

FISH BAC Probe Selection using the UCSC Genome Browser WebLink: <u>UCSC Genome Browser</u>

1. Once on the genome browser page, hover over the 'Genomes' Tab to reveal available genome builds and select your genome build, most FISH probes currently utilize GRCh37/hg19 build.



2. Enter the chromosome region in the search box below and hit Enter or click on the Go button. For example, type in 18q12.1.

UCSC Genome Browser on Human (GRCh37/hg19)											
move <<< < > >> >>> zo <u>on in 1.5x - 5x - 10x base zoom out 1.5x 3x 10x 4990 - 10x base zoom out 1.5x 3x 10x 4990 - 10x 10x 10x 10x 10x 10x 10x 10x 10x 10x</u>											
multi-region chr2:25,383,722-25,391,559 7,838 brt. gene, chromosome range, search terms, help pages, see example go examples											
ch2 (p23.3) 26.5 25.1 26.5 26.1 27.2 16.6 20.6 15.0 15.0 15.0 15.0 12.0 12.0 12.0 12.0 10.0 15.0 12.0 10.0 12.0 12.0 12.0 12.0 12.0 12											

3. You may arrive at this page, select your region under the "Chromosome Bands Localized by FISH Mapping Clones" section.

Search across the Genome Browser site	Search Results on hg38 (Human Dec. 2013 (GRCh38/hg38))
Search Human Human Dec. 2013 (GRCh38/hg38) Image: Graph of the search o	Chromosome Bands Localized by FISH Mapping Clones: 18q12.1 - chr18:27500001-35100000 Arobsus4 Alignments in Human Aligned mRNAs: • AF069054 - chr18:31624666-31684571 - 2125 99.8% 18 - 31624666 31684571 AF069054 1 2127 2147

4. For a larger region or segment: type in the region of interest with a semicolon (;) separating the proximal and distal segments of the region.

multi-region chr1	5:19,000,001-33	3,600,000 14,600,000	bp. 15q11;15q13			go <u>examples</u>
chr15 (q11	.1-q13.3) p13 p12	2 p11.2 11.2 12	15q14 21.1	q21.3 22.2 q23	25.3 <mark>q26.1</mark> 2	26.2 <mark>26.3</mark>
Scale		5 N	lb		hg19	
chr15:			25,000,000	30	,000,000	
		R	eference Assembly Fix	Patch Sequence Alignment	s	
		Refere	nce Assembly Alternate	Haplotype Sequence Align	ments	
				chr15_gl383554_alt		
		Ch	romosome Bands Loca	lized by FISH Mapping Clon	es	
	15q11.1			15q12	15q13	3.2
		15q11.2	2	15	iq13.1	15q13.3
			Clones Placed on Cyt	ogenetic Map Using FISH		
RP11-79A23		RP11-11H9	RP11-441B20	RP11-94G7	RP11-54I3	RP11-38E12
RP11-23B24		RP11-80H14	RP11-171C8	CTD-2264C5 RP1	1-680F8	RP11-115G22
RP11-452L16		RP11-228M15	RP11-1081A4		RP11-540B	6 RP11-54I3
	DD44 coDa		oth paralle			

5. Below the Browser track, in the Mapping and Sequencing tab (which is categorized in alphabetical order) unhide the FISH Clones if hidden - select pack, squish, dense or full display and click on the Refresh button in the top right of the Mapping and Sequencing tab.

•			Mapping and	Sequencing			refresh
Base Position dense ▼	P14 Fix Patches pack V	P14 <u>Alt Haplotype</u> S pack ▼	Assembly hide v	Centromeres hide ✔	Chromosome Ban d pack	■ <u>Clone Ends</u> hide ▼	Exome Probe sets hide V
B <u>FISH Clones</u> squish ✓ hide	Gap hide ✓	GC Percent hide v	GRC Contigs hide ▼	GRC Incident hide ✔	Hg19 Diff hide ❤	INSDC hide ✔	■ <u>LiftOver & Re</u> <u>Map</u> hide ▼
dense <u>ONS</u> squish pack full <u>STSTMITKEIS</u> hide ✓	■ <u>Mappability</u> hide ▼	■ <u>Problematic R</u> egions hide ▼	■ <u>Recomb Rate</u> hide ✓	RefSeq Acc hide	Restr Enzymes hide	Scaffolds hide V	Short Match hide

a) Full: aligns each probe on a track as its own entity

	Reference Assembly Alternate Naplotype Sequence Aligoments Chromosome Bands Localized by FISH Mapping Clones
00	Clones Placed on Cytogenetic Map Using FISH
HP11-676016	
RP11-1L4	
RP11-1L4	
RP11-90G7	
RP11-297N1	
RP11-79G13	
RP11-81J17	
RP11-111H24	
RP11-19F14	—
RP11-63N12	—
	UCSC Genes (BelSen, GenBank, CCDS, Bfam, IBNAs & Comparative Genomics)

b) Dense: aligns all probes in the region on one row/track and you can hover to see the name of each probe.



c) Pack: aligns the probes on multiple tracks in overlapping regions, don't need to hover to see the probe name.

	chr18 (q12.1) p1	1.32 18p11.31	p11.22 18p1	1.21	18q11.2	18q12.1	18q12.2	18q12.3	18q21.1 18	(q21.2 q21.31	g21.32 q21.33	18q22.1 q22.2	18q22.3 1	8q23	
Scale chr18:	25,500,000	26,000,000]	26,500,000]	27,000,000	27,500,000	2 Mb 28,000,000	28,500,000	29,000,000 bly Fix Patch Se	29,500,000] quence Alignments	hg19 30,000,000	30,500,000	31,000,000	31,500,000]	32,000,000	32,500,000]
						Re	eference Assembly i	Uternate Haplotys	e Sequence Alignm	ents					
							Chromosome Ban	is Localized by F	ISH Mapping Clones						
-								18q12.1							
							Clones Place	on Cytogenetic	Map Using FISH						
RP11-676D16		RP11-90G7				RP11	-79G13		RP11	-19F14			RP11	-81J17	RP11-63N12
	RP11-1L4	RP11-29	7N1												
	RP11-1L4														
RP11-111H24															

d) Squish: similar to dense but displays overlapping probes on a different track, without the probe name.

Heterance Assembly Pix Patch Sequence Alignments Reference Assembly Alternate Highlighting Sequence Alignments Chromosome Bands Localized by FISH Macing Comes	
18g12, 1	
Clanes Placed on Cytogenetic Map Using FISH	-

e) The track displayed below shows the FISH BAC Clones when the 'pack' display is selected, it also shows you the location of each probe relative to your region.



6) Determine which probe is appropriate for your region duplication or deletion by also correlating with the <u>eFISH</u> website for possible cross-hybridization to other locations in the genome. eFISH is similar to in-silico PCR tool testing using BLAST, the software will display a peak for regions your selected probe can hybridize to. In the example below, I chose RP11-19F14, one of the suggested probes from our search.

a) Upon arrival at the <u>eFISH</u> website, type in the probe name as shown below.

Search for FIS	H Probes											
Searching: Human Ger	Searching: Human Genome - Feb. 2009 Assembly (GRCh37/hg19) ✔ Keyword: Search											
Examples: Ctd-2089N14 chr7:74,940,08075,040,079 7p22.2												
Submit New												
Genome:	Human Genome - Feb. 2009 Assembly (GRCh37/hg19) 🗸											
Probes:	Paste probe list below: (e.g. <u>AC073062; RP11-668D21 chr7:7131260771482932</u> Not DNA sequence.) RP11-19F14											
	Note: please use the standardized clone name!											
	Submit Reset											

b) Click on the Submit button.

Genome:	Human Genome - Feb. 2009 Assembly (GRCh37/hg19)
Mapped Probes:	RP11-19F14 (chr18:2978436229973029 BAC_End) <u>DGV</u> <u>UCSC</u>
Show Chromosomes:	Chr18
	Check All Uncheck All
Show Probes:	☑ <u>RP11-19F14</u> [chr18]
Max Score (Y axis):	
Image Width:	○ 1000
	Refresh



7) In the result window, click on the hyperlinked probe name to see the areas that your probe hybridizes to. In the Megablast result window, all the regions are located on chromosome 18, and the peaks are centered at the region of interest.

Back to main page

Genome:	Human Genome - Feb. 2009 Assembly (GRCh37/hg19)]									
Mapped Probes:	RP11-19F14 (chr18:2978436229973029 BAC_End) DGV UCSC														
Show Chromosomes:	Check All Uncheck All	🕒 efish -	davinci -	Work - Microsof	t Edge	1 	Disc	ari2anaka Par		DD11_1	054400-6-6-4	U	4646.0	-	
Show Probes	[chr18]	A Not	secure	projects.tca	ig.ca/cgi-	bin/efish/ge	blast.	cgi/probe=Pro	be i ccreainar	ne=KPTT-D	9F14&Job_Id=	Untitled_r21	victsœuser_	ia=75et56	26 (iii) A"
Max Score (Y axis):	$\mathbf{E} = 100 \circ 50 \circ 10 \circ 6$														
Image Width:	dth. 0 1000 @ 2000 0 4000 KF 11-19F 14 Megadlast Kesult														
	Refresh	subject	target	Perc. Ident.	Length	Mismatch	Gap	Subject Chr.	sStart	sStop	Target Chr.	tStart	tStop	E-value	Score
		Probe1	chr18	100	15639	0	0	chr18	29784362	29800000	chr18	29784362	29800000	0.0	1.847e 05
RP11-19F14	<u> </u>	Probe1	chr18	100	65639	0	0	chr18	29784362	29850000	chr18	29784362	29850000	0.0	1.847e 05
100		Probe1	chr18	100	100000	0	0	chr18	29800001	29900000	chr18	29800001	29900000	0.0	1.847e 05
-		Probe1	chr18	98.85	86	0	1	chr18	29820142	29820227	chr18	61297445	61297531	3e-34	154
50-		Probe1	chr18	100	100000	0	0	chr18	29850001	29950000	chr18	29850001	29950000	0.0	1.847e 05
-		Probe1	chr18	100	73029	0	0	chr18	29900001	29973029	chr18	29900001	29973029	0.0	1.847e 05
-		Probe1	chr18	100	23029	0	0	chr18	29950001	29973029	chr18	29950001	29973029	0.0	1.847e 05
04 (++++++++++++++++++++++++++++++++++++	20M 30M 40M 50M 60M	Probe1	chr18	94.17	103	6	0	chr18	29950652	29950754	chr18	29950739	29950841	2e-35	158
chr18		Probe1	chr18	94.17	103	6	0	chr18	29950739	29950841	chr18	29950652	29950754	2e-35	158
11 301 31 11 21	11 2 12 1 12 2 12 3 21 1 21 2 22 1				* Start	and Stop co	ordin	ates are absolu	ite, based or	1 the actual	location on th	ie genome.			

8) Finally, when ordering from your lab's preferred vendor, be sure to have selected an appropriate control region probe with your region's probe for confirmation.

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