The dark matter of the genome and blood pressure regulation – modeling non-coding genetic mechanisms in cellular models and rats

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RODENT MODEL RESOURCE

Shawn Kalloway (past)

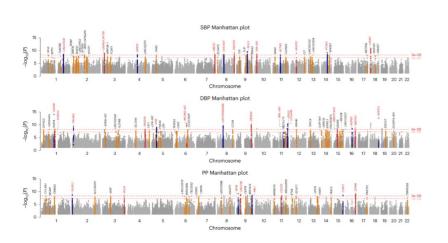
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Human BP SNPs -> rat orthology & human iPSC-derived cell types

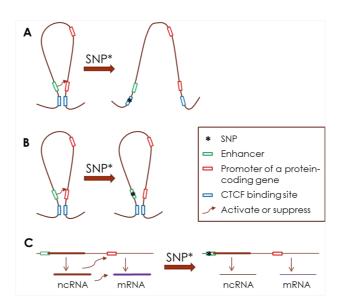
Overall hypothesis: Non-coding, non-transcribed SNPs must exert their effects on phenotypes by modifying expression of gene(s) in some tissue(s) to modify one or more physiological mechanisms relevant to the trait.

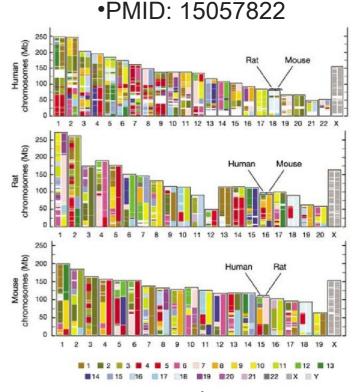
•PMCID: PMC11096100



- <1% missense or nonsense variants,
- >20% >10-kbp from nearest gene

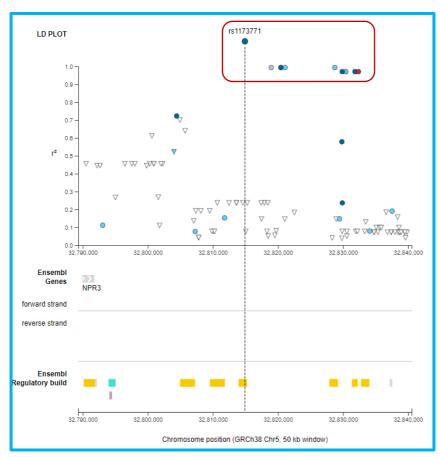
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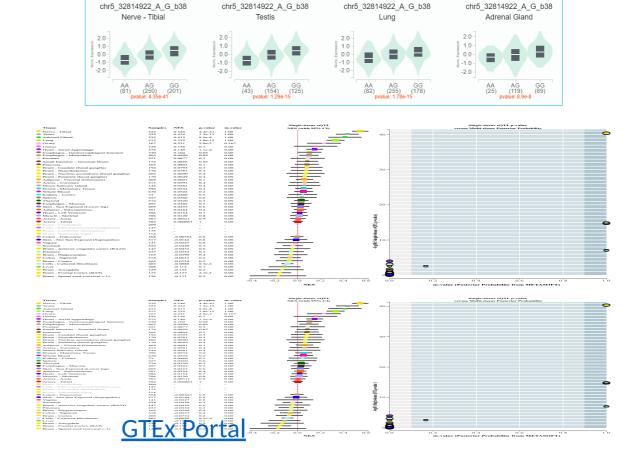




Synteny and sequencelevel conservation

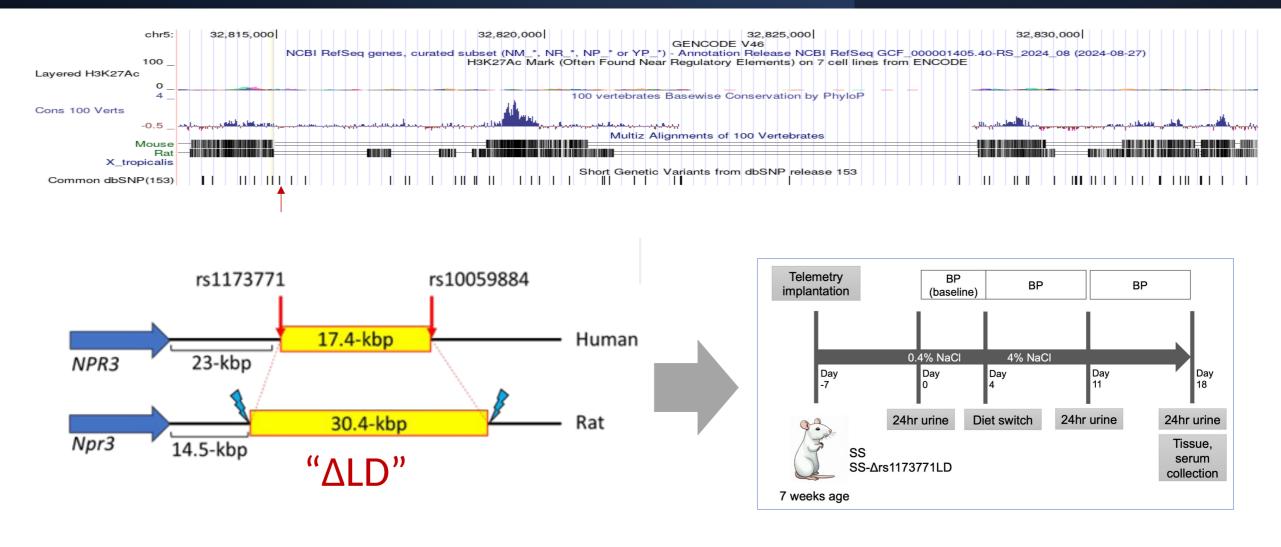
rs1173771 (rs771)



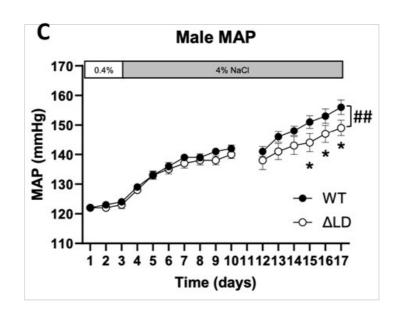


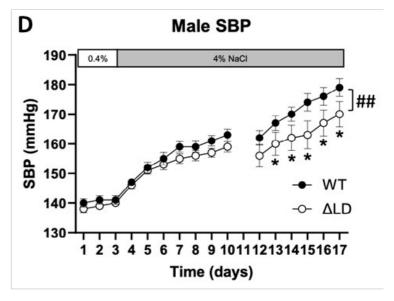
GWAS Catalog (ebi.ac.uk)

We deleted the entire homologous noncoding region in SS using CRISPR-Cas9

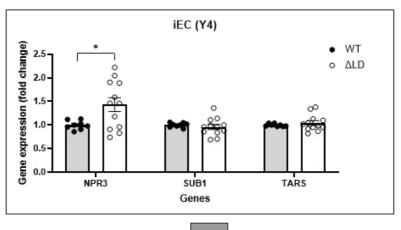


Systolic blood pressure was reduced in Δ LD male rats

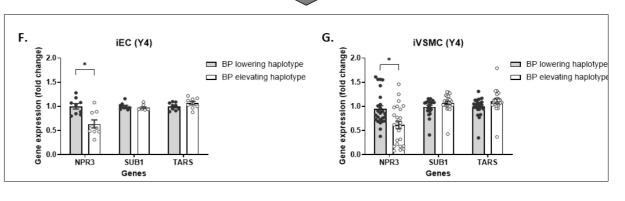




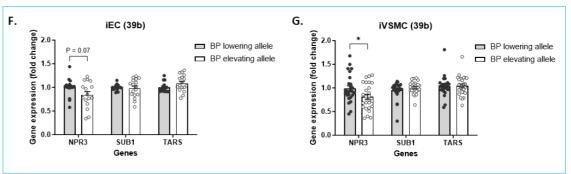
CRISPR-SpCas9 gene edited iPSC models reveal similar effects of the haplotype and single rs771 on Npr3



Deletion model



Haplotype reconstituted models



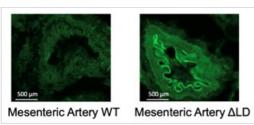
Single rs1173771 edited model

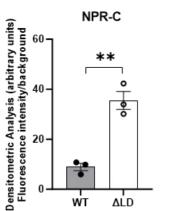
NPR3 encodes NPR-C, a multifunctional receptor

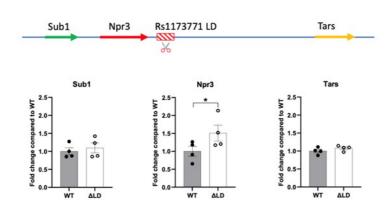
- In the vasculature, NPR-C binds C-type natriuretic peptide (CNP), mediates the effect of CNP on vascular function and structure, and plays an important role in preserving vascular homeostasis in vivo.
 - Moyes, et al. J Clin Invest. 2014; PMID: 25105365
 - Villar, et al. Cardiovasc Res. 2007; PMID: 17391657
- In the kidney, NPR-C facilitates the clearance of atrial, Btype, and C-type natriuretic peptides (ANP, BNP, CNP) from the circulation via endocytosis.
 - Maack, et al. Science, 1987; PMID: 2823385
 - Almeida, et al. Am J Physiol. 1989; PMID: 2537040

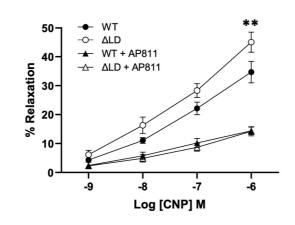
ΔLD has tissue-specific effects on Npr3 expression and function

Mesenteric Artery

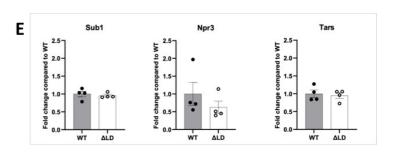


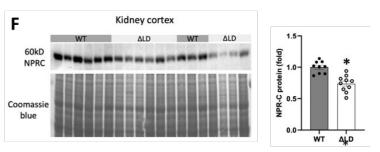


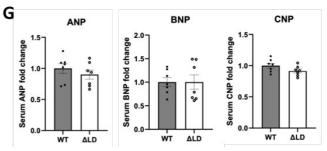




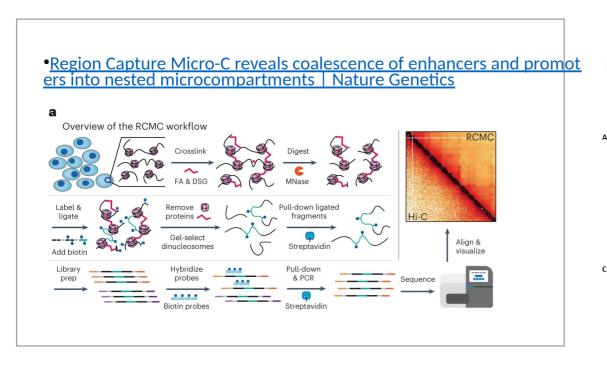
Kidney

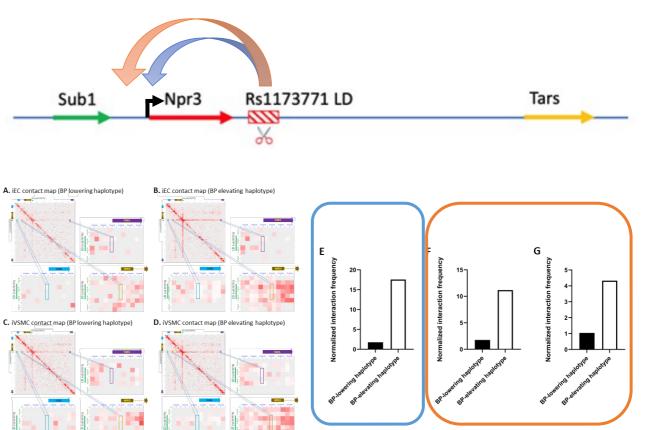






The BP elevating haplotype increases contact frequency between the LD region and the Npr3 promoter

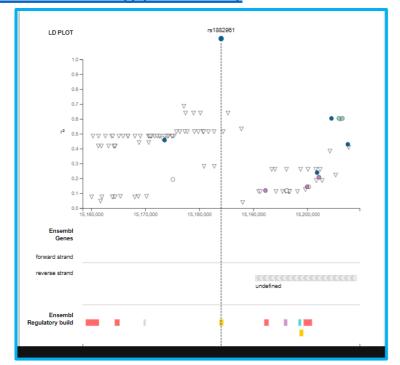




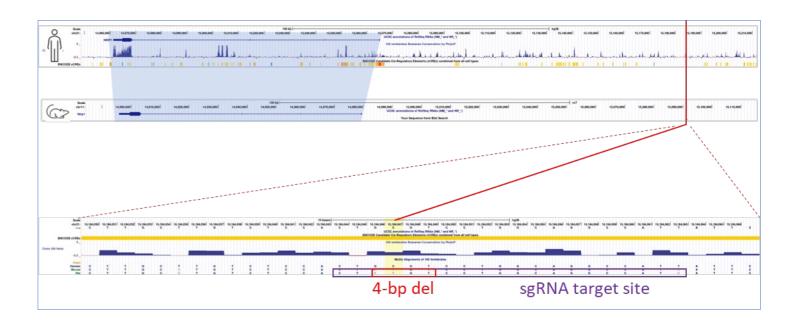
rs1882961 C->T (rs961)

riskAllele	pValue pValueAnnotation	riskFrequency	orValue	beta	ci	Mapped Genes	traitName	Traits	bkgTraits	accessionId	locations	pubmedId	author
							Systolic blood	systolic blood					
rs1882961-?	3.00E-13 -	NR	-	-	-	LINC02920,CYCSP42	pressure	pressure	-	GCST007087	21:15184047	30595370	Kichaev G

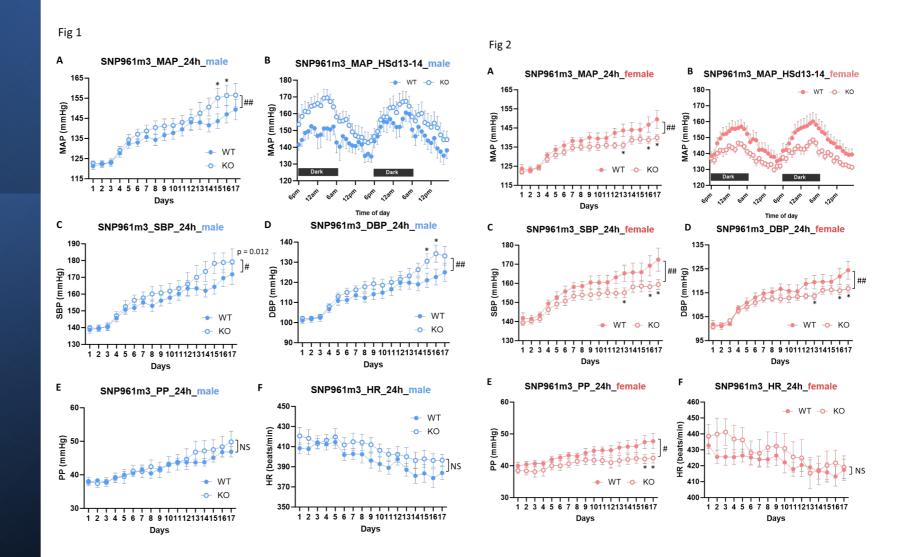
GWAS Catalog (ebi.ac.uk)



No evidence of eQTL, 120-kb away from nearest gene

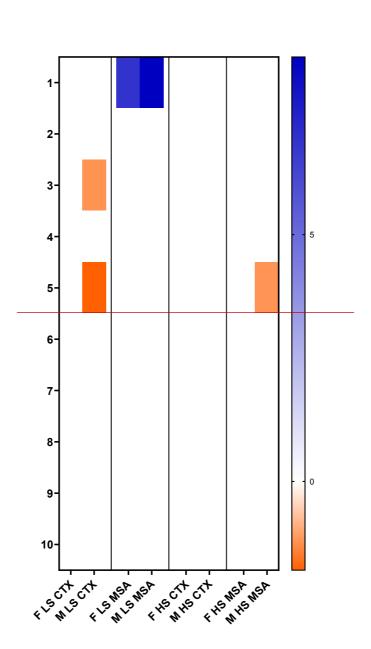


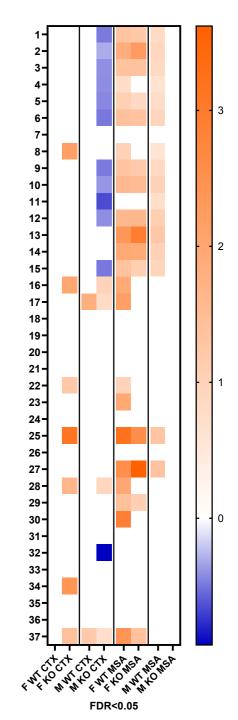
Editing this conserved region in SS rats results in sex-divergent effects on blood pressure traits



Effects on local genes (very preliminary data)

log2FC KO/WT, FDR<0.05





Overall conclusions

- The majority of loci (now >2,000) associated with blood pressure are non-coding and hundreds of functional SNP may be quite distant from the genes they regulate
- Human iPSCs can be engineered to harbor blood pressure elevating and lowering alleles and haplotypes then differentiated to study their effects on gene expression
- At least some human non-coding loci can be manipulated in animal models to provide functional evidence of their role in complex traits
- Unlike knockout models, each engineered SNP model will have unique tissue(s)-specific (and sex-specific!) effects on gene(s) expression and phenotypes, leading to complex hypotheses about their mechanisms

Thanks! Questions?

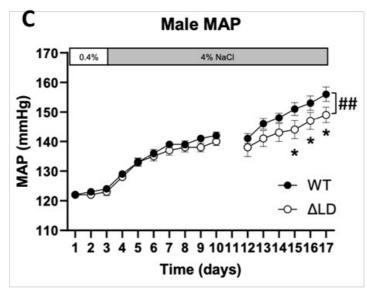


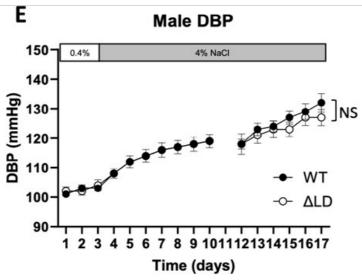
After all, aren't we all just fat rats, stuck in the manhole covers of life?

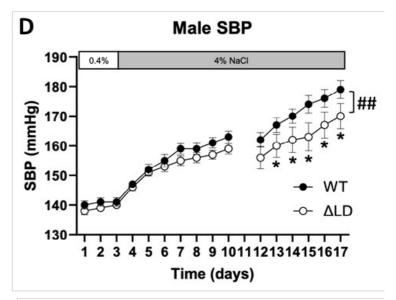


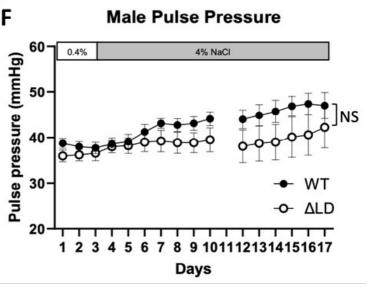
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Systolic blood pressure was reduced in ΔLD male rats

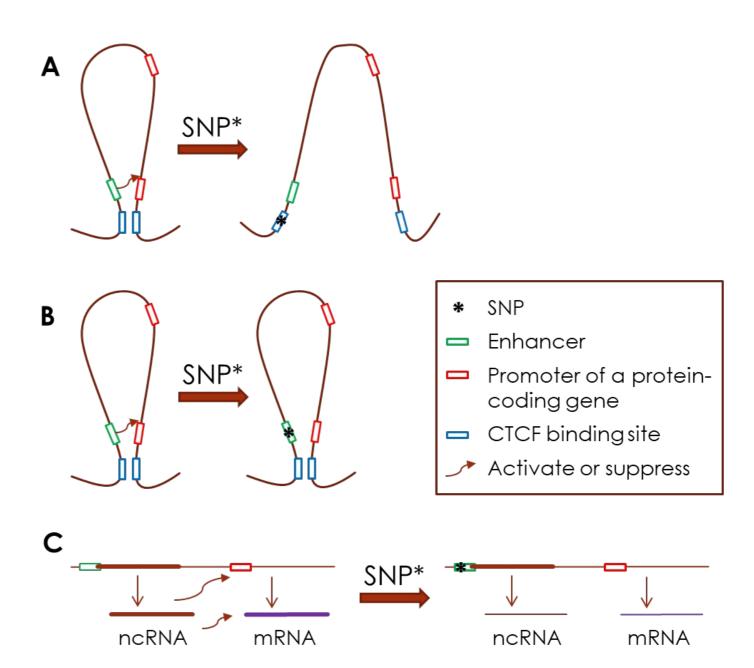








Proposed mechanisms by which non-coding SNPs could influence genes and blood pressure



<u>Lift Genome Annotations (ucsc.edu)</u>

Conservation n in rats extends to a ~30.4-kbp region

