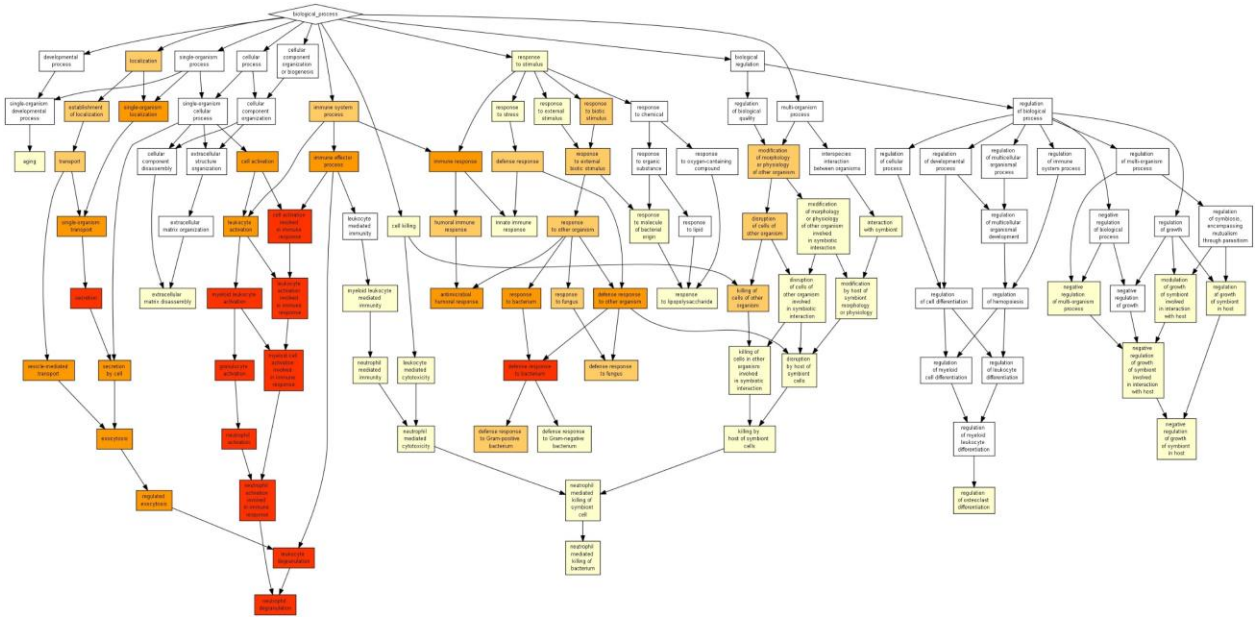

Figure 1 **Flowchart GOrilla process downregulated signature**

This flowchart shows the GO processes that are downregulated in the group ‘responders’. The gene signature mainly impacts processes involved in myeloid cell and leukocyte activation, defence against bacteria and secretion/degranulation. This indicates that these processes are downregulated in the ‘responders’-group in response to tyrosine kinase inhibitors. Which is to be expected because tyrosine kinase inhibitors are meant to supress immune cells from the myeloid lineage to proliferate.

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0043312	neutrophil degranulation	2.8E-11	1.47E-7	2.52 (608,122,91,46)	[+] Show genes
GO:0002283	neutrophil activation involved in immune response	4.04E-11	1.06E-7	2.50 (608,123,91,46)	[+] Show genes
GO:0002275	myeloid cell activation involved in immune response	5.68E-11	9.89E-8	2.48 (608,124,91,46)	[+] Show genes
GO:0036230	granulocyte activation	8.18E-11	1.07E-7	2.46 (608,125,91,46)	[+] Show genes
GO:0043299	leukocyte degranulation	8.18E-11	8.55E-8	2.46 (608,125,91,46)	[+] Show genes
GO:0042119	neutrophil activation	8.18E-11	7.13E-8	2.46 (608,125,91,46)	[+] Show genes
GO:0002366	leukocyte activation involved in immune response	1.57E-10	1.17E-7	1.79 (608,131,200,77)	[+] Show genes
GO:0002263	cell activation involved in immune response	1.57E-10	1.02E-7	1.79 (608,131,200,77)	[+] Show genes
GO:0046903	secretion	4.46E-10	2.59E-7	2.59 (608,151,59,38)	[+] Show genes
GO:0042742	defense response to bacterium	6.36E-10	3.33E-7	7.85 (608,35,31,14)	[+] Show genes
GO:0002274	myeloid leukocyte activation	6.8E-10	3.23E-7	2.35 (608,131,91,46)	[+] Show genes
GO:0045055	regulated exocytosis	1.27E-9	5.53E-7	2.31 (608,133,91,46)	[+] Show genes
GO:0032940	secretion by cell	1.44E-9	5.77E-7	2.58 (608,148,59,37)	[+] Show genes
GO:0045321	leukocyte activation	1.79E-9	6.69E-7	2.56 (608,149,59,37)	[+] Show genes
GO:0009617	response to bacterium	2.62E-9	9.13E-7	7.23 (608,38,31,14)	[+] Show genes
GO:0002252	immune effector process	3.75E-9	1.23E-6	1.65 (608,150,206,84)	[+] Show genes
GO:0006887	exocytosis	5.32E-9	1.64E-6	2.61 (608,138,59,35)	[+] Show genes
GO:0098542	defense response to other organism	5.8E-9	1.68E-6	5.74 (608,53,32,16)	[+] Show genes
GO:0001775	cell activation	1.17E-8	3.21E-6	2.43 (608,157,59,37)	[+] Show genes
GO:0044765	single-organism transport	2.18E-8	5.7E-6	1.92 (608,189,92,55)	[+] Show genes
GO:0006955	immune response	3.17E-8	7.89E-6	1.88 (608,109,172,58)	[+] Show genes

Table 1 **GOrilla process downregulated signature**

This table shows the GO terms and their description that are enriched in the list of genes from the downregulated signature. The P-values and the adjusted P-values are reasonably significant, for a random set of genes one might observe P-values in the range of E-8. The enrichment scores are also mostly intermediate.

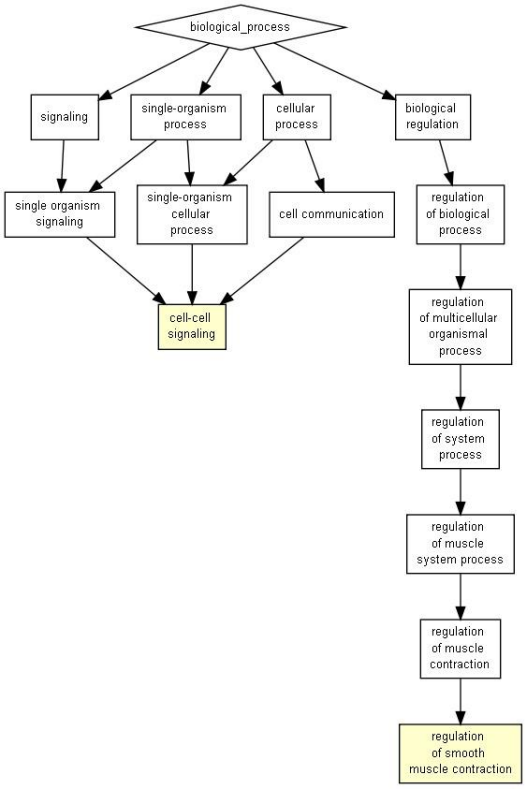

Figure 2 ***Flowchart GOrilla process upregulated signature***

This flowchart shows the GO processes that are upregulated in the group 'responders'. The terms are very broad, and there are no processes that are enriched in a highly significant manner. This indicates that there is no real signature for upregulated genes in patients responding to tyrosine kinase inhibitors.

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0006940	regulation of smooth muscle contraction	6.08E-4	1E0	4.27 (559,6,131,6)	[+] Show genes
GO:0007267	cell-cell signaling	6.5E-4	1E0	3.29 (559,11,139,9)	[+] Show genes

Table 2 **GOrilla process upregulated signature**

This table shows the GO terms and their description that are enriched in the list of genes from the upregulated signature. The P-values and the adjusted P-values are statistically insignificant. The enrichment scores are intermediate. This also indicates that there is no real signature for upregulated genes in patients responding to tyrosine kinase inhibitors.

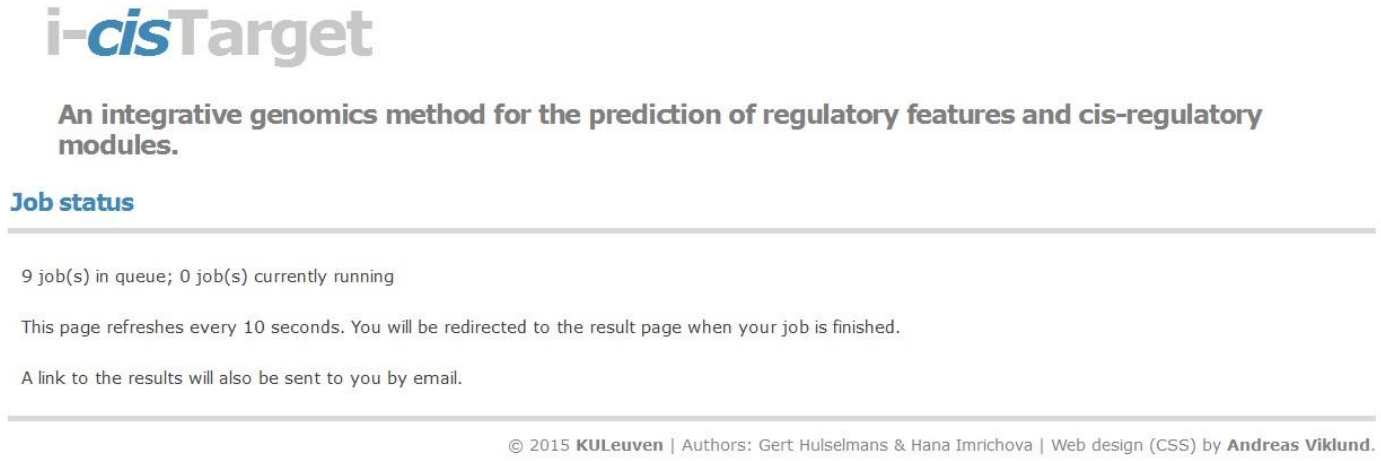

Figure 3 **Results from i-cisTarget**

This image shows i-cisTarget running, as may be observed there are 9 jobs in que and none are running. Even if left running for several hours, this does not change



Figure 4 **Visualisation GATA2 binding sites in IGV**

When visualizing the sorted bam file and the gff track obtained from fuzznuc, one can observe the position of the predicted GATA2 binding sites on the gff track and the mapped reads can be found on the sorted bam track. If GATA2 indeed binds the sequence "AGATCTTA", then we would expect peaks on the sorted bam track at the same position as the gff track. As this is not the case for most of the binding sequence positions, we doubt whether "AGATCTTA" is a true GATA2 binding sequence.

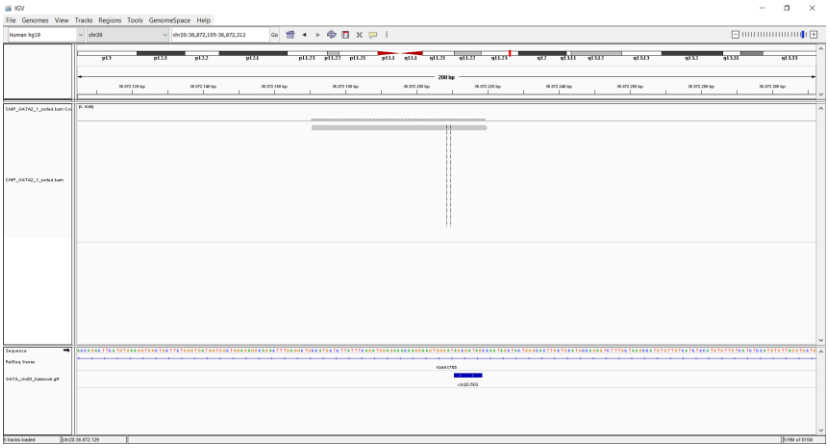

Figure 5 **Visualisation GATA2 binding sites in IGV**

Figure 5 again shows both the sorted bam track and the gff track. In this case we observe our sequence "AGATCTTA" is inside of a mapped read, therefore we hypothesize that GATA2 may have been associated with another transcription factor.

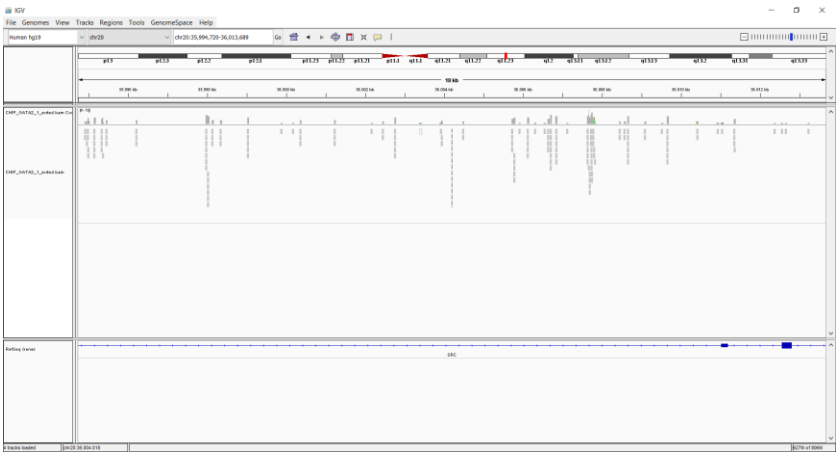

Figure 6 **Visualisation GATA2 binding sites in IGV**

Figure 6 shows several promising peaks within the gene SRC. SRC is a proto-oncogene tyrosine protein kinase (non-receptor), of which an elevated activity is correlated with poor prognosis and advancing malignancy in human cancer (http://theoncologist.alphamedpress.org/content/14/7/667). This could indicate an interaction between GATA2 and SRC, and this could be implicated in leukaemia.