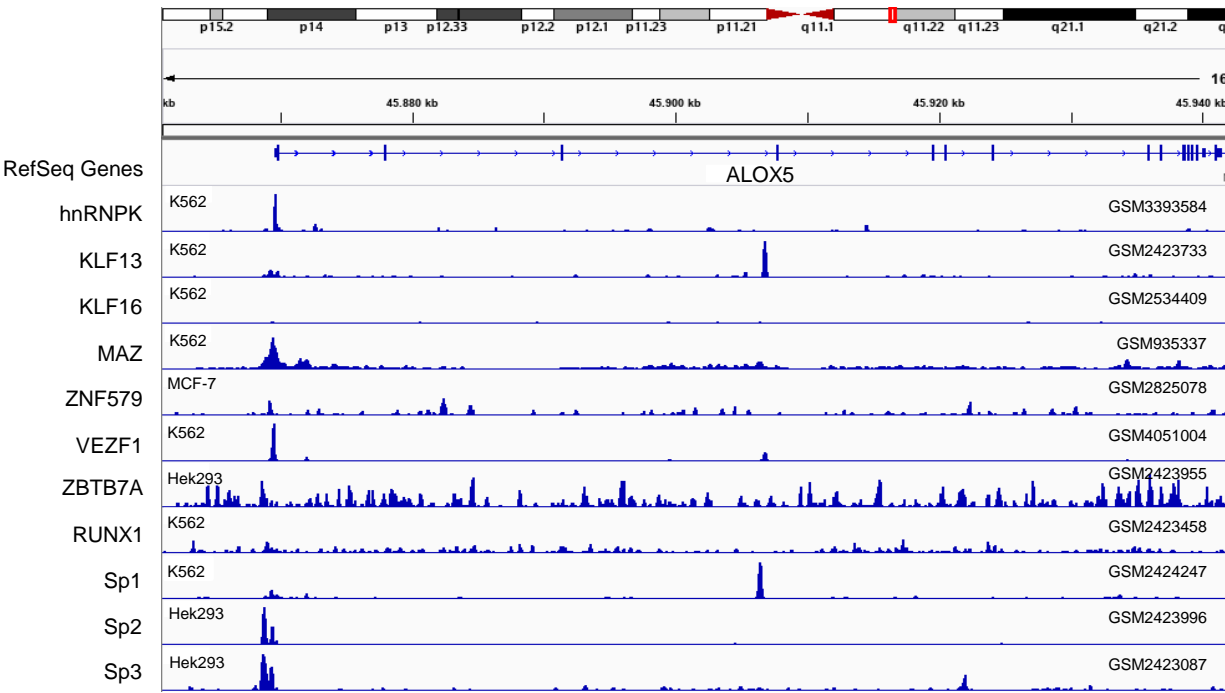


## **Analysis of proximal *ALOX5* promoter binding proteins by quantitative proteomics**

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**Suppl. Fig. 1**



**Suppl. Figure 1: ChIP-seq data showing binding of various transcription factors within the *ALOX5* gene.**

Chip-seq data were taken from the GEO database and visualized by the Integrative Genomics Viewer [72].

View of transcription factor binding to the *ALOX5* gene, with signals in the promoter region as shown for hnRNPK [73], KLF13 and KLF16 [74], ZNF579, VEZF1, ZBTB7A, RUNX1 [74], Sp1, Sp2 and Sp3 [74] and MAZ. The GEO accession numbers and the cell lines used are given for each dataset.

Suppl. Table 1

Oligonucleotide	sequence
Wildtype (WT) fwd	ACC CAG GAG CGA GGC CCC TGC CCC GCC CGA GGC GAG GTC CCG CCC AGT CGG CGC CGC GTG AAG AGT GGG AGA GAA GTA CTG CGG <b>GGG CGG GGG CGG GGG CGG GGG CGG</b> <b>GGG CGG</b> GGG CAG
WT rev	CTG CCC CCG CCC CCG CCC CCG CCC CCG CCC CCG CCC CCG CAG TAC TTC TCT CCC ACT CTT CAC GCG GCG CCG ACT GGG CGG GAC CTC GCC TCG GGC GGG GCA GGG GCC TCG CTC CTG GGT
Scrambled (SCR)	ACG CGT CCG AGG CCT GCG AGC CGG CCG TGC AGC GCT GCC GAG GGG TGC GAG CCC ACG CGG ACG CGC GAG GCC CGC ACC CTG CGA GGG TCG GAC GGA GCG ACG GTC CCC CAG CCT CGC GAG
SCR rev	CTC GCG AGG CTG GGG GAC CGT CGC TCC GTC CGA CCC TCG CAG GGT GCG GGC CTC GCG CGT CCG CGT GGG CTC GCA CCC CTC GGC AGC GCT GCA CGG CCG GCT CGC AGG CCT CGG ACG CGT

**Suppl. Table 1: 120-mer single-stranded forward and reverse oligonucleotide sequences used for pulldown experiments.** The wildtype (WT) sequence corresponds to position -260 to -141 of the proximal *ALOX5* promoter, the scrambled (SCR) sequence contains the same nucleotides in random order (checked for the inadvertent occurrence of consensus binding sites for transcription factors). The 5-fold tandem GC-box is marked in bold.

**Suppl. Table 2**

protein	HL60	dHL60	THP1	dTHP1	MM6	dMM6	Rec-1	BL41
1. APOBEC3C				x				
2. BLM	x	x						
3. CIRBP							x	
4. CYP7B1			x					
5. CUL4A	x							
6. DDB2		x						
7. DHX36				x	x	x		
8. POLB		x						
9. ETV6	x							
10. FAM120A							x	x
11. FAF1						x		
12. FOSL2		x						
13. FOSL2	x							
14. hnRNPD	x		x		x			
15. hnRNPK	x	x		x			x	x
16. hnRNPU								x
17. JUND	x							
18. KLF13	x						x	
19. KLF16	x	x	x	x	x		x	
20. MAZ	x			x	x			
21. METTL17			x					
22. MDK					x			
23. MSANTD2						x		
24. MSH2	x							
25. MSH3	x	x						
26. MTF2	x							
27. NIP7			x					
28. NUP133	x							
29. NUP214	x							
30. NUP53	x							
31. NUP93	x							
32. THAP12							x	
33. PCBP2		x						
34. PRDM10		x		x				
35. RBM3	x							
36. RBMS1						x		
37. RANBP2	x							
38. RECQL	x							
39. RPA1	x							

**Suppl. Table 2**

protein	HL60	dHL60	THP1	dTHP1	MM6	dMM6	Rec-1	BL41
40. RPA2	x					x		
41. RPA3	x	x						
42. RFC1	x	x						
43. RUNX1		x						
44. SLC35A5			x					
45. SF3B1	x							
46. SMARCA1		x						
47. Sp1	x	x	x	x	x		x	x
48. Sp2			x					x
49. Sp3	x			x	x	x		
50. Sp4				x				
51. SUZ12	x							
52. SUB1	x							
53. GTF3C5	x							
54. TFAM	x							
55. TMEM209	x							
56. VEZF1	x	x						
57. WDR76	x							
58. YBX1		x						
59. ZBTB7A	x	x		x				
60. ZFP64			x					
61. ZFP91					x			x
62. ZNF148		x						
63. ZNF281	x	x				x		
64. ZNF316				x				
65. ZNF444	x							
66. ZNF579	x	x		x				

**Suppl. Table 2: Overview of all significant *ALOX5* interacting proteins identified from DNA pulldowns with myeloid and B-lymphocytic cell lines****References**

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