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		GenBank	Graphics	Distance tree of results			
<input checked="" type="checkbox"/>	select all 22 sequences selected						
	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate Bat-CoV/Phuhu/Itav/206645-63/2011 .complete genome	767	767	14%	0.0	70.58%	MG596803.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate Bat-CoV/H.says/Itav/206645-49/2011 .complete genome	765	765	13%	0.0	70.68%	MG596802.1
<input checked="" type="checkbox"/>	Coronavirus Neoromicia/PHL-PHF11/RSA/2011 .complete genome	758	945	14%	0.0	70.93%	KC889978.4
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus strain Neoromicia/5038 .complete genome	730	912	14%	0.0	70.83%	MF593268.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate NL13845 .complete genome	689	689	13%	0.0	70.24%	MG021451.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate NL140422 .complete genome	632	632	11%	2e-179	70.46%	MG021452.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate NL140455 .complete genome	628	628	12%	2e-178	70.30%	MG097421.1
<input checked="" type="checkbox"/>	BTVs-BetaCoV/SC2013 .complete genome	542	542	11%	3e-152	70.15%	KJ473821.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome coronavirus isolate D389/15 .complete genome	442	442	5%	3e-122	72.03%	KX108942.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate camel/MERS/Amibara/118/2017 .complete genome	178	178	1%	1e-42	72.65%	MG364474.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome coronavirus isolate Hu/Khari-KSA-2598/2015 .complete genome	178	178	1%	1e-42	72.65%	KT806053.1
<input checked="" type="checkbox"/>	Middle East respiratory syndrome-related coronavirus isolate camel/MERS/Amibara/126/2017 .complete genome	172	172	1%	5e-41	72.48%	MG364475.1

Fig. 3.1 BLAST analysis of the whole genome sequence of novel corona virus with the MERS CoV genome

3.1 ORF1ab Protein Sequence comparison of NCoV and MERS CoV

MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSVEEVLSEARQ
 HLKDGTCGLVEVEKGVLPQLEQPYVFIKRS DARTAPHGHVMVELVAELEGIQYGRSGE
 TLGVLVPHVGEIPVAYRKVLLRKNKNGKAGGHSYGADLKSFDLGDDELGTDPEYDFQEN
 WNTKHSSGV TRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQ
 LDFIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNCEPCNFVFP
 LNSIIKTIQPRVEKKKLDGFMGRIRSVYPV ASPNECNQMCLSTLMKCDHCGETSWQTG
 DFKVATCEFCGTENLTKEGATTCGYLPQNAVVKIYCPACHNSEVGPHEHSLAEYHNESG
 LKTILRKGGRTIAFGGCVFVSYVGCHNKCA YWVPRASANIGCNHTGVVGESEGLNDNL
 LEILQKEKVNINIVGDFKLNEEIAIILASFSASTSAFVETVKGLDYKAFKQIVESCNG
 FKVTKGKAKKGAWNIGEQKSILSPLYAFASEAARVVRSIFSRTLETAQNSVRVLQKAA
 ITILDGISQYSRLIDAMMFTSDLATNNLVVMA YITGGVVQLTSQWLNIFGTVVEKLV
 KPVLDWLEEKFKEDGVEFLRDGWEIFKFI STACEIVGGQVLTCAKEIKESVQTFFYKLV
 NKFLALCADSIIGGAKLALNLGETFVTHSKGLYRKCQVKSREETGLMLPLKAPKEI
 FLEGETLPTEVLTEEVLKGTDLQPLEQPTSEAVEAPLVGTPVCINGLMLLEIKDTEK
 YCALAPNMMVTNNTFTLKGGA PTKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEK
 CSAYTVELGTEVNEFACV VADAVIKTLQPVSELLTPLGIDLDEWSMATYYLFDSEGEF
 KLASHMYCSFYPPDEDEEEGDCEEEEFEPSTQY EYGTEDDYQGKPLEFGATSAAALQPE
 EEQEEDWLDDDSQQT VGGQDGEDNQTTTIQTIVEVQPQLEMELTPVVQTIEVNSFSG
 YLKLTDNVYIKNADIVEEAKKVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESD