To do before handing in:

~~Abbreviations add~~ just review if any goes out

GSO3 form-finish filling it in

Abstract

Acknowledgements

\*Numbers letter of number

\*Margins if printing double side

\*Reduce space between chapter name and top of the page ~~I have added \vskip-3em~~

\*Only include sections and remove subsections

**Introduction:**

* ~~Gene regulation figure~~
* ~~Check aims again-Ask Anna~~ and Antonio to check
* ~~Reduce length of integrative methods-Ask Anna~~
* ~~Other cell type figure (only if time)~~
* Stuart 2015 table

**Material and methods**

* ~~Change whatever is needed for the single-cell analysis final version~~
* ~~Remove network analysis if taking it out~~

**Results 1**

* ~~Shorten Julian’s paragraph-Katie~~
* ~~Change master list by consensus peak~~ ~~also in the figure~~
* ~~Paragraph of limitations that Antonio suggested~~
* ~~Indicate statistical significance from the MT and TSS across all the samples of the cohort with~~ ~~ATAC-seq and Fast-ATAC~~
  + ~~Core CD14 and CD4 fresh~~
  + ~~Psoriasis~~
  + ~~PsA~~
* ~~Check change of chromatin segmentation map names~~
* ~~TSS variation upon sequencing depth in CD14 and one CD4 sample, make graph~~ ~~and decide where to include~~
* ~~Length fragment ratio values and how to link to TSS ratios~~
* One paragraph discussion from Katie
* Optimise space
* ~~To remove to from aims~~ keep it
* NHEKS optimization-Andy

﻿

**Results 2**

* ~~Pathway analysis table re-design~~
* ~~Shorten QC~~
* ~~Remove ChIPm metrics from appendix~~
* Figures size make sure and reshuffle
* ~~Fine-mapping add locus that I left out~~ and also indicate 5 as a more stringent cut off
* ~~TNFRSF9 association plot, read LD matrix, merge and then make plot~~
* See where or if to include the TNFRSF9 plot
* In fine-mapping
  + Sentence about this strategy being better than the LD one
  + That limitation of not having entire cohort is precisely the fact that in some instances the credible set of SNPs may be bigger than the one using high LD (difficult to decide on cut off)
  + Better fine-mapping for those loci with bigger OR: state example
  + Mention that those loci with only one SNP in the credible set not in LD with GWAS may be due to the sensitivity of the association analysis with sample size
  + Incorporate expression data: none for TNFRSF9 or nearby or STAT3
  + In TNFRSF9 and also mention STAT3 about not evidence of modulation of gene expression for any of those genes
* ~~Ola’s corrections~~
  + ~~Currently RNA-seq~~
* ~~Alasoo paper reads properly for changing sentence in discussion-red~~
  + ~~No evidence of colocalization of caWQTL-eQTL that is accessible in naïve and goes to no accessible in stimulated although there is effect on expression,but could still happen for some regions where the SNP modulating accessibility is not exactly the same as the eQTL,but then it doesn’t really makes sense.~~
  + ~~Read calderon paper~~
* ~~ATAC master lists enrichment for eQTLs barplot?no~~
* In discussion:
  + Fine-mapping points and Kasela eQTL no in B3GNT2 may be due to power-either here or in results
  + NOD-like paragraph revise or fold changes
  + TIAM1 paragraph link

**Results 3**

* Re-write single-cell
* Repeat ATAC correlation with gene expression maybe only TSS
* Adapt discussion
* Shorten QC part
* ~~Maybe remove network analysis~~ removed for the moment
* ~~Fine-mapping RUNX3 association plot to put it together with the chr5q30~~
* Point out which loci are genome-wide associated with PsA in Stuart 2015 and check which is the cohort used and if I may have it. Potential combined analysis to present in the viva
* ~~Mention about BF 5 and consider~~
* ~~Not to remove supplementary table with failing ones and add it to the main table~~
* ~~Incorporate Anna and Andy’s changes~~
  + ~~I am at the RUNX3 association plot~~
  + ~~Missing single-cell~~
  + ~~Missing limitations~~
  + ~~Missing conclusions~~

**Final discussion**

* Possibility of large scale testing of SNPs effects on enhancers or regulatory regions MPSS

Appendix

* ~~Remove ChIPm QC table decided to leave it in otherwise something is missing~~
* ~~Remove Enrichment of eQTL SNPs for the consensus list of ATAC peaks used to perform differential chromatin accessibility analysis in each cell type figure~~
* Make point about hypoxia effect in the joint as the driver of those changes

Bibliograpgy

* Merge with the new readcube and compile
* Add journal to the missing ones