

Murine osteosarcoma model reproduces the complex genomic rearrangements and heterogeneity of human disease

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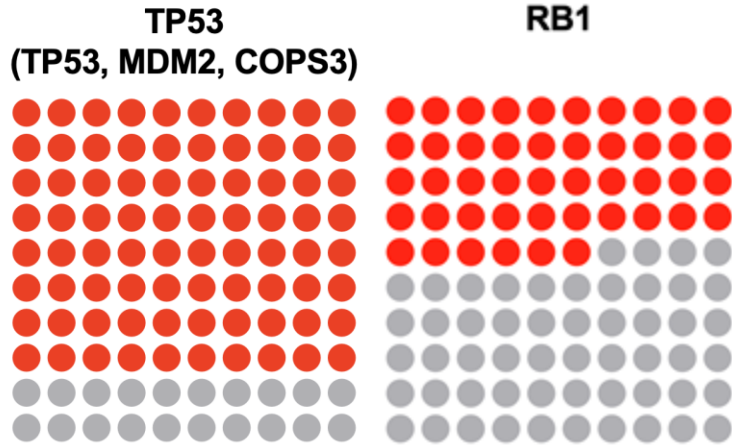


KOCH INSTITUTE
for Integrative Cancer Research at MIT

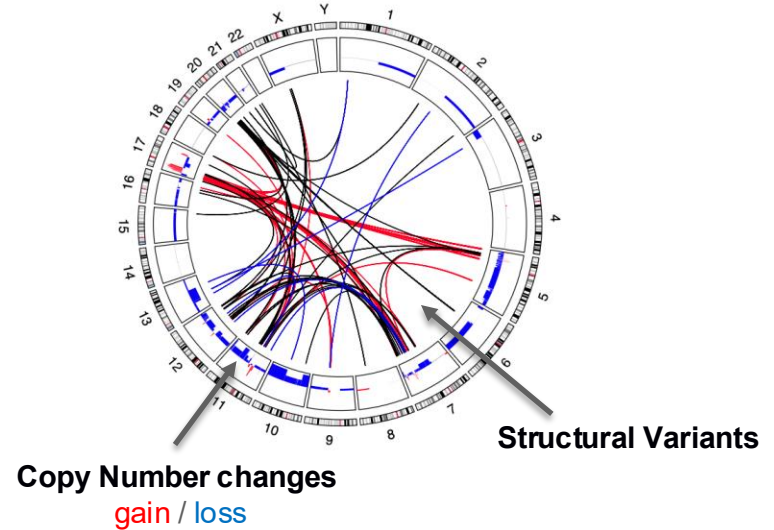


Genomic Hallmarks of Osteosarcoma

Tumor suppressor loss

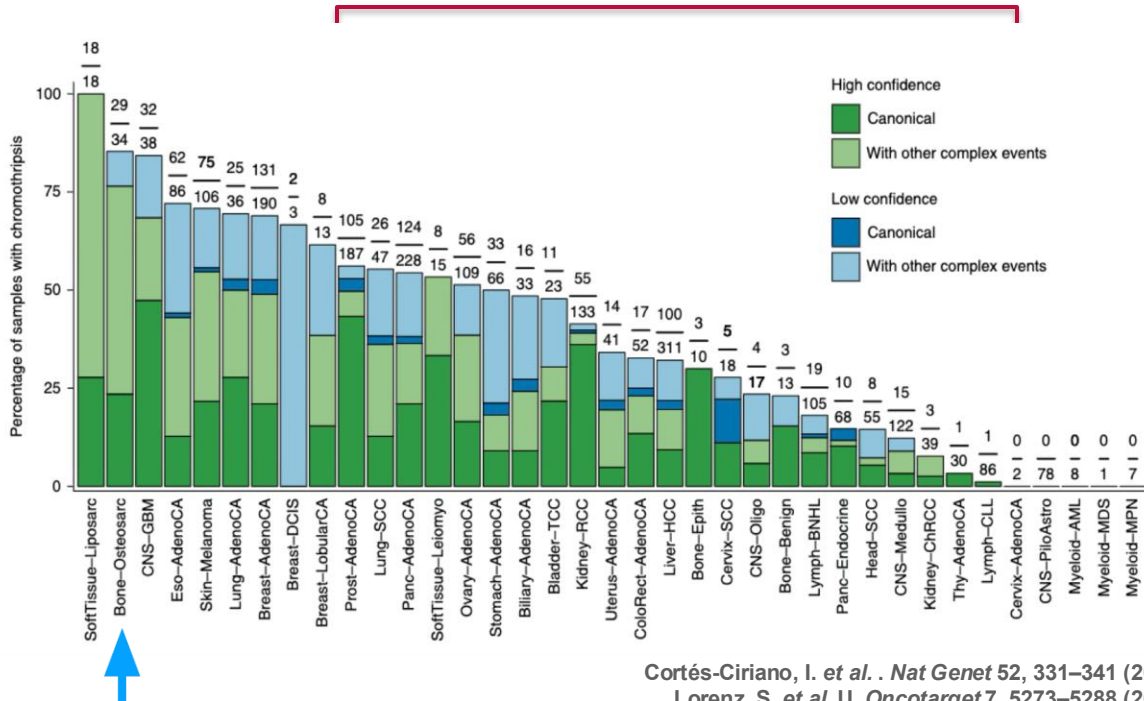
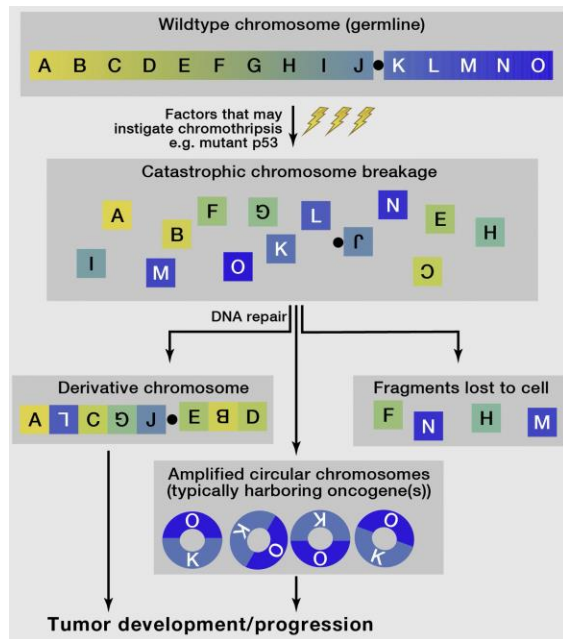


Highly rearranged genomes



Lorenz, S. et al. *U. Oncotarget* 7, 5273–5288 (2015).

Chromothripsis generates complex genomic rearrangements



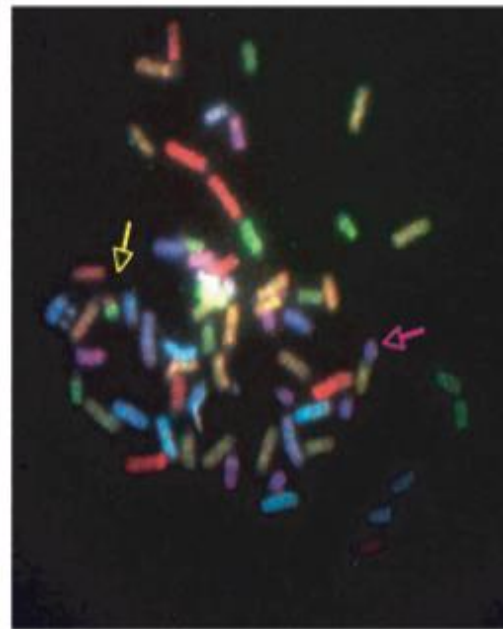
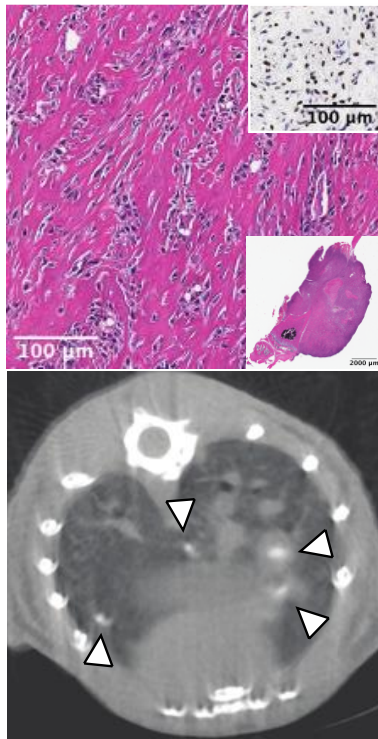
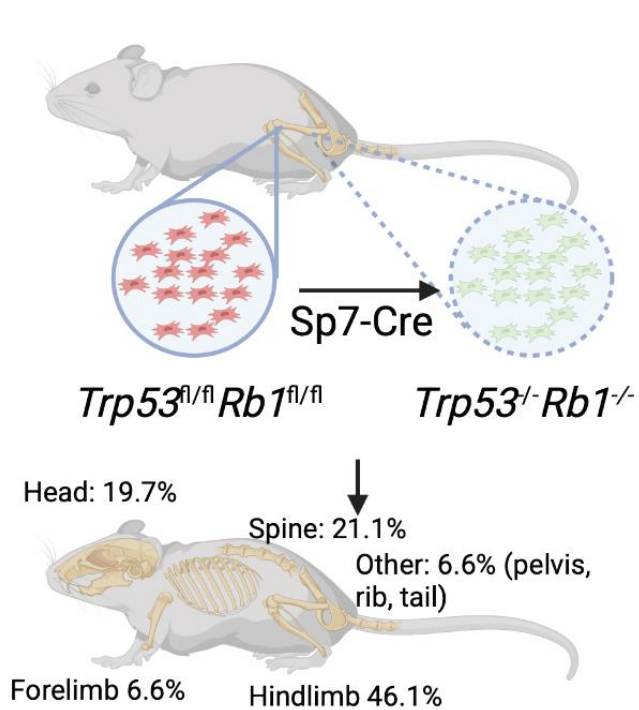
Cortés-Ciriano, I. et al. . *Nat Genet* 52, 331–341 (2020).

Lorenz, S. et al. *U. Oncotarget* 7, 5273–5288 (2015).

Korbel, J. O. & Campbell, P. J. *Cell* 152, 1226–1236 (2013)

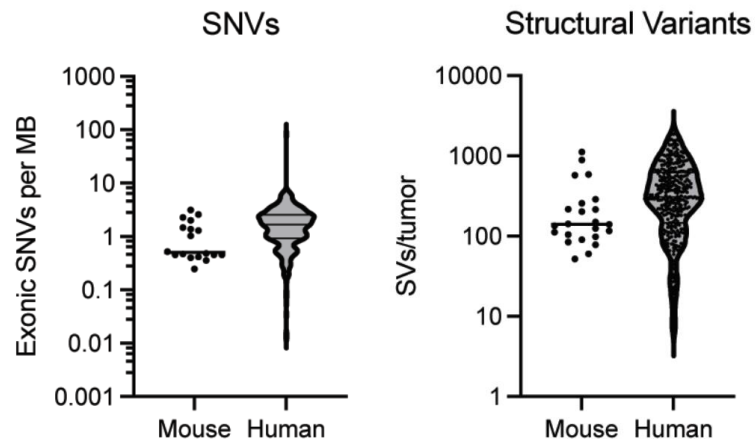
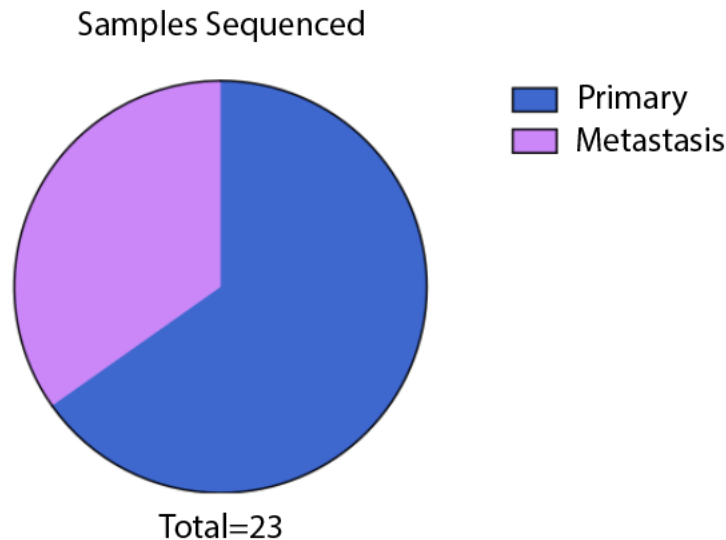


Murine Osteosarcoma reproduces key features of human disease



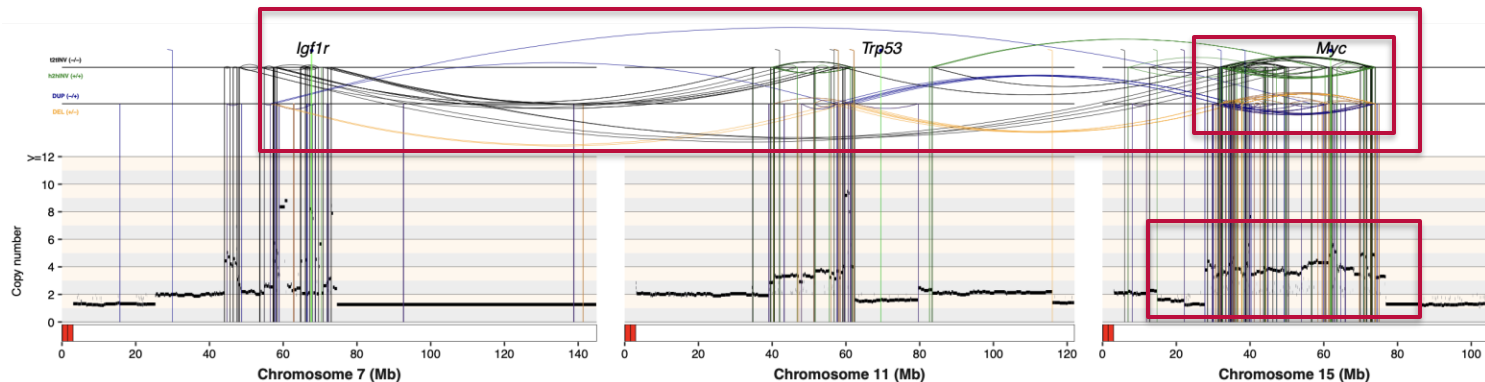
Walkley, C. R. ...Orkin, S *Gene Dev* 22, 1662–1676 (2008).

mOS bears a comparable single nucleotide variant and structural variant burden to human disease

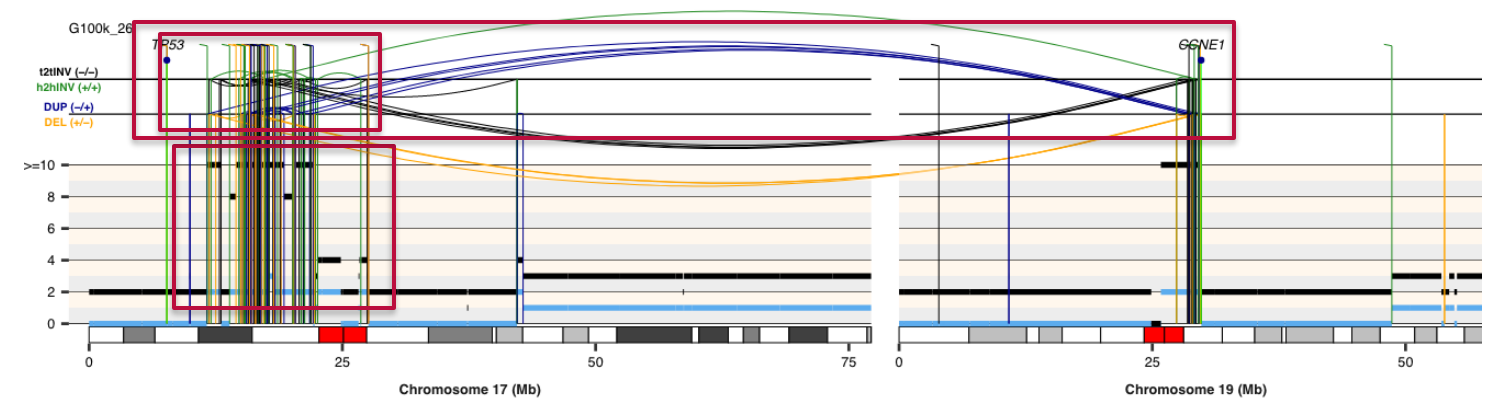


	mOS	Human (Valle-Inclan)
TMB (SNV/mb)	0.50 (0.25 - 1.61)	1.67 (0.93 - 2.54)
SVs (/tumor)	140 (98 - 256)	309 (146 - 621)

mOS recapitulates complexity of rearrangements found in human osteosarcoma



Mouse OS

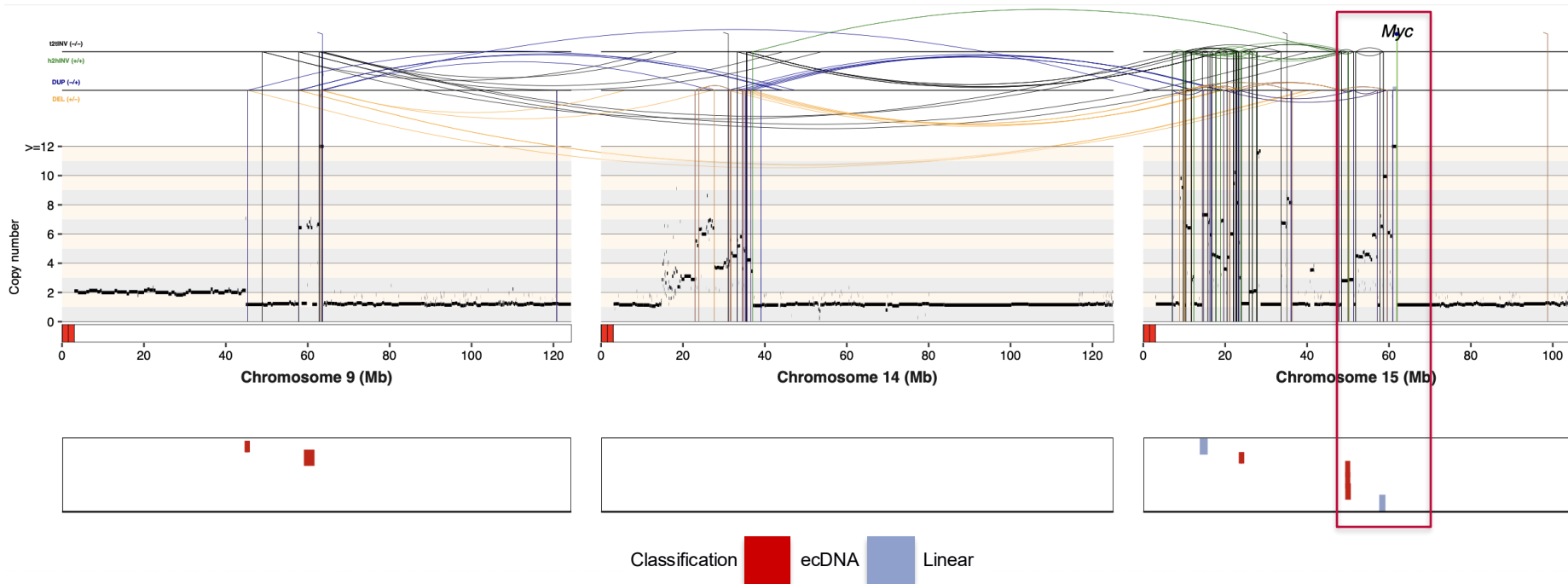


Human OS

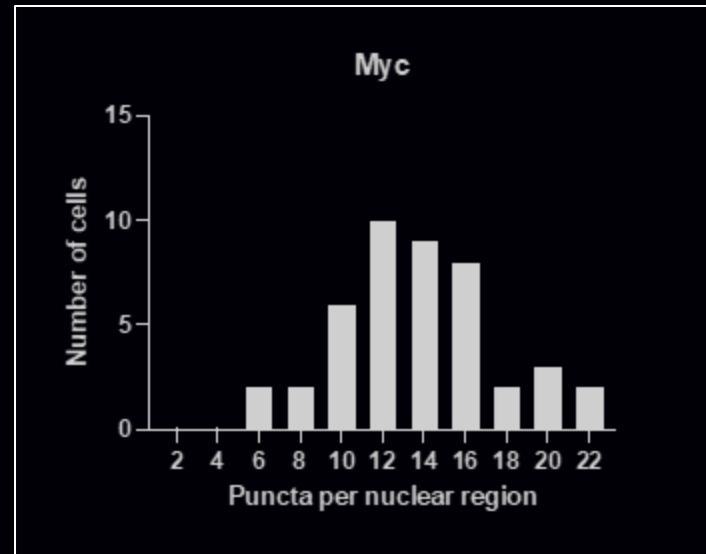
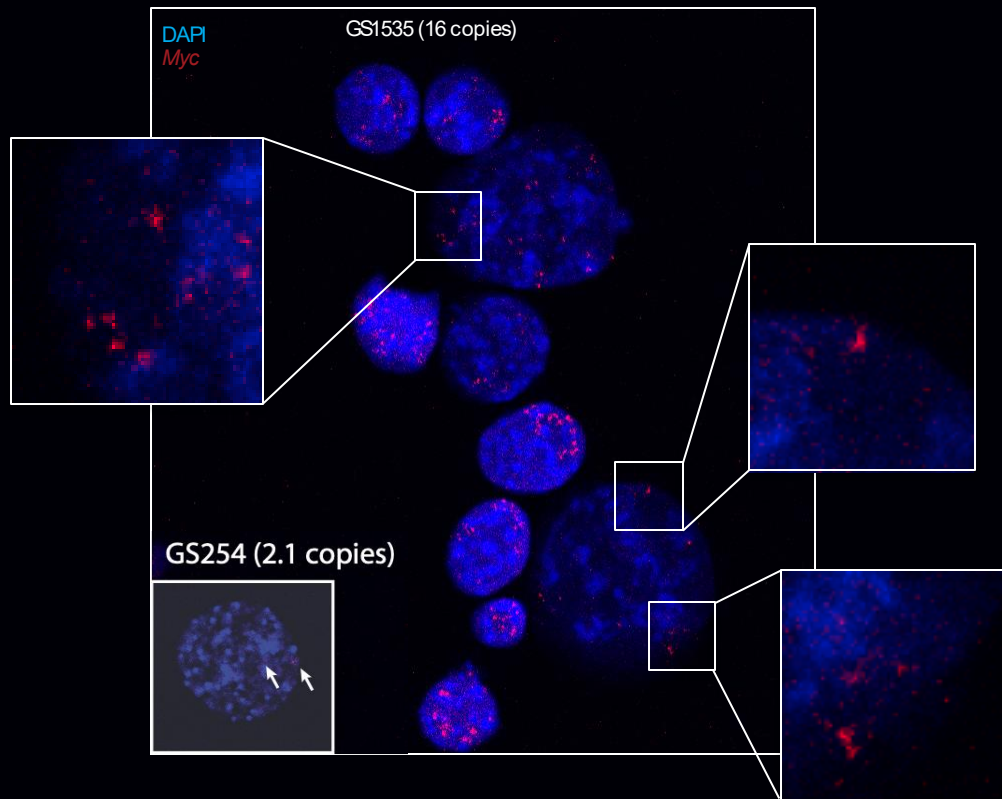
Ianthe Van Belzen



Complex genomic rearrangements can amplify oncogenes

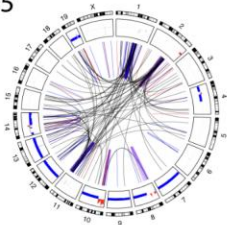


MYC is amplified in ecDNA

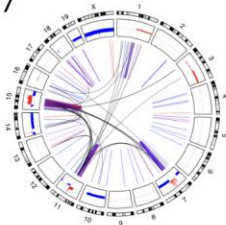


mOS generates a range of genomic complexity, including complex genomic rearrangements

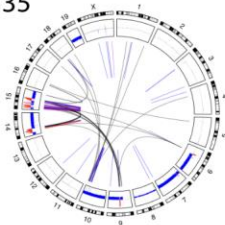
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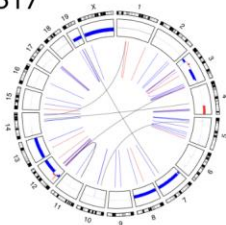
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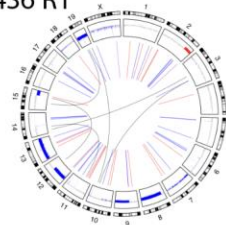
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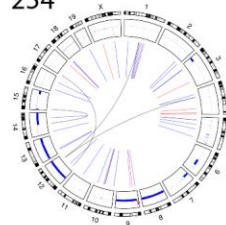
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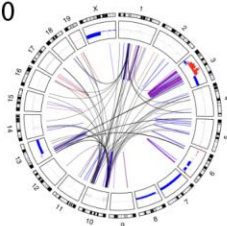
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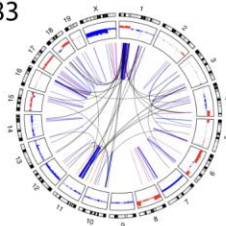
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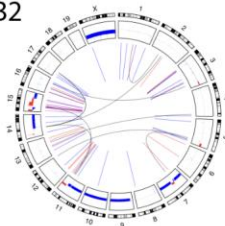
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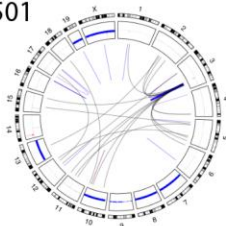
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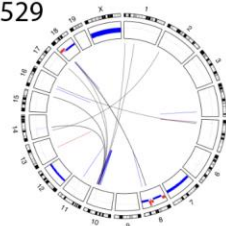
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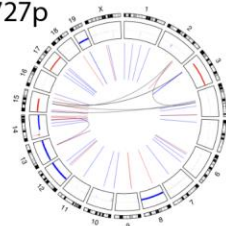
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1529



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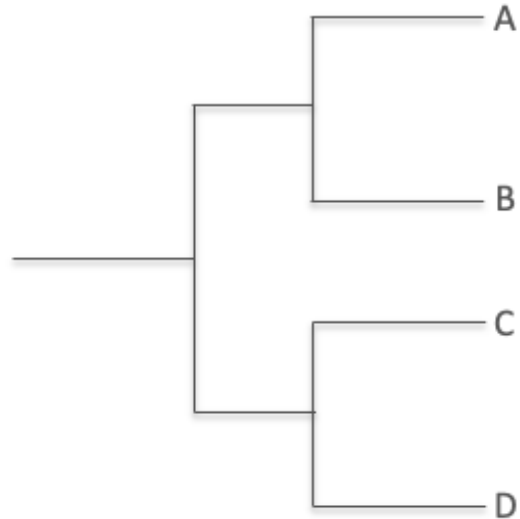
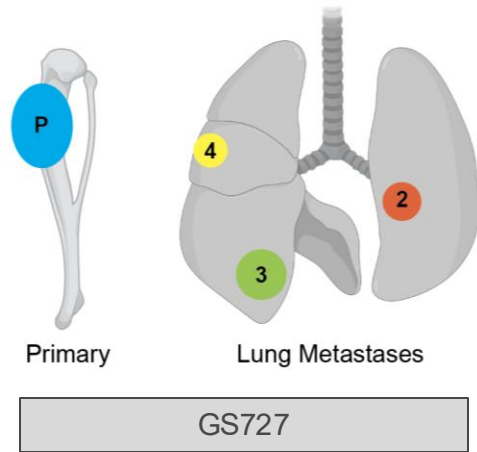


High genomic
complexity

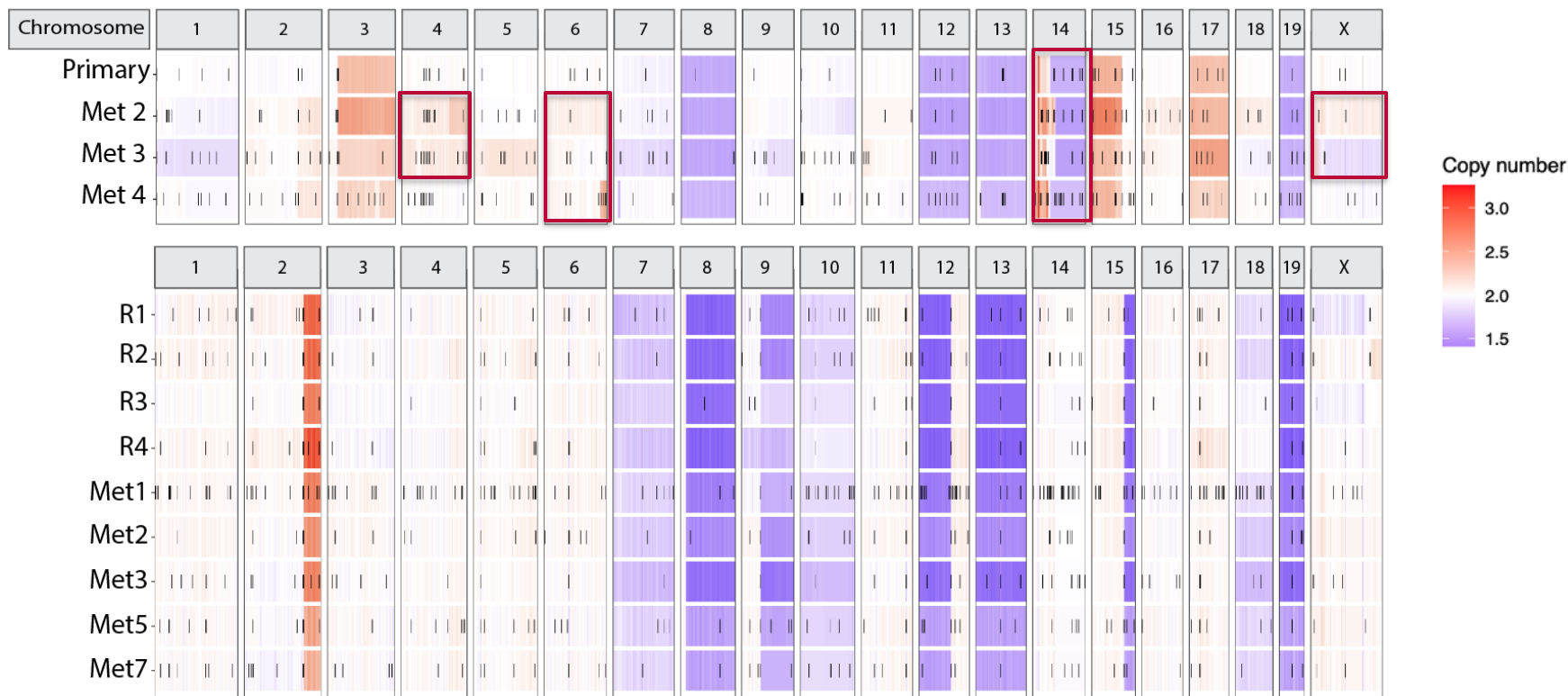
Low genomic
complexity



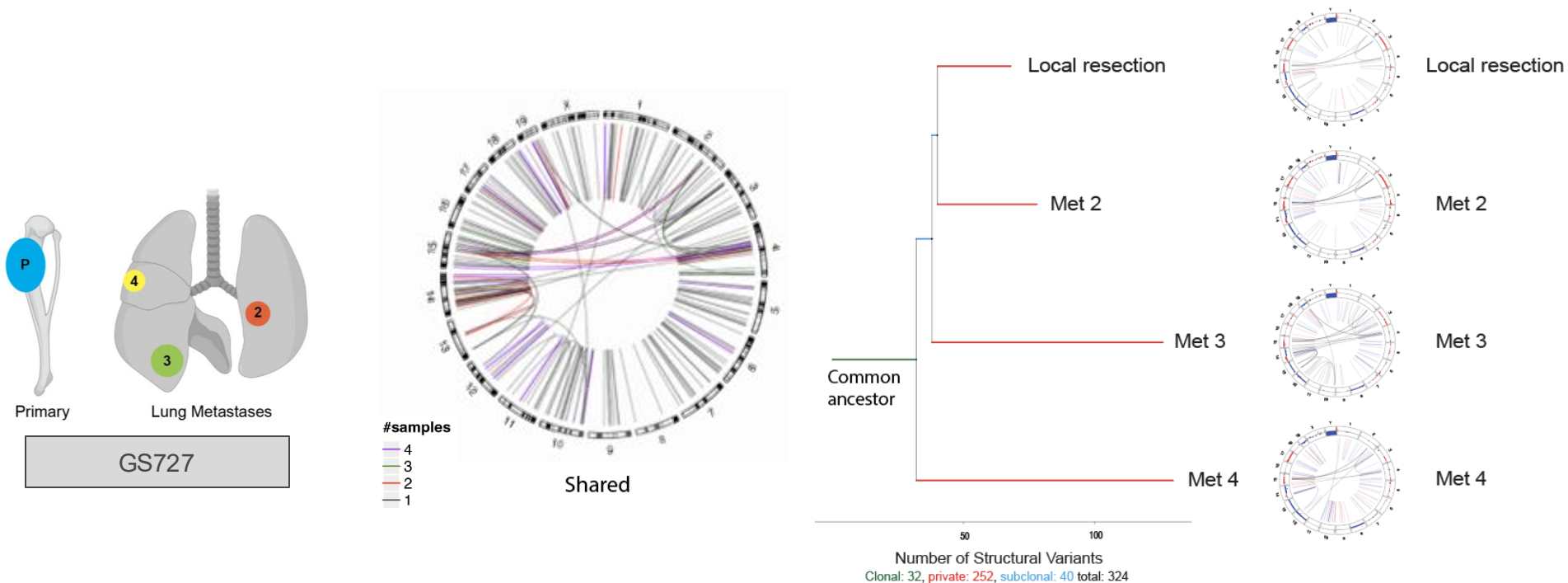
Multi-region sequencing reveals tumor evolution and heterogeneity



mOS maintains initial karyotype and displays ongoing evolution

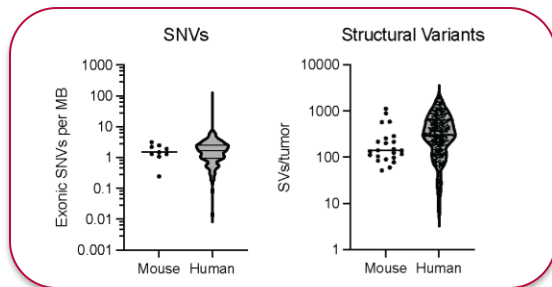


Metastatic murine osteosarcoma can undergo continuous structural rearrangement

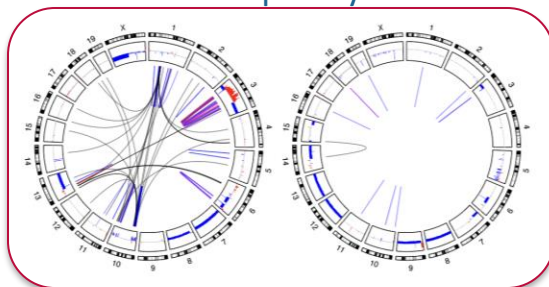


Conclusions from the model

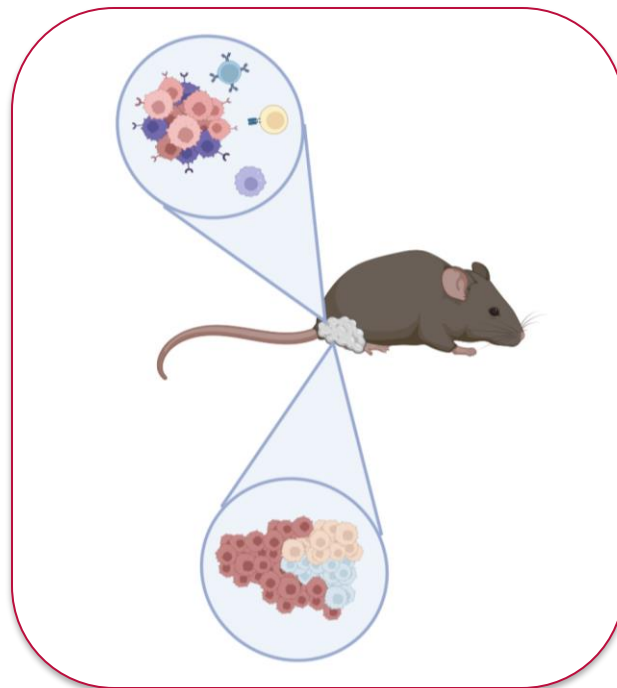
Similar TMB and SV burden to human OS



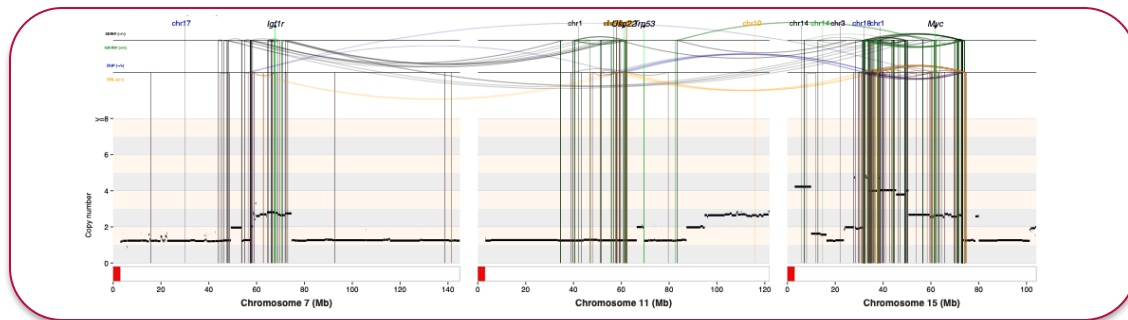
Generates a range of genomic complexity



Tool to study chromothripsis and immunogenomics



Mechanisms of genomic instability mirror the human disease



Acknowledgments

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Shalom Beyene

KI Histology Core

Kathy Cormier

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