cBioPortal query report: **NRAS**

2019-05-17

NRAS metadata

Gene symbol: **NRAS**
UniProtKB ID: **P01111**
Gene product name: **GTPase NRas**
Chromosome: **1**
Strand: **-1**
Number of unique Ensembl transcripts: **1**
Number of unique Ensembl exons for all transcripts: **7**

Primary representative transcript:

Ensembl transcript ID **ENST00000369535**
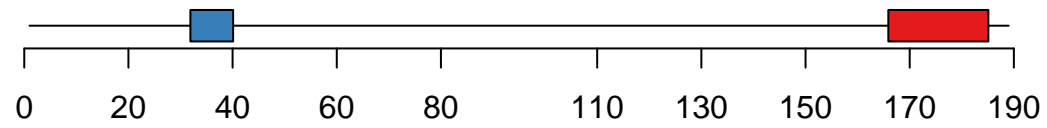Number of exons: **7**
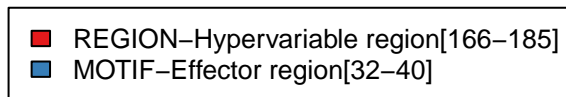Transcript length: **4326**
Coding sequence length: **570**
Transcript start position: **114704469**
Transcript end position: **114716771**

# Protein features: Domains, Regions, Motifs and Modifications

Color legend

- ■ REGION−Hypervariable region[166−185]
- ■ MOTIF−Effector region[32−40]

All features (minus variants and sequence conflicts)

TYPE	AA_start	AA_end	LABEL
CHAIN	1	186	GTPase NRas
PROPEP	187	189	Removed in mature form
NP_BIND	10	18	GTP
NP_BIND	29	30	GTP
NP_BIND	57	61	GTP
NP_BIND	116	119	GTP
REGION	166	185	Hypervariable region
MOTIF	32	40	Effector region
MOD_RES	89	89	Phosphoserine; by STK19
LIPID	181	181	S-palmitoyl cysteine
LIPID	186	186	S-farnesyl cysteine
CROSSLNK	170	170	Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)
MUTAGEN	89	89	S->A: Abolished phosphorylation by STK19
MUTAGEN	164	164	R->A: Loss of GTP-binding activity
MUTAGEN	181	181	C->S: Loss of plasma membrane localization

Ensembl Transcripts

All transcripts are ploted to their relative genomic positions with all shared intronic regions removed. Transcription start sites are always on the left regardless of strand. **'Main' representative transcript used for variant alignment is in red**


```
0      480     960    1440    1920    2400    2880    3360    3850    4330
```
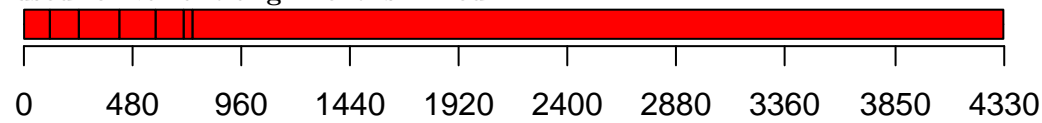
Query metadata

Total number of studies returned by cBioPortal: **249**
Total number of unique case IDs returned by cBioPortal: **47642**

Total number of studies with mutation/variant data available: **194**
Total number of cases queried for **NRAS** variants: **35693**
Total number of studies with **NRAS** variants: **82**
Total number of unique cases represented in filtered mutation data: **894**
Total number of unique variants for **NRAS** returned: **113**

Table 2: Cases with multiple variants

Number of samples	Number of mutations per sample
868	1
42	2
9	3
4	4
7	7

Table 3: Tissue types in all cases

Primary Tissue	Total cases in database	Total cases sequenced	Total altered cases	Percent altered
Myeloid	25	25	5	20.00
Skin	2696	1861	272	14.62
Thyroid	1871	864	85	9.84
Other	1383	1383	75	5.42
Bowel	4719	2714	100	3.68
Testis	462	399	13	3.26
Thymus	297	142	4	2.82
Lymphoid	8190	6282	150	2.39
Soft Tissue	1428	800	18	2.25
Germ Cell	318	232	5	2.16
Liver	1310	663	10	1.51
Uterus	2272	1121	16	1.43
Bladder/Urinary Tract	2750	1400	16	1.14
Ampulla of Vater	187	187	2	1.07
Bone	365	258	2	0.78
Lung	7804	4723	35	0.74
Peripheral Nervous System	1675	408	3	0.74
Ovary/Fallopian Tube	2003	843	6	0.71
Head and Neck	2446	1053	7	0.66
Esophagus/Stomach	3711	1386	8	0.58
Biliary Tract	1049	744	4	0.54
Pancreas	1710	959	5	0.52
CNS/Brain	5802	2126	9	0.42
Kidney	4111	889	3	0.34
Cervix	662	365	1	0.27
Breast	10535	7010	10	0.14
Prostate	5569	719	0	0.00
Pleura	320	107	0	0.00
Adrenal Gland	211	27	0	0.00

Primary Tissue	Total cases in database	Total cases sequenced	Total altered cases	Percent altered
Eye	84	4	0	0.00
Appendix	83	83	0	0.00
Pituitary	3	3	0	0.00

Gene fusions returned:

case_id	amino_acid_change	genetic_profile_id
P-0003805-T01-IM5	CSDE1-NRAS fusion	msk_impact_2017_mutations
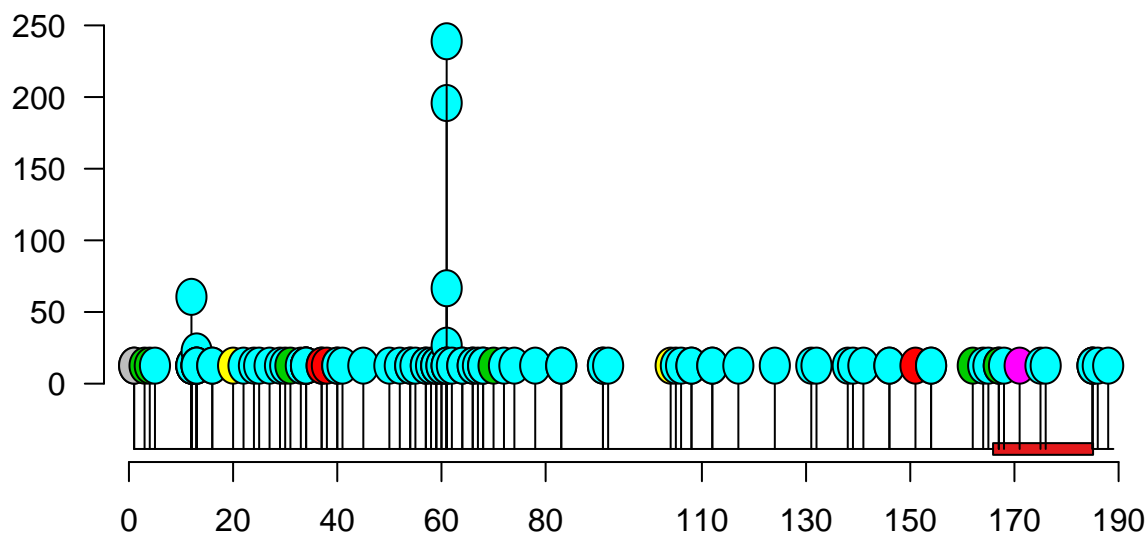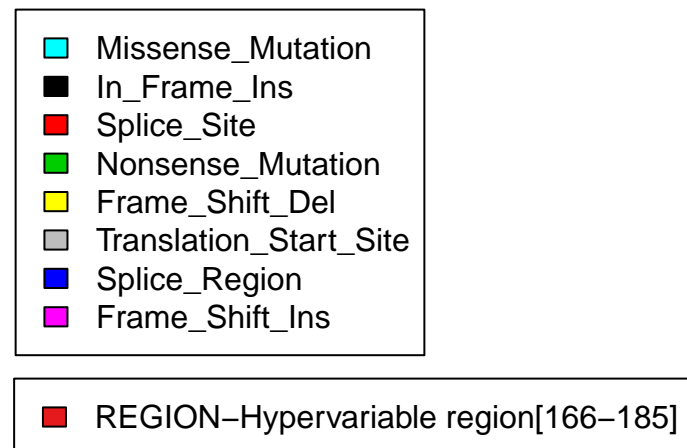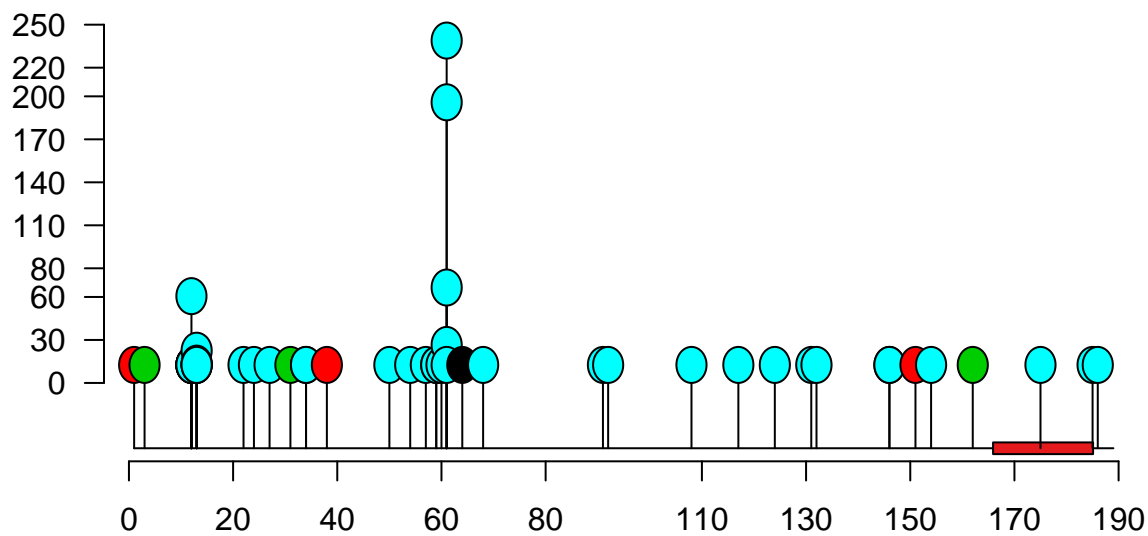
R session info:

```
## R version 3.6.0 (2019-04-26)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 18.04.2 LTS
##
## Matrix products: default
## BLAS:    /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.7.1
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.7.1
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
##  [1] grid      parallel  stats4    stats     graphics  grDevices utils
##  [8] datasets  methods   base
##
## other attached packages:
##  [1] RColorBrewer_1.1-2
##  [2] knitr_1.22
##  [3] markdown_0.9
##  [4] trackViewer_1.19.28
##  [5] BSgenome.Hsapiens.NCBI.GRCh38_1.3.1000
##  [6] BSgenome_1.51.0
##  [7] Biostrings_2.51.5
##  [8] XVector_0.23.2
##  [9] rjson_0.2.20
## [10] biomaRt_2.39.4
## [11] rtracklayer_1.43.4
## [12] GenomicRanges_1.35.1
## [13] GenomeInfoDb_1.19.3
## [14] IRanges_2.17.5
## [15] S4Vectors_0.21.24
## [16] BiocGenerics_0.29.2
## [17] cgdsr_1.2.10
##
## loaded via a namespace (and not attached):
##  [1] ProtGenerics_1.15.0       bitops_1.0-6
##  [3] matrixStats_0.54.0        bit64_0.9-7
##  [5] progress_1.2.0            httr_1.4.0
##  [7] InteractionSet_1.11.2     Rgraphviz_2.27.0
##  [9] tools_3.6.0               backports_1.1.4
## [11] R6_2.4.0                  rpart_4.1-15
## [13] Hmisc_4.2-0               DBI_1.0.0
## [15] lazyeval_0.2.2            Gviz_1.27.7
## [17] colorspace_1.4-1          nnet_7.3-12
## [19] gridExtra_2.3             prettyunits_1.0.2
## [21] bit_1.1-14                curl_3.3
## [23] compiler_3.6.0            graph_1.61.1
```

```
## [25] Biobase_2.43.1             htmlTable_1.13.1
## [27] DelayedArray_0.9.9         grImport_0.9-1.1
## [29] scales_1.0.0               checkmate_1.9.3
## [31] stringr_1.3.1              digest_0.6.18
## [33] Rsamtools_1.99.6           foreign_0.8-71
## [35] rmarkdown_1.12             base64enc_0.1-3
## [37] dichromat_2.0-0            pkgconfig_2.0.2
## [39] htmltools_0.3.6            plotrix_3.7-5
## [41] highr_0.8                  ensembldb_2.7.12
## [43] htmlwidgets_1.3            rlang_0.3.4
## [45] rstudioapi_0.10            RSQLite_2.1.1
## [47] BiocParallel_1.17.19       acepack_1.4.1
## [49] R.oo_1.22.0                VariantAnnotation_1.29.25
## [51] RCurl_1.95-4.12            magrittr_1.5
## [53] GenomeInfoDbData_1.2.1     Formula_1.2-3
## [55] Matrix_1.2-17              Rcpp_1.0.1
## [57] munsell_0.5.0              R.methodsS3_1.7.1
## [59] yaml_2.2.0                 stringi_1.2.4
## [61] SummarizedExperiment_1.13.0 zlibbioc_1.29.0
## [63] plyr_1.8.4                 blob_1.1.1
## [65] crayon_1.3.4               lattice_0.20-38
## [67] splines_3.6.0              GenomicFeatures_1.35.11
## [69] hms_0.4.2                  pillar_1.3.1
## [71] XML_3.98-1.19              evaluate_0.13
## [73] biovizBase_1.31.1          latticeExtra_0.6-28
## [75] data.table_1.12.2          gtable_0.3.0
## [77] assertthat_0.2.1           ggplot2_3.1.1
## [79] xfun_0.6                   AnnotationFilter_1.7.0
## [81] survival_2.44-1.1          tibble_2.1.1
## [83] GenomicAlignments_1.19.1   AnnotationDbi_1.45.1
## [85] memoise_1.1.0              cluster_2.0.9
```