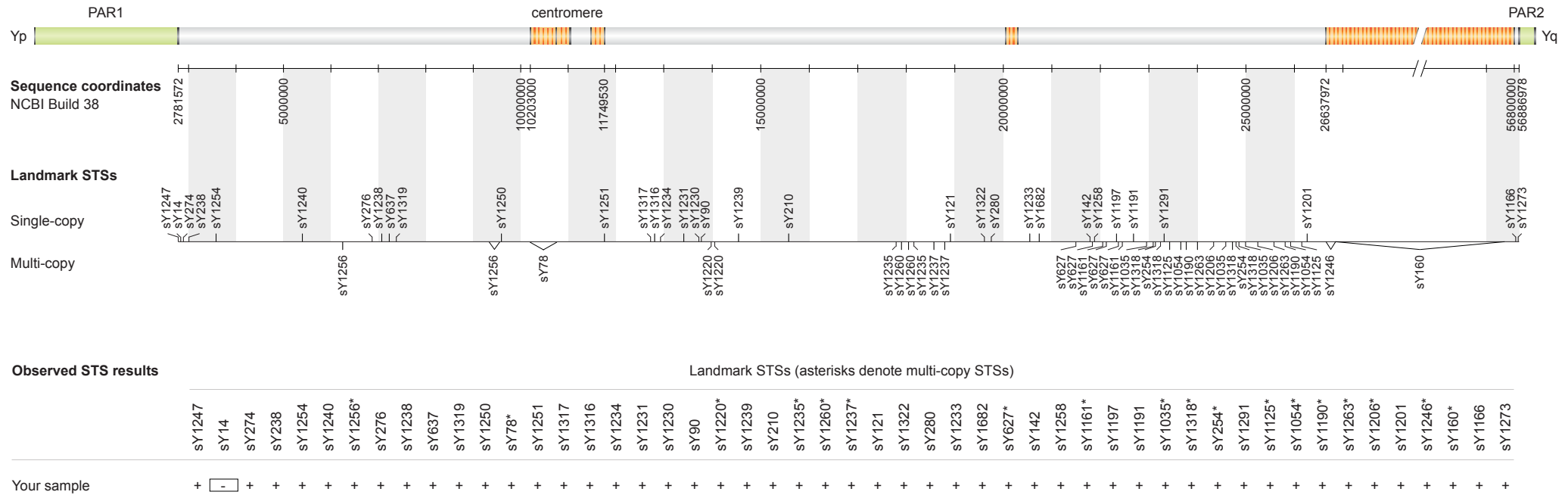


1. By testing your sample with 51 landmark STSs,¹ you have identified the following result: absence of a single STS, sY14.



2. To confirm the result for sY14 and to further delineate the deletion in your sample, you wish to assay additional STSs in the vicinity of sY14. To generate a catalog of STSs in a 50-kilobase interval surrounding sY14, select [sY14] and [50 kb] from pull-down menus, and click on the [Get STSs within interval] button.

Reference Tools

Table of landmark STSs

STS maps of common interstitial deletions

STS maps of idicY and isoY chromosomes

Retrieve STSs Between Two Loci Example

Landmark STSs Select to Select
 Any two STSs Select to Select
 chrY coordinates* to

Output format html text

*NCBI Build 38

Retrieve STSs Near One Locus Example

Landmark STS sY14 and 50 kb
 Any one STS Select and Select interval
 chrY coordinate* and Select interval

Output format html text

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Notes

¹ See Table of landmark STSs under Reference Tools. Landmark STSs consist of sY1247 and sY1273, located at the boundaries between MSY and pseudoautosomal (PAR) sequences on Yp and Yq, respectively, and a previously published panel of 49 STS (see Supplementary Methods Table SM-2 in Repping et al., 2006).

3. STSs in the 50-kb interval surrounding sY14 are displayed as a table and in a customized UCSC Genome Browser. For each STS, the table indicates: multi-copy with an asterisk, start and end sequence coordinates, PCR product length, primer sequences, amplification conditions, GenBank accession number, and in the case of a multi-copy STS, sequence coordinates of co-amplified loci. A custom track in the browser displays the 50-kb region encompassing the catalogued STSs. The positions of each STS and of each protein-coding gene, as well as of other genomic features within the interval, are indicated.

The following STSs are within chrY:2762300-2812299:

STS Identifier	Multi-copy	STS Start	STS End	STS Length	Primer 1	Primer 2	PCR Conditions	GenBank	Co-amplified Loci
sY1247		2781333	2781765	433	GAACTCTGCAAACCTCCTGG	TTTTGAGGCGGAGTCTCG	Standard PCR	G75493	
SRY-1-5		2786756	2787553	798	CAGTCCAGCTGTGCAAGAGA	ATAGGCAGGCTCACTTCTGG	Touchdown PCR	BV679099	
SRY-1-6		2786969	2787654	686	TTTCGAACTCTGGCACCTT	GCCAATGTTACCCGATTGTC	Touchdown PCR	BV679100	
sY14		2787066	2787535	470	GAATATCCCGCTCTCCGGA	GCTGGTGCTCCATTCTGAG	Standard PCR	G38356	
SRY-1-4		2787414	2788203	790	AGCCATCTAGAAGTTGGGC	TGGGTCGCTTCACTCTATCC	Touchdown PCR	BV679098	
SRY-1-3		2787928	2788723	796	AGGAATTGTGGCATCATTAG	TCACAAAACGAGAGGACACAA	Touchdown PCR	BV679097	
SRY-1-2		2788583	2789272	690	TCCCCACAACCTCTTTCATC	AAATGGGAGGAAAGTCCCC	Touchdown PCR	BV679096	
SRY-1-1		2789093	2789866	774	CGTGTAACCTCTCCATAGCC	AAATGACACAAGGCACCACA	Touchdown PCR	BV679095	
SRY-flank-4		2791198	2791992	795	CCCAACATCTTGAAAGGACA	GGGCTTAACCAACAGCAAAA	Touchdown PCR	BV679094	
SRY-flank-3		2791807	2792472	666	TGAAACCTTGTTTTACAGGCA	GCAGGTCACCAAGACACAA	Touchdown PCR	BV679093	
SRY-flank-2		2792245	2793009	765	GATTTGACCAAGCCTTTGGA	ATGAAGTAGGGTGCACTGGG	Touchdown PCR	BV679092	
SRY-flank-1		2792828	2793577	750	CCAAGCTATGAGAGAGGCAG	CAGCAGCTGTTTGACCAAGA	Touchdown PCR	BV679091	
sY2045		2795255	2795359	105	AGCTTAACTGGTGCT	GAACCTAAAGTGCAAGCAT	Standard PCR	G66044	
sY2901		2796260	2796482	223	GATTATGGGCCGAAATAGCA	GAATACAGCCCTTTGGTCA	Standard PCR	BV703768	

