**Homo sapiens chromosome 7, GRCh38.p14 Primary Assembly**

NCBI Reference Sequence: NC_000007.14

FASTA Graphics

LOCUS NC_000007 211602 bp DNA linear CON 07-OCT-2023
DEFINITION Homo sapiens chromosome 7, GRCh38.p14 Primary Assembly.
ACCESSION NC_000007 REGION: complement(140713328..140924929)
VERSION NC_000007.14
DBLINK BioProject: PRJNA168
Assembly: GCF_000001405.40
KEYWORDS RefSeq.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 211602)
CONSRTM International Human Genome Sequencing Consortium
TITLE Finishing the euchromatic sequence of the human genome
JOURNAL Nature 431 (7011), 931-945 (2004)
PUBMED 15496913
REFERENCE 2 (bases 1 to 211602)
AUTHORS Hillier,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H.,
Wagner-McPherson,C., Layman,D., Maas,J., Jaeger,S., Walker,R.,
Wylie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.E.,
Fewell,G.A., Delehaunty,K.D., Miner,T.L., Nash,W.E., Cordes,M.,
Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S.,
Isak,A., Vanbrunt,A., Nguyen,C., Du,F., Lamar,B., Courtney,L.,
Kalicki,J., Ozersky,P., Bielicki,L., Scott,K., Holmes,A.,
Harkins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C.,
Dauphin-Kohlberg,S., Kozlowicz-Reilly,A., Leonard,S., Rohlfing,T.,
Rock,S.M., Tin-Wollam,A.M., Abbott,A., Minx,P., Maupin,R.,
Strowmatt,C., Latreille,P., Miller,N., Johnson,D., Murray,J.,
Woessner,J.P., Wendl,M.C., Yang,S.P., Schultz,B.R., Wallis,J.W.,
Spieth,J., Bieri,T.A., Nelson,J.O., Berkowicz,N., Wohldmann,P.E.,
Cook,L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,J.A.,
Mardis,E.R., Clifton,S.W., Chissoe,S.L., Marra,M.A., Raymond,C.,
Haugen,E., Gillett,W., Zhou,Y., James,R., Phelps,K., Iadanoto,S.,
Bubb,K., Simms,E., Levy,R., Clendenning,J., Kaul,R., Kent,W.J.,
Furey,T.S., Baertsch,R.A., Brent,M.R., Keibler,E., Flicek,P.,
Bork,P., Suyama,M., Bailey,J.A., Portnoy,M.E., Torrents,D.,
Chinwalla,A.T., Gish,W.R., Eddy,S.R., McPherson,J.D., Olson,M.V.,
Eichler,E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.
TITLE The DNA sequence of human chromosome 7
JOURNAL Nature 424 (6945), 157-164 (2003)

PUBMED 12853948

REFERENCE 3 (bases 1 to 211602)

AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C., Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R., Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J., LeVine,R., McEwan,P., McKernan,K., Meldrim,J., Mesirov,J.P., Miranda,C., Morris,W., Naylor,J., Raymond,C., Rosetti,M., Santos,R., Sheridan,A., Sougnez,C., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Wyman,D., Rogers,J., Sulston,J., Ainscough,R., Beck,S., Bentley,D., Burton,J., Clee,C., Carter,N., Coulson,A., Deadman,R., Deloukas,P., Dunham,A., Dunham,I., Durbin,R., French,L., Grafham,D., Gregory,S., Hubbard,T., Humphray,S., Hunt,A., Jones,M., Lloyd,C., McMurray,A., Matthews,L., Mercer,S., Milne,S., Mullikin,J.C., Mungall,A., Plumb,R., Ross,M., Shownkeen,R., Sims,S., Waterston,R.H., Wilson,R.K., Hillier,L.W., McPherson,J.D., Marra,M.A., Mardis,E.R., Fulton,L.A., Chinwalla,A.T., Pepin,K.H., Gish,W.R., Chissoe,S.L., Wendl,M.C., Delehaunty,K.D., Miner,T.L., Delehaunty,A., Kramer,J.B., Cook,L.L., Fulton,R.S., Johnson,D.L., Minx,P.J., Clifton,S.W., Hawkins,T., Branscomb,E., Predki,P., Richardson,P., Wenning,S., Slezak,T., Doggett,N., Cheng,J.F., Olsen,A., Lucas,S., Elkin,C., Uberbacher,E., Frazier,M., Gibbs,R.A., Muzny,D.M., Scherer,S.E., Bouck,J.B., Sodergren,E.J., Worley,K.C., Rives,C.M., Gorrell,J.H., Metzker,M.L., Naylor,S.L., Kucherlapati,R.S., Nelson,D.L., Weinstock,G.M., Sakaki,Y., Fujiyama,A., Hattori,M., Yada,T., Toyoda,A., Itoh,T., Kawagoe,C., Watanabe,H., Totoki,Y., Taylor,T., Weissenbach,J., Heilig,R., Saurin,W., Artiguenave,F., Brottier,P., Bruls,T., Pelletier,E., Robert,C., Wincker,P., Smith,D.R., Doucette-Stamm,L., Rubenfield,M., Weinstock,K., Lee,H.M., Dubois,J., Rosenthal,A., Platzer,M., Nyakatura,G., Taudien,S., Rump,A., Yang,H., Yu,J., Wang,J., Huang,G., Gu,J., Hood,L., Rowen,L., Madan,A., Qin,S., Davis,R.W., Federspiel,N.A., Abola,A.P., Proctor,M.J., Myers,R.M., Schmutz,J., Dickson,M., Grimwood,J., Cox,D.R., Olson,M.V., Kaul,R., Raymond,C., Shimizu,N., Kawasaki,K., Minoshima,S., Evans,G.A., Athanasiou,M., Schultz,R., Roe,B.A., Chen,F., Pan,H., Ramser,J., Lehrach,H., Reinhardt,R., McCombie,W.R., de la Bastide,M., Dedhia,N., Blocker,H., Hornischer,K., Nordsiek,G., Agarwala,R., Aravind,L., Bailey,J.A., Bateman,A., Batzoglou,S., Birney,E., Bork,P., Brown,D.G., Burge,C.B., Cerutti,L., Chen,H.C., Church,D., Clamp,M., Copley,R.R., Doerks,T., Eddy,S.R., Eichler,E.E., Furey,T.S., Galagan,J., Gilbert,J.G., Harmon,C., Hayashizaki,Y., Haussler,D., Hermjakob,H., Hokamp,K., Jang,W., Johnson,L.S., Jones,T.A., Kasif,S., Kaspryzk,A., Kennedy,S., Kent,W.J., Kitts,P.,

Koonin,E.V., Korf,I., Kulp,D., Lancet,D., Lowe,T.M., McLysaght,A., Mikkelsen,T., Moran,J.V., Mulder,N., Pollara,V.J., Ponting,C.P., Schuler,G., Schultz,J., Slater,G., Smit,A.F., Stupka,E., Szustakowski,J., Thierry-Mieg,D., Thierry-Mieg,J., Wagner,L., Wallis,J., Wheeler,R., Williams,A., Wolf,Y.I., Wolfe,K.H., Yang,S.P., Yeh,R.F., Collins,F., Guyer,M.S., Peterson,J., Felsenfeld,A., Wetterstrand,K.A., Patrinos,A., Morgan,M.J., de Jong,P., Catanese,J.J., Osoegawa,K., Shizuya,H., Choi,S. and Chen,Y.J.

CONSRTM International Human Genome Sequencing Consortium

TITLE Initial sequencing and analysis of the human genome

JOURNAL Nature 409 (6822), 860-921 (2001)

PUBMED 11237011

REMARK Erratum:[Nature 2001 Aug 2;412(6846):565]

COMMENT REFSEQ INFORMATION: The reference sequence is identical to CM000669.2.

On Feb 3, 2014 this sequence version replaced NC_000007.13.
Assembly Name: GRCh38.p14 Primary Assembly
The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see: https://genomereference.org.

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI RefSeq
Annotation Status :: Updated annotation
Annotation Name :: GCF_000001405.40-RS_2023_10
Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline
Annotation Software Version :: 10.2
Annotation Method :: Best-placed RefSeq; Gnomon; RefSeqFE; cmsearch; tRNAscan-SE
Features Annotated :: Gene; mRNA; CDS; ncRNA
Annotation Date :: 10/02/2023
##Genome-Annotation-Data-END##

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Derived by automated computational analysis using gene
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with support for all annotated introns"
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gene prediction method: Gnomon. Supporting evidence

includes similarity to: 1 mRNA, 5 ESTs, 204 long SRA reads, 4 Proteins, and 98% coverage of the annotated genomic feature by RNAseq alignments, including 2 samples with support for all annotated introns"
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/note="Derived by automated computational analysis using gene prediction method: Gnomon. Supporting evidence includes similarity to: 1 mRNA, 2 ESTs, 200 long SRA reads, 4 Proteins, and 100% coverage of the annotated genomic feature by RNAseq alignments, including 4 samples with support for all annotated introns"
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170697..170743,171537..171655,175512..175643,
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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130463..130622,137346..137382,141773..141909,
143237..143354,146855..146939,147842..148018,
170697..170743,171537..171655,175512..175643,
184984..185118,198414..198563)
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/note="isoform 6 is encoded by transcript variant 7;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."

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/db_xref="MIM:164757"
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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130463..130622,137346..137382,139122..139241,
141773..141909,143237..143354,146855..146939,
147842..148018,170697..170743,171537..171655,
175512..175643,184984..185118,198414..198563)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="Derived by automated computational analysis using
gene prediction method: Gnomon."
/codon_start=1
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/db_xref="MIM:164757"
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CDS join(227..364,90058..90321,115935..116038,116868..116970,
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137346..137382,141773..141909,143237..143354,
146855..146939,147842..148018,170697..170743,
171537..171655,175512..175643,184984..185118,
190160..190313,198414..198436)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 8 is encoded by transcript variant 9;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."
/codon_start=1
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/protein_id="NP_001365399.1"
/db_xref="GeneID:673"
/db_xref="HGNC:HGNC:1097"
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/translation="MAALSGGGGGGAEPGQALFNGDMEPEAGAGAGAAASSAADPAIP
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CDS join(227..364,74718..74819,115935..116038,116868..116970,
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137346..137382,141773..141909,143237..143354,
146855..146939,147842..148018,170697..170743,
171537..171655,175512..175643,184984..185118,
190160..190313,198414..198436)

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/note="isoform 13 is encoded by transcript variant 14;
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prediction method: BestRefSeq."
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/db_xref="MIM:164757"
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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130463..130622,141847..141909,143237..143354,
146855..146939,147842..148018,170697..170743,
171537..171655,175512..175643,184984..185118,
190160..190313,198414..198436)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 9 is encoded by transcript variant 10;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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130463..130622,137346..137382,141773..141909,
143237..143354,146855..146939,147842..148018,
170697..170743,171537..171655,175512..175643,
184984..185118,190160..190313,198414..198436)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 2 is encoded by transcript variant 2;
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prediction method: BestRefSeq."
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/db_xref="MIM:164757"
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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130463..130622,137346..137382,139122..139241,
141773..141909,143237..143354,146855..146939,
147842..148018,170697..170743,171537..171655,
175512..175643,184984..185118,190160..190313,
198414..198436)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 4 is encoded by transcript variant 5;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."
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CDS join(227..364,74718..74819,90058..90321,115935..116047,
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130463..130622,137346..137382,141773..141909,
143237..143354,146855..146939,147842..148018,
170697..170743,171537..171655,175512..175643,
184984..185118,190160..190313,198414..198436)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 5 is encoded by transcript variant 6;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."

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/db_xref="HGNC:HGNC:1097"
/db_xref="MIM:164757"
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
116868..116970,123370..123518,124449..124568,
130463..130622,137346..137382,141839..141909,
143237..143354,146855..146939,147842..148018,
170697..170743,171537..171655,175512..175643,
184984..185118,190160..190333)
/gene="BRAF"
/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 7 is encoded by transcript variant 8;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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130463..130622,137346..137382,141773..141909,
143237..143354,146855..146939,147842..148018,
170697..170743,171537..171655,175512..175643,
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/gene_synonym="B-raf; B-RAF1; BRAF-1; BRAF1; NS7; RAFB1"
/note="isoform 1 is encoded by transcript variant 1;
Derived by automated computational analysis using gene
prediction method: BestRefSeq."
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CDS join(227..364,74718..74819,90058..90321,115935..116038,
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141773..141909,143237..143354,146855..146939,
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184984..185118,190160..190313,198414..205593)
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gene prediction method: Gnomon. Supporting evidence
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with support for all annotated introns"
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/note="Derived by automated computational analysis using
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170697..170743,171537..171655,175512..175643,
184984..185118,190160..190333)
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184984..185118,190160..190313,198414..205593)
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ORIGIN

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