

FasterDB

Find your Gene : ?  Human

Paste a sequence (>24nucleotides) to find your gene :



Search provided for : Human

[Download customized exons lists](#)

Result Number	Gene Description
1	WNK1 HSAN2, HSN2, PRKWNK1 ENSG00000060237 WNK lysine deficient protein kinase 1 

Figure 1. FasterDB “SEARCH PAGE” corresponding to human WNK1 gene. In the search page, gene searching, in the mouse or human genome, can be done: 1- By keywords (ENSEMBL ID, HUGO gene name, synonyms or gene description) or chromosomal localization; 2- By perfect match sequence search against fasterDB genes. The result of the request will be displayed in 3. Clicking on help icon will display search criteria for users.

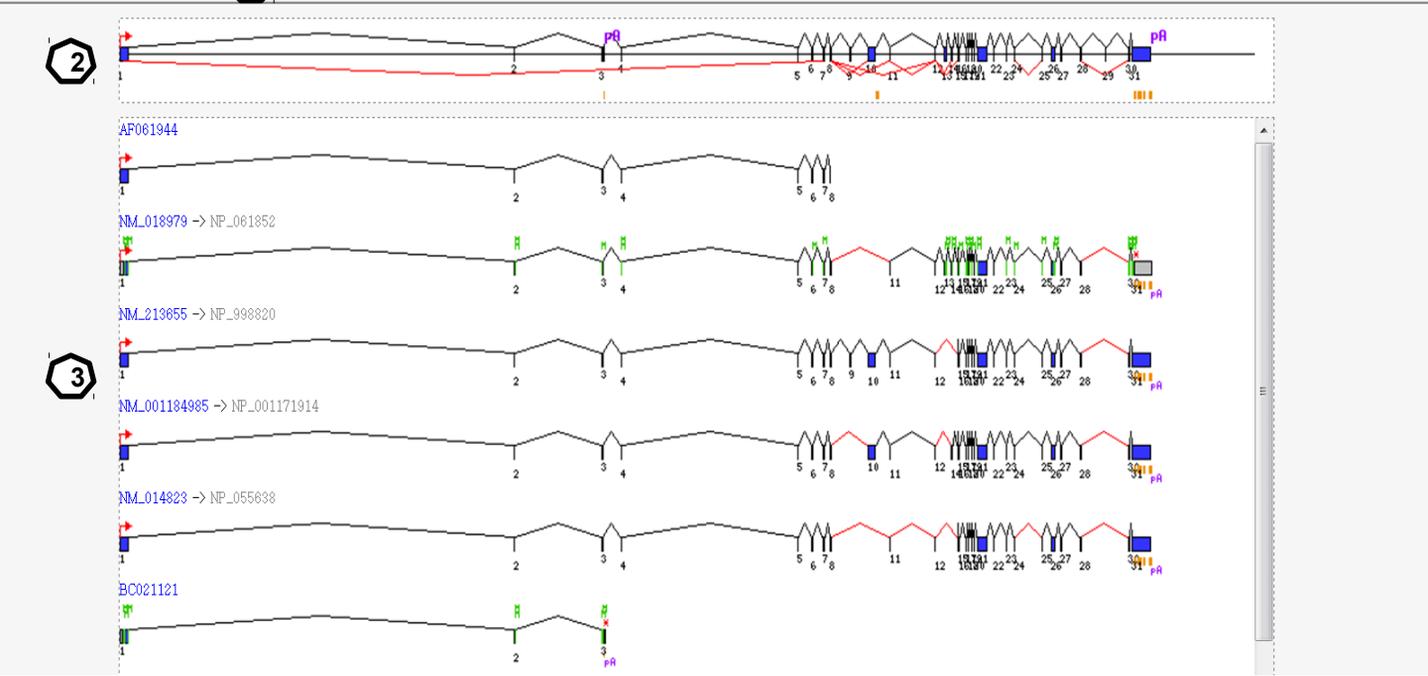


Figure 2. FasterDB “MAIN PAGE” corresponding to human WNK1 gene. WNK1 gene main page in fasterDB. 1- Information about the gene (fasterDB id, HUGO name and synonyms), clicking on the left arrow allows to go to the upstream gene while clicking on the right arrow leads to downstream gene; 2- Schematic representation of the gene. Alternative splicing events are also presented. In orange are presented micro-RNAs binding sites; 3- Transcripts of the gene with the splicing pattern of each transcript. Transcript names are clickable, allowing to get more information about the transcript in NCBI. 4- Panel with different tabs, each providing additional information about gene (See Supplementary Fig 1-9 for more information); 5- Link to the fasterDB human’s orthologous gene in the mouse genome; 6- Link to download the graphical representation of the gene and its transcripts; 7- Link to fasterDB “SEARCH PAGE”. Clicking on the help icon displays a legend of the page. Each exon or intron is clickable to display its sequence in fasta format.

A

Experiments	Expressed	<Gene Expression Level	<Ni	<Global Si	<Local Si	P-value
hESC T0	Yes	1071	1.09	3.71	2.12	0.0000
HSMM	Yes	1524	-1.27	2.68	1.97	0.0000
A549	Yes	1861	-1.59	2.14	1.54	0.0000
WI38	Yes	977	-1.89	1.79	1.51	0.0000
HConF	Yes	1409	-2.44	1.37	1.36	0.0000
NHA	Yes	1202	-2.70	1.24	1.34	0.0002
HEPG	Yes	432	-2.70	1.24	-1.33	0.0106
HRE	Yes	560	-3.03	1.13	-1.33	0.0005
RPTEC	Yes	1323	-3.85	-1.14	-1.39	0.0002
HAc	Yes	1087	-4.76	-1.41	-1.39	0.0009
HGF	Yes	649	-5.56	-1.64	-1.39	0.0050
HPF	Yes	936	-4.35	-1.30	-1.41	0.0001
AG09309	Yes	884	-6.25	-1.89	-1.43	0.0001
SKNS	Yes	587	-2.08	1.64	-1.45	0.0003
LNCAP	Yes	1080	-3.85	-1.15	-1.47	0.0007
HEK293	Yes	1243	-3.45	-1.05	-1.56	0.0000
CACO2	Yes	681	-2.38	1.43	-1.69	0.0000

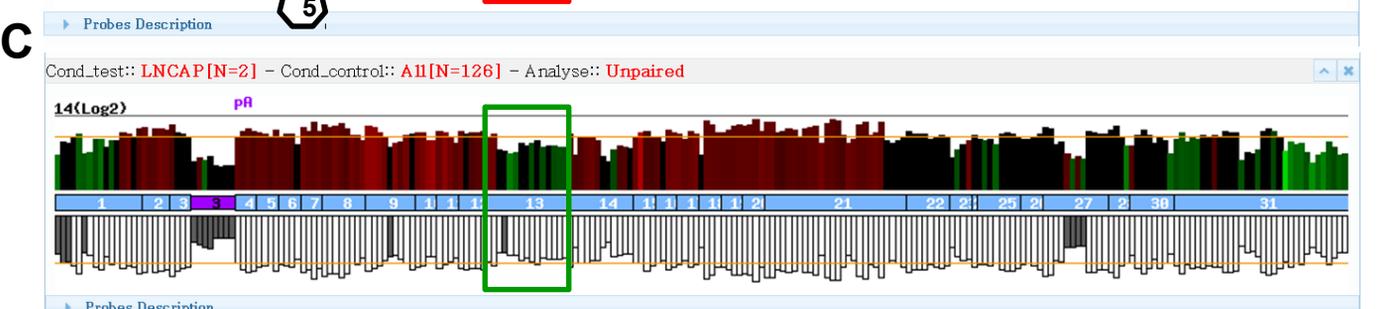
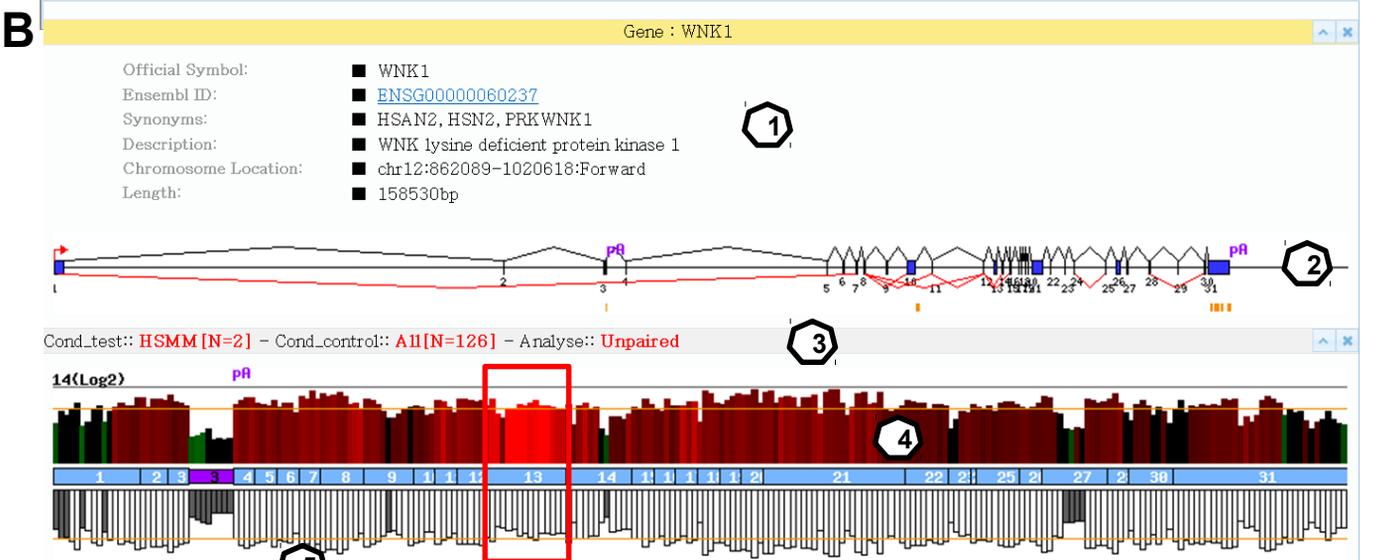


Figure 3. Expression table of exon 13 in the WNK1 gene among human cell lines (A) and visualization of exon arrays probes intensities in the HSMM (B) and LNCAP (C) cell lines for WNK1. **A.** For each cell line, we computed gene expression level which represents the median of the intensity of all the probes associated to the exons of the gene and determine if the gene is expressed or not. We also compute Normalized Intensity (NI), Global Splicing Index (SI) and Local Splicing index (Si) which represent different methods to calculate the inclusion level of an exon. The table can be sorted according to these values. Finally, a P-value is given for each local Si value. **B.** Graphical representation of the WNK1 gene in exon-arrays visualization: 1- Information about the gene; 2- Graphical representation of the gene; 3- Information about the analysis; 4- Graphical representation of the probes among the exons of the WNK1 gene. The height of each probe corresponds to its intensity level. Red probes indicate inclusion in test condition while green probes indicate its exclusion (inclusion in control condition). Black probes point no difference between both conditions. 5- Descriptions of the probes. Red rectangle corresponds to exon 13 which is highly included in HSMM (test condition) compared to all the other cell lines. **C.** Green rectangle indicates the exclusion of the exon 13 in the LNCAP cell line compared to remaining cell lines.

A

Gene	
Symbol:	WNK1
Synonyms:	HSAN2, HSN2, PRKWNK1
Description:	WNK lysine deficient protein kinase 1
Ensembl ID Link:	ENSG00000060237
Chromosome:	12 - Forward Strand
Chromosomal Location: (UCSC Link)	862089 - 1020618 (158530bp)
Sequence:	sequence
Associated Transcripts:	AF061944 NM_018979 NM_213655 NM_001184985 NM_014823 BC021121 BC071959 BC094862 AJ296290 BC141881 AB002342 DQ925669 BC013629

B

Exon-Intron						
Position	Type	Gene Coordinate	Chromosomal Coordinate	Length	Sequence	Features
1	Exon	1 - 1402	862089 - 863490	1402	sequence	download
1	Intron	1403 - 60719	863491 - 922807	59317	sequence	-
2	Exon	60720 - 60892	922808 - 922980	173	sequence	download
2	Intron	60893 - 74119	922981 - 936207	13227	sequence	-
3	Exon	74120 - 74340	936208 - 936428	221	sequence	download
3	Intron	74341 - 77080	936429 - 939168	2740	sequence	-
4	Exon	77081 - 77238	939169 - 939326	158	sequence	download
4	Intron	77239 - 104238	939327 - 966326	27000	sequence	-
5	Exon	104239 - 104327	966327 - 966415	89	sequence	download
5	Intron	104328 - 106322	966416 - 968410	1995	sequence	-
6	Exon	106323 - 106542	968411 - 968630	220	sequence	download
6	Intron	106543 - 108090	968631 - 970178	1548	sequence	-
7	Exon	108091 - 108421	970179 - 970509	331	sequence	download
7	Intron	108422 - 109160	970510 - 971248	739	sequence	-
8	Exon	109161 - 109348	971249 - 971436	188	sequence	download
8	Intron	109349 - 112187	971437 - 974275	2839	sequence	-
9	Exon	112188 - 112442	974276 - 974530	255	sequence	download
9	Intron	112443 - 114943	974531 - 977031	2501	sequence	-
10	Exon	114944 - 116182	977032 - 978270	1239	sequence	download
10	Intron	116183 - 118342	978271 - 980430	2160	sequence	-
11	Exon	118343 - 118426	980431 - 980514	84	sequence	download
11	Intron	118427 - 125289	980515 - 987377	6863	sequence	-
12	Exon	125290 - 125439	987378 - 987527	150	sequence	download
12	Intron	125440 - 126650	987528 - 988738	1211	sequence	-
13	Exon	126651 - 127109	988739 - 989197	459	sequence	download
13	Intron	127110 - 127798	989198 - 989886	689	sequence	-
14	Exon	127799 - 128077	989887 - 990165	279	sequence	download
14	Intron	128078 - 128769	990166 - 990857	692	sequence	-
15	Exon	128770 - 128867	990858 - 990955	98	sequence	download
15	Intron	128868 - 128988	990956 - 991076	121	sequence	-

Figure 4. Gene (A) and Exon-Intron (B) tables. **A-** The gene table shows general information about the studied gene (official symbol, synonyms, description, chromosomal location and associated transcripts). Links to other resources of the gene are also available: clicking on the Ensembl ID of the gene leads to its Ensembl page while clicking on chromosomal coordinates directs to the UCSC page of the gene. Finally, clicking on sequence displays the sequences of each of the exons and introns of the gene. **B-** Summary table of the exon/intron structure of the gene. For each element, gene and chromosomal coordinates are displayed as well as its length. Clicking on sequence link displays the nucleotidic sequence of the element. For exons only, clicking on download link in the features column results in a file containing further information about the exon of interest.

A

Report	
Exon	Number of Evidence
Transcription Initiation & First Exon(s)	
1	1
Transcription Termination & Last Exon(s)	
3	3
31	4
Exon Skipping	
2	1
3	1
4	1
5	1
6	1
9	6
10	5
11	1
13	5
14	4
29	7
Alternative 3' Splice Site	
7	1
12	1
Alternative 5' Splice Site	
1	1
24	1

B

Polyadenylation								
ID	Position	Gene Coordinate of Cleavage Site	Chromosomal Coordinate of Cleavage Site	Pattern	PolyA Tail	Accession Number	Type	
PA1	3	74575	936663	AATAAA	yes	BC021121	Cdna	
PA2	3	74575	936663	AATAAA	yes	BC071959	Cdna	
PA3	3	74575	936663	AATAAA	yes	BC094862	Cdna	
PA4	31	158530	1020618	AATAAA	yes	NM_018979	Cdna	
PA5	31	158530	1020618	AATAAA	no	NM_213655	Cdna	
PA6	31	158530	1020618	AATAAA	no	NM_001184985	Cdna	
PA7	31	158530	1020618	AATAAA	yes	NM_014823	Cdna	

C

Exon Skipping		
ID	Position	Transcript
ES1	2	BC141881
ES2	3	BC141881
ES3	4	BC141881
ES4	5	BC141881
ES5	6	BC141881
ES6	9	NM_018979 NM_001184985 NM_014823 AJ296290 BC141881 AB002342
ES7	10	NM_018979 NM_014823 AJ296290 BC141881 AB002342
ES8	11	BC141881
ES9	13	NM_213655 NM_001184985 NM_014823 BC141881 AB002342
ES10	14	NM_213655 NM_014823 BC141881 AB002342
ES11	29	NM_018979 NM_213655 NM_001184985 NM_014823 AJ296290 BC141881 AB002342

Figure 5. Report (A), polyadenylation (B) and Exon skipping (C) tables. **A-** Features relative to alternative splicing events are summarized in the report table. For each type of AS event, the exon concerned and the number of transcripts having this AS event (number of evidence) are displayed. Clicking on a given AS event displays further information about this event. Two examples of transcription end and exon skipping events tables are shown in **B** and **C** respectively. **B-** The “Transcription Termination & last Exons” link shows polyadenylation sites. For each polyadenylation site, we display its exonic position, gene and chromosomal coordinates. Moreover information about the signal pattern, the accession number and the type of sequence (cDNA/Est) of the transcript used to define the polyadenylation site are displayed. Finally, the presence of a polyA tail is tested and notified when present in the sequence. **C-** The “Exon Skipping” table shows information about skipped exons displaying their position and the transcripts that have been used to make this annotation.

Splice Site Strength

ID	Site	Exon	Strength	Alternative	Sequence
S1	5'(Donor)	1	9.65	no	CAGgtaaag
S2	5'(Donor)	1	-19.55	yes	GCAgagcag
S3	5'(Donor)	2	10.74	no	AACgtaagt
S4	3'(Acceptor)	2	9.34	no	gtttggttttgatttagGAT
S5	5'(Donor)	3	7.76	no	TAGgtatgt
S6	3'(Acceptor)	3	9.33	no	gtatacttgccttttctagGTA
S7	5'(Donor)	4	8.46	no	AGTgtaagt
S8	3'(Acceptor)	4	7.73	no	aatcgttctttaatttaagGTA
S9	5'(Donor)	5	11	no	AAGgtaagt
S10	3'(Acceptor)	5	8.5	no	tttctgttatggtttcagGGG
S11	5'(Donor)	6	6.41	no	ATGgtaaat
S12	3'(Acceptor)	6	5.68	no	ctttccctctgtttggaagATA
S13	5'(Donor)	7	3.41	no	TATgtacgt
S14	3'(Acceptor)	7	11.24	no	tttaccctttattctgtagGTA
S15	3'(Acceptor)	7	-8.49	yes	agcggcagttggtacgggagGAG
S16	5'(Donor)	8	10.36	no	GTGgtaagt
S17	3'(Acceptor)	8	7.51	no	gcgattcattttcctcagCTG
S18	5'(Donor)	9	5.19	no	ACTgtatgt
S19	3'(Acceptor)	9	1.05	no	tggtttgtttgtgtgagCCT
S20	5'(Donor)	10	1.5	no	CAGgttata
S21	3'(Acceptor)	10	5.1	no	tcttattcattgtgatacagCCT
S22	5'(Donor)	11	9.22	no	CAGgtgaga
S23	3'(Acceptor)	11	10.05	no	tggtcactctttcctcagGCA
S24	5'(Donor)	12	7.82	no	CAGgtaaac
S25	3'(Acceptor)	12	4.39	no	tcattgtattttattcttagCAG
S26	5'(Donor)	13	8.35	no	CAGgtattg
S27	3'(Acceptor)	13	7.24	no	gttttctttaccctccagCTT
S28	5'(Donor)	14	8.39	no	GAGgtaaat
S29	3'(Acceptor)	14	10.47	no	cttcctcatttctgtcacagGGC
S30	5'(Donor)	15	10.65	no	CAGgtacgt
S31	3'(Acceptor)	15	7.45	no	gttatctttcattcacagAGT

Figure 6. Splice site strength table. All the splice sites of the WNK1 gene are showed in this table. For each splice site, we display its type (donor or acceptor), its strength according to MaxEntScan computation method and if the site is alternative or not. Furthermore, the sequence (9 and 23 nucleotides for donor and acceptor sites respectively) is showed with capital letters corresponding to the exonic part of the site while intronic part is represented in minuscule letters.

A

	Five prime untranslated region	
	UTR1	UTR2
Genbank Accession	NM_018979 BC021121 BC071959 BC094862	BC141881
Length	643	701
Number of ATG in frame	0	0
Number total of ATG	4	5
Number of GTG in frame	6	0
Number total of GTG	15	12
Number of CTG in frame	5	4
Number total of CTG	13	9
Number of Micro ORF in frame	0	0
Number total of Micro ORF	2	3
Percentage of GC	77	50
Number of Pyrimidine Track	6	3

B

	Three prime untranslated region	
	UTR1	UTR2
Genbank Accession	BC021121 BC071959 BC094862	NM_018979 BC013629
Length	206	2660
Number of ATG in frame	0	15
Number total of ATG	1	44
Number of GTG in frame	1	15
Number total of GTG	4	52
Number of CTG in frame	1	17
Number total of CTG	4	44
Percentage of GC	33	39
Number of Pyrimidine Track	1	22

Figure 7. 5'UTR (A) and 3'UTR (B) tables. **A-** Several information about each of the 5' Untranslated regions (UTR) are given. For each UTR, the subset of transcripts having this UTR is displayed as well as the number of motifs ATG, GTG and CTG found either globally in the UTR sequence or in frame. The length and the GC content are also computed for each UTR. Finally, the number of pyrimidine tracks as well as the number of Micro ORF is displayed. **B-** Same information as in **A** for the 3'UTR region.

Micro RNA				
ID	Name	Gene Coordinate	Chromosomal Coordinate	Method
M1	hsa-miR-613	74370 - 74388	936458 - 936476	miranda
M2	hsa-miR-206	74370 - 74388	936458 - 936476	miranda
M3	hsa-miR-1	74370 - 74388	936458 - 936476	miranda
M4	hsa-miR-146b-5p	74475 - 74498	936563 - 936586	miranda
PolyA				
M1	hsa-miR-19b	116213 - 116230	978301 - 978318	miranda
M2	hsa-miR-19a	116213 - 116230	978301 - 978318	miranda
M3	hsa-miR-448	116328 - 116348	978416 - 978436	miranda
M4	hsa-miR-136	116344 - 116367	978432 - 978455	miranda
M5	hsa-miR-23a	116346 - 116366	978434 - 978454	miranda
M6	hsa-miR-23b	116346 - 116366	978434 - 978454	miranda
M7	hsa-miR-153	116439 - 116463	978527 - 978551	miranda
M8	hsa-miR-217	116442 - 116466	978530 - 978554	miranda
M9	hsa-miR-374a	116631 - 116653	978719 - 978741	miranda
M10	hsa-miR-374b	116632 - 116653	978720 - 978741	miranda
PolyA				
M1	hsa-miR-1244	155956 - 155962	1018044 - 1018050	pita
M2	hsa-miR-325	155958 - 155964	1018046 - 1018052	pita
M3	hsa-miR-107	155965 - 155972	1018053 - 1018060	targetscan
M4	hsa-miR-103	155965 - 155972	1018053 - 1018060	targetscan
M5	hsa-miR-31	155975 - 155993	1018063 - 1018081	miranda
M6	hsa-miR-31	155986 - 155994	1018074 - 1018082	targetscan
M7	hsa-miR-31	155986 - 155992	1018074 - 1018080	pita
M8	hsa-miR-543	155999 - 156006	1018087 - 1018094	targetscan
M9	hsa-miR-543	155999 - 156005	1018087 - 1018093	pita
M10	hsa-miR-136	156030 - 156038	1018118 - 1018126	targetscan
M11	hsa-miR-320d	156082 - 156088	1018170 - 1018176	pita
M12	hsa-miR-320b	156082 - 156088	1018170 - 1018176	pita
M13	hsa-miR-320a	156082 - 156088	1018170 - 1018176	pita
M14	hsa-miR-320c	156082 - 156088	1018170 - 1018176	pita
M15	hsa-miR-215	156424 - 156431	1018512 - 1018519	pita
M16	hsa-miR-192	156424 - 156431	1018512 - 1018519	pita
M17	hsa-miR-192	156425 - 156432	1018513 - 1018520	targetscan
M18	hsa-miR-215	156425 - 156432	1018513 - 1018520	targetscan
M19	hsa-miR-889	156450 - 156456	1018538 - 1018544	pita

Figure 8. Micro RNA table. This table summarizes information about micro RNA binding sites found among the WNK1 gene sequence. For each miRNA, we display its ID, gene and chromosomal coordinates, and the algorithm which allowed predicting this miRNA (Miranda, pita, targetscan). When a polyadenylation site is present, a blue bar is displayed between miRNA binding sites.

Conserved Exons

ID Gene Mouse	Position Human	Position Mouse
4851	1	1
4851	2	2
4851	3	3
4851	4	4
4851	5	7
4851	6	8
4851	7	9
4851	8	10
4851	9	11
4851	10	12
4851	11	13
4851	12	14
4851	13	15
4851	14	16
4851	15	17
4851	16	18
4851	17	19
4851	18	20
4851	19	21
4851	20	22
4851	21	23
4851	22	24
4851	23	25
4851	24	26
4851	25	27
4851	26	28
4851	27	29
4851	28	30
4851	30	31

Figure 9. Conservation table. For each human gene, we display, in the first column, its orthologous in the mouse genome as provided by Ensembl. Furthermore, we display for each human exon its orthologous, if exists, in the mouse genome.

A

Exon Position	Tissues	Cell Lines
1	Expression	Expression
2	Expression	Expression
3	Expression	Expression
4	Expression	Expression
5	Expression	Expression
6	Expression	Expression
7	Expression	Expression
8	Expression	Expression
9	Expression	Expression
10	Expression	Expression
11	Expression	Expression
12	Expression	Expression
13	Expression	Expression
14	Expression	Expression
15	Expression	Expression
16	Expression	Expression
17	Expression	Expression
18	Expression	Expression
19	Expression	Expression
20	Expression	Expression
21	Expression	Expression
22	Expression	Expression
23	Expression	Expression
24	Expression	Expression
25	Expression	Expression
26	Expression	Expression
27	Expression	Expression
28	Expression	Expression
29	Expression	Expression
30	Expression	Expression
31	Expression	Expression

← FasterID: 18112 - WNK lysine deficient protein kinase 1 (WNK1) ENSG0000060237 --> Exon: 13 →

B

Experiments	Expressed	<Gene Expression Level	<Ni	<Global Si	<Local Si	P-value
Heart	Yes	415	1.67	3.26	3.08	0.0000
Thyroid	Yes	244	-1.10	1.79	1.50	0.0000
Muscle	Yes	262	-1.03	1.91	1.39	0.0004
Testis	Yes	215	-1.11	1.76	1.21	0.0007
Cerebellum	Yes	188	-1.69	1.16	-1.33	0.0000
Pancreas	No	120	-3.33	-1.96	-1.39	0.0040
Kidney	Yes	457	-1.75	1.10	-1.69	0.0000
Prostate	Yes	174	-2.22	-1.30	-2.04	0.0000
Liver	Yes	189	-2.70	-1.56	-2.22	0.0000
Breast	Yes	207	-3.45	-2.04	-2.27	0.0000
Spleen	Yes	204	-4.00	-2.38	-3.23	0.0000

Figure10. Expression table. **A-** In this table, we display for each exon of the WNK1 gene two links: the first link leads to a table summarizing the expression of the exon in the tissues while the second link displays a table summarizing exon expression in the cell lines (see Material and Methods for more information about tissues and cell lines included in these analyses). **B-** Example of the expression of the human exon 13 of the WNK1 gene in human tissues. For each tissue, we computed gene expression level which represents the median of the intensity of all the probes associated to the exons of the gene and determine if the gene is expressed or not. We also compute Normalized Intensity (NI), Global Splicing Index (SI) and Local Splicing index (Si) which represent different methods to calculate the inclusion level of an exon. The table can be sorted according to these values. Finally, we show the p-value of the student test based on the local Si values. The table can be sorted according to any of the columns

A

← FasterID : 18112 - WNK lysine deficient protein kinase 1 (WNK1) ENSG0000060237 --> Exon : 13 →

Experiments	Expressed	<Gene Expression Level	<Ni	<Global Si	<Local Si	P-value
Heart	Yes	415	1.67	3.26	3.08	0.0000
Thyroid	Yes	244	-1.10	1.79	1.50	0.0000
Muscle	Yes	262	-1.03	1.91	1.39	0.0004
Testis	Yes	215	-1.11	1.76	1.21	0.0007
Cerebellum	Yes	188	-1.69	1.16	-1.33	0.0000
Pancreas	No	120	-3.33	-1.96	-1.39	0.0040
Kidney	Yes	457	-1.75	1.10	-1.69	0.0000
Prostate	Yes	174	-2.22	-1.30	-2.04	0.0000
Liver	Yes	189	-2.70	-1.56	-2.22	0.0000
Breast	Yes	207	-3.45	-2.04	-2.27	0.0000
Spleen	Yes	204	-4.00	-2.38	-3.23	0.0000

B

← FasterID : 4851 - WNK lysine deficient protein kinase 1 Gene (Hsm2) ENSMUSG0000045962 --> Exon : 15 →

Experiments	Expressed	<Gene Expression Level	<Ni	<Global Si	<Local Si	P-value
Testicle	Yes	368	1.39	4.76		
Brain	Yes	221	-1.41	2.44		
Heart	Yes	520	-1.67	2.07		
Muscle	Yes	281	-2.70	1.26		
Embryo	Yes	279	-2.86	1.21		
Spleen	Yes	546	-3.12	1.01		
Kidney	Yes	504	-3.70	-1.25		
Thymus	Yes	468	-4.35	-1.43		
Ovary	Yes	271	-4.55	-1.49		
Liver	Yes	256	-6.25	-2.13		
Lung	Yes	533	-7.69	-2.50		

Figure 11. Expression of human exon 13 (A) and mouse exon 15 (B) in tissues. **A-** Expression levels of the exon 13 in the WNK1 gene across human tissues. Red rectangles correspond to heart and muscle tissues where exon 13 has high global Si values. **B-** Expression table of the exon 15 in the HSN2 gene (orthologous of the human exon 13 in the WNK1 gene) among mouse tissues. Red rectangles correspond to heart and muscle tissues where exon 15 has also high global Si values.

A

Motifs

← FasteID : 18112 WNK lysine deficient protein kinase 1 (WNK1) - Exon :: 13 →

```

CTTCCAGTTTCCCAGCCAGTACCAACTATCCAAGGCAACCTCAGATCCAGTTGCGACACAACCCCTCGGTTGTTCCAGTCCACTCTGGTGCTCATTTC
TCCAGTGGGACAGCCGCTCCCTACTCCCTTCTACTCCACAGTATCCTGTCTCTCAAAATCCCATATCGACTCCTCATGTGTACGGCTCAGACAGGTTT
CTCATCCCTCCCATCACAATGGCAGCTGGCATTACTCAGCCTCTGCTCAGCTTGGCTTCATCTGCTACAACAGCTCGATCCCGGGGTATCAACTGTG
GTTCCTAGTCAGCTTCCAACCCCTCTCAGCCTGTGACTCAGTCCCAAGTCAGGTTCAACCCAGAGCTCCTCAACCCAGCTCCTCAACCCAGCTCAGTCCATGGGAATC
CAGTCAACCTTGACAAAGTGTGAGTTCCACTTTCCTCTGGAGATGTTCTGTACCAAG

```

Mouse Exon(s) :

FasteID : 4851 WNK lysine deficient protein kinase 1 Gene (Hsn2) - Exon :: 15

```

CTTCCAGTTTCCCAGCAGTAGCAACTGCCAAGGGAACCTCAGATCCAGTTTCAACACAACCCCTCAGTGTTCAGTCCACTCTGGTGCTCATTTC
TTCCTATGGGACGCCAATCCCTACTCTTACTCCACAGTATCCTGTCTCTCAAAATCCCATATCGACTCCTCATGTGTACGGCTCAGACAGGTTT
CTCATCCCTCCCATCACAATGGCAGCTGGCATTACTCAGCCTCTGCTCAGCTTGGCTTCATCTGCTACAACAGCTCGATCCCGGGGTATCAACTGTG
GTTCCTAGTCAGCTTCCAACCCCTCTCAGCCTGTGACTCAGTCCCAAGTCAGGTTCAACCCAGAGCTCCTCAACCCAGCTCCTCAACCCAGCTCAGTCCATGGGA
TACCAGTCACTTGGCAAGTGTGAGGTTCCACTTTCCTCTGGAGATGTTTGTACCAAG

```

Exon Arrays :

Hsn2 → C2C12 :: siPTB_vs.SIG12

WNK1 → HeLa :: PTB_RNAi_vs.Mock_RNAi

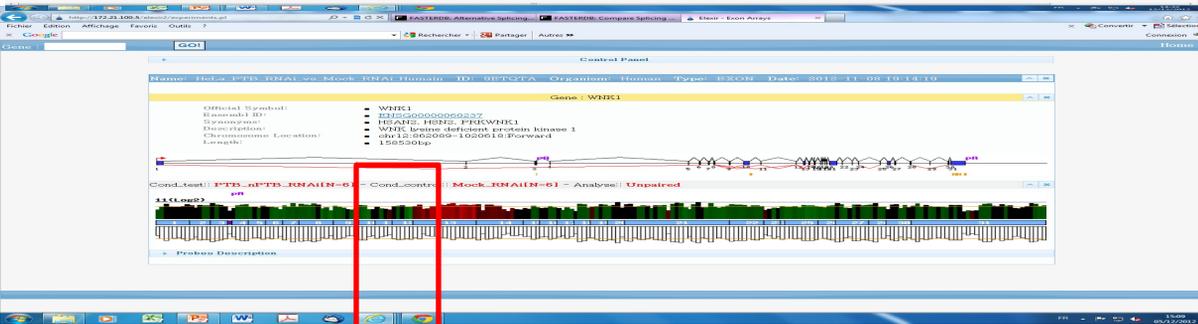
CLIP Data :

Experiments for PTB

B



C



D

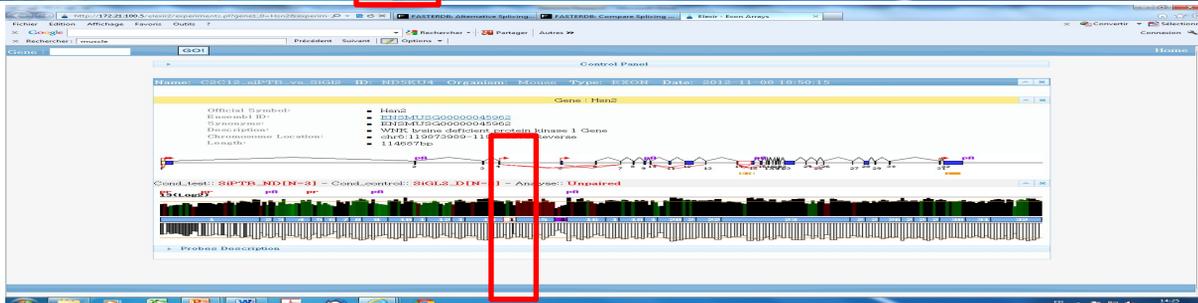


Figure 12. Comparison of PTB Binding Sites between Human exon 13 and its orthologous exon in the mouse genome (exon 15) among the WNK gene (A). CLIP-seq data for PTB at the exon level (B). Exon Arrays visualization when PTB is depleted in the Human (C) and Mouse (D). **A.** For each exon and 200 nucleotides of its intronic neighborhood on both sides, motifs corresponding to PTB binding sites are represented by yellow lines. The sequence of each exon can be retrieved by clicking on it. Furthermore, clicking on “Motifs” in the blue panel, allows displaying exact position of each motif and its sequence. Finally, links to CLIP-seq data or Exon-arrays experiments concerning the motif are also proposed. **B.** Reads from CLIP-seq experiment corresponding to PTB binding sites are represented as a raw signal below exon’s schematic presentation while motifs (A) are represented by orange lines on exonic graphical presentation. The exon of interest is represented in black while neighboring exons are grey. **C.** Graphical representation of the human WNK1 gene in exon-arrays visualization when PTB is depleted. The height of each probe corresponds to its intensity level. Red probes indicate inclusion in test condition (PTB depletion) while green probes indicate its exclusion (inclusion in control condition). Red square corresponds to exon 13 which has PTB binding sites. **D.** Graphical representation of the mouse HSN2 gene in exon-arrays visualization when PTB is depleted. Red square corresponds to exon 15, the orthologous of the exon 13 in the human WNK1 gene. Exon 15 has also PTB binding sites.

A

Splicing Factor		
Exon Position	Motif & Conservation	
1	9G8	Go
2	9G8	Go
3	9G8	Go
4	9G8	Go
5	9G8	Go
6	9G8	Go
7	9G8	Go
8	9G8	Go
9	9G8	Go
10	9G8	Go
11	9G8	Go
12	9G8	Go
13	PTB	Go
14	9G8	Go
15	9G8	Go

B

← FasterID : 18112 WNK lysine deficient protein kinase 1 (WNK1) - Exon ::: 13 →

```
CTTCCAGTTTCCAGCCAGTACCAACTATCCAAGGCGAACCTCAGATCCCAGTTGCGACACAACCCTCGGTTGTTCCAGTCCACTCTGGTGTCTATTTCT
TCCAGTGGGACAGCCGCTCCCTACTCCCTTGTCCCTCAGTACCTGTCTCTCAGATCCCATATCAACTCCTCATGTGTCTACGGCTCAGACAGGTTTCT
CATCCCTTCCATCACATGGCAGCTGGCATTACTCAGCCTCTGCTCAGGTTGGCTTTCATCTGCTACAACAGCTGCGATCCCAGGGGATCAACTGTGGTT
CCTAGTCAGCTTCAACCTTCTGAGCCTGTGACTCAGCTGCCAAGTCAGGTTACCCACAGCTCTACAACCAGCAGTTCAGTCCATGGGAATACCAGC
TAACCTTGGACAAGCTGCTGAGGTTCCACTTTCCTCTGGAGATGTTCTGTACCAG
```

Mouse Exon(s) :

FasterID : 4851 WNK lysine deficient protein kinase 1 Gene (Hsn2) - Exon ::: 15

```
CTTCCAGTTTCCAGACAGTAGCAACTGTCCAAGGTGAACCTCACATCCCAGTTTCAACACAACCCTCAGTTGTTCCAGTCCACTCTGGTGTCTATTTCT
TCCTATGGGACAGCCAACTCCCTACTCTTTACTCCACAGTATCTGTCTCAAATCCCATATCGACTCCTCATGTGTCCACGGCCGACAGAGGTTTCT
CATCCGTTCTATAACAATGGCTGCTGGCATTAAACCAGCCTCTGCTCACCTGGCTTTCATCTGCTACAGCATCTTCAATCCCAGGGGATCACCTGTAGTT
CCTAATCAGCTTCAACTCTTCTGCAGCCTGTGAATCAGCTGCAGAGTCAGGTTACCCACAGCTTCTACAGCCAAACAGTTCAGTCCATAGGAATACC
AGCTAACCTTGGACAAGCTGCTGAGGGTCCACTTCCCTCTGGAGATGTTTTGTACCAG
```

Exon Arrays :

Hsn2 -> C2C12 :: siPTB_vs_SiG12

WNK1 -> HeLa :: PTB_RNAi_vs_Mock_RNAi

CLIP Data :

Experiments for PTB

Figure 13. Splicing factor table. **A-** Splicing factor table displays for each exon, the motifs found for a list of splicing factors in the exon and 200 nucleotides in the bordering introns. For this, considering an exon of interest, the user should choose in the list the splicing factor and then click the “Go” button. **B-** Example result showing PTB motifs for exon 13 of the WNK1 gene. Motifs are represented by yellow lines on the graphical presentation of the exon and its intronic neighborhood. The motifs found in the corresponding orthologous exon are showed also (exon 15 of HSN2 mouse gene). Sequences of exon or introns (upstream and downstream the exon) can be displayed simply by clicking on exon or intron in the graphical presentation. Finally, links of CLIP-seq or exon arrays experiments associated to the splicing factor of interest are displayed, if exist, at the bottom.