

WP3 28.01.22

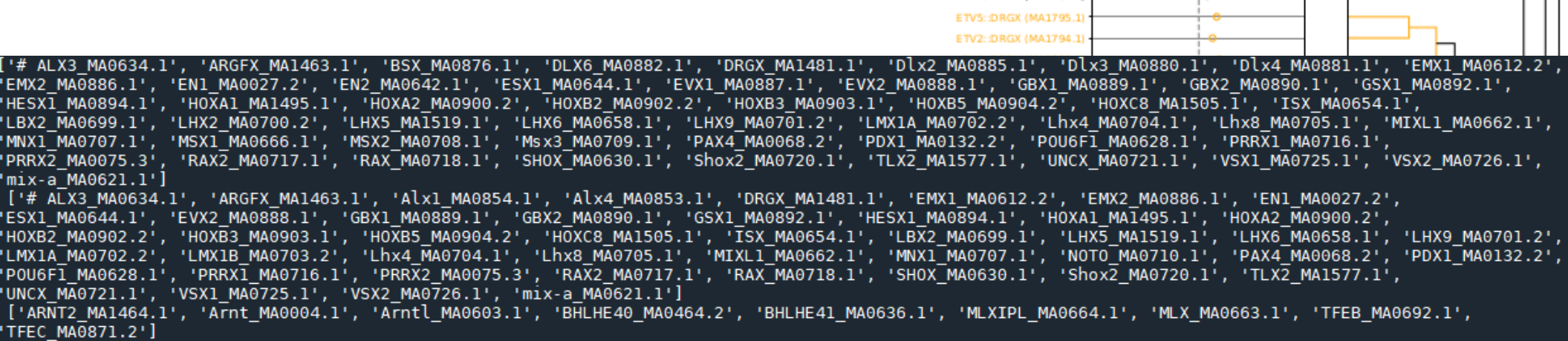
Tasks done since last week

- Successfully ran the snakemake pipeline
 - Takes about 3 days
 - Clustering creates a file for easy snakemake import
- Started to attempt Transcription factor grouping by family
- Got bam files from WP2

cluster5_Score	cluster7_Score	cluster9_Score	cluster10_Score
ATOH1(var.2)	ATF7	Ar	CLOCK
BARHL2	BACH2(var.2)	CENPB	CREM
EBF1	BHLHE22	DPYX	EOMES
Ebf2	CEBPA	Egr3	HOXD12
EN2	CEBPB	GATA1	IRF5
FOXA1	CEBPG	GATA6	MGA
FOXC1	CEBPG(var.2)	Gmeb1	MYF5
FOXC2	Creb5	Hic1	MYF6
FOXD2	DBP	HMBOX1	NKX2-3
FOXD3	DMRT	LEF1	NKX2-5
FOXC1	FOS::JUN(var.2)	NFKB1	Pax2
GATA1	FOSB::JUN	NFKB2	PAX3(var.2)
HAND2	FOSB::JUNB(var.2)	NR1I2	PAX9
HNF4A(var.2)	FOSL1::JUN(var.2)	NR2C2	PKNOX2
HOXA13	FOSL1::JUND(var.2)	ONECUT2	Rhox11
HOXC13	FOSL2::JUN(var.2)	OSR1	RUNX1
ISL2	FOSL2::JUNB(var.2)	PBX1	RUNX3
NEUROG1	FOSL2::JUND(var.2)	PBX1	SMAD1::SMAD3::SMAD4
NEUROG2(var.2)	HOXA9	NFX1	SREBF1
Nkx3-1	HOXC10	RFX4	SREBF2
NR1I3	HOXC12	RXRA::VDR	TBR1
Me2a3	HOXC8	SNAT1	TBX1
ONC113	HOXC9	SNAT3	TBX15
OSR2	HOXD10	SOX10	TBX18
Ptf1a	HOXD11	SOX12	TBX2
RARA::RXRA	JDP2(var.2)	Spz1	TBX20
RARB(var.3)	JUN::JUNB(var.2)	TCF4	TBX21
RELA	MZF1	TCF7	TBX3
RXRG	NFATC1	TCF7L1	TBX4
SOX14	NFATC2	TCF7L2	TBX5
SRF	NFATC3	THAP11	TBX6
TAL1::TCF3	PAX1	TP73	TBXT
TBP	PITX3	VEZF1	Tcf21
TCF21(var.2)	PKNOX1	ZBTB6	TFEC
TFCP2	Six3	ZEB1	TGIF1
THRB	TEF	ZNF135	TGIF2
VENTX	TFEB	ZNF143	THRB(var.2)
ZBTB18	ZNF652	ZNF354C	ZNF382

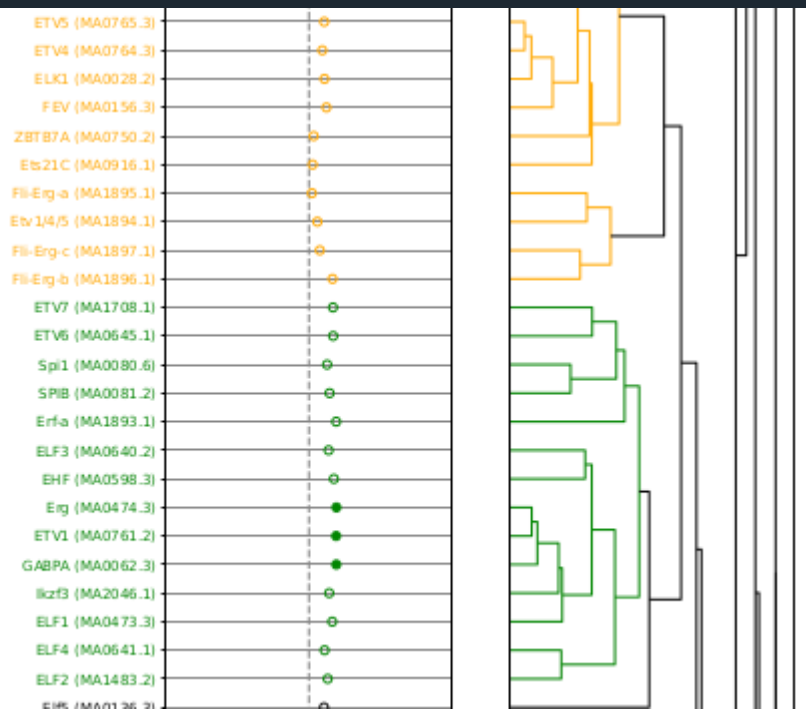
Problems

- Snakemake pipeline runs some tools we don't need for our analyses
 - Might be able to reduce runtime through that
- Snakemake pipeline output is different; adaptation of scripts required
- Ran into problems with TF family grouping
- Bam files from WP2 cause peak calling error



Some TFs have overlap with multiple different families

Fix this issues by working with grouping to shortest Distance?



ToDos

- Fix the errors
- Finish TF family grouping
- Run pipeline with Data from WP2