

gene			<i>Rv3376</i>					<i>Rv3377c</i>										<i>Rv3378c</i>				
coordinate (H37Rv)			3790459	3790491	3790652	3790688	3790694	3790929	3791117	3791129	3791133	3791136	3791195	3791261	3791576	3791598	3792135	3792263	3792523	3792712	3792840	3793102
mutation			dupT	G>T	C>T	T>A	G>T	T>C	G>A	T>C	C>X	T>C	G>T	A>C	G>T	T>C	T>C	C>A	T>G	CC>TT	A>G	C>A
change			X	V>F	T>M	V>D	G>C	K>E	T>M	X	X15	I>V	T>K	I>S	P>H	T>A	M>V	G>V	I>L	X	V>A	D>Y
MTb complex species	total genomes	synteny (%)	Number of genomes with mutation																			
<i>africanum</i>	34	101	2		4		4		1				1		1			29				1
<i>bovis</i>	130	99									129			1		1			1			50
<i>orygis</i>	2	101						1														
<i>caprae</i>	4	100								4	4											
<i>microti</i>	6	100				6			1													
<i>pinnipedii</i>	3	100		3		3																
<i>munji</i>	1	99														1				1		
<i>canetti</i>	14	97	100% coverage; 99% identity																			
<i>lacus</i>	2	43	97% coverage; 77% identity																			
<i>decipiens</i>	1	52	97% coverage; 79% identity																			