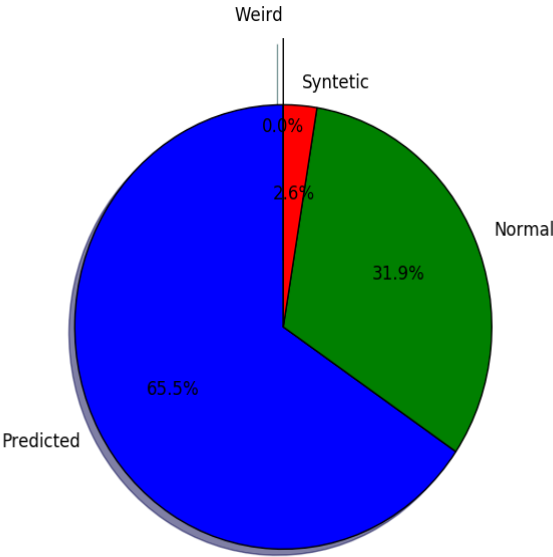
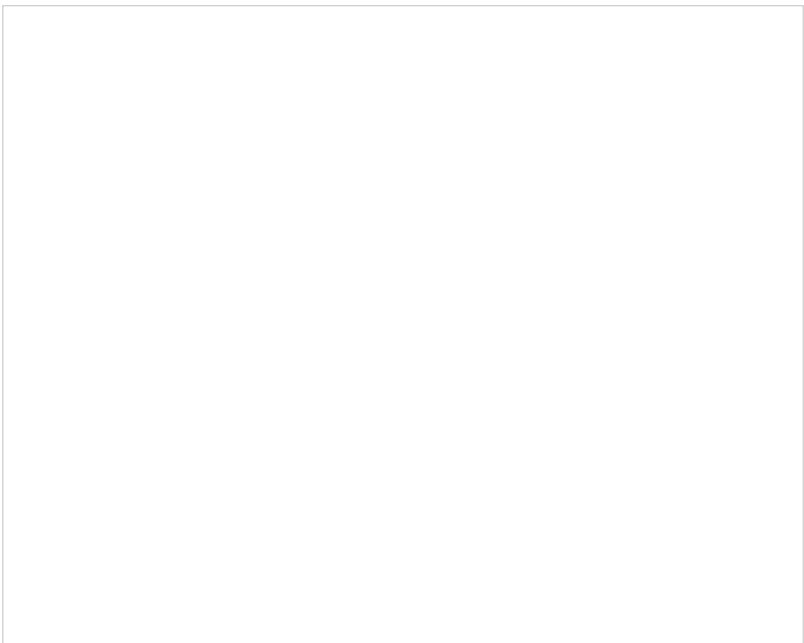
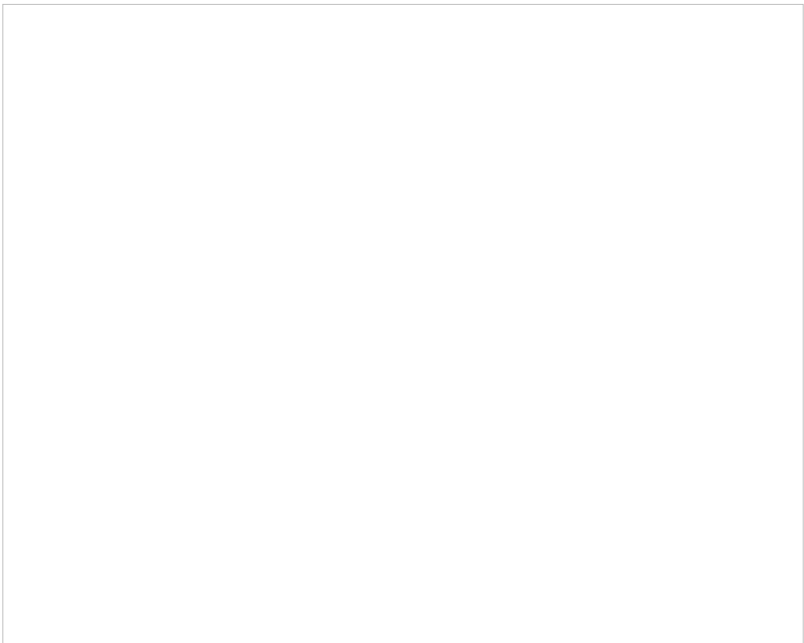
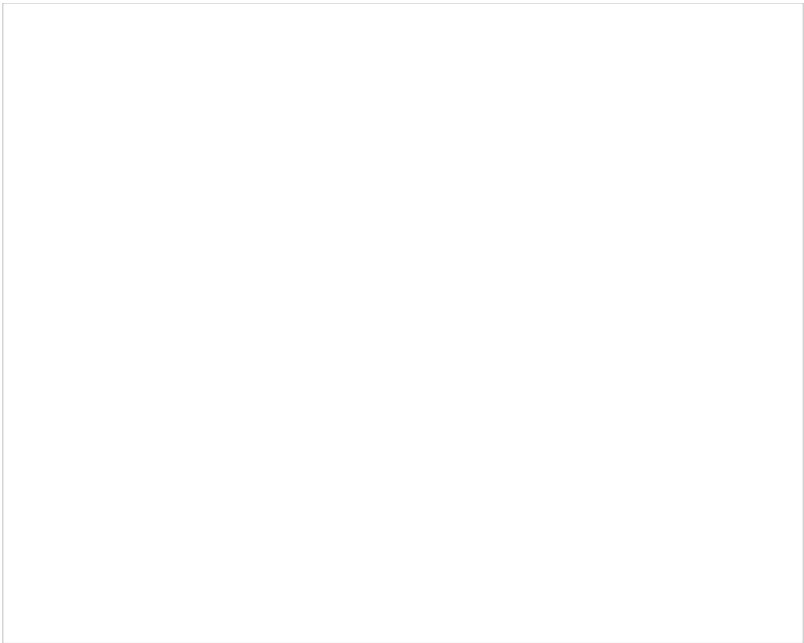


Result of Blast

Summary

Number of all alignments	Number of predicted	Number of normal alignments	Number of syntetic	Number of weird	Number of species	Number of species in predicted
116	76	37	3	0	18	10





Means for all data

Mean length	Mean identities	Mean score	Mean percent
6209.62068966	1330.84482759	2325.20811638	97.4052586207

Normal alignments

Means for normal alignments

Mean length	Mean identities	Mean score	Mean percent
6032.94423792	1332.44609665	2336.99456022	97.5768401487

Details

Hylobates pileatus

Gap	Percent	Title
6	98.19	Hylobates pileatus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Pongo pygmaeus

Gap	Percent	Title
0	98.39	Pongo pygmaeus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Pan paniscus

Gap	Percent	Title
0	99.4	Pan paniscus BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713686 gb KM017616.1 Pan paniscus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Macaca mulatta

Gap	Percent	Title
3	96.45	Macaca mulatta BRCA1, DNA repair associated (BRCA1), mRNA

Nomascus leucogenys

Gap	Percent	Title
0	98.59	Nomascus leucogenys BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713708 gb KM017627.1 Nomascus leucogenys breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Cercopithecus wolffi

Gap	Percent	Title
3	96.32	Cercopithecus wolffi breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Symphalangus syndactylus

Gap	Percent	Title
6	98.39	Symphalangus syndactylus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Homo sapiens

Gap	Percent	Title
0	100.00	Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 1, mRNA
0	100.00	Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 2, mRNA
0	100.00	Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:4804551), partial cds
0	100.00	Homo sapiens cDNA, FLJ98032
0	100.00	Homo sapiens breast and ovarian cancer susceptibility protein 1 (BRCA1) mRNA, complete cds

Gap	Percent	Title
0	100.00	Homo sapiens breast and ovarian cancer susceptibility protein (BRCA1) mRNA, BRCA1-2201T/2430C/2731T/3232G/3667G/4427C/4956G allele, partial cds
0	100.00	Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:40017569), partial cds
0	100.00	Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 3, mRNA
0	100.00	Homo sapiens cDNA clone IMAGE:7961445 >gi 146147644 gb BC115038.1 Homo sapiens cDNA clone IMAGE:7961448
0	100.00	Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:40017573)
0	100.00	Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:40017573)
0	99.94	Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone MGC:131629 IMAGE:7961446), complete cds
0	99.94	Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:3996658), with apparent retained intron
0	99.93	Homo sapiens cDNA, FLJ98032
1	99.69	Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA, complete cds
7	99.52	Homo sapiens cDNA clone IMAGE:40017575, containing frame-shift errors
0	99.42	Homo sapiens IRIS mRNA, complete cds; alternatively spliced
6	97.52	Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 3, mRNA
6	97.03	Homo sapiens cDNA clone IMAGE:7961445 >gi 146147644 gb BC115038.1 Homo sapiens cDNA clone IMAGE:7961448

Colobus guereza

Gap	Percent	Title
0	96.45	Colobus guereza breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Miopithecus talapoin

Gap	Percent	Title
3	96.45	Miopithecus talapoin breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Hylobates agilis

Gap	Percent	Title
6	98.13	Hylobates agilis breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Papio anubis

Gap	Percent	Title
3	96.39	Papio anubis BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713712 gb KM017629.1 Papio anubis breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Lophocebus albigena

Gap	Percent	Title
6	96.06	Lophocebus albigena breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Pan troglodytes

Gap	Percent	Title
0	99.4	Pan troglodytes BRCA1 (BRCA1) mRNA, partial cds
0	99.2	Pan troglodytes BRCA1, DNA repair associated (BRCA1), mRNA

Trachypithecus francoisi

Gap	Percent	Title
2	96.25	Trachypithecus francoisi breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Nomascus gabriellae

Gap	Percent	Title
0	98.59	Nomascus gabriellae breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Macaca fascicularis

Gap	Percent	Title
3	96.45	Macaca fascicularis BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713702 gb KM017624.1 Macaca fascicularis breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Hylobates lar

Gap	Percent	Title
6	98.06	Hylobates lar breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds

Predicted alignments

Means for predicted alignments

Mean length	Mean identities	Mean score	Mean percent
6214.95072464	1329.42608696	2321.42723043	97.3826956522

Details

Cercocebus atys

Gap	Percent	Title
6	96.17	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA
6	96.17	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X6, mRNA
6	95.83	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA
13	95.65	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X11, mRNA
13	95.65	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA
12	95.47	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA
16	95.47	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA
0	92.31	PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA

Pongo abelii

Gap	Percent	Title
0	98.55	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA
0	98.55	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA
0	98.52	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X10, mRNA
0	98.46	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X12, mRNA
0	98.46	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X13, mRNA
1	98.45	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X11, mRNA
0	98.31	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA
0	98.29	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X15, mRNA
0	98.29	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X14, mRNA
0	98.29	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA
6	97.95	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA
13	97.45	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X6, mRNA
19	97.05	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X7, mRNA
6	94.63	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X13, mRNA
6	94.37	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X12, mRNA
0	93.33	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X10, mRNA
0	93.26	PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA

Callithrix jacchus

Gap	Percent	Title
13	92.62	PREDICTED: Callithrix jacchus BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA
13	92.62	PREDICTED: Callithrix jacchus BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA
13	92.62	PREDICTED: Callithrix jacchus BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA

Macaca nemestrina

Gap	Percent	Title
3	96.37	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA
3	96.36	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA
3	96.14	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X11, mRNA
3	96.14	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA
3	96.14	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA
6	95.95	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X6, mRNA
9	95.77	PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA

Nomascus leucogenys

Gap	Percent	Title
0	98.38	PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA
0	98.21	PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA
0	98.10	PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA
0	98.07	PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA
0	98.07	PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA
6	93.39	PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA

Macaca mulatta

Gap	Percent	Title
3	96.26	PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X3, mRNA
3	96.26	PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X1, mRNA
6	96.07	PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X4, mRNA
9	95.89	PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X2, mRNA

Cebus capucinus

Gap	Percent	Title
13	92.80	PREDICTED: Cebus capucinus initiator BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA
13	92.80	PREDICTED: Cebus capucinus initiator BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA
16	92.62	PREDICTED: Cebus capucinus initiator BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA

Pan troglodytes

Gap	Percent	Title
0	99.41	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X12, misc_RNA
0	99.41	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X8, mRNA
0	99.41	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA
0	99.41	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA
0	99.40	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X2, mRNA
0	99.30	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X12, misc_RNA
0	99.30	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X8, mRNA
0	99.30	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA

Gap	Percent	Title
0	99.30	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA
0	99.30	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X5, mRNA
3	99.21	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X6, mRNA
3	99.21	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X5, mRNA
6	99.03	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA
9	98.85	PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X7, mRNA

Macaca fascicularis

Gap	Percent	Title
3	96.50	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X3, mRNA
3	96.50	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X4, mRNA
3	96.26	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X2, mRNA
9	95.89	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X6, mRNA
9	95.89	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X1, mRNA
12	95.71	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X7, mRNA
16	95.47	PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X5, mRNA

Ptilocolobus tephrosceles

Gap	Percent	Title
0	98.00	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA
0	96.17	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X5, mRNA
0	96.17	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA
0	96.17	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA
0	96.14	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA
3	95.97	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X6, mRNA
4	95.60	PREDICTED: Ptilocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X2, mRNA

Divided by species in normal alignments

	0
Cercopithecus wolffi	1
Colobus guereza	1
Homo sapiens	15
Hylobates agilis	1
Hylobates lar	1
Hylobates pileatus	1
Lophocebus albigena	1
Macaca fascicularis	1
Macaca mulatta	1
Miopithecus talapoin	1
Nomascus gabriellae	1
Nomascus leucogenys	1
Pan paniscus	1
Pan troglodytes	2
Papio anubis	1
Pongo pygmaeus	1
Symphalangus syndactylus	1
Trachypithecus francoisi	1

Divided by species in predicted alignments

	0
Callithrix jacchus	3
Cebus capucinus	3
Cercocebus atys	7
Macaca fascicularis	7
Macaca mulatta	4
Macaca nemestrina	7
Nomascus leucogenys	5
Pan troglodytes	9
Ptilocolobus tephrosceles	6
Pongo abelii	13