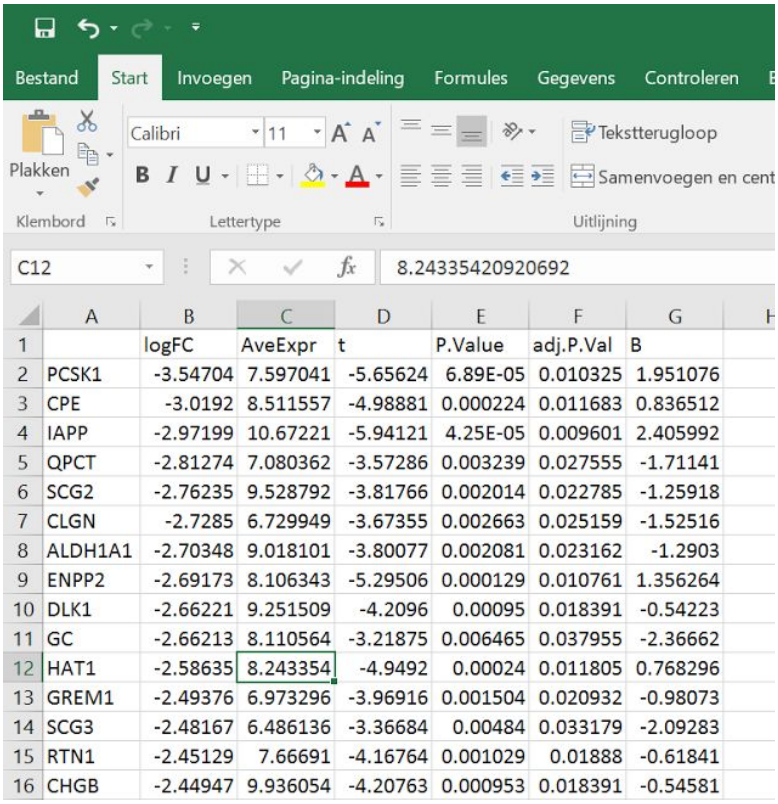
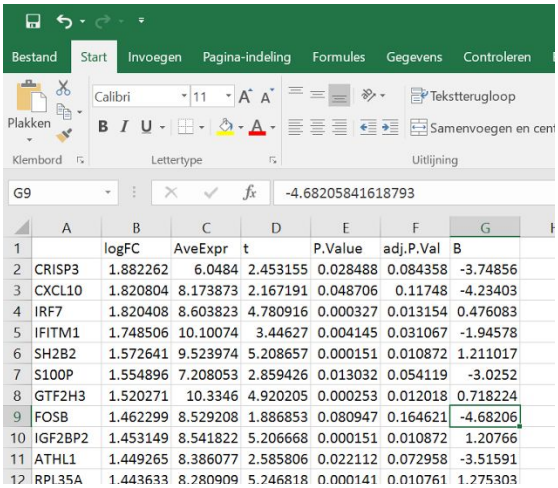
Supplementary Data



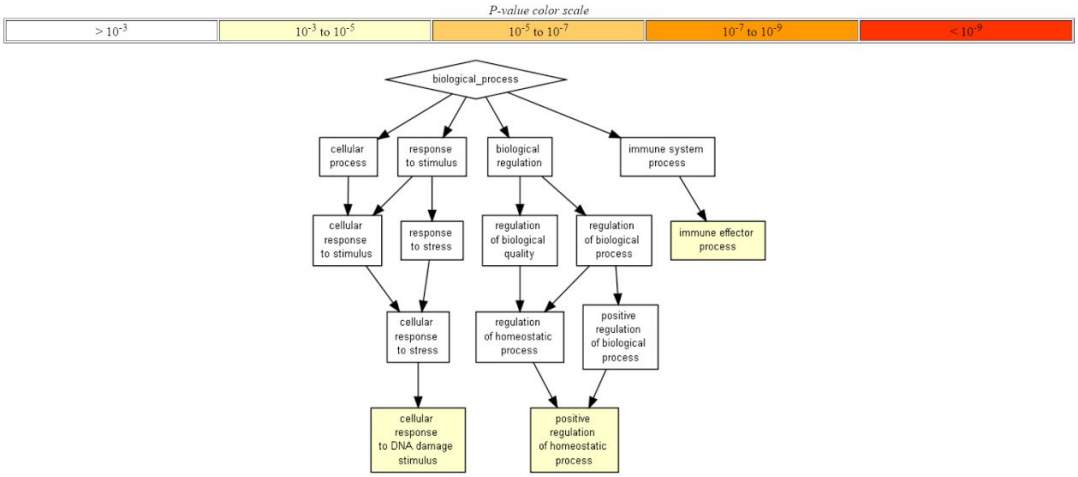
	A	B	C	D	E	F	G
1		logFC	AveExpr	t	P.Value	adj.P.Val	B
2	PCSK1	-3.54704	7.597041	-5.65624	6.89E-05	0.010325	1.951076
3	CPE	-3.0192	8.511557	-4.98881	0.000224	0.011683	0.836512
4	IAPP	-2.97199	10.67221	-5.94121	4.25E-05	0.009601	2.405992
5	QPCT	-2.81274	7.080362	-3.57286	0.003239	0.027555	-1.71141
6	SCG2	-2.76235	9.528792	-3.81766	0.002014	0.022785	-1.25918
7	CLGN	-2.7285	6.729949	-3.67355	0.002663	0.025159	-1.52516
8	ALDH1A1	-2.70348	9.018101	-3.80077	0.002081	0.023162	-1.2903
9	ENPP2	-2.69173	8.106343	-5.29506	0.000129	0.010761	1.356264
10	DLK1	-2.66221	9.251509	-4.2096	0.00095	0.018391	-0.54223
11	GC	-2.66213	8.110564	-3.21875	0.006465	0.037955	-2.36662
12	HAT1	-2.58635	8.243354	-4.9492	0.00024	0.011805	0.768296
13	GREM1	-2.49376	6.973296	-3.96916	0.001504	0.020932	-0.98073
14	SCG3	-2.48167	6.486136	-3.36684	0.00484	0.033179	-2.09283
15	RTN1	-2.45129	7.66691	-4.16764	0.001029	0.01888	-0.61841
16	CHGB	-2.44947	9.936054	-4.20763	0.000953	0.018391	-0.54581

Figure A1:
After getting the TSV file of the ‘tophits’ significant genes, a list was made of the upregulated and downregulated genes. The Log fold change column showed positive as well as negative number. Positive gene numbers were upregulated and negatives were downregulated; The 5 most significant downregulated genes here include PCSK1, CPE, IAPP, QPCT, SCG2 and CLGN



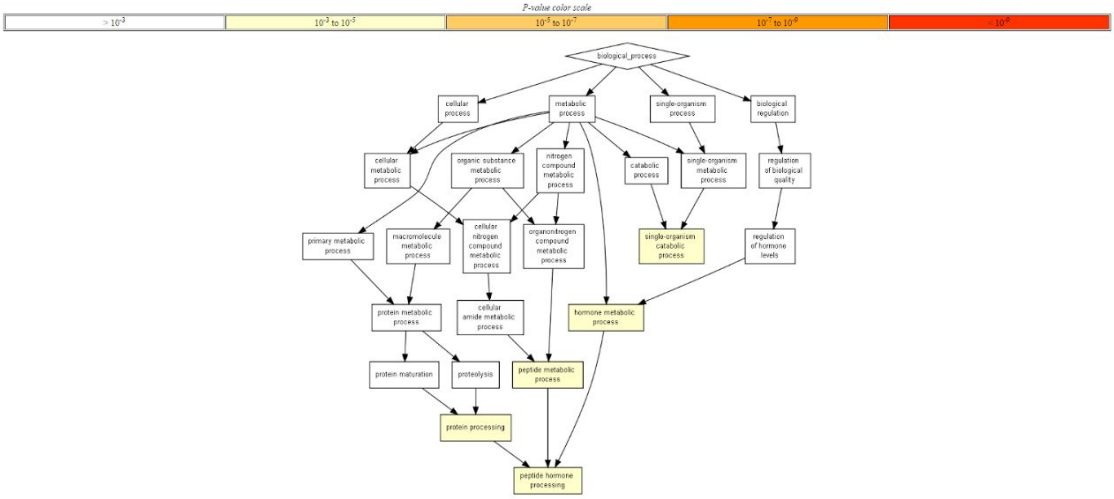
	A	B	C	D	E	F	G
1		logFC	AveExpr	t	P.Value	adj.P.Val	B
2	CRISP3	1.882262	6.0484	2.453155	0.028488	0.084358	-3.74856
3	CXCL10	1.820804	8.173873	2.167191	0.048706	0.11748	-4.23403
4	IRF7	1.820408	8.603823	4.780916	0.000327	0.013154	0.476083
5	IFITM1	1.748506	10.10074	3.44627	0.004145	0.031067	-1.94578
6	SH2B2	1.572641	9.523974	5.208657	0.000151	0.010872	1.211017
7	S100P	1.554896	7.208053	2.859426	0.013032	0.054119	-3.0252
8	GTF2H3	1.520271	10.3346	4.920205	0.000253	0.012018	0.718224
9	FOSB	1.462299	8.529208	1.886853	0.080947	0.164621	-4.68206
10	IGF2BP2	1.453149	8.541822	5.206668	0.000151	0.010872	1.20766
11	ATHL1	1.449265	8.386077	2.585806	0.022112	0.072958	-3.51591
12	RPL35A	1.443633	8.280909	5.246818	0.000141	0.010761	1.275303

Figure 2: The 5 most significant upregulated genes here include CRISP3, CXCL10, IRF7, IFITM1, SH2B2



GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0002252	immune effector process	3.9E-4	1E0	2.20 (187,30,51,18)	[+] Show genes
GO:0032846	positive regulation of homeostatic process	4.4E-4	7.29E-1	7.48 (187,4,25,4)	[+] Show genes
GO:0006974	cellular response to DNA damage stimulus	6.13E-4	6.77E-1	6.68 (187,7,20,5)	[+] Show genes

Figure 3: The first 200 upregulated and downregulated genes were pasted into GOrilla for functional enrichment analysis. The most upregulated genes are shown here.



GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0006518	peptide metabolic process	2.46E-4	7.43E-1	8.57 (197,4,23,4)	[+] Show genes
GO:0016486	peptide hormone processing	2.46E-4	3.71E-1	8.57 (197,4,23,4)	[+] Show genes
GO:0016485	protein processing	2.46E-4	2.48E-1	8.57 (197,4,23,4)	[+] Show genes
GO:0042445	hormone metabolic process	2.6E-4	1.97E-1	7.14 (197,6,23,5)	[+] Show genes
GO:0044712	single-organism catabolic process	8.53E-4	5.16E-1	2.74 (197,12,60,10)	[+] Show genes

Figure 4: GOrilla analysis of the most downregulated genes.

	A	B	C	D	E	F	G
1	Geneid	SRR3313326.bam	SRR3313327.bam	SRR3313328.bam	SRR3313329.bam	SRR3313330.bam	SRR3313331.bam
2	5S_rRNA	0	0	0	0	0	0
3	7SK	0	0	0	0	0	0
4	A1BG	0	0	0	0	0	0
5	A1BG-AS1	0	0	0	0	0	0
6	A1CF	0	0	0	0	0	0
7	A2M	0	0	0	0	0	0
8	A2M-AS1	0	0	0	0	0	0
9	A2ML1	0	0	0	0	0	0
10	A2ML1-AS1	0	0	0	0	0	0
11	A2ML1-AS2	0	0	0	0	0	0
12	A3GALT2	0	0	0	0	0	0
13	A4GALT	0	0	0	0	0	0
14	A4GNT	0	0	0	0	0	0
15	AAAS	0	0	0	0	0	0
16	AACS	0	0	0	0	0	0
17	AADAC	0	0	0	0	0	0
18	AADACL2	0	0	0	0	0	0
19	AADACL3	0	0	0	0	0	0
20	AADACL4	0	0	0	0	0	0
21	AADAT	0	0	0	0	0	0
22	AAED1	0	0	0	0	0	0

Figure 5: tsv file for the RNA seq gene counts

	A	B	C	D	E	F	G
1	Geneid	SRR3313326.bam	SRR3313327.bam	SRR3313328.bam	SRR3313329.bam	SRR3313330.bam	SRR3313331.bam
2	MT1G	167	48	46	104	104	83
3	MT1H	116	29	37	67	67	55
4	POTEF	65	99	62	155	155	88
5	MT1X	50	19	8	37	37	28
6	POTEI	11	10	9	19	19	9
7	FAM127A	10	7	4	5	5	8
8	FAM127C	8	5	3	2	2	5
9	ZNF878	6	8	11	4	4	7
10	NBPF12	6	5	14	6	6	6
11	CTD-3099C6.9	6	4	3	1	1	6
12	AL627309.1	6	1	7	2	2	3
13	RP4-669L17.10	6	3	9	4	4	3
14	ZNF730	6	3	1	4	4	1
15	ZNF844	5	9	10	7	7	7
16	POTEE	5	8	4	11	11	7
17	ZNF708	5	7	15	4	4	6
18	ZNF273	5	2	1	2	2	1
19	ZNF525	4	3	2	4	4	9
20	ZNF98	4	1	4	0	0	6

Figure 6: Columns sorted by highest expression value: