Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Ut purus elit, vestibulum ut, placerat ac, adipiscing vitae, felis. Curabitur dictum gravida mauris. Nam arcu libero, nonummy eget, consectetuer id, vulputate a, magna. Donec vehicula augue eu neque. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Mauris ut leo. Cras viverra metus rhoncus sem. Nulla et lectus vestibulum urna fringilla ultrices. Phasellus eu tellus sit amet tortor gravida placerat. Integer sapien est, iaculis in, pretium quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec varius orci eget risus. Duis nibh mi, congue eu, accumsan eleifend, sagittis quis, diam. Duis eget orci sit amet orci dignissim rutrum.

To reference this table within the text: **??**

Nam dui ligula, fringilla a, euismod sodales, sollicitudin vel, wisi. Morbi auctor lorem non justo. Nam lacus libero, pretium at, lobortis vitae, ultricies et, tellus. Donec aliquet, tortor sed accumsan bibendum, erat ligula aliquet magna, vitae ornare odio metus a mi. Morbi ac orci et nisl hendrerit mollis. Suspendisse ut massa. Cras nec ante. Pellentesque a nulla. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Aliquam tincidunt urna. Nulla ullamcorper vestibulum turpis. Pellentesque cursus luctus mauris.

To reference this table : **??**

Table 1: Stats of different assemblies. Some explanation of the dummy values which are shown below.

	Assembly 1 / Assembly 7	Assembly 2	Assembly 3	Assembly 4 / Assembly 8	Assembly 5	Assembly 6
assembly length [Mb]	1244	1270	1280	1290	1231	1232
ambiguous bases [Mb]	0.2	790	273	238	237	135
number of contigs ($>$ 10kb)	1328	13817	18461	13746	13751	13864
number of contigs	13647	14776	14767	14619	15354	13716
median contig length	0.013	0.0183	0.013	0.048	0.074	0.099
longest contig or scaffold [Mb]	3.147	1.89	13.13	139.10	28.24	139.41
L50	1384	777	5	5	5	5
N50 [Mb]	0.149	1.148	153.1498	13.3309	14.463	99.463
CL50	65	13	4	4	1	1
CN50 [Mb]	1.1398	16.12	13.2725	48.485	45.6215	138.0284

chr	marker	ext	best blast	2nd best blast	notes
1	bla	axo	chrchr1	-	
1	bli	axo	chrchr4		
1	bla	axo	chrchr1		
2	gene1		Super-Scaffold_28	Super-Scaffold_28	
2	IGUAS	eoN	chr2		
2	LOL	oN	chrchr2		lower scored match on chr2
2	PIU	el			lower scored match on another location in the genome, 96.75 percent identity. Some longer explanation because some text is needed in this place.
2	Schnu	gi	chr7		
3	SHAD	bu	chrchr3		
3	algo	ax	chr3		lower scored match on chr8, bit score 350, but only 189 bp long and 100 percent identity
3	Mol2	eo	chr3		
3	Myb111	axN	chrchr3		
4	das	mxs	chr3		lower scored match on chr4, 91.01 percent identity
4	F3H	ara	chrchr4		
4	k9	at	chrchr6		
4	m3	at	Chrchr4:16928437089-13029707494802	Chrchr4:231847-2987408702	
4	My0		chrchr1	-	bit score 222, but only 146 bp long and percent identity 100 duplication? Both 479bp long and same scores
1	bla	axo	chrchr4		
1	bli	axo	chrchr1		
1	bla	axo	Super-Scaffold_28	Super-Scaffold_28	
2	gene1		chr2		lower scored match on chr2
2	IGUAS	eoN			
2	LOL	oN			

2	PIU	el	chrchr2		lower scored match on another location in the genome, 96.75 percent identity. Some longer explanation because some text is needed in this place.
2	Schnu	gi	chr7		
3	SHAD	bu	chrchr3		
3	algo	ax	chr3		lower scored match on chr8, bit score 350, but only 189 bp long and 100 percent identity
3	Mol2	eo	chr3		
3	Myb111	axN	chrchr3		
4	das	mxs			lower scored match on chr4, 91.01 percent identity
4	F3H	ara	chr3		
4	k9	at	chrchr4		
4	m3	at	chrchr6		bit score 222, but only 146 bp long and percent identity 100
4	My0		Chrchr4:16928437089-13029707494802	Chrchr4:231847-2987408702	duplication? Both 479bp long and same scores

Table 2: This table shows fantasy blast results in order to show how a long table could look like.