

FrOGG ChromoAGN

29.01.2026

Liste des présents

	GUERMOUCHE Helene Organisateur	
	ABERMIL Nassera (Externe)	
	Audrey Bidet (Non vérifié)	
	AUGER Nathalie (Externe)	
	Barbara Dewaele (Non vérifié)	
	Christine (Non vérifié)	
	dom (Non vérifié)	
	Faten Hsoumi (Non vérifié)	
	GAILLARD JEAN BAPTI... (Externe)	
	GENTIEN David (Externe)	
	Hadjer LAzga (Non vérifié)	
	Nathalie Nadal (Non vérifié)	
	roynard_pauline (Externe)	
	TUEUR Giulia (Externe)	

	TOUJANI Saloua (Non vérifié)	
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Profil complexe en COG Lymphome

Grenoble

29 janvier 2026

T25-6153

Lymphome folliculaire, grade 1/2, au diagnostic

Forte masse tumorale

Clone en CMF dans le ganglion tumoral = 60%

Echec du caryotype.

FISH : BCL2 réarrangé

T25-6153

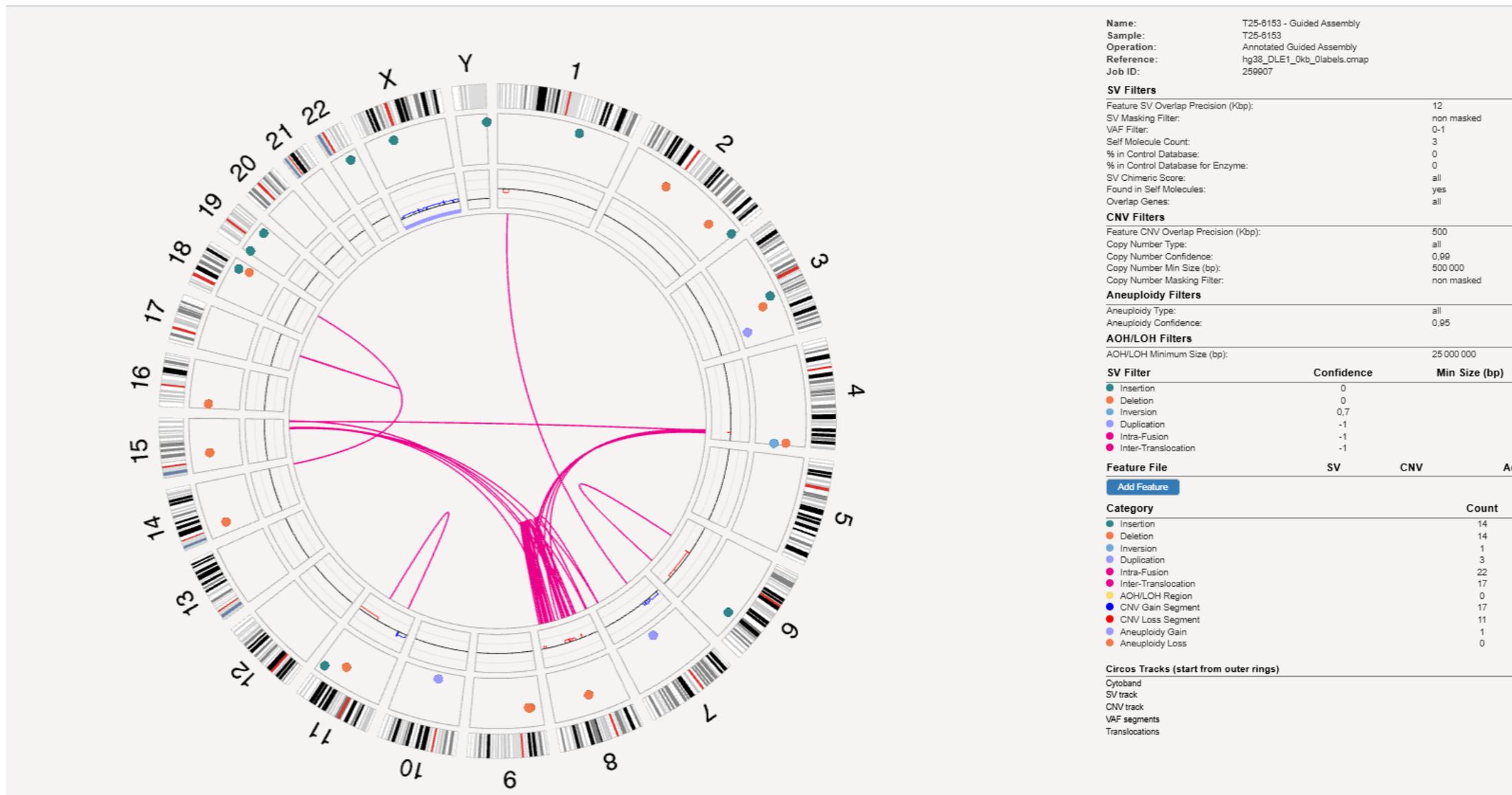
Guided assembly

N50 = 324

LD = 14,1

Map rate = 68

Effective coverage = 290



T25-6153

Bed lymphomes B :

t(14;18) IGH::BCL2

VAF = 0,31

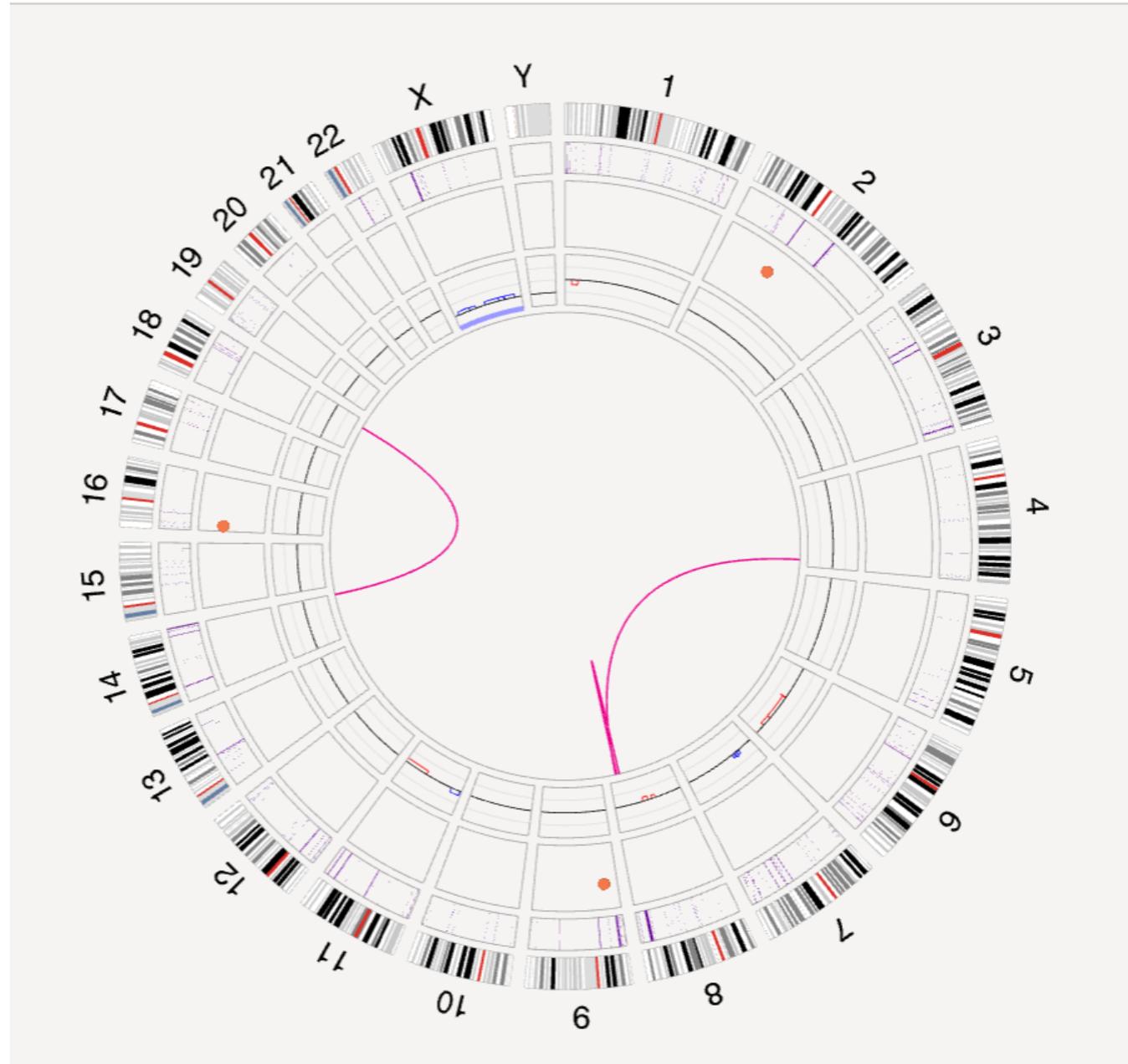
t(4;8) et inv(8)(q24q24)

MYC::non-Ig

VAF = 0,12

Del 9p21.3 : CDKN2A (200 kb)

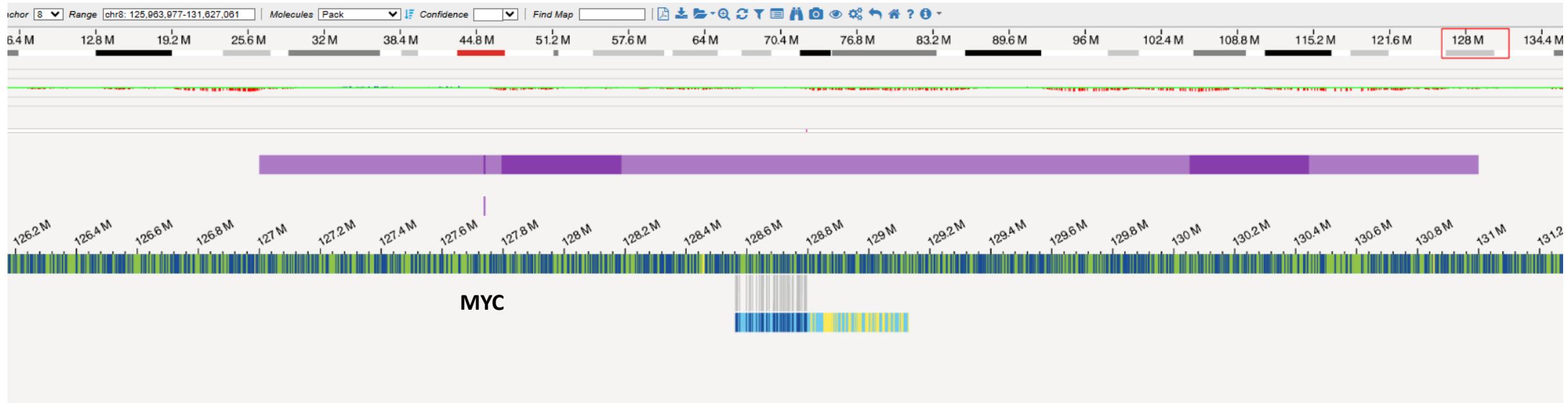
Del 16p13.3 : CIITA (3,1 Mb)



T25-6153

Map 1442

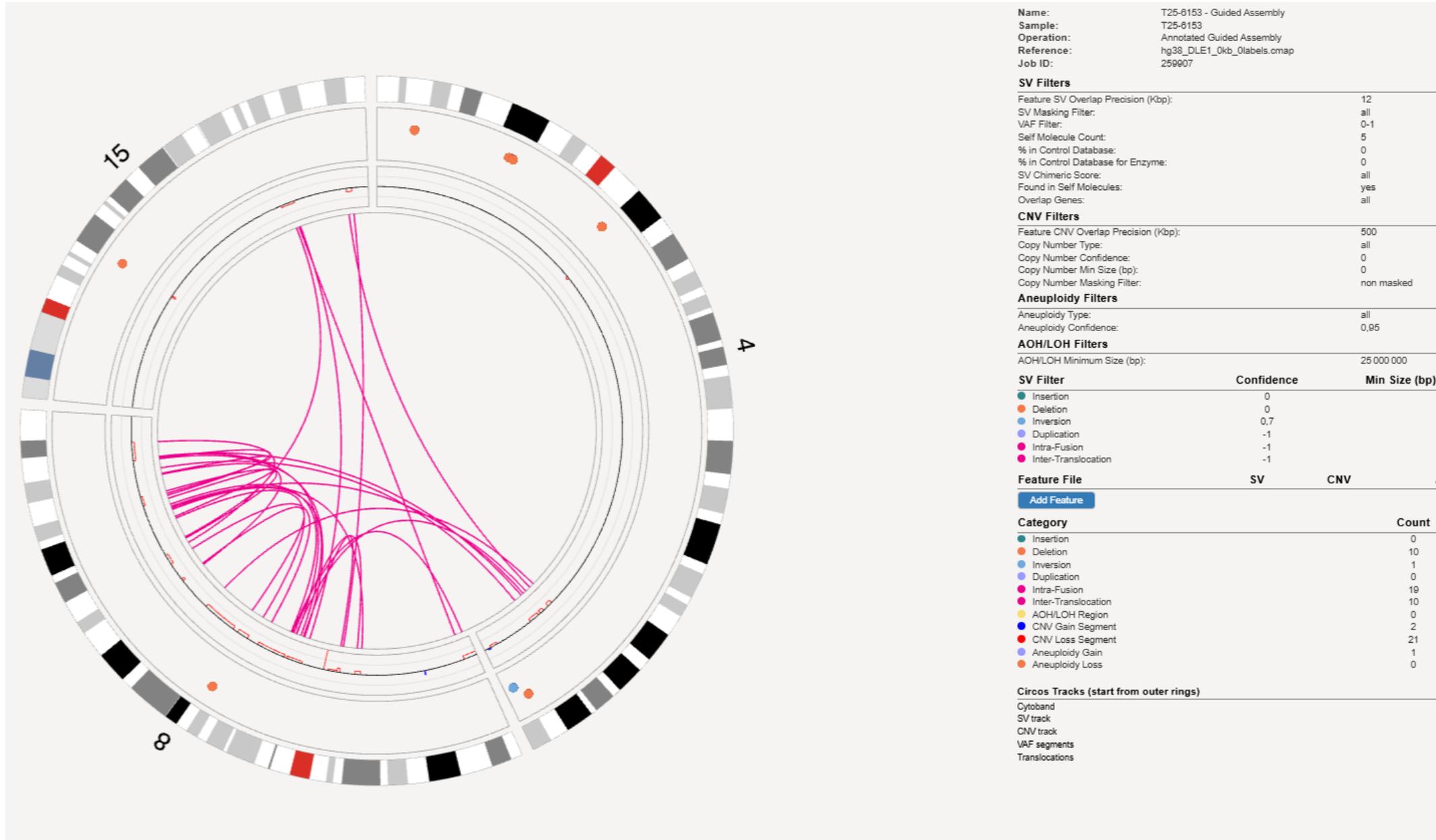
MYC réarrangé : t(4;8)
Partenaire ? FBXO8



T25-6153

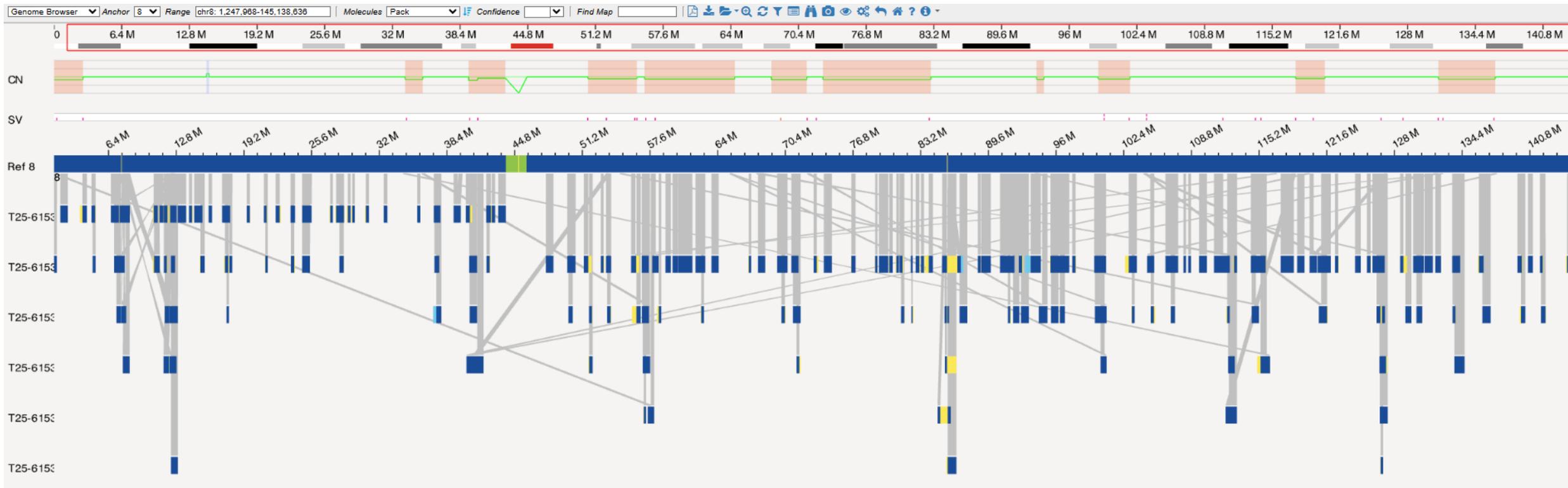
CNV : size =0, confidence All

VAF des SV =
0,12 à 0,22



T25-6153

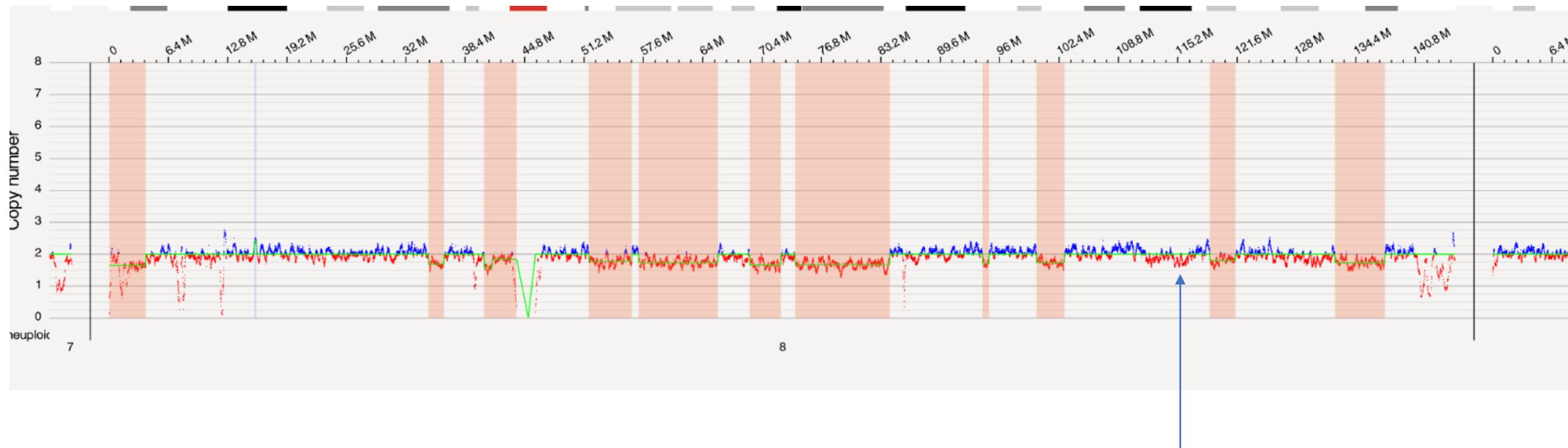
Chromosome 8 ...



T25-6153

Chromosome 8 ...

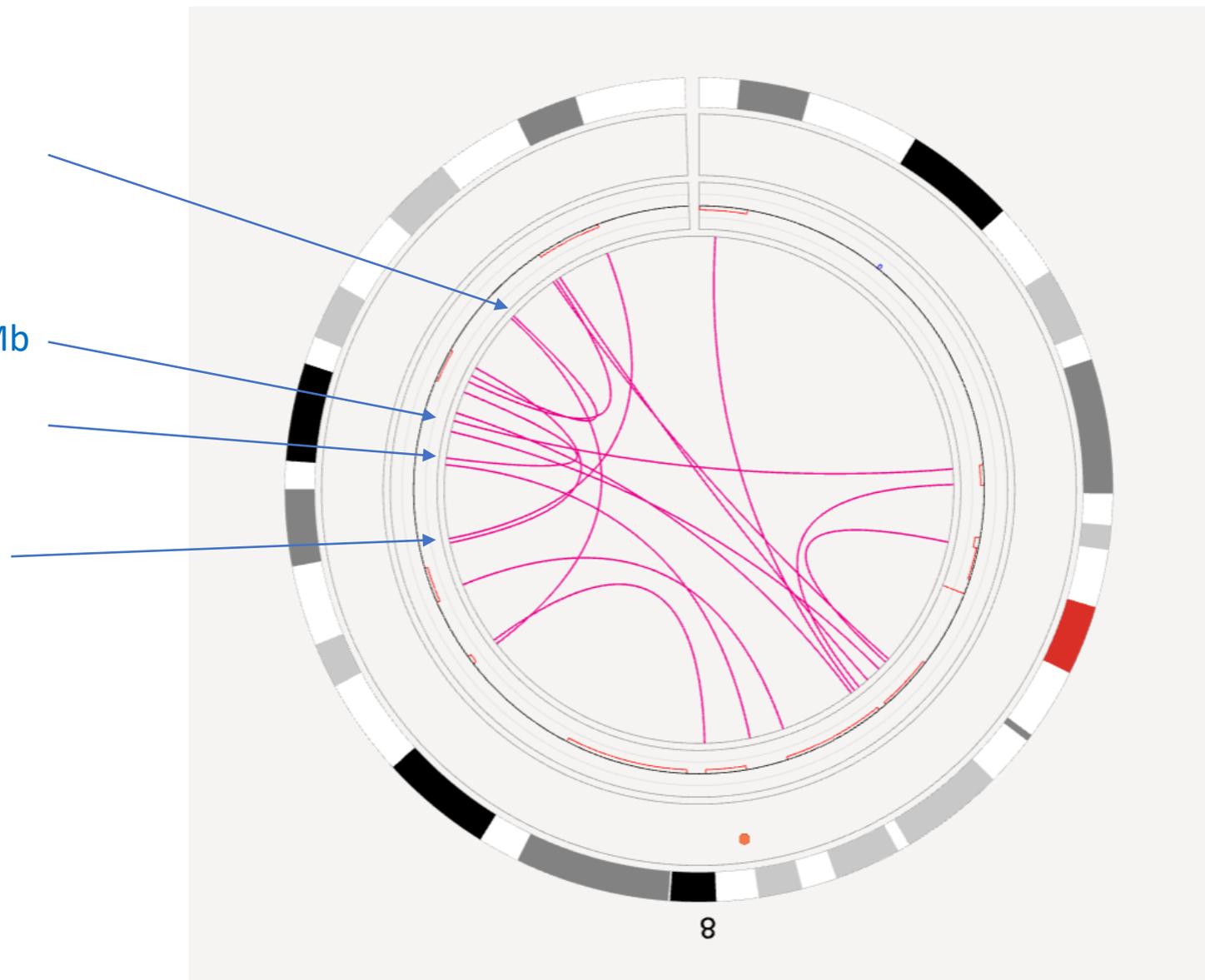
CNV : size =0, confidence All



T25-6153

Chromosome 8 ...

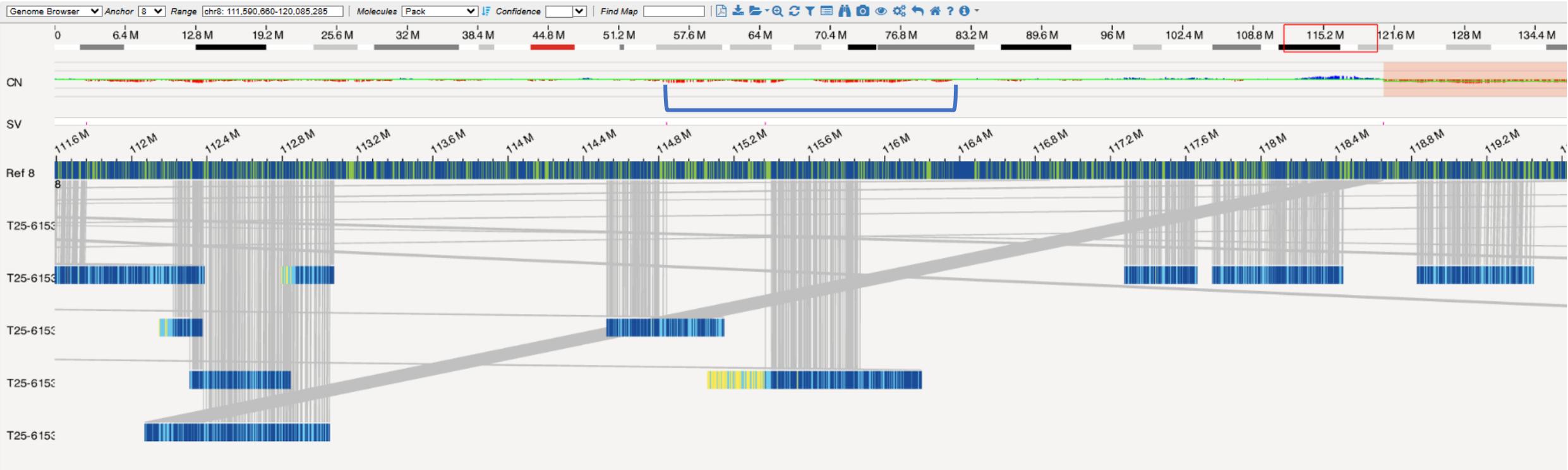
114,8 – 116,3 Mb



T25-6153

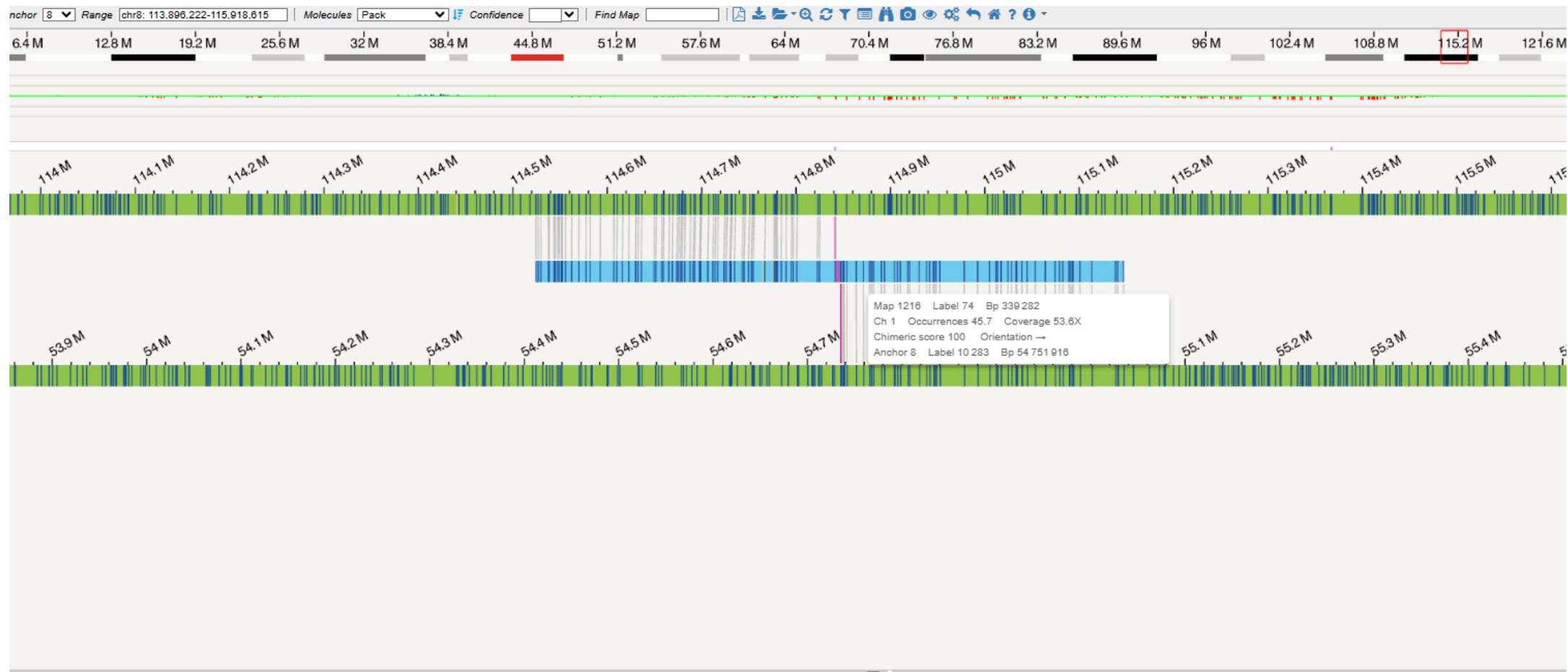
8q

114,8 – 116,3 Mb



?? CNV aux bornes des SV

Map 1216



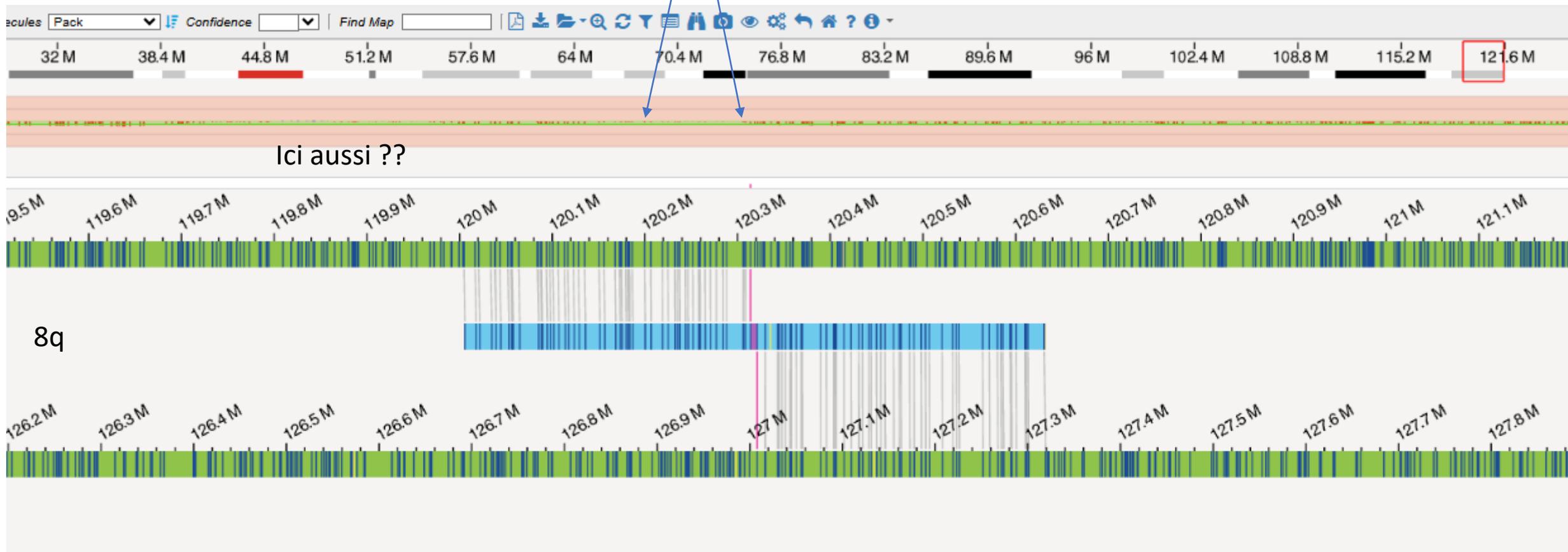
CNV Annotation													
	RefoontigID1	RefoontigID2	RelStartPos...	RelEndPos ...	Size (bp)	Zygosity	Confide...	SmaplId	VAF	Present in % of control db samples	Present in % of control db samples with the same enzyme	Fail assembly chimeric score	
fusion	8	8	104 556 227	121 114 235	-1	heterozygous	0,94	1454	0,180	0,0	0,0	pass	
fusion	8	8	104 556 227	121 114 235	-1	heterozygous	0,91	1455	0,180	0,0	0,0	pass	
fusion	8	8	111 780 447	88 289 655	-1	heterozygous	0,82	1456	0,180	0,0	0,0	pass	
fusion	8	8	114 841 514	54 735 306	-1	heterozygous	0,96	1459	0,160	0,0	0,0	pass	

T25-6153

Map 1181

Entre ces deux points,
Nb copies = 2 ??

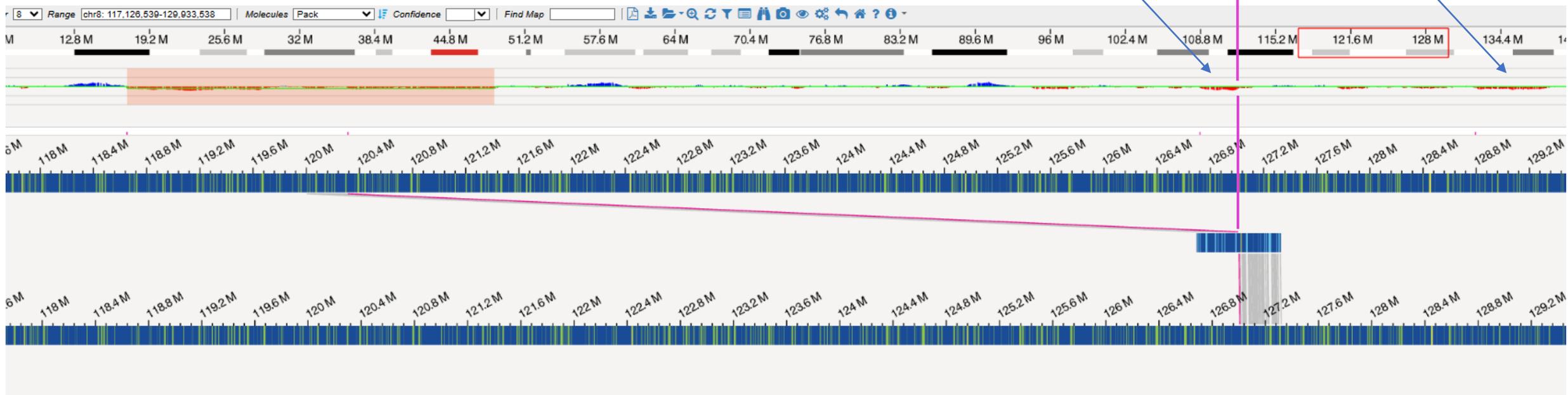
8q



T25-6153

Map 1181

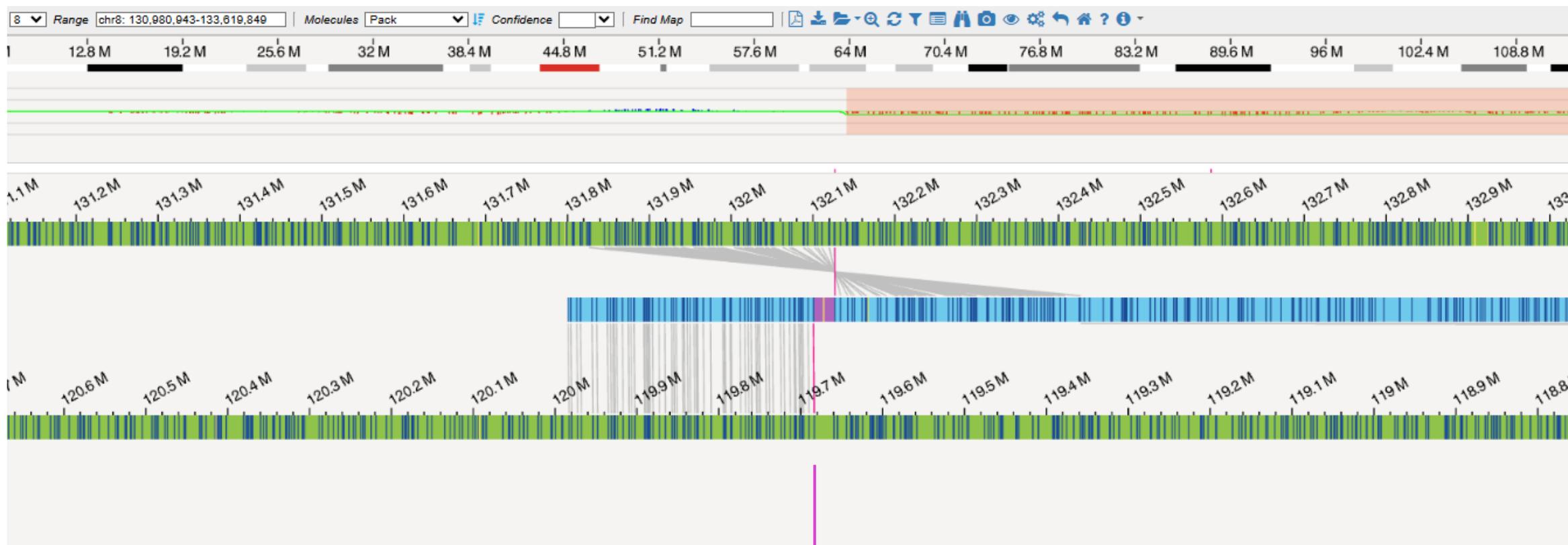
Position SV / borne CNV =
identique = 127 008 058



T25-6153

Map 112

8q



Position SV / borne CNV =
identique = 119 683 408

T25-6153

Map 112

Position SV = 119 683 408

8q

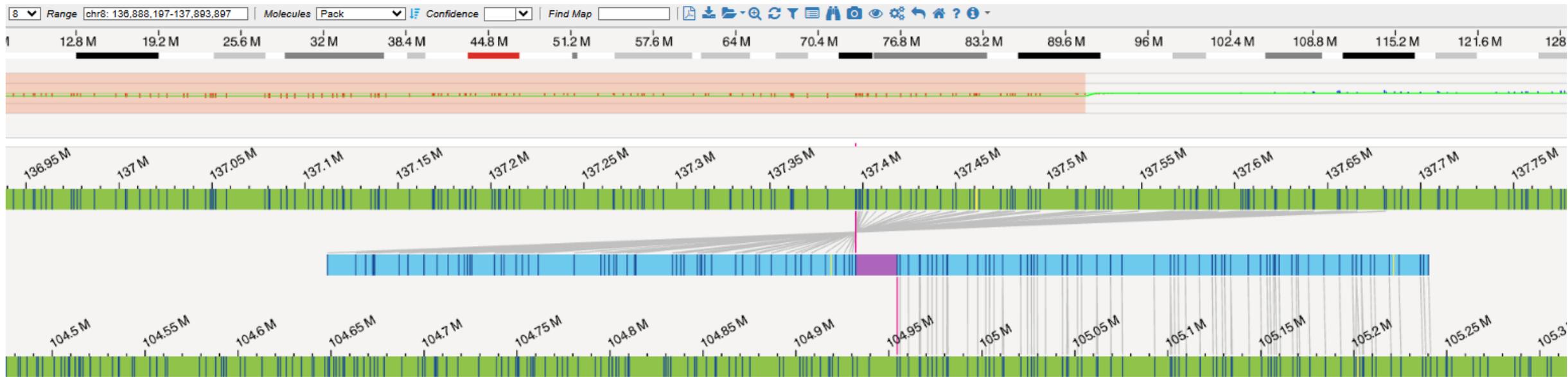


?? CNV 2 copies dans cet intervalle

T25-6153

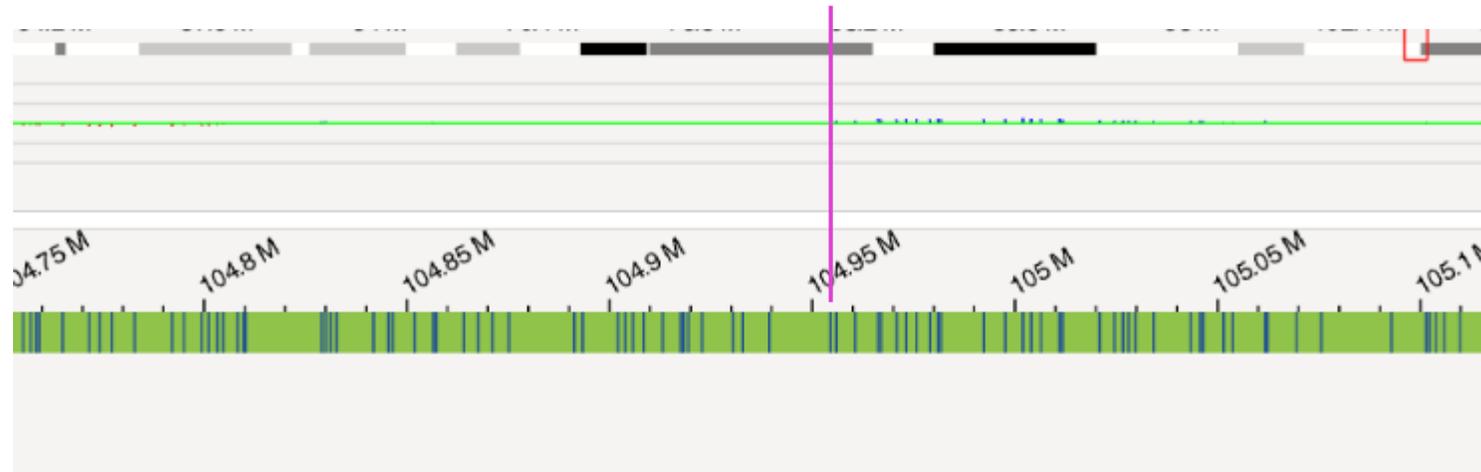
Map 1349

8q



Position SV = 104 954 456

Pas de CNV, ni SV proche de cette position



CONCLUSIONS... Hypothèses !

Evènement complexe sous-clonal (~30% des cellules) avec réarrangement MYC

Limite de détection des CNV

Difficile d'établir avec certitude le(s) mécanisme(s) sous-jacent(s)

ChromolymphoB?

FrOGG – 29/01/26

Giulia TUEUR

• Cas clinique 1

Mr M. 72 ans

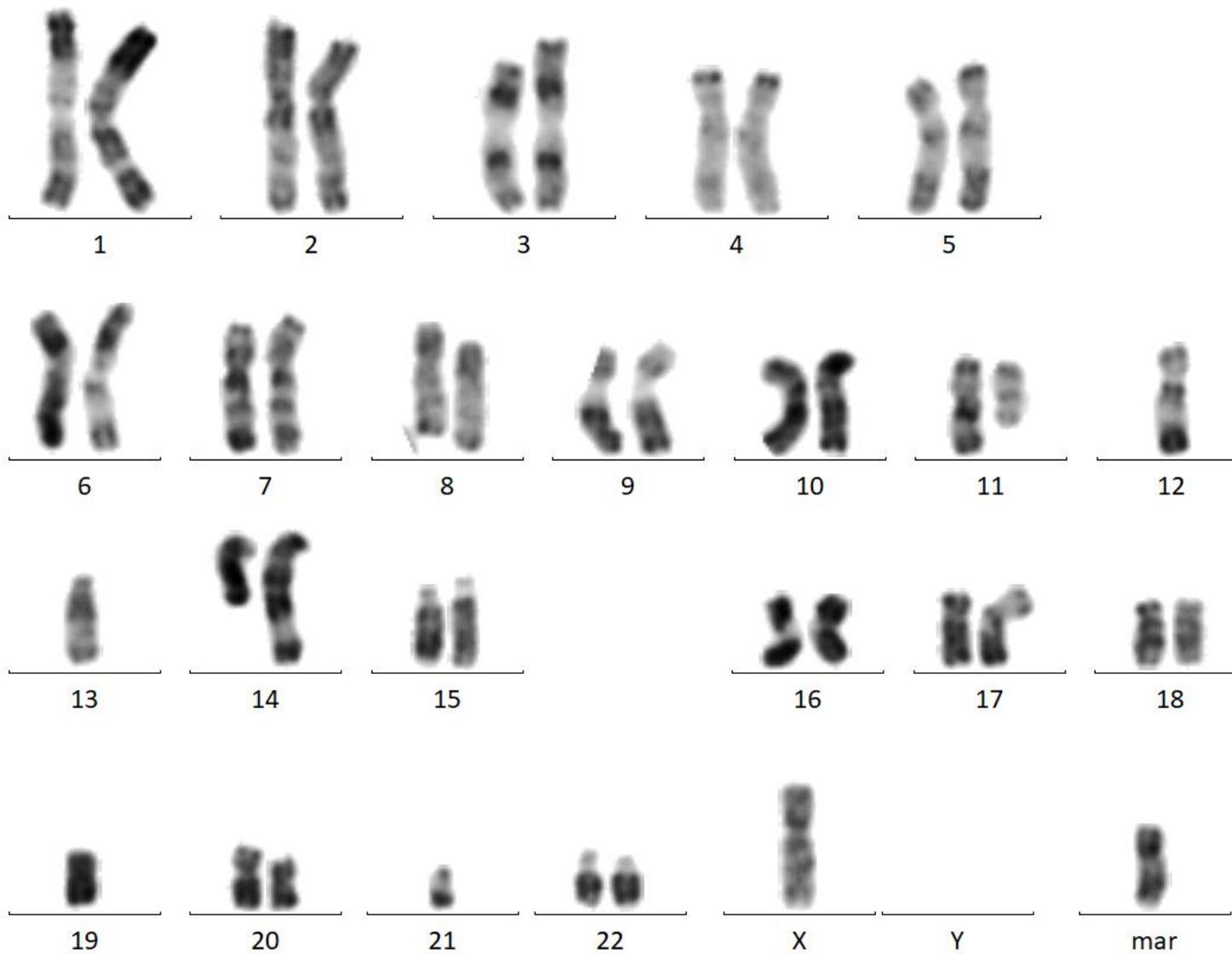
ATCD : Nombreux dont TE compliquée de myélofibrose. Blastose à 7%

Juin 2024 : Apparition lymphocytose à 38 G/L

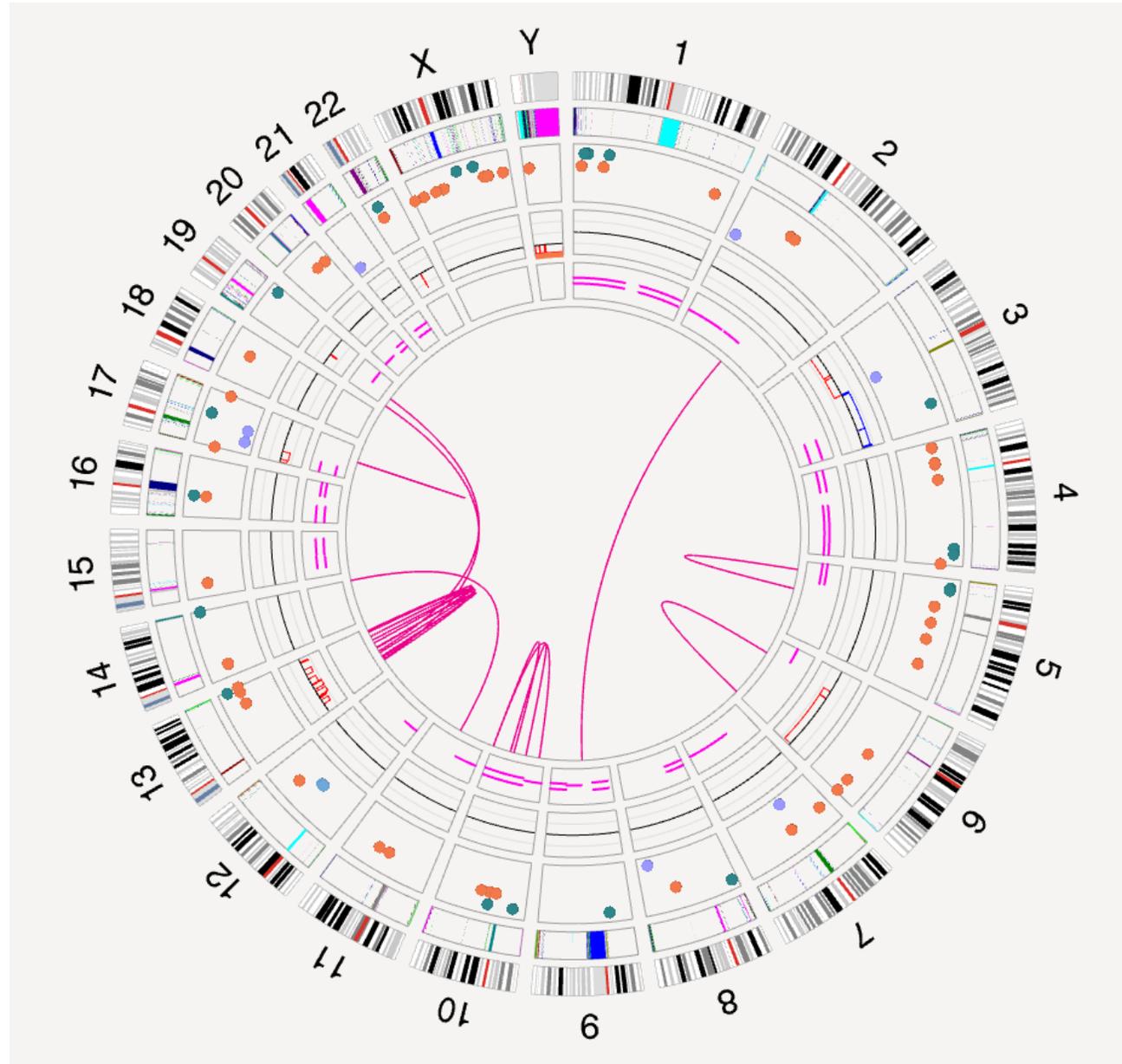
CMF retrouvant 2 populations :

- Une majoritaire (98% des LyB) CD5+, lambda, CD20+ → LCM
- Une minoritaire (0,6% des Ly B) CD5+, kappa dim, CD20dim → LLC

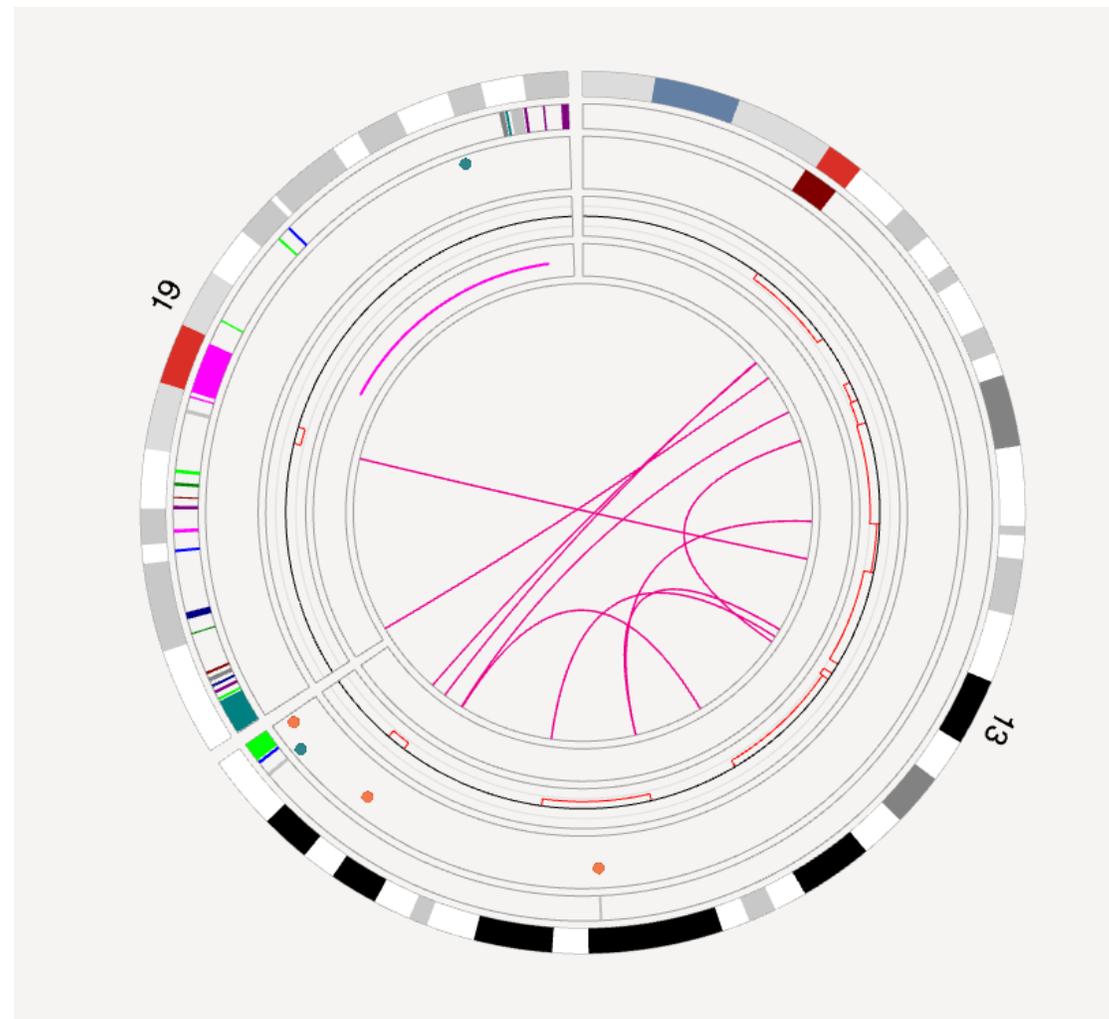
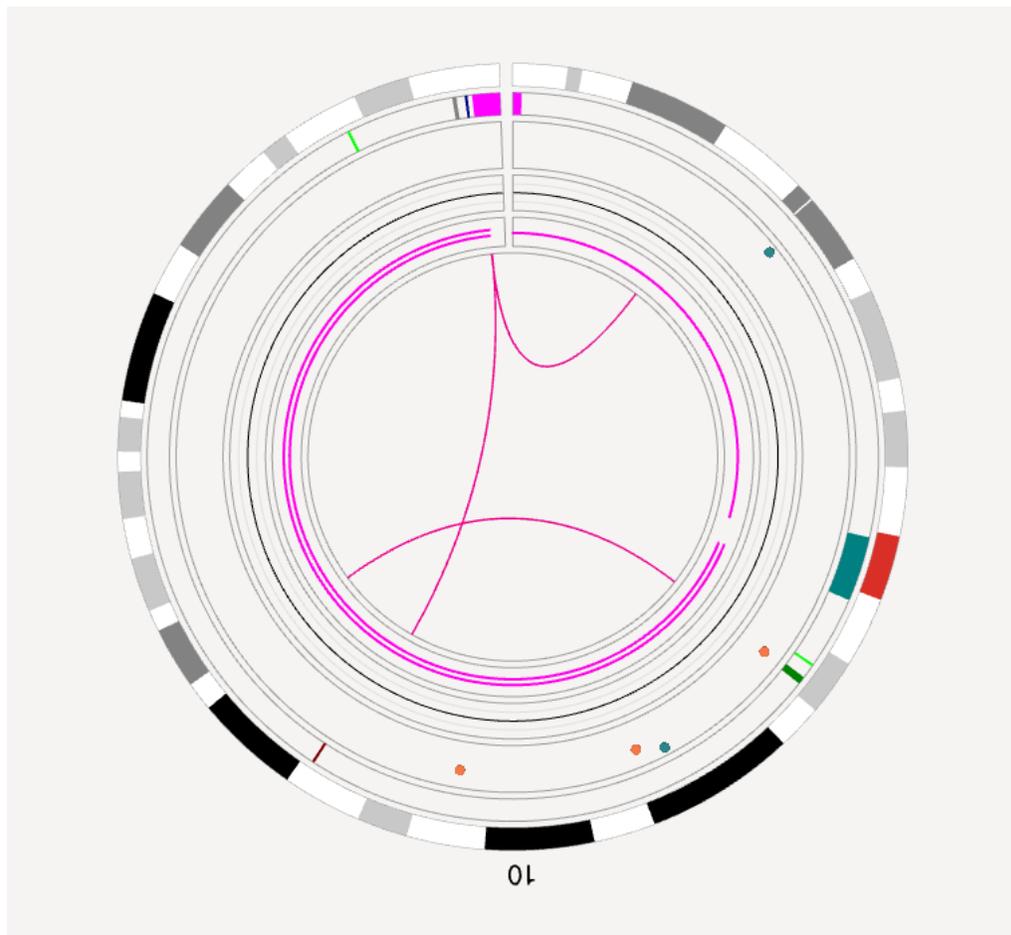
Cytogé



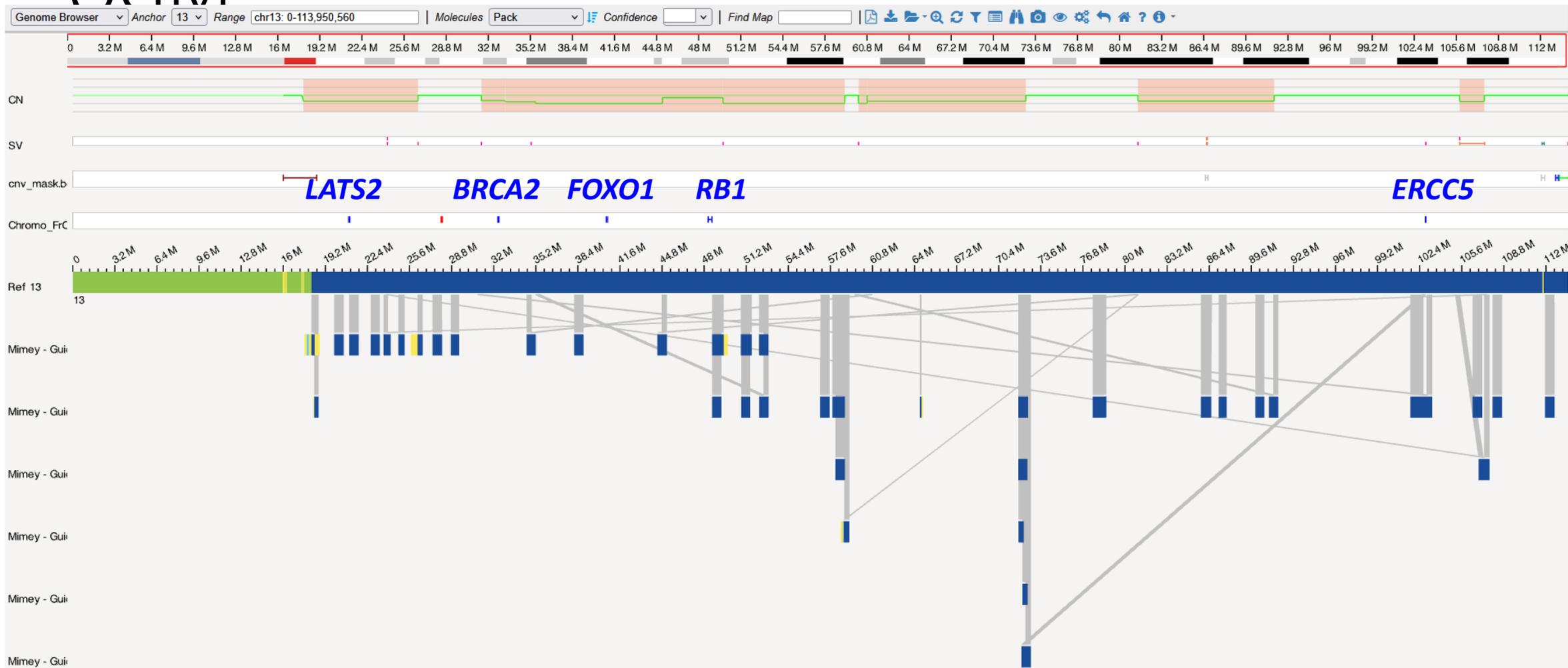
OGM



OGM



OGM



OCMA

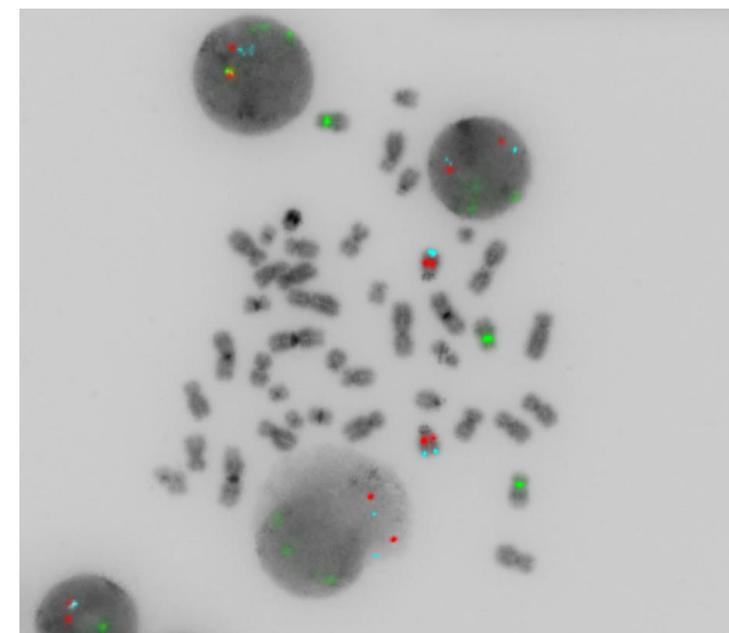
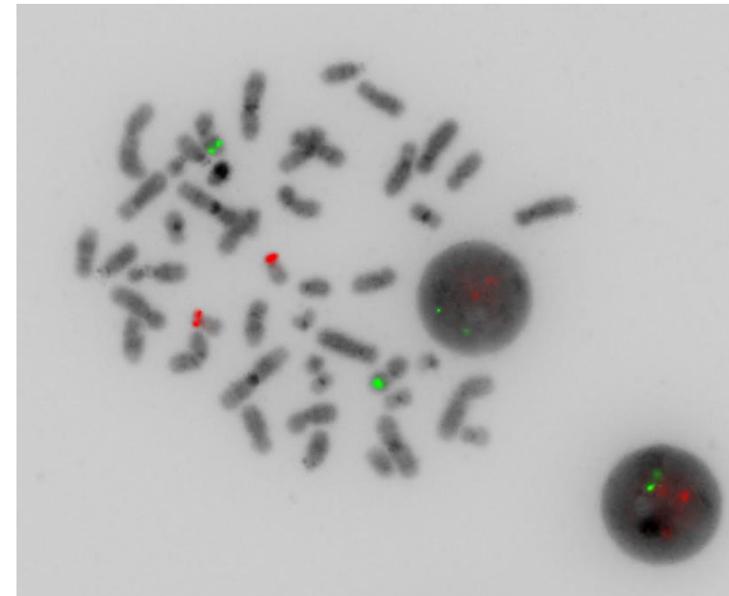
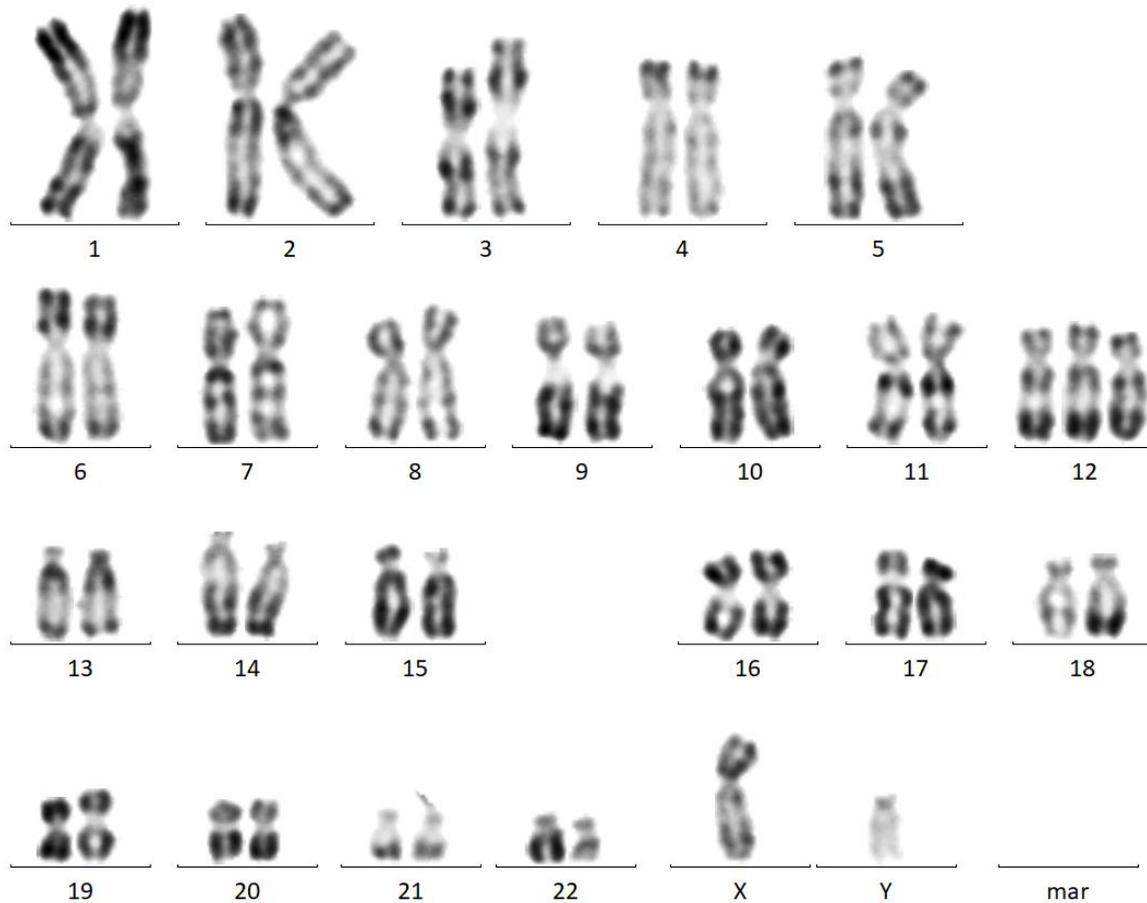
<i>deletion</i>	13	13	105 440 223	107 342 356	1 779 339	0,79	0,310
<i>intrachr_fusion</i>	13	13	23 920 058	107 342 356	-1	0,96	0,350
<i>intrachr_fusion</i>	13	13	23 920 058	107 342 356	-1	0,79	0,350
<i>intrachr_fusion</i>	13	13	31 077 413	102 969 418	-1	0,95	0,300
<i>intrachr_fusion</i>	13	13	34 849 859	60 475 107	-1	0,97	0,120
<i>translocation_i...</i>	13	19	49 445 273	22 468 414	-1	0,97	0,380
<i>intrachr_fusion</i>	13	13	59 743 327	91 300 986	-1	0,96	0,330
<i>intrachr_fusion</i>	13	13	80 973 777	44 818 391	-1	0,98	0,340
<i>intrachr_fusion</i>	13	13	80 991 839	58 702 319	-1	0,81	0,310
<i>intrachr_fusion</i>	13	13	102 871 114	72 476 858	-1	0,98	0,370
<i>intrachr_fusion</i>	13	13	105 440 223	23 825 400	-1	0,76	0,320
<i>translocation_i...</i>	13	19	26 253 286	1 036 799	-1	0,96	0,300

OGM

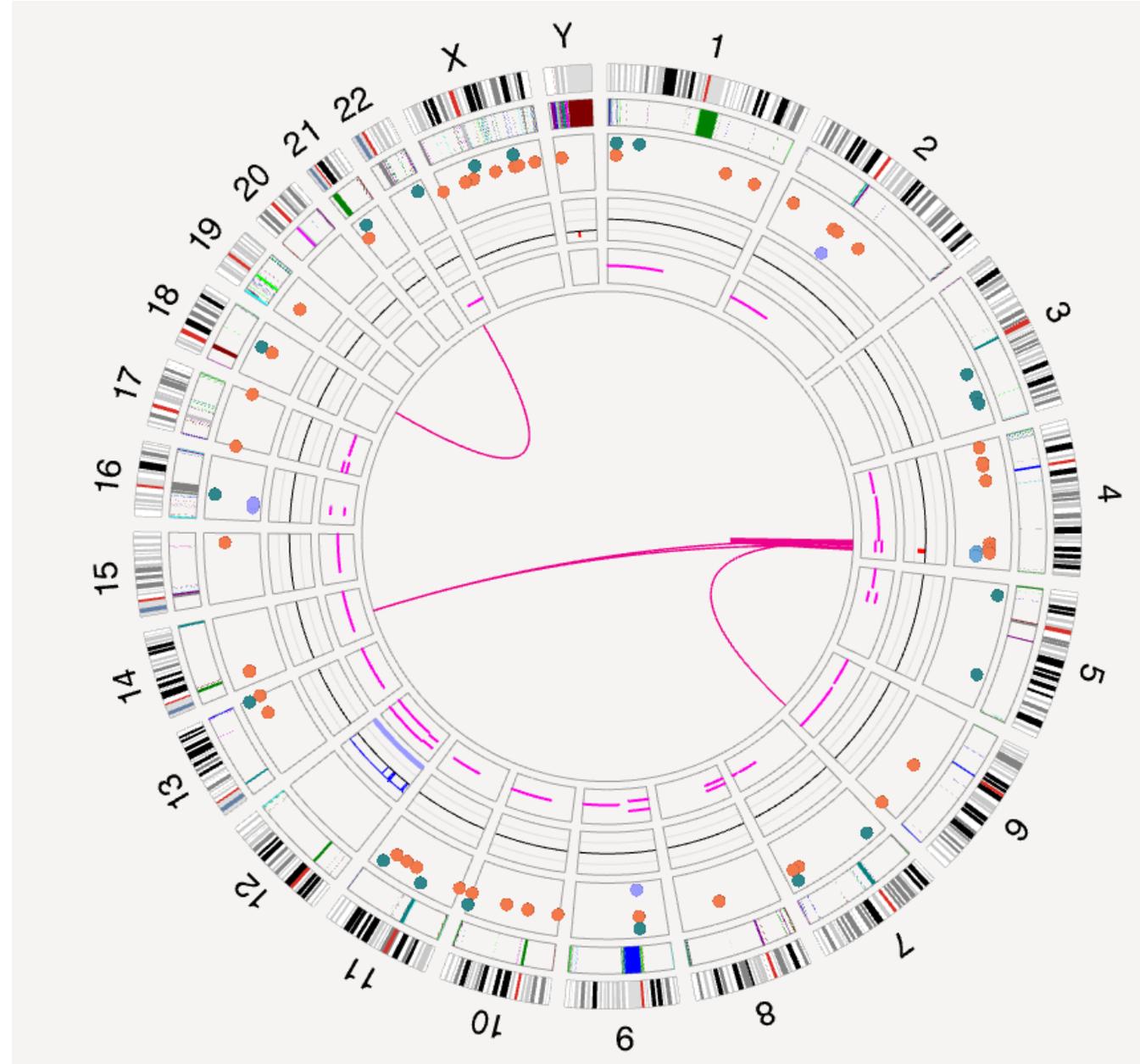
17 542 017	26 250 299	8 708 283	loss	1,288	1,00	0,356
31 077 413	32 870 738	1 793 326	loss	1,349	1,00	0,325
32 881 974	35 167 434	2 285 461	loss	1,213	1,00	0,394
35 170 997	44 829 790	9 658 794	loss	1,032	1,00	0,484
44 833 979	49 428 152	4 594 174	loss	1,726	0,99	0,137
49 445 273	58 690 160	9 244 888	loss	1,017	1,00	0,491
59 738 477	60 390 776	652 300	loss	1,009	1,00	0,496
60 392 350	72 464 842	12 072 493	loss	1,285	1,00	0,357
80 973 777	91 344 315	10 370 539	loss	1,295	1,00	0,352
105 440 223	107 309 921	1 869 699	loss	1,239	1,00	0,381

• Cas clinique n°2

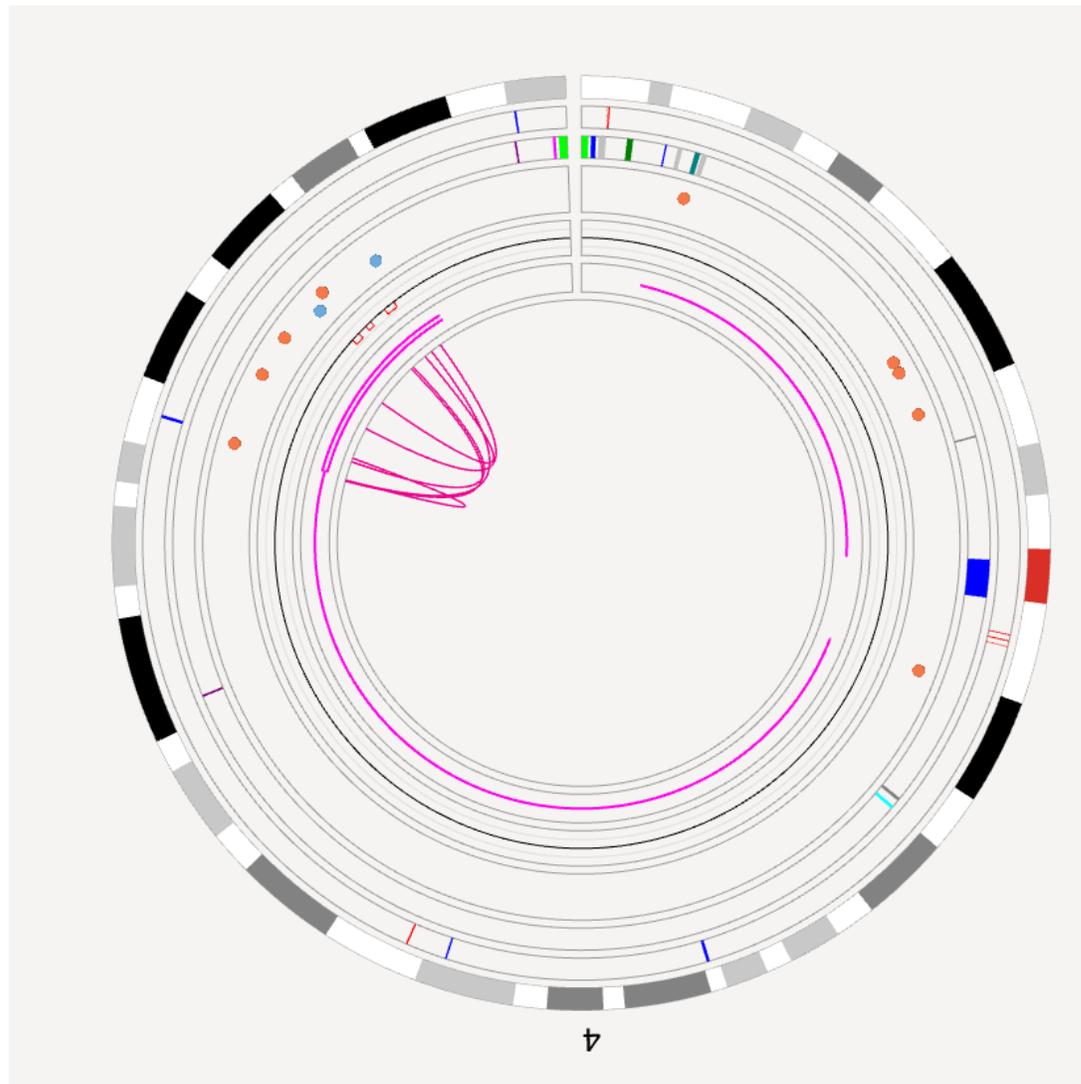
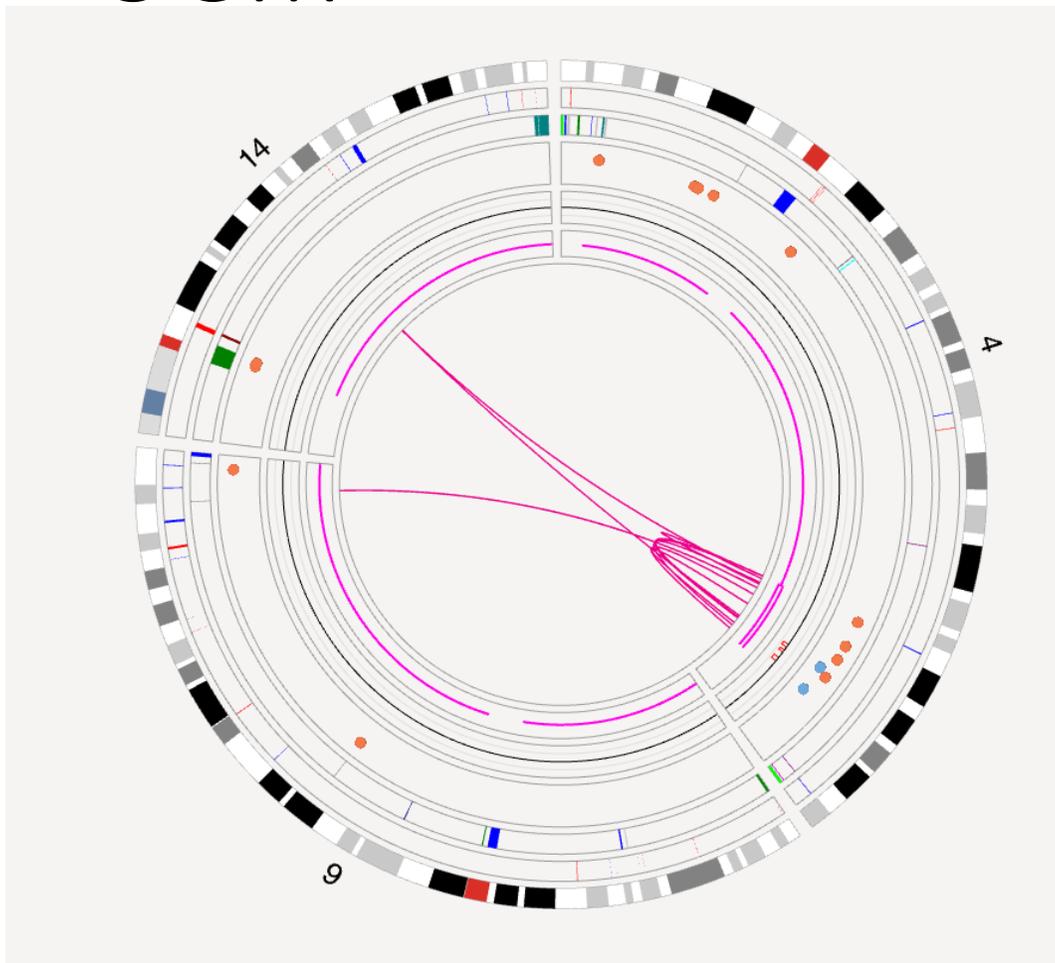
Patient suivi pour LLC



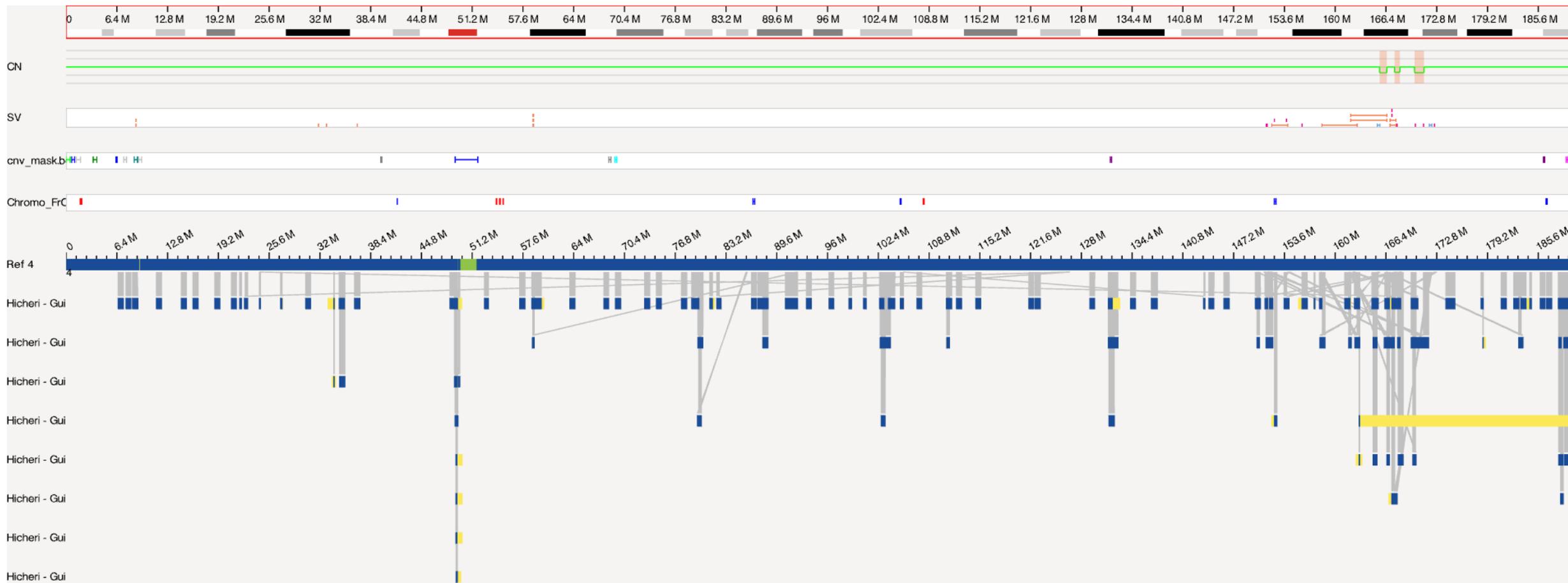
OGM



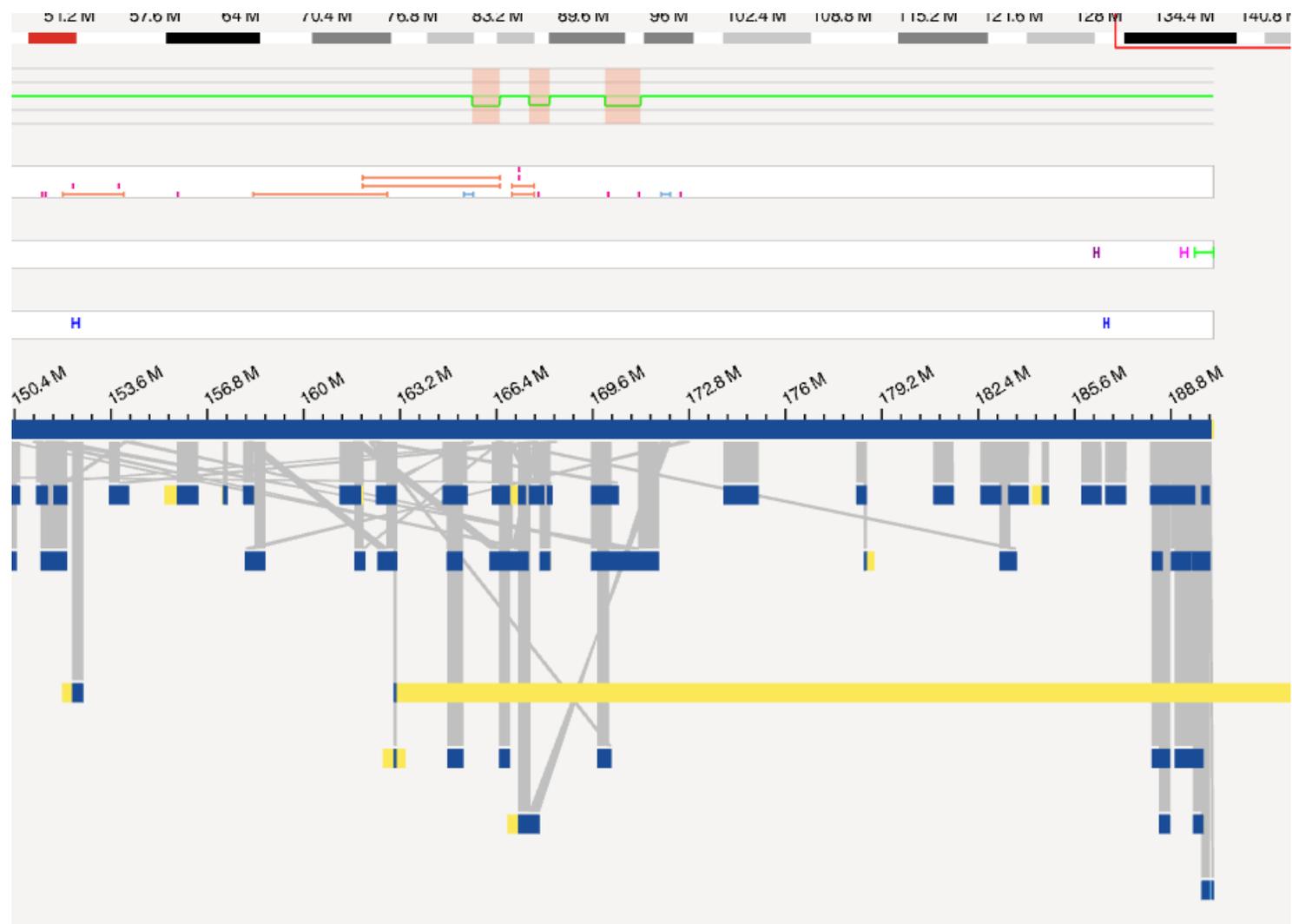
OGM



OGM



OGM



OGM

Type	RefcontigID1	RefcontigID2	RefStartPos...	RefEndPos ...	Size (bp)	Zygoty	Confide...	SmaplId	VAF	Pres
<i>intrachr_fusion</i>	4	4	151 312 150	167 798 455	-1	<i>heterozygous</i>	0,99	687	0,320	
<i>intrachr_fusion</i>	4	4	151 431 426	154 321 689	-1	<i>heterozygous</i>	0,98	699	0,200	
<i>translocation_i...</i>	4	14	152 337 386	49 298 483	-1	<i>heterozygous</i>	0,99	692	0,350	
<i>intrachr_fusion</i>	4	4	153 859 590	168 117 374	-1	<i>heterozygous</i>	0,99	693	0,340	
<i>intrachr_fusion</i>	4	4	167 798 455	151 312 150	-1	<i>heterozygous</i>	0,99	713	0,320	
<i>intrachr_fusion</i>	4	4	170 122 414	162 171 774	-1	<i>heterozygous</i>	0,99	715	0,320	
<i>intrachr_fusion</i>	4	4	170 112 133	162 171 774	-1	<i>heterozygous</i>	0,60	729	0,320	
<i>intrachr_fusion</i>	4	4	171 134 314	151 431 426	-1	<i>heterozygous</i>	0,97	727	0,360	
<i>intrachr_fusion</i>	4	4	172 518 365	158 393 352	-1	<i>heterozygous</i>	0,99	724	0,310	
<i>translocation_i...</i>	4	6	155 820 999	162 035 038	-1	<i>heterozygous</i>	0,97	1039	0,050	
<i>translocation_i...</i>	4	14	167 152 876	49 127 727	-1	<i>heterozygous</i>	0,99	2095	0,350	
<i>translocation_i...</i>	4	14	167 152 876	49 127 727	-1	<i>heterozygous</i>	0,99	2097	0,350	

SV Annotation	Match	CNV Annotation	Feature										
Id.	RefId	Start (bp)	End (bp)	Size (bp)	Type	Fractional Copy Nu...	Copy Nu...	Confidence	VAF	Algorithm	Overlap Genes	Nearest NonOverlap Ge...	Nearest No
27	4	165 597 692	166 502 038	904 347	loss	1,290	1	1,00	0,355	Region-based	LINC01179;LOC101928131;TLL1	CPE	
29	4	167 483 404	168 160 926	677 523	loss	1,357	1	1,00	0,322	Region-based	ANXA10	DDX60	
30	4	170 010 615	171 187 219	1 176 605	loss	1,299	1	1,00	0,350	Region-based	MFAP3L;LOC101928198;AADAT;LINC01612;...	LINC02275	

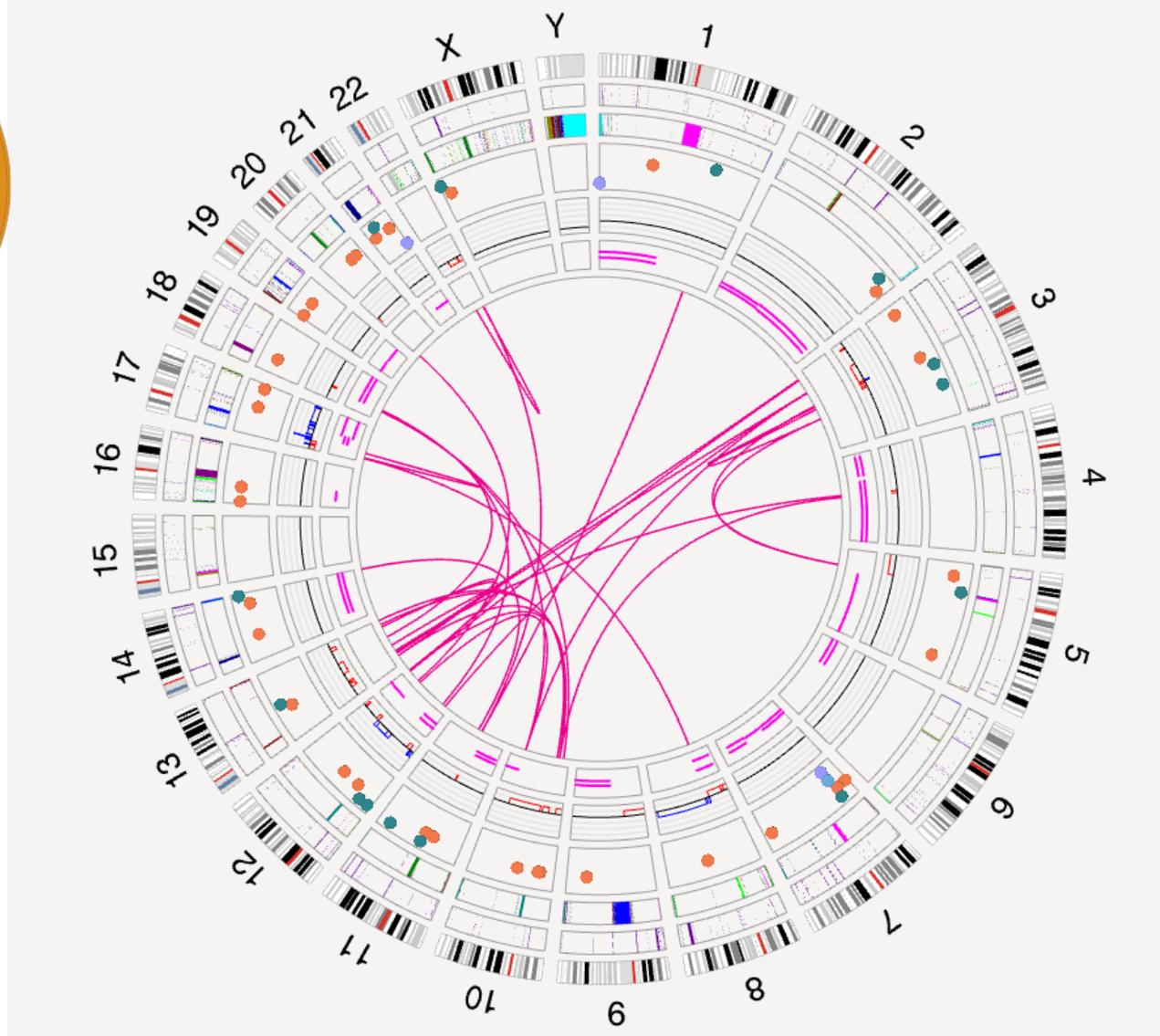
VAFs similaires → chromotrypsis ok?

Cas n°3

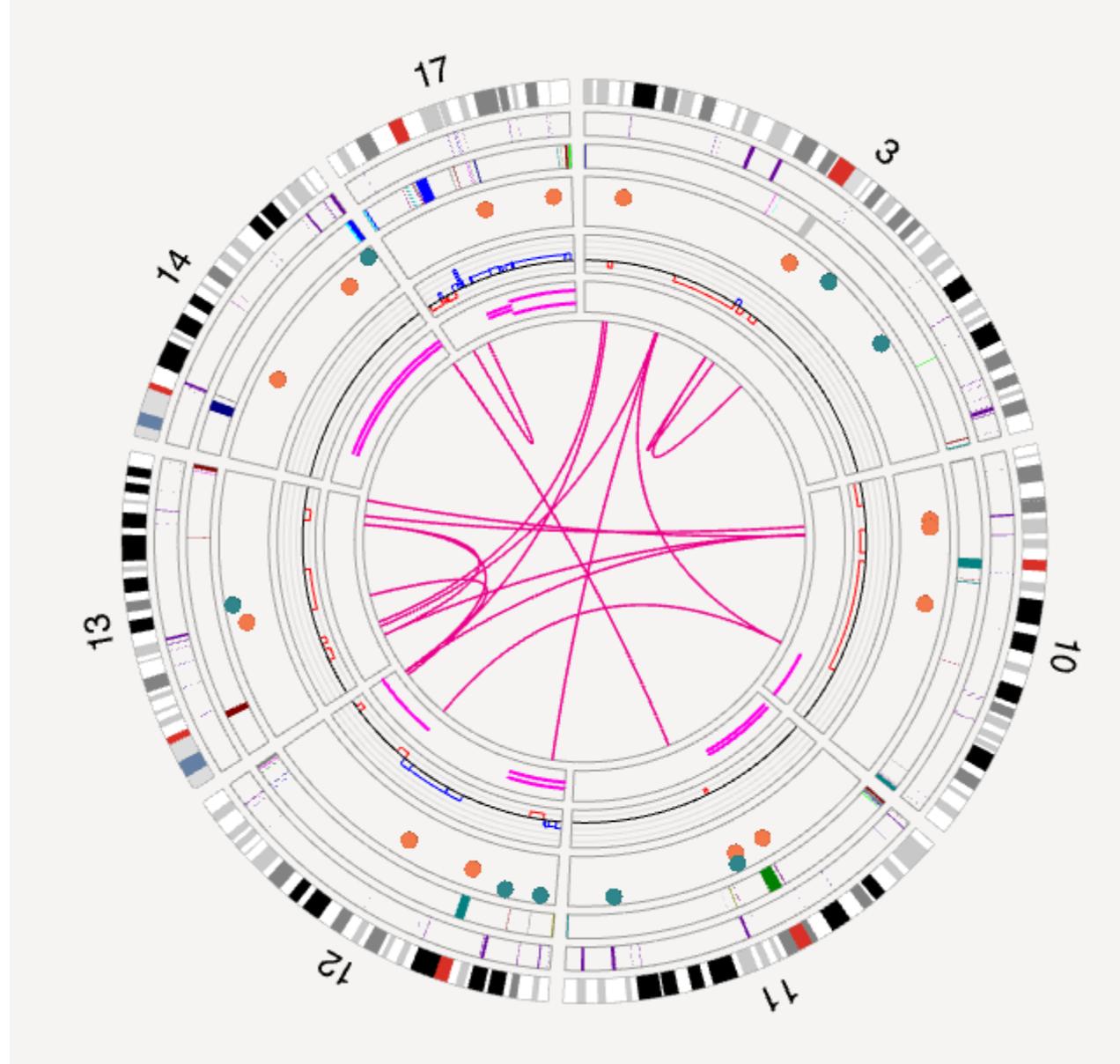
- Rechute LCM
- 43~45,XY,der(3)add(3)(p?)add(3q?),t(11;14)(q13;q32),-17,+1~7mar,inc[cp22]
.ish t(11;14)(CCND1+,IGH+;IGH+,CCND1+)[12],mar(TP53-,D17Z1+)x2[47]
.nuc ish(CCND1,IGH)x3(CCND1 con IGHx2)[184/200],(TP53x1,D17Z1x2)[172/200]

Caryotype hypodiploïde à 43~45 chromosomes, très complexe, composite et très difficilement classable retrouvant la t(11;14)(q13;q32) (avec fusion IGH-CCND1 confirmée en FISH) associée à de façon variable à de nombreuses anomalies (non identifiables).

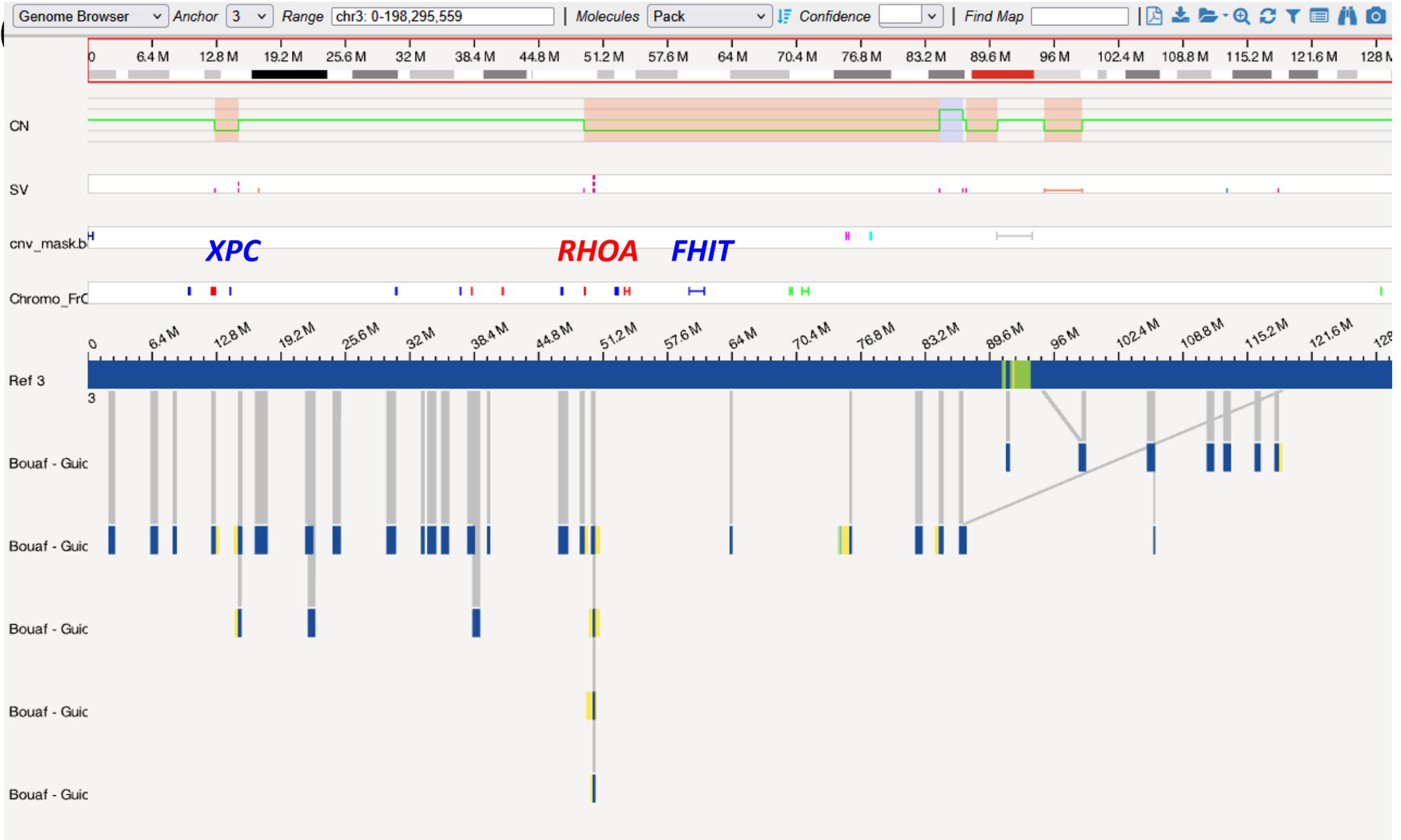
OGM



OGM



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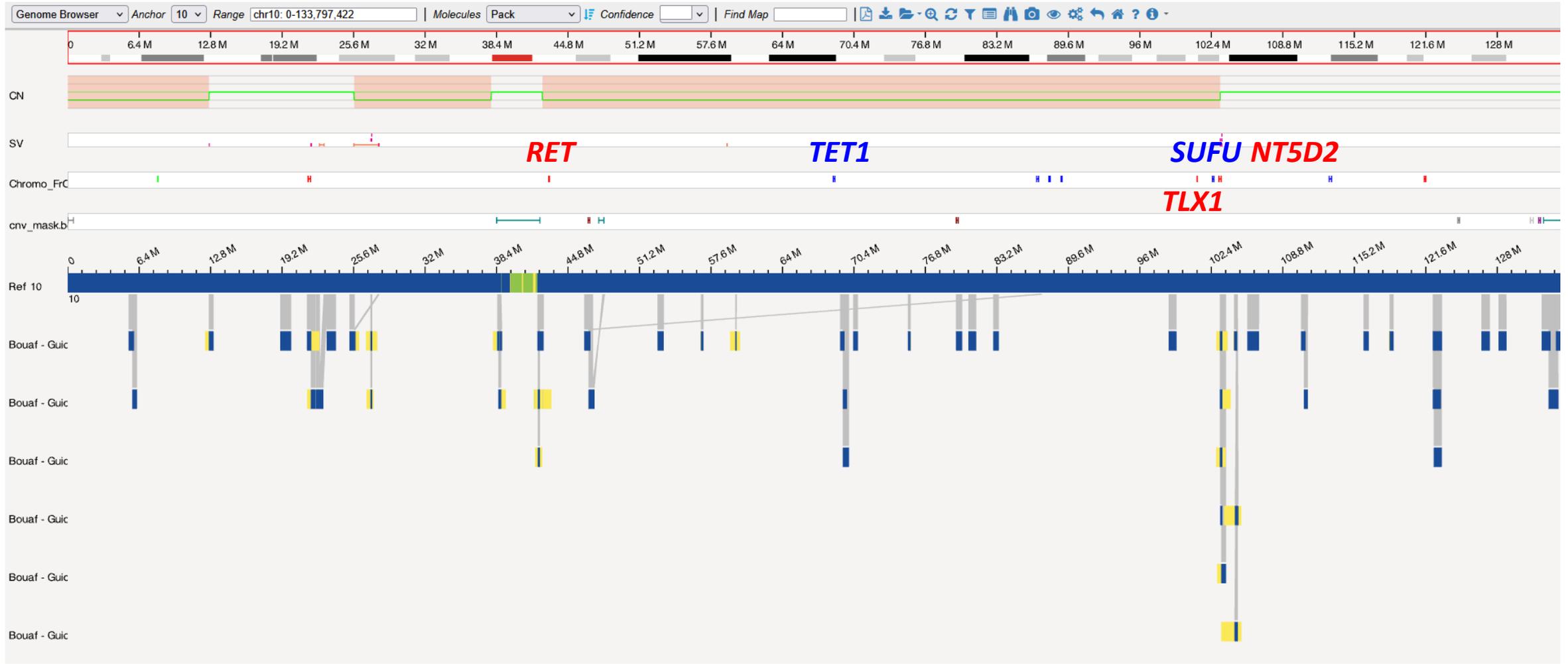
OCM

Type	RefconfigID1	RefconfigID2	RefStartPos...	RefEndPos ...	Size (bp)	Confide...	VAF
insertion	3	3	147 176 776	147 188 128	2 809	0,99	0,600
insertion	3	3	113 174 917	113 175 389	17 153	0,99	0,440
deletion	3	3	16 976 706	16 992 117	4 689	0,95	0,530
deletion	3	3	95 035 939	98 784 047	3 744 678	0,79	0,440
translocation_i...	3	13	12 644 364	28 889 845	-1	0,99	0,450
translocation_i...	3	13	49 293 716	25 723 253	-1	0,99	0,430
translocation_i...	3	10	50 334 098	103 347 007	-1	0,70	0,630
translocation_i...	3	12	50 225 777	9 861 501	-1	0,89	0,670
translocation_i...	3	5	84 615 999	38 939 881	-1	0,99	0,590
intrachr_fusion	3	3	86 925 264	118 421 112	-1	0,97	0,360
intrachr_fusion	3	3	87 264 109	93 727 966	-1	0,83	0,530
translocation_i...	3	5	118 256 796	39 277 619	-1	0,99	0,380
translocation_i...	3	10	50 334 098	103 347 007	-1	0,81	0,630
translocation_i...	3	10	50 334 098	103 347 007	-1	0,99	0,630
translocation_i...	3	12	50 225 777	9 861 501	-1	0,91	0,670
translocation_i...	3	12	50 225 777	9 861 501	-1	0,95	0,670
translocation_i...	3	12	14 980 476	126 389 241	-1	0,99	0,500
translocation_i...	3	12	14 980 476	126 389 241	-1	0,99	0,500

OGM

RefId	Start (bp)	End (bp)	Size (bp)	Type	Fractional Copy Nu...	Copy Nu...	Confidence	VAF
3	12 604 415	14 980 476	2 376 062	loss	1,031	1	1,00	0,485
3	49 293 716	84 605 876	35 312 161	loss	1,022	1	1,00	0,489
3	84 613 347	86 938 375	2 325 029	gain	2,937	3	1,00	0,469
3	87 264 109	90 375 086	3 110 978	loss	1,000	1	1,00	0,500
3	95 007 676	98 777 193	3 769 518	loss	1,002	1	1,00	0,499

OGM

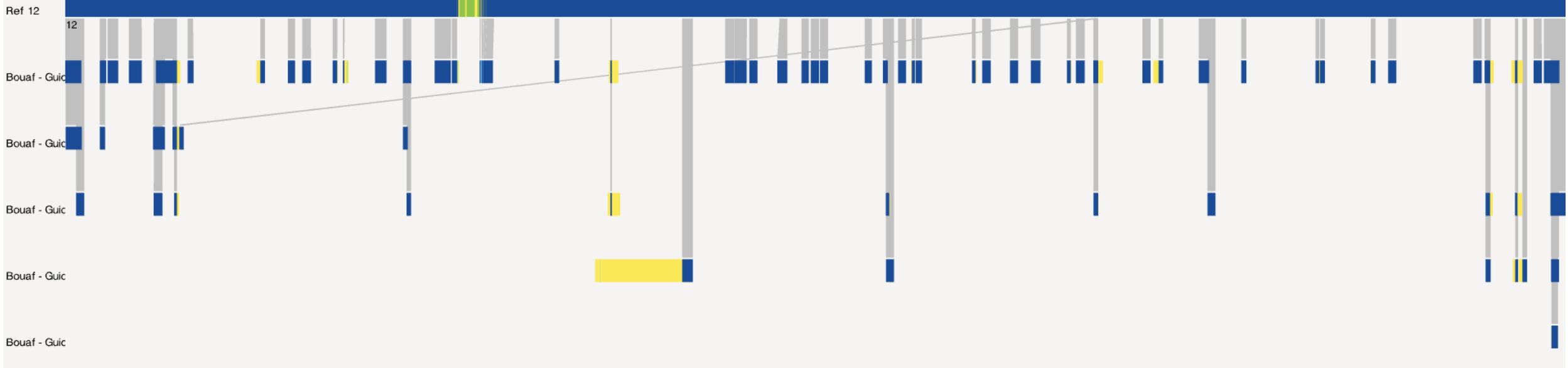
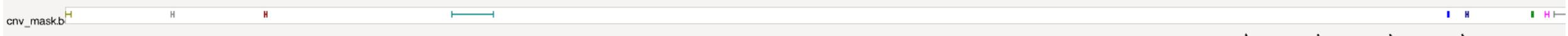
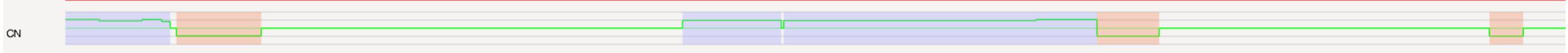


OGM

Type	RefcontigID1	RefcontigID2	RefStartPos...	RefEndPos ...	Size (bp)	Confide...	VAF
deletion	10	10	22 539 507	22 960 629	416 743	0,98	0,450
deletion	10	10	25 630 248	27 807 260	2 158 916	0,79	0,470
deletion	10	10	59 035 596	59 039 728	2 267	0,82	1,000
translocation_i...	10	3	103 347 007	50 334 098	-1	0,70	0,630
translocation_i...	10	4	21 817 566	91 344 129	-1	0,99	0,440
translocation_i...	10	13	21 776 362	102 312 284	-1	0,99	0,490
translocation_i...	10	12	27 227 344	128 807 858	-1	0,55	0,470
translocation_i...	10	12	27 227 344	128 807 858	-1	0,68	0,470
translocation_i...	10	12	103 210 928	91 602 925	-1	0,98	0,570
translocation_i...	10	3	103 347 007	50 334 098	-1	0,81	0,630
translocation_i...	10	3	103 347 007	50 334 098	-1	0,99	0,630
translocation_i...	10	12	103 210 928	91 602 925	-1	0,98	0,570
translocation_i...	10	13	27 157 788	19 464 724	-1	0,06	0,460
translocation_i...	10	13	27 883 233	112 972 062	-1	0,93	0,460
translocation_i...	10	18	12 678 213	22 518 361	-1	0,99	0,430
translocation_i...	10	18	103 342 626	22 977 796	-1	0,99	0,380

OGM

RefId	Start (bp)	End (bp)	Size (bp)	Type	Fractional Copy Nu...	Copy Nu...	Confidence	VAF
10	18 514	12 657 543	12 639 030	loss	1,033	1	1,00	0,484
10	25 647 798	37 918 235	12 270 438	loss	1,030	1	1,00	0,485
10	42 505 001	103 198 284	60 693 284	loss	1,025	1	1,00	0,487

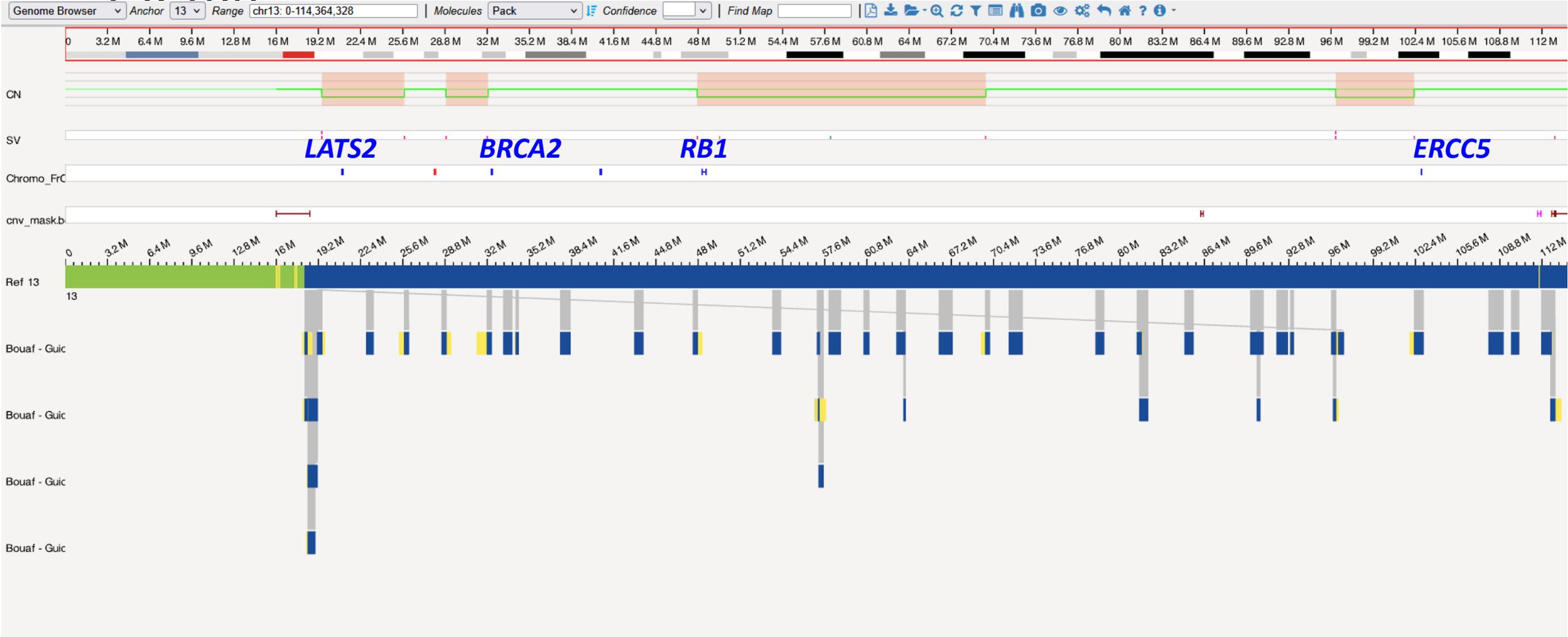


Type	RefcontigID1	RefcontigID2	RefStartPos...	RefEndPos ...	Size (bp)	Confide...	VAF
<i>insertion</i>	12	12	6 421 072	6 423 443	7 638	0,96	0,330
<i>insertion</i>	12	12	21 412 692	21 413 179	23 820	0,98	0,390
<i>deletion</i>	12	12	36 989 490	37 133 651	93 135	0,99	1,000
<i>deletion</i>	12	12	67 328 329	67 344 099	5 552	0,93	0,290
<i>translocation_i...</i>	12	3	9 861 501	50 225 777	-1	0,89	0,670
<i>translocation_i...</i>	12	10	128 807 858	27 227 344	-1	0,55	0,470
<i>translocation_i...</i>	12	10	128 807 858	27 227 344	-1	0,68	0,470
<i>translocation_i...</i>	12	10	91 602 925	103 210 928	-1	0,98	0,570
<i>translocation_i...</i>	12	3	9 861 501	50 225 777	-1	0,91	0,670
<i>translocation_i...</i>	12	3	9 861 501	50 225 777	-1	0,95	0,670
<i>translocation_i...</i>	12	18	17 351 356	26 374 385	-1	0,96	0,440
<i>translocation_i...</i>	12	10	91 602 925	103 210 928	-1	0,98	0,570
<i>translocation_i...</i>	12	20	97 072 405	3 107 871	-1	0,93	0,490
<i>translocation_i...</i>	12	3	126 389 241	14 980 476	-1	0,99	0,500
<i>translocation_i...</i>	12	3	126 389 241	14 980 476	-1	0,99	0,500
<i>translocation_i...</i>	12	13	128 694 113	96 354 989	-1	0,87	0,450
<i>translocation_i...</i>	12	13	129 345 461	47 939 833	-1	0,93	0,440
<i>translocation_i...</i>	12	13	128 712 870	96 354 989	-1	0,96	0,450

OGM

12	14 568	3 026 969	3 012 402	gain	3,086	3	1,00	0,543
12	3 030 268	6 804 654	3 774 387	gain	2,883	3	1,00	0,441
12	6 808 792	8 555 525	1 746 734	gain	3,076	3	1,00	0,538
12	8 557 345	9 313 494	756 150	gain	2,827	3	1,00	0,413
12	9 861 501	17 390 827	7 529 327	loss	1,044	1	1,00	0,478
12	54 781 001	63 530 226	8 749 226	gain	2,965	3	1,00	0,483
12	63 752 357	86 160 784	22 408 428	gain	2,938	3	1,00	0,469
12	86 162 372	91 549 322	5 386 951	gain	3,071	3	1,00	0,535
12	91 551 121	97 072 405	5 521 285	loss	1,018	1	1,00	0,491
12	126 381 363	129 371 981	2 990 619	loss	1,017	1	1,00	0,492

OGM



OGM

Type	RefcontigID1	RefcontigID2	RefStartPos...	RefEndPos ...	Size (bp)	Confide...	VAF
<i>insertion</i>	13	13	58 035 491	58 035 973	27 339	0,98	0,950
<i>deletion</i>	13	13	49 615 061	49 630 844	2 170	0,82	1,000
<i>translocation_i...</i>	13	3	28 889 845	12 644 364	-1	0,99	0,450
<i>translocation_i...</i>	13	3	25 723 253	49 293 716	-1	0,99	0,430
<i>translocation_i...</i>	13	4	32 005 312	87 089 531	-1	0,99	0,470
<i>translocation_i...</i>	13	10	102 312 284	21 776 362	-1	0,99	0,490
<i>translocation_i...</i>	13	12	96 354 989	128 694 113	-1	0,87	0,450
<i>intrachr_fusion</i>	13	13	19 464 724	96 354 989	-1	0,05	0,340
<i>translocation_i...</i>	13	10	19 464 724	27 157 788	-1	0,06	0,460
<i>translocation_i...</i>	13	12	47 939 833	129 345 461	-1	0,93	0,440
<i>translocation_i...</i>	13	12	96 354 989	128 712 870	-1	0,96	0,450
<i>translocation_i...</i>	13	10	112 972 062	27 883 233	-1	0,93	0,460
<i>translocation_i...</i>	13	18	69 793 267	23 578 751	-1	0,95	0,450

OGM

Refid	Start (bp)	End (bp)	Size (bp)	Type	Fractional Copy Nu...	Copy Nu...	Confidence	VAF
13	19 456 455	25 712 851	6 256 397	loss	1,042	1	1,00	0,479
13	28 873 996	32 072 597	3 198 602	loss	1,058	1	1,00	0,471
13	47 926 760	69 824 871	21 898 112	loss	1,044	1	1,00	0,478
13	96 349 351	102 299 359	5 950 009	loss	0,986	1	1,00	0,507

OGM



OGM

Type	RelContigID1	RelContigID2	RelStartPos...	RelEndPos...	Size (bp)	Confide...	VAI
<i>deletion</i>	17	17	45 283 546	46 141 455	851 973	0,79	0,280
<i>deletion</i>	17	17	45 283 546	46 141 455	851 955	0,79	0,280
<i>deletion</i>	17	17	75 417 746	75 454 528	13 538	0,91	0,280
<i>translocation_i...</i>	17	8	8 338 672	38 964 942	-1	0,99	0,670
<i>translocation_i...</i>	17	8	8 338 672	38 964 942	-1	0,99	0,670
<i>intrachr_fusion</i>	17	17	9 833 650	20 853 187	-1	0,84	0,490

Refid	Start (bp)	End (bp)	Size (bp)	Type	Fractional Copy Nu...	Copy Nu...	Confidence	VAF
17	1 315 080	8 295 051	6 979 972	loss	1,087	1	1,00	0,457
17	8 304 000	9 807 973	1 503 974	gain	2,927	3	1,00	0,464
17	9 813 180	11 229 675	1 416 496	loss	1,083	1	1,00	0,458
17	11 715 697	16 723 925	5 008 229	loss	1,013	1	1,00	0,493
17	16 727 463	19 497 284	2 769 822	gain	3,016	3	1,00	0,508
17	19 505 676	20 853 187	1 347 512	gain	2,867	3	1,00	0,433
17	20 855 789	22 079 438	1 223 650	gain	5,154	5	1,00	1,577
17	22 080 575	22 732 567	651 993	gain	3,049	3	1,00	0,525

Merci de votre attention