Reference Name	Reference Start	Reference End	Type	Alternate Sequence	Alternate Start	Alternate End
1	153673007	153838214	PATCH_NOVEL	HSCHR1_1_CTG31	153673007	153855445
1	155180173	155275036	PATCH_NOVEL	HSCHR1_2_CTG31	155180173	155290440
1	198339213	198694304	PATCH_NOVEL	HSCHR1_3_CTG31	198339213	198705791
1	248865779	248908210	PATCH_FIX	HG999_1_PATCH	248865779	248915094
1	249058211	249098883	PATCH_FIX	HG999_2_PATCH	249058211	249107562
2	36453102	36590458	PATCH_NOVEL	HSCHR2_1_CTG1	36453102	36596491
2	149790583	149880633	PATCH_NOVEL	HSCHR2_2_CTG12	149790583	149886714
2	169686873	169793704	PATCH_NOVEL	HSCHR2_1_CTG12	169686873	169810693
3	51416109	51584055	PATCH_FIX	HG186_PATCH	51416109	51587470
3	57369478	57399969	PATCH_FIX	HG280_PATCH	57369478	57448270
3	66270271	66308065	PATCH_FIX	HG991_PATCH	66270271	66335333
3	151307154	151477286	PATCH_NOVEL	HSCHR3_1_CTG2_1	151307154	151487824
4	34519577	34885480	PATCH_NOVEL	HSCHR4_1_CTG6	34519577	34895763
4	62777687	62877254	PATCH_NOVEL	HSCHR4_2_CTG9	62777687	62899031
4	69170077	69878175	HAP	HSCHR4_1	69170077	69760502
4	75382210	75689879	PATCH_FIX	HG706_PATCH	75382210	75630386
4	156756530	156908416	PATCH_NOVEL	HSCHR4_1_CTG12	156756530	156921065
5	12681538	12744122	PATCH_NOVEL	HSCHR5_2_CTG1	12681538	12764265
5	68505250	70910270	PATCH_NOVEL	HSCHR5_1_CTG1	68505250	70125573
5	94505561	94590195	PATCH_NOVEL	HSCHR5_1_CTG2	94505561	94606801
5	161800673	161968654	PATCH_NOVEL	HSCHR5_1_CTG5	161800673	161974131
6	28477797	33351542	HAP	HSCHR6_MHC_COX	28477797	33273167
6	28659143	33448354	HAP	HSCHR6_MHC_SSTO	28659143	33587709
6	28696604	33225977	HAP	HSCHR6_MHC_MANN	28696604	33379866
6	28696604	33329076	HAP	HSCHR6_MHC_DBB	28696604	33306999
6	28696604	33335493	HAP	HSCHR6_MHC_APD	28696604	33318893
6	28696604	33359642	HAP	HSCHR6_MHC_MCF	28696604	33530001
6	28696604	33379750	HAP	HSCHR6_MHC_QBL	28696604	33308587
6	80059725	80156628	PATCH_NOVEL	HSCHR6_1_CTG5	80059725	80184460
7	56835596	57190579	PATCH_FIX	HG736_PATCH	56835596	57190565
7	57342227	57586048	PATCH_FIX	HG14_PATCH	57342227	57594049
7	98260131	98556215	PATCH_FIX	HG946_PATCH	98260131	98587904
7	101718951	102072447	PATCH_FIX	HG115_PATCH	101718951	102075280

7	141333209	141446583	PATCH_NOVEL	HSCHR7_1_CTG6	141333209	141452591
7	141557850	142778624	PATCH_FIX	HG7_PATCH	141557850	142842133
8	144743526	145146062	PATCH_FIX	HG104_HG975_PATCH	144743526	145173331
8	145285645	145659901	PATCH_FIX	HG243_PATCH	145285645	145489421
9	7428994	7577169	PATCH_NOVEL	HSCHR9_1_CTG1	7428994	7591981
9	72028659	72092013	PATCH_NOVEL	HSCHR9_1_CTG35	72028659	72100209
9	72639029	72804234	PATCH_NOVEL	HSCHR9_2_CTG35	72639029	72810314
9	90793962	90842895	PATCH_NOVEL	HSCHR9_3_CTG35	90793962	90853993
9	136049442	136369192	PATCH_FIX	HG79_PATCH	136049442	136379605
9	139136890	139166997	PATCH_FIX	HG998_1_PATCH	139136890	139199324
9	139216998	139252828	PATCH_FIX	HG998_2_PATCH	139216998	139266278
10	17613209	18252930	PATCH_FIX	HG544_PATCH	17613209	18006000
10	27574584	27706537	PATCH_NOVEL	HSCHR10_1_CTG2	27574584	27753837
10	45670681	45964419	PATCH_NOVEL	HSCHR10_1_CTG5	45670681	45980482
10	133258319	133381404	PATCH_FIX	HG995_PATCH	133258319	133386696
11	25191953	25340626	PATCH_NOVEL	HSCHR11_1_CTG1_1	25191953	25346359
11	49862648	50121284	PATCH_FIX	HG281_PATCH	49862648	50183651
12	60001	282464	PATCH_FIX	HG858_PATCH	60001	223298
12	28148967	28263711	PATCH_NOVEL	HSCHR12_1_CTG2	28148967	28269770
12	58326520	58486538	PATCH_NOVEL	HSCHR12_1_CTG2_1	58326520	58495697
12	59323046	59454651	PATCH_NOVEL	HSCHR12_2_CTG2_1	59323046	59461700
12	101503370	101652073	PATCH_NOVEL	HSCHR12_3_CTG2_1	101503370	101658250
12	126711744	126890020	PATCH_NOVEL	HSCHR12_1_CTG5	126711744	126896062
12	132806993	132967794	PATCH_FIX	HG996_PATCH	132806993	132972239
13	115085142	115109878	PATCH_FIX	HG531_PATCH	115085142	115119803
15	28557187	28842093	PATCH_NOVEL	HSCHR15_1_CTG4	28557187	28853713
15	66200521	66577156	PATCH_NOVEL	HSCHR15_1_CTG8	66200521	66589293
16	55822434	56002460	PATCH_NOVEL	HSCHR16_1_CTG3_1	55822434	56014895
16	69174054	69258593	PATCH_NOVEL	HSCHR16_2_CTG3_1	69174054	69263725
17	1	252428	PATCH_NOVEL	HSCHR17_1_CTG1	1	270261
17	252429	296626	PATCH_FIX	HG990_PATCH	252429	297979
17	21250948	21566608	PATCH_FIX	HG987_PATCH	21250948	21657910
17	34442621	35005379	PATCH_FIX	HG75_PATCH	34442621	34976908
17	36372617	36711255	PATCH_FIX	HG745_PATCH	36372617	36711256

17	39463362	39589187	PATCH_NOVEL	HSCHR17_1_CTG4	39463362	39596512
17	39869611	40277911	PATCH_FIX	HG185_PATCH	39869611	40282145
17	43384864	44913631	HAP	HSCHR17_1	43384864	45065691
17	62273514	62649312	PATCH_FIX	HG183_PATCH	62273514	62730554
17	68302419	68520360	PATCH_NOVEL	HSCHR17_2_CTG4	68302419	68526413
17	75216812	75295408	PATCH_NOVEL	HSCHR17_3_CTG4	75216812	75307030
18	47818564	48101162	PATCH_NOVEL	HSCHR18_1_CTG1_1	47818564	48108394
18	49189306	49348012	PATCH_NOVEL	HSCHR18_2_CTG1_1	49189306	49354094
18	65090960	65219788	PATCH_NOVEL	HSCHR18_2_CTG2	65090960	65289237
18	70600357	70692016	PATCH_NOVEL	HSCHR18_1_CTG2	70600357	70704908
18	76253467	76412030	PATCH_NOVEL	HSCHR18_1_CTG2_1	76253467	76421416
18	76694886	76848997	PATCH_NOVEL	HSCHR18_2_CTG2_1	76694886	76854432
19	20193557	20845946	PATCH_FIX	HG730_PATCH	20193557	20773949
19	20845947	21225187	PATCH_NOVEL	HSCHR19_1_CTG3	20845947	21231603
19	21831092	21991838	PATCH_NOVEL	HSCHR19_2_CTG3	21831092	22001318
19	22303652	22483468	PATCH_NOVEL	HSCHR19_3_CTG3	22303652	22491675
19	34643165	34791855	PATCH_NOVEL	HSCHR19_1_CTG3_1	34643165	34799028
20	17751747	17874115	PATCH_NOVEL	HSCHR20_1_CTG1	17751747	17880131
20	61031539	61213369	PATCH_FIX	HG506_HG1000_1_PATCH	61031539	61200126
20	61263370	61267733	PATCH_FIX	HG1000_2_PATCH	61263370	61270629
21	15796462	15847792	PATCH_NOVEL	HSCHR21_1_CTG1_1	15796462	15860378
21	23474793	23669288	PATCH_NOVEL	HSCHR21_2_CTG1_1	23474793	23675990
21	34141390	34210247	PATCH_NOVEL	HSCHR21_3_CTG1_1	34141390	34216041
21	34777735	34884866	PATCH_NOVEL	HSCHR21_4_CTG1_1	34777735	34894424
22	39280299	39407165	PATCH_NOVEL	HSCHR22_1_CTG2	39280299	39377222
22	42477964	42648568	PATCH_NOVEL	HSCHR22_1_CTG1	42477964	42636470