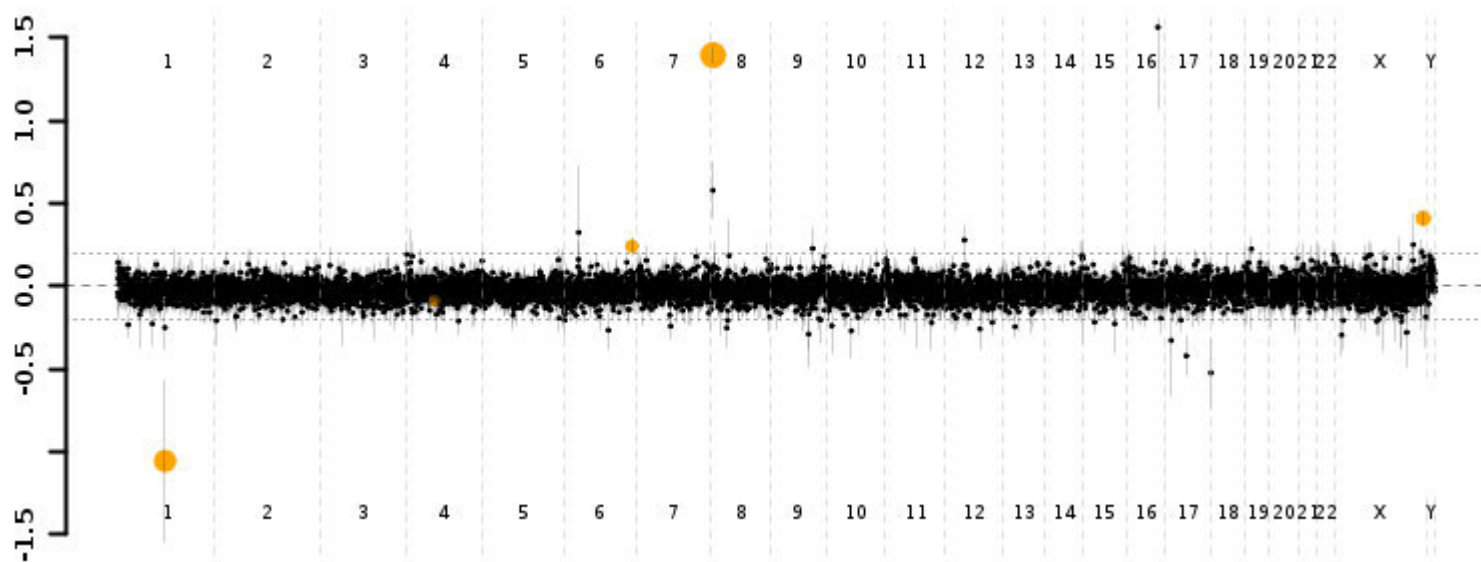


# Normal result on direct amnio and whole genome amplification



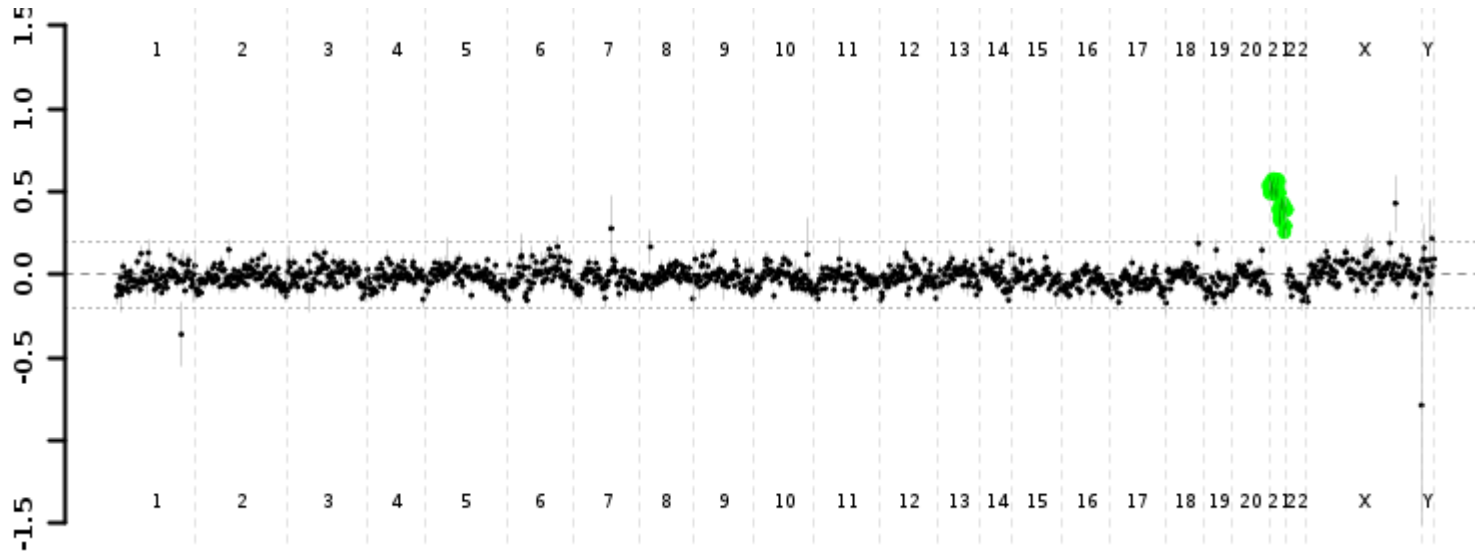
**Red = loss/deletion**

**Green = gain/duplication**

**Orange = internal control**

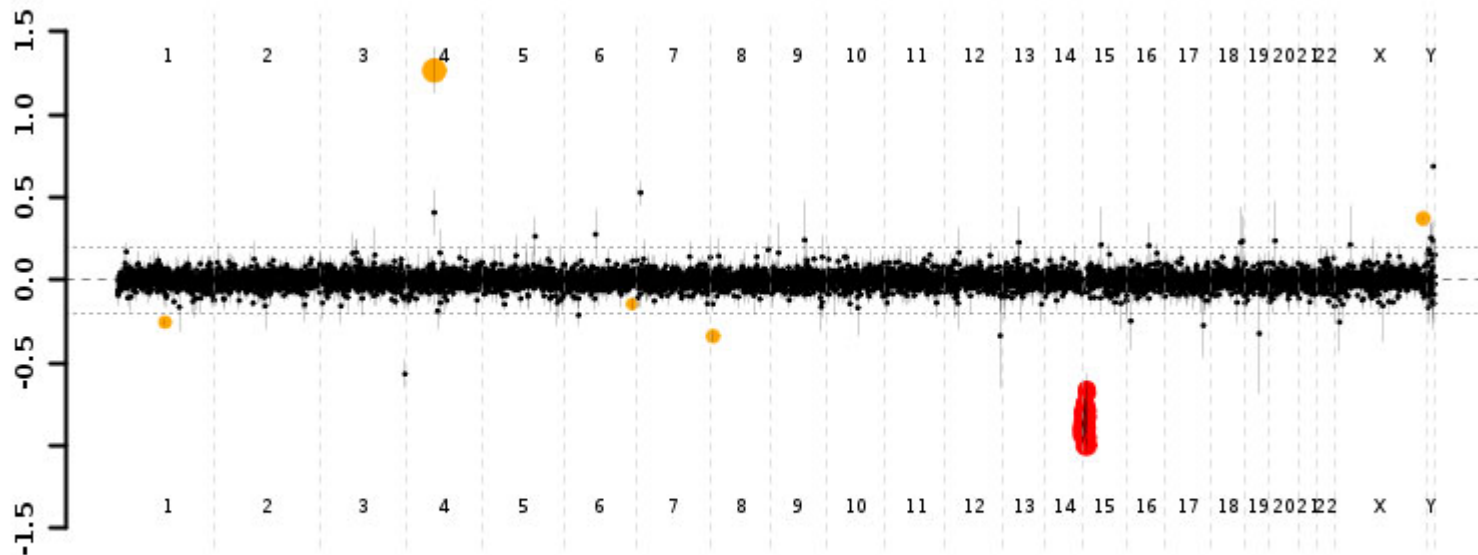
# Abnormal CMA Images

# Trisomy 21



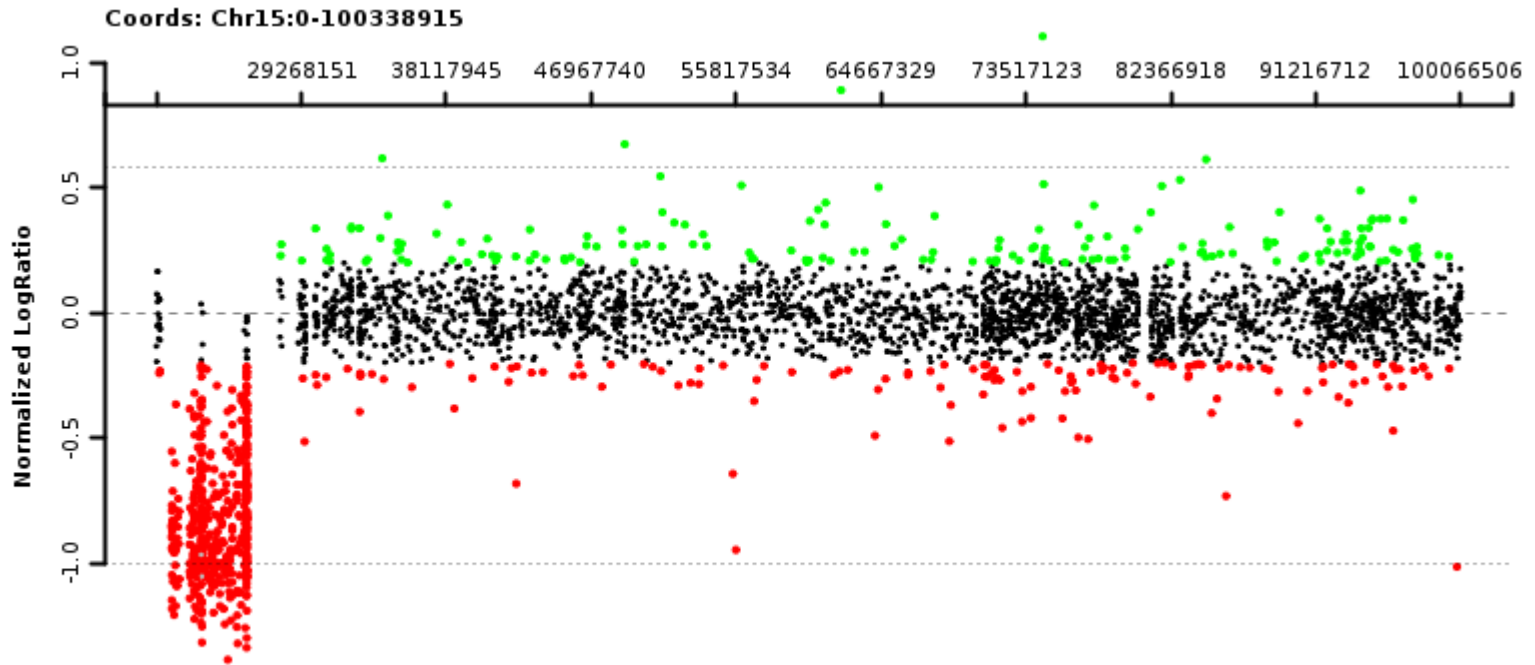
Chr	Min. Start	Min. Stop	RefSeq Genes (max. 50)	Value	Status	-
	Max. Start	Max. Stop				
	Min. Size	Max. Size				
21:q11.2-q22.3	14,445,069	46,913,787	LIPI, RBM11, HSPA13, SAMSN1, NRIP1, USP25, C21orf34, CXADR, BTG3, C21orf91, CHODL, PRSS7, NCAM2, MRPL39, JAM2, ATP5J, GABPA, APP, CYR1, ADAMTS1, ADAMTS5, N6AMT1, ZNF294, RWDD2B, USP16, CCT8, C21orf7, BACH1, GRIK1, CLDN17, CLDN8, KRTAP24-1, KRTAP25-1, KRTAP26-1, KRTAP27-1, KRTAP23-1, KRTAP13-2, KRTAP13-1, KRTAP13-3, KRTAP13-4, KRTAP15-1, KRTAP19-1, KRTAP19-2, KRTAP19-3, KRTAP19-4, KRTAP19-5, KRTAP19-6, KRTAP19-7, KRTAP6-3, KRTAP6-2	GAIN	ABNORMAL (POSITIVE FINDING)	Plot UCSC Similar Cases
	1	46,944,323				
	32.469	46.944				

# Prader-Willi/Angelman deletion



Chr	Min. Start	Min. Stop	RefSeq Genes	Value
	Max. Start	Max. Stop		
	Min. Size	Max. Size		
<a href="#">15:q11.2-q13.1</a>	21,365,890	25,950,338	<a href="#">MAGEL2</a> , <a href="#">NDN</a> , <a href="#">C15orf2</a> , <a href="#">SNRPN</a> , <a href="#">SNURF</a> , <a href="#">UBE3A</a> , <a href="#">ATP10A</a> , <a href="#">GABRB3</a> , <a href="#">GABRA5</a> , <a href="#">GABRG3</a> , <a href="#">OCA2</a>	LOSS
	20,642,827	27,938,509		
	4.584	7.296		

# Prader-Willi/Angelman deletion



# Prader-Willi/Angelman deletion

Coords: Chr15:20443316-28087557

