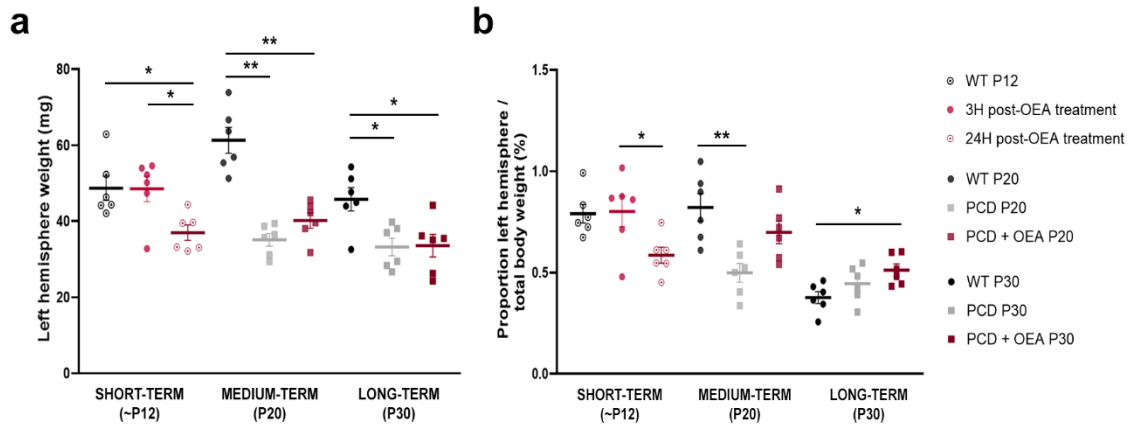


This document includes the following Supplementary Material:

- Figure S1: Graphs of the left hemi-cerebellum weight (a) and the proportion between the left hemi-cerebellum weight respect to the total body weight (b) in the short- (~P12), medium- (P20) and long-term (P30).
- Figure S2: Micrographs of detailed marker-based characterization of microglia in the cerebellum of untreated PCD and OEA-treated PCD mice at P30.
- Table S1: Comparisons and specific p-values from hemi-cerebellar weight and relation to the total body weight.
- Supplementary Information: Specificity and efficiency analyses of qPCR primers

Figure S1



**Figure S1. (a, b) Graphs of the left hemi-cerebellum weight (a) and the proportion between the left hemi-cerebellum weight respect to the total body weight (b) in the short- (~P12), medium- (P20) and long-term (P30).** Analysis of left hemicerebellum weight revealed differences, in the short term, between WT untreated mice and WT mice 3 and 24 hours after OEA treatment, with the weight being lower in mice 24 hours after OEA treatment (WT:  $49 \pm 3$  mg; 3 hours:  $49 \pm 3$  mg; 24 hours:  $37 \pm 2$  mg). At P20 and P30 (i.e., medium and long term) differences were found between WT animals and the two experimental groups of PCD mice, with the weight of the mutants being less (P20, WT:  $61 \pm 3$  mg, PCD:  $35 \pm 1$  mg, PCD+OEA:  $40 \pm 2$  mg; P30, WT:  $45 \pm 3$  mg, PCD:  $33 \pm 2$  mg, PCD+OEA:  $33 \pm 3$  mg). However, when the ratio of hemicerebellum weight to total body weight was analyzed, differences were only detected between the groups 3 and 24 hours after treatment in the short term, with the percentage being lower after 24 hours (WT:  $0.79 \pm 0.04\%$ , 3 hours:  $0.80 \pm 0.07\%$ , 24 hours:  $0.58 \pm 0.04\%$ ). Regarding the medium term, differences were found between WT and untreated PCD mice, the percentage being lower in mutants compared to the wild type (WT:  $0.82 \pm 0.06\%$ , PCD:  $0.49 \pm 0.04\%$ , PCD+OEA:  $0.69 \pm 0.05\%$ ). Concerning long-term analysis, differences were limited to WT *vs.* OEA-treated PCD mice at P30, with the percentage being higher in those PCD mice treated with OEA (WT:  $0.37 \pm 0.02\%$ , PCD:  $0.44 \pm 0.03\%$ , PCD+OEA:  $0.51 \pm 0.03\%$ ). Due to the non-anorexigenic effect on the total body weight reported for the dose of OEA used in our study (Pérez-Martín, *et al.*, 2021), these results suggest that the weight of the hemicerebellum of OEA-treated PCD mice was greater than their total body weight; that is, cerebellar atrophy in these treated animals was lower than in the untreated mice. n=6 animals per experimental group. One-way ANOVA followed by Bonferroni's post hoc test. \*  $p < 0.05$ ; \*\*  $p < 0.01$

Figure S2

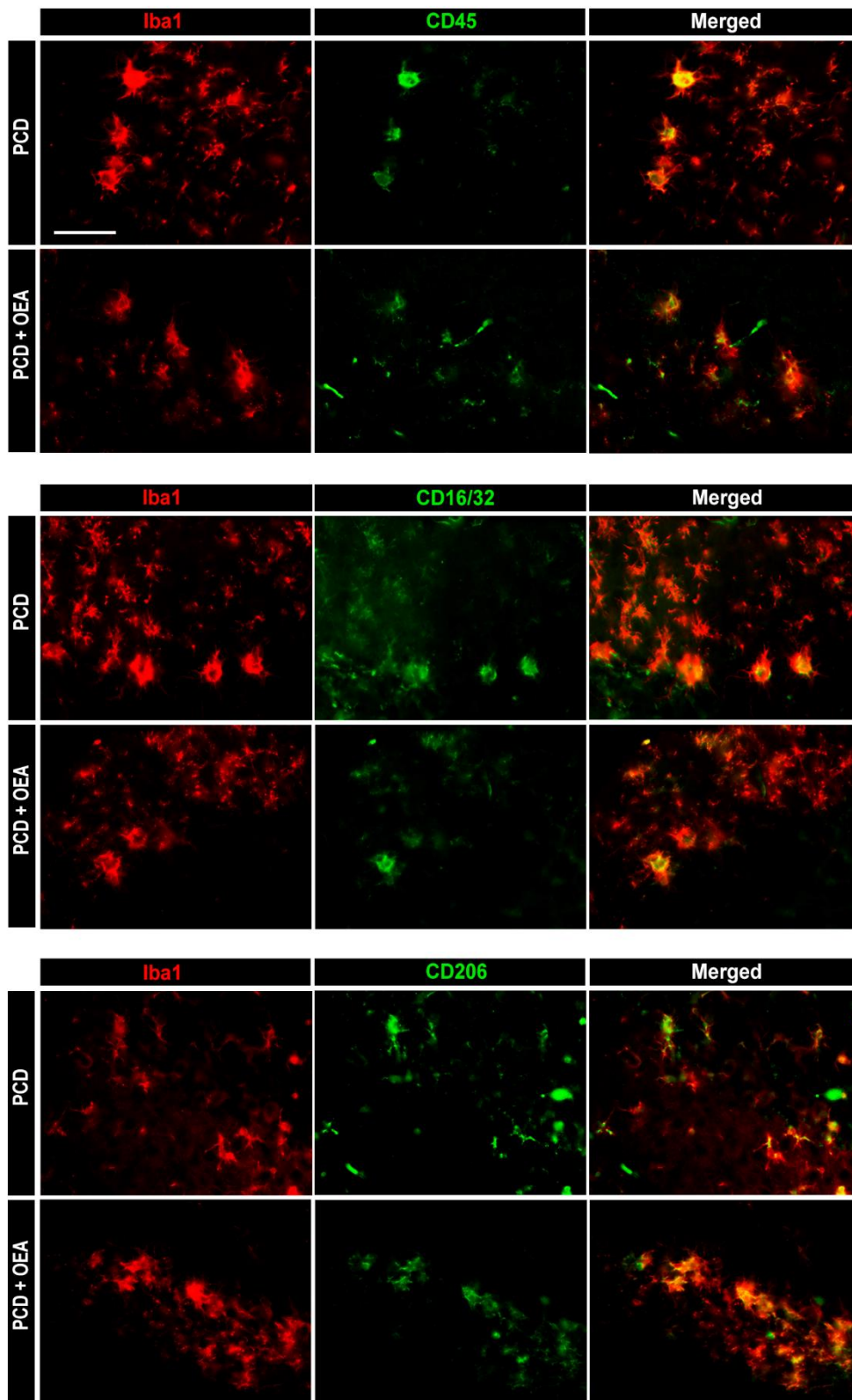


Figure S2. Micrograph of detailed marker-based characterization of microglia in the cerebellum of untreated PCD and OEA-treated PCD mice at P30. At the top, immunolabeling for Iba1 (red) and CD45 (green), i.e., reactive microglial cells. In the center, immunolabeling for Iba1 (red) and CD16/32

(green), i.e., proinflammatory microglial cells. At the bottom, immunolabeling for Iba1 (red) and CD206 (green), i.e., neuroprotective or tissue reparative microglial cells. Scale bar: 20  $\mu\text{m}$ .

**Table S1.** Comparisons and specific *p*-values from hemi-cerebellar weight and relation to the total body weight.

Variables	Comparisons	<i>p</i> -values
Hemi-cerebellar weight ~P12-P13	WT <i>vs.</i> WT 3H Post-OEA	1.000
	WT <i>vs.</i> WT 24H Post-OEA	<b>0.036</b>
	WT 3H Post-OEA <i>vs.</i> WT 24H Post-OEA	<b>0.039</b>
Hemi-cerebellar weight P20	WT <i>vs.</i> PCD	<b>&lt; 0.001</b>
	WT <i>vs.</i> PCD+OEA	<b>&lt; 0.001</b>
	PCD <i>vs.</i> PCD+OEA	0.521
Hemi-cerebellar weight P30	WT <i>vs.</i> PCD	<b>0.019</b>
	WT <i>vs.</i> PCD+OEA	<b>0.023</b>
	PCD <i>vs.</i> PCD+OEA	1.000
Hemi-cerebellum/ Total Body weight ~P12-P13	WT <i>vs.</i> 3H Post-OEA	1.000
	WT <i>vs.</i> WT 24H Post-OEA	0.061
	WT 3H Post-OEA <i>vs.</i> WT 24H Post-OEA	<b>0.046</b>
Hemi-cerebellum/ Total Body weight P20	WT <i>vs.</i> PCD	<b>0.004</b>
	WT <i>vs.</i> PCD+OEA	0.451
	PCD <i>vs.</i> PCD+OEA	0.081
Hemi-cerebellum/Total Body weight P30	WT <i>vs.</i> PCD	0.472
	WT <i>vs.</i> PCD+OEA	<b>0.029</b>
	PCD <i>vs.</i> PCD+OEA	0.477

Bold values indicate statistical significance at the  $p < 0.05$ .

Supplementary Information. Specificity and efficiency analyses of qPCR primers

Gene	<i>Bdnf</i>
MGI/NCBI ID	<a href="#">88145/12064</a>
Forward primer	GTGGTGTAAGCCGCAAAGA
Reverse primer	AACCATAGTAAGGAAAAGGATGGTC

Job name Job 2: RBDNF\_1L  
Species Mouse (Mus musculus)  
Assembly GRCh38  
Search type BLASTN (NCBI Blast)  
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Results table

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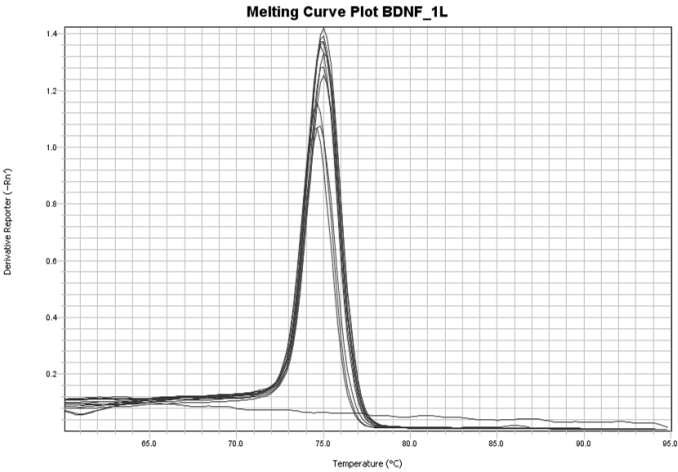
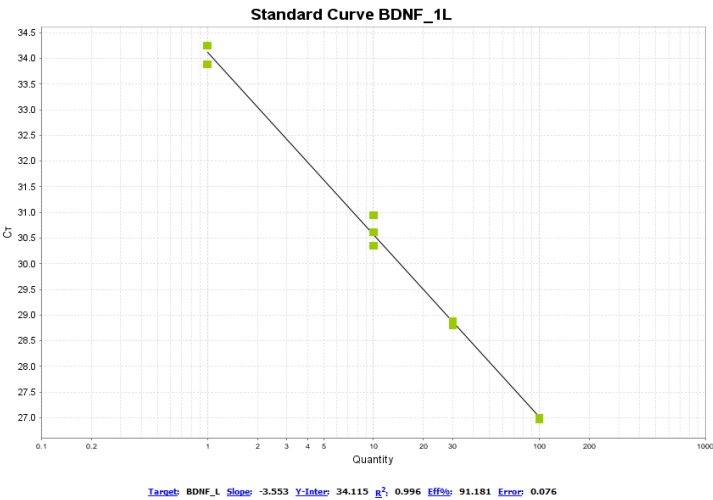
Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
2:109723405-109723429 (Sequence)	<i>Bdnf</i>	Reverse	1	25	25 (Sequence)	49.9	7e-05	100.00 (aligned)
X:115466059-115466076 (Sequence)		Reverse	4	21	18 (Sequence)	36.1	1.0	100.00 (aligned)
16:59726024-59726041 (Sequence)	<i>Epha5</i>	Reverse	4	21	18 (Sequence)	36.1	1.0	100.00 (aligned)

Job name Job 1: FBDNF\_1L  
Species Mouse (Mus musculus)  
Assembly GRCh38  
Search type BLASTN (NCBI Blast)  
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Results table

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
2:109676375-109676393 (Sequence)	<i>Gm45346</i> , <i>Bdnf</i>	Forward	1	19	19 (Sequence)	38.1	0.087	100.00 (aligned)
X:145325531-145325549 (Sequence)	<i>Lthf1</i>	Forward	1	19	19 (Sequence)	30.2	21	94.74 (aligned)
17:44550474-44550488 (Sequence)	<i>Rano2</i>	Reverse	5	19	15 (Sequence)	30.2	21	100.00 (aligned)



Gene	Cox2 (Ptgs2)
MGI/NCBI ID	<a href="#">977798/19225</a>
Forward primer	GGTCATTGGTGGAGAGGTGTA
Reverse primer	TGAGTCTGCTGGTTTGAATAG

Job name

Job 3: FCOX2\_2

Species

Mouse (Mus musculus)

Assembly

GRCm38

Search type

BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
1.150103068-150103389 (Sevenset)	Epxa2	Forward	1	21	21 (Sevenset)	42.9	0.008	100.00 (Sevenset)
1.93679078-93679093 (Sevenset)	Gat3a2	Forward	4	19	16 (Sevenset)	32.1	8.0	100.00 (Sevenset)
1.94004506-94004521 (Sevenset)	Gat3a2	Forward	4	19	16 (Sevenset)	32.1	8.0	100.00 (Sevenset)

Job name

Job 4: RCOX2\_2

Species

Mouse (Mus musculus)

Assembly

GRCm38

Search type

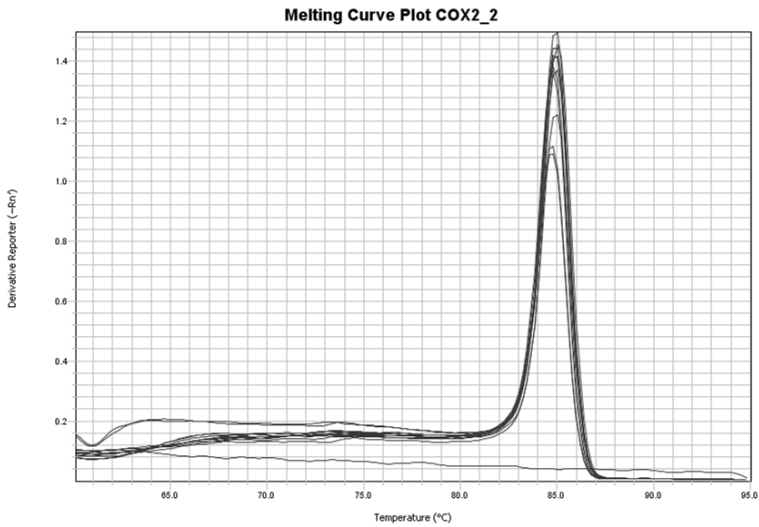
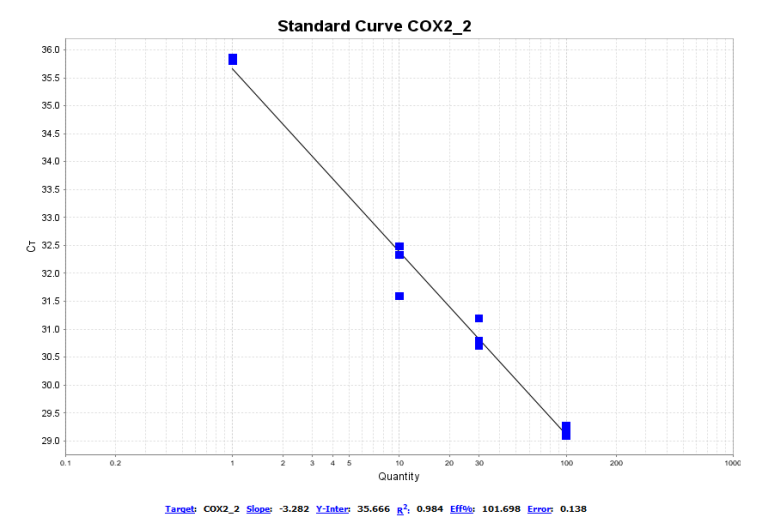
BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
1.150104085-150104106 (Sevenset)	Epxa2	Reverse	1	22	22 (Sevenset)	44.0	0.002	100.00 (Sevenset)
11.61875986-61875983 (Sevenset)	Spoec1	Forward	1	16	16 (Sevenset)	36.1	0.51	100.00 (Sevenset)
13.9821178-9821195 (Sevenset)		Forward	1	17	17 (Sevenset)	34.1	2.0	100.00 (Sevenset)



Gene	<i>Gap43</i>
MGI/NCBI ID	<a href="#">95639/14432</a>
Forward primer	GCTGGTGCATCACCCTTCT
Reverse primer	TGGTGTCAAGCCGGAAGATAA

Job name: Job 1: FGAP43\_1  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)  
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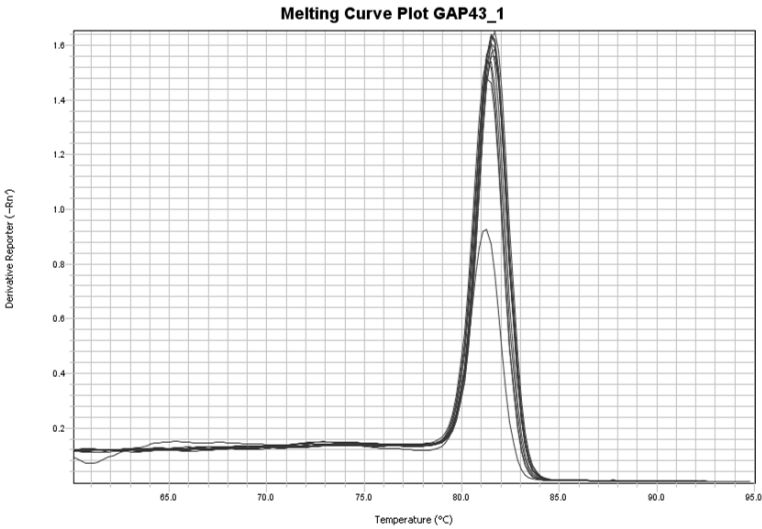
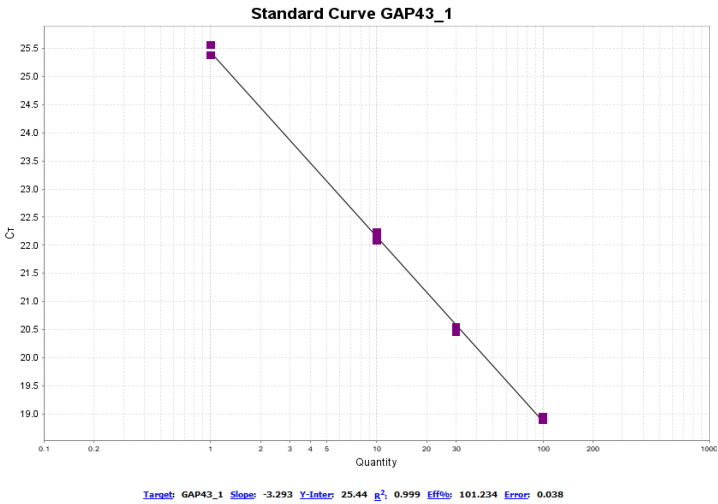
Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
16,422,923,08-42,292,328 (Sequence)	Gap43	Reverse	1	21	21 (Sequence)	42.0	0.008	100.00 (aligned)
12,247,391,80-247,391,94 (Sequence)		Forward	5	19	15 (Sequence)	30.2	31	100.00 (aligned)
8,606,365,13-606,365,31 (Sequence)	Mia3	Reverse	3	21	19 (Sequence)	30.2	31	94.74 (aligned)

Job name: Job 2: RGAP43\_1  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)  
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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
16,422,922,15-42,292,233 (Sequence)	Gap43	Forward	1	19	19 (Sequence)	30.1	0.007	100.00 (aligned)
18,606,670,36-606,670,51 (Sequence)		Reverse	2	17	16 (Sequence)	32.1	5.3	100.00 (aligned)
11,482,698,78-482,698,93 (Sequence)		Forward	2	17	16 (Sequence)	32.1	5.3	100.00 (aligned)





Gene	<i>Ifny</i>
MGI/NCBI ID	<a href="#">107656/15978</a>
Forward primer	CAGCAACAGCAAGGCGAAAAAGG
Reverse primer	TTTCCGCTTCCTGAGGCTGGAT

Job name: Job 3: F IFNg\_5  
 Species: Mouse (Mus musculus)  
 Assembly: GRCh38  
 Search type: BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
10.118442744-118442765 (Sequenced)	<i>Ifng</i> , <i>Gm49751</i>	Forward	1	23	23 (Sequenced)	46.0	7e-04	100.00 (Sequenced)
6.88084544-88084560 (Sequenced)	<i>Rpn1</i>	Reverse	1	17	17 (Sequenced)	34.1	2.7	100.00 (Sequenced)
6.122602286-122602301 (Sequenced)	<i>Apobec1</i>	Reverse	1	16	16 (Sequenced)	32.1	11	100.00 (Sequenced)

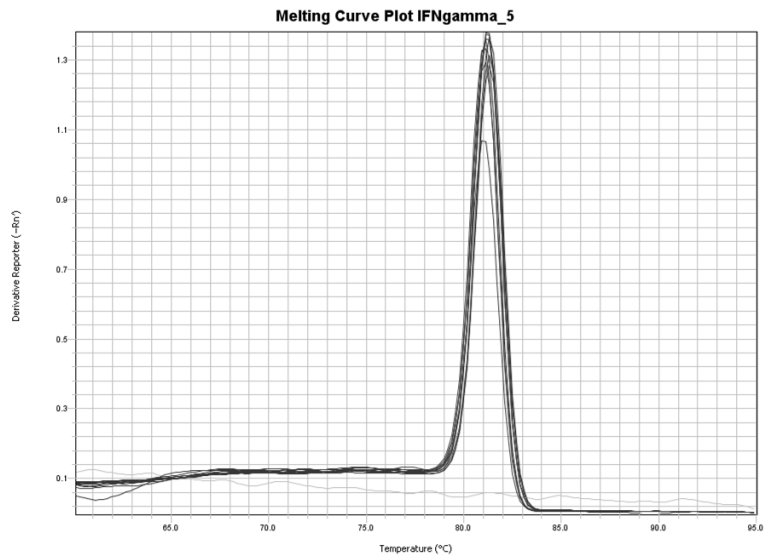
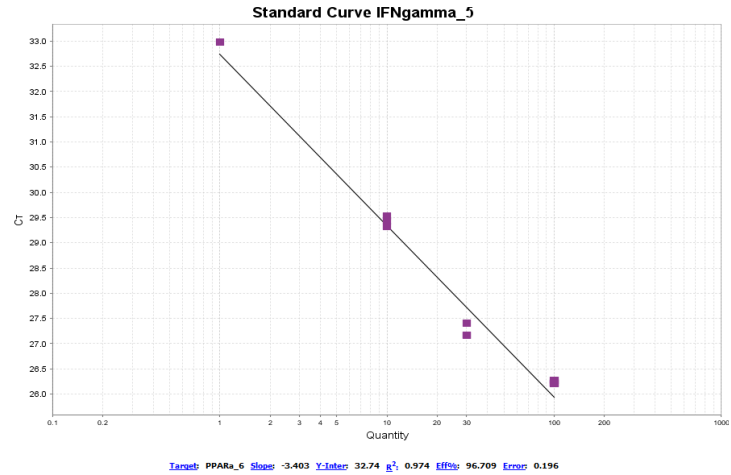
Job name: Job 4: R IFNg\_5  
 Species: Mouse (Mus musculus)  
 Assembly: GRCh38  
 Search type: BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
10.118445226-118445246 (Sequenced)	<i>Ifng</i>	Reverse	1	22	22 (Sequenced)	44.0	0.002	100.00 (Sequenced)
15.97777534-97777550 (Sequenced)		Forward	6	22	17 (Sequenced)	34.1	2.0	100.00 (Sequenced)
7.127866783-127866799 (Sequenced)	<i>Zfp658</i>	Forward	6	22	17 (Sequenced)	34.1	2.0	100.00 (Sequenced)



Gene	<i>Il1b</i>
MGI/NCBI ID	<a href="#">96543/16176</a>
Forward primer	TGCTCATGTCCTCATCCTGGAAGG
Reverse primer	TCGCAGCAGCACATCAACAAGAG

Job name

Job 3: FIL-1B\_2

Species

Mouse (Mus musculus)

Assembly

GRCm38

Search type

BLASTN (NCBI Blast)

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Results table

Show All entries									
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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID	
2:129368079-129368101 (Sequence)	Il1b	Reverse	1	23	23 (Sequence)	46.0	7e-04	100.00	<a href="#">Alignment</a>
CHR_MG4198_PATCH.7486517:7486532 (Sequence)		Reverse	8	23	16 (Sequence)	32.1	11	100.00	<a href="#">Alignment</a>
17:7535084-7535099 (Sequence)		Reverse	8	23	16 (Sequence)	32.1	11	100.00	<a href="#">Alignment</a>

Job name

Job 4: RIL-1B\_2

Species

Mouse (Mus musculus)

Assembly

GRCm38

Search type

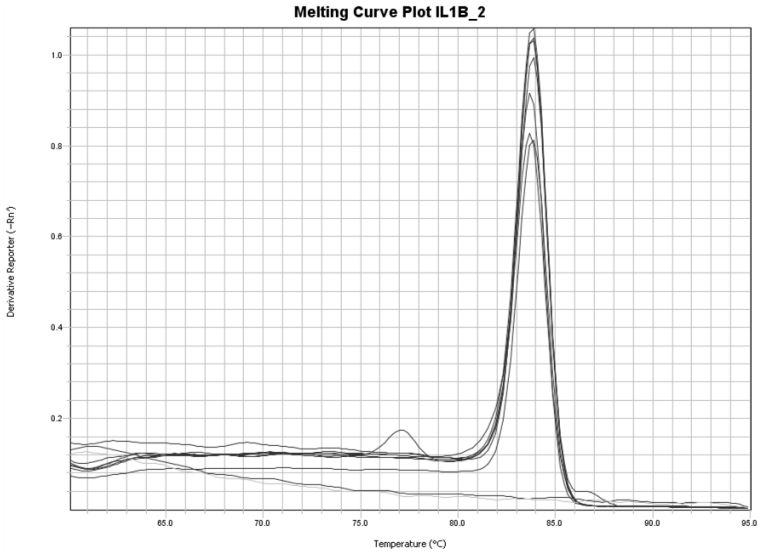
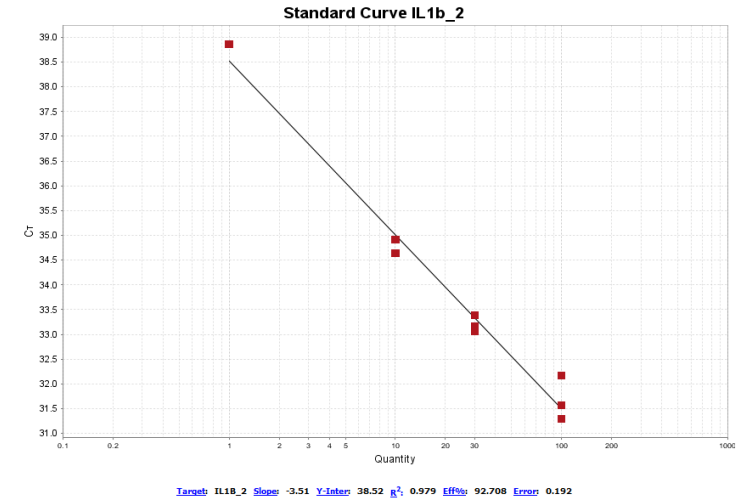
BLASTN (NCBI Blast)

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Results table

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2:129367394-129368007 (Sequence)	Il1b	Forward	1	24	24 (Sequence)	48.0	2e-04	100.00	<a href="#">Alignment</a>
2:24873612-24873628 (Sequence)	Chnrl1	Forward	6	22	17 (Sequence)	34.1	3.4	100.00	<a href="#">Alignment</a>
2:50624565-50624581 (Sequence)		Forward	3	19	17 (Sequence)	34.1	3.4	100.00	<a href="#">Alignment</a>



Gene	<i>Il6</i>
MGI/NCBI ID	<a href="#">96559/16193</a>
Forward primer	GAGGATACCACTCCCAACAGACC
Reverse primer	AAGTGCATCATCGTTGTTTCATACA

Job name: Job 5: FIL-6\_3  
 Species: Mouse (Mus musculus)  
 Assembly: GRCh38  
 Search type: BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
5,300,134,655-300,134,827 (Sequenced)	<i>Il6</i>	Forward	1	23	23 (Sequenced)	46.0	7e-04	100.00
7,133,653,834-133,653,851 (Sequenced)	<i>Edrt1</i>	Reverse	6	23	18 (Sequenced)	36.1	0.69	100.00
CHR_MG3530_PATCH67271492-67271508 (Sequenced)	<i>Nbt2</i>	Forward	3	19	17 (Sequenced)	34.1	2.7	100.00

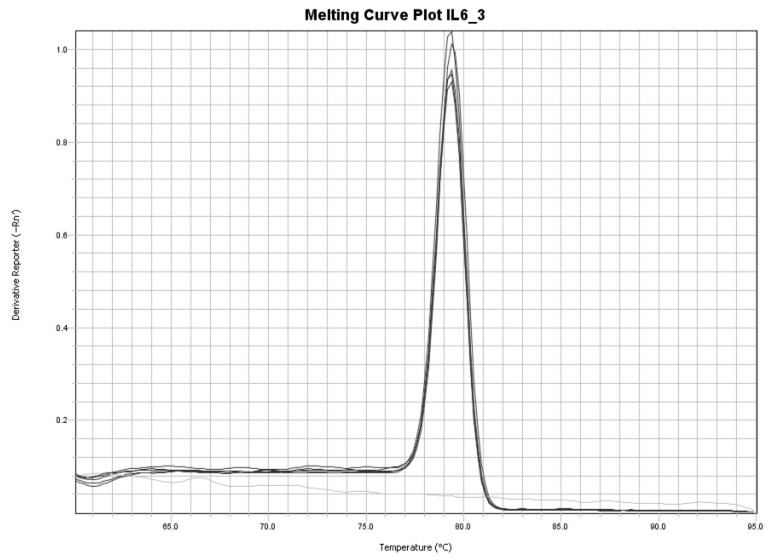
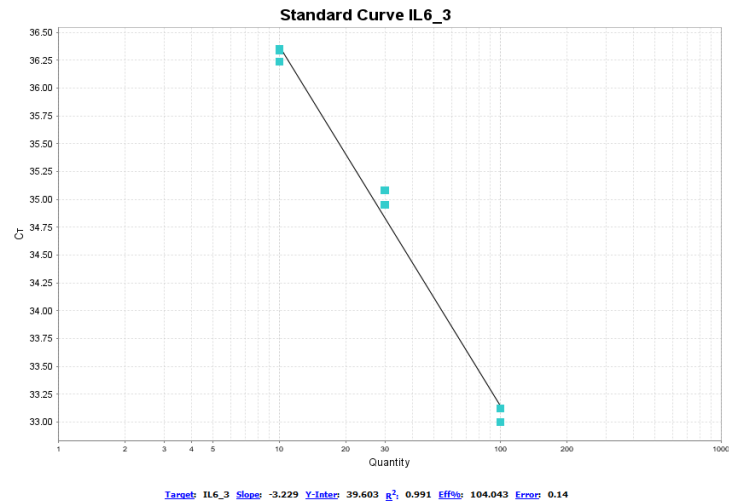
Job name: Job 6: RIL-6\_3  
 Species: Mouse (Mus musculus)  
 Assembly: GRCh38  
 Search type: BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
5,300,148,533-300,148,726 (Sequenced)	<i>Il6</i>	Reverse	1	24	24 (Sequenced)	48.0	2e-04	100.00
16,161,978,688-16,197,883 (Sequenced)		Forward	6	21	16 (Sequenced)	32.1	13	100.00
3,716,233,226-716,233,411 (Sequenced)		Reverse	9	24	16 (Sequenced)	32.1	13	100.00




Gene	<i>iNos (Nos2)</i>
MGI/NCBI ID	<a href="#">97361/18126</a>
Forward primer	CTTTGCCACGGACGAGAC
Reverse primer	AACTTCCAGTCATTGTACTCTGAGG

Job name

Job 1: FINOS\_D

Species

 Mouse (Mus musculus)

Assembly

GRCm38

Search type

BLASTN (NCBI Blast)

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Results table

Show All entries									
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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID	
11:78951210-78951227 (Sequence)	Nos2	Forward	1	18	18 (Sequence)	36.1	0.34	100.00	(Alignment)
5:37554037-37554051 (Sequence)	Srk32b	Forward	4	18	15 (Sequence)	30.2	21	100.00	(Alignment)
3:17677861-17677874 (Sequence)		Reverse	5	18	14 (Sequence)	28.2	82	100.00	(Alignment)

Job name

Job 2: RINOS\_D

Species

 Mouse (Mus musculus)

Assembly

GRCm38

Search type

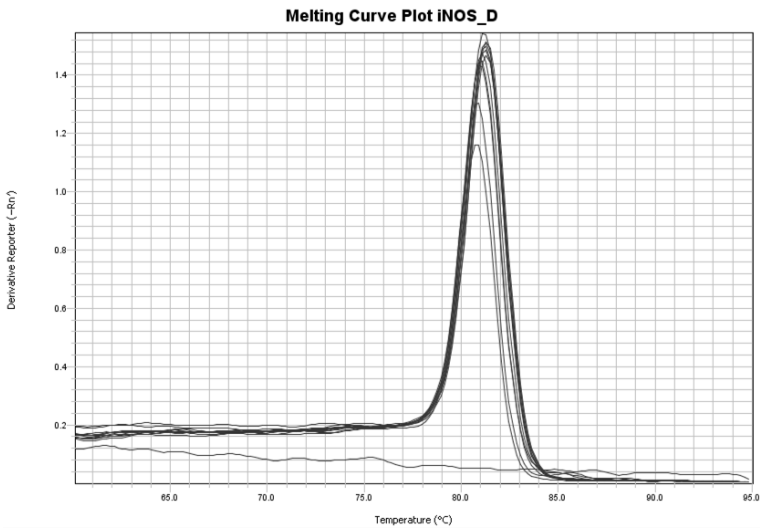
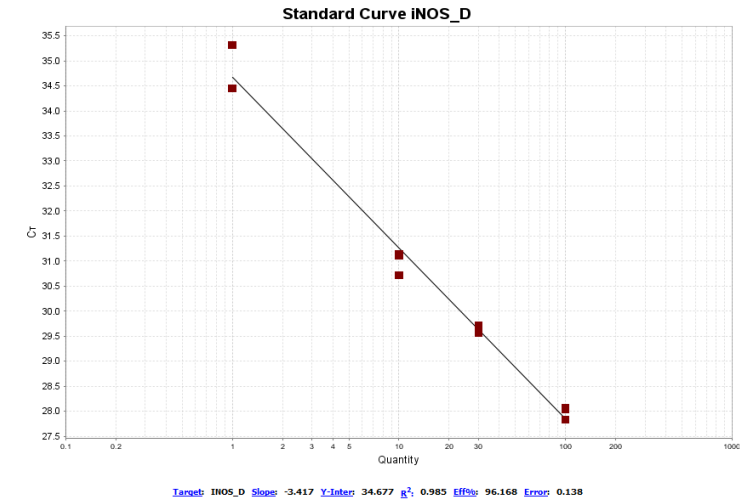
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Results table

Show All entries									
Show/hide columns (2 hidden)									
Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID	
11:78952804-78952828 (Sequence)	Nos2	Reverse	1	25	25 (Sequence)	49.9	7e-05	100.00	(Alignment)
9:25633893-25633910 (Sequence)	Epxd1	Forward	8	25	18 (Sequence)	36.1	1.0	100.00	(Alignment)
X:99111652-99111673 (Sequence)		Reverse	2	22	22 (Sequence)	34.1	4.0	95.45	(Alignment)




Gene	<i>Map2</i>
MGI/NCBI ID	<a href="#">97175/17756</a>
Forward primer	GCTGTAGCAGTCCTGAAAGGTG
Reverse primer	CTTCCTCCACTGTGGCTGTTTG

Job name

Job 1: F MAP2\_8

Species

 Mouse (Mus musculus)

Assembly

GRCm38

Search type

BLASTN (NCBI Blast)

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Results table

Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	v	E-val	%ID
1,663,994,430-56,399,451 (Sequence)	Map2	Forward	1	22	22 (Sequence)	44.0		0.002	100.00 (Alignment)
13,109,053,951-109,053,967 (Sequence)	Pde4d	Forward	4	20	17 (Sequence)	34.1		2.0	100.00 (Alignment)
5,518,975,97-5,189,7613 (Sequence)		Forward	4	20	17 (Sequence)	34.1		2.0	100.00 (Alignment)

Job name

Job 2: R MAP2\_8

Species

 Mouse (Mus musculus)

Assembly

GRCm38

Search type

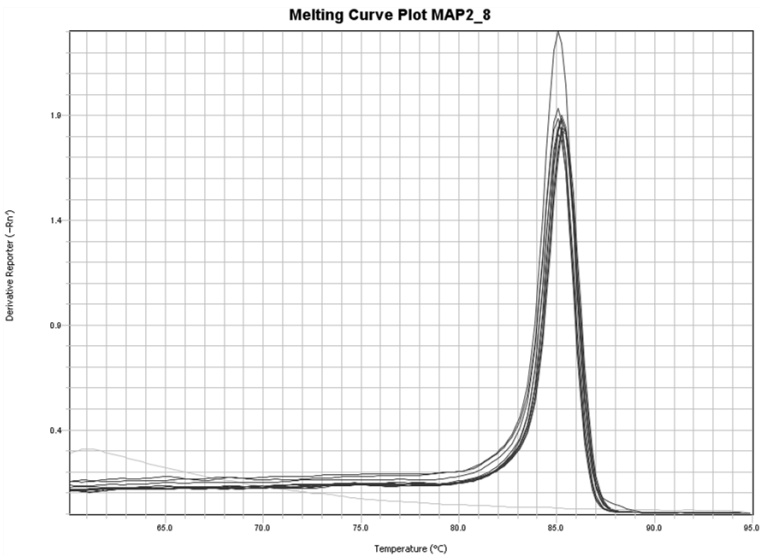
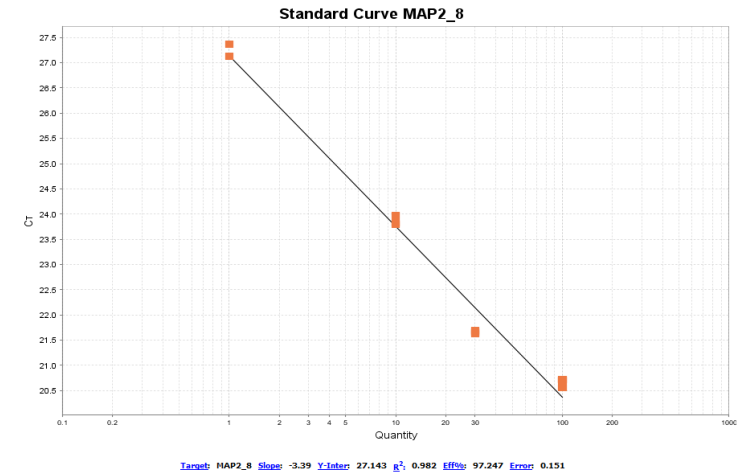
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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	v	E-val	%ID
1,664,015,00-66,401,521 (Sequence)	Map2	Reverse	1	22	22 (Sequence)	44.0		0.002	100.00 (Alignment)
7,110,892,973-110,892,990 (Sequence)	Mot1	Reverse	1	18	18 (Sequence)	36.1		0.51	100.00 (Alignment)
5,127,433,533-127,433,550 (Sequence)	Tmem132c	Forward	1	18	18 (Sequence)	36.1		0.51	100.00 (Alignment)



Gene	<i>Nfkb</i>
MGI/NCBI ID	<a href="#">1914300/67050</a>
Forward primer	GCTGCCAAAGAAGGACACGACA
Reverse primer	GGCAGGCTATTGCTCATCACAG

Job name: Job 5: F NFKB\_3  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)

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Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
3.135594931-135594952 (Sequence)	Nfkb1	Reverse	1	22	22 (Sequence)	44.0	0.002	100.00 (alignment)
12.84380205-84380221 (Sequence)	Entpd5	Reverse	1	17	17 (Sequence)	34.1	2.0	100.00 (alignment)
11.82735770-82735786 (Sequence)	Cd8b	Forward	2	18	17 (Sequence)	34.1	2.0	100.00 (alignment)

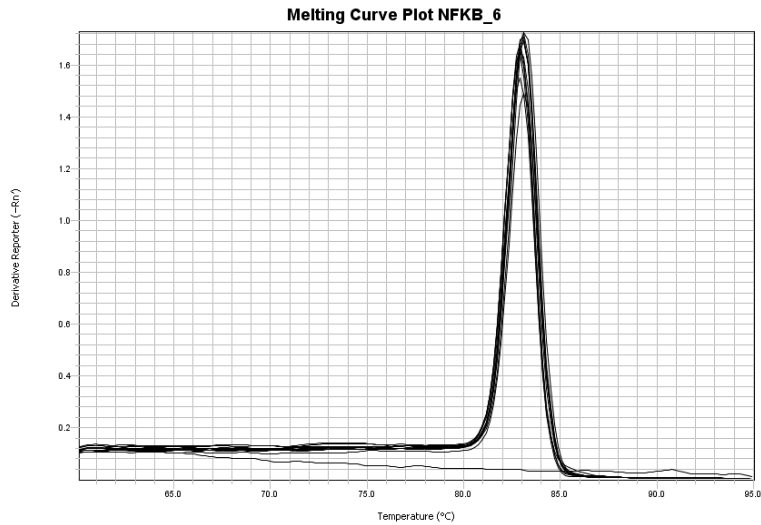
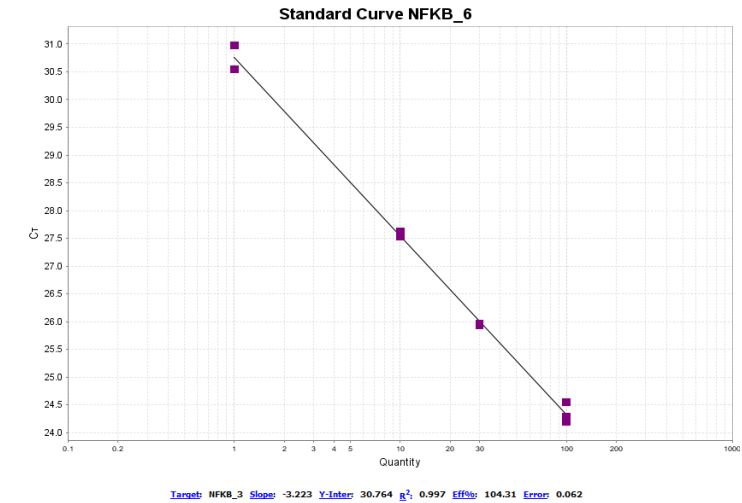
Job name: Job 6: R NFKB\_3  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)

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Results table

Show All entries Show/hide columns (2 hidden) Filter

Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
3.135594336-135594357 (Sequence)	Nfkb1	Forward	1	22	22 (Sequence)	44.0	0.002	100.00 (alignment)
9.112092346-112092362 (Sequence)	Arpe21	Forward	6	22	17 (Sequence)	34.1	2.0	100.00 (alignment)
3.7679587-7679592 (Sequence)	Gm16685	Reverse	5	20	16 (Sequence)	32.1	8.0	100.00 (alignment)



Gene	<i>Ppara</i>
MGI/NCBI ID	<a href="#">104740/19013</a>
Forward primer	ATGCCAGTACTGCCGTTTTC
Reverse primer	TTGCCCAGAGATTGAGGTC

Job name: Job 9: FPPAR-alpha\_6  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)

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Results table

Show All Entires

Show/hide columns (2 hidden)

Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
15,857,80955-857,89584 (sequence)	Ppara	Forward	1	20	20 (sequence)	40.0	0.022	100.00 (aligned)
1,374,89565-374,99580 (sequence)	Musfa	Forward	5	20	16 (sequence)	32.1	5.3	100.00 (aligned)
1,182,904643-182,904657 (sequence)		Forward	1	15	15 (sequence)	30.2	21	100.00 (aligned)

Job name: Job 10: RPPAR-alpha\_6  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)

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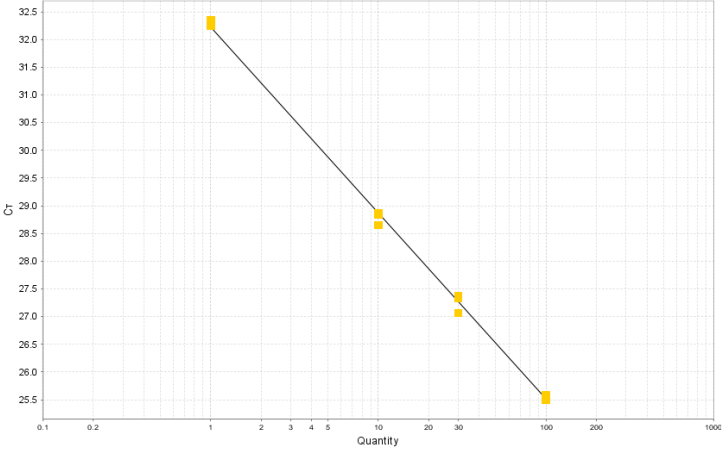
Results table

Show All Entires

Show/hide columns (2 hidden)

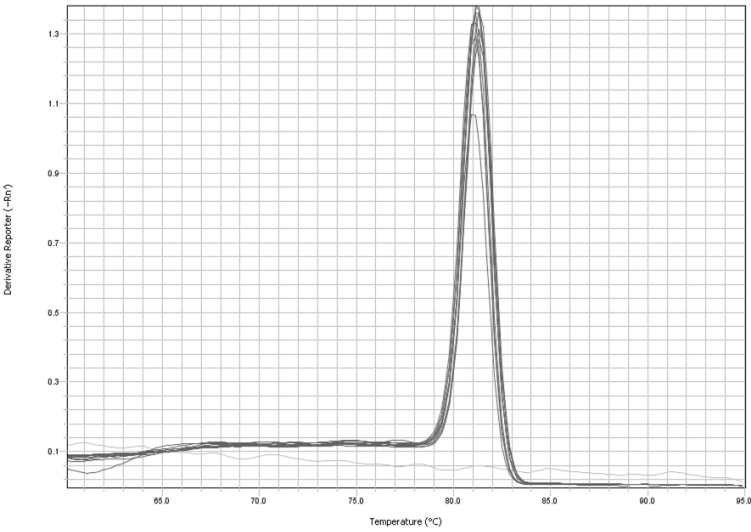
Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
15,857,80935-857,86954 (sequence)	Ppara	Reverse	1	20	20 (sequence)	40.0	0.022	100.00 (aligned)
16,915,6095-915,6022 (sequence)		Reverse	3	19	17 (sequence)	34.1	1.3	100.00 (aligned)
12,28453633-28453649 (sequence)	Dcdc2c	Reverse	1	17	17 (sequence)	34.1	1.3	100.00 (aligned)

Standard Curve PPARalpha\_6



Target: PPARa\_6 Slope: -3.362 Y-inter: 32.23 R<sup>2</sup>: 0.998 Eff%: 98.346 Error: 0.054

Melting Curve Plot PPARalpha\_6



Gene	<i>Tnf<math>\alpha</math></i>
MGI/NCBI ID	<a href="#">104798/21926</a>
Forward primer	GCTTGTCACTCGAATTTTGAGA
Reverse primer	ATGTCTCAGCCTCTTCTCATTC

Job name: Job 1: FTFN-alpha\_4  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)

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Results table

Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
17:35281727-35281748 (Sequenced)	Tnf	Reverse	1	22	22 (Sequenced)	44.0	0.002	100.00 (Aligned)
15:192735245-192735262 (Sequenced)		Reverse	5	22	18 (Sequenced)	36.1	0.51	100.00 (Aligned)
9:114945435-114945452 (Sequenced)		Reverse	1	18	18 (Sequenced)	36.1	0.51	100.00 (Aligned)

Job name: Job 2: RTNF-alpha\_4  
 Species: Mouse (Mus musculus)  
 Assembly: GRCm38  
 Search type: BLASTN (NCBI Blast)

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Results table

Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
17:352809876-352809897 (Sequenced)	Tnf	Forward	1	22	22 (Sequenced)	44.0	0.002	100.00 (Aligned)
X:82477467-82477560 (Sequenced)		Reverse	5	20	16 (Sequenced)	32.1	8.0	100.00 (Aligned)
X:82459583-82459589 (Sequenced)		Reverse	5	20	16 (Sequenced)	32.1	8.0	100.00 (Aligned)

