location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr11:84867425-84942100	74676	73,814	45,409	41,288	51,061	36,027	51,258	38,725	73,814	46,392	46,353	47,628	40,018	26,939	Locus contains a 28S rRNA-like element, line elements, and high conservation in an intron of mRNA DLG2.
chr11:65022925-65031750	8826	20,255	11,279	13,377	7,422	11,233	3,986	20,255	1,504	19,810	14,704	11,628	12,850	7,301	Locus contains ncRNA MALAT1.
chr2:202890425-202914025	23601	2,716	1,523	1,726	823	1,204	2,716	1,260	1,758	1,800	843	927	1,979	1,720	Locus contains a SRP_RNA-related
chr21:14365075-14379325	14251	2,229	842	2,229	1,512	606	845	611	492	774	368	522	440	865	Locus contains a 28S_rRNA-related
chr11:64946775-64971250	24476	2,137	868	1,155	1,044	623	342	1,295	179	2,137	458	1,128	693	493	Locus contains ncRNA NEAT1.
chr15:22809575-22919700	110126	1,816	557	114	186	430	1,816	1,006	114	287	783	516	357	520	PWS locus, including snoRNA clusters HBII-85 and HBII-52, IPW (ncRNA), and more
chr12:39871225-40111600	240376	1,446	566	464	334	1,446	587	1,274	283	199	363	454	217	606	Locus contains mRNA PDZRN4 but reads are elsewhere
chr8:67992975-68000050	7076	1,339	621	299	405	290	293	367	253	1,049	822	1,029	1,339	681	Locus contains ncRNA SNHG6, snoRNA HBII-276, and mRNA C8orf45. Reads are from HBII-276.
chr4:113827100-114091750	264651	1,197	490	436	356	452	369	223	523	342	1,197	556	609	330	Locus contains hY3_RNA-related, SRP_RNA-related, and mRNA.
chr7:130178825-130451400	272576	1,188	418	202	213	217	105	299	152	668	1,188	482	742	330	Locus contains ncRNA FLJ43663 (NR_015431.1)
chr12:126216200-126231125	14926	792	391	792	541	274	638	388	565	275	191	230	205	207	Locus contains a 28S rRNA-like gene.
chr8:125239925-125298400	58476	726	95	4	105	9	5	12	726	32	10	12	109	15	Locus contains ESTs
chrX:73336425-73429775	93351	618	253	231	239	164	84	325	68	310	618	127	406	208	Locus contains misRNA NCRNA00182, miRNAs, and ESTs.
chr6:21774653-22329825	555173	597	154	80	123	79	132	118	86	141	597	65	124	150	Locus contains no known genes but many ESTs and mRNAs.
chr2:106659950-106724850	64901	586	261	170	117	207	94	341	129	393	586	83	459	295	Locus contains ESTs
chr2:209099000-209402250	303251	567	83	22	42	22	19	567	13	41	65	19	49	53	
chr4:88997950-89088100	90151	550	249	165	84	355	550	148	138	144	477	293	207	180	
chr2:186421575-187045450	623876	543	192	104	165	97	91	272	47	162	543	120	246	270	Interesting -- locus contains no genes but high conservation and general transcription.
chrX:72949400-72989313	39914	480	127	1	235	74	1	241	0	156	480	208	1	7	Locus contains ncRNA XIST.
chr3:62910725-63091200	180476	464	96	7	464	87	5	121	209	94	24	3	21	25	
chr8:32905675-33033300	127626	456	79	16	15	38	19	456	7	20	13	236	19	26	
chrX:93434300-94126850	692551	455	107	33	49	35	25	279	25	455	86	28	60	99	
chr6:72128125-72186342	58218	392	63	21	11	34	18	392	11	92	26	29	34	30	Locus contains ncRNA C6orf155 and miRNAs
chr20:34091925-34103650	11726	386	190	141	88	229	386	172	79	202	274	191	168	162	Locus contains ESTs and ncRNA LOC647979 (NR_027451).
chr1:220524025-220686875	162851	376	174	376	200	162	97	181	41	315	55	68	51	367	
chr5:148767275-148793000	25726	368	81	40	368	52	6	27	4	34	193	13	79	70	Locus contains ncRNA LOC728264 and miRNAs.
chr14:100364750-100405275	40526	367	69	11	27	18	170	17	4	13	367	8	49	76	Locus contains ncRNA MEGS.
chrX:110643475-110767925	124451	358	196	147	107	198	121	157	107	195	358	332	230	200	
chr8:134423875-134497625	73751	358	137	137	57	95	131	140	110	84	358	151	92	156	
chr19:20755700-20823525	67826	354	73	29	40	27	45	58	11	46	354	22	94	77	
chr7:137497625-137771725	274101	338	155	86	134	124	99	123	78	276	210	78	338	162	
chr10:19970175-20140000	169826	336	78	24	105	43	34	61	336	27	149	23	21	33	
chrX:64126100-64618150	492051	334	144	74	197	80	87	188	41	136	334	58	226	163	
chr6:77666425-78134625	468201	300	89	44	58	63	25	146	19	62	300	22	109	138	Locus containsno genes or ESTs
chr4:67977175-68014325	37151	294	113	140	42	54	294	85	204	89	90	62	105	73	
chr6:106965550-107033200	67651	290	146	79	62	217	290	122	118	175	146	123	191	83	
chr4:12676250-12957000	280751	290	128	89	97	132	290	118	75	83	185	77	134	130	Locus contains ncRNA HSP90AB2P
chr14:70858200-71037050	178851	284	91	45	88	48	37	97	33	187	67	11	284	100	Locus contains ESTs
chr5:60665775-60714725	48951	277	78	33	66	47	32	78	36	102	277	18	118	55	Locus contains ESTs
chr14:100459225-100609600	150376	275	82	24	23	34	242	24	18	26	275	20	92	121	Locus contains snoRNA cluster 14q
chr3:175644725-176014550	369826	264	72	73	50	45	27	82	11	55	264	44	66	74	Locus contains ESTs and mRNAs
chr17:67895375-68098675	203301	264	35	5	264	5	21	12	4	31	10	3	8	20	
chr8:17399650-17430625	30976	231	36	4	5	9	5	13	74	9	231	29	7	13	Locus contains ESTs
chr5:88250875-88580200	329326	214	54	20	34	21	26	31	8	44	214	84	64	48	
chrX:114863475-114997900	134426	200	78	20	118	69	48	169	16	59	200	12	44	102	
chr5:33032900-33307175	274276	197	83	56	73	76	40	52	62	78	197	62	128	84	
chr10:6228325-6278100	49776	194	82	71	67	47	194	59	71	63	85	75	122	48	
chr2:134595725-134694600	98876	190	56	30	91	43	18	51	9	69	64	9	190	37	
chr22:25386775-25639800	253026	183	100	71	146	63	99	90	58	97	134	55	183	105	
chrX:55952950-56258125	305176	174	86	61	92	48	35	129	20	89	174	37	136	119	
chr1:172098475-172103825	5351	174	101	104	106	39	89	80	96	149	174	53	153	66	Locus contains ncRNA GAS5 snoRNA RNA C/D box cluster, including U44, U47, U74-81. U76 is highest expressed.
chr8:58277700-58297325	19626	172	27	1	0	0	1	118	0	0	0	0	0	172	
chrX:73081400-73149600	68201	172	60	33	41	40	29	80	20	59	172	54	77	59	
chr7:18241000-18493675	252676	168	37	32	23	27	20	16	7	31	28	8	168	49	
chr20:36470500-36515575	45076	161	73	59	149	25	51	48	60	93	51	21	83	161	Looks great!! Contains ncRNA ACA60, U71a, and U71d
chrX:135771475-135783050	11576	160	73	29	35	68	24	70	19	68	108	79	160	141	
chr2:127007450-127034900	27451	159	60	62	32	52	159	49	22	66	45	20	96	56	
chr10:67000950-67213100	212151	158	40	10	24	13	10	74	17	23	158	7	75	33	
chr5:144793925-145104175	310251	156	61	29	156	70	18	38	9	64	145	21	55	67	
chr1:141730725-141862525	131801	156	80	59	47	68	28	57	17	88	156	58	153	143	
chrX:148863050-149024650	161601	156	57	29	69	22	24	93	7	57	156	30	52	89	
chr11:86297350-86316725	19376	151	36	151	9	23	12	31	1	30	79	19	15	24	Locus contains ESTs
chr9:2442800-2542025	99226	150	23	31	7	14	7	11	4	10	150	4	7	7	
chr6:119718475-120097975	379501	144	52	54	35	30	22	85	8	44	83	18	144	53	
chrX:97432775-97543875	111101	142	84	141	80	47	62	74	87	87	142	24	104	72	
chr3:115526175-115535575	9401	141	54	41	10	64	30	78	36	35	141	51	48	62	Locus contains ESTs, conserved blocks, and a possible 3' UTR extension of a nearby mRNAs
chr10:46514400-46569425	55026	141	57	53	43	45	78	31	59	44	141	32	60	38	
chr8:130300925-130810225	509301	139	35	18	40	14	13	31	17	33	37	13	139	29	
chr11:39456550-40064650	608101	137	61	31	64	33	28	62	18	61	137	32	106	101	
chr5:60715925-60749750	33826	136	57	37	56	44	33	51	33	83	136	12	92	55	
chr8:127908350-128572000	663651	133	68	39	72	41	35	133	62	90	73	33	90	77	
chr1:206037850-206108750	70901	133	66	42	70	45	22	101	9	85	105	58	133	51	
chr3:64987550-65012925	25376	131	19	3	6	4	2	20	2	15	131	4	6	12	
chr16:83806950-84141650	334701	127	62	49	127	29	14	48	36	40	125	81	50	79	
chrX:74681500-74831575	150076	127	50	24	45	32	39	67	13	45	127	23	54	82	
chr8:135860125-135912450	52326	126	49	23	29	47	8	126	33	72	78	48	41	31	
chr12:90890975-91048525	157551	124	32	17	14	15	6	24	18	56	48	11	124	15	
chrX:62523600-62696725	173126	123	63	37	62	49	35	95	20	68	123	34	95	71	
chr18:35328475-35629325	300851	122	23	7	38	7	5	11	3	13	20	7	15	122	
chr1:245418575-245440175	21601	122	35	31	22	24	14	35	9	50	25	11	122	37	
chr21:29671250-29823325	152076	122	48	26	38	36	20	63	21	73	39	65	122	28	
chr7:80790500-80803425	12926	119	44	83	119	31	74	33	26	31	17	20	20	33	
chr3:152670000-152720900	50901	119	19	8	9	7	5	9	2	18	119	5	12	12	
chr20:53108150-53174325	66176	116	58	46	49	53	25	32	52	51	116	78	92	50	
chr7:33631025-33852800	221776	115	34	22	31	17	12	44	5	37	115	9	49	32	
chr22:44829900-44895200	65301	114	35	21	64	26	14	40	4	29	114	12	35	22	
chr7:19918100-20126725	208626	114	74	67	61	67	51	76	79	82	114	47	107	63	
chr13:23456900-23626575	169676	114	72	51	32	111	84	72	59	70	64	114	83	54	
chr7:63370950-63480450	109501	113	46	26	24	26	38	52	7	36	113	18	94	77	
chr1:121029075-121187200	158126	110	35	24	39	21	110	18	23	24	11	11	41	65	
chr4:106079150-106264700	185551	110	23	9	17	9	7	110	6	17	29	10	19	21	
chr21:28840100-29136975	296876	109	50	23	52	28	19	42	15	76	89	36	109	57	
chr1:65291650-65304400	12751	109	24	19	12	11	6	17	3	21	109	23	30	15	
chr6:29809950-29848275	38326	108	41	28	18	42	108	24	40	48	36	28	53	23	
chr15:19183225-19203975	20751	108	52	48	28	51	40	41	57	49	49	36	108	63	
chr2:54096175-54165975	69801	106	72	64	55	71	74	68	53	60	95	63	106	87	
chr10:119231725-119242550	10826	106	21	16	3	3	34	106	0	0	41	5	0	27	Locus contains ncRNA EMX2OS
chr8:92141050-92151400	10351	103	50	28	10	87	103	57	27	30	42	40	53	78	Locus contains ESTs and mRNAs. Data suggest a novel, strand-specific ncRNA.
chr14:52757725-52912850	155126	103	31	26	32	13	9	25	5	28	54	11	34	103	
chr6:3121200-3139125	17926	101	14	14	8	2	101	8	10	1	1	1	1	2	
chrX:45482950-45595350	112401	101	32	21	32	11	25	25	10	73	101	8	27	20	
chr6:34352100-34361825	9726	99	36	23	12	32	99	41	15	21	47	48	34	23	
chr8:60225475-60995275	769801	99	57	38	60	33	32	99	33	80	91	29	68	68	
chr14:85408675-85959800	551126	98	52	35	60	34	28	60	15	61	86	35	98	61	
chr17:42482352-42533565	51214	98	45	27	49	32	39	54	10	42	98	21	71	55	
chr5:102119525-102221625	102101	97	46	27	22	49	11	46	9	97	77	54	79	33	
chr13:49793725-49890200	96476	97	51	53	31	50	37	32	39	56	97	40	77	46	
chr12:45112400-45261050	148651	97	47	17	45	16	19	90	45	40	97	39	56	53	
chrX:101911200-102072375	161176	96	47	38	46	31	33	71	14	48	96	22	65	54	
chr10:49590325-49693725	103401	96	23	17	28	11	9	14	14	21	21	10	96	9	
chr12:32445125-32538825	93701	95	36	15	86	19	9	95	11	41	59	5	18	40	
chr13:49555025-49595650	40626	95	35	22	23	28	9	30	13	61	42	42	95	25	
chrX:112699025-113202875	503851	93	38	20	93	20	18	41	15	42	57	20	51	42	
chr22:29695634-29706450	10817	93	57	45	37	52	58	68	29	47	88	31	82	93	Locus contains ncRNA TUG1.
chr6:86438525-86452775	14251	93	43	29	30	26	33	25	13	63	93	72	55	30	Locus contains ncRNA U50
chr5:92890475-92942875	52401	92	20	6	7	5	25	17	2	18	92	1	21	29	
chr8:128891450-129010774	119325	92	25	12	27	12	7	9	5	22	92	15	48	31	
chr2:123438725-124477200	1038476	91	57	40	66	34	38	64	31	82	91	32	72	73	
chr14:95576925-95731700	154776	91	20	8	16	8	91	10	3	35	17	4	14	10	
chr3:64872075-64896750	24676	90	14	5	7	5	3	14	1	15	90	4	5	10	
chr6:14338050-14736875	398826	89	36	25	34	25	15	40	14	89	33	23	65	31	
chr7:66441725-66470800	29076	88	14	3	8	4	4	13	1	5	11	88	8	6	
chr18:72307325-72331925	24601	88	20	6	12	7	3	15	6	18	88	10	23	30	
chr1:93548254-93583962	35709	88	33	22	20	14	17	46	4	38	88	9	56	51	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr1:174109725-174170025	60301	86	54	58	86	38	46	25	82	47	73	38	78	24	
chr6:42833450-42867750	34301	86	34	18	46	17	13	34	4	27	86	32	69	29	
chr13:81905500-83297700	1392201	86	56	34	76	34	56	70	20	61	86	28	75	76	
chr3:13011600-13315275	303676	86	46	61	59	27	65	22	33	55	20	23	86	51	
chrX:149113300-149357500	244201	85	42	34	30	29	31	39	26	59	85	24	35	69	
chr13:99372350-99383275	10926	82	35	82	63	8	68	13	49	24	8	11	25	35	
chr1:197068975-197174200	105226	81	21	10	5	12	14	16	5	56	12	2	81	15	
chr3:196904200-196928625	24426	80	41	16	74	23	31	80	9	29	71	34	34	44	
chr10:42319800-42366925	47126	80	36	23	20	25	46	36	7	34	75	13	80	34	
chr7:135330850-135602275	271426	79	29	17	27	14	12	19	7	37	28	10	79	68	
chr7:104403400-104440275	36876	79	32	15	41	18	8	43	9	24	69	15	79	29	
chr1:173389275-173428400	39126	79	25	35	12	23	12	26	18	43	12	6	79	10	
chr5:131713500-131731950	18451	78	31	18	41	19	11	78	6	15	39	60	16	31	
chr19:32905775-33020475	114701	78	44	31	35	32	37	56	19	32	75	15	78	72	
chrX:139623150-139637100	13951	78	10	3	10	4	78	1	0	2	2	3	6	4	Locus contains ncRNA RP1-177G6.2
chr8:129045250-129106528	61279	77	20	6	24	8	3	5	2	16	77	12	39	29	
chr6:30364275-30401550	37276	77	34	21	35	25	22	49	13	28	77	13	58	30	
chr4:3542725-3692050	149326	76	10	2	7	2	2	76	3	4	4	1	3	5	
chr2:217838575-218189250	350676	76	35	44	34	45	16	30	5	34	54	13	76	37	
chr13:39764925-39866925	102001	74	29	60	17	14	9	17	74	43	27	20	16	20	
chr5:127320775-127407525	86751	73	36	24	24	29	29	42	12	25	69	25	73	38	
chr8:90781700-90817050	35351	72	26	17	20	21	16	38	5	26	72	7	40	31	
chr16:10338750-10419300	80551	72	21	8	15	12	8	16	10	27	23	3	33	72	
chr13:66853600-67679750	826151	71	38	27	38	26	24	43	15	44	71	22	49	55	
chr11:27551550-27606750	55201	71	32	23	15	33	22	28	26	26	71	42	43	26	
chr1:191490425-191504575	14151	70	31	25	9	26	36	35	6	30	70	29	41	33	
chr5:141048275-141198325	150051	69	20	18	30	17	23	25	2	69	10	12	5	12	
chr3:64827825-64839350	11526	69	10	3	3	3	2	11	0	11	69	3	3	7	
chr8:52950675-53051275	100601	68	30	16	21	20	10	33	7	34	57	33	68	31	
chr5:67121850-67148800	26951	68	8	0	1	1	0	2	68	6	2	2	1	7	
chr1:237661375-237853250	191876	67	17	5	26	6	11	18	6	19	67	5	13	17	
chr7:78921550-78942375	20826	66	38	50	9	36	41	66	16	27	65	15	51	41	
chrX:53141125-53204125	63001	66	33	24	29	23	23	41	9	31	66	33	43	37	
chr8:114557150-115165825	608676	66	36	21	42	24	21	41	15	48	66	20	56	43	
chr1:83879475-84089425	209951	66	22	4	17	10	10	66	17	14	26	6	37	37	
chr8:61960000-62228150	268151	65	33	22	51	29	25	26	15	30	35	18	65	50	
chr7:55494425-55505775	11351	65	20	22	16	18	16	23	11	16	17	10	65	11	
chr7:22570350-22697250	126901	65	15	7	12	12	6	6	6	25	6	9	65	16	
chr5:27086125-27661000	574876	65	31	17	30	23	18	65	13	55	37	11	36	39	
chr3:8312700-8451425	138726	64	22	21	17	11	21	34	4	16	64	11	19	26	
chrX:71049200-71256150	206951	64	40	33	59	36	34	27	32	64	59	22	46	33	
chr11:121514300-121586150	71851	63	16	6	7	15	12	25	4	16	63	3	3	17	
chr2:177854175-177922425	68251	63	14	11	8	7	11	63	2	8	12	5	12	13	
chr3:3963675-4110125	146451	62	38	25	37	29	27	48	19	33	54	33	55	62	
chr16:71044100-71322025	277926	62	32	17	43	18	17	43	14	28	54	15	45	62	
chr6:155200400-155254075	53676	62	30	13	29	23	13	31	8	29	62	33	59	27	
chr6:11226350-11254175	27826	62	16	7	8	14	62	9	15	9	14	10	14	11	
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location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
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chr21:34451725-34596450	144726	31	13	6	14	7	7	31	3	12	23	10	14	14	
chr3:195671625-195688075	16451	31	16	20	9	21	6	19	10	31	29	5	19	12	
chr7:140065900-140073425	7526	31	16	10	7	10	31	17	9	18	21	9	22	19	
chr10:9685125-9966750	281626	31	16	9	18	9	13	17	4	20	28	8	18	31	
chr6:131664050-131812075	148026	30	11	5	14	6	4	10	3	30	12	4	25	12	
chrX:109471950-109537125	65176	30	7	2	4	6	5	4	2	3	11	3	5	30	
chr2:218542550-218575300	32751	30	8	14	10	5	3	6	0	5	30	2	4	6	
chr1:199749575-199812300	62726	30	19	16	30	15	21	16	18	23	17	9	24	18	
chrX:56788625-56810725	22101	30	12	6	9	7	4	16	1	18	30	3	27	11	
chr8:104008750-104088225	79476	29	14	8	11	6	12	26	3	17	29	10	17	17	
chr2:138865825-138928025	62201	29	14	10	10	12	9	17	5	11	29	7	26	19	
chr5:38858825-38880150	21326	29	11	4	5	8	5	16	4	18	29	4	13	15	
chr9:131276675-131307550	30876	29	17	16	18	12	12	29	9	24	28	6	16	16	
chr20:48468950-48485200	16251	29	9	8	2	6	29	9	12	22	2	2	1	7	
chr13:64705550-64987675	282126	29	16	11	18	8	8	15	10	29	26	8	19	25	
chr11:22854575-22984925	130351	29	13	11	15	9	4	16	9	12	29	7	18	18	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr18:40170025-40351650	181626	29	18	10	20	11	9	26	11	21	29	10	24	26	
chr11:133854275-133909025	54751	29	8	2	29	2	2	27	3	6	6	2	5	5	
chr3:172974575-173020300	45726	29	8	6	17	4	4	3	3	5	29	1	14	5	
chr1:70914525-71011625	97101	28	8	5	5	5	3	28	3	9	10	4	7	9	
chr3:36894500-36969325	74826	28	13	8	23	7	7	6	4	18	27	2	28	12	
chr13:21470600-21702150	231551	28	13	9	15	6	3	28	7	17	6	2	23	27	
chr1:59032550-59113800	81251	28	10	6	12	3	7	12	1	10	28	9	19	8	
chr2:157897775-157942400	44626	28	10	6	8	5	4	8	3	18	13	4	28	9	
chr4:53272125-53310900	38776	28	10	3	10	6	5	10	7	17	11	4	9	28	
chr4:54914475-55161475	247001	28	15	8	23	9	7	18	7	20	28	6	19	21	
chr3:163927725-164333150	405426	28	15	9	22	10	9	17	4	15	28	9	19	21	
chr6:2198150-2222350	24201	28	15	11	19	10	6	27	7	15	28	7	22	15	
chr9:2193975-2294325	100351	28	10	5	6	4	4	7	7	28	22	4	12	9	
chrX:50921225-51011000	89776	27	10	5	9	5	6	10	2	9	27	6	20	11	
chr2:46863875-46966525	102651	27	10	7	10	4	7	7	5	27	17	7	12	9	
chr11:115542275-115819825	277551	27	10	6	15	5	11	27	10	8	7	3	8	13	
chr7:7895500-7963275	67776	27	12	7	8	6	4	15	2	16	27	14	20	16	
chrX:6755350-6907125	151776	27	17	13	22	11	8	25	6	18	26	12	27	20	
chr22:16799450-16847225	47776	27	13	5	27	11	7	21	3	12	14	7	21	14	
chr12:9371350-9397650	26301	27	4	1	2	1	1	3	1	2	2	1	2	27	
chr1:118176175-118202375	26201	27	13	10	5	16	18	27	4	10	14	13	16	12	
chr6:147231675-147541450	309776	26	15	6	22	9	14	12	4	16	26	6	25	26	
chrX:100582750-100611900	29151	26	10	7	10	5	4	14	2	9	26	7	15	13	
chr10:97629600-97656950	27351	26	10	5	7	8	4	14	2	12	15	4	26	10	
chr2:74066300-74115525	49226	26	11	10	26	8	3	10	3	17	11	2	25	6	
chr6:126421650-126451675	30026	26	10	3	5	6	4	21	11	5	26	10	14	8	
chr4:116354750-116650400	295651	26	15	10	20	11	9	17	5	18	23	7	19	26	
chr19:52838475-52873175	34701	26	10	7	26	7	5	9	2	14	9	10	13	9	
chr2:81715400-81955300	239901	26	14	10	17	9	8	18	5	13	26	9	19	20	
chr13:37514150-37567175	53026	26	13	6	8	23	6	26	4	11	22	6	12	15	
chr2:216786600-216817600	31001	26	10	10	6	6	26	9	3	11	9	10	11	7	
chr11:23093750-23240675	146926	26	14	7	21	8	14	17	5	17	26	7	19	17	
chr2:31919400-31946050	26651	25	11	4	7	8	5	9	4	9	19	16	25	12	
chr14:60598575-60663800	65226	25	14	16	13	7	8	18	2	16	25	16	14	19	
chr4:24126625-24137100	10476	25	10	2	5	7	9	10	2	10	25	8	21	7	
chr1:171471125-171555075	83951	25	13	6	9	8	7	15	6	16	25	8	23	14	
chr2:91630925-91689500	58576	25	15	19	23	16	17	17	8	7	13	12	3	25	
chr6:127722975-127746550	23576	25	11	6	7	10	5	12	8	13	25	6	15	15	
chr5:123269425-123559950	290526	25	15	10	17	12	12	15	5	18	25	10	19	20	
chr13:109079875-109141250	61376	25	8	3	6	4	5	5	2	12	7	3	25	13	
chr7:63559775-63598600	38826	25	8	4	6	5	6	9	2	9	25	3	11	12	
chr4:7154500-7226600	72101	25	13	8	9	10	23	25	9	13	11	11	16	10	
chr14:95058100-95070625	12526	25	12	9	15	5	8	10	7	11	25	7	23	13	
chr2:40800500-41088800	288301	25	14	12	19	10	9	12	5	23	25	7	12	23	
chr6:6628525-6756250	127726	25	11	11	10	7	4	25	5	13	12	13	9	18	
chr1:85705400-85746650	41251	25	10	5	3	13	4	7	5	18	13	6	25	8	
chrX:62428575-62446375	17801	24	11	8	5	9	24	8	4	7	18	8	11	14	
chr7:37575125-37663375	88251	24	13	5	12	7	19	13	7	12	18	8	24	23	
chr11:120733150-120748050	14901	24	13	10	13	19	13	10	6	10	20	11	6	24	
chr1:93931500-94066425	134926	24	16	11	16	14	8	19	4	19	24	23	20	20	
chr5:169491450-169587275	95826	24	5	2	4	1	1	24	1	5	4	1	4	3	
chr12:45330500-45384750	54251	24	10	3	8	4	5	24	7	9	19	10	11	12	
chr11:12937650-12965350	27701	24	4	0	1	1	3	24	0	2	1	2	1	6	
chr19:11961475-11976575	15101	24	7	5	7	4	3	5	7	24	5	3	6	10	
chr22:30445350-30475986	30637	24	13	12	23	9	10	13	4	10	22	4	24	15	
chr7:12729150-12829100	99951	24	9	4	10	12	3	5	4	9	10	24	6	9	
chr12:5102450-5197825	95376	24	7	6	24	3	5	6	2	11	5	3	5	6	
chr1:209631400-209656375	24976	24	9	5	8	5	4	12	5	7	13	3	13	24	
chr1:23477400-23492375	14976	24	10	4	7	5	3	11	3	8	24	10	20	14	
chr13:83475500-83726025	250526	24	9	5	9	4	5	7	5	18	10	4	11	24	
chr8:29402750-29731425	328676	24	16	13	20	10	11	16	8	17	24	23	23	14	
chr2:63825225-63857575	32351	24	6	23	2	2	3	2	3	2	5	24	3	4	
chr2:111674975-111729375	54401	23	9	6	5	9	5	9	1	14	14	3	23	6	
chr2:183740700-183793025	52326	23	9	4	9	6	3	8	3	9	23	9	17	10	
chr5:148209825-148249425	39601	23	9	10	4	11	3	3	2	23	3	20	13	2	
chr9:131132400-131148400	16001	23	6	4	4	3	4	23	1	8	3	1	10	3	
chr3:158291000-158313675	22676	23	3	1	1	23	1	1	1	3	1	1	1	1	
chr12:61283950-61301575	17626	23	9	5	5	7	4	13	4	10	15	8	23	6	
chr2:193651275-193911400	260126	23	13	10	14	8	7	15	5	14	23	7	21	15	
chr5:111819800-111931900	112101	23	13	10	14	8	6	16	4	14	21	6	23	16	
chr6:33913800-33955400	41601	23	3	1	2	1	1	23	0	1	1	0	1	4	
chr18:31720150-31782325	62176	23	8	4	7	6	3	15	2	5	10	3	7	23	
chr13:31411725-31443975	32251	23	6	5	3	23	1	7	3	6	7	3	5	4	
chr7:92358275-92489825	131551	23	14	10	16	9	8	15	8	23	21	6	16	20	
chr3:114236500-114337000	100501	23	11	5	13	9	7	12	3	9	23	7	21	14	
chr19:7320850-7339925	19076	23	5	1	11	2	2	2	0	4	3	1	23	2	
chrX:119236975-119259025	22051	23	8	12	5	4	5	8	4	7	23	4	13	7	
chr2:165216625-165235250	18626	23	7	11	2	3	1	23	5	6	8	2	11	2	
chr7:96103850-96148750	44901	23	9	3	7	9	4	12	2	7	23	9	19	7	
chr18:51712175-51765200	53026	23	4	0	1	1	1	3	1	3	23	0	11	3	
chr6:111912800-111930550	17751	23	10	11	7	5	5	10	3	14	23	7	15	12	
chrX:64926450-65001925	75476	23	15	11	13	14	11	18	9	15	22	12	23	21	
chr18:34964525-35098275	133751	23	6	3	6	2	2	9	2	6	7	3	6	23	
chr11:59416375-59538600	122226	23	11	6	12	8	7	18	4	10	23	6	16	15	
chr5:52567275-52762975	195701	22	11	7	15	7	5	11	3	11	22	7	15	15	
chr4:15266300-15304725	38426	22	15	17	7	11	19	22	9	15	16	6	22	17	
chr1:58845000-58872925	27926	22	9	9	8	7	5	22	12	8	6	5	9	7	
chr20:57146000-57188600	42601	22	5	0	4	1	2	2	0	11	2	0	22	4	
chr2:64956975-65041825	84851	22	10	7	12	4	6	9	3	10	11	6	22	14	
chr5:117175975-117309050	133076	22	14	6	13	15	9	19	4	18	21	6	22	20	
chr21:16915600-16926550	10951	22	4	3	1	2	1	4	1	2	22	3	0	5	
chr11:34675025-34851400	176376	22	14	8	19	10	12	14	4	15	20	8	21	22	
chr1:203936725-203948947	12223	22	7	2	5	4	3	5	2	4	16	6	22	6	
chr10:110110175-110275525	165351	22	11	6	14	6	6	22	3	9	18	6	17	16	
chr8:8814750-8878550	63801	22	10	7	11	5	7	22	2	19	9	3	14	8	
chr1:191151850-191212425	60576	22	9	6	5	6	4	5	5	17	6	22	11	13	
chr4:108966225-109026800	60576	22	9	5	9	12	4	16	10	22	7	3	9	6	
chr6:3944675-3963450	18776	22	10	5	9	5	3	11	3	22	16	6	18	12	
chr13:107690275-107702750	12476	22	8	5	3	7	3	9	4	12	8	5	22	5	
chrX:130649675-130814125	164451	22	11	8	12	7	8	9	5	18	18	5	22	11	
chr6:111946650-111981100	34451	21	11	12	9	7	9	10	2	13	21	10	16	11	
chr10:112658400-112668025	9626	21	6	2	3	3	3	4	1	5	21	2	12	7	
chr11:130235450-130250500	15051	21	12	15	7	10	21	14	6	8	14	7	13	12	
chr1:110606700-110664300	57601	21	11	14	6	11	7	7	8	8	21	17	12	9	
chr9:2746150-2763400	17251	21	10	5	8	6	10	21	1	5	17	11	10	10	
chr2:24208525-24239425	30901	21	9	6	7	7	6	8	1	9	21	9	10	13	
chr3:13663800-13793125	129326	21	9	9	9	5	8	8	8	21	10	3	8	12	
chr4:74354350-74381575	27226	21	9	5	6	4	5	15	4	10	21	4	11	11	
chr7:20842975-21086525	243551	21	13	9	19	7	8	14	6	14	18	8	16	21	
chr13:50001250-50161600	160351	21	11	4	21	6	4	8	3	9	12	20	14	19	
chr21:15555275-15773775	218501	21	12	21	9	4	5	13	18	10	10	18	11	12	
chr3:9403550-9411575	8026	21	11	6	9	9	6	14	5	9	17	6	21	15	
chr7:30386175-30420575	34401	21	11	8	18	4	5	19	3	13	9	12	21	8	
chr5:98293600-98305025	11426	21	9	4	3	6	6	10	2	6	21	18	21	6	
chr11:38040175-38218375	178201	21	13	7	18	7	5	20	6	19	21	7	13	21	
chr19:63509250-63520475	11226	21	13	9	11	10	16	14	9	12	21	5	20	12	
chr11:58486575-58554025	67451	21	13	8	13	7	8	18	7	13	21	6	21	17	
chr13:55006675-55166650	159976	21	11	6	11	6	6	14	3	13	20	6	21	11	
chr5:134953975-135046175	92201	21	5	3	5	2	2	21	2	5	3	1	3	7	
chr20:56260575-56317475	56901	21	11	8	21	6	4	13	2	15	19	1	19	11	
chr2:39574775-39654150	79376	21	13	18	9	12	12	21	6	14	18	12	10	7	
chr4:109632100-109739300	107201	20	11	5	11	16	6	20	5	13	15	5	15	13	
chr1:32287575-32302500	14926	20	8	5	11	4	4	6	2	14	20	5	11	8	
chr18:5222477-5236926	14450	20	14	15	9	20	14	11	11	10	20	14	20	14	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr7:9904850-10020150	115301	20	6	3	6	3	2	6	2	6	8	3	7	20	
chr17:30860150-30875450	15301	20	5	3	3	3	1	3	2	12	5	2	20	2	
chr3:71738000-71797250	59251	20	8	4	7	3	3	6	2	18	15	2	20	6	
chr5:175530325-175540750	10426	20	3	0	1	0	0	1	0	0	12	0	2	20	
chr1:22292500-22313675	21176	20	8	3	10	6	2	7	2	8	18	6	20	6	
chr13:30077400-30089300	11901	20	5	3	2	1	2	5	0	2	20	4	6	4	
chr11:17334725-17362725	28001	20	8	2	11	3	17	20	1	5	10	10	6	7	
chr9:21481050-21587675	106626	20	11	6	9	5	5	17	8	20	15	4	12	16	
chr6:129882650-129921300	38651	20	8	7	5	6	3	14	1	20	11	4	9	5	
chr18:4368300-4442750	74451	20	7	2	6	2	12	2	0	7	20	1	6	20	
chr10:71853850-71860875	7026	20	13	19	6	14	8	20	9	12	14	11	18	11	
chr2:187712425-187798175	85751	20	6	6	4	4	2	7	1	7	12	2	7	20	
chr1:101291125-101334500	43376	20	6	3	3	4	2	7	1	6	9	3	20	6	
chr18:956025-1015450	59426	20	7	4	8	4	3	7	2	7	20	3	9	8	
chr1:158198825-158225975	27151	20	3	2	20	1	1	1	1	1	2	1	1	1	
chr8:142313025-142336125	23101	20	8	4	8	7	16	12	1	8	6	3	8	20	
chr21:38511875-38532825	20951	19	5	3	1	2	1	2	5	19	1	1	12	7	
chr18:66398450-66514300	115851	19	10	5	11	4	6	17	7	15	9	4	8	19	
chr7:32919525-32950200	30676	19	11	11	16	9	10	8	4	16	19	8	12	10	
chrX:64727500-64769875	42376	19	7	4	10	4	3	7	1	11	19	3	10	7	
chr4:14744675-14820275	75601	19	11	8	11	12	9	15	3	12	19	6	16	14	
chr2:43167775-43268825	101051	19	9	5	19	7	4	6	3	14	9	5	16	9	
chr7:45950100-46055950	105851	19	10	4	10	5	5	11	4	10	19	6	18	15	
chr7:65806575-65829700	23126	19	9	6	15	5	5	8	6	15	19	3	11	9	
chr3:186480050-186516225	36176	19	8	4	5	5	6	13	4	6	19	2	10	15	
chr2:207387650-207464200	76551	19	10	7	8	5	11	19	7	13	14	11	6	10	
chr4:24416150-24422275	6126	19	7	6	4	7	19	5	3	6	12	3	5	9	
chr18:43586600-43607850	21251	19	8	5	4	4	7	8	2	9	19	5	13	7	
chr4:9776300-10014350	238051	19	8	3	9	4	4	8	3	8	15	5	11	19	
chr5:53893950-54004750	110801	19	9	6	6	8	6	11	6	19	16	4	12	11	
chr12:58277175-58299650	22476	19	5	1	2	5	1	6	1	6	7	2	19	3	
chr5:141750225-141851975	101751	19	7	7	8	4	5	7	2	19	5	4	8	5	
chr6:167309700-167331675	21976	19	7	4	8	2	3	10	2	7	10	2	14	19	
chr12:71550025-71815050	265026	19	10	7	12	7	6	14	4	10	19	6	15	16	
chr15:54850700-54891650	40951	19	6	5	4	3	3	6	1	6	19	3	8	8	
chr19:21530650-21577025	46376	19	8	7	11	4	3	7	1	7	19	7	7	14	
chr7:134416925-134469600	52676	19	12	11	7	9	10	16	4	8	16	12	17	19	
chr15:28935575-28965125	29551	19	6	4	5	4	4	3	5	19	4	1	7	13	
chr2:62348300-62566800	218501	19	12	8	19	8	6	16	7	19	16	5	18	12	
chr2:60086175-60209975	123801	19	11	7	12	9	6	14	5	11	19	6	14	14	
chr3:87221775-87276850	55076	19	6	3	9	3	4	5	1	5	19	3	7	7	
chr2:86718725-86789500	70776	19	9	5	12	5	6	10	3	8	19	5	14	11	
chr3:39600250-39734000	133751	19	12	10	14	10	8	15	6	17	19	8	13	15	
chr2:156711975-156818525	106551	19	10	4	19	4	4	14	7	17	12	3	9	12	
chr20:35569025-35576975	7951	19	8	10	11	3	2	9	2	7	10	19	8	4	
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chr3:16120050-16171700	51651	16	4	3	2	2	3	4	1	2	6	16	3	3	
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chr4:76201975-76270600	68626	16	10	5	16	5	4	13	4	14	15	5	14	12	
chr12:67055575-67125325	69751	16	6	4	11	2	1	8	1	10	5	2	16	5	
chrX:138078900-138094350	15451	16	5	6	4	2	1	7	1	2	6	16	4	7	
chr1:33641707-33668475	26769	16	8	4	6	9	6	8	2	6	13	5	16	8	
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chr10:47057100-47109425	52326	16	4	1	5	1	0	5	1	5	1	0	16	6	
chr16:78259025-78345200	86176	16	7	4	5	3	3	10	4	16	15	2	3	13	
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chr17:26911725-26949250	37526	16	5	16	8	5	1	4	4	3	12	1	3	2	
chr13:110206850-110287225	80376	16	4	2	3	2	2	3	3	8	3	1	4	16	
chr19:41757025-41772825	15801	16	8	5	6	5	8	10	2	9	14	2	16	9	
chr12:7153400-7167400	14001	16	6	3	9	3	2	14	3	6	4	2	16	4	
chr5:12678075-12800025	121951	16	7	6	6	4	4	7	4	11	9	3	16	13	
chr4:37873600-38109850	236251	16	9	6	13	5	9	16	4	9	12	4	11	11	
chr7:155933475-155996100	62626	16	5	2	16	2	2	7	2	4	5	3	4	6	
chr1:191667675-191731275	63601	16	6	2	4	2	2	4	8	7	16	2	8	5	
chr3:88209750-88229200	19451	16	7	4	4	4	3	7	2	10	16	3	10	9	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr9:33001575-33014725	13151	16	8	6	7	4	4	10	2	8	16	8	11	14	
chr4:26418775-26459200	40426	16	5	1	6	2	2	16	1	4	12	1	4	6	
chr4:9729950-9746600	16651	16	2	0	0	0	0	1	0	0	1	0	1	16	
chr14:38898625-38914350	15726	16	5	1	4	3	1	16	3	4	6	4	9	4	
chr8:126604125-126708875	104751	16	8	4	9	5	4	16	8	10	12	4	9	10	
chr2:183481775-183495675	13901	15	8	3	5	8	5	9	3	13	14	15	6	6	
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chr5:6882550-6906100	23551	15	7	4	2	4	8	12	6	8	5	4	15	7	
chr3:6508350-6577400	69051	15	7	5	10	4	3	9	3	6	10	3	9	15	
chr6:32970575-32980325	9751	15	4	1	2	3	4	3	1	5	4	2	15	5	
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chr3:22263700-22385225	121526	15	4	3	4	1	3	3	2	4	7	2	5	15	
chr6:125271300-125315975	44676	15	6	3	5	3	3	4	1	7	10	15	4	6	
chr15:38123550-38145575	22026	15	11	7	14	12	11	13	2	9	15	11	15	14	
chr6:45632625-45776550	143926	15	8	5	11	4	4	8	2	13	13	3	15	11	
chr8:134678950-134886525	207576	15	9	7	15	6	6	9	3	11	14	6	13	10	
chr8:96366700-96483000	116301	15	8	3	9	4	3	13	2	10	15	6	14	10	
chr13:50430725-50449550	18826	15	5	3	3	3	2	4	1	6	10	2	15	5	
chr10:39116700-39194725	78026	15	3	1	15	1	1	1	0	0	1	0	2	7	
chr3:109306850-109354500	47651	15	2	1	2	1	1	1	0	1	1	1	15	1	
chr9:238650-254175	15526	15	4	4	3	2	2	5	1	9	1	1	15	3	
chr9:2768700-2781525	12826	15	7	3	6	4	7	14	2	6	15	7	7	4	
chr8:20314425-20440800	126376	15	5	2	6	3	2	6	2	15	4	2	4	6	
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chr12:30619850-30648175	28326	14	6	3	6	4	3	7	2	4	14	6	7	7	
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chr12:64277400-64357675	80276	13	8	7	5	8	11	8	6	9	13	6	12	7	
chr13:19075800-19097525	21726	13	6	3	6	3	3	7	2	7	13	4	7	8	
chrX:127995400-128076925	81526	13	8	6	12	6	6	10	3	11	13	5	11	9	
chr5:150289375-150308950	19576	13	5	2	2	4	2	9	0	3	13	2	4	9	
chrX:75319875-75330775	10901	13	7	5	3	5	3	9	12	7	6	7	13	5	
chr3:37389200-37409350	20151	13	7	4	7	4	2	10	3	13	8	12	8	6	
chr7:125329375-125521800	192426	13	9	8	12	6	5	11	3	12	12	5	13	10	
chr14:95413500-95462925	49426	13	2	0	1	0	13	0	0	0	0	0	0	2	
chr5:25365475-25481600	116126	13	7	4	9	7	4	10	2	10	13	5	10	10	
chr14:27161250-27210900	49651	13	4	2	3	1	5	13	1	2	4	1	3	4	
chr10:118564075-118598450	34376	13	5	2	5	3	6	13	1	5	8	1	11	6	
chr2:167280525-167386875	106351	13	6	3	6	3	3	6	1	6	13	5	8	7	
chr8:118749225-118816450	67226	13	6	5	6	5	2	4	4	13	8	2	12	9	
chr3:177467675-177586425	118751	12	7	3	8	5	4	9	3	10	12	4	10	10	
chrX:67684350-67726050	41701	12	8	4	8	5	4	9	3	10	12	5	12	9	
chr19:57268625-57289533	20909	12	5	4	5	4	2	5	2	5	12	2	10	6	
chr4:55363650-55399250	35601	12	6	4	7	4	3	7	2	5	12	5	10	9	
chrX:102738075-102748350	10276	12	3	1	2	2	2	4	1	2	12	3	5	4	
chr12:123664425-123811800	147376	12	7	9	12	4	3	5	8	8	7	3	6	7	
chr12:41907575-41950125	42551	12	5	3	5	3	3	5	1	4	12	2	6	6	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr1:22450050-22467875	17826	12	3	1	4	1	1	1	12	2	2	1	1	1	
chr1:9129450-9164075	34626	12	7	10	8	5	3	4	1	12	12	4	6	11	
chr8:110241350-110293300	51951	12	5	1	3	5	2	5	1	6	9	10	12	4	
chr3:67820975-67872650	51676	12	6	4	7	4	2	12	6	5	12	3	6	8	
chr1:245000875-245012875	12001	12	5	4	8	3	5	7	3	2	12	4	3	7	
chr9:32926300-32939200	12901	12	3	2	1	1	2	12	4	1	3	1	3	2	
chr13:72807725-72937000	129276	12	6	3	12	3	3	6	2	6	10	2	8	7	
chr6:126028200-126084725	56526	12	6	3	4	3	3	10	2	7	9	4	12	6	
chr8:130092325-130220700	128376	12	6	4	8	2	3	6	5	12	8	2	12	7	
chr13:79335200-79412750	77551	12	7	6	6	4	4	7	2	6	12	6	9	9	
chr2:121545350-121619175	73826	12	6	6	10	4	7	6	2	6	12	4	6	6	
chr2:192461425-192508825	47401	12	5	2	5	6	2	3	1	9	12	1	4	5	
chr4:4962125-5022325	60201	12	7	5	10	4	4	7	4	12	10	3	9	11	
chr8:79929700-79960525	30826	12	5	2	4	2	2	9	4	12	4	1	12	5	
chr13:50544475-50665475	121001	12	6	4	7	3	4	8	2	7	9	5	10	12	
chr12:50511350-50526675	15326	12	2	0	1	1	0	12	0	2	1	0	1	1	
chr13:49455650-49466250	10601	12	5	3	4	3	2	3	0	5	5	12	11	5	
chr18:52870875-52909150	38276	12	7	4	8	5	4	9	2	8	12	4	8	9	
chr17:21373950-21390575	16626	12	4	4	3	4	12	2	3	2	4	2	4	4	
chr3:37839075-37851625	12551	12	5	2	3	7	1	5	2	2	10	2	12	4	
chr18:37312775-37462750	149976	12	6	3	12	4	5	4	4	5	11	2	5	7	
chr4:109327675-109455425	127751	12	6	4	8	2	3	7	1	5	8	3	12	12	
chr12:111269000-111299725	30726	12	6	2	12	5	3	8	2	9	10	2	9	8	
chr19:35205200-35223675	18476	12	5	2	3	2	5	6	2	3	12	5	10	5	
chr1:199858800-199883250	24451	12	5	11	11	5	7	2	1	12	2	2	4	3	
chr3:139242175-139254800	12626	12	4	3	3	2	1	6	0	4	12	1	5	2	
chr13:53710800-53826900	116101	12	5	3	4	4	3	7	2	5	12	3	7	7	
chr2:19091050-19143450	52401	12	7	5	5	4	3	12	3	8	11	6	8	8	
chr5:95329600-95376075	46476	12	5	4	4	3	2	6	3	10	12	3	6	7	
chr4:9413775-9428250	14476	12	2	1	1	1	0	12	1	1	1	0	2	1	
chr12:45538425-45587250	48826	12	5	2	3	3	3	10	1	4	12	11	4	7	
chr14:96479600-96696875	217276	12	7	5	12	4	5	7	2	10	9	2	10	8	
chr3:180146275-180207400	61126	12	6	5	5	5	5	7	5	6	4	4	12	6	
chr1:113341575-113352750	11176	12	4	2	4	3	2	2	1	2	12	4	5	3	
chr12:46324075-46343100	19026	12	5	2	3	3	5	4	2	2	12	5	8	6	
chr19:21811825-21825825	14001	12	5	2	8	3	2	5	1	5	12	1	11	5	
chr13:75944675-76053050	108376	12	6	5	6	4	3	5	4	11	10	3	6	12	
chr8:90285550-90313750	28201	12	6	3	6	4	4	9	1	4	12	4	7	7	
chr13:37380475-37450700	70226	12	5	3	5	5	2	12	2	5	11	2	7	6	
chr2:218521300-218534150	12851	12	3	5	5	2	0	2	0	2	12	1	2	2	
chr6:141206225-141265250	59026	12	7	12	8	8	3	6	2	10	9	4	10	9	
chr3:103307650-103425850	118201	12	7	6	8	5	3	9	2	7	12	5	11	9	
chr8:83217050-83316925	99876	11	6	3	9	4	3	6	2	6	9	4	8	11	
chr17:34952496-34983927	31432	11	7	5	9	4	3	10	3	8	11	5	11	8	
chr6:167232425-167255350	22926	11	3	1	2	1	3	1	0	4	3	0	9	11	
chr1:105438075-105481400	43326	11	3	1	2	1	1	2	3	11	2	1	2	3	
chr12:84499575-84625775	126201	11	5	2	6	3	3	5	3	6	6	2	5	11	
chr14:84031800-84050525	18726	11	6	3	7	4	6	11	1	9	11	3	6	8	
chr2:101190700-101222900	32201	11	5	2	4	3	1	6	1	3	11	4	11	4	
chr2:73789225-73801625	12401	11	2	0	1	0	1	5	0	1	4	0	11	2	
chr12:3767950-3783200	15251	11	4	2	2	2	3	3	1	3	11	2	10	3	
chr2:105547175-105636100	88926	11	3	2	4	2	1	3	4	11	2	1	2	6	
chr6:155257875-155278175	20301	11	6	3	7	5	2	5	1	5	11	7	11	5	
chr5:74363725-74384025	20301	11	5	2	6	2	3	9	1	5	11	1	8	7	
chrX:49575900-49588600	12701	11	3	1	3	1	1	11	1	2	7	1	3	3	
chr1:196813275-196869300	56026	11	3	1	1	1	1	4	2	11	2	0	3	5	
chr4:82382450-82416400	33951	11	3	2	11	1	1	2	6	7	1	1	1	2	
chr7:105333950-105351950	18001	11	4	6	8	1	6	11	1	1	5	1	1	4	
chr21:43576100-43643725	67626	11	4	2	6	3	3	5	0	3	5	2	11	2	
chr3:152871900-152886900	15001	11	3	2	3	2	1	2	3	11	2	1	2	4	
chr3:59325725-59437400	111676	11	7	5	9	5	4	9	2	5	11	5	9	9	
chr15:39365175-39377125	11951	11	7	5	10	4	3	10	4	10	11	5	11	5	
chr14:87558425-87570400	11976	11	3	1	1	1	1	2	11	4	2	1	6	2	
chr17:15326100-15332950	6851	11	4	2	8	2	3	4	1	3	11	1	5	2	
chr6:41475450-41577700	102251	11	5	3	11	3	4	4	2	6	7	2	5	7	
chr12:59462625-59500450	37826	11	6	4	6	4	4	7	1	6	11	3	7	10	
chr1:66644600-66679850	35251	11	5	3	5	4	2	6	3	5	11	5	7	6	
chr4:125047300-125156250	108951	11	6	3	7	11	2	7	1	5	8	7	5	6	
chr4:5953425-5987275	33851	11	2	0	1	0	11	1	0	1	1	0	2	1	
chr1:72768625-72851975	83351	11	4	2	3	2	3	3	2	8	11	1	2	4	
chr2:158279100-158295500	16401	11	4	1	3	3	1	11	1	2	6	5	3	3	
chr21:14711200-14767900	56701	11	3	2	2	1	1	2	2	11	3	0	2	3	
chr10:54913075-54953825	40751	11	6	3	7	4	4	9	1	7	11	3	9	8	
chr8:142095575-142171400	75826	11	3	2	6	2	1	3	2	11	4	1	3	3	
chr11:2404925-2415425	10501	11	2	0	11	0	0	3	0	1	0	0	2	2	
chr12:129625700-129695450	69751	11	5	1	9	2	9	9	1	3	11	1	3	5	
chr6:57029975-57042500	12526	11	4	1	3	2	4	3	1	3	11	2	7	4	
chr6:166166775-166177900	11126	11	2	0	1	1	2	8	0	0	11	0	0	3	
chr1:226324900-226335050	10151	11	3	1	3	2	1	2	0	2	11	1	6	3	
chr5:68020875-68039900	19026	11	6	4	7	4	3	6	5	5	11	4	7	7	
chr6:81204400-81225475	21076	11	4	2	4	1	2	8	2	3	11	2	3	4	
chr8:72732550-72834350	101801	11	6	4	8	4	4	8	2	7	11	3	9	9	
chr3:113609400-113639400	30001	11	4	2	3	2	3	7	1	6	7	2	11	4	
chr21:34226200-34287850	61651	11	6	2	10	4	2	11	3	9	7	6	10	5	
chr7:63682825-63758200	75376	10	6	2	8	3	4	5	2	10	10	2	7	10	
chr16:53502500-53520209	17710	10	4	5	0	6	2	4	1	8	6	2	1	10	
chr8:70066100-70122500	56401	10	6	5	7	5	3	7	3	5	10	4	9	10	
chr8:104430300-104445100	14801	10	5	5	10	5	9	4	3	6	4	4	6	3	
chr8:27472050-27491175	19126	10	3	1	7	1	1	10	1	1	4	2	1	1	
chr8:9004100-9020950	16851	10	2	1	1	1	1	1	2	10	2	2	2	2	
chr8:67007800-67084250	76451	10	7	5	9	4	3	8	2	9	10	3	10	10	
chr8:75469125-75486275	17151	10	5	2	5	3	4	8	1	5	10	3	9	5	
chr2:191398300-191442800	44501	10	3	2	4	2	1	3	1	5	3	2	10	5	
chr12:58495000-58544275	49276	10	5	3	5	3	2	6	3	10	8	2	7	8	
chrX:106618050-106664800	46751	10	3	1	4	1	5	2	0	3	10	1	3	3	
chr6:3842475-3856791	14317	10	2	1	1	10	0	0	1	1	0	3	1	1	
chr15:49996975-50010800	13826	10	4	1	5	5	1	4	1	5	10	3	10	3	
chr13:39913400-39947425	34026	10	4	3	5	3	1	4	0	5	10	5	4	3	
chr19:39973225-40013800	40576	10	3	1	4	2	1	3	1	3	4	1	5	10	
chr1:199822075-199856100	34026	10	4	5	8	4	4	2	1	10	2	2	3	3	
chr4:24772175-24788500	16326	10	5	4	4	2	2	7	2	5	6	3	10	6	
chr13:43721900-43784850	62951	10	3	2	2	1	1	6	1	1	2	10	2	2	
chr7:65959125-65978250	19126	10	4	3	4	2	1	4	1	4	6	3	7	10	
chr11:45007750-45055500	47751	10	2	1	1	1	0	1	0	2	10	1	1	1	
chr10:48090350-48146425	56076	10	2	10	2	1	1	1	0	1	2	1	1	1	
chr1:114594500-114609650	15151	10	1	0	0	0	0	10	0	0	0	0	0	0	
chr18:57387175-57433350	46176	10	3	2	3	3	1	10	0	3	3	2	2	2	
chr6:143375000-143402275	27276	10	5	3	4	2	3	10	2	3	8	3	6	6	
chr1:143238675-143262750	24076	10	3	1	2	10	3	1	0	3	1	3	2	1	
chr1:164701025-164758425	57401	10	6	4	6	4	2	6	3	10	8	3	8	8	
chr2:64438550-64482125	43576	10	3	1	4	1	1	4	0	3	3	5	10	3	
chr21:22804275-22835300	31026	10	3	2	3	1	1	2	3	10	2	1	4	5	
chr6:30889850-30922825	32976	10	3	1	4	1	2	2	1	4	4	1	10	3	
chr8:58900375-58914400	14026	10	2	2	1	1	0	1	4	10	1	0	0	2	
chr2:207788050-207840375	52326	10	2	2	2	1	1	1	0	2	2	0	3	10	
chr4:101852975-101870350	17376	10	2	2	1	1	1	1	3	10	1	1	1	3	
chr6:155282650-155328225	45576	10	5	3	10	4	1	4	2	7	7	6	7	3	
chrX:137166825-137196100	29276	10	5	3	6	4	3	8	1	5	10	4	6	6	
chr8:128640050-128779150	139101	10	5	3	7	3	2	4	4	10	5	2	5	6	
chr7:127705000-127725825	20826	10	5	4	6	4	4	7	2	5	10	4	7	6	
chr8:138400700-138502875	102176	10	5	4	6	3	3	7	1	6	10	3	5	5	
chr3:184643050-184657550	14501	10	4	2	2	3	6	5	2	3	2	2	4	10	
chr1:236697975-236712250	14276	10	2	1	1	1	0	10	0	1	2	0	1	1	
chr6:57636750-57672625	35876	10	5	4	4	3	3	5	4	10	8	3	7	7	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr6:126461350-126482675	21326	10	4	1	2	2	1	9	4	2	10	5	4	4	
chr7:155386625-155451325	64701	10	3	1	4	1	1	10	1	2	3	1	2	2	
chr14:22834350-22839975	5626	10	4	2	1	2	4	3	2	10	4	5	5	4	
chr7:20477725-20548875	71151	10	5	3	3	3	2	4	4	10	7	3	6	8	
chr8:124540800-124568875	28076	10	5	1	5	4	3	6	3	7	10	4	9	4	
chr16:25178750-25189800	11051	10	4	1	6	2	1	3	0	1	10	2	8	4	
chr3:37861975-37876925	14951	10	3	1	6	1	2	7	0	2	10	0	3	3	
chr4:53376500-53401675	25176	10	5	2	5	3	3	5	1	4	10	4	7	6	
chr6:84732350-84748000	15651	10	3	1	1	2	1	2	2	4	2	3	10	3	
chr1:35058475-35091575	33101	10	7	5	10	5	4	7	4	8	9	5	9	7	
chr5:94014600-94029225	14626	10	4	2	2	3	2	3	2	6	6	1	8	10	
chr5:127435825-127445650	9826	10	4	2	3	2	2	5	1	3	10	1	7	4	
chr2:177947475-177965575	18101	10	4	4	2	4	2	7	1	3	6	2	10	8	
chr1:191884000-191929100	45101	10	3	1	3	1	0	2	10	3	6	1	5	2	
chr20:971000-1032775	61776	10	5	4	5	2	2	10	2	4	9	1	6	8	
chr4:26657100-26713550	56451	9	5	4	9	3	3	5	1	7	7	2	9	5	
chr2:122483375-122493675	10301	9	4	2	5	2	1	4	0	4	9	2	6	7	
chr13:30254825-30309675	54851	9	3	2	3	2	1	1	0	6	2	1	9	2	
chr3:160049375-160087675	38301	9	7	4	6	9	3	6	1	7	9	9	9	9	
chr8:551925-588750	36826	9	4	3	4	2	1	6	1	4	5	1	9	6	
chr8:110304925-110316200	11276	9	4	1	1	4	2	4	2	3	7	6	9	3	
chr1:227077300-227144400	67101	9	3	2	3	2	2	2	1	9	4	1	5	3	
chr2:191748300-191787275	38976	9	4	3	3	2	1	3	3	9	7	1	6	4	
chr2:23485150-23511825	26676	9	5	5	9	3	2	6	1	6	8	4	8	3	
chr11:117173700-117185525	11826	9	2	1	2	0	0	6	0	1	9	0	2	2	
chr11:129074200-129114425	40226	9	5	3	7	2	2	6	1	4	8	3	7	9	
chr5:1759400-1776250	16851	9	5	3	7	3	1	5	1	4	9	3	6	9	
chr18:40517050-40532650	15601	9	4	2	5	2	2	9	1	4	7	2	9	3	
chr1:48285375-48309925	24551	9	1	0	1	0	0	9	0	0	0	0	0	1	
chr8:20871025-20973775	102751	9	4	3	3	2	3	2	5	9	3	1	3	5	
chr14:45824500-45861375	36876	9	2	1	2	1	1	9	0	1	2	1	2	1	
chr2:155952550-156008475	55926	9	4	2	4	2	1	3	2	5	5	1	5	9	
chr3:88191225-88208250	17026	9	5	3	3	3	1	5	1	9	9	2	9	7	
chr6:1395175-1499250	104076	9	5	5	5	4	4	4	3	6	9	4	6	9	
chr15:23112925-23128125	15201	9	5	2	4	3	7	5	1	3	7	9	6	3	
chr15:46800350-46810550	10201	9	3	3	1	3	9	4	2	3	3	3	4	4	
chr4:6714950-6738350	23401	9	5	3	6	3	9	4	1	4	6	3	5	6	
chrX:42677625-42779075	101451	9	4	2	5	2	2	4	1	3	9	2	6	4	
chr2:19395750-19410525	14776	9	3	3	2	2	2	4	1	2	9	2	5	5	
chr2:145589275-145631750	42476	9	3	1	0	1	0	9	0	2	5	1	1	7	
chr5:54056975-54069450	12476	9	1	0	0	1	1	0	0	0	0	0	9	1	
chr6:154759925-154767025	7101	9	3	0	2	2	1	9	5	2	3	0	4	3	
chrX:138783749-138795925	12177	9	4	2	6	2	1	4	1	4	7	1	9	4	
chrX:68001200-68090950	89751	9	3	2	9	3	2	3	1	4	4	2	4	3	
chr14:86260825-86341250	80426	9	5	3	6	3	3	7	2	6	9	5	6	7	
chr9:124209250-124254675	45426	9	5	3	8	3	2	6	1	5	9	4	8	8	
chr15:52749925-52822450	72526	9	5	3	6	3	3	9	1	4	8	4	7	7	
chr5:39280900-39292500	11601	9	2	1	2	2	1	1	1	1	1	1	9	1	
chr7:11275675-11302400	26726	9	4	7	2	2	1	2	6	8	9	1	2	4	
chrX:13885025-13926975	41951	9	4	2	4	3	2	5	1	4	9	2	7	6	
chr7:63143400-63159850	16451	9	2	1	2	1	1	2	0	1	9	1	3	2	
chr13:56129650-56140775	11126	9	2	2	1	1	1	2	3	9	2	1	1	3	
chr8:76283650-76351975	68326	9	4	2	4	2	2	9	2	4	5	2	4	4	
chr7:115726625-115762575	35951	9	3	9	1	2	1	1	0	3	5	1	3	3	
chr12:18869375-18895800	26426	9	2	1	1	1	1	9	1	2	2	1	2	2	
chr1:113301525-113321425	19901	9	4	2	5	4	2	2	1	2	9	6	8	5	
chr10:116533050-116566275	33226	9	3	3	4	1	2	3	2	3	9	1	4	5	
chr5:153455300-153511350	56051	9	5	4	5	4	4	6	3	5	9	4	8	6	
chr11:129695825-129745775	49951	9	4	2	5	2	1	7	1	3	5	1	5	9	
chr3:3878525-3899175	20651	9	5	3	4	3	3	6	1	4	8	4	7	9	
chr9:101603550-101614575	11026	9	3	1	1	1	1	4	0	1	9	7	2	5	
chr8:21389625-21523225	133601	9	5	6	9	2	3	4	2	4	4	7	8	4	
chr2:107594300-107750025	155726	9	5	4	6	4	2	5	2	5	8	3	7	9	
chr13:70096550-70376150	279601	9	6	3	8	3	3	6	3	9	8	3	7	8	
chr6:114828600-114909700	81101	9	6	3	9	3	7	6	2	7	8	4	7	7	
chr17:49425-59050	9626	9	3	1	3	1	0	3	1	3	6	1	9	1	
chr5:1183775-1239275	55501	9	2	0	3	1	1	3	1	1	1	1	2	9	
chr18:33065350-33076375	11026	9	2	1	1	0	1	1	0	2	9	2	2	2	
chr4:1162925-1175425	12501	9	4	2	3	1	2	8	1	4	9	1	4	4	
chr5:77321525-77331525	10001	9	2	1	1	2	0	3	1	2	3	2	9	2	
chr8:122409075-122455775	46701	9	5	4	6	3	2	6	2	5	9	6	7	6	
chr1:194117800-194158050	40251	9	2	2	2	1	1	1	3	9	1	1	1	3	
chr2:207931600-208000325	68726	9	4	5	5	2	3	4	1	4	6	2	9	7	
chr6:30109600-30121550	11951	9	4	3	2	2	3	4	1	4	6	2	5	9	
chr18:65797050-65814575	17526	9	3	0	1	1	0	8	0	1	9	5	5	2	
chr15:40538400-40556025	17626	9	5	2	5	6	3	4	2	5	6	4	9	5	
chr3:8816950-8886100	69151	9	4	2	8	2	4	3	1	4	7	3	9	7	
chr3:27841100-27880125	39026	9	4	3	4	2	1	4	4	9	3	2	4	6	
chr7:93425600-93443100	17501	9	3	3	1	3	1	3	1	5	3	2	9	2	
chr14:60832450-60851000	18551	9	4	2	5	2	1	4	1	4	9	4	8	5	
chr1:51794250-51821775	27526	9	3	1	9	1	1	3	2	2	2	3	2	3	
chr15:72566300-72592700	26401	9	4	3	9	2	2	4	1	3	7	3	8	6	
chr16:63817525-63848450	30926	9	4	2	4	3	3	6	1	4	9	2	6	5	
chr12:95534400-95556825	22426	9	2	1	2	1	2	1	2	9	2	0	2	4	
chr15:77428250-77465075	36826	9	3	2	4	2	2	3	2	9	4	1	7	3	
chr10:129903575-129998050	94476	9	4	2	5	2	2	5	1	5	9	2	6	5	
chr2:239460050-239536125	76076	9	2	3	4	1	0	1	0	1	9	1	1	1	
chr5:82197325-82250800	53476	8	5	3	5	3	2	8	1	5	8	3	6	5	
chr14:20977125-20993325	16201	8	4	2	8	3	2	6	1	3	7	1	8	4	
chr15:86833575-86843600	10026	8	2	1	2	1	0	2	0	0	8	1	1	2	
chr18:11646850-11658050	11201	8	1	0	0	0	0	0	0	0	0	0	0	8	
chr14:75762425-75799950	37526	8	3	2	3	3	1	8	1	2	2	3	4	4	
chr14:98529150-98680525	151376	8	4	2	7	2	2	4	1	5	5	1	8	4	
chr12:92829775-92882150	52376	8	5	2	4	3	3	8	2	3	8	8	5	5	
chr3:154164450-154202725	38276	8	4	3	6	3	2	4	1	6	8	3	6	7	
chr5:170105175-170132700	27526	8	4	2	4	2	3	7	1	5	8	2	6	4	
chr1:179329700-179339750	10051	8	2	1	1	1	1	1	2	8	1	1	1	2	
chr1:94958600-94969225	10626	8	2	0	8	1	1	6	0	2	1	0	1	1	
chr8:2545200-2594500	49301	8	3	3	2	1	1	8	0	1	4	1	4	7	
chr9:2673000-2701050	28051	8	5	3	5	2	3	8	1	4	8	4	6	6	
chr13:75491350-75542100	50751	8	4	2	2	2	2	3	3	8	6	2	3	5	
chr18:51549225-51625400	76176	8	5	3	6	5	4	5	2	6	8	3	7	8	
chr5:88659975-88751600	91626	8	4	2	4	2	2	3	2	6	8	4	5	4	
chr15:67738650-67775700	37051	8	2	1	8	1	0	8	0	3	2	0	1	3	
chr1:184733575-184761100	27526	8	4	3	3	3	3	5	2	7	6	3	8	5	
chr15:70415750-70422125	6376	8	4	3	3	2	2	8	0	4	8	2	6	3	
chr2:75001325-75029025	27701	8	3	0	8	0	3	4	4	3	1	3	1	4	
chr4:52952325-52974425	22101	8	5	3	7	7	3	4	2	8	6	3	8	5	
chr10:119256775-119270300	13526	8	2	1	1	0	1	7	0	1	8	0	0	2	
chr12:75176700-75230575	53876	8	4	4	4	4	3	4	1	4	4	8	6	4	
chr12:96435000-96447575	12576	8	2	0	0	0	1	8	0	3	1	0	0	4	
chrX:119347600-119374125	26526	8	4	3	6	3	3	5	2	4	8	3	6	7	
chr18:18732600-18754800	22201	8	2	1	2	1	1	4	1	2	2	0	2	8	
chr3:72239600-72471675	232076	8	5	3	8	2	8	8	3	5	8	2	5	5	
chr6:36223550-36259875	36326	8	4	2	4	2	4	3	1	3	8	4	8	7	
chr2:90959050-90986900	27851	8	1	0	8	0	0	0	0	1	0	1	1	1	
chr2:113075625-113090775	15151	8	4	2	4	2	2	4	1	4	6	3	8	5	
chr18:70941800-71033250	91451	8	4	2	7	4	3	3	1	4	8	2	6	5	
chrX:47769775-47794250	24476	8	3	2	6	2	2	3	0	3	8	1	4	3	
chr3:84058675-84073875	15201	8	2	1	1	0	0	1	3	8	1	1	0	2	
chr2:114283350-114336075	52726	8	3	2	4	2	2	2	1	3	5	2	8	5	
chr7:115859275-115880850	21576	8	3	8	1	4	0	1	0	5	8	1	3	2	
chr19:15279000-15289200	10201	8	5	3	8	3	2	6	2	7	7	3	8	5	
chr3:12995350-13009850	14501	8	2	1	3	2	1	1	0	4	2	1	8	1	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr11:14889900-14935000	45101	8	3	3	2	1	1	7	2	4	4	1	8	3	
chr14:96996650-97122525	125876	8	3	1	4	2	1	3	1	5	3	1	8	3	
chr18:46799075-46810100	11026	8	4	3	3	3	2	4	2	3	8	4	5	4	
chrX:57912775-57943025	30251	8	3	1	3	1	3	3	1	3	8	1	4	2	
chr11:121425850-121455950	30101	8	3	1	3	5	8	2	1	3	7	2	2	3	
chr1:210367025-210384325	17301	8	2	2	2	1	1	2	1	2	8	2	3	2	
chr10:31608475-31625250	16776	8	4	2	4	2	2	5	1	5	8	3	5	4	
chr4:111456725-111486750	30026	8	4	4	6	3	2	5	1	4	8	2	6	6	
chr3:195446400-195513525	67126	8	3	2	3	1	1	3	8	8	4	1	1	4	
chr2:77168475-77216350	47876	8	3	2	3	2	8	3	1	4	4	1	3	3	
chr9:36409075-36421725	12651	8	4	2	5	1	1	5	0	4	6	1	6	8	
chr5:147308325-147389600	81276	8	4	3	5	3	2	7	0	4	8	3	6	6	
chr8:125541150-125555450	14301	8	3	1	2	2	2	3	1	2	8	1	7	2	
chr15:75573800-75655225	81426	8	4	2	6	4	8	3	0	3	4	3	7	3	
chr12:69889725-69989850	100126	8	5	3	6	3	2	5	3	8	6	4	4	8	
chr10:120422300-120428500	6201	8	3	2	1	2	4	2	0	3	8	5	5	4	
chr4:77361150-77383100	21951	8	3	1	3	1	2	3	8	2	3	3	2	8	
chr7:5433575-5444700	11126	8	2	1	5	1	2	2	0	2	8	1	2	1	
chr3:167355350-167366325	10976	8	2	1	2	1	1	8	0	2	3	1	3	1	
chrX:113528900-113613550	84651	8	4	3	6	3	4	6	1	5	8	3	5	5	
chr6:28189525-28199325	9801	8	4	4	3	3	4	5	2	3	8	3	8	4	
chr1:179196475-179208700	12226	8	3	3	3	2	3	4	1	3	8	2	5	2	
chr14:68133150-68148025	14876	8	2	2	2	0	1	1	0	2	8	1	4	1	
chr8:108150775-108322000	171226	8	5	4	6	3	4	4	2	6	8	5	6	7	
chr11:96952375-97086200	133826	8	5	3	6	4	2	7	2	4	8	3	8	6	
chr22:27033450-27045625	12176	8	3	2	3	2	1	3	1	3	8	2	4	4	
chr1:212579525-212590244	10720	8	4	4	3	5	2	7	1	3	6	8	4	4	
chr2:30968700-30980475	11776	8	1	0	0	0	0	8	0	0	0	0	0	0	
chr16:47237250-47265300	28051	8	5	3	8	3	2	6	2	6	8	3	8	7	
chr2:16335875-16523025	187151	8	4	3	8	2	2	3	1	3	5	2	4	6	
chr20:58089800-58106500	16701	8	1	0	1	0	1	0	0	0	0	0	1	8	
chr12:29121750-29172275	50526	8	5	4	5	5	4	7	2	5	8	3	8	6	
chr10:4934575-4967950	33376	8	3	2	2	3	2	2	6	2	4	1	3	8	
chr2:217088775-217129475	40701	8	3	1	2	1	2	1	1	8	2	3	3	5	
chr11:106680375-106691525	11151	8	3	1	1	2	3	6	1	3	4	4	8	3	
chr5:133796150-133810875	14726	8	2	0	1	3	1	1	0	1	0	8	1	1	
chr13:96654250-96665325	11076	8	2	1	3	1	1	1	3	8	2	0	0	5	
chr14:33522725-33553200	30476	8	3	1	4	3	2	2	1	8	4	2	6	3	
chr5:100411875-100464525	52651	8	4	3	7	3	3	5	2	5	8	2	5	5	
chrX:39654075-39718125	64051	8	2	1	8	1	1	1	0	1	3	1	2	2	
chr6:29346025-29356300	10276	8	4	4	5	3	2	4	1	3	8	3	5	6	
chr7:125011450-125108750	97301	8	3	2	4	2	1	2	2	8	2	1	2	3	
chr14:34498300-34508825	10526	8	4	1	3	2	1	8	1	6	6	1	7	4	
chr14:97192075-97236700	44626	8	4	3	4	3	3	6	8	5	5	3	4	5	
chr4:75129050-75167025	37976	8	3	2	1	1	1	2	3	8	2	1	2	4	
chr7:129031750-129038650	6901	8	4	3	7	2	3	7	1	3	7	1	8	6	
chr9:5129600-5146200	16601	8	3	2	2	3	1	4	1	4	5	4	8	5	
chr6:98783950-98895400	111451	8	4	2	6	2	5	5	1	5	6	2	5	8	
chr1:221252075-221314050	61976	8	5	3	5	4	4	6	2	8	7	5	6	5	
chr7:80594925-80732275	137351	8	4	2	6	3	3	5	2	4	8	2	6	6	
chr2:157739200-157801400	62201	8	3	2	3	2	3	3	1	2	3	2	4	8	
chr22:33904725-33953150	48426	8	4	2	4	7	4	4	3	4	8	3	5	6	
chr2:105915600-105995825	80226	8	4	2	5	2	3	5	5	8	5	2	6	6	
chr7:30517800-30529075	11276	8	4	4	3	3	2	7	1	4	6	4	8	4	
chr1:119352575-119365400	12826	8	3	2	1	2	1	4	1	5	8	1	3	3	
chr10:6663500-6677950	14451	8	2	1	2	0	3	3	0	3	2	8	4	1	
chr14:50799425-50830400	30976	7	4	2	2	2	2	4	1	7	4	1	7	6	
chr6:132319775-132332075	12301	7	2	1	2	1	1	1	0	1	7	0	1	2	
chr7:77147550-77161525	13976	7	4	2	7	3	3	6	4	5	5	2	3	4	
chr11:72124275-72140250	15976	7	2	1	3	1	1	1	1	3	2	0	7	0	
chr5:49667825-49697900	30076	7	2	1	2	2	1	2	1	4	2	1	7	2	
chr10:80162000-80341225	179226	7	3	4	6	2	7	3	1	3	3	2	2	3	
chrX:125218650-125243775	25126	7	5	3	7	2	4	5	2	6	6	2	6	5	
chr2:167180050-167221900	41851	7	3	2	2	2	1	3	2	7	4	1	4	5	
chr15:47173125-47199050	25926	7	4	3	3	3	5	4	2	5	4	6	7	2	
chr5:1597500-1620100	22601	7	2	1	2	0	1	2	0	7	2	0	3	1	
chr8:50277200-50391700	114501	7	5	4	5	4	3	6	1	6	7	5	5	7	
chr7:7252400-7267000	14601	7	2	0	1	2	2	4	1	3	1	2	7	1	
chrX:138752200-138762250	10051	7	4	2	6	2	1	4	1	4	6	2	7	5	
chrX:6577525-6619425	41901	7	3	1	2	2	1	4	1	3	7	2	3	3	
chr2:7917975-7969300	51326	7	4	2	4	2	2	5	2	7	6	2	4	5	
chr14:80950175-80970975	20801	7	3	1	2	1	2	7	0	1	3	1	7	2	
chr5:92788525-92800450	11926	7	2	0	0	0	1	3	1	1	7	0	2	2	
chrX:115823450-115840525	17076	7	3	1	3	2	2	6	0	4	7	1	4	4	
chr6:53704600-53744825	40226	7	3	1	4	1	2	7	0	4	5	1	5	5	
chr12:130395250-130407325	12076	7	2	2	1	1	1	1	3	7	1	0	0	2	
chr2:46288525-46300250	11726	7	2	1	1	1	1	2	3	7	2	1	2	3	
chr1:81414200-81494775	80576	7	4	3	5	3	2	4	3	5	7	2	5	4	
chrX:44194775-44217950	23176	7	2	1	7	1	1	2	0	2	2	0	1	1	
chr1:229087100-229097900	10801	7	4	3	5	2	4	2	2	4	4	4	5	7	
chr6:2737475-2768400	30926	7	3	3	2	3	2	3	1	3	7	3	6	3	
chr8:108779875-108813100	33226	7	4	3	6	2	2	5	1	4	7	2	6	4	
chrX:38601375-38677625	76251	7	4	2	5	2	2	4	1	5	7	3	5	5	
chr8:105676400-105757350	80951	7	3	2	4	2	2	3	1	3	5	1	4	7	
chr6:12007000-12022300	15301	7	3	2	1	4	7	6	3	6	1	0	1	5	
chr16:11464875-11492800	27926	7	3	2	3	1	1	2	1	4	2	3	7	3	
chr8:6541450-6552025	10576	7	3	1	5	1	1	5	0	2	4	1	7	4	
chr3:47182200-47192800	10601	7	4	2	4	2	3	7	1	5	6	3	4	6	
chr4:368275-378300	10026	7	3	2	2	2	2	2	1	1	7	3	4	4	
chrX:10963875-11001100	37226	7	4	3	6	3	2	5	1	3	7	2	5	6	
chr2:239994925-240122575	127651	7	3	3	7	2	2	3	1	5	5	1	4	4	
chr5:56013475-56103075	89601	7	4	2	5	3	2	4	1	4	7	2	7	5	
chrX:102885925-102902750	16826	7	2	2	1	1	1	1	2	7	2	0	1	3	
chr17:7716675-7728025	11351	7	4	2	3	5	5	4	0	3	7	4	7	6	
chr5:95945275-96020850	75576	7	4	3	3	4	4	5	1	4	7	2	6	4	
chr9:15989575-16042100	52526	7	2	1	2	1	2	4	0	2	7	1	2	4	
chr20:5134450-5152500	18051	7	5	2	5	4	7	4	1	4	7	6	7	4	
chr2:101422625-101454925	32301	7	4	3	4	2	2	5	1	4	7	2	6	5	
chr5:44862425-44872625	10201	7	3	1	1	2	3	5	1	2	5	7	4	2	
chr12:45939700-45986400	46701	7	4	2	4	2	3	3	1	4	7	1	6	5	
chr2:42416350-42427850	11501	7	3	2	4	2	1	6	1	3	7	1	7	3	
chr4:125320325-125379400	59076	7	3	2	3	2	1	3	1	4	4	1	3	7	
chr2:167967500-168003750	36251	7	4	2	7	2	4	3	1	3	6	3	5	5	
chr21:19714950-19740475	25526	7	3	2	2	2	2	3	1	2	6	1	5	7	
chr17:71097925-71111875	13951	7	3	2	7	1	1	3	0	4	6	1	6	2	
chr5:36729300-36761900	32601	7	1	1	2	1	1	1	0	1	1	1	7	1	
chr5:53692150-53755875	63726	7	4	3	4	2	3	6	2	5	7	3	5	5	
chr1:236138375-236165900	27526	7	4	3	4	3	3	4	2	4	7	2	5	4	
chr6:169521225-169539250	18026	7	1	0	0	0	1	2	0	2	7	0	1	2	
chr9:460700-475275	14576	7	2	1	2	1	0	7	0	1	1	1	2	6	
chr3:115417750-115427925	10176	7	1	0	1	0	0	0	0	3	0	0	7	0	
chr5:74941275-74952975	11701	7	3	1	7	1	1	7	1	4	4	1	2	3	
chr17:10598925-10629325	30401	7	3	2	5	1	2	4	3	2	7	1	3	4	
chr1:161532100-161545575	13476	7	3	1	1	1	1	4	1	2	7	2	4	7	
chr11:119530475-119566750	36276	7	2	1	7	1	1	5	2	1	4	0	2	1	
chr5:153788925-153803825	14901	7	3	1	4	2	1	3	1	2	5	1	7	2	
chr3:24611450-24674150	62701	7	3	1	2	1	3	7	2	4	4	2	3	3	
chr5:93465825-93476900	11076	7	3	2	2	2	1	3	1	2	7	0	6	3	
chr13:79861975-79897575	35601	7	3	2	3	2	2	3	2	6	3	2	7	4	
chr8:94562350-94588700	26351	7	3	2	4	2	1	3	2	3	6	2	6	7	
chr3:136560550-136594175	33626	7	2	2	1	1	2	2	3	7	2	1	4	2	
chrX:74466525-74477225	10701	7	2	2	2	1	1	2	2	7	2	1	2	2	
chr8:103749000-103836675	87676	7	4	3	7	2	3	4	1	5	4	2	5	4	
chr4:12579600-12608800	29201	7	2	2	1	2	3	2	7	2	2	0	2	2	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr10:1085825-1091600	5776	7	2	1	2	1	1	4	1	2	3	1	7	4	
chr2:57699575-57740425	40851	7	3	2	1	1	1	2	1	2	6	2	7	4	
chr8:28538200-28593425	55226	7	4	2	6	3	3	3	2	5	7	2	4	4	
chr11:68926100-69048700	122601	7	3	2	7	2	2	3	2	3	3	1	3	2	
chr7:99948500-99966925	18426	7	4	4	7	2	2	4	2	6	3	2	4	6	
chr6:2414150-2484475	70326	7	4	3	4	2	5	7	4	4	4	1	3	3	
chr11:7855925-7880950	25026	7	2	1	1	1	1	2	1	7	1	0	2	4	
chr6:48152775-48178175	25401	7	2	1	1	3	0	2	1	7	2	1	1	2	
chr16:85445825-85562825	117001	7	4	3	7	2	5	4	1	4	4	2	4	6	
chr2:181636500-181651275	14776	7	4	1	4	2	3	6	1	2	7	3	6	7	
chr3:130058000-130074800	16801	7	2	4	2	1	1	1	0	1	2	0	1	7	
chrX:79626350-79664125	37776	7	4	2	4	4	2	6	2	4	6	2	5	7	
chr11:61150700-61162450	11751	7	4	4	4	4	1	4	7	4	4	3	6	3	
chr10:113880000-113890875	10876	7	2	7	6	1	0	0	1	1	1	0	0	0	
chr8:104323575-104358050	34476	7	3	2	2	3	5	7	1	5	4	1	5	4	
chr9:114007475-114015775	8301	7	3	1	2	3	1	4	1	4	3	1	7	4	
chr6:56917375-56926575	9201	7	2	1	0	1	4	1	1	7	1	0	1	1	
chr7:63000650-63023550	22901	7	4	2	3	4	3	3	3	7	6	1	5	5	
chr6:37180500-37212625	32126	6	2	2	5	2	2	2	1	6	2	1	2	2	
chr22:26646350-26652975	6626	6	3	2	3	2	2	3	2	3	6	2	5	5	
chr7:29552375-29568225	15851	6	1	0	6	0	0	2	0	1	2	0	0	1	
chr12:64452900-64492900	40001	6	2	1	2	1	0	2	0	1	6	1	1	1	
chr21:39415875-39444300	28426	6	3	2	3	2	3	2	3	3	6	4	5	4	
chr10:116460425-116473650	13226	6	3	4	4	3	2	6	0	2	3	2	2	2	
chr12:2733775-2756550	22776	6	3	2	4	2	1	2	1	3	6	2	4	4	
chr12:5248100-5298825	50726	6	3	2	6	2	2	4	1	3	6	2	4	5	
chr5:139072325-139135900	63576	6	4	3	6	2	3	3	2	6	3	2	5	4	
chr2:237685400-237732100	46701	6	3	1	2	2	0	2	0	1	6	3	3	6	
chr1:85836625-85880575	43951	6	4	1	5	2	2	5	2	3	6	4	6	3	
chr1:91132500-91146825	14326	6	3	1	2	2	1	3	1	3	6	2	6	2	
chr10:76728025-76749800	21776	6	3	2	4	2	2	4	2	6	4	3	6	3	
chr6:11758275-11776200	17926	6	2	1	1	1	1	1	2	6	2	0	1	2	
chr6:74040350-74054750	14401	6	2	1	3	1	2	2	1	2	6	0	3	3	
chr6:18142500-18217725	75226	6	4	2	6	2	3	4	3	6	5	1	5	6	
chr1:120940875-120953875	13001	6	4	3	2	5	4	5	6	3	5	3	6	3	
chr4:72215925-72232750	16826	6	4	3	4	4	4	5	3	5	6	2	4	5	
chr4:125759125-125791075	31951	6	3	1	3	3	1	2	1	4	6	1	4	2	
chr8:106235775-106344550	108776	6	4	3	4	3	2	4	1	5	6	3	5	5	
chr5:134493025-134619900	126876	6	3	2	5	1	1	3	0	2	5	6	3	4	
chr9:127207725-127218875	11151	6	1	1	2	0	1	1	1	2	6	0	1	1	
chr14:99267075-99297500	30426	6	2	1	6	2	1	4	0	5	2	1	2	2	
chr13:19287250-19304250	17001	6	3	2	3	3	2	3	1	3	5	3	6	4	
chr5:8490875-8526025	35151	6	4	5	2	6	3	6	1	3	3	3	4	6	
chr13:38747350-38802275	54926	6	3	2	3	3	1	2	1	4	6	2	5	4	
chr15:79036700-79049525	12826	6	3	2	4	2	2	4	1	3	6	2	4	4	
chr12:95477300-95516900	39601	6	2	0	1	1	2	1	0	5	3	0	2	6	
chr17:39456275-39467525	11251	6	4	3	6	3	2	5	2	3	6	2	6	5	
chr13:47534400-47540050	5651	6	2	1	1	3	0	4	1	3	6	2	5	2	
chr4:8541575-8566850	25276	6	3	2	3	1	3	4	1	3	6	2	2	4	
chr7:36737750-36788825	51076	6	2	1	1	1	2	4	0	5	3	0	6	3	
chr15:79524225-79548025	23801	6	2	0	1	1	1	1	2	1	6	1	3	4	
chr8:111817150-111883075	65926	6	3	2	4	4	2	3	1	3	6	1	5	4	
chr6:139674475-139684850	10376	6	1	0	1	0	0	0	0	1	3	0	6	2	
chr3:43162175-43282975	120801	6	3	2	6	2	2	3	2	3	6	2	3	4	
chr1:39776600-39792825	16226	6	3	2	3	1	2	3	0	2	6	5	3	3	
chr4:54483050-54499200	16151	6	2	1	1	1	1	2	2	6	2	2	2	2	
chr9:137244375-137371000	126626	6	2	2	6	2	2	2	1	4	3	1	3	2	
chr16:3113750-3124850	11101	6	3	2	5	2	2	4	1	2	6	2	5	2	
chr5:57860400-57875950	15551	6	3	1	4	2	2	4	1	4	6	2	5	4	
chr5:90759300-90789150	29851	6	3	1	4	1	1	3	1	3	3	3	5	6	
chr21:43712475-43723950	11476	6	2	1	2	1	0	0	6	2	3	1	1	2	
chr10:62726900-62746900	20001	6	1	1	1	1	0	1	3	6	0	0	0	2	
chr2:146013750-146223325	209576	6	4	2	5	2	3	4	2	6	5	2	4	4	
chr12:7324400-7339725	15326	6	3	2	2	2	2	3	2	3	6	2	4	4	
chr13:74376150-74419100	42951	6	3	2	4	2	2	3	1	3	6	2	4	4	
chr2:42002850-42053225	50376	6	2	2	3	1	1	2	0	4	6	1	3	3	
chr9:14575325-14587525	12201	6	2	1	2	1	2	3	0	2	3	1	6	3	
chr13:84444275-84578075	133801	6	4	2	6	2	2	3	2	5	5	2	4	6	
chr2:41924000-41937475	13476	6	3	4	3	3	2	2	3	3	6	2	4	4	
chr7:37800325-37812150	11826	6	2	1	1	1	0	1	2	6	1	0	3	2	
chr12:30814550-30854925	40376	6	3	3	2	2	3	4	1	2	6	3	3	4	
chr15:55822375-55857650	35276	6	1	1	1	1	1	1	1	6	1	0	1	1	
chr4:99326125-99342425	16301	6	1	1	1	0	1	1	0	6	1	0	2	2	
chr6:83161900-83211150	49251	6	3	3	3	4	2	5	0	5	4	1	6	4	
chr4:124718875-124749675	30801	6	2	1	1	1	1	1	1	6	2	1	2	4	
chr6:3926525-3939100	12576	6	3	2	3	1	2	4	1	6	5	2	6	4	
chr8:37109300-37205775	96476	6	3	1	5	2	1	3	1	3	6	2	4	4	
chr11:30371700-30382775	11076	6	2	1	1	1	3	6	1	1	1	2	1	1	
chr2:145689775-145757350	67576	6	2	1	2	1	1	6	2	6	2	1	1	3	
chr7:35750875-35764150	13276	6	3	2	2	1	6	5	1	1	3	2	2	5	
chr6:44114325-44170550	56226	6	2	1	2	1	1	1	0	5	4	6	3	2	
chr19:47466700-47476275	9576	6	4	2	5	3	3	4	2	5	4	3	6	5	
chr5:79329500-79349525	20026	6	2	0	1	1	3	6	0	1	5	2	3	6	
chrX:58337500-58371350	33851	6	2	5	1	1	3	2	0	1	2	1	2	6	
chr13:42278100-42340125	62026	6	4	4	6	4	2	4	2	5	5	3	4	5	
chr22:22567775-22575550	7776	6	2	1	6	1	1	1	2	1	3	1	2	4	
chr7:8311175-8366500	55326	6	3	2	4	3	2	4	1	4	6	2	4	5	
chr15:77191800-77204850	13051	6	1	1	0	1	1	1	2	6	0	0	0	2	
chr8:90958775-90977600	18826	6	3	1	3	1	2	4	2	3	5	1	6	2	
chr10:27288300-27300050	11751	6	2	2	2	1	1	6	1	2	4	1	3	2	
chr8:80224875-80250800	25926	6	3	2	4	2	2	3	2	5	6	2	3	5	
chr4:90216125-90233175	17051	6	4	3	6	2	2	6	1	4	5	2	5	5	
chr13:49658575-49701625	43051	6	2	0	5	1	1	3	2	2	2	1	6	3	
chr8:26350000-26365750	15751	6	3	2	2	2	1	5	0	5	6	1	3	2	
chrX:48460225-48477975	17751	6	3	1	6	1	2	3	0	2	6	1	5	6	
chr14:80937850-80948425	10576	6	2	1	1	1	1	6	0	1	3	0	6	1	
chr13:29410325-29519200	108876	6	4	2	5	3	3	3	2	5	6	2	4	5	
chr4:79780850-79806375	25526	6	2	2	1	1	6	1	0	1	1	1	3	1	
chr16:11375775-11386450	10676	6	1	0	1	1	0	0	0	1	1	1	6	1	
chr8:123572275-123648225	75951	6	2	1	2	6	1	2	1	2	3	1	2	2	
chr2:59545675-59619200	73526	6	4	2	6	2	2	5	3	5	5	2	4	4	
chr1:179407300-179428500	21201	6	2	1	1	1	1	1	2	6	1	0	1	2	
chr4:90584375-90650325	65951	6	2	1	2	1	1	2	1	2	4	1	3	6	
chr4:93394950-93417950	23001	6	3	1	4	2	2	4	1	3	6	2	2	3	
chr5:99862475-99884050	21576	6	2	1	3	1	1	3	1	2	4	1	3	6	
chr11:37603350-37656150	52801	6	3	1	4	2	2	4	1	4	5	3	5	6	
chr8:47941875-47969750	27876	6	1	0	0	0	0	0	0	0	0	0	6	1	
chr16:87351225-87378000	26776	6	2	1	6	1	0	3	0	2	2	0	3	1	
chr12:118517650-118534025	16376	6	2	1	1	1	1	2	2	6	3	4	2	2	
chr4:107142375-107160000	17626	6	3	2	3	1	1	3	2	6	5	1	3	3	
chrX:36682025-36716325	34301	6	2	2	1	0	1	1	2	6	4	1	5	2	
chr11:128956550-128999900	43351	6	3	1	2	3	2	3	1	2	4	2	4	6	
chr11:72539200-72584250	45051	6	2	1	2	4	0	1	0	2	5	0	2	6	
chr3:72727375-72817150	89776	6	3	2	6	2	2	3	1	4	4	2	4	5	
chr13:47479700-47493175	13476	6	4	3	5	2	2	4	4	5	6	2	3	4	
chr4:6046775-6060425	13651	6	2	1	3	1	1	1	0	2	1	0	6	1	
chr7:39733400-39765800	32401	6	3	2	5	2	2	4	1	3	5	1	6	3	
chr16:49755350-49769950	14601	6	1	0	1	0	1	6	1	0	5	0	0	1	
chr11:64825000-64835850	10851	6	2	3	6	1	1	1	0	2	3	0	4	1	
chr16:66082250-66096075	13826	5	3	2	5	1	2	4	0	2	5	1	5	2	
chr2:91040800-91059550	18751	5	3	2	5	2	2	2	1	3	3	1	5	3	
chr1:235143375-235157150	13776	5	2	0	1	2	1	5	0	1	2	4	1	2	
chr21:35616700-35632175	15476	5	1	0	0	0	0	2	0	0	0	0	0	5	
chr4:106466500-106490525	24026	5	3	2	4	3	2	5	1	3	5	5	5	2	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr14:49172775-49179275	6501	5	2	1	4	2	1	4	0	1	4	1	5	2	
chr2:48342900-48376875	33976	5	2	1	2	1	1	2	1	3	2	1	5	4	
chr5:120635200-120699075	63876	5	3	2	5	2	2	4	5	3	5	2	3	4	
chr10:90729225-90740200	10976	5	2	3	1	2	5	1	1	4	4	1	3	2	
chr4:2757175-2787100	29926	5	2	1	5	2	1	5	1	4	1	0	5	1	
chr4:85418625-85432325	13701	5	3	2	3	2	1	3	1	2	5	2	4	3	
chr8:2683850-2700525	16676	5	2	2	1	0	1	5	0	2	3	0	3	2	
chr2:85975525-86007075	31551	5	3	3	3	2	5	2	0	4	3	1	4	2	
chr5:92830575-92842275	11701	5	1	0	1	1	1	2	1	1	5	0	2	2	
chr13:100010550-100034475	23926	5	3	3	3	2	1	4	0	2	3	1	5	3	
chr5:55919625-55956375	36751	5	2	1	1	1	0	5	0	1	2	1	3	2	
chr2:136680450-136726125	45676	5	1	1	2	1	0	1	0	2	2	1	5	2	
chr4:45434200-45475850	41651	5	3	2	3	2	1	2	1	2	5	2	4	3	
chr10:5146300-5161275	14976	5	2	1	1	1	0	2	5	1	3	0	1	5	
chr1:59255200-59301300	46101	5	2	2	2	1	1	2	0	2	5	4	4	1	
chrX:56824125-56848925	24801	5	2	1	4	2	1	3	0	2	5	1	5	3	
chr8:24112325-24140875	28551	5	1	0	1	0	0	5	0	1	1	0	2	2	
chr3:131414550-131449200	34651	5	2	0	2	1	1	3	0	2	5	1	2	3	
chr1:89521625-89559825	38201	5	2	1	2	1	1	2	1	2	4	1	5	3	
chr8:96278825-96304600	25776	5	1	0	2	1	0	5	0	1	1	0	1	1	
chr5:42794450-42825750	31301	5	3	1	2	2	4	2	1	1	4	2	4	5	
chr12:68755950-68789750	33801	5	3	3	4	2	4	3	1	4	5	3	3	5	
chr2:37838875-37869900	31026	5	2	1	2	0	1	1	1	5	1	3	1	1	
chr8:117182000-117203125	21126	5	1	1	1	0	0	0	1	5	0	0	0	1	
chr1:201273200-201284425	11226	5	1	0	1	1	5	1	0	0	0	4	0	2	
chr13:111594475-111683250	88776	5	2	2	3	1	2	2	1	3	3	1	3	5	
chr6:27771225-27791475	20251	5	2	1	3	1	1	1	0	2	5	1	4	2	
chr2:134424550-134510625	86076	5	2	2	2	5	2	1	1	1	2	1	2	4	
chr5:142064125-142106675	42551	5	2	2	3	2	1	2	1	4	2	1	5	2	
chr12:92933675-92975575	41901	5	3	2	5	2	3	4	1	3	5	1	4	3	
chr2:53906400-53920900	14501	5	3	2	2	2	3	4	1	4	5	4	4	3	
chr6:155702975-155724025	21051	5	2	1	3	1	1	4	0	2	5	1	3	3	
chrX:38748625-38829075	80451	5	2	1	2	1	1	3	0	2	5	1	2	4	
chr7:15034875-15075100	40226	5	3	3	4	2	2	5	2	2	4	1	3	3	
chr8:67466625-67481800	15176	5	2	1	1	1	1	5	2	1	2	1	1	5	
chr5:133864950-133875950	11001	5	1	1	5	1	0	1	0	1	0	1	1	1	
chr1:91072125-91085975	13851	5	1	0	1	1	2	1	1	1	5	0	1	1	
chr4:35648950-35702775	53826	5	2	1	4	1	2	2	1	4	1	1	5	2	
chr5:138990975-139005450	14476	5	2	0	4	1	0	2	0	1	3	1	5	1	
chr6:4111525-4130600	19076	5	1	1	2	1	1	1	0	1	1	1	5	1	
chr10:126423300-126430700	7401	5	2	1	3	1	3	2	0	2	5	1	3	4	
chr2:84550150-84567200	17051	5	2	1	3	1	1	5	1	1	2	1	2	3	
chr2:47589325-47600350	11026	5	2	0	1	1	5	2	0	1	5	1	1	3	
chr2:120176200-120227875	51676	5	3	2	3	1	2	4	0	2	5	1	3	5	
chr5:149961075-149975750	14676	5	1	1	5	1	0	1	0	1	1	1	1	0	
chr13:29782300-29797600	15301	5	2	2	2	1	1	2	0	3	4	1	5	1	
chr1:191511500-191522500	11001	5	2	3	1	2	2	3	1	3	3	5	4	1	
chr13:26522125-26538050	15926	5	2	1	2	1	0	2	0	5	2	1	4	1	
chr5:141603100-141658125	55026	5	3	2	5	2	2	4	2	4	4	1	4	2	
chr10:44150000-44171575	21576	5	2	3	3	2	1	2	0	1	1	1	5	1	
chr6:27484175-27507175	23001	5	2	3	2	1	3	2	0	5	3	2	2	3	
chr11:37861200-37931225	70026	5	2	1	2	1	1	1	0	1	5	1	2	2	
chr14:76534800-76551800	17001	5	1	1	1	1	1	1	0	2	0	1	5	0	
chr5:114562825-114570725	7901	5	2	2	2	2	3	2	1	2	3	3	5	3	
chr8:55512850-55528575	15726	5	1	1	1	0	0	1	0	1	1	0	5	1	
chr6:43923350-44037900	114551	5	2	2	3	1	2	3	1	3	5	1	4	3	
chr11:84662925-84675450	12526	5	1	1	0	1	0	2	0	1	5	1	1	1	
chr12:124248075-124327650	79576	5	2	1	3	2	5	1	0	2	3	1	2	4	
chr2:174393650-174464925	71276	5	3	1	5	2	2	4	1	3	4	2	4	3	
chr6:74607850-74640200	32351	5	3	2	4	2	1	3	1	5	3	1	3	3	
chr14:33403725-33434925	31201	5	2	1	5	2	1	3	1	3	3	2	3	2	
chr12:129125675-129208050	82376	5	3	2	5	2	2	2	1	3	5	2	3	3	
chr18:33500650-33550675	50026	5	2	1	3	1	2	1	0	2	5	1	3	2	
chr7:50198525-50260725	62201	5	2	1	3	1	1	3	1	2	5	1	3	3	
chr8:86963950-87054175	90226	5	3	2	4	2	2	3	1	3	5	2	3	3	
chr4:128977825-128988500	10676	5	2	0	2	1	5	4	1	1	3	1	1	1	
chr10:17290425-17301825	11401	5	1	1	1	0	0	1	0	2	2	0	5	1	
chr9:36392125-36402600	10476	5	2	1	2	1	1	3	1	2	3	1	5	3	
chr8:16431250-16489400	58151	5	2	5	2	1	0	4	0	5	1	1	2	4	
chrX:40136950-40206350	69401	5	2	1	4	1	1	2	1	3	5	2	3	2	
chr7:124655325-124692375	37051	5	3	1	4	2	2	4	1	3	5	1	4	2	
chr22:26399650-26467825	68176	5	2	1	4	2	1	2	1	5	2	3	2	2	
chr2:235183250-235262900	79651	5	2	1	3	1	1	2	5	3	3	1	2	3	
chr4:76679425-76695050	15626	5	3	3	1	2	2	4	1	2	5	2	4	3	
chr8:125829300-125904725	75426	5	3	2	4	2	1	3	1	3	5	2	4	3	
chr11:76132025-76162975	30951	5	1	2	1	0	0	5	1	0	2	0	1	1	
chr13:37779325-37804375	25051	5	2	1	2	1	0	5	2	2	3	0	2	2	
chr1:227445225-227455500	10276	5	1	1	2	1	1	1	0	5	1	1	3	2	
chr14:103403900-103436425	32526	5	1	1	5	1	1	2	1	2	1	0	2	1	
chr4:10302925-10319675	16751	5	1	0	1	0	0	5	0	0	0	0	1	0	
chrX:55818100-55829600	11501	5	2	1	1	1	1	3	0	1	5	1	4	2	
chr7:61383725-61394675	10951	5	1	0	5	0	0	0	0	0	0	0	0	0	
chrX:21818800-21841025	22226	5	2	2	2	2	2	3	1	2	3	5	4	2	
chr2:48237675-48250500	12826	5	2	1	2	1	1	2	1	2	5	2	3	3	
chr3:111003125-111018900	15776	5	1	0	1	1	0	5	0	0	0	0	0	1	
chr5:54198250-54243900	45651	5	2	1	1	1	1	5	0	1	3	1	2	2	
chr12:4829050-4840850	11801	5	1	0	1	1	5	0	0	1	1	0	1	0	
chr14:104347300-104362400	15101	5	2	1	5	1	1	2	1	4	3	1	3	2	
chr7:149967450-150001750	34301	4	2	1	2	1	1	1	0	2	3	1	4	2	
chr13:89971500-90052625	81126	4	2	1	2	1	1	2	0	2	3	1	2	4	
chr1:100787025-100809750	22726	4	2	1	2	1	1	4	0	1	3	2	4	1	
chr10:112068400-112115800	47401	4	2	1	4	1	1	2	0	1	2	1	3	2	
chr6:20445050-20482600	37551	4	2	1	4	1	1	1	0	1	4	1	3	3	
chr2:10614350-10628300	13951	4	3	2	2	3	3	3	2	2	4	4	4	3	
chr9:117281075-117332525	51451	4	2	1	3	1	1	1	0	1	2	1	2	4	
chr1:118021050-118060375	39326	4	2	1	3	1	1	4	0	3	3	2	3	2	
chr2:224419425-224431400	11976	4	2	2	4	2	1	2	1	3	3	2	4	3	
chrX:51150500-51160675	10176	4	2	0	1	1	4	1	0	1	4	0	4	3	
chr14:69792625-69829600	36976	4	2	1	2	1	0	2	0	1	2	1	2	4	
chr4:76853725-76868150	14426	4	2	0	3	1	1	2	1	1	2	4	2	2	
chr2:175621975-175641350	19376	4	2	1	1	1	0	3	1	2	2	0	4	1	
chr2:38224625-38236425	11801	4	2	2	3	1	1	3	0	1	2	2	4	2	
chr5:626650-642950	16301	4	1	0	1	0	0	1	0	0	1	0	1	4	
chr10:74428350-74435575	7226	4	1	0	0	1	0	1	0	2	3	4	2	0	
chr4:106491125-106505350	14226	4	2	1	2	2	2	4	1	2	4	4	3	1	
chr10:31098800-31139450	40651	4	3	3	4	2	3	2	4	4	2	1	2	2	
chr13:79054625-79103425	48801	4	3	2	3	2	1	4	1	4	4	2	4	4	
chr5:159600-182725	23126	4	2	1	2	1	1	3	0	1	4	1	2	2	
chr18:51434050-51464400	30351	4	1	1	2	0	0	1	0	1	1	1	1	4	
chr6:14808225-14856150	47926	4	2	2	3	1	1	2	1	4	2	1	2	4	
chr1:89153625-89168975	15351	4	2	1	2	1	2	2	1	3	4	1	4	2	
chr17:66488275-66507650	19376	4	1	0	1	0	1	1	0	1	4	1	1	1	
chr1:38655800-38689600	33801	4	2	1	1	1	1	4	0	2	3	1	4	2	
chr2:3151200-3164600	13401	4	2	1	4	1	1	4	0	0	2	1	4	2	
chr5:148435300-148452150	16851	4	2	1	3	2	2	3	1	2	4	1	3	4	
chr8:95986900-96001825	14926	4	2	1	3	1	0	1	0	2	4	2	3	1	
chr2:3671525-3682050	10526	4	2	2	3	2	1	4	0	4	2	0	2	2	
chr1:185637825-185716750	78926	4	2	1	2	0	1	2	1	2	4	1	3	2	
chr9:123192750-123210375	17626	4	2	1	2	1	1	2	1	2	4	1	4	4	
chr1:94851700-94869225	17526	4	2	2	3	2	2	4	1	2	4	1	2	2	
chr4:5594075-5607075	13001	4	2	1	2	1	1	4	1	1	4	1	2	2	
chr20:48336525-48346625	10101	4	1	1	0	0	0	0	1	1	0	0	4	0	
chr8:75160600-75178150	17551	4	1	1	1	2	1	0	0	1	1	1	4	1	
chr15:65581525-65598300	16776	4	2	2	2	1	1	4	1	2	4	2	3	3	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr11:113096775-113107650	10876	4	2	2	1	1	1	2	1	2	4	3	3	3	
chr11:28328725-28349150	20426	4	2	2	1	1	1	3	1	3	4	2	3	4	
chr17:37055675-37077700	22026	4	1	0	4	0	1	1	0	1	1	0	1	1	
chr5:5410650-5437825	27176	4	2	1	2	1	2	3	1	2	4	1	3	4	
chr4:11108100-11128250	20151	4	2	1	2	1	1	3	0	2	2	1	3	4	
chr1:154326000-154341900	15901	4	1	1	3	1	1	1	0	1	4	1	1	1	
chr21:20864700-20924525	59826	4	2	2	3	1	1	3	0	2	4	2	2	2	
chr3:135322675-135340275	17601	4	2	1	2	1	1	2	0	1	4	3	4	2	
chr15:64997350-65018875	21526	4	2	4	1	2	0	3	0	2	2	1	1	2	
chr13:29572725-29629450	56726	4	2	2	4	1	1	1	1	2	3	1	2	2	
chr2:120936925-121024600	87676	4	2	2	4	1	1	2	1	3	3	2	2	3	
chr13:98845000-98872975	27976	4	3	2	4	1	2	2	1	3	4	2	4	3	
chr4:41790675-41800725	10051	4	2	1	1	1	1	3	1	3	3	2	4	2	
chr20:56582075-56648350	66276	4	2	1	3	1	2	4	0	1	2	0	1	2	
chr4:24423850-24436150	12301	4	2	2	2	4	4	2	1	2	3	1	2	2	
chr4:25707575-25774725	67151	4	2	3	4	2	2	2	0	4	3	2	2	3	
chr9:123914275-123933950	19676	4	1	1	2	0	0	4	0	1	1	1	1	1	
chr10:89817350-89828825	11476	4	1	0	0	0	0	0	0	1	0	0	4	0	
chr5:171206800-171220925	14126	4	2	2	2	2	0	2	0	2	3	1	4	1	
chr10:17544300-17574475	30176	4	2	1	2	1	1	2	1	4	3	1	2	2	
chr5:141712700-141725675	12976	4	1	1	2	1	1	1	0	4	1	0	1	2	
chr12:1511350-1531175	19826	4	2	1	4	1	1	1	0	2	4	1	1	2	
chr2:8625475-8656675	31201	4	1	0	4	0	0	2	1	1	1	0	2	1	
chr1:33624900-33640125	15226	4	2	1	2	2	1	2	0	2	3	2	4	1	
chr2:68184950-68197450	12501	4	2	1	1	1	2	1	0	1	4	2	2	3	
chr2:238241425-238260675	19251	4	2	1	2	3	1	4	1	4	4	3	4	1	
chr11:109591300-109599000	7701	4	2	1	1	1	1	1	0	2	4	3	2	1	
chr5:67711025-67754775	43751	4	1	1	1	1	1	2	4	1	2	0	1	2	
chr8:94942275-94989225	46951	4	1	1	2	1	0	1	0	1	2	1	2	4	
chr1:27717600-27729175	11576	4	2	0	3	1	0	1	0	1	3	4	2	1	
chr6:44054725-44073196	18472	4	1	1	2	1	1	1	0	1	1	4	1	0	
chr1:161547975-161558200	10226	4	2	2	1	1	1	3	0	1	4	1	3	3	
chr1:197692000-197775950	83951	4	2	3	3	2	1	3	1	3	4	1	3	3	
chr12:55531725-55548275	16551	4	1	1	1	1	0	1	1	1	4	1	1	1	
chr13:35836025-35848350	12326	4	1	0	1	1	1	1	0	1	4	0	1	1	
chr12:108546875-108559575	12701	4	1	0	4	1	1	1	0	1	1	1	2	1	
chr6:15803725-15840100	36376	4	2	1	4	1	1	3	1	2	3	1	2	4	
chr1:237448850-237518300	69451	4	2	1	3	0	0	2	1	2	2	1	2	4	
chr4:65264625-65308600	43976	4	2	2	4	1	1	3	1	2	4	2	3	3	
chr5:167625475-167637500	12026	4	1	1	2	1	1	4	1	4	1	0	1	1	
chr8:121151225-121164350	13126	4	1	1	1	1	0	1	0	0	1	4	1	1	
chr12:4015975-4071825	55851	4	2	1	3	1	1	3	1	2	4	1	3	3	
chr12:59079125-59174275	95151	4	2	1	3	2	1	3	1	3	4	2	3	3	
chr2:127375700-127418650	42951	4	2	1	1	1	2	2	1	2	4	1	4	2	
chr8:37300175-37362850	62676	4	2	2	3	1	1	2	4	1	3	1	1	3	
chr14:95273700-95291125	17426	4	1	0	1	0	1	1	1	1	1	0	4	1	
chr16:83714775-83742000	27226	4	2	1	4	1	1	3	0	1	2	1	4	1	
chr5:81999675-82050175	50501	4	2	1	2	2	1	3	0	4	2	1	1	2	
chr6:132493825-132536700	42876	4	2	2	2	1	2	2	1	2	4	0	3	4	
chr12:46439750-46452350	12601	4	1	1	1	1	1	4	0	1	4	0	1	1	
chr5:40478375-40500725	22351	4	2	1	3	2	1	2	1	2	4	1	4	3	
chr10:102320175-102331900	11726	4	1	0	1	1	4	0	0	2	1	1	1	1	
chr4:285700-301175	15476	4	2	1	3	2	2	4	1	1	4	1	4	4	
chrX:111827950-111846700	18751	4	2	1	2	1	1	2	0	1	4	2	2	3	
chr13:104871700-104904225	32526	4	1	1	4	1	0	1	0	1	3	0	0	1	
chr10:44057525-44069225	11701	4	2	1	2	1	1	2	0	2	3	1	2	4	
chr2:28505600-28531825	26226	4	1	1	2	0	0	1	0	1	1	4	1	1	
chr6:131076150-131124300	48151	4	2	1	2	1	1	3	1	3	4	1	4	3	
chrX:57018625-57030000	11376	4	2	1	2	1	1	3	1	1	4	1	3	1	
chr5:158747225-158807525	60301	4	2	1	3	1	1	2	0	1	2	1	4	3	
chr3:195235225-195254025	18801	4	1	1	1	1	1	1	1	3	1	1	1	4	
chr14:98364250-98474750	110501	4	2	1	4	1	2	3	2	2	4	1	3	2	
chr12:12775375-12786225	10851	4	1	1	2	0	1	1	0	1	4	0	3	1	
chr2:62229225-62239350	10126	4	2	1	2	1	1	3	1	1	4	2	4	2	
chr2:202531900-202562225	30326	4	1	1	2	1	1	1	2	4	1	0	1	1	
chr18:69451350-69507600	56251	4	2	3	4	3	1	3	1	3	3	2	2	3	
chr9:5564750-5571550	6801	4	2	1	2	1	2	1	0	1	1	4	3	2	
chr10:114927875-114959800	31926	4	2	1	2	1	1	2	1	1	2	1	4	2	
chr11:10696225-10707675	11451	4	2	1	2	2	1	2	0	2	1	1	4	2	
chr7:86800800-86810825	10026	4	2	1	1	2	2	3	1	2	2	1	4	2	
chr21:43744000-43763000	19001	4	1	1	1	0	1	1	0	1	2	1	0	4	
chr3:31131575-31154225	22651	4	1	0	1	0	1	1	0	1	4	0	0	1	
chr4:119994100-120020550	26451	4	2	1	2	1	1	2	1	2	4	1	4	3	
chrX:42991675-43019825	28151	4	2	0	2	1	1	2	0	1	4	1	2	2	
chr2:57876000-57907450	31451	4	1	1	1	1	0	0	0	1	3	0	4	3	
chr10:54673950-54691500	17551	4	1	1	1	1	0	1	1	4	1	1	0	1	
chr21:18370050-18390050	20001	4	2	1	1	1	1	2	0	2	2	1	3	4	
chr10:44839900-44867575	27676	4	2	3	2	1	1	2	2	2	4	0	2	3	
chr14:40496250-40534675	38426	4	2	1	2	1	1	2	1	2	4	1	3	2	
chr6:31363000-31416375	53376	4	2	1	3	1	2	2	1	3	4	2	2	2	
chr9:5300525-5316625	16101	4	2	2	3	2	3	3	1	2	4	1	3	2	
chrX:124133150-124148375	15226	4	1	0	1	0	1	4	0	1	0	0	1	1	
chr1:198597975-198611175	13201	4	1	1	1	0	1	2	1	3	1	1	4	1	
chr1:203671525-203684250	12726	4	1	0	0	0	0	1	0	1	1	0	0	4	
chr11:9738200-9748525	10326	4	2	2	3	1	1	2	0	2	4	1	2	2	
chr14:55229950-55253225	23276	4	2	1	1	1	1	2	0	1	1	4	3	2	
chr10:3964425-3977400	12976	4	1	0	1	1	0	0	0	0	1	1	1	4	
chr12:28607450-28619725	12276	4	2	3	1	2	1	2	1	1	3	3	4	1	
chr10:80394300-80443425	49126	4	2	3	4	0	2	1	0	2	2	1	2	1	
chr4:55462350-55525325	62976	4	2	1	3	2	1	2	1	2	4	1	2	2	
chr14:76222450-76238625	16176	4	1	1	1	1	1	1	1	2	2	0	2	4	
chr2:200692850-200728325	35476	4	1	1	2	1	1	1	0	1	2	1	2	4	
chr8:21766900-21799225	32326	4	2	1	4	1	1	1	0	1	1	2	2	1	
chr5:32567225-32584425	17201	4	1	1	2	1	1	1	1	4	2	0	3	2	
chr11:94007350-94057525	50176	4	2	2	2	1	3	2	2	3	2	1	3	4	
chr11:127925850-127944925	19076	4	1	1	1	1	0	1	0	3	1	0	4	0	
chr5:66581100-66618700	37601	4	2	1	2	1	1	2	1	2	3	1	4	2	
chr1:226142500-226163525	21026	4	1	0	4	0	1	0	0	1	1	2	1	1	
chr2:76662200-76684675	22476	4	2	1	4	1	1	2	1	3	3	1	3	3	
chr13:43541700-43575500	33801	4	2	1	2	1	1	2	1	4	1	1	2	3	
chr17:14447875-14462575	14701	4	1	1	1	1	0	1	2	4	1	0	1	1	
chr2:193983125-194058900	75776	4	2	1	3	1	1	2	1	4	3	1	2	3	
chr15:81191300-81205175	13876	4	2	1	2	1	1	2	1	3	2	1	4	3	
chr3:144386625-144409775	23151	4	1	1	1	0	1	1	0	1	1	1	4	1	
chr17:50603800-50615775	11976	4	1	0	0	1	1	4	0	1	4	1	1	2	
chr1:192286275-192304050	17776	4	1	0	1	0	0	1	4	1	2	0	1	1	
chr2:161805425-161819450	14026	4	1	0	1	0	0	1	4	3	0	0	3	2	
chr11:47579600-47590300	10701	4	2	2	3	1	4	2	3	1	3	2	3	2	
chr2:177202562-177210548	7987	4	1	1	1	0	0	3	0	0	3	0	2	4	
chr12:32083800-32099625	15826	4	2	1	3	1	0	1	0	2	3	1	4	1	
chrX:112428775-112448300	19526	4	2	1	2	1	1	2	0	2	4	1	2	2	
chr18:43736200-43765550	29351	4	2	1	4	1	1	2	1	2	3	1	2	2	
chr4:6554025-6576400	22376	4	1	0	4	1	3	1	0	1	1	0	2	1	
chr1:38952425-38967525	15101	4	1	0	1	0	0	4	0	0	1	0	1	1	
chr11:2316375-2338500	22126	4	2	1	2	1	2	2	0	2	4	1	2	2	
chr5:61966575-61986950	20376	4	2	1	1	2	1	2	1	4	4	3	2	2	
chr11:68711325-68782100	70776	4	2	1	4	1	1	2	1	3	3	1	2	3	
chrX:7876450-7886700	10251	4	2	0	2	1	1	4	2	1	3	1	2	3	
chrX:119142325-119155025	12701	4	1	1	1	0	1	1	0	1	4	0	1	1	
chr8:118825700-118840650	14951	4	1	1	1	1	0	1	0	2	3	1	4	2	
chr1:43203850-43224600	20751	3	2	1	3	1	2	2	0	2	3	0	2	2	
chr3:32802975-32815650	12676	3	1	1	3	1	1	2	0	1	2	1	2	2	
chr7:64833500-64843700	10201	3	2	0	3	1	2	2	0	1	3	0	3	1	
chr2:155447775-155502825	55051	3	2	1	2	1	0	1	0	1	3	1	2	3	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr16:83762925-83776250	13326	3	1	0	2	0	0	2	0	0	3	2	1	1	
chr2:158472500-158484150	11651	3	1	1	1	0	1	2	0	1	3	0	1	1	
chr10:77993900-78008175	14276	3	1	1	0	1	0	2	0	1	3	0	3	2	
chr6:143711975-143724400	12426	3	2	2	1	1	1	3	1	1	3	0	2	1	
chr12:109859650-109871275	11626	3	1	0	0	0	3	0	0	1	0	3	0	1	
chr2:128803850-128856725	52876	3	1	1	2	1	1	2	1	1	2	0	3	1	
chr17:60528775-60538900	10126	3	2	1	3	1	1	1	2	3	2	2	1	2	
chr4:37438825-37458300	19476	3	1	1	2	0	0	0	0	1	1	0	3	0	
chr4:56497950-56508950	11001	3	1	1	0	1	1	1	1	1	1	0	3	1	
chr16:83112375-83139300	26926	3	1	1	3	1	1	1	1	3	1	0	2	2	
chr2:188216850-188242950	26101	3	2	1	3	1	1	1	0	3	2	1	2	3	
chr2:231927600-231939325	11726	3	1	1	2	0	1	1	0	1	3	0	0	1	
chr1:82690075-82738225	48151	3	1	1	1	0	0	1	1	3	0	0	0	2	
chr14:72115775-72140300	24526	3	1	1	1	1	1	1	2	3	2	1	0	1	
chr20:29267675-29298475	30801	3	1	1	3	0	0	1	0	1	0	0	0	1	
chr2:104872525-104884550	12026	3	1	0	2	0	1	3	0	1	0	0	0	0	
chr6:91443800-91462575	18776	3	1	0	0	0	0	0	0	0	0	1	3	0	
chr2:128912250-128946725	34476	3	2	1	1	1	0	3	1	2	3	0	3	2	
chr21:10142425-10168325	25901	3	2	1	3	1	2	2	1	1	2	1	1	3	
chr5:142858650-142910425	51776	3	2	1	3	2	1	3	0	2	3	1	2	2	
chr20:1594825-1615675	20851	3	1	0	1	0	1	1	0	1	1	0	3	0	
chr5:86440850-86461100	20251	3	1	0	1	0	3	0	0	0	0	0	1	0	
chr6:164108650-164125500	16851	3	1	0	0	0	0	0	0	1	0	0	1	3	
chr6:126536000-126549075	13076	3	2	1	1	1	1	3	2	1	3	1	2	2	
chr5:78088475-78102000	13526	3	1	0	1	0	0	3	0	0	1	0	1	1	
chr12:91259775-91314700	54926	3	1	2	1	1	1	2	0	1	2	1	3	1	
chr4:57290325-57305175	14851	3	2	1	2	1	2	2	1	2	2	1	3	2	
chr4:14873975-14887950	13976	3	2	1	2	2	1	3	0	3	3	1	3	2	
chr6:56857225-56873850	16626	3	2	3	3	1	1	2	1	3	3	1	2	2	
chr4:84754000-84780025	26026	3	2	2	3	2	2	3	2	2	3	2	3	2	
chr21:39131050-39141200	10151	3	1	0	1	0	0	0	3	1	1	1	1	1	
chr1:231084925-231131050	46126	3	1	1	3	1	1	1	0	1	2	1	1	2	
chr4:24273450-24285525	12076	3	1	1	1	0	0	0	0	0	0	0	0	3	
chr1:157219375-157229975	10601	3	1	0	1	1	0	1	0	1	0	0	3	0	
chrX:43070225-43119975	49751	3	2	1	2	1	1	2	1	3	3	1	3	3	
chr13:72717475-72744200	26726	3	1	0	3	0	1	1	0	1	2	0	1	1	
chr6:135461825-135493175	31351	3	2	1	3	1	1	1	1	3	3	0	1	2	
chr15:89814100-89836700	22601	3	1	1	1	0	0	3	0	1	2	1	1	2	
chr21:32528625-32540925	12301	3	1	1	1	1	1	1	0	1	3	2	3	1	
chr14:50080825-50091175	10351	3	1	1	2	1	1	3	0	1	2	0	3	2	
chrX:70452900-70467450	14551	3	1	0	3	1	1	2	0	2	3	1	2	2	
chr9:117609800-117640825	31026	3	1	2	2	1	0	1	0	1	1	0	1	3	
chr1:110140000-110161150	21151	3	1	1	1	1	1	1	1	2	3	1	1	1	
chr2:67455100-67475300	20201	3	1	1	1	1	0	2	0	1	3	0	1	2	
chr2:145391450-145406075	14626	3	1	0	0	0	0	0	0	0	0	0	0	3	
chr3:120042175-120054600	12426	3	1	0	1	1	1	3	1	1	1	1	1	3	
chr2:47707900-47740825	32926	3	1	1	3	1	1	2	0	1	2	1	1	1	
chr7:115705750-115719100	13351	3	1	3	0	1	0	0	0	1	1	0	1	1	
chr5:120503325-120556975	53651	3	1	1	1	1	0	1	0	2	2	0	1	3	
chr17:13902350-13912750	10401	3	1	0	1	1	1	1	1	1	3	1	3	0	
chr3:156892700-156920200	27501	3	1	0	3	1	1	2	0	3	1	0	1	3	
chr1:180367800-180398625	30826	3	2	1	2	1	1	1	3	2	2	1	2	3	
chr6:140930925-140944025	13101	3	1	1	0	0	0	0	0	0	3	0	0	1	
chr5:126209425-126222425	13001	3	1	1	2	1	0	1	0	2	1	0	3	1	
chr1:38349575-38436300	86726	3	2	1	3	1	3	2	1	2	2	1	2	3	
chr10:63244600-63290375	45776	3	2	1	3	1	1	2	0	1	2	0	2	3	
chr6:163707275-163722675	15401	3	1	2	3	1	1	1	0	1	2	1	3	1	
chr11:68866050-68876750	10701	3	1	3	1	0	0	0	1	0	0	0	0	1	
chr8:17033050-17043750	10701	3	1	1	1	1	1	1	1	3	1	1	3	2	
chr14:65329850-65390700	60851	3	1	1	3	1	1	3	1	1	2	0	2	2	
chr2:129013175-129078275	65101	3	2	1	3	1	1	3	3	2	1	0	1	2	
chr2:19934400-19954800	20401	3	1	0	1	1	1	3	1	1	2	1	3	1	
chr10:11477175-11516650	39476	3	1	1	2	1	1	2	0	1	3	1	2	2	
chrX:16349775-16384450	34676	3	2	2	3	1	1	1	1	2	2	1	3	2	
chr11:125559275-125576425	17151	3	2	0	2	2	1	2	0	1	2	3	2	2	
chr16:85173525-85183625	10101	3	1	1	3	2	1	3	0	2	1	0	1	2	
chr18:71155200-71236250	81051	3	2	1	3	1	1	2	0	2	3	1	2	3	
chr6:48613250-48635850	22601	3	1	0	1	1	0	1	0	1	3	1	1	1	
chr14:95159375-95182150	22776	3	1	0	2	0	0	1	1	1	1	0	2	3	
chr7:135091600-135161700	70101	3	2	1	3	2	3	2	0	3	2	1	2	2	
chr12:3887700-3912800	25101	3	1	0	1	0	0	0	3	1	0	0	1	1	
chrX:121189550-121211000	21451	3	2	1	1	1	1	2	1	2	3	2	3	2	
chr4:75405950-75439100	33151	3	1	1	1	1	1	1	1	2	3	1	3	2	
chr5:5376800-5390800	14001	3	1	0	1	0	0	1	0	0	3	0	0	1	
chr7:140858550-140880350	21801	3	1	1	1	1	1	1	0	0	3	0	1	2	
chr5:6309175-6335000	25826	3	1	0	1	0	2	2	0	1	3	1	2	2	
chr7:152227150-152252575	25426	3	2	1	3	1	1	3	1	2	2	2	2	1	
chrX:47499275-47526100	26826	3	2	1	2	1	1	2	0	1	3	1	2	2	
chr12:92102025-92112725	10701	3	2	3	2	1	1	1	0	2	2	1	1	2	
chr14:61092950-61102975	10026	3	1	1	1	1	0	1	1	3	1	0	2	1	
chr10:79477000-79490450	13451	3	1	1	2	1	0	1	0	2	1	0	2	3	
chr9:109835775-109863175	27401	3	1	0	0	1	0	0	0	1	1	0	1	3	
chr5:171169700-171196400	26701	3	2	1	3	1	0	2	0	2	2	2	3	2	
chr5:36449325-36493325	44001	3	2	1	3	1	2	3	1	3	2	1	2	2	
chr8:117452225-117463525	11301	3	1	1	2	1	1	1	0	1	3	1	2	1	
chrX:128656625-128669100	12476	3	1	0	1	0	1	1	3	1	0	1	1	1	
chr2:856250-875200	18951	3	1	0	1	0	1	2	0	0	3	0	1	3	
chr10:90790650-90810150	19501	3	1	1	1	1	1	1	0	3	3	1	2	1	
chr2:59760925-59778075	17151	3	1	1	2	1	1	2	0	1	3	1	2	2	
chr6:37852300-37874075	21776	3	1	0	1	0	1	2	0	1	3	0	1	1	
chr14:70218275-70241100	22826	3	1	0	3	1	1	1	0	1	1	1	3	1	
chr1:83290500-83321125	30626	3	1	1	1	0	0	3	1	1	1	1	2	2	
chrX:45204175-45226275	22101	3	1	1	1	1	1	2	1	2	3	1	1	2	
chrX:106809250-106830375	21126	3	1	1	1	1	0	1	1	3	2	1	1	1	
chr14:20357225-20368875	11651	3	2	1	3	1	1	2	1	3	2	1	3	3	
chr9:132216250-132228100	11851	3	1	1	3	0	0	0	0	0	0	1	0	0	
chr1:157733100-157744550	11451	3	1	0	0	1	0	1	3	0	1	0	0	0	
chr12:28147950-28179550	31601	3	1	0	1	1	2	3	1	1	1	0	1	1	
chr8:101561650-101582050	20401	3	1	1	3	1	0	3	1	1	1	1	2	1	
chr8:96764575-96799350	34776	3	2	1	3	1	1	2	0	2	2	1	2	2	
chr1:219344150-219386650	42501	3	1	1	1	1	1	2	0	2	1	1	2	3	
chr4:129807075-129835750	28676	3	2	1	2	2	1	3	1	2	1	1	2	1	
chr21:25773375-25797750	24376	3	1	1	2	1	1	2	0	1	3	1	2	2	
chrX:12985100-12999000	13901	3	1	1	1	1	1	1	1	2	3	1	1	1	
chr20:30614850-30628550	13701	3	1	0	2	0	0	1	0	1	0	0	3	0	
chr2:74047225-74063900	16676	3	1	0	3	1	0	1	0	1	1	1	1	1	
chr6:44551950-44649875	97926	3	1	1	3	1	1	1	1	1	2	0	1	2	
chr10:43321675-43337750	16076	3	1	1	2	1	1	1	0	1	2	0	3	1	
chr2:18650725-18664975	14251	3	2	1	2	1	1	3	1	1	2	1	3	2	
chr18:10967400-10990075	22676	3	2	1	3	1	1	2	0	2	3	1	2	3	
chr13:85112300-85176950	64651	3	2	1	3	1	1	1	0	2	3	0	3	2	
chr18:24926225-24960300	34076	3	1	1	3	0	1	1	0	2	1	1	1	1	
chr3:154613700-154630125	16426	3	1	1	1	1	0	1	0	3	2	1	1	2	
chr3:9316650-9327225	10576	3	1	1	1	1	1	3	0	2	2	1	1	2	
chr4:21970900-21980925	10026	3	1	0	3	0	1	2	0	0	1	3	0	0	
chr13:93951875-93969425	17551	3	2	2	3	2	2	2	3	3	2	1	2	2	
chr3:128335025-128366725	31701	3	2	2	2	2	2	2	3	2	2	1	1	2	
chr6:47497200-47512025	14826	3	1	1	2	0	1	2	0	1	3	1	1	1	
chr10:119334750-119346225	11476	3	1	0	0	0	0	3	0	0	1	0	0	1	
chr12:109163775-109180275	16501	3	1	1	3	1	1	2	0	1	2	1	1	1	
chr3:67392950-67407275	14326	3	1	1	1	1	1	3	1	2	2	1	2	1	
chr12:27251975-27262525	10551	3	1	0	1	0	0	1	0	1	1	1	1	3	
chr5:25161275-25192725	31451	3	1	0	1	1	1	1	0	1	2	0	1	3	
chr14:68342850-68361800	18951	3	1	1	1	0	0	1	1	1	1	0	3	1	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr2:235007225-235027750	20526	3	1	1	2	1	1	1	0	2	1	0	3	2	
chr2:235436300-235461250	24951	3	1	0	2	0	1	2	1	1	2	0	3	2	
chr5:72582075-72621975	39901	3	1	0	1	1	3	2	1	1	1	0	1	1	
chr7:17050950-17064125	13176	3	2	1	2	1	1	1	1	3	3	1	2	2	
chr21:43431675-43445875	14201	3	1	1	2	1	1	3	0	1	2	1	2	2	
chr3:138221350-138270375	49026	3	2	1	2	1	0	1	1	3	2	1	1	3	
chr4:108912750-108928175	15426	3	1	0	1	1	0	2	1	2	2	1	3	1	
chr18:51844825-51856000	11176	3	1	0	0	0	0	2	0	0	3	0	2	1	
chr1:55603825-55618950	15126	3	1	0	0	0	0	3	0	0	0	0	1	0	
chr7:44985750-44993250	7501	3	1	0	1	0	1	0	0	2	2	0	3	1	
chr1:170043625-170063325	19701	3	1	0	1	0	0	1	0	1	3	1	2	2	
chrX:112520800-112559300	38501	3	1	1	1	1	1	2	1	2	3	1	1	2	
chr6:113779025-113797250	18226	3	1	0	0	0	0	1	0	3	0	0	0	1	
chrX:7521975-7555900	33926	3	2	1	2	1	1	2	1	3	2	1	2	2	
chr10:82403500-82422325	18826	3	1	0	3	0	0	1	0	1	1	0	1	1	
chr12:84376050-84390000	13951	3	1	1	3	1	1	1	1	1	2	1	2	2	
chr8:23401500-23433375	31876	3	1	1	1	0	1	1	0	1	2	1	3	1	
chr4:60197375-60231625	34251	3	2	1	2	1	1	2	1	2	3	1	3	2	
chr7:132000925-132019600	18676	3	1	1	2	1	1	1	0	1	3	1	2	1	
chr1:54700800-54715125	14326	3	1	1	2	1	0	1	1	3	1	0	1	1	
chr17:35920625-35944325	23701	3	1	1	2	1	1	1	0	3	1	1	3	1	
chr14:82180425-82193800	13376	3	1	1	3	0	0	1	0	1	2	0	2	2	
chr15:68264425-68364650	100226	3	2	2	3	1	1	2	1	2	2	1	2	2	
chr6:24848150-24866900	18751	3	1	1	3	1	1	1	0	1	2	0	2	1	
chr20:38277400-38346375	68976	3	2	1	2	1	1	2	1	2	3	1	2	2	
chr7:3112050-3122375	10326	3	1	0	0	0	0	0	0	0	3	0	2	1	
chr13:54046725-54067800	21076	3	1	1	1	1	1	1	1	1	3	0	0	1	
chr11:123446150-123461375	15226	3	1	0	1	0	0	1	0	0	0	0	0	3	
chr1:110967750-110987075	19326	3	1	1	3	1	0	1	0	2	1	0	1	1	
chr2:145044975-145101650	56676	3	1	1	2	1	0	1	0	2	3	1	2	1	
chrX:113383525-113403350	19826	3	1	1	3	1	1	1	0	1	2	1	1	1	
chr12:112666800-112695075	28276	3	1	0	1	0	2	0	0	1	1	1	0	3	
chr6:107039875-107055450	15576	3	1	2	1	1	0	3	0	1	1	0	1	1	
chrX:39545025-39558350	13326	3	1	1	1	0	1	3	0	1	1	0	1	1	
chr2:209877875-209898250	20376	3	1	1	1	1	1	1	0	2	2	1	3	1	
chr8:98281700-98293000	11301	3	1	0	2	1	2	2	0	2	3	1	1	2	
chr13:20795375-20806850	11476	3	1	1	1	1	1	2	0	1	1	1	3	2	
chr16:64354175-64369575	15401	3	1	0	1	0	0	1	0	3	1	0	1	1	
chr4:97862925-97919950	57026	3	1	1	2	1	1	2	0	3	1	1	2	2	
chr6:45930950-45960325	29376	3	0	0	1	1	0	0	0	3	0	1	0	0	
chr2:113338800-113367300	28501	3	1	1	1	0	0	0	1	2	0	0	0	3	
chr5:100029775-100049925	20151	2	1	1	2	1	1	1	0	2	2	1	2	2	
chr6:40364375-40431825	67451	2	1	0	2	1	1	1	2	1	1	1	2	1	
chr12:66382725-66396775	14051	2	1	0	1	1	0	1	0	1	1	2	2	1	
chr8:8448600-8464875	16276	2	1	1	2	1	0	1	1	1	1	0	2	2	
chr10:5323425-5346050	22626	2	1	1	1	1	1	2	2	2	1	1	2	1	
chr11:61497150-61510050	12901	2	1	0	1	0	0	2	1	1	1	0	1	1	
chr16:82518800-82529525	10726	2	1	1	2	1	0	2	0	0	2	1	1	1	
chr17:52638425-52662275	23851	2	1	1	2	1	1	2	0	1	2	1	2	2	
chr18:19102650-19116400	13751	2	1	1	2	1	1	1	0	1	2	0	2	2	
chr2:15837300-15865800	28501	2	1	1	2	1	1	1	1	2	2	0	1	1	
chr2:208068275-208086800	18526	2	1	1	1	0	0	1	0	1	1	0	2	1	
chr5:130418650-130430500	11851	2	1	0	2	0	0	1	0	1	2	0	2	1	
chr6:23772575-23786650	14076	2	1	1	1	1	0	1	0	2	2	1	1	1	
chr2:129171850-129204875	33026	2	1	1	2	0	1	1	0	1	2	1	2	1	
chr2:207882050-207916600	34551	2	1	2	2	0	0	1	0	2	1	0	1	2	
chr10:31640150-31647375	7226	2	1	1	0	1	1	1	0	1	2	1	1	1	
chr13:32944875-32958750	13876	2	1	1	1	0	0	1	0	1	2	0	1	1	
chr10:8185475-8199525	14051	2	1	1	1	1	1	2	0	2	1	0	2	1	
chr1:37631125-37664925	33801	2	1	1	2	1	1	1	0	2	1	2	1	2	
chr13:37652175-37671200	19026	2	1	1	1	1	0	2	0	1	1	1	1	1	
chr13:30514900-30551075	36176	2	1	1	1	0	2	0	0	1	1	0	1	1	
chr3:52030875-52042150	11276	2	0	0	0	0	0	1	0	0	0	2	0	0	
chr4:13433500-13445875	12376	2	1	0	1	2	0	1	0	0	1	0	1	2	
chr12:74122750-74141150	18401	2	1	0	1	1	0	1	0	1	2	2	1	2	
chr3:191350675-191373100	22426	2	1	1	1	0	1	2	0	1	2	0	2	2	
chr4:13280500-13304225	23726	2	1	0	0	0	0	2	0	0	2	0	0	2	
chr9:99670975-99681450	10476	2	1	1	1	0	1	1	1	2	1	1	2	1	
chr12:99650125-99682025	31901	2	1	0	1	0	0	0	0	0	1	0	0	2	
chr11:118872950-118890300	17351	2	1	1	2	1	1	2	0	1	2	1	1	1	
chr14:63186050-63201475	15426	2	1	1	2	1	0	2	1	2	2	1	2	2	
chr14:37627700-37638050	10351	2	1	0	1	1	1	1	0	1	2	1	2	2	
chr3:174419600-174446075	26476	2	1	1	2	1	0	2	0	2	2	1	2	1	
chr3:15547200-15558900	11701	2	1	1	1	0	1	2	1	1	2	1	2	2	
chr9:101349675-101362675	13001	2	1	0	0	1	0	2	0	1	2	1	1	2	
chr2:197532200-197543775	11576	2	1	0	0	1	0	0	0	1	0	0	2	1	
chr13:23020375-23031325	10951	2	1	0	1	2	1	0	0	1	1	0	1	1	
chr12:46293050-46303950	10901	2	1	0	0	0	1	1	0	0	2	1	1	1	
chr1:226983650-227005375	21726	2	1	1	2	1	1	1	0	2	1	1	1	1	
chr4:24088325-24111350	23026	2	1	0	2	0	0	1	0	1	2	1	1	1	
chr5:126425050-126439050	14001	2	1	1	1	0	0	1	0	0	1	0	2	2	
chr12:28059800-28074275	14476	2	1	1	0	0	0	1	0	2	0	0	0	1	
chr6:114419675-114434275	14601	2	1	2	1	1	2	1	1	2	2	1	2	1	
chr10:46439775-46457625	17851	2	1	0	2	0	0	0	0	1	1	0	0	1	
chr10:72470575-72517275	46701	2	1	1	2	1	1	1	0	1	1	0	1	1	
chr17:21173800-21193125	19326	2	1	0	2	1	0	1	0	1	1	0	1	1	
chr5:151402350-151417950	15601	2	1	2	1	1	1	2	1	2	1	1	1	2	
chr5:67021350-67033475	12126	2	1	0	1	0	0	1	1	2	0	2	0	1	
chr2:46610375-46622325	11951	2	1	2	1	2	1	2	0	2	2	1	2	1	
chr2:68699850-68713300	13451	2	1	1	1	1	1	1	0	1	2	1	1	2	
chr2:1582100-1606250	24151	2	1	1	2	1	1	1	0	2	1	0	1	1	
chr3:15903550-15915000	11451	2	1	0	1	1	0	1	0	0	2	1	1	1	
chr2:48144125-48183025	38901	2	1	1	1	0	1	1	0	1	1	1	2	2	
chr8:125928050-125946450	18401	2	1	0	1	1	1	1	1	1	1	0	2	2	
chr11:35030825-35051075	20251	2	1	1	2	1	0	1	0	2	2	1	2	1	
chr14:99762875-99774250	11376	2	1	0	1	0	0	1	0	1	2	0	1	0	
chr4:11175800-11186900	11101	2	1	0	0	0	0	1	0	1	2	0	1	1	
chrX:44865675-44877100	11426	2	1	0	1	1	1	1	1	1	2	1	1	1	
chr15:68593550-68621775	28226	2	1	0	2	0	1	1	0	1	1	1	2	2	
chr6:158103850-158116625	12776	2	1	2	1	0	0	1	0	0	0	1	1	0	
chr1:115446650-115482075	35426	2	1	1	2	1	1	2	0	1	2	0	1	1	
chr1:5284450-5323200	38751	2	1	0	2	1	0	0	0	1	1	0	1	1	
chr6:28803400-28817200	13801	2	1	1	2	1	1	1	0	1	2	1	2	2	
chr2:143529050-143548825	19776	2	1	0	1	0	0	1	1	1	1	0	2	1	
chr6:83144225-83155775	11551	2	1	0	1	1	1	1	0	1	1	0	2	0	
chr5:95612950-95629950	17001	2	1	1	1	1	0	2	0	2	2	1	1	1	
chr6:132270225-132303825	33601	2	1	1	2	1	0	1	0	1	2	1	1	1	
chr8:80982575-80993550	10976	2	1	0	1	1	1	2	1	1	2	2	2	1	
chr4:97596350-97637675	41326	2	1	1	2	1	1	2	1	2	2	0	2	2	
chr15:77908600-77919075	10476	2	1	1	1	1	1	2	1	1	2	1	2	1	
chr1:219188650-219213500	24851	2	1	0	2	0	0	1	0	1	1	1	2	2	
chr5:108581425-108615525	34101	2	1	1	1	0	0	2	1	1	1	1	2	1	
chr8:8935475-8948675	13201	2	1	1	1	1	0	1	1	1	2	0	2	1	
chr1:58946300-58965675	19376	2	1	1	1	1	1	1	0	2	1	0	0	1	
chr7:12309550-12324625	15076	2	1	1	1	0	0	1	0	1	2	0	2	2	
chr8:99470550-99481825	11276	2	1	1	0	0	0	1	1	1	2	0	1	2	
chr14:21939225-21987475	48251	2	1	0	2	0	1	2	0	1	1	0	2	1	
chr1:79669875-79726875	57001	2	1	1	1	0	1	1	0	1	2	1	2	2	
chr15:27756650-27770700	14051	2	1	0	1	0	1	2	0	0	1	0	0	2	
chr13:44167650-44182450	14801	2	1	1	2	1	1	1	1	1	2	1	1	1	
chrX:39865200-39876225	11026	2	1	1	2	1	0	1	1	1	1	0	1	1	
chr8:28599675-28613975	14301	2	1	0	1	1	1	1	0	1	2	1	1	2	
chr4:109840575-109856475	15901	2	1	1	1	1	1	2	0	1	1	1	1	1	
chr1:110890825-110912275	21451	2	0	2	0	0	0	0	0	1	0	0	0	0	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr5:65651750-65665975	14226	2	1	0	1	2	0	1	0	0	1	1	0	2	
chr7:134059975-134078575	18601	2	1	1	2	1	1	1	0	1	2	2	1	2	
chr10:14583425-14595550	12126	2	1	0	0	0	0	2	1	1	0	0	2	1	
chr14:59839275-59854025	14751	2	1	0	1	1	0	1	1	1	1	1	2	1	
chr1:227938125-227966450	28326	2	1	1	2	1	1	1	0	1	2	0	1	2	
chr1:192052425-192067650	15226	2	1	0	1	1	0	1	2	1	2	1	1	1	
chr14:103819375-103843275	23901	2	0	0	1	0	1	1	0	0	2	0	0	0	
chr16:86886600-86897900	11301	2	0	0	0	0	0	0	0	0	2	0	0	0	
chr7:129874900-129897725	22826	2	1	1	2	1	0	1	0	1	1	2	1	1	
chr7:36085575-36119300	33726	2	1	0	1	0	0	1	0	1	1	2	1	0	
chr1:229493875-229512225	18351	2	1	1	2	0	1	1	0	1	2	1	1	1	
chr17:45292550-45303650	11101	2	1	1	2	0	1	1	0	2	1	2	1	1	
chr7:156071100-156081325	10226	2	1	1	2	0	1	2	1	0	1	0	1	1	
chrX:16485950-16503000	17051	2	1	0	2	1	0	1	0	1	2	1	1	1	
chr12:1905425-1919900	14476	2	1	0	1	1	1	1	0	1	2	1	2	2	
chr2:173862575-173875725	13151	2	1	1	1	1	1	1	2	1	1	1	1	1	
chr5:7315850-7326875	11026	2	1	0	1	1	0	2	0	2	1	1	1	2	
chr14:102278900-102297625	18726	2	1	0	2	1	0	1	1	1	1	0	1	1	
chr2:102247075-102260750	13676	2	1	0	1	0	0	0	0	2	0	0	2	0	
chr9:110220050-110234450	14401	2	1	0	1	1	0	1	0	1	2	1	1	1	
chr2:112100575-112126675	26101	2	1	1	2	1	0	2	0	2	1	2	1	1	
chr1:108668675-108685775	17101	2	1	0	0	0	0	0	0	0	1	0	1	2	
chr14:96861925-96885100	23176	2	1	0	1	0	0	1	0	1	2	0	0	1	
chr2:68414075-68436975	22901	2	1	0	2	1	1	1	0	1	2	1	2	1	
chr8:59599400-59611475	12076	2	1	1	1	1	1	1	0	1	2	1	1	1	
chr1:111258200-111271650	13451	2	1	0	1	0	0	1	1	2	1	0	2	1	
chr3:28780450-28795425	14976	2	1	1	2	0	0	1	0	1	1	0	1	1	
chr8:107124300-107141200	16901	2	1	1	2	0	0	1	0	0	2	0	0	1	
chr7:154880875-154899050	18176	2	0	0	0	0	2	0	0	0	0	0	0	0	
chr4:119116800-119129925	13126	2	1	0	1	0	0	1	0	1	1	0	2	1	
chr4:109537600-109559575	21976	2	1	1	2	1	1	2	0	1	1	0	1	1	
chr7:63974350-63986200	11851	2	1	0	2	0	1	0	0	1	0	0	0	2	
chr9:110453000-110477975	24976	2	1	1	1	1	1	2	0	1	1	0	1	2	
chr2:177413225-177449975	36751	2	1	0	1	0	1	1	0	0	2	0	0	1	
chr6:3720750-3734450	13701	2	0	0	0	0	0	0	2	0	0	0	0	0	
chr3:127457650-127470750	13101	2	0	2	0	0	0	1	0	1	0	0	0	0	
chr16:1370125-1384875	14751	2	1	1	2	0	1	1	0	2	2	0	2	1	
chr7:154956450-154968800	12351	2	1	1	2	0	1	1	1	1	1	0	1	1	
chr8:86661875-86704300	42426	2	1	1	2	1	1	1	0	1	2	0	1	1	
chr15:35840950-35861750	20801	2	1	1	1	1	0	2	1	1	2	1	1	1	
chr12:27470200-27503925	33726	2	1	1	2	1	2	1	1	2	1	1	1	2	
chr16:85209025-85242650	33626	2	1	0	1	2	1	2	0	1	1	1	1	1	
chr1:230946300-230968050	21751	2	1	1	1	0	0	1	0	0	1	0	1	2	
chr5:153310925-153336875	25951	2	1	1	1	1	0	2	0	1	1	1	2	2	
chr16:64844625-64859475	14851	2	1	0	0	0	0	1	0	1	2	0	0	1	
chr2:75102425-75113500	11076	2	1	0	0	0	0	1	0	0	2	0	1	1	
chr3:140070825-140082475	11651	2	1	0	2	1	0	1	0	1	2	1	1	1	
chr3:72052025-72073225	21201	2	1	0	2	0	0	1	0	1	1	0	1	1	
chr21:26566775-26598525	31751	2	1	0	1	1	1	1	1	2	1	1	1	1	
chr4:6803950-6814375	10426	2	1	0	1	0	0	1	1	2	1	0	0	1	
chrX:46061075-46074800	13726	2	1	2	1	1	0	2	0	1	1	0	1	1	
chr1:198069025-198095775	26751	2	1	0	1	0	0	1	0	1	1	1	1	2	
chr6:28257900-28284400	26501	2	1	0	1	1	0	1	0	1	2	0	1	1	
chr8:133765050-133775675	10626	2	1	1	1	1	0	0	0	1	1	0	2	0	
chrX:68155600-68165750	10151	2	0	0	2	0	0	1	0	1	0	0	1	0	
chr16:85714350-85726850	12501	2	1	0	1	0	1	1	0	0	1	0	0	2	
chr14:58685825-58705500	19676	2	1	0	2	0	0	1	0	1	1	0	1	1	
chr12:37070650-37099175	28526	2	1	1	1	0	1	1	0	1	2	1	1	1	
chr14:50957850-50968625	10776	2	0	0	0	0	0	0	0	0	2	0	0	0	
chr2:208088275-208101600	13326	2	1	1	1	1	0	0	0	1	2	0	2	1	
chr16:24382475-24394475	12001	2	1	0	1	1	1	1	0	2	1	0	1	2	
chr12:91114125-91124300	10176	2	1	1	0	0	0	1	0	2	1	0	1	1	
chr3:14365525-14403925	38401	2	1	1	1	1	0	1	0	2	1	2	1	1	
chr3:18718325-18755600	37276	2	1	1	2	1	0	1	0	2	2	1	2	1	
chrX:9188975-9205300	16326	2	1	0	1	0	1	0	0	2	0	0	0	1	
chr17:31380950-31404075	23126	2	1	0	2	1	1	2	1	1	2	0	1	2	
chrX:8034225-8044325	10101	2	1	0	1	0	0	1	0	0	2	1	1	1	
chr1:89972700-89985275	12576	2	1	1	1	0	0	1	0	1	1	0	2	1	
chr14:75090375-75100625	10251	2	1	1	1	1	1	1	0	1	0	0	2	1	
chr7:17693175-17708075	14901	2	1	0	1	0	0	0	0	0	0	1	2	0	
chr1:186622825-186667625	44801	2	1	1	2	0	1	1	0	1	1	0	1	1	
chr14:54626650-54641500	14851	2	1	0	2	0	0	0	0	0	1	0	1	1	
chr2:195714425-195743825	29401	2	1	0	1	1	0	1	0	1	1	2	1	2	
chr10:120025775-120037250	11476	2	1	1	2	1	0	2	0	1	1	1	1	1	
chrX:108755875-108765750	9876	2	0	0	0	0	0	0	0	1	0	1	2	0	
chr5:170925150-170938100	12951	2	1	0	2	0	1	0	0	0	0	0	1	1	
chr8:123180400-123245250	64851	2	1	1	2	2	1	1	0	1	2	0	1	1	
chrX:45935775-45952650	16876	2	1	1	2	1	0	1	0	1	1	0	1	1	
chr9:108063575-108084000	20426	2	1	0	1	0	0	1	0	0	1	2	1	1	
chr10:21588375-21603075	14701	2	1	0	1	0	0	1	0	1	2	0	0	1	
chr8:116879400-116915750	36351	2	1	1	1	1	1	2	0	1	2	1	1	2	
chr13:90287700-90298800	11101	2	1	0	1	1	1	2	0	1	1	1	1	1	
chr5:172802300-172835075	32776	2	1	1	1	1	1	1	0	1	1	1	0	2	
chr6:319725-331650	11926	2	1	0	0	0	0	0	1	1	1	1	2	1	
chr1:190336425-190386300	49876	2	1	0	2	1	1	1	0	1	2	0	1	1	
chr1:32953825-32968200	14376	2	1	1	2	0	2	2	1	1	1	0	1	1	
chr10:46461825-46483150	21326	2	1	0	2	0	1	1	0	1	1	0	1	1	
chr18:69428125-69440375	12251	2	1	1	2	1	0	0	0	1	0	1	0	0	
chr8:135270400-135285950	15551	2	1	1	2	1	1	1	0	1	2	0	1	1	
chr11:12061300-12075325	14026	2	1	0	1	0	0	0	0	1	0	0	1	2	
chr7:148684475-148711675	27201	2	1	1	1	1	1	1	0	1	2	1	1	2	
chr7:37491050-37501225	10176	2	1	1	1	0	0	1	0	1	1	0	1	2	
chr20:21494900-21542475	47576	2	1	1	2	0	1	2	1	1	1	1	1	1	
chr4:12494675-12506850	12176	2	1	1	1	1	0	2	0	0	1	0	1	1	
chr1:209780925-209794325	13401	2	1	1	1	1	2	1	1	1	2	1	1	1	
chr11:44514100-44530500	16401	2	1	0	1	1	1	1	0	1	2	0	1	1	
chr7:19668825-19689525	20701	2	1	0	0	1	0	1	0	0	2	1	1	1	
chr21:23019950-23043675	23726	2	0	0	1	0	0	0	0	1	0	0	0	2	
chr1:116599350-116640475	41126	2	1	0	2	0	1	1	0	1	1	0	0	1	
chr12:12899550-12917075	17526	2	1	1	2	1	1	1	0	1	1	1	2	2	
chr4:84501725-84520225	18501	2	1	0	2	1	1	1	0	1	1	2	1	1	
chr2:19843425-19853775	10351	2	1	1	1	1	0	2	1	0	1	1	1	1	
chr6:88777300-88787350	10051	2	0	0	0	0	0	2	0	0	0	0	0	0	
chr7:45237050-45257100	20051	2	1	0	1	2	0	1	0	1	1	0	1	0	
chr3:162490600-162502750	12151	2	1	1	1	1	0	1	0	0	1	1	1	2	
chr6:95297000-95320325	23326	2	1	0	1	0	2	0	0	0	1	0	0	1	
chr3:67211075-67230650	19576	2	1	1	1	1	1	2	0	1	1	0	1	1	
chr8:90569375-90582100	12726	2	1	0	1	1	1	2	0	0	2	1	0	1	
chr15:52877675-52913225	35551	2	1	1	1	1	0	1	1	2	1	1	1	2	
chr11:127666200-127694325	28126	2	1	1	1	0	0	1	0	1	0	0	2	0	
chr16:65001425-65016550	15126	2	1	1	1	0	0	0	0	0	0	0	2	1	
chr7:107281875-107305375	23501	2	1	0	2	0	0	1	0	0	1	0	1	1	
chr16:72642800-72653775	10976	2	1	1	1	1	0	1	1	1	2	1	1	1	
chrX:47435100-47446900	11801	2	0	0	0	0	0	1	0	0	2	0	0	0	
chr17:6706675-6717550	10876	2	1	0	1	0	1	2	1	1	1	0	0	1	
chr7:139125175-139135400	10226	2	1	1	1	0	0	2	0	1	1	0	1	1	
chr3:178961675-178979250	17576	2	1	0	2	0	0	0	0	2	0	0	1	0	
chr4:74767950-74796275	28326	2	1	1	1	0	0	2	0	1	2	0	1	0	
chr21:39892800-39905250	12451	2	1	0	1	0	2	0	0	0	1	0	0	0	
chr4:105886425-105897000	10576	2	0	0	0	0	0	2	0	0	0	0	0	1	
chr8:20714075-20728800	14726	2	0	0	0	0	0	0	2	0	0	0	0	1	
chr1:211527625-211546900	19276	2	1	0	1	1	2	1	0	1	2	2	1	1	
chr7:127535725-127551125	15401	2	1	1	1	0	1	1	0	1	1	2	1	1	
chr14:56622350-56632675	10326	2	0	0	0	0	0	0	0	0	2	0	0	1	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr11:11610275-11623250	12976	2	1	1	2	1	1	1	0	2	1	1	1	1	
chr2:20228225-20252075	23851	2	1	1	2	0	0	1	0	2	1	0	1	1	
chr13:94099200-94126650	27451	2	1	1	2	1	1	1	0	1	1	1	1	1	
chr12:60293850-60330425	36576	2	1	0	1	1	1	1	0	1	2	0	1	1	
chr15:86016750-86031775	15026	2	0	0	0	0	0	0	0	0	0	0	0	2	
chr12:130862425-130873450	11026	2	1	1	2	1	0	1	0	1	1	1	1	1	
chr8:49497300-49508350	11051	2	0	0	2	0	0	0	0	0	0	0	0	0	
chrX:13179325-13195650	16326	2	0	0	0	0	0	0	0	2	0	0	0	0	
chr2:60308225-60325275	17051	2	1	0	1	1	1	1	0	1	2	0	1	2	
chr10:33295350-33306125	10776	2	1	1	1	0	0	0	0	1	2	1	1	1	
chr4:28047250-28057975	10726	2	0	0	0	0	0	0	0	0	2	0	0	0	
chr2:118070075-118082125	12051	2	1	1	1	1	1	2	1	1	2	1	2	2	
chr7:126966450-126978000	11551	2	1	0	1	0	0	1	1	1	1	0	1	2	
chr2:191182625-191194800	12176	2	1	1	1	1	1	1	0	1	1	1	2	2	
chr12:71402075-71451500	49426	2	1	1	2	1	1	1	0	1	2	2	2	2	
chr20:41540650-41550875	10226	2	1	0	1	1	0	1	0	1	2	1	1	0	
chr7:25945000-25956500	11501	2	1	0	1	0	0	1	1	1	2	0	1	0	
chr2:140320750-140345675	24926	2	1	1	2	0	0	1	0	1	2	0	1	1	
chr5:123989500-124000000	10501	2	1	0	2	1	0	1	0	2	1	1	1	0	
chr2:100743825-100764825	21001	2	0	0	1	0	0	2	0	0	1	0	0	0	
chr4:123259225-123275150	15926	2	1	1	0	0	1	0	0	1	1	0	2	0	
chrX:97117325-97138975	21651	2	1	1	0	1	1	1	0	1	1	1	2	1	
chr13:62527475-62547500	20026	2	0	0	1	0	0	0	0	0	0	0	0	2	
chr2:3018400-3029600	11201	2	1	0	2	0	1	0	0	0	0	0	1	1	
chr5:67639050-67653625	14576	2	1	0	2	0	0	1	1	1	0	0	1	1	
chr8:126534450-126548675	14226	2	1	0	2	1	0	1	0	1	1	0	1	1	
chr9:136478450-136494350	15901	2	1	0	2	0	0	0	0	0	0	2	1	0	
chr3:140886175-140908425	22251	2	1	0	0	0	0	1	0	0	2	1	1	1	
chr5:71698825-71709925	11101	2	1	0	0	1	1	1	0	0	2	0	2	1	
chrX:17692075-17705000	12926	2	0	0	0	0	1	0	0	0	2	0	0	1	
chr18:52269550-52287850	18301	2	1	1	1	0	0	0	0	0	1	0	2	1	
chr2:239386225-239398275	12051	2	1	0	0	0	0	0	2	1	1	0	1	1	
chr11:75618975-75681950	62976	2	1	0	2	0	1	1	0	1	1	0	1	1	
chr12:12035425-12048075	12651	2	1	0	2	1	0	1	0	1	1	0	1	0	
chr13:76119825-76133875	14051	2	1	1	2	1	0	1	1	1	1	0	2	2	
chr4:75749750-75816175	66426	2	1	1	2	1	1	1	0	1	1	0	1	1	
chr6:105257475-105276750	19276	2	1	0	1	0	0	1	0	1	1	1	1	2	
chr4:82927700-82939425	11726	2	1	1	1	1	1	2	0	1	1	0	1	1	
chr13:73143700-73156425	12726	2	0	0	0	0	0	1	0	0	1	1	2	0	
chr4:45663225-45675625	12401	2	1	0	0	1	0	1	0	1	1	1	2	1	
chrX:42589900-42605225	15326	2	0	0	1	0	0	0	0	0	0	0	1	2	
chr1:117139575-117159550	19976	2	1	0	2	0	0	0	0	1	1	0	2	1	
chr10:124096325-124117225	20901	2	1	0	2	0	0	1	0	1	1	0	1	1	
chr16:73375750-73388725	12976	2	1	1	2	0	0	0	0	1	1	0	1	1	
chr8:49339350-49364275	24926	2	1	0	2	1	1	1	0	1	1	1	1	1	
chr10:116737575-116751575	14001	2	1	0	1	0	0	1	0	0	1	0	1	2	
chr6:167563325-167591625	28301	2	1	0	0	0	1	1	0	1	1	0	1	2	
chr13:26929500-26940825	11326	2	0	0	1	0	0	0	1	2	0	0	0	0	
chr8:101497275-101508975	11701	2	1	0	1	0	0	1	0	2	0	0	0	1	
chr8:55859150-55874925	15776	2	1	0	0	0	0	2	0	2	1	0	1	1	
chr12:66122475-66133100	10626	2	1	0	0	0	0	0	0	1	1	2	0	1	
chr2:102818025-102837000	18976	2	1	0	1	2	0	1	0	1	1	2	1	1	
chr2:60939000-60949925	10926	2	0	0	0	0	0	1	0	0	2	0	0	0	
chr21:40002450-40025400	22951	2	1	1	1	1	1	1	0	1	2	0	1	1	
chr6:168840750-168858250	17501	2	0	0	0	0	0	0	0	0	2	0	0	1	
chrX:33839175-33855650	16476	2	1	0	0	1	0	0	0	0	2	1	0	1	
chr4:122340200-122357975	17776	2	1	0	1	0	0	1	0	1	1	0	2	1	
chr8:134223000-134240175	17176	2	1	0	1	0	0	1	0	1	0	0	2	0	
chr1:233083800-233131200	47401	2	1	0	2	1	1	1	1	1	1	1	1	1	
chr10:79868075-79885175	17101	2	1	0	2	0	1	0	0	1	1	0	1	1	
chr12:22424300-22444300	20001	2	1	0	2	0	1	1	0	1	1	1	1	1	
chr10:74794275-74801925	7651	2	1	0	1	1	1	1	0	1	2	1	1	1	
chr3:129629700-129653875	24176	2	1	1	1	1	1	1	0	1	2	1	1	1	
chr6:168228500-168281475	52976	2	1	0	1	0	0	1	0	2	0	0	1	1	
chr3:40633100-40647875	14776	2	1	0	1	0	0	1	0	0	1	0	2	1	
chr6:56831150-56842350	11201	2	1	1	2	0	1	0	0	0	1	0	1	0	
chr1:233176125-233186700	10576	2	1	0	1	1	0	0	2	1	1	0	1	0	
chr2:83365875-83377675	11801	2	1	0	1	1	0	0	0	1	2	0	1	1	
chr3:39253550-39266600	13051	2	1	0	1	0	0	0	0	1	2	0	1	1	
chr4:103259950-103278600	18651	2	1	0	1	1	0	1	0	1	2	1	1	1	
chr15:95199150-95215225	16076	2	0	0	1	0	0	0	1	2	0	0	0	1	
chr2:33927975-33955425	27451	2	1	0	1	1	0	1	0	1	1	1	1	2	
chr3:165381975-165394700	12726	2	0	0	0	0	0	2	0	1	0	0	0	0	
chr12:129742550-129761400	18851	2	1	0	1	1	1	1	0	1	2	0	1	1	
chr11:93342525-93370800	28276	2	1	0	2	0	0	1	0	1	1	1	1	1	
chr13:111038175-111051075	12901	2	1	0	2	0	0	0	0	1	1	0	1	1	
chr18:10217025-10229050	12026	2	1	0	2	1	0	0	0	1	0	0	1	1	
chr7:64405850-64428525	22676	2	1	1	2	0	1	1	0	1	1	1	1	1	
chr11:113400350-113410875	10526	2	0	0	0	0	0	0	0	0	0	2	0	0	
chr13:77485575-77499475	13901	2	0	0	0	0	1	2	0	0	0	0	0	1	
chr8:87388450-87400450	12001	1	1	0	1	0	0	1	0	0	1	0	1	1	
chr15:72297100-72307675	10576	1	1	0	1	0	0	0	0	1	1	0	1	1	
chr18:31270875-31282100	11226	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr7:1314975-1333125	18151	1	1	0	1	0	0	0	0	1	1	0	1	1	
chr12:62078650-62106025	27376	1	1	1	1	1	1	1	0	1	1	0	1	1	
chr7:38128125-38146550	18426	1	1	0	1	0	0	1	0	1	1	0	1	0	
chr18:45525275-45537075	11801	1	1	0	0	0	0	1	0	0	1	0	1	1	
chr5:123734825-123757500	22676	1	1	1	1	1	1	1	0	1	1	1	1	1	
chr2:131299475-131330850	31376	1	1	0	1	0	1	0	0	0	0	0	1	1	
chr15:34482575-34514925	32351	1	1	0	1	0	0	1	0	0	1	0	1	1	
chr4:100514375-100532350	17976	1	1	1	0	1	0	1	1	1	1	0	1	0	
chr3:59513350-59536300	22951	1	1	0	1	0	0	1	0	1	1	0	0	1	
chr5:172551525-172566225	14701	1	1	0	1	0	1	1	0	1	1	0	1	1	
chr6:106317650-106342450	24801	1	0	0	1	0	0	0	0	1	1	0	1	1	
chr8:143050700-143089375	38676	1	1	0	1	0	1	1	0	1	0	0	1	0	
chr7:10108575-10127025	18451	1	1	0	1	1	1	1	0	1	1	0	1	1	
chr1:94192050-94206150	14101	1	1	0	0	0	0	1	0	1	1	0	1	1	
chr10:72048325-72060125	11801	1	1	0	1	0	1	1	0	1	1	0	1	0	
chr13:65073950-65093750	19801	1	1	1	1	1	0	1	0	1	1	1	1	1	
chrX:42410125-42420750	10626	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr10:9125775-9138650	12876	1	0	1	0	0	1	1	0	0	0	0	0	1	
chr6:137747450-137784475	37026	1	1	1	1	0	1	1	1	1	1	0	1	1	
chr8:58422575-58434950	12376	1	1	1	1	1	0	1	1	1	1	0	1	1	
chr8:6504100-6520650	16551	1	1	0	1	1	1	1	0	0	1	1	0	1	
chrX:47681075-47693375	12301	1	1	1	1	0	1	1	1	1	1	0	1	1	
chr12:4208850-4236425	27576	1	1	1	1	1	1	1	0	1	1	0	1	1	
chr14:65527250-65542300	15051	1	1	1	1	0	0	1	1	1	1	0	0	1	
chr7:12555150-12568375	13226	1	1	0	1	0	0	1	0	1	1	0	0	1	
chr13:32328175-32365200	37026	1	1	0	1	0	0	1	0	1	1	1	1	1	
chr5:131205050-131217175	12126	1	1	0	0	0	0	0	0	1	1	0	1	1	
chr8:127174725-127195150	20426	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr1:41622050-41638350	16301	1	1	0	1	0	1	1	0	1	1	1	0	1	
chr7:139990575-140001525	10951	1	1	0	1	0	0	0	0	0	1	0	1	1	
chr5:147208200-147229425	21226	1	1	1	1	1	1	1	0	1	1	0	1	1	
chr10:58632875-58649825	16951	1	1	0	1	1	0	1	0	0	1	0	0	1	
chr7:26058825-26077900	19076	1	1	0	1	0	1	1	0	1	1	0	0	1	
chr1:47977525-47990050	12526	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr9:136969250-136980175	10926	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr12:103278000-103288275	10276	1	0	0	0	0	0	1	0	0	1	1	1	0	
chr4:92760700-92774625	13926	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr18:71295125-71308850	13726	1	1	0	0	1	1	0	0	0	1	0	0	1	
chr1:36804800-36856000	51201	1	1	0	1	0	0	1	0	1	1	0	1	0	
chr13:102433875-102457175	23301	1	1	1	1	1	0	1	0	1	1	1	1	1	
chr15:32723275-32748900	25626	1	1	1	1	0	1	1	0	1	1	1	0	1	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr9:110587325-110599600	12276	1	1	1	1	0	0	0	0	0	1	0	1	1	
chr4:126684025-126702050	18026	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr1:227336900-227362675	25776	1	1	1	1	1	1	1	0	1	1	0	0	1	
chr9:20275050-20313050	38001	1	1	0	0	0	0	0	0	1	1	0	1	1	
chr10:43662450-43681050	18601	1	1	1	0	1	1	0	0	0	0	0	1	1	
chr10:95690050-95706050	16001	1	1	0	1	0	0	0	0	0	1	0	1	1	
chr8:107241625-107255900	14276	1	1	1	1	0	0	1	0	1	1	0	1	1	
chr5:172935725-172946925	11201	1	1	1	0	1	0	1	0	0	1	1	1	1	
chr1:61790650-61807975	17326	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr18:12755775-12765850	10076	1	0	0	1	0	0	0	0	1	1	0	1	1	
chr3:34601800-34619400	17601	1	1	0	0	1	1	1	0	1	1	0	1	1	
chr12:123289800-123300925	11126	1	0	0	0	1	0	0	1	0	1	0	0	1	
chr1:210766975-210778775	11801	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr4:3267300-3280150	12851	1	1	0	1	0	0	0	0	1	1	0	0	1	
chr13:25892925-25912325	19401	1	1	0	0	1	0	1	0	1	1	1	1	1	
chr16:11202325-11213275	10951	1	1	0	1	0	0	1	0	1	1	1	1	1	
chr16:85636250-85652025	15776	1	0	0	1	0	1	0	0	0	0	0	0	1	
chr18:65815775-65821875	6101	1	1	0	0	0	0	1	0	0	1	1	1	1	
chr7:131200300-131215700	15401	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr18:62495250-62511675	16426	1	1	0	0	1	0	1	0	1	1	0	1	1	
chr11:3318675-3329000	10326	1	0	0	0	0	0	1	0	0	0	0	1	0	
chr18:50499900-50530325	30426	1	1	1	1	1	0	1	0	1	1	0	1	1	
chr21:36918225-36929075	10851	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr1:184977425-184989700	12276	1	0	0	1	0	0	1	0	0	1	0	1	1	
chr10:20704225-20728925	24701	1	1	1	1	1	0	1	0	1	1	0	1	1	
chr8:102116975-102146725	29751	1	1	0	1	0	0	0	0	1	1	0	1	1	
chr8:62947050-62968950	21901	1	0	0	1	0	0	1	0	0	0	0	0	1	
chr6:160265000-160304725	39726	1	1	0	1	0	1	1	0	1	1	1	1	1	
chr7:106011900-106044800	32901	1	1	1	1	0	0	1	0	0	0	1	1	1	
chr3:1054400-1066350	11951	1	1	1	1	1	0	1	0	0	1	1	0	1	
chr13:96567750-96587100	19351	1	0	0	0	0	1	0	0	0	1	1	0	1	
chr15:75776925-75798350	21426	1	1	0	1	0	1	1	0	1	1	0	0	1	
chr5:138004150-138033350	29201	1	1	0	1	0	0	0	0	1	1	0	1	1	
chr6:169980975-170009950	28976	1	0	0	1	0	0	1	0	0	1	0	0	1	
chr2:65553800-65571600	17801	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr3:14234200-14253875	19676	1	1	0	1	1	0	1	0	1	1	1	1	1	
chr3:151675700-151689700	14001	1	1	0	1	1	0	1	0	1	1	1	1	1	
chr13:36774375-36786575	12201	1	0	0	1	0	0	0	0	0	0	0	1	1	
chr4:60023500-60045050	21551	1	1	0	1	1	1	1	0	1	1	0	1	1	
chr5:82720450-82740300	19851	1	1	0	1	0	0	1	0	1	1	1	1	1	
chr11:70708525-70763300	54776	1	1	1	1	1	1	1	0	1	1	0	1	1	
chr8:129364550-129425050	60501	1	1	1	1	0	1	1	0	1	1	0	1	1	
chr2:174618925-174633575	14651	1	0	0	1	0	0	0	0	0	1	0	0	1	
chr3:162956025-162984275	28251	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr4:80131600-80143150	11551	1	1	0	1	1	1	0	0	1	1	0	1	1	
chr5:82352125-82366025	13901	1	1	0	0	1	1	1	0	0	1	0	1	1	
chr1:232846750-232871450	24701	1	1	0	1	0	0	1	0	1	1	1	1	1	
chr18:3275925-3287175	11251	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr18:73132350-73145125	12776	1	1	1	1	0	0	1	0	0	1	0	0	1	
chr5:171039675-171075250	35576	1	0	0	1	0	0	1	0	0	1	0	0	1	
chr7:133743150-133761500	18351	1	1	1	1	0	1	0	0	0	0	0	0	1	
chr1:157866600-157887050	20451	1	1	0	1	0	0	1	0	1	1	0	0	1	
chr14:100893675-100910100	16426	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr8:67374100-67384800	10701	1	0	0	0	0	0	1	0	1	1	0	0	1	
chr11:76004575-76019350	14776	1	1	0	1	0	0	1	0	1	1	1	1	1	
chr5:150980275-150993600	13326	1	1	1	1	1	1	1	0	1	1	1	1	1	
chr1:242144675-242161200	16526	1	0	0	0	0	1	0	0	0	1	0	1	0	
chr13:109450900-109474050	23151	1	0	0	0	0	1	0	0	0	0	0	0	1	
chr14:88668550-88683450	14901	1	0	0	0	0	0	0	0	1	1	1	1	0	
chr1:242224475-242238875	14401	1	0	0	1	0	1	0	0	0	1	0	0	1	
chr1:196602575-196613925	11351	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr5:65527325-65546300	18976	1	1	1	1	0	0	1	0	1	0	1	0	1	
chr11:60195475-60207650	12176	1	0	0	1	0	0	0	0	0	0	0	1	1	
chr17:13668000-13679475	11476	1	1	0	1	0	0	1	0	0	1	0	1	0	
chr1:232737950-232749825	11876	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr16:80725025-80730300	5276	1	0	0	1	0	1	0	0	0	0	0	0	0	
chr4:11720650-11746750	26101	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr5:172072175-172091825	19651	1	0	0	1	0	0	1	1	1	0	0	1	0	
chr11:64016000-64031350	15351	1	1	1	1	0	1	0	0	1	1	0	1	1	
chr5:93854775-93865400	10626	1	0	0	0	0	0	1	0	0	1	0	1	1	
chr8:99411775-99424650	12876	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr11:86907850-86918625	10776	1	0	0	0	0	0	0	0	1	0	0	1	1	
chr7:142857900-142879425	21526	1	1	0	1	0	0	0	0	1	1	0	1	1	
chr18:66573100-66583300	10201	1	0	0	1	0	0	1	0	0	0	0	0	1	
chr11:118079725-118089900	10176	1	1	0	1	1	0	1	1	1	1	0	1	1	
chr2:127221550-127268625	47076	1	1	1	1	0	0	1	0	1	0	0	0	0	
chr6:12422400-12439200	16801	1	1	0	1	0	0	0	0	1	1	0	1	1	
chr8:29955875-29977325	21451	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr13:57331500-57346525	15026	1	0	0	0	0	0	1	0	0	1	0	1	1	
chr3:107753000-107766100	13101	1	0	0	0	0	1	1	0	0	1	0	0	0	
chr3:190099900-190110100	10201	1	1	0	1	1	0	1	0	1	1	1	1	0	
chr3:53080350-53090725	10376	1	1	1	1	0	1	1	0	1	1	1	1	0	
chr12:53675775-53689275	13501	1	1	0	1	1	0	0	0	0	1	0	1	1	
chr6:164379775-164403250	23476	1	1	0	1	0	1	1	0	1	1	0	1	1	
chr10:79685025-79696100	11076	1	0	0	0	0	1	0	0	0	0	0	0	0	
chr4:103556475-103569975	13501	1	1	0	1	0	1	1	0	1	1	0	1	0	
chr2:173956250-173969375	13126	1	0	0	1	1	0	0	0	0	1	1	0	1	
chr4:24699025-24711050	12026	1	1	1	1	0	0	1	0	1	1	1	1	0	
chr10:63773225-63790825	17601	1	1	0	1	0	1	1	0	1	1	0	1	0	
chr13:70805100-70838950	33851	1	1	1	1	0	0	1	0	1	1	0	1	1	
chr20:47658050-47669650	11601	1	1	0	1	0	0	1	0	1	0	0	1	1	
chr1:232962350-232985575	23226	1	1	0	1	0	1	1	0	1	0	0	0	1	
chr13:80149275-80161275	12001	1	0	0	1	0	0	0	0	0	0	0	1	1	
chr5:15074475-15098700	24226	1	0	0	1	0	0	1	0	1	1	0	1	1	
chr12:88147075-88171675	24601	1	1	0	0	1	0	1	0	1	1	1	1	1	
chr20:12132900-12146175	13276	1	0	0	0	0	0	1	0	1	1	0	0	1	
chr3:151267675-151279475	11801	1	0	0	0	0	1	0	0	0	1	1	0	0	
chr5:153865150-153884225	19076	1	1	1	1	0	0	1	0	1	1	0	1	1	
chr8:131665675-131689950	24276	1	1	1	1	1	1	1	0	1	1	0	1	1	
chr10:58524700-58561000	36301	1	1	1	1	0	0	1	1	1	1	0	1	1	
chr3:188285650-188297650	12001	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr6:94572500-94596150	23651	1	0	0	1	0	0	1	0	0	0	0	0	0	
chr11:8260275-8275625	15351	1	0	0	1	0	0	1	0	0	0	0	0	0	
chr2:172916050-172928325	12276	1	0	0	1	0	0	0	0	0	0	0	1	0	
chr3:67036325-67048375	12051	1	0	0	1	0	0	0	0	0	1	0	0	0	
chr8:143175675-143202700	27026	1	1	1	1	0	1	1	0	0	1	0	1	1	
chrX:13390150-13402350	12201	1	0	0	1	0	0	0	0	1	1	0	0	0	
chrX:149445825-149463350	17526	1	0	0	1	0	0	0	0	0	1	0	1	1	
chr11:129971550-129983400	11851	1	1	1	0	0	0	1	0	0	1	0	1	1	
chr2:10067850-10080200	12351	1	0	1	1	0	0	0	1	0	1	1	0	1	
chr6:27356350-27374325	17976	1	1	1	1	0	0	1	0	1	1	0	1	1	
chr13:70523025-70535900	12876	1	1	1	1	0	0	1	0	1	1	0	1	1	
chr5:174407925-174419375	11451	1	1	0	1	0	0	1	0	1	1	0	1	1	
chrX:22623000-22636625	13626	1	0	0	0	0	0	0	0	0	0	1	1	1	
chr10:83047075-83063275	16201	1	0	0	1	0	0	1	0	0	1	0	0	1	
chr16:32487800-32498825	11026	1	1	0	1	0	0	1	0	1	1	1	1	1	
chrX:96977850-96994250	16401	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr10:120357125-120373825	16701	1	1	0	1	0	0	1	0	0	1	0	1	1	
chr12:95328975-95344075	15101	1	0	0	1	1	0	1	0	1	1	0	1	0	
chr13:26444150-26456575	12426	1	0	0	1	0	1	0	0	0	0	0	1	0	
chr18:75510350-75521775	11426	1	0	0	1	0	0	0	0	0	0	1	1	0	
chr2:234448625-234460150	11526	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr9:30285875-30296925	11051	1	0	0	1	0	0	0	0	0	1	0	1	1	
chr7:93318600-93332975	14376	1	0	0	1	1	0	1	0	0	1	0	0	0	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr10:119185750-119206425	20676	1	1	0	1	1	0	1	0	1	1	0	1	1	
chr1:206192400-206213400	21001	1	1	1	1	0	0	1	0	1	1	0	1	1	
chr3:129747975-129758550	10576	1	0	0	0	0	0	0	0	1	0	0	1	0	
chr5:20567625-20582975	15351	1	1	0	0	0	1	1	0	1	1	1	1	1	
chr5:58269850-58284050	14201	1	0	0	0	0	0	0	0	1	0	0	0	1	
chr7:107961175-107971925	10751	1	1	0	0	1	0	1	0	1	1	1	1	1	
chr10:79649925-79660825	10901	1	0	0	0	0	1	0	0	0	0	0	0	0	
chr12:131342275-131366850	24576	1	0	0	0	0	1	1	0	0	0	0	1	0	
chr6:141828150-141851300	23151	1	1	0	1	1	1	1	0	1	1	0	1	1	
chr9:115624525-115638900	14376	1	0	0	0	0	0	0	0	0	1	0	1	1	
chrX:130474825-130486100	11276	1	0	0	1	0	0	1	0	0	1	0	0	1	
chr15:54368275-54379425	11151	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr20:23933300-23963300	30001	1	0	0	0	0	0	1	0	0	0	0	0	1	
chr20:23069750-23081475	11726	1	0	0	1	0	0	0	0	1	0	1	0	0	
chr14:100655175-100665700	10526	1	0	0	0	0	0	0	0	0	0	0	1	0	
chr11:125478700-125489900	11201	1	0	0	0	0	1	0	0	1	1	0	0	1	
chr8:143698500-143708725	10226	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr1:211844700-211858375	13676	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr7:132089250-132105750	16501	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr1:142366925-142378900	11976	1	0	0	1	0	0	0	0	0	1	0	0	1	
chr10:125967200-125988150	20951	1	0	0	1	0	0	0	0	1	0	0	0	0	
chr12:125949425-125960625	11201	1	1	0	1	0	1	1	0	0	1	0	1	1	
chr5:158952700-158963825	11126	1	0	0	1	0	1	0	0	0	1	0	1	0	
chr10:5063025-5074225	11201	1	0	1	0	0	0	0	0	0	0	0	1	1	
chr2:130348325-130363275	14951	1	1	0	1	1	1	0	0	1	1	0	1	1	
chr7:85086825-85104450	17626	1	0	0	1	0	1	0	0	0	0	0	1	1	
chr12:83580475-83606200	25726	1	1	0	1	0	0	1	0	1	1	0	0	1	
chr13:21926150-21946050	19901	1	1	0	1	1	0	1	0	1	1	0	1	0	
chr4:55732800-55750175	17376	1	0	0	1	0	1	0	0	1	1	0	1	1	
chr6:137544875-137554925	10051	1	1	0	1	0	1	1	1	1	1	0	1	1	
chr1:84998125-85009475	11351	1	0	0	1	0	0	0	0	1	1	0	0	1	
chrX:13066500-13084525	18026	1	0	0	0	0	0	1	0	0	1	0	1	1	
chr6:137463000-137483475	20476	1	0	0	0	0	0	0	0	0	1	0	1	0	
chr6:40057500-40082950	25451	1	0	1	1	0	1	0	0	1	0	0	1	0	
chrX:107150775-107167475	16701	1	0	0	0	0	0	0	0	1	0	0	1	0	
chr18:18297450-18310625	13176	1	0	0	0	0	0	1	1	0	0	0	0	1	
chr8:115369100-115387225	18126	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr1:18263675-18285975	22301	1	0	0	1	0	0	1	0	1	1	0	0	0	
chr1:56367475-56378825	11351	1	1	0	1	0	0	1	0	1	1	0	1	0	
chr13:110967175-110979375	12201	1	0	0	1	0	0	0	0	0	0	0	0	1	
chr2:112179825-112193875	14051	1	0	0	1	0	0	1	0	0	1	1	0	0	
chr7:86596600-86613925	17326	1	0	0	0	0	0	1	0	0	1	0	1	1	
chr8:124686250-124701500	15251	1	0	0	0	0	0	0	0	1	1	0	1	1	
chr2:206825950-206841100	15151	1	0	0	1	0	0	0	0	1	1	0	1	1	
chr2:148061475-148073025	11551	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr5:68249800-68267150	17351	1	0	0	0	0	1	1	0	1	1	0	1	1	
chr1:212355225-212367225	12001	1	0	0	0	0	1	0	0	0	0	0	0	0	
chr2:100672675-100683975	11301	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr2:177566750-177577650	10901	1	0	0	1	0	0	0	0	0	1	0	1	1	
chr8:135113725-135131100	17376	1	0	0	0	0	0	0	0	0	1	0	1	0	
chr1:245015075-245029300	14226	1	1	0	1	0	0	1	0	0	1	1	1	0	
chr10:102392025-102402450	10426	1	0	0	1	0	0	0	0	0	0	0	1	0	
chr11:39334375-39350600	16226	1	0	0	1	0	0	0	0	1	0	0	1	0	
chr15:97788575-97799125	10551	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr18:74488625-74501875	13251	1	1	0	1	0	1	1	0	1	1	0	1	0	
chr13:44374400-44385800	11401	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr2:72003825-72014850	11026	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr21:44053175-44063175	10001	1	0	1	0	0	0	0	0	0	1	0	1	1	
chr12:113054050-113092400	38351	1	0	0	0	0	0	0	0	1	0	0	0	1	
chr1:4325150-4335375	10226	1	0	0	0	0	0	0	0	0	0	0	0	1	
chrX:45440850-45465775	24926	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr11:44677300-44698225	20926	1	1	0	1	1	0	0	0	1	1	1	1	0	
chr16:26291625-26301925	10301	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr15:77299925-77310325	10401	1	0	0	0	0	1	0	0	0	0	0	0	0	
chr5:122085725-122100025	14301	1	0	0	1	0	0	0	0	1	1	0	0	1	
chr8:143507200-143521850	14651	1	1	0	1	0	0	1	0	1	1	1	1	0	
chr8:8654675-8664850	10176	1	1	0	1	0	0	1	1	0	1	1	1	1	
chr2:68059800-68077075	17276	1	0	0	0	0	0	0	0	0	1	0	1	1	
chr5:32651700-32662150	10451	1	0	0	0	0	0	1	0	1	0	0	1	0	
chr4:25052450-25069275	16826	1	0	0	1	0	0	1	0	1	1	0	0	0	
chr14:70669500-70682000	12501	1	0	0	1	0	0	1	0	1	1	0	1	0	
chr13:90193525-90216950	23426	1	0	0	0	0	0	1	0	1	0	0	0	1	
chr4:108726075-108736900	10826	1	0	0	0	0	0	0	0	1	1	0	1	0	
chr6:112406400-112459300	52901	1	1	1	1	0	0	0	0	1	1	0	1	1	
chr11:127550150-127566775	16626	1	0	0	0	0	0	1	0	1	1	0	1	1	
chr18:45392375-45412075	19701	1	1	0	1	1	0	0	0	1	1	0	1	1	
chr8:24784000-24803475	19476	1	1	0	1	0	1	0	0	1	0	0	1	1	
chr9:125140075-125157500	17426	1	1	0	1	0	1	1	0	1	0	0	1	0	
chr4:102845400-102859100	13701	1	0	0	1	0	0	1	0	1	1	1	1	0	
chr2:176938125-176952700	14576	1	0	0	0	0	0	0	0	1	0	0	0	1	
chr1:190448450-190465925	17476	1	0	0	1	0	0	0	0	1	0	0	0	1	
chr12:115292100-115302600	10501	1	0	0	1	0	0	0	0	1	0	0	0	0	
chr15:47839050-47854350	15301	1	0	0	1	0	0	1	0	1	0	0	1	1	
chr16:82854175-82865325	11151	1	0	0	1	0	1	0	0	0	1	0	0	1	
chr2:223543900-223554575	10676	1	0	0	1	0	0	0	0	0	1	0	0	0	
chr2:231458400-231474450	16051	1	0	0	1	0	1	0	0	0	0	0	0	1	
chr2:237208375-237219525	11151	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr2:71085625-71099625	14001	1	0	0	1	0	0	0	0	1	1	0	1	1	
chr20:2090500-2103375	12876	1	0	0	1	0	0	0	0	1	1	0	0	1	
chr9:110109500-110126925	17426	1	0	0	0	1	0	0	0	0	0	0	0	1	
chr12:97320125-97330750	10626	1	0	0	0	0	0	0	0	0	1	0	1	1	
chr7:79757325-79769550	12226	1	1	1	0	1	0	1	1	1	1	0	0	1	
chr18:37965050-37976600	11551	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr2:206943350-206958650	15301	1	0	0	1	0	0	0	0	1	1	0	1	1	
chr8:79243350-79253700	10351	1	0	1	1	0	0	0	0	1	0	0	1	0	
chr5:81125650-81136150	10501	1	0	0	1	0	0	0	1	0	0	0	0	0	
chr7:155540650-155553700	13051	1	0	0	1	0	0	0	0	0	0	0	0	1	
chr6:150647775-150661325	13551	1	0	0	0	0	0	0	0	1	1	1	0	1	
chr3:31017300-31040525	23226	1	0	0	1	0	0	0	0	0	1	0	0	1	
chr4:4855350-4865400	10051	1	0	0	0	0	1	1	0	0	1	0	0	0	
chr2:192023525-192035025	11501	1	1	0	1	0	0	1	0	1	1	0	1	1	
chr20:56824850-56837175	12326	1	0	0	1	0	0	1	0	0	0	1	0	1	
chr6:140260300-140278725	18426	1	0	0	0	0	0	1	0	0	1	0	1	1	
chr6:78243750-78269775	26026	1	0	0	1	0	1	0	0	0	0	0	1	1	
chr14:70369075-70380850	11776	1	0	0	1	0	0	1	0	1	0	0	0	0	
chr18:22231500-22244975	13476	1	0	0	1	0	0	0	0	0	1	0	1	1	
chr21:26974675-27001175	26501	1	0	0	1	0	0	1	0	1	1	0	0	1	
chr3:140313275-140326250	12976	1	0	0	1	0	0	0	0	0	1	0	0	1	
chr3:158712275-158734225	21951	1	1	1	1	0	0	1	0	1	0	0	1	1	
chrX:102123350-102139900	16551	1	0	0	1	0	0	1	0	0	1	0	0	0	
chr1:225586950-225598475	11526	1	1	0	1	0	0	1	0	1	1	0	1	0	
chr7:25285175-25303700	18526	1	0	0	0	0	0	1	0	1	0	0	0	0	
chr20:56126025-56136400	10376	1	0	0	0	0	0	0	0	1	1	0	0	1	
chr1:201504525-201520825	16301	1	0	0	1	0	0	0	0	0	1	0	1	0	
chr1:86455725-86478575	22851	1	0	0	1	0	0	1	0	1	1	0	1	1	
chr4:67908675-67922125	13451	1	0	0	1	0	0	0	0	0	0	1	1	1	
chr14:93405000-93415700	10701	1	0	0	0	0	0	0	0	0	0	1	0	1	
chr11:8171725-8184025	12301	1	0	0	0	0	0	1	0	0	0	0	0	1	
chr9:99536025-99552150	16126	1	0	0	0	0	0	0	0	0	0	0	1	1	
chr2:31234450-31256675	22226	1	0	0	1	0	0	0	0	0	1	0	1	1	
chr2:31769200-31779600	10401	1	0	0	0	0	0	0	1	0	0	0	0	1	
chr5:124845325-124857875	12551	1	0	0	1	0	0	0	0	0	1	0	0	0	
chr2:238009325-238034900	25576	1	0	0	1	0	0	0	0	0	0	1	0	0	
chr2:88735550-88749975	14426	1	0	0	0	0	0	1	0	1	1	1	1	1	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chrX:148733000-148752575	19576	1	0	0	0	0	0	1	0	0	0	0	1	0	
chr11:127986200-127997625	11426	1	0	0	1	1	0	0	0	0	0	0	0	0	
chr8:140183025-140239350	56326	1	0	0	1	0	0	1	0	0	0	0	0	1	
chr1:233220100-233231000	10901	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr14:71447525-71461400	13876	1	0	0	1	0	0	0	0	1	0	0	1	1	
chr3:40986025-41002750	16726	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr5:102017350-102033375	16026	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr1:38888750-38900850	12101	1	0	0	1	0	0	1	0	0	0	0	0	0	
chr10:7584675-7594825	10151	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr18:44239350-44253025	13676	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr2:187440075-187467625	27551	1	0	0	1	0	0	0	0	1	0	0	1	0	
chr2:45358400-45376050	17651	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr4:102619950-102632850	12901	1	0	0	1	0	0	1	0	0	0	0	1	0	
chr5:109275850-109296200	20351	1	0	1	1	0	0	1	0	0	1	0	1	1	
chr2:66891375-66902150	10776	1	0	0	0	0	0	0	0	0	1	0	1	1	
chr1:61193225-61207625	14401	1	0	0	0	0	1	0	0	0	1	0	1	1	
chr2:151418900-151431450	12551	1	0	0	0	0	0	1	0	1	1	0	1	1	
chr10:112221425-112232275	10851	1	0	0	0	0	0	0	0	1	1	0	1	1	
chr13:76807675-76829275	21601	1	0	0	1	0	0	1	0	1	0	0	1	0	
chr21:35050150-35061650	11501	1	0	0	1	0	0	0	0	0	0	0	1	0	
chr8:18025325-18043650	18326	1	0	0	0	0	0	1	0	1	1	0	1	0	
chr6:167428450-167439825	11376	1	0	0	0	0	0	1	0	0	0	0	1	1	
chr1:108865050-108879725	14676	1	0	0	0	0	0	1	0	0	1	1	0	1	
chr7:46184850-46198900	14051	1	0	0	0	0	0	1	0	0	1	0	0	0	
chr18:42451550-42482700	31151	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr3:138272725-138291175	18451	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr4:1743950-1756700	12751	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr8:123825700-123843275	17576	1	0	0	1	0	0	1	0	0	0	0	0	1	
chr2:136867875-136878800	10926	1	0	0	1	1	0	0	0	1	1	0	1	0	
chr1:87457500-87472250	14751	1	0	0	1	0	0	1	0	1	0	0	0	0	
chrX:115315750-115327875	12126	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr8:21182750-21199450	16701	1	0	0	1	0	0	0	0	0	0	0	0	1	
chr8:43637850-43650650	12801	1	0	0	0	0	0	0	0	1	0	0	1	0	
chr20:55589775-55605050	15276	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr8:127449850-127469100	19251	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr1:157472725-157487250	14526	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr10:115138875-115151400	12526	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr14:94916400-94934950	18551	1	0	0	1	0	0	0	0	0	0	0	1	0	
chr5:126931200-126948250	17051	1	0	0	0	0	0	0	0	1	0	0	1	0	
chr18:60131975-60143950	11976	1	0	0	0	1	0	1	0	0	1	0	1	0	
chr4:114929225-114940000	10776	1	0	0	0	1	0	1	0	0	1	0	0	0	
chr1:242310200-242327800	17601	1	0	0	1	0	0	0	0	1	0	0	0	0	
chr1:221930725-221941025	10301	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr1:246337475-246347500	10026	1	0	0	0	0	0	0	0	1	0	0	0	1	
chr13:80059725-80075900	16176	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr4:13730175-13740250	10076	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr8:66160600-66171525	10926	1	0	0	0	0	0	1	0	0	1	0	0	1	
chr15:68065575-68082800	17226	1	0	1	1	0	1	0	0	0	0	0	0	1	
chr1:10834200-10846175	11976	1	0	0	1	0	0	1	0	0	0	0	0	0	
chr18:57739625-57750700	11076	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr2:142652025-142668175	16151	1	0	0	1	0	0	0	0	0	1	0	0	0	
chr2:237859350-237869800	10451	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr4:1021700-1040275	18576	1	0	0	1	0	0	1	0	0	1	0	0	1	
chr4:1589400-1605200	15801	1	0	0	0	0	0	0	0	0	1	1	0	1	
chr6:44847950-44860775	12826	1	0	0	0	0	0	1	0	0	0	0	0	1	
chr18:8443475-8460025	16551	1	0	0	0	0	0	0	0	0	1	0	1	0	
chr5:3790400-3802175	11776	1	0	0	1	0	0	1	0	1	1	0	1	0	
chrX:112619875-112636550	16676	1	0	0	0	0	0	0	0	1	0	0	1	0	
chr4:35430750-35443150	12401	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr5:10822825-10832850	10026	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr1:34594000-34611425	17426	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr11:27837225-27857975	20751	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr4:84893350-84907125	13776	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr5:134674675-134685525	10851	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr2:2821100-2843950	22851	1	0	1	0	0	1	0	0	0	0	0	0	0	
chr1:197930275-197948150	17876	1	0	0	0	0	0	0	0	0	1	0	1	0	
chr21:24182150-24197250	15101	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr6:125885000-125895925	10926	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr3:154809400-154830550	21151	1	0	0	0	0	0	0	0	1	1	0	0	1	
chr13:24548975-24561125	12151	1	0	0	1	1	0	1	0	1	1	0	0	0	
chr13:46522450-46536325	13876	1	0	0	0	0	0	1	0	0	0	0	0	1	
chr6:168331950-168343050	11101	1	0	0	0	0	0	0	1	0	0	0	0	0	
chr3:113997225-114007525	10301	1	0	0	0	0	1	0	0	1	0	0	0	1	
chr2:85812350-85823000	10651	1	0	0	1	0	0	0	0	0	1	0	0	1	
chr13:21203525-21215225	11701	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr4:23939275-23950400	11126	1	0	0	1	0	1	0	0	0	0	0	0	0	
chr8:26092850-26111900	19051	1	0	0	1	0	1	0	0	0	0	0	0	0	
chrX:30716225-30736150	19926	1	0	0	1	0	0	0	0	0	0	0	0	0	
chrX:5192350-5206925	14576	1	0	0	1	0	0	0	0	0	1	0	0	1	
chr3:188363175-188375850	12676	1	0	0	1	0	0	0	0	1	0	0	1	0	
chr7:106276275-106286550	10276	1	0	0	0	0	0	0	0	0	1	0	1	0	
chr1:29914900-29928125	13226	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr2:134177450-134192075	14626	1	0	0	0	1	0	0	0	1	0	0	0	0	
chr12:115504200-115514350	10151	1	0	0	1	0	0	0	0	1	0	0	0	0	
chr13:94306375-94318750	12376	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr5:54380675-54392025	11351	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr6:130952300-130967925	15626	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr3:177853550-177864125	10576	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr7:175450-189200	13751	1	0	0	0	0	0	0	0	0	0	0	1	0	
chr2:201342075-201354925	12851	1	0	0	1	0	1	0	0	0	0	0	0	0	
chr2:151669825-151682775	12951	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr8:23664975-23675150	10176	1	0	0	0	0	0	0	0	0	1	0	0	0	
chrX:20329325-20341425	12101	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr2:145864000-145902775	38776	1	0	0	1	0	0	1	0	0	1	0	1	0	
chr6:34632150-34647850	15701	1	0	0	0	0	0	1	0	1	1	0	0	1	
chr5:176041950-176075125	33176	1	0	0	1	0	0	0	0	0	1	0	1	0	
chr2:235906000-235923850	17851	1	0	0	1	0	0	0	0	0	0	0	0	1	
chr14:24222400-24234725	12326	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr6:47425050-47444950	19901	1	0	0	1	0	0	0	0	0	1	0	0	0	
chr10:72360000-72376125	16126	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr16:86135375-86147125	11751	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr18:73358625-73372325	13701	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr18:75427775-75446650	18876	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr4:79842650-79853700	11051	1	0	0	1	0	0	0	0	0	0	0	0	1	
chr9:136571925-136590625	18701	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr8:38628300-38642625	14326	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr12:66812300-66822625	10326	1	0	0	0	0	0	0	0	0	0	0	1	0	
chr3:188521875-188539200	17326	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr8:113083525-113098000	14476	1	0	0	0	0	0	0	0	0	1	0	0	1	
chr13:54457650-54471175	13526	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr1:41728875-41743675	14801	1	0	0	0	0	0	0	0	1	1	0	0	0	
chr2:144839850-144851925	12076	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr5:169663425-169690075	26651	1	0	0	0	0	0	0	0	0	1	0	0	0	
chr1:155641250-155657075	15826	1	0	0	0	0	0	0	0	1	0	0	0	0	
chr18:10498025-10508725	10701	1	0	0	0	0	0	0	0	1	0	0	0	0	
chr10:120265025-120275550	10526	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr13:42662375-42676425	14051	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr21:28521775-28537600	15826	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr3:45182150-45196400	14251	1	0	0	1	0	0	0	0	0	0	0	0	1	
chrX:45353850-45364375	10526	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr2:204255125-204267050	11926	1	0	0	0	0	1	0	0	0	0	0	0	0	
chr16:31588925-31601750	12826	1	0	0	0	0	0	1	0	1	0	0	0	0	
chr13:102352250-102366025	13776	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr5:72743475-72759550	16076	1	0	0	0	0	0	0	0	0	0	0	0	1	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr11:2185000-2195750	10751	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr13:103304175-103316475	12301	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr2:118641200-118655550	14351	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr4:117477050-117499075	22026	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr5:3618525-3632100	13576	1	0	0	1	0	0	0	0	0	0	0	0	0	
chr9:12944125-12955625	11501	1	0	0	0	0	0	0	0	1	0	0	0	0	
chr18:58292100-58302600	10501	1	0	0	0	0	0	0	0	0	0	0	1	0	
chr5:65876625-65888825	12201	1	0	0	0	0	0	0	0	0	0	0	1	0	
chr8:102348200-102365375	17176	1	0	0	0	0	0	0	0	0	0	0	1	0	
chr10:64272675-64282950	10276	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr18:74372500-74382950	10451	1	0	0	0	0	0	0	0	0	0	0	0	1	
chr2:59937350-59959625	22276	1	0	0	0	0	0	1	0	0	0	0	0	0	
chr13:68163750-68188075	24326	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr14:60768300-60778400	10101	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr16:77894925-77907775	12851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr12:36728900-36740300	11401	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr16:49113275-49131950	18676	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:16732325-16743650	11326	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:97235825-97246525	10701	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:171923650-171936650	13001	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:235101975-235113800	11826	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr11:101930825-101946125	15301	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:1006500-1016800	10301	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:33691650-33706325	14676	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:2915250-2928275	13026	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:37650675-37661525	10851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:35727600-35746750	19151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:19779350-19799600	20251	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:21343525-21353675	10151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:107085125-107104250	19126	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:49778575-49789975	11401	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:97516400-97526500	10101	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:59170525-59185400	14876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:25523625-25539425	15801	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:46758275-46770275	12001	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:99827550-99842325	14776	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:92334500-92344850	10351	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:89328975-89341875	12901	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:62230700-62240900	10201	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:20493075-20506350	13276	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:124822950-124833175	10226	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:3799050-3822500	23451	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr14:100197725-100219000	21276	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:41141450-41165950	24501	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:155711350-155725225	13876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:169303700-169322700	19001	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:100547525-100561800	14276	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr12:66912600-66922875	10276	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:3426225-3440625	14401	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:154606775-154624950	18176	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr21:22930950-22941850	10901	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:10070425-10083725	13301	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:41915550-41927950	12401	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:6608650-6619000	10351	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr9:6054675-6064900	10226	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:4568200-4583225	15026	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:226789375-226804525	15151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chrX:68323375-68348925	25551	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr11:29287925-29298875	10951	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr12:90728475-90738500	10026	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:9972325-9986625	14301	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:109813675-109824100	10426	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:230573375-230588800	15426	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:27285150-27300025	14876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr16:84629500-84646475	16976	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:71985450-71997700	12251	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:47056500-47068675	12176	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:151317425-151330125	12701	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr20:24726575-24738550	11976	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:129258125-129268825	10701	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:115617300-115634500	17201	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:117684425-117694800	10376	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr15:75899850-75913050	13201	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:980375-1000225	19851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chrX:136212300-136224525	12226	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:124766050-124776075	10026	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:54356225-54366425	10201	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:79782425-79793050	10626	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:80083325-80095925	12601	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr17:44887200-44904100	16901	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:20526500-20537775	11276	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:53148200-53163075	14876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:75360325-75373025	12701	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr11:13877025-13889575	12551	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:29804225-29817650	13426	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:104555125-104567000	11876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:31280650-31291700	11051	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:242433950-242449875	15926	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr14:98295825-98307425	11601	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:71002675-71016650	13976	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:91184500-91207375	22876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:129188850-129205475	16626	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:63131625-63144250	12626	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:84487175-84498675	11501	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:150676175-150689200	13026	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:234704700-234716175	11476	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr11:12043925-12055650	11726	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:69751425-69764700	13276	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:185828975-185840500	11526	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr12:33624000-33638850	14851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:2350825-2395175	44351	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:71468300-71482450	14151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:3881075-3894525	13451	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:112343150-112361000	17851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:201431425-201441525	10101	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr3:153975125-153989575	14451	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:102800100-102810350	10251	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:41596600-41607700	11101	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:48021375-48033500	12126	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:163349950-163361375	11426	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:20622500-20634450	11951	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:100217575-100229800	12226	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:133140825-133161650	20826	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:142857525-142870300	12776	0	0	0	0	0	0	0	0	0	0	0	0	0	
chrX:45030125-45040475	10351	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:120864150-120877825	13676	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:130131950-130145525	13576	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr12:59599600-59621750	22151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:140419225-140429850	10626	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr13:52409200-52419600	10401	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:32000350-32014075	13726	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:231247700-231258825	11126	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr21:41969525-41979600	10076	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:158012750-158032025	19276	0	0	0	0	0	0	0	0	0	0	0	0	0	

location	span (nt)	max	mean	adipose	colon	heart	hypothalamus	kidney	liver	lung	ovary	skeletal muscle	spleen	testes	Comments
chr7:139158975-139169025	10051	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:66380600-66391625	11026	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:168412975-168429225	16251	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:143272275-143284725	12451	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:113800850-113811850	11001	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr1:190265225-190278725	13501	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr6:44743250-44755800	12551	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:70288175-70298975	10801	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr9:31332775-31343225	10451	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:159281300-159295375	14076	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:84045950-84056500	10551	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:122289675-122301200	11526	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:143487875-143498025	10151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chrX:68211200-68232250	21051	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:42792000-42802200	10201	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr11:38356650-38373850	17201	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:15520650-15531025	10376	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr14:92422900-92433575	10676	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:71159500-71173350	13851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:149073750-149085000	11251	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:60376250-60386500	10251	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:127914425-127929275	14851	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr9:136300550-136313775	13226	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr12:44764175-44775050	10876	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr18:37147675-37159675	12001	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:3276050-3292025	15976	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr2:239599675-239614825	15151	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr8:140577700-140593825	16126	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr14:101121575-101132150	10576	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr7:54998325-55008375	10051	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:81264400-81281800	17401	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr4:121140275-121151000	10726	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr5:107200075-107210175	10101	0	0	0	0	0	0	0	0	0	0	0	0	0	
chr10:1842775-1853600	10826	0	0	0	0	0	0	0	0	0	0	0	0	0	