Figures

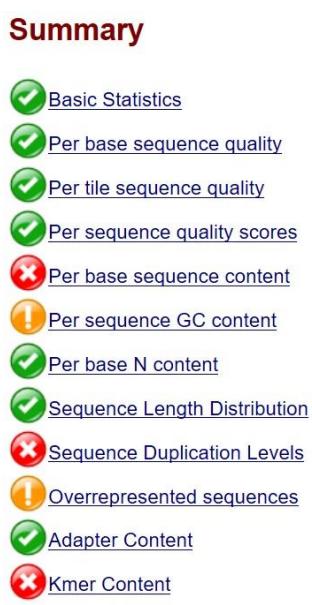

Figure 1. Summary of quality control Control_1.

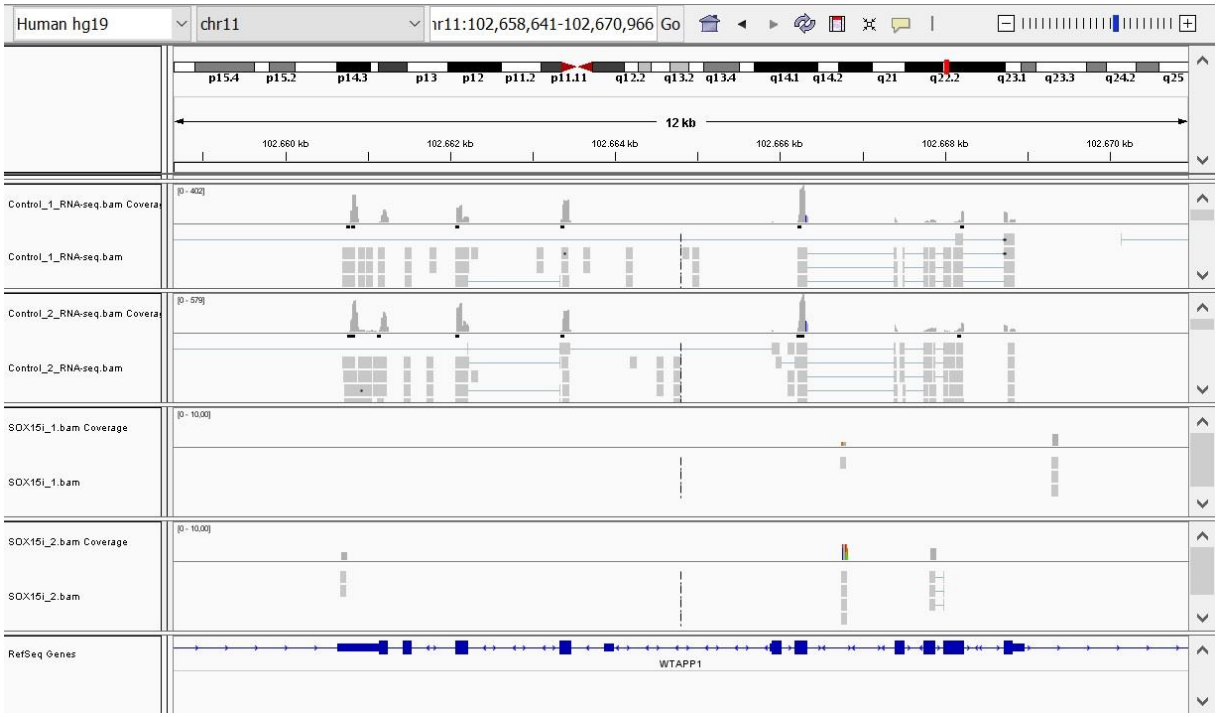

Figure 2. IGV demonstrating the difference in aligned reads to the reference sequence for all conditions (WTAPP1 gene).

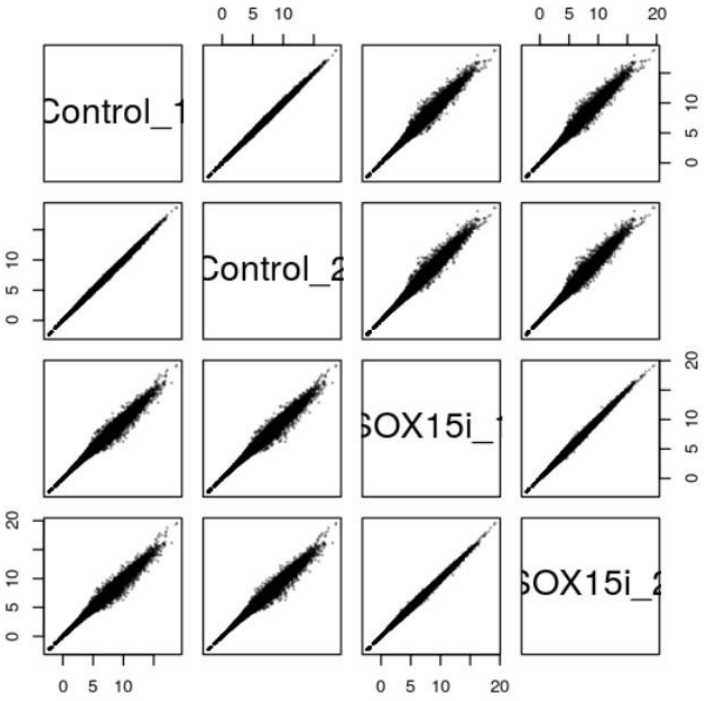

Figure 3. Log transformed variance between all conditions.

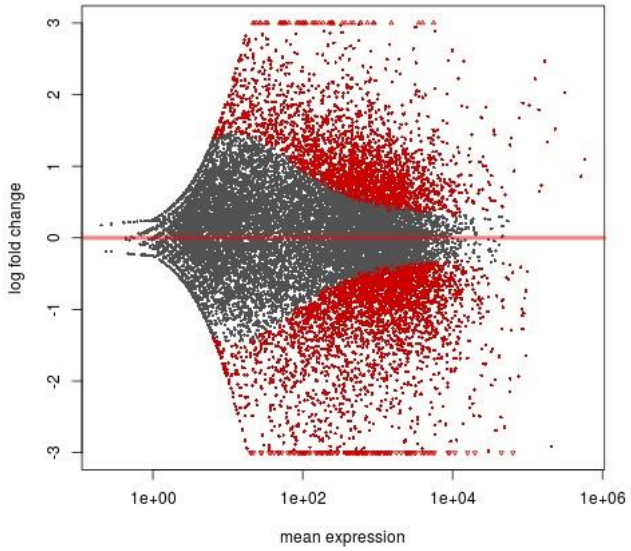

Figure 4. MA-plot of the differential expression data.

GO Term	p-Value	Matches
positive regulation of cell motility [GO:2000147]	1.263241e-5	66
positive regulation of cellular component movement [GO:0051272]	1.758692e-5	67
epithelium development [GO:0060429]	2.169064e-5	139
positive regulation of cell migration [GO:0030335]	2.307168e-5	64
locomotion [GO:0040011]	6.626329e-5	178
positive regulation of locomotion [GO:0040017]	7.242179e-5	66

Figure 5. GO enrichment results for the downregulated genes.

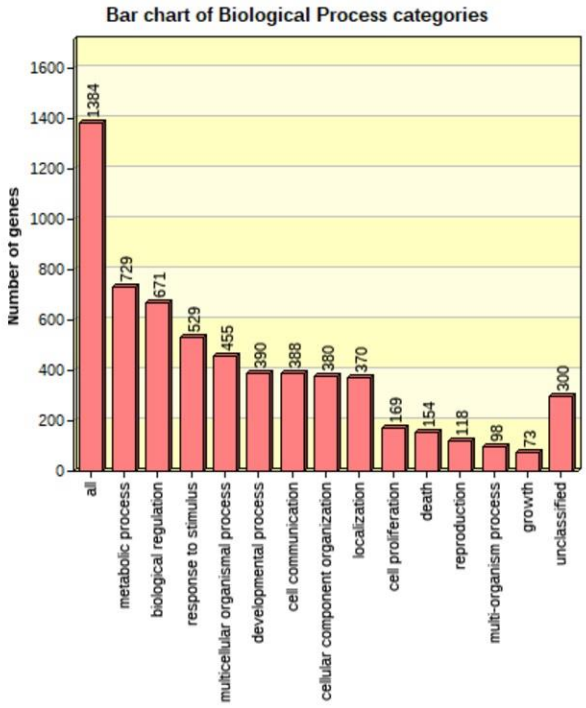

Figure 6. Bar chart of the biological processes defined by related genes.

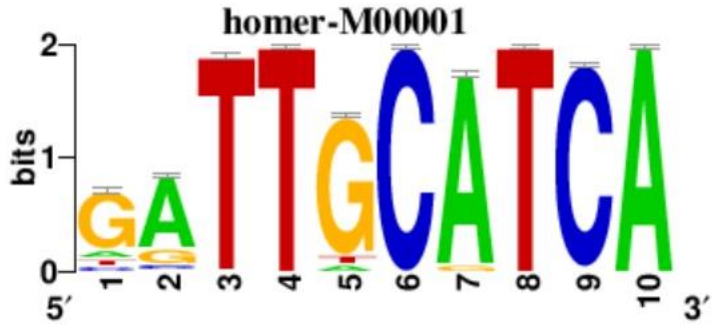

Figure 7. DDIT3 motif identified by applying the downregulated genes in iRegulon.

GO Term	p-Value	Matches
tissue development [GO:0009888]	1.261593e-7	84
epithelium development [GO:0060429]	1.458342e-5	58
single-organism developmental process [GO:0044767]	1.664534e-5	179
developmental process [GO:0032502]	1.724076e-5	181
multicellular organism development [GO:0007275]	2.230905e-4	155
cell differentiation [GO:0030154]	3.673651e-4	123

Figure 8. GO terms of gene targets DDIT3.

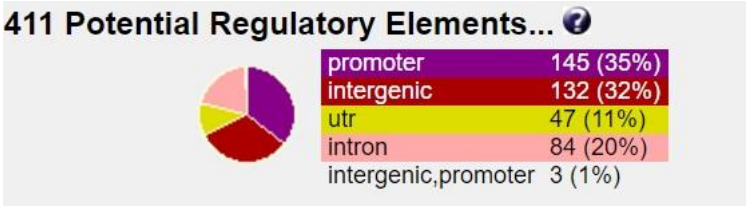

Figure 9. Potential regulatory elements ChIP-seq analysis of SOX15.

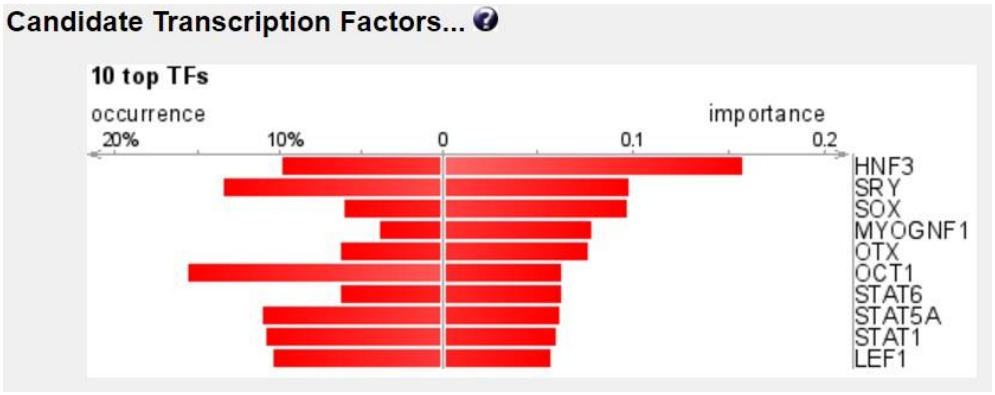

Figure 10. TOP 10 candidate TFs based on ChIP-seq analysis of SOX15.

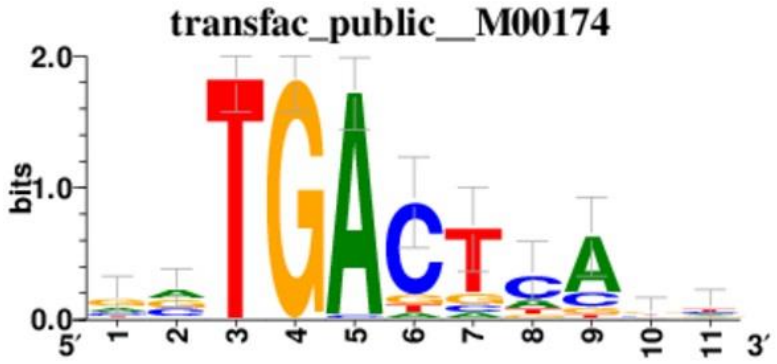

Figure 11. Motif of the highest ranked TFs (JUN and FOS)) based on ChIP-seq analysis.

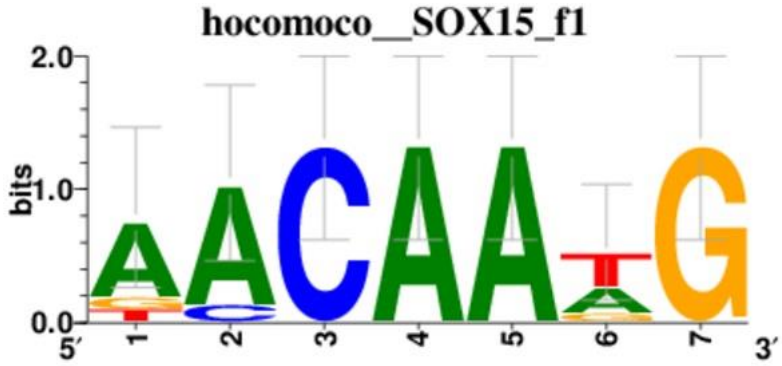

Figure 12. Motif of SOX15 based on ChIP-seq analysis.