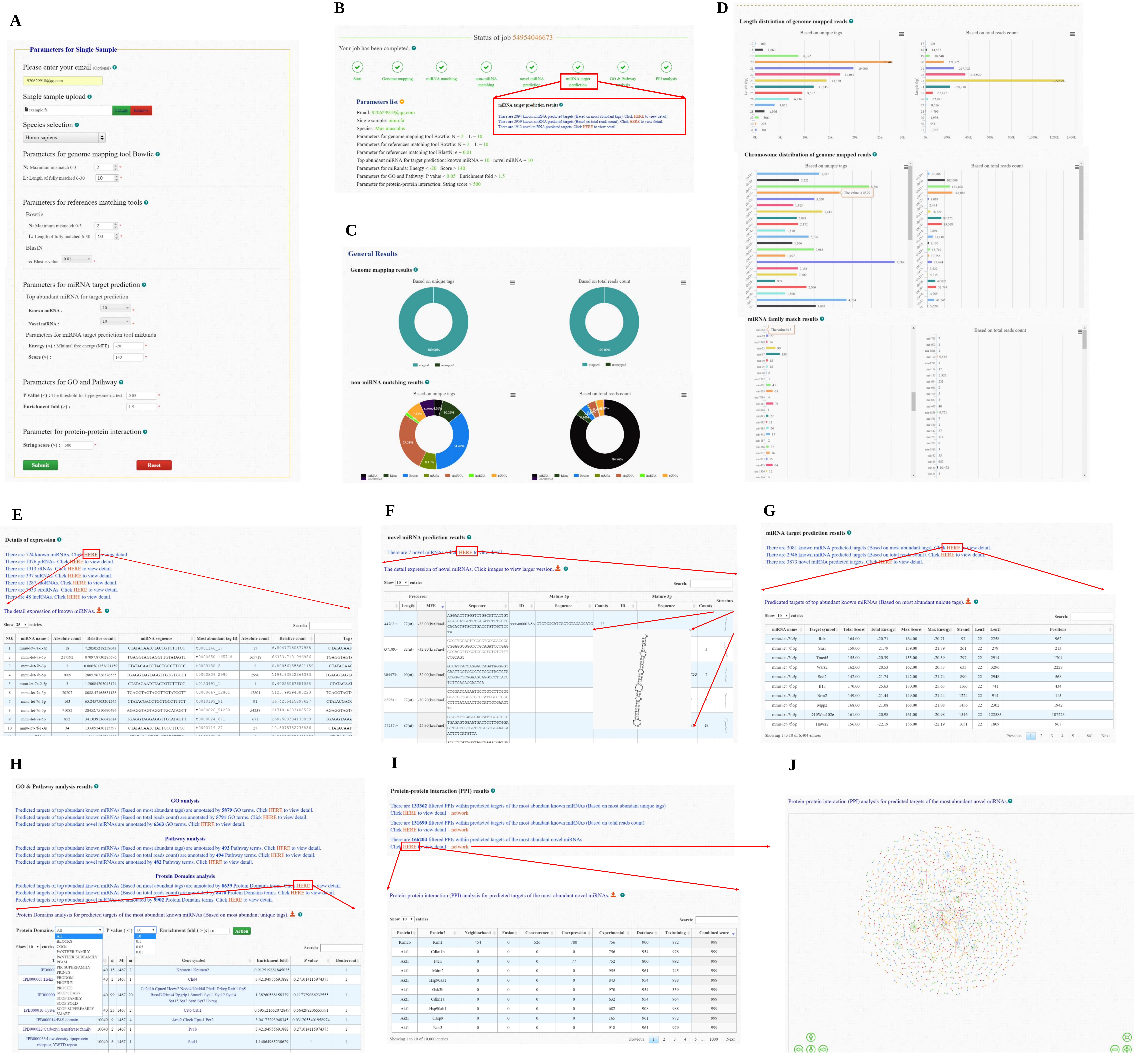
Supplementary Figure 2



Parameters for Single Sample

Please enter your email (Optional)

920629918@qq.com

Single sample upload

example.fa Change Remove

Species selection

Homo sapiens

Parameters for genome mapping tool Bowtie

N: Maximum mismatch 0-3 2 *

L: Length of fully matched 6-30 10 *

Parameters for references matching tools

Bowtie

N: Maximum mismatch 0-3 2 *

L: Length of fully matched 6-30 10 *

BlastN

e: Blast e-value 0.01 *

Parameters for miRNA target prediction

Top abundant miRNA for target prediction

Known miRNA : 10 *

Novel miRNA : 10 *

Parameters for miRNA target prediction tool miRanda

Energy (<) : Minimal free energy (MFE) -20 *

Score (>) : 140 *

Parameters for GO and Pathway

P value (<) : The threshold for hypergeometric test 0.05 *

Enrichment fold (>) : 1.5 *

Parameter for protein-protein interaction

String score (>) : 500 *

Submit Reset

Status of job 54954046673

Your job has been completed.

Start — Genome mapping — miRNA matching — non-miRNA matching — novel miRNA prediction — miRNA target prediction — GO & Pathway analysis — PPI analysis

Parameters list

Email: 920629919@qq.com
Single sample: mmu.fa
Species: Mus musculus
Parameters for genome mapping tool Bowtie: N = 2 L = 10
Parameters for references matching tool Bowtie: N = 2 L = 10
Parameter for references matching tool BlastN: e = 0.01
Top abundant miRNA for target prediction: known miRNA = 10 novel miRNA = 10
Parameters for miRanda: Energy < -20 Score > 140
Parameters for GO and Pathway: P value < 0.05 Enrichment fold > 1.5
Parameter for protein-protein interaction: String score > 500

miRNA target prediction results

There are 2894 known miRNA predicted targets (Based on most abundant tags). Click HERE to view detail.
There are 2959 known miRNA predicted targets (Based on total reads count). Click HERE to view detail.
There are 1912 novel miRNA predicted targets. Click HERE to view detail.

General Results

Genome mapping results

Based on unique tags — Based on total reads count

non-miRNA matching results

Based on unique tags — Based on total reads count

Length distriution of genome mapped reads

Based on unique tags — Based on total reads count

Chromosome distribution of genome mapped reads

Based on unique tags — Based on total reads count

miRNA family match results

Based on total reads count

Details of expression

There are 724 known miRNAs. Click HERE to view detail.
There are 1076 piRNAs. Click HERE to view detail.
There are 1913 rRNAs. Click HERE to view detail.
There are 397 snRNAs. Click HERE to view detail.
There are 1287 snoRNAs. Click HERE to view detail.
There are 7033 circRNAs. Click HERE to view detail.
There are 48 lncRNAs. Click HERE to view detail.

The detail expression of known miRNAs.

Show 25 entries Search:

NO.	miRNA name	Absolute count	Relative count	miRNA sequence	Most abundant tag ID	Absolute count	Relative count	Tag s
1	mmu-let-7a-1-3p	18	7.20505218259043	CTATACAATCTACTGTCTTTCC	t0001166_17	17	6.80477150577985	CTATACAAT
2	mmu-let-7a-5p	217592	87097.8730285676	TGAGGTAGTAGGTTGTATAGTT	t0000650_165718	165718	66333.7131996956	TGAGGTAGTA
3	mmu-let-7b-3p	2	0.800561353621159	CTATACAACCTACTGCCTTCCC	t0088138_2	2	0.800561353621159	CTATACAAC
4	mmu-let-7b-5p	7009	2805.56726376535	TGAGGTAGTAGGTTGTGTGGTT	t0000509_2990	2990	1196.83922366363	TGAGGTAGTA
5	mmu-let-7c-2-3p	3	1.20084203043174	CTATACAATCTACTGTCTTTCC	t0123991_1	1	0.40028067681058	CTATACAAT
6	mmu-let-7c-5p	20207	8088.47163631138	TGAGGTAGTAGGTTGTATGGTT	t0000667_12801	12801	5123.99294385223	TGAGGTAGTA
7	mmu-let-7d-3p	163	65.2457503201245	CTATACGACCTGCTGCCTTTCT	t0010199_91	91	36.4255415897627	CTATACGACC
8	mmu-let-7d-5p	71082	28452.7510690496	AGAGGTAGTAGGTTGCATAGTT	t0000826_54238	54238	21710.4233488522	AGAGGTAGTA
9	mmu-let-7e-5p	852	341.039136642614	TGAGGTAGGAGGTTGTATAGTT	t0000024_671	671	268.588334139899	TGAGGTAGGA
10	mmu-let-7f-1-3p	34	13.6095430115597	CTATACAATCTATTGCCTTCCC	t0000119_27	27	10.8075782738856	CTATACAAT

novel miRNA prediction results

There are 7 novel miRNAs. Click HERE to view detail.

The detail expression of novel miRNAs. Click images to view larger version.

Show 10 entries Search:

Precursor				Mature-5p			Mature-3p			Structur
	Length	MFE	Sequence	ID	Sequence	Counts	ID	Sequence	Counts	
44763:+	77(nt)	-33.00(kcal/mol)	AGGAACTTGGGTCTGGCATTACTGTAGAGCATGGTCTCAGATGTCTGCTCCACACTGTGCCTGACCTGTTGTTCCTA	xxx-m0002-5p	GTCTGGCATTACTGTAGAGCATG	23				
37189:-	82(nt)	-32.80(kcal/mol)	CGCTTGGAGTTCCCGTGGGCAGGCGCGGAGGCGGGTCCGCAGATCCCGAGCGGAGCTTGCCTGGCGTCTCTGTTTCCGTAGT						3	
304473:-	90(nt)	-32.00(kcal/mol)	GTCATTACCAGGACCAGATAGGGGTGAATTCCTCGCCTGTCGCTAGTCTAACGGGCTCGGAAGCAGGCCCTTATCTCTTGAGAGCAATGA					TG	7	
63981:+	77(nt)	-30.70(kcal/mol)	CTGGATCAGAATGCCTGTCTTTGGGGGATGCTGGATGTGCATGGCCTGGCCCTCTATAGACTGGCATTGTGAAGTTG						3	
57237:+	87(nt)	-25.90(kcal/mol)	GTACTTTCAGGCAGTATTGCATCCCTGAGAGTGGAATGACTCCTTGTGGAGTTGGTCCTGGTCTGGGTGCAAACAATTTTCATGTTA						19	

miRNA target prediction results

There are 3081 known miRNA predicted targets (Based on most abundant tags). Click HERE to view detail.
There are 2946 known miRNA predicted targets (Based on total reads count). Click HERE to view detail.
There are 3873 novel miRNA predicted targets. Click HERE to view detail.

Predicated targets of top abundant known miRNAs (Based on most abundant unique tags).

Show 10 entries Search:

miRNA name	Target symbol	Total Score	Total Energy	Max Score	Max Energy	Strand	Len1	Len2	Positions
mmu-let-7f-5p	Rdx	164.00	-20.71	164.00	-20.71	97	22	2258	962
mmu-let-7f-5p	Sra1	159.00	-21.79	159.00	-21.79	261	22	279	213
mmu-let-7f-5p	Tmed5	155.00	-20.39	155.00	-20.39	297	22	2914	1704
mmu-let-7f-5p	Wars2	162.00	-20.53	162.00	-20.53	633	22	3296	2228
mmu-let-7f-5p	Sod2	142.00	-21.74	142.00	-21.74	890	22	2948	568
mmu-let-7f-5p	Il13	170.00	-25.63	170.00	-25.63	1166	22	741	434
mmu-let-7f-5p	Rrm2	149.00	-21.44	149.00	-21.44	1224	22	914	115
mmu-let-7f-5p	Mpp2	168.00	-21.08	168.00	-21.08	1456	22	2302	1942
mmu-let-7f-5p	D10Wsu102e	161.00	-20.98	161.00	-20.98	1546	22	122583	107223
mmu-let-7f-5p	Havcr2	156.00	-22.19	156.00	-22.19	1651	22	1809	967

Showing 1 to 10 of 6,404 entries Previous 1 2 3 4 5 … 641 Next

GO & Pathway analysis results

GO analysis

Predicted targets of top abundant known miRNAs (Based on most abundant tags) are annotated by **5879** GO terms. Click HERE to view detail.
Predicted targets of top abundant known miRNAs (Based on total reads count) are annotated by **5791** GO terms. Click HERE to view detail.
Predicted targets of top abundant novel miRNAs are annotated by **6363** GO terms. Click HERE to view detail.

Pathway analysis

Predicted targets of top abundant known miRNAs (Based on most abundant tags) are annotated by **493** Pathway terms. Click HERE to view detail.
Predicted targets of top abundant known miRNAs (Based on total reads count) are annotated by **494** Pathway terms. Click HERE to view detail.
Predicted targets of top abundant novel miRNAs are annotated by **482** Pathway terms. Click HERE to view detail.

Protein Domains analysis

Predicted targets of top abundant known miRNAs (Based on most abundant tags) are annotated by **8639** Protein Domains terms. Click HERE to view detail.
Predicted targets of top abundant known miRNAs (Based on total reads count) are annotated by **8470** Protein Domains terms. Click HERE to view detail.
Predicted targets of top abundant novel miRNAs are annotated by **9902** Protein Domains terms. Click HERE to view detail.

Protein Domains analysis for predicted targets of the most abundant known miRNAs (Based on most abundant unique tags).

Protein Domains: All **P value (<):** 1.0 **Enrichment fold (>):** 1.0 Action

Show 10 entries Search:

T		n	M	m	Gene symbol	Enrichment fold	P value	Bonferroni
IPB000(	40	15	1467	2	Kremen1 Kremen2	0.912519881845035	1	1
IPB000005:Helix-	40	2	1467	1	Chd4	3.42194955691888	0.271014115974375	1
IPB00000	40	99	1467	20	Cc2d1b Cpne6 Hecw2 Nedd4 Nedd4l Plcd1 Prkcg Rab11fip5 Rasal3 Rims4 Rpgrip1 Smurf1 Syt11 Syt12 Syt14 Syt15 Syt2 Syt6 Syt7 Uvrag	1.38260588158339	0.117329086232555	1
IPB000010:Cyste	40	23	1467	2	Cst6 Cstl1	0.595121662072849	0.564298206555591	1
IPB000014:PAS domain	10040	9	1467	4	Arnt2 Clock Epas1 Per2	3.04173293948345	0.0312055401958974	1
IPB000022:Carboxyl transferase family	10040	2	1467	1	Pccb	3.42194955691888	0.271014115974375	1
IPB000033:Low-density lipoprotein receptor, YWTD repeat	10040	6	1467	1	Sorl1	1.14064985230629	1	1

Protein-protein interaction (PPI) results

There are **133362** filtered PPIs within predicted targets of the most abundant known miRNAs (Based on most abundant unique tags)
Click HERE to view detail network

There are **131690** filtered PPIs within predicted targets of the most abundant known miRNAs (Based on total reads count)
Click HERE to view detail network

There are **166204** filtered PPIs within predicted targets of the most abundant novel miRNAs
Click HERE to view detail network

Protein-protein interaction (PPI) analysis for predicted targets of the most abundant novel miRNAs.

Show 10 entries Search:

Protein1	Protein2	Neighborhood	Fusion	Cooccurence	Coexpression	Cxperimental	Database	Textmining	Combined score
Rrm2b	Rrm1	454	0	526	780	756	900	882	999
Akt1	Cdkn1b	0	0	0	0	756	954	978	999
Akt1	Pten	0	0	0	77	752	800	992	999
Akt1	Mdm2	0	0	0	0	955	961	745	999
Akt1	Hsp90aa1	0	0	0	0	843	954	988	999
Akt1	Gsk3b	0	0	0	0	970	954	359	999
Akt1	Cdkn1a	0	0	0	0	632	954	964	999
Akt1	Hsp90ab1	0	0	0	0	682	908	988	999
Akt1	Casp9	0	0	0	0	165	961	972	999
Akt1	Nos3	0	0	0	0	918	961	979	999

Showing 1 to 10 of 10,000 entries Previous 1 2 3 4 5 … 1000 Next

Protein-protein interaction (PPI) analysis for predicted targets of the most abundant novel miRNAs.