

# Analysis of CNV around RHT for stitching

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Testing that we can get all the chromosome:

```
regions <- getFullChromosomes(covs_db)
kable(regions)
```

seqnames	start	end	width	strand
chr1A_part1	1	471268514	471268514	*
chr1A_part2	1	122700062	122700062	*
chr1B_part1	1	438710978	438710978	*
chr1B_part2	1	251131730	251131730	*
chr1D_part1	1	452132239	452132239	*
chr1D_part2	1	43247170	43247170	*
chr2A_part1	1	461985541	461985541	*
chr2A_part2	1	318408600	318408600	*
chr2B_part1	1	453189109	453189109	*
chr2B_part2	1	348037928	348037928	*
chr2D_part1	1	462213638	462213638	*
chr2D_part2	1	189609282	189609282	*
chr3A_part1	1	453944834	453944834	*
chr3A_part2	1	296650429	296650429	*
chr3B_part1	1	448149495	448149495	*
chr3B_part2	1	382653875	382653875	*
chr3D_part1	1	476202024	476202024	*
chr3D_part2	1	139247838	139247838	*
chr4A_part1	1	452361832	452361832	*
chr4A_part2	1	291985939	291985939	*
chr4B_part1	1	450934365	450934365	*
chr4B_part2	1	222522897	222522897	*
chr4D_part1	1	450983086	450983086	*
chr4D_part2	1	58852321	58852321	*
chr5A_part1	1	453009176	453009176	*
chr5A_part2	1	256532231	256532231	*
chr5B_part1	1	451214723	451214723	*
chr5B_part2	1	261770196	261770196	*
chr5D_part1	1	451892688	451892688	*
chr5D_part2	1	114152980	114152980	*
chr6A_part1	1	452282082	452282082	*
chr6A_part2	1	165497012	165497012	*
chr6B_part1	1	452040062	452040062	*
chr6B_part2	1	268910784	268910784	*
chr6D_part1	1	450491070	450491070	*
chr6D_part2	1	23010327	23010327	*
chr7A_part1	1	450010157	450010157	*
chr7A_part2	1	286652930	286652930	*

seqnames	start	end	width	strand
chr7B_part1	1	453799701	453799701	*
chr7B_part2	1	296791078	296791078	*
chr7D_part1	1	453789122	453789122	*
chr7D_part2	1	184858467	184858467	*
chrUn	1	480870096	480870096	*

First we want to stitch all the coverages for a single group.

seqnames	start	end	width	strand	norm_cov	cnv_level
chr4D_part1	18174768	18177343	2576	*	1.7185726	2
chr4D_part1	18461838	18465037	3200	*	0.9087390	1
chr4D_part1	18467438	18468037	600	*	0.0000000	0
chr4D_part1	18688131	18691130	3000	*	0.8821596	1
chr4D_part1	18696131	18698530	2400	*	1.4545589	1
chr4D_part1	18723885	18724284	400	*	2.5076514	3
chr4D_part1	18781062	18785418	4357	*	1.6233020	2
chr4D_part1	18961637	18962036	400	*	2.6892301	3

seqnames	start	end	width	strand	norm_cov	cnv_level
chr4D_part1	18173768	18177343	3576	*	2.0574271	2
chr4D_part1	18461838	18465437	3600	*	1.3768191	1
chr4D_part1	18465638	18467837	2200	*	0.0377604	0
chr4D_part1	18468638	18474386	5749	*	0.3035551	0
chr4D_part1	18686931	18687530	600	*	0.4059689	0
chr4D_part1	18688331	18697530	9200	*	0.5804821	1
chr4D_part1	18697931	18700102	2172	*	2.0290139	2
chr4D_part1	18721885	18726884	5000	*	0.9446813	1
chr4D_part1	18727685	18728824	1140	*	2.1105920	2
chr4D_part1	18778862	18785418	6557	*	2.0949333	2
chr4D_part1	18961637	18964436	2800	*	0.2380148	0

seqnames	start	end	width	strand	norm_cov	cnv_level
chr4D_part1	18464238	18465437	1200	*	1.907877	2
chr4D_part1	18465638	18469037	3400	*	1.673495	2

seqnames	start	end	width	strand	norm_cov	cnv_level
chr4D_part1	18696931	18697130	200	*	1.927437	2