

Example of Multiple Variant Annotation: Contig 6.3 Zyx102EF(CG32018)- RA, RB, RC, RD, RE, RF, RG

>variant A

1.) MESVAQQLRELSLPKGDGTSPLVCIGHGKVAKLVAKISNNQNASVKRRLDIPPKPIKYN
EMPQ

2.) VPSSRQVLCREPLYSQPLIGVEKTMRGHMPFRKYLSSSEFGVADTQINRKTTLNDP
AILEQQLEALAYHKLQMEKKGLLGVAQKPTQPLNSFTKPLSKTLSKSLIYNSLGSVRKEI
ETLELLTDETKISASTYSNVNETD

3.) DNEKDELPPPPSPESAVSSSYSELRHATLEFNKPIDY
LQNNQTTNPLQIYANQYAMQHDATGK

4.) SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNART
TFYDVNSIHRNDKEGLKNYISIPTEPVQELENYG

5.) GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDY
LQTLEKCSVCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK

6.) KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE

7.) DCGLLLSSEAEGRCYPLDDHVLCKSCNAKRVQALTNRMTSEH

>variant B

MESVAQQLRELSLPKGDGTSPLVCIGHGKVAKLVAKISNNQNASVKRRLDIPPKPIKYN
EMPQ/a1 <-- Note that this exon is found in variant A and does not need to be reannotated.

B1.) VPSSRQVLCREPLYSQPLIGVEKTMRGHMPFRKYLSSSEFGVADTQINRKTTLNDP
AILEQQLEALAYHKLQMEKKGLLGVAQKPTQPLNSFTKPLSKTLSKSLIYNSLGSVRKEI
ETLELLTDETKISASTYSNVNETA <-- Note that this a new exon not found in variant A.

B2.) AMDSSHSTQKMLSVCTNFISDNEKDELPPPPSPESAVSSSYSELRHATLEFNKPIDYLQNN
QTTNPLQIYANQYAMQHDATGK <-- Note that this a new exon not found in variant A.

SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNARTTF
YDVNSIHRNDKEGLKNYISIPTEPVQELENYG/a4

GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDYLQTLEKCS
 VCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK/a5

KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE/a6

DCGLLSSEAEGRCYPLDDHVLCKSCNAKRVQALTNRMTSEH/a7

>variant C <-- Note that variant has no new exons.

MESVAQQLRELSLPKGDTGSPLVCIGHGKVAKLVAKISNNQNASVKRRLDIPPKPIKYNEMPQ/a

1

VPSSRQVLCREPLYSQPLIGVEKTMRGHMPFRKYLSSSEFGVADTQINRKTTLDNP
 AILEQQLEALAYHKLQMEKKGLLGVAQKPTQPLNSFTKPLSKTLSKSLIYNSLGSVRKEI
 ETLELLTDETKISASTYSNVNETA/b1

AMDSSHSTQKMLSVCTNFISDNEKDELPPPPSPESAVSSSYSELRHATLEFNKPIDYLQNNQTT
 NPLQIYANQYAMQHDATGK/b2

SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNARTTF
 YDVNSIHRNDKEGLKNYISIPTEPVQELENYG/a4

GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDYLQTLEKCS
 VCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK/a5

KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE/a6

DCGLLSSEAEGRCYPLDDHVLCKSCNAKRVQALTNRMTSEH/a7

>variant D

MESVAQQLRELSLPKGDTGSPLVCIGHGKVAKLVAKISNNQNASVKRRLDIPPKPIKYN

EMPQ/a1

VPSSRQVLCREPLYSQPLIGVEKTMRGHMPFRKYLSSSEFGVADTQINRKTTLDNPAILEQQLEA
 LAYHKLQMEKKGLLGVAQKPTQPLNSFTKPLSKTLSKSLIYNSLGSVRKEIETLELLTDETKISAST
 YSNVNETD/a2

DNEKDELPPPPSPESAVSSSYSELRHATLEFNKPIDYLQNNQTTNPLQIYANQYAMQH DATGK/a
3

SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNARTTF
YDVNSIHRNDKEGLKNYISIPTEPVQELENYG/a4

GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDYLQTLEKCS
VCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK/a5

KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE/a6

DCGLLLSSEAEGRCYPLDDHVLCKSCNAKRVQALTNRMTSEH/a7

>variant E

MESVAQQLRELSLPKGDTGSPLVCIGHGKVAKLVAKISNNQNASVKRRLDIPPKPIKYN
EMPQ/a1

VPSSRQVLCREPLYSQPLIGVEKTMRGHMPFRKYLSSSEFGVADTQINRKTTLDNP
AILEQQLEALAYHKLQMEKKGLLGVQAKPTQPLNSFTKPLSKTLSKSLIYSNLGSVRKEI
ETLELLTDETKISASTYSNVNETA/b1

AMDSSHSSTQKMLSVCTNFISDNEKDELPPPPSPESAVSSSYSELRHATLEFNKPIDYLQNNQTT
NPLQIYANQYAMQH DATGK/b2

SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNARTTF
YDVNSIHRNDKEGLKNYISIPTEPVQELENYG/a4

GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDYLQTLEKCS
VCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK/a5

KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE/a6

DCGLLLSSEAEGRCYPLDDHVLCKSCNAKRVQALTNRMTSEH/a7

>variant F

MESVAQQLRELSLPKGDTGSPLVCIGHGKVAKLVAKISNNQNASVKRRLDIPPKPIKYN
EMPQ/a1

GK/NY-LMU

VPSSRQVLC\$REPLY\$SQPLIGVEKTMRGHMPFRKYL\$SSEFGVADTQINRKTTLDNP
 AILEQQLEALAYHKLQMEKKGLLGVQAKPTQPLNSFTKPLSKTLSKSLIYSNLG\$SVRKEI
 ETLELLTDETKISASTYSNVNETD/a2

DNEKDELPPPP\$PESAVSSSYSELRHATLEFNKPIDYLQNNQTTNPLQIYANQY
 AMQH\$DATGK/a3

SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNARTTF
 YDVNSIHRNDKEGLKNYISIPTEPVQELENYG/a4

GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDYLQTLEKCS
 VCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK/a5

KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE/a6

DCGLLLSSEAEGRCYPLDDHVLC\$KSCNAKRVQAL\$TNRMTSEH/a7

>variant G

G1.) MQ <-- **Note that this a new exon not found in earlier variants. It is also very short and will require more work to locate.**

VPSSRQVLC\$REPLY\$SQPLIGVEKTMRGHMPFRKYL\$SSEFGVADTQINRKTTLDNPAI
 LEQQLEALAYHKLQMEKKGLLGVQAKPTQPLNSFTKPLSKTLSKSLIYSNLG\$SVRKEIET
 LELLTDETKISASTYSNVNETA/b1

AMDSSHSSTQKML\$VCTNFISDNEKDELPPPP\$PESAVSSSYSELRHATLEFNKPIDYLQNNQTT
 NPLQIYANQYAMQH\$DATGK/b2

SSSTYDSIYEPINPRPCVADTLPRESYNLHNSYVNDNNPNISHEYNISNSIEANQTLYIHGNARTTF
 YDVNSIHRNDKEGLKNYISIPTEPVQELENYG/a4

GRCVKCNSRVLGESSGCTAMDQIYHIFCFTCTDCQINLQGKPFYALDGKPYCEYDYLQTLEKCS
 VCMEPILERILRATGKPYHPQCFTCVVCGKSLDGLLFTVDATNQNYCITDFHK/a5

KKFAPRCCVCKQPIMPDPGQEETIRVVALDRSFHLECYKCE/a6

GK/NY-LMU

DCGLLLSSEAEGRGCYPLDDHVLCKSCNAKRVQALTNRMTSEH/a7

How many different exons are present?

A1-A7, B1-B2, G1. Therefore, there are only 10 coding exons to annotate for a gene with 7 variants and 49 coding exons.

**Please direct any questions or concerns to:
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