.0000	18.9192827
CHR_HSCHR6_1_CTG4	22591.7143	5.8432931
CHR_HSCHR6_1_CTG5	16519.5556	2.3802366
CHR_HSCHR6_1_CTG7	713.0000	14.8303165
CHR_HSCHR6_1_CTG8	204876.5000	2.1728625
CHR_HSCHR6_1_CTG9	15742.0000	1.6874674
CHR_HSCHR6_8_CTG1	27155.5000	2.0353743
CHR_HSCHR6_MHC_APD_CTG1	32086.4625	0.8409252
CHR_HSCHR6_MHC_COX_CTG1	16241.7790	0.4966280
CHR_HSCHR6_MHC_DBB_CTG1	17577.6747	0.5049966
CHR_HSCHR6_MHC_MANN_CTG1	18491.7793	0.5202857
CHR_HSCHR6_MHC_MCF_CTG1	17280.9259	0.4485155
CHR_HSCHR6_MHC_QBL_CTG1	18862.2000	0.5036147
CHR_HSCHR6_MHC_SSTO_CTG1	19720.4800	0.4389742
CHR_HSCHR7_1_CTG1	17529.5000	2.5473211
CHR_HSCHR7_1_CTG4_4	19438.3333	7.4917721
CHR_HSCHR7_1_CTG6	20766.0000	1.0031720
CHR_HSCHR7_1_CTG7	6126.6154	2.7871034
CHR_HSCHR7_2_CTG1	23620.5000	1.6704492
CHR_HSCHR7_2_CTG4_4	29544.4000	1.0493543
CHR_HSCHR7_2_CTG6	14736.9592	0.6718175
CHR_HSCHR7_2_CTG7	21245.2000	4.8167154
CHR_HSCHR7_3_CTG6	26115.7500	2.2374090
CHR_HSCHR8_1_CTG1	15851.3077	2.3027657
CHR_HSCHR8_1_CTG6	46897.5000	1.3851596
CHR_HSCHR8_1_CTG7	68927.0000	1.3888607
CHR_HSCHR8_2_CTG1	18450.9091	3.3987307
CHR_HSCHR8_2_CTG7	25128.3333	3.5300769
CHR_HSCHR8_3_CTG1	9292.0000	2.1082672
CHR_HSCHR8_3_CTG7	10563.5263	1.5539042
CHR_HSCHR8_4_CTG1	21105.2000	5.6059970
CHR_HSCHR8_4_CTG7	15182.2500	3.2710861
CHR_HSCHR8_5_CTG1	25269.7778	2.3645613
CHR_HSCHR8_5_CTG7	12228.8889	2.1716530
CHR_HSCHR8_6_CTG1	18570.8000	1.9508802
CHR_HSCHR8_6_CTG7	19793.0000	5.8190434
CHR_HSCHR8_7_CTG1	34953.0000	3.3864559
CHR_HSCHR8_8_CTG1	24860.6923	1.5244919

Group.1	x	sterr
CHR_HSCHR8_9_CTG1	295414.0000	0.9075555
CHR_HSCHR9_1_CTG1	21201.6667	9.3548698
CHR_HSCHR9_1_CTG2	57651.0000	1.7110620
CHR_HSCHR9_1_CTG3	57157.0000	2.3138766
CHR_HSCHR9_1_CTG4	8145.0000	7.5095719
CHR_HSCHR9_1_CTG5	61839.6667	1.5447815
CHR_HSCHRX_1_CTG3	14196.8333	2.0505401
CHR_HSCHRX_2_CTG12	14807.0000	1.3926955
CHR_HSCHRX_2_CTG3	15236.0909	2.1628191
GL000008.2	13911.0000	1.9175550
GL000009.2	34425.0000	1.5564201
GL000194.1	19552.6000	1.7479385
GL000195.1	20012.8333	1.5990353
GL000205.2	14508.7143	1.7468081
GL000213.1	7898.5000	2.7780378
GL000214.1	29148.6667	2.6417544
GL000216.2	2317.3667	1.2519264
GL000218.1	17385.2500	1.6572159
GL000219.1	14087.8000	2.5358994
GL000220.1	40440.0000	4.1584722
GL000221.1	34246.5000	1.8118949
GL000224.1	16046.8000	1.8625018
GL000225.1	23050.0000	2.5672001
KI270330.1	192.0000	NA
KI270435.1	428.0000	NA
KI270438.1	938.0714	0.8492870
KI270442.1	45939.0000	3.4372081
KI270519.1	185.0000	NA
KI270528.1	795.0000	3.2135970
KI270706.1	63843.0000	1.3193450
KI270708.1	21926.6667	5.7168369
KI270709.1	590.0909	1.9208307
KI270711.1	25967.0000	1.4063224
KI270712.1	9435.1429	7.1060688
KI270713.1	12980.0000	1.3592794
KI270714.1	10396.5000	1.7218315
KI270716.1	578.0000	1.6308141
KI270717.1	7474.0000	11.7396323
KI270718.1	941.5000	2.2957991
KI270719.1	54154.5000	1.6263810
KI270720.1	7587.0000	1.5894286
KI270721.1	12249.5000	1.3840790
KI270722.1	61204.0000	3.5464678
KI270723.1	9846.0000	2.8669398
KI270724.1	5881.0000	4.1142169
KI270725.1	22660.7500	4.4729189
KI270726.1	17058.0000	2.1769372
KI270727.1	13463.8235	1.4874710
KI270728.1	26830.7105	1.0228750
KI270729.1	705.6091	0.6726096
KI270730.1	1017.5625	0.8974439
KI270731.1	11046.1250	3.0478640

Group.1	x	sterr
KI270732.1	445.0000	NA
KI270733.1	35641.5000	3.9444475
KI270734.1	15543.8571	2.2461385
KI270735.1	576.5000	6.1848162
KI270736.1	440.0000	NA
KI270737.1	546.5536	0.8092471
KI270738.1	700.8409	0.5895912
KI270741.1	93756.0000	4.2056742
KI270742.1	47580.5000	1.9327752
KI270743.1	19314.2000	1.7074009
KI270744.1	16689.6667	2.0282471
KI270745.1	3710.0000	3.0571544
KI270746.1	9526.0000	7.4585567
KI270747.1	1577.9118	0.8031156
KI270748.1	27924.0000	1.4478195
KI270749.1	18103.6667	4.3157798
KI270750.1	62365.0000	3.9478050
KI270751.1	21026.6667	5.2180775
KI270752.1	19326.0000	1.1919079
KI270753.1	10166.6667	9.5109358
KI270754.1	11464.0000	4.3667028
KI270755.1	24050.0000	3.0165009
KI270756.1	550.0741	0.9775761
X	49383.0133	0.1869751
Y	41082.2401	0.3239418

```r
library(ggplot2)
ExonX <- subset(Homo_sapien_exon, chromosome == "X")
ExonY <- subset(Homo_sapien_exon, chromosome == "Y")
hist(ExonX$length)
```
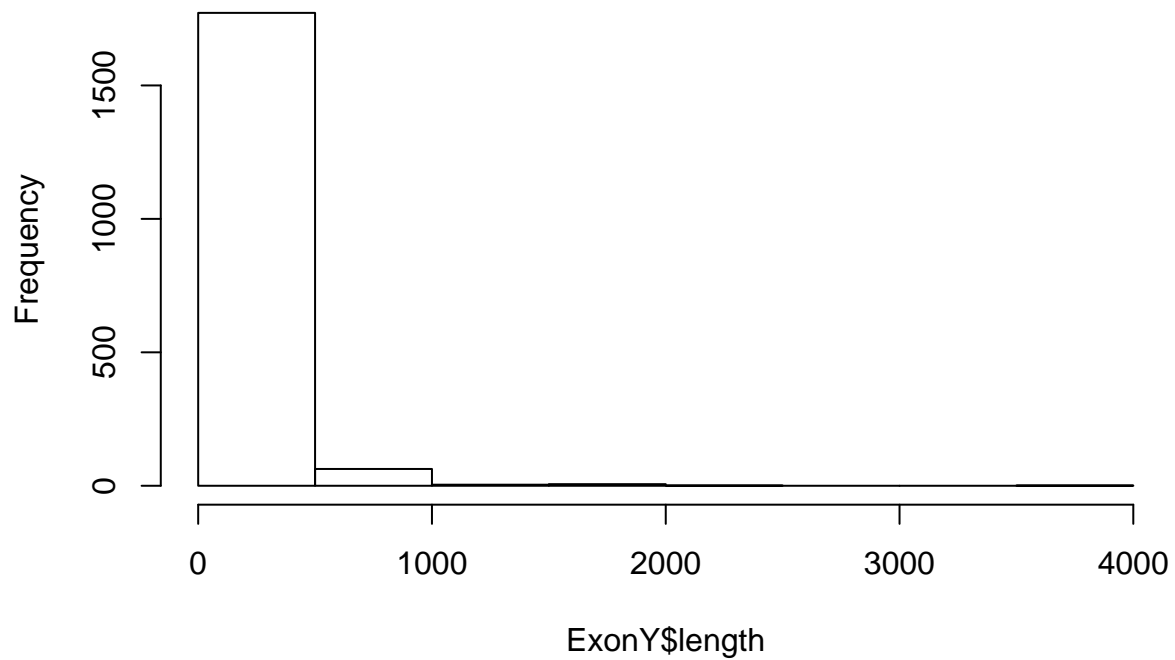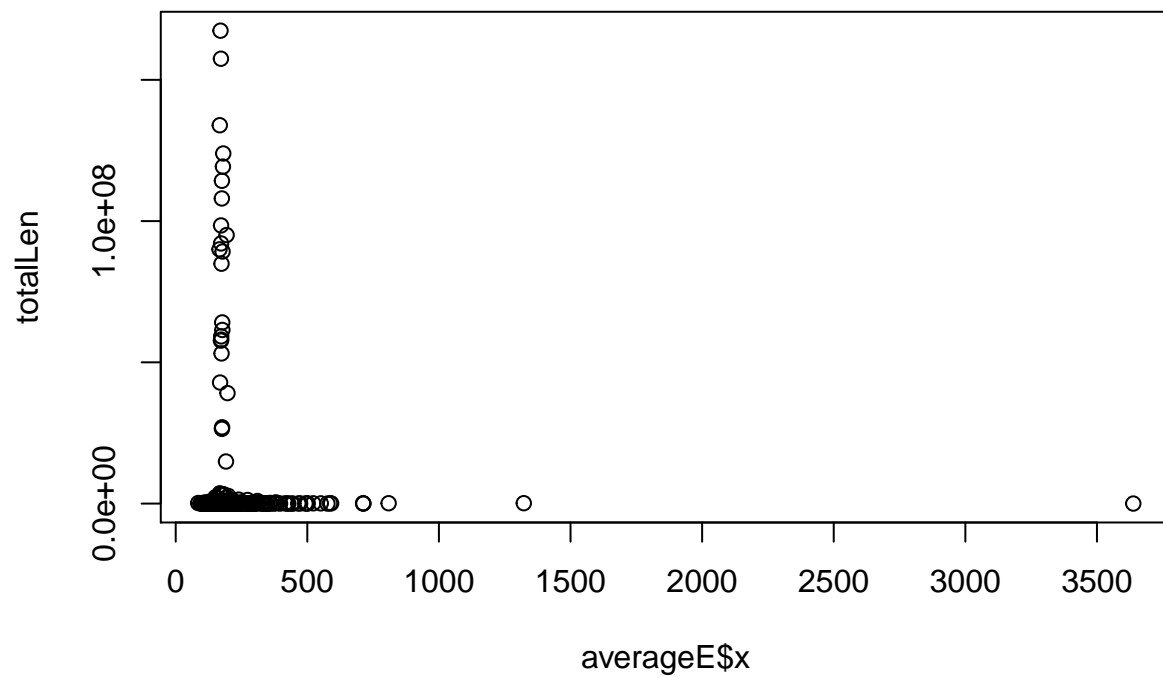
Histogram of ExonX$length
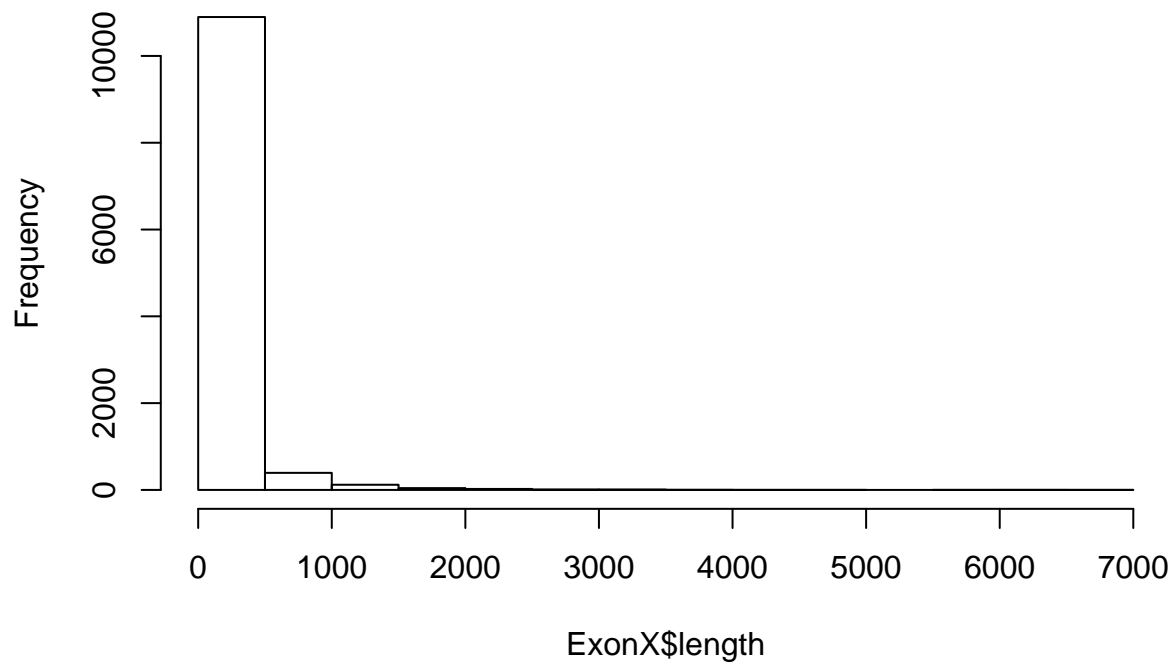

```r
hist(ExonY$length)
```

Histogram of ExonY$length


```r
totalLen <- sumE$x + sumTran$x
plot(averageE$x, totalLen)
```

There is no relationship between total chromosome length and average exon length