

Table with multiple columns and rows, containing extensive data. Several rows are highlighted in yellow.

Chromosome	Start (Mb)	End (Mb)	RefSeq	Gene	Start (Mb)	End (Mb)	RefSeq	Gene	Start (Mb)	End (Mb)	RefSeq	Gene	Start (Mb)	End (Mb)	RefSeq	Gene	Start (Mb)	End (Mb)	RefSeq	Gene
1	100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000	
1	100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000		100000000	100000000	chr1:100000000	

The table consists of approximately 20 columns and thousands of rows. Each row contains a series of numerical values, likely representing statistical parameters such as p-values, odds ratios, or beta coefficients. The columns are densely packed with numbers. Several rows are highlighted in a light yellow color, indicating specific points of interest. The overall appearance is that of a comprehensive data table from a genetic study.

Chromosome	Position (Mb)	Gene	RefSeq ID	Ensembl ID	Transcript Start (kb)	Transcript End (kb)	Transcript Orientation	Transcript Type	Transcript Status	Transcript Length (bp)	Transcript GC Content (%)	Transcript GC Content (95% CI)	Transcript GC Content (90% CI)	Transcript GC Content (99% CI)	Transcript GC Content (99.99% CI)
1	1.5	ABO	ABO	ABO	0	1	+	Protein Coding	Confirmed	210	41.9	41.4-42.4	41.2-42.6	41.1-42.7	41.0-42.8
1	1.5	ABO	ABO	ABO	0	1	+	Protein Coding	Confirmed	210	41.9	41.4-42.4	41.2-42.6	41.1-42.7	41.0-42.8
1	1.5	ABO	ABO	ABO	0	1	+	Protein Coding	Confirmed	210	41.9	41.4-42.4	41.2-42.6	41.1-42.7	41.0-42.8
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1	1.5	ABO	ABO	ABO	0	1	+	Protein Coding	Confirmed	210	41.9	41.4-42.4	41.2-42.6	41.1-42.7	41.0-42.8