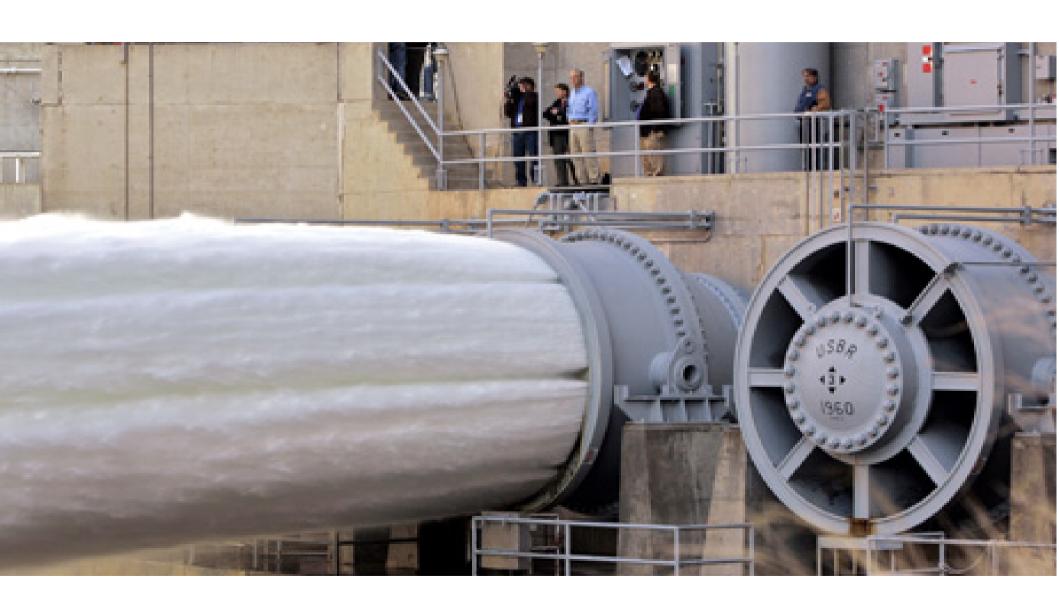


"data flood"







>1500

and so many more ...





>1500

and so many more ...

- * Metadata is critical
 - assay type
 - sample
 - processing methods





>1500

and so many more ...

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* Web display solution is nice

A lab's own data, Array/sequencing data sets Files amount to **1TB**





>1500

and so many more ...

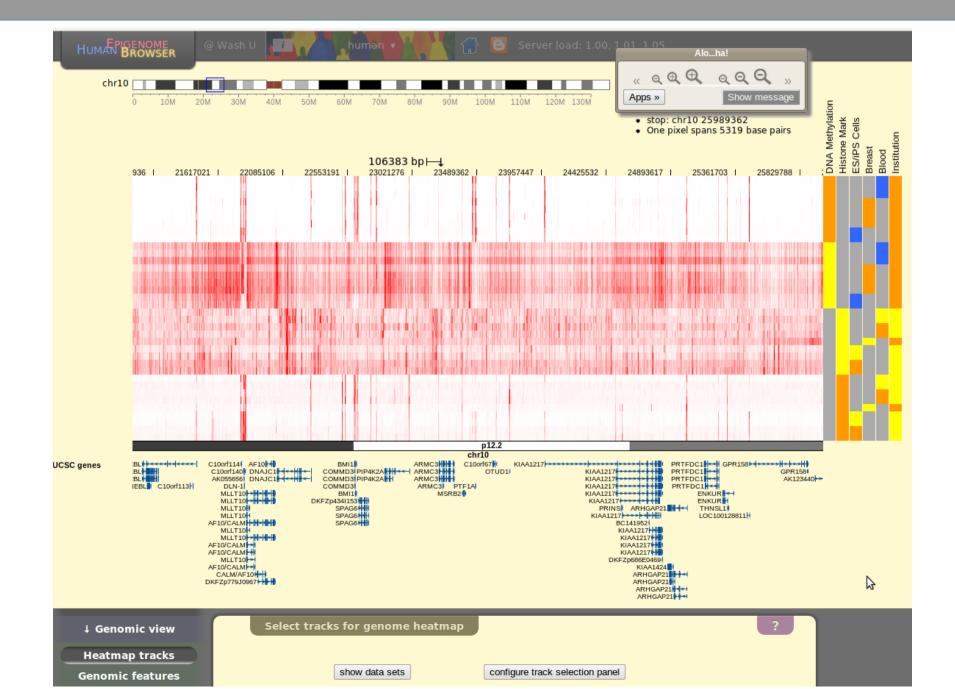
- * Metadata is critical
 - assay type
 - sample
 - processing methods

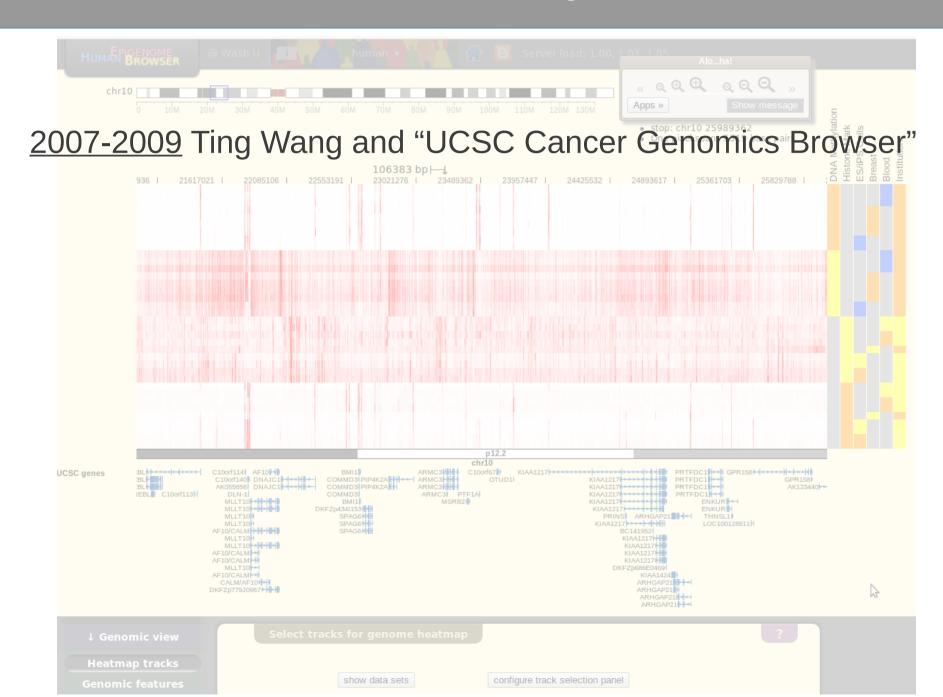
* Integrate with public data sets

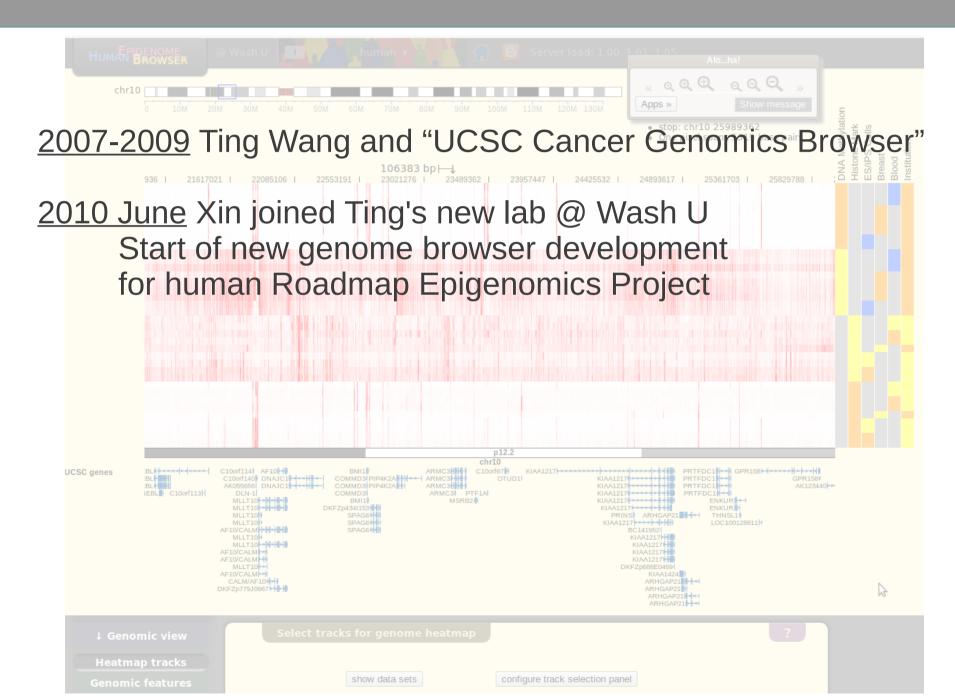
* Web display solution is nice

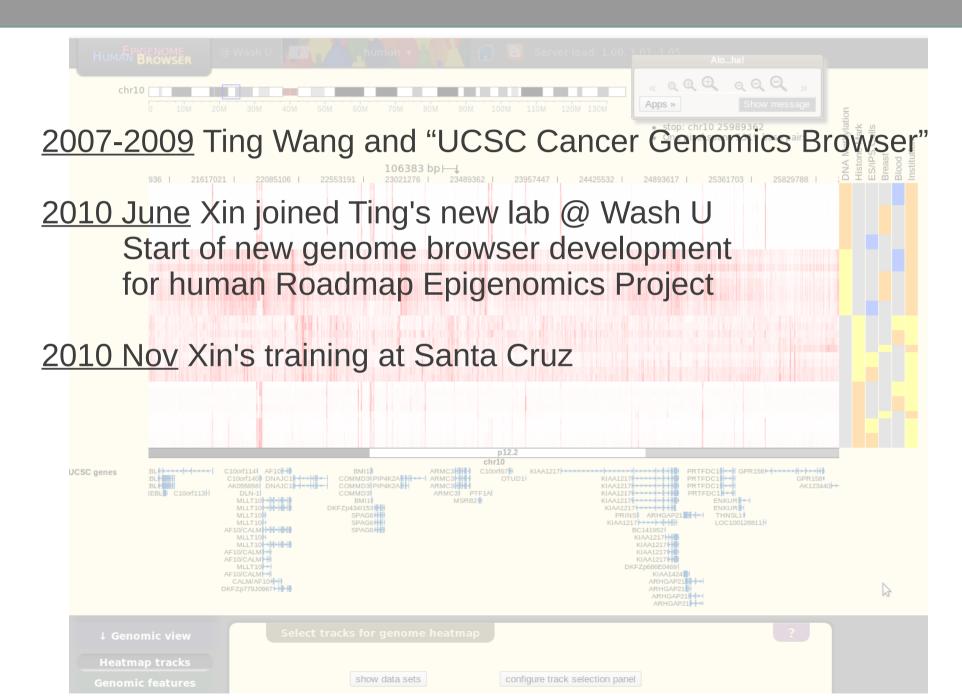
A lab's own data, Array/sequencing data sets Files amount to **1TB**

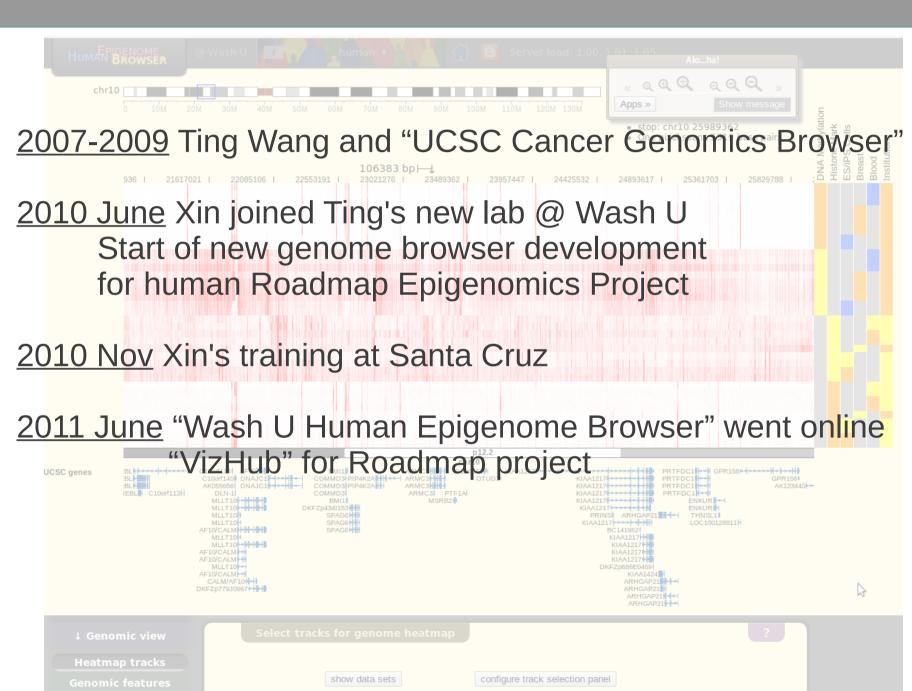
Our solution

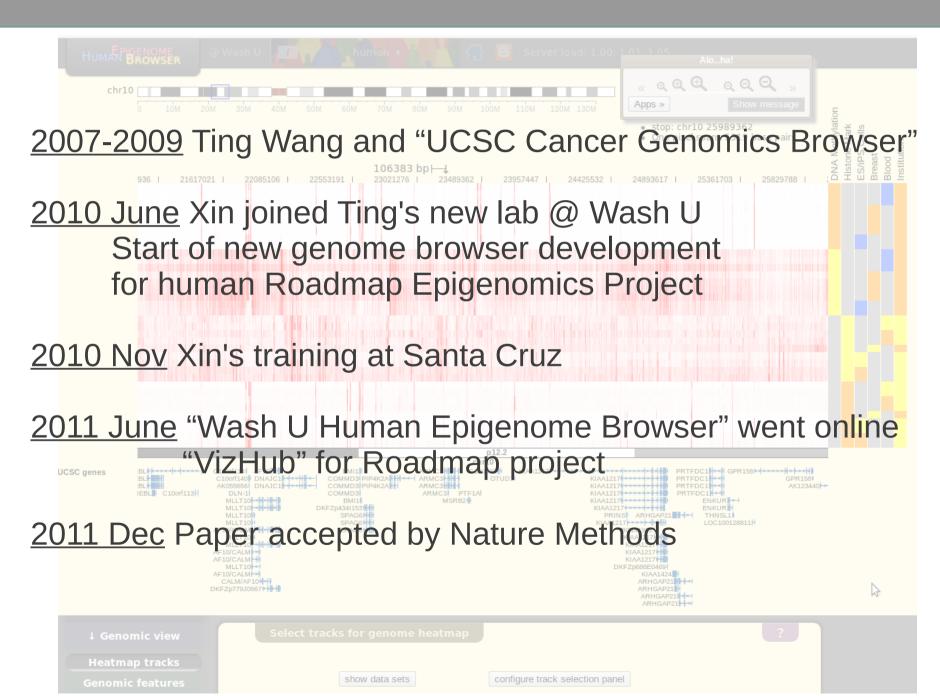












- "Need for Speed"
 - BigWig, bigBed
 - Parallel programming

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- Custom track

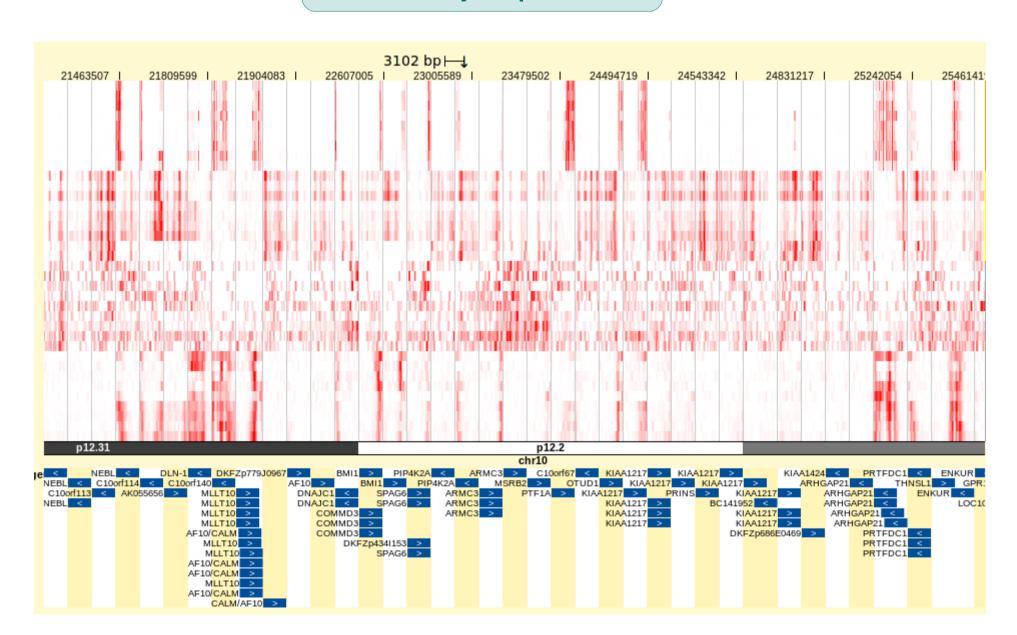
Bells and whistles

Genomic juxtaposition

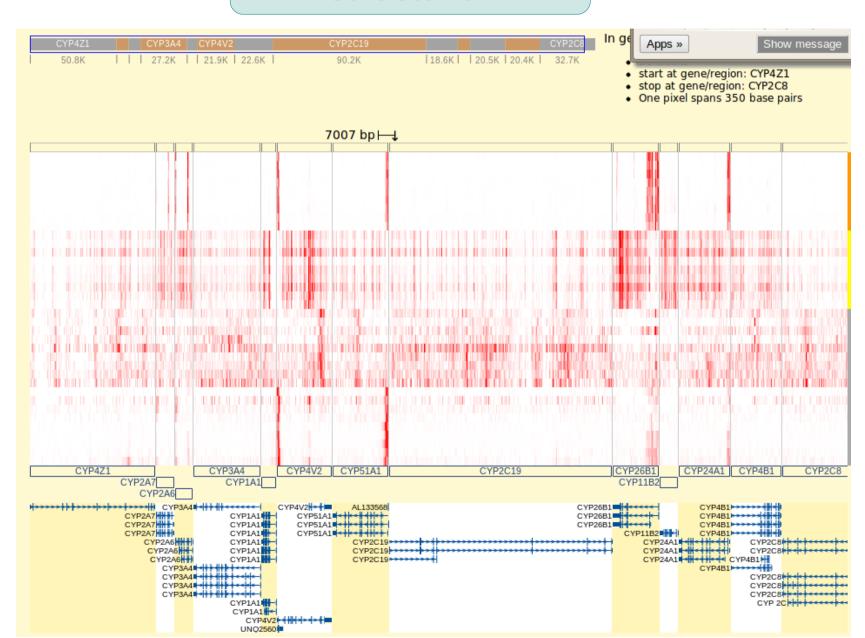
Gene Set View

Genome Snapshot

Genomic juxtaposition



Gene Set View



Genome Snapshot



Future work



Acknowledgement



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