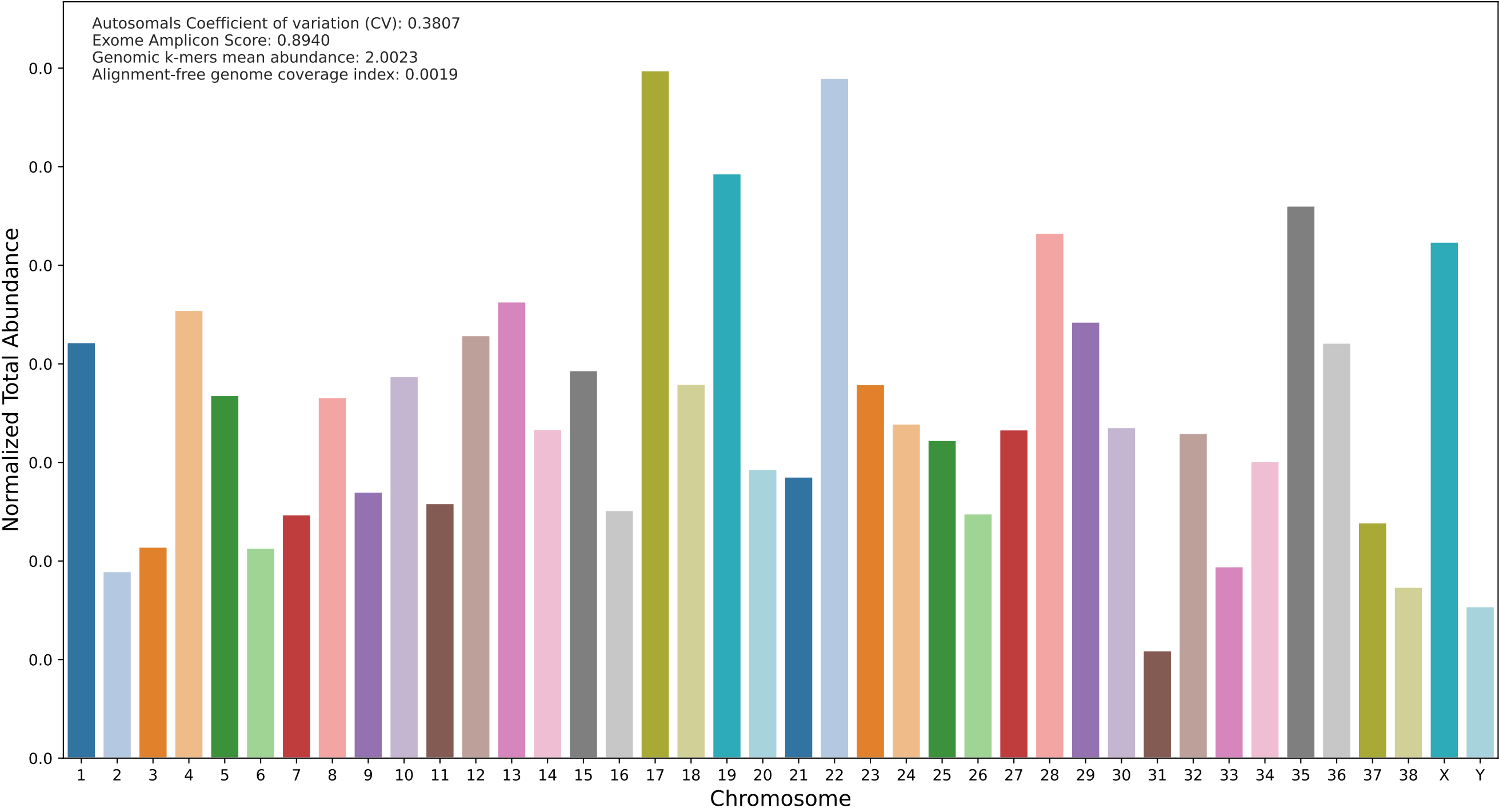
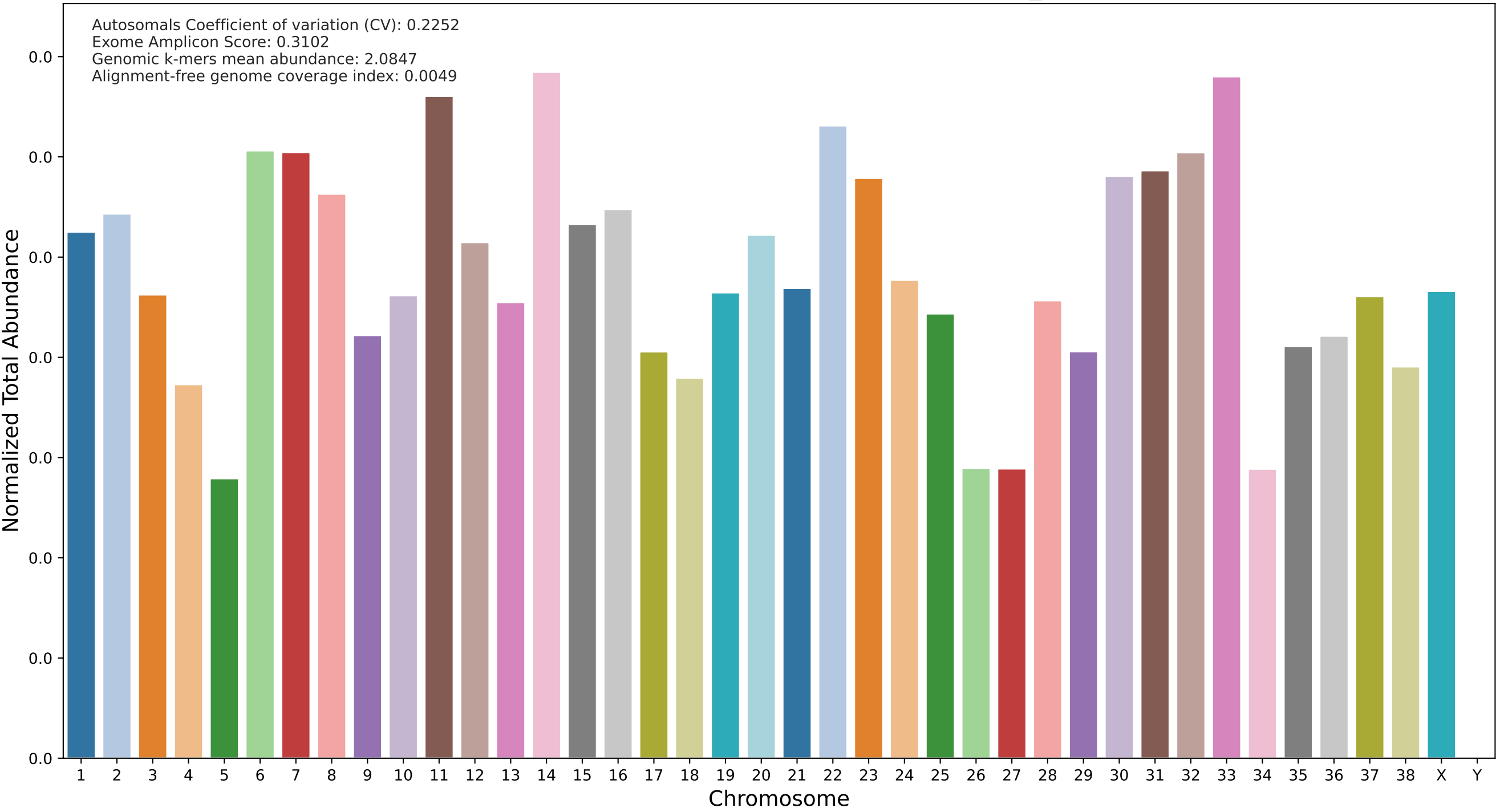


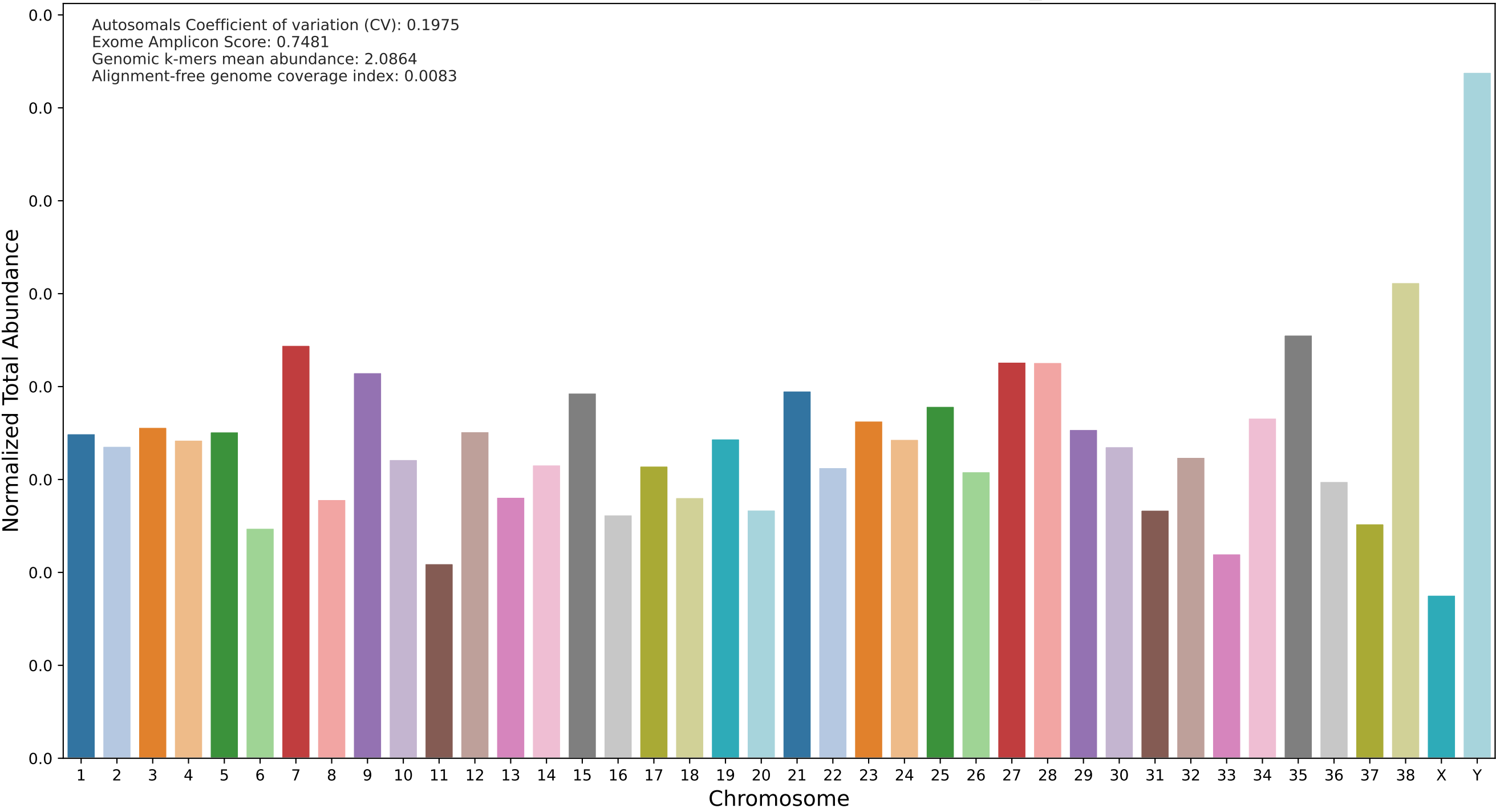
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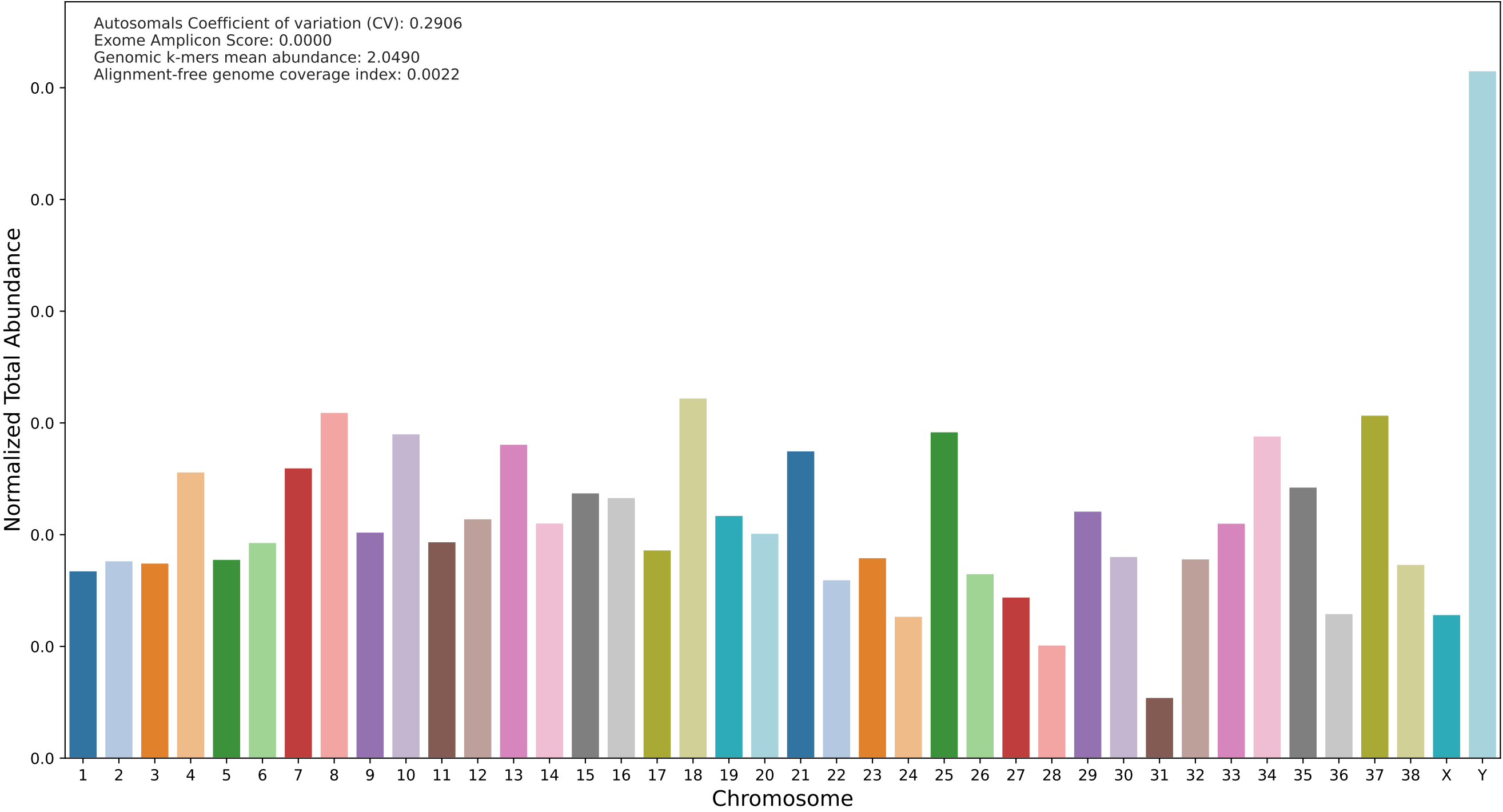
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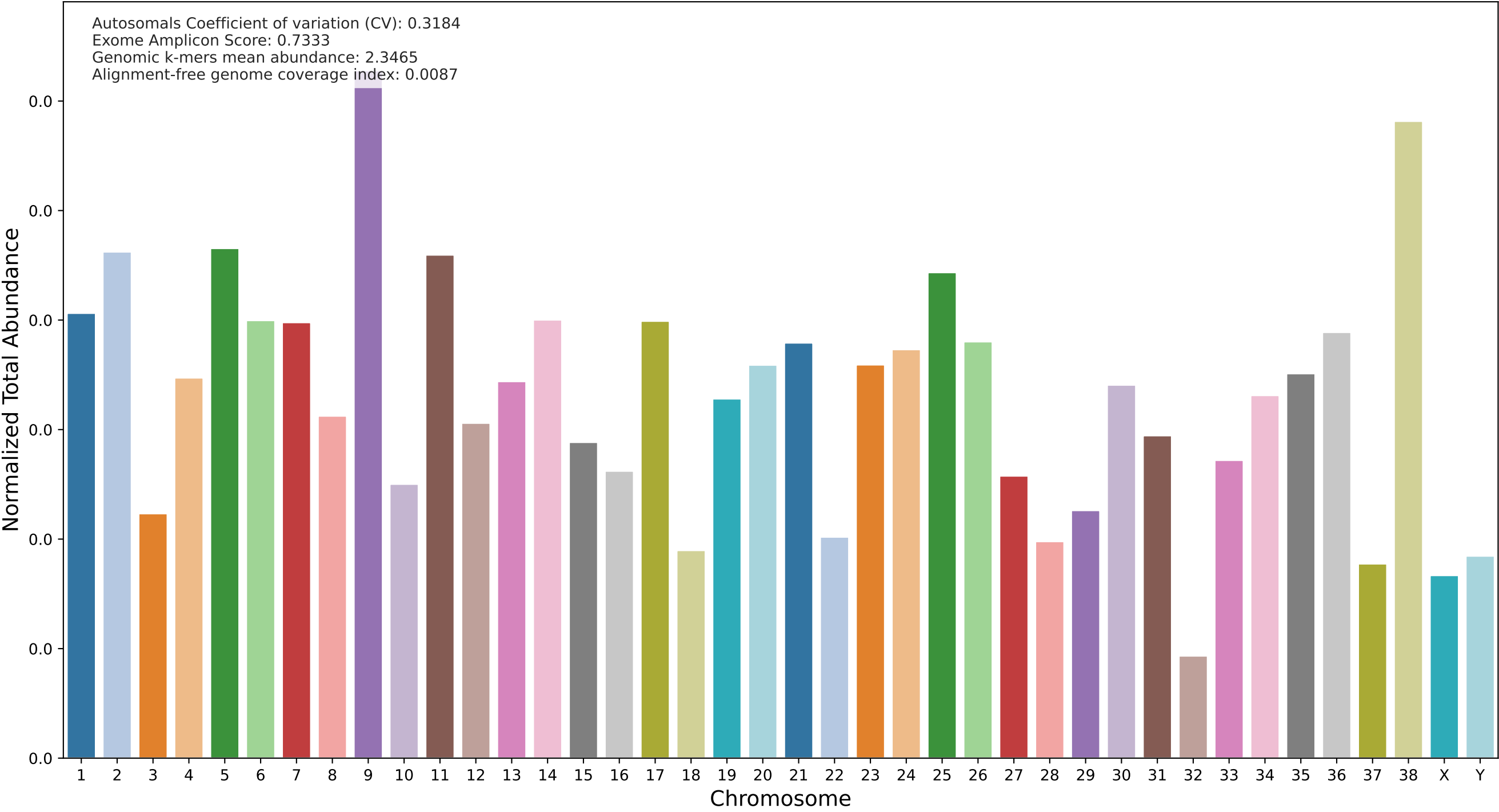
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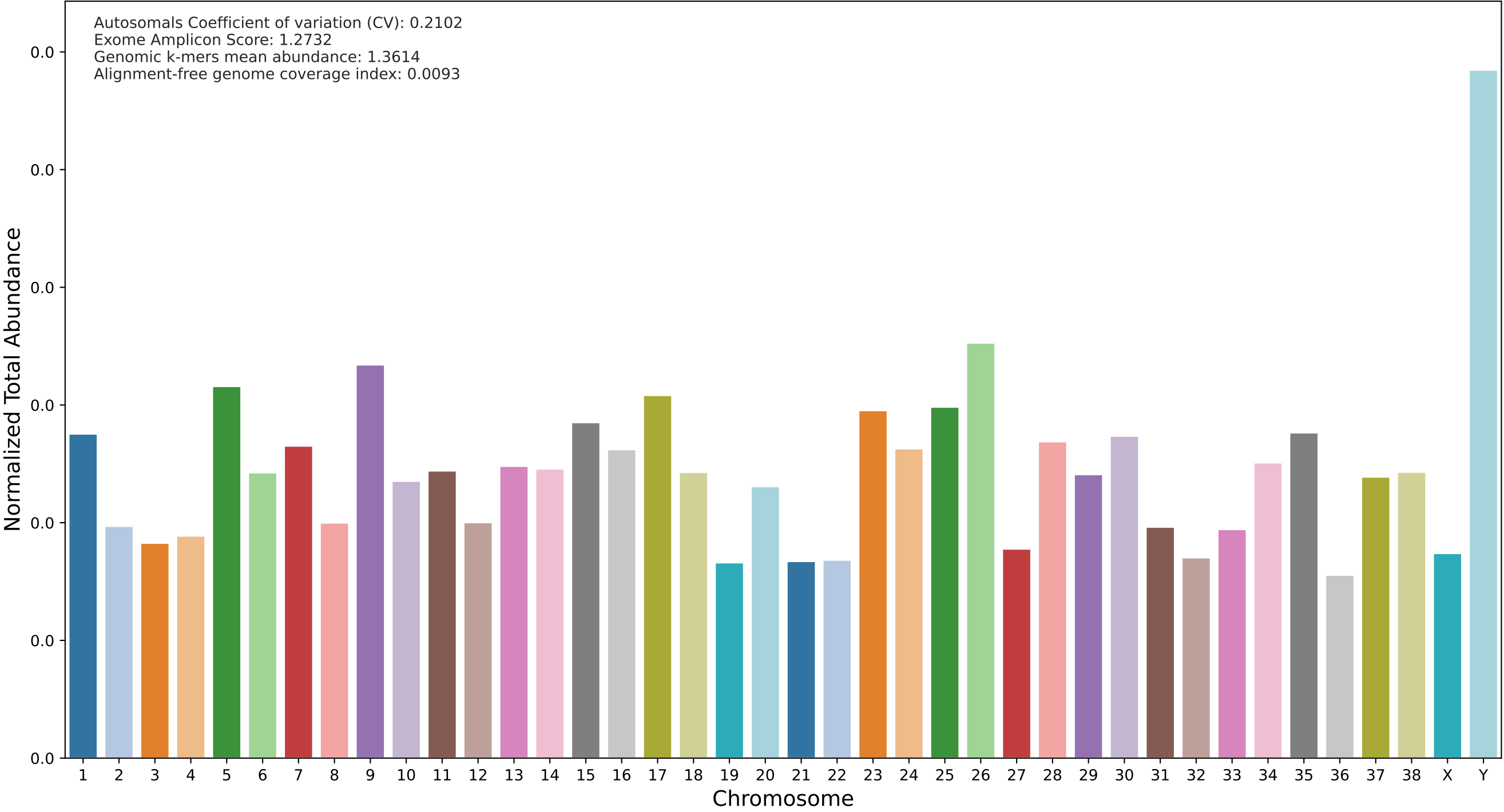
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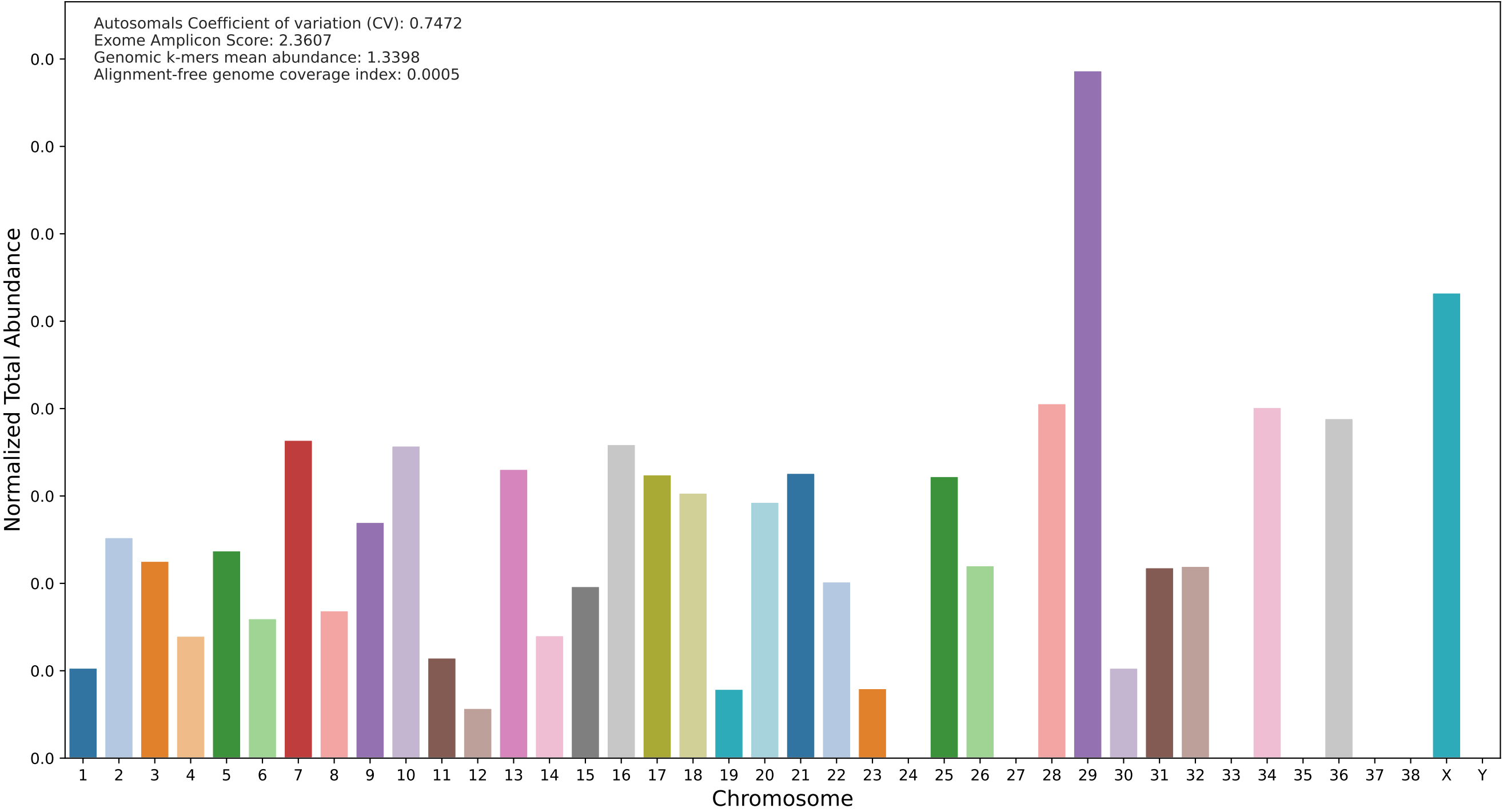
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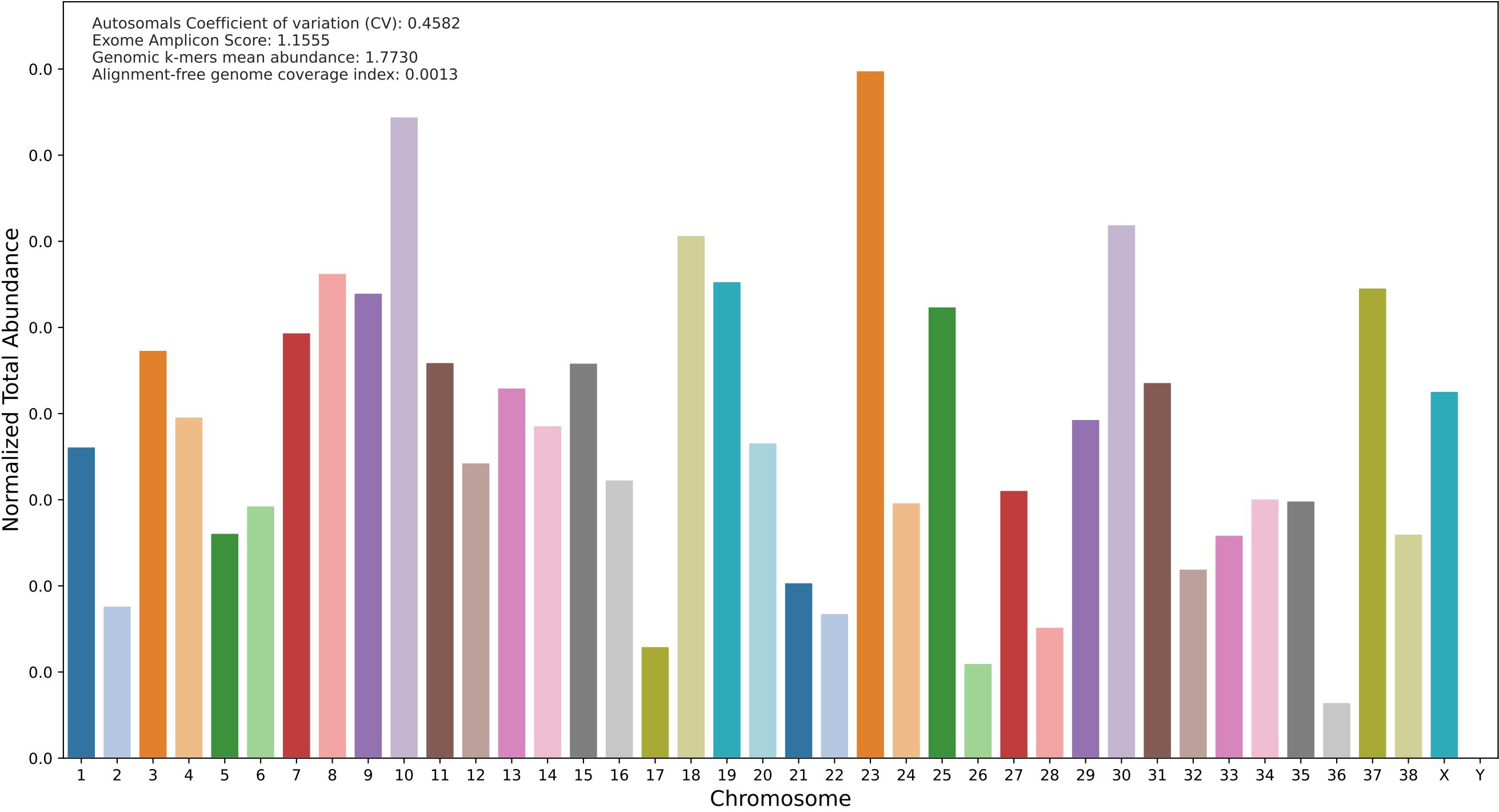
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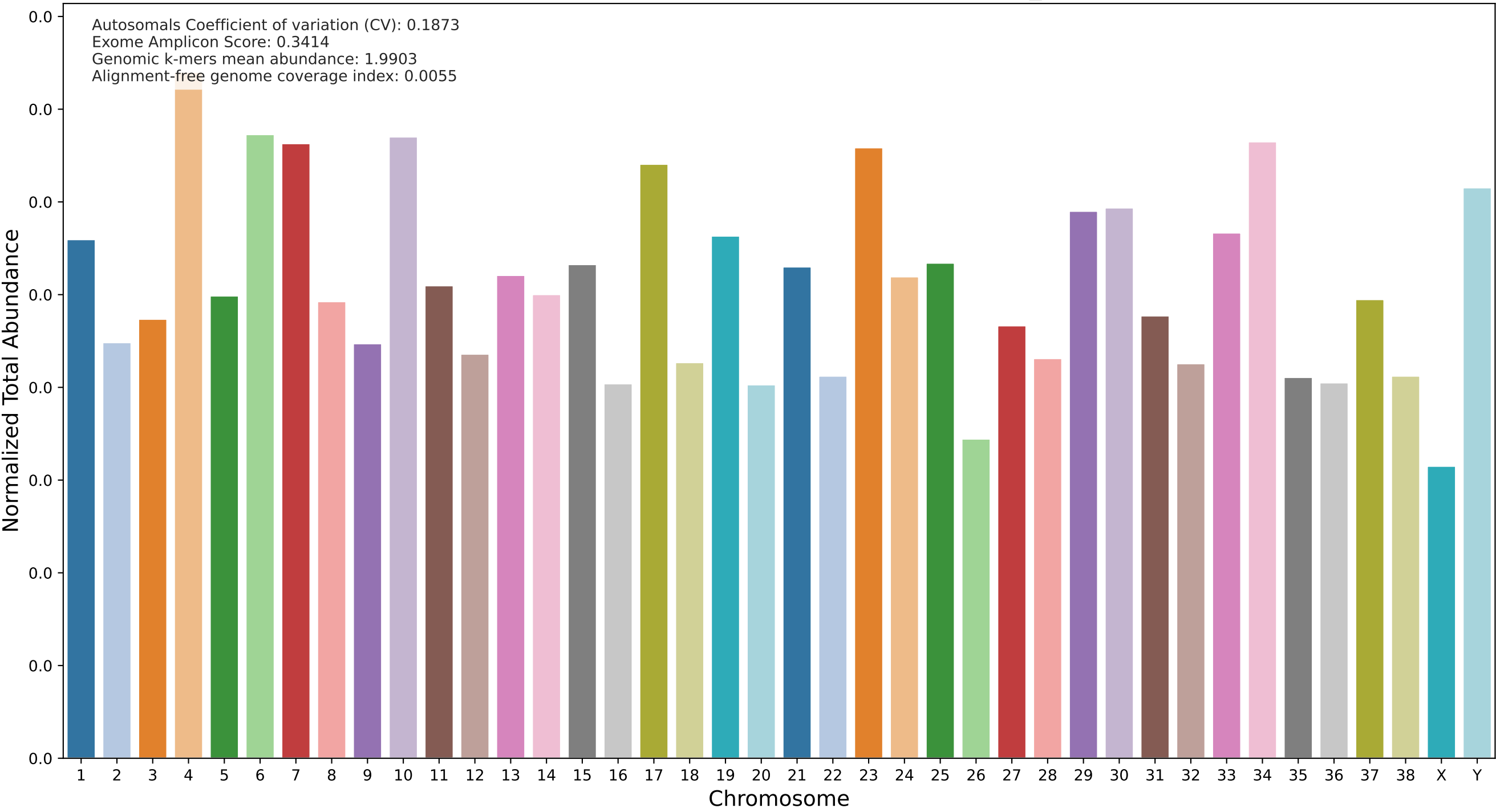
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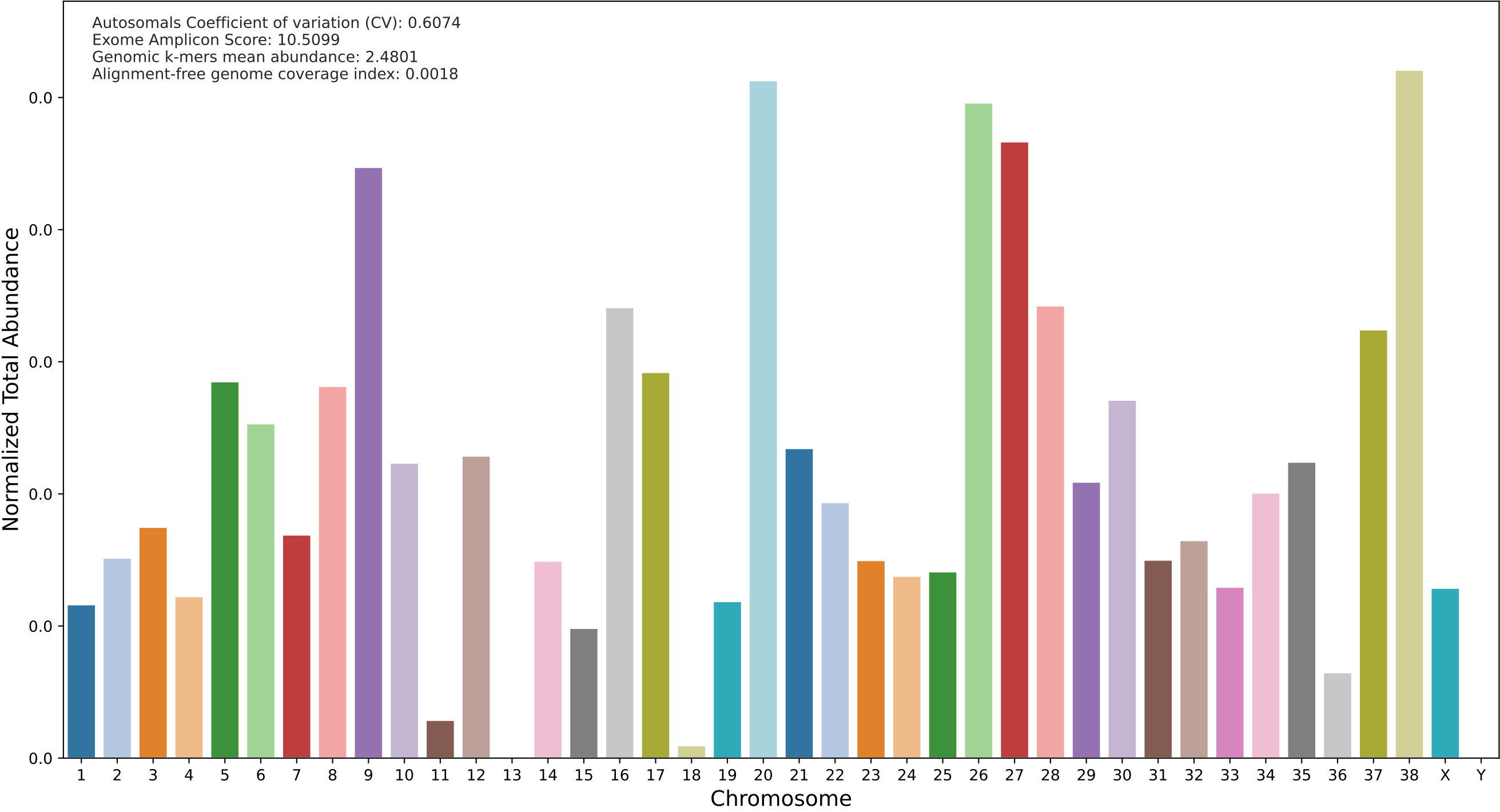
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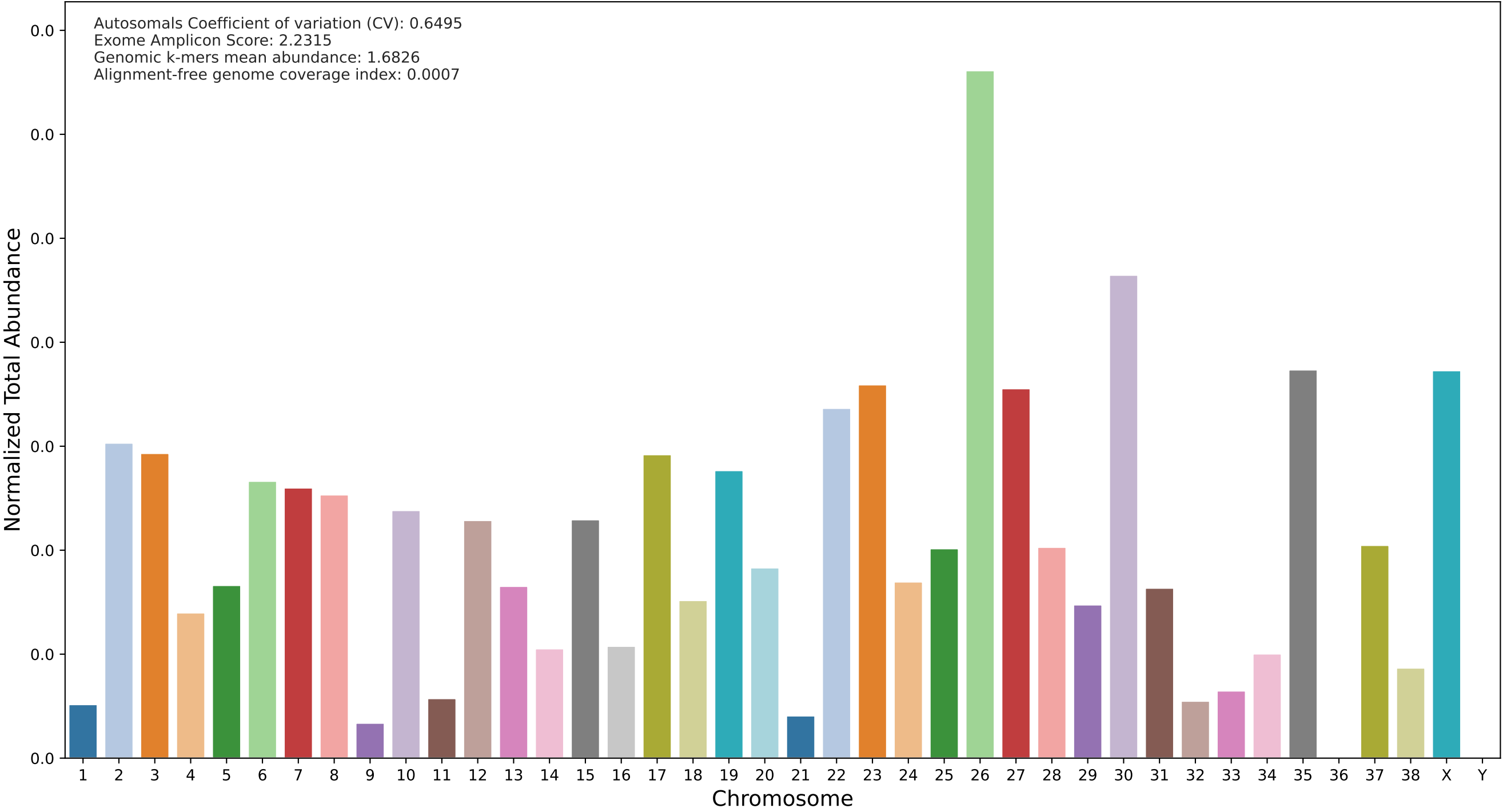
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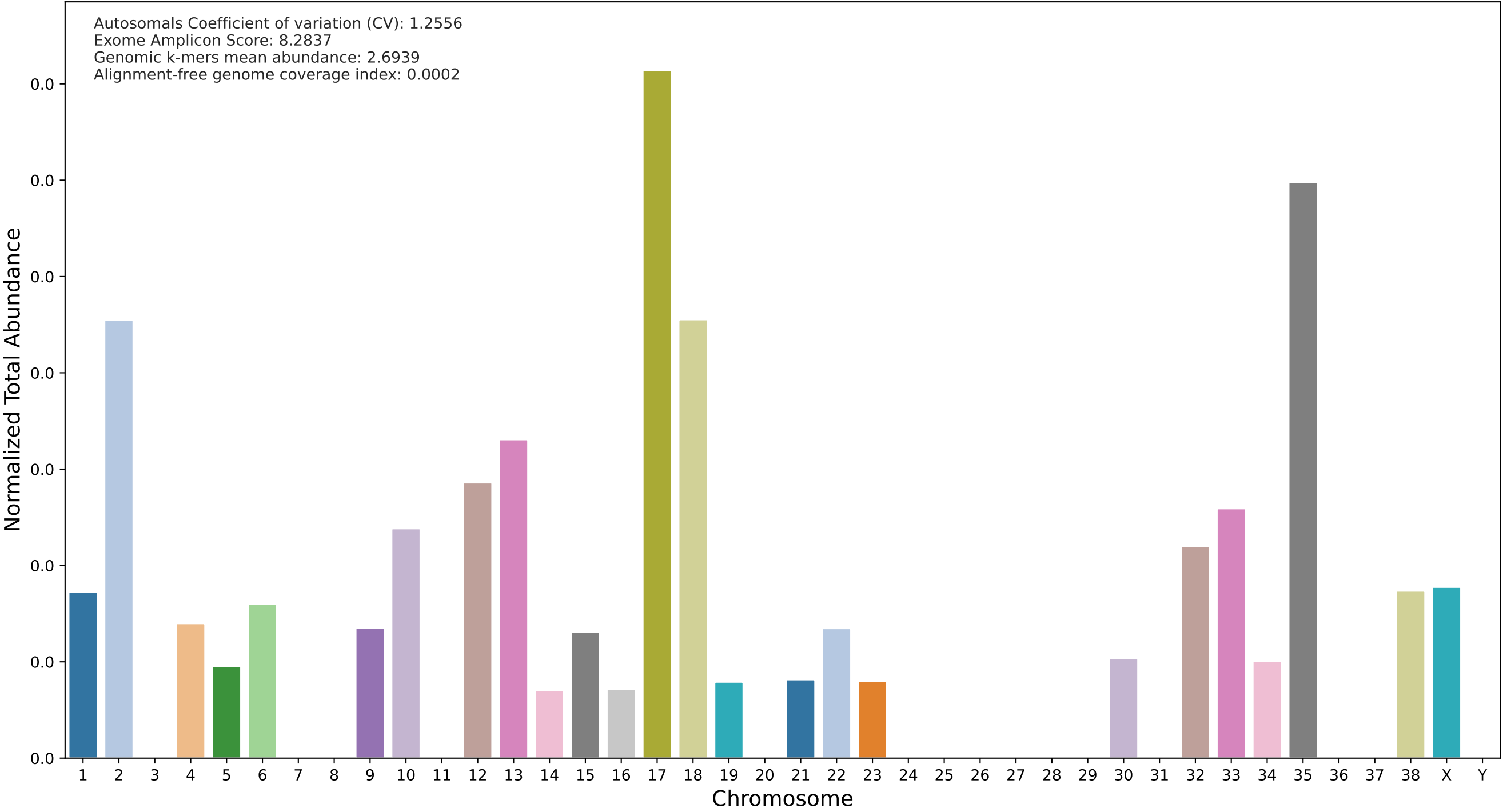
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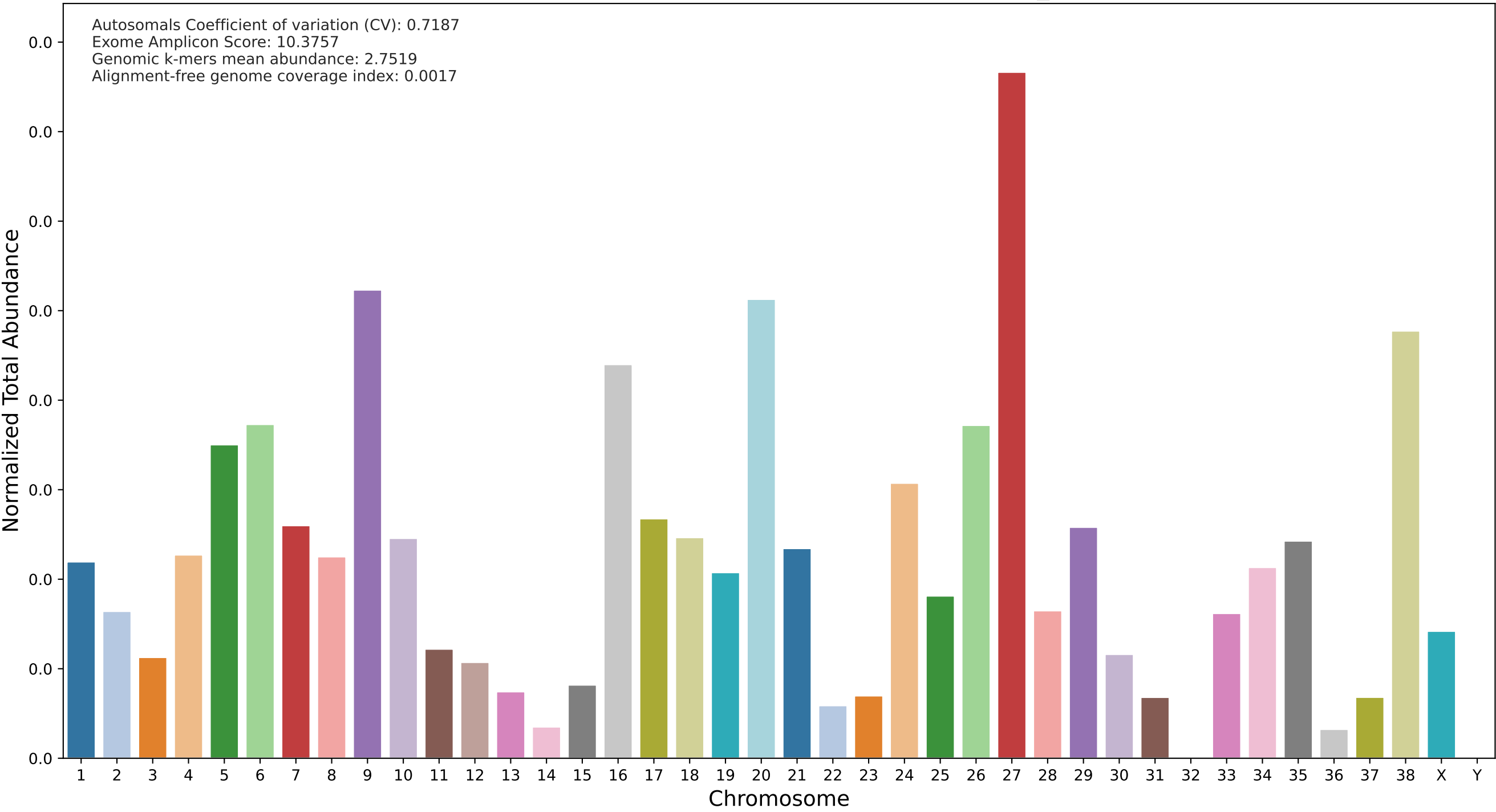
Normalized Chromosome Abundance - SAMN25331201_SRX17765634



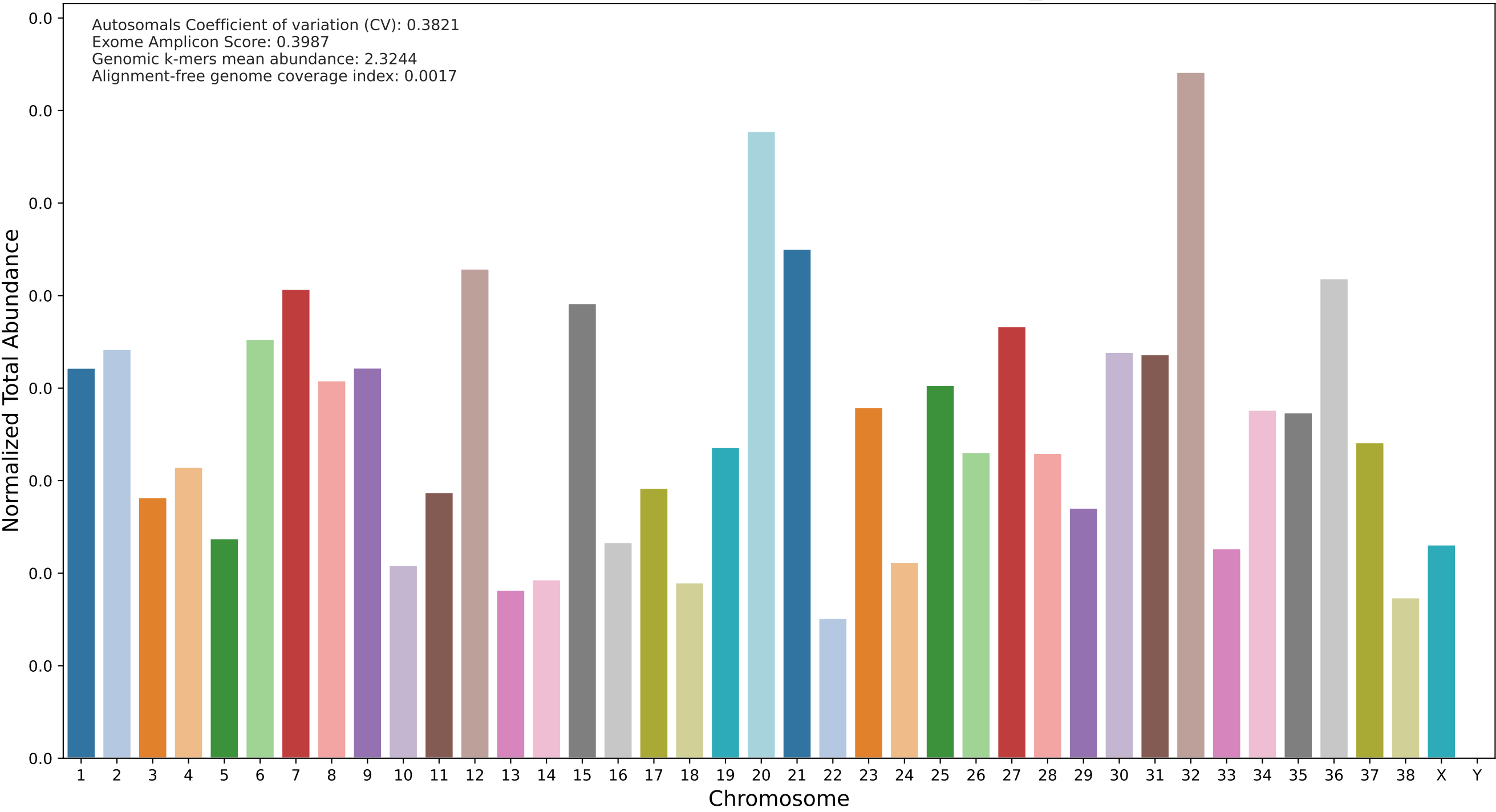
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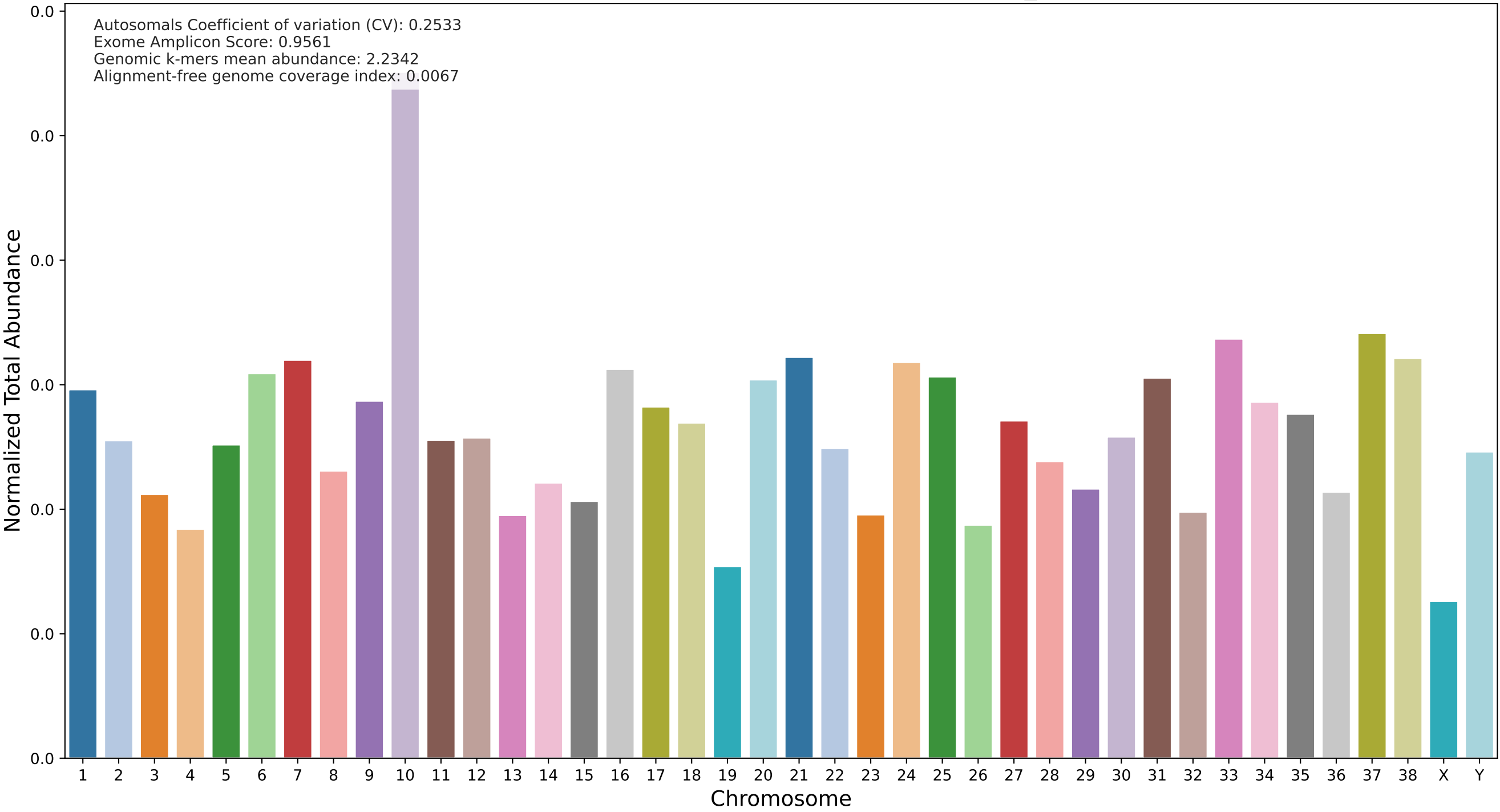
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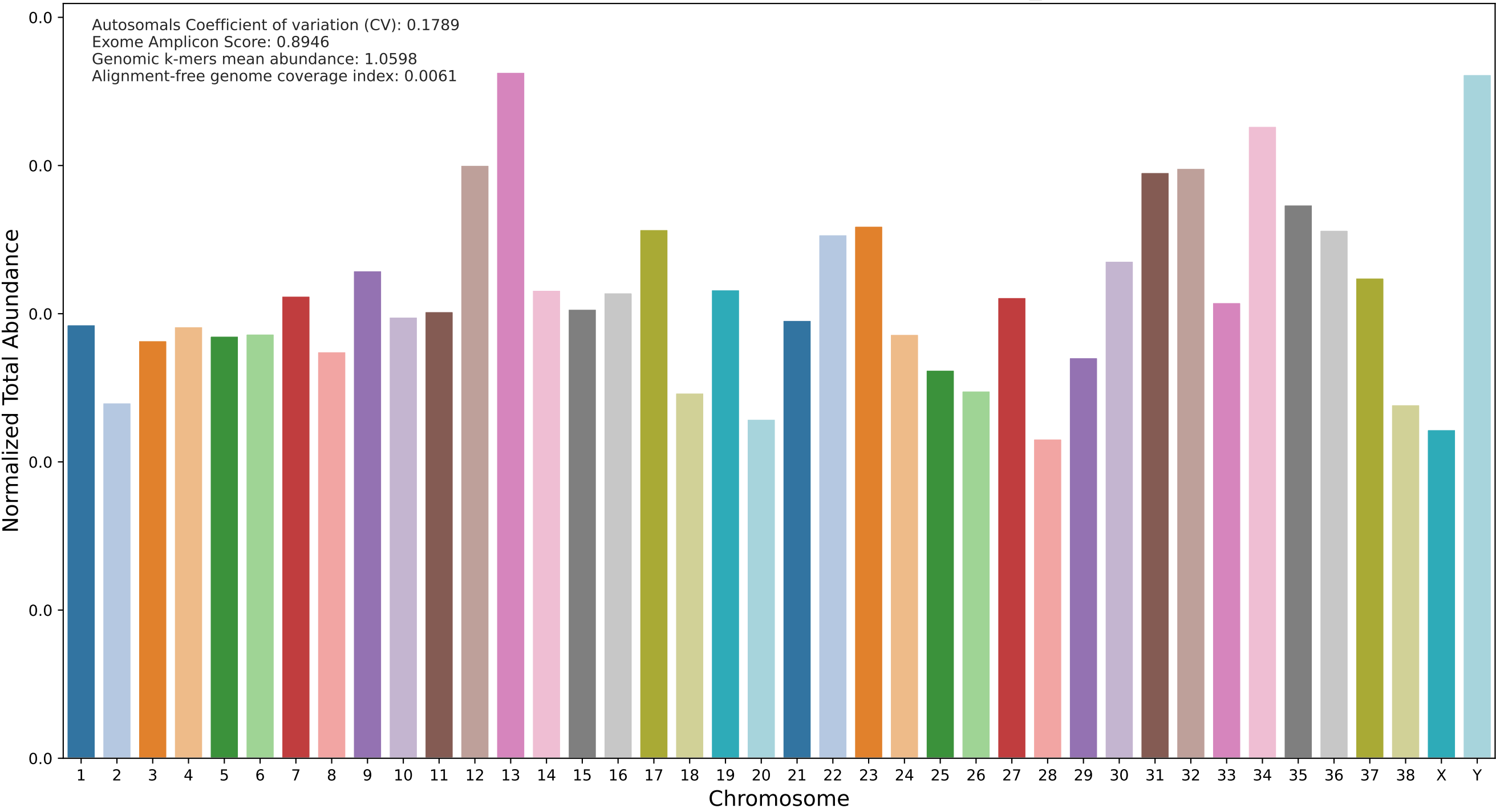
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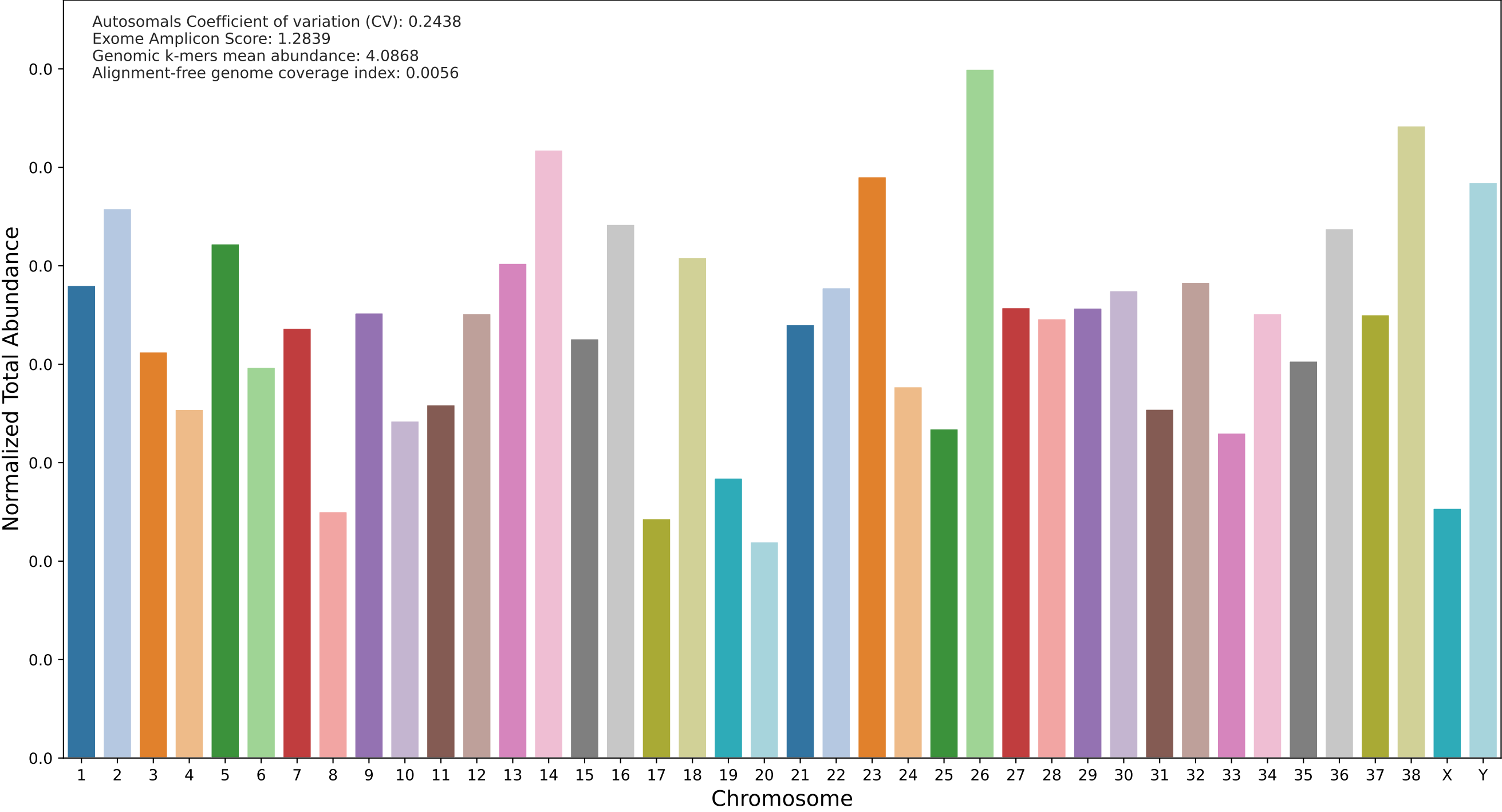
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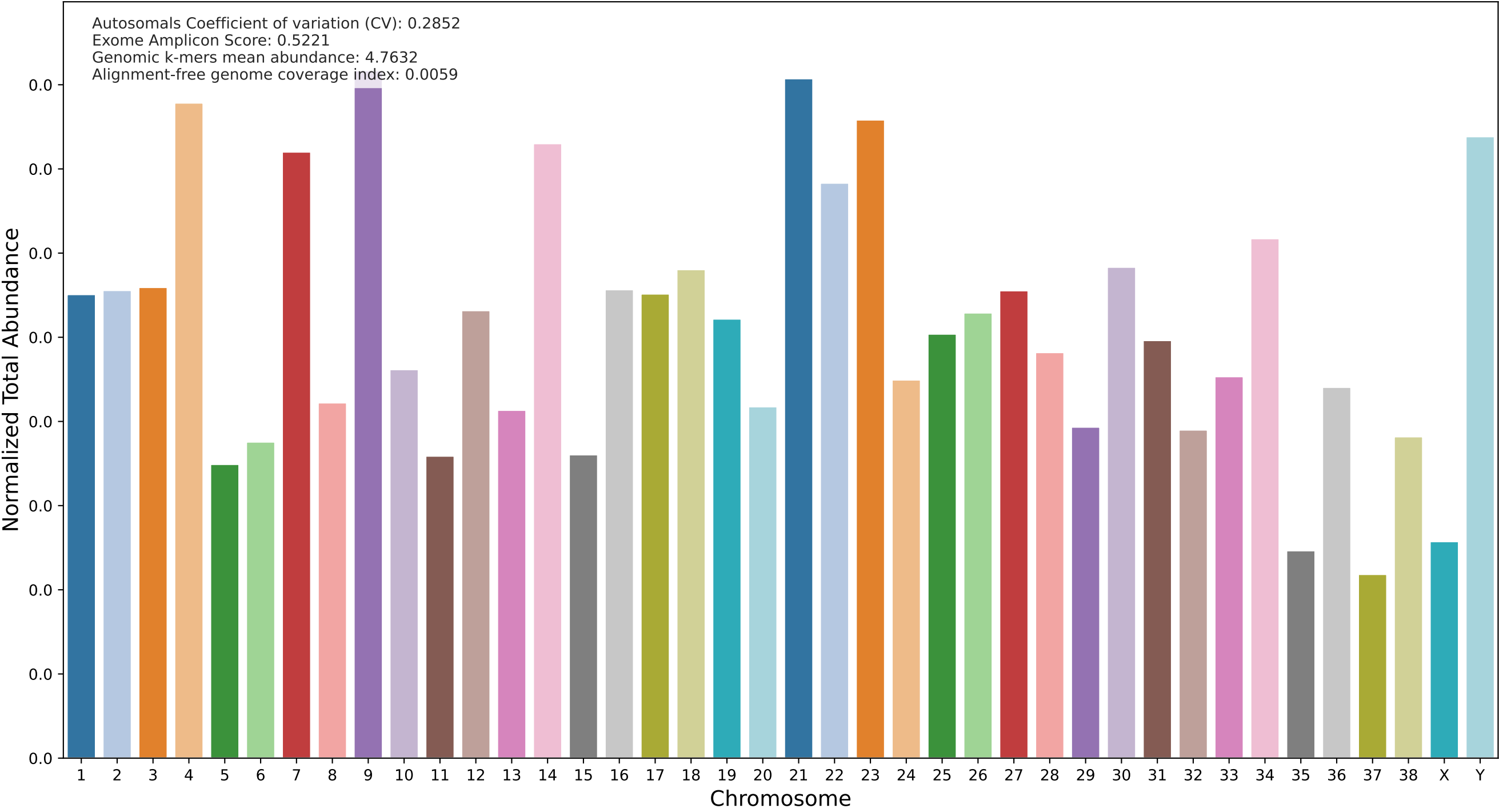
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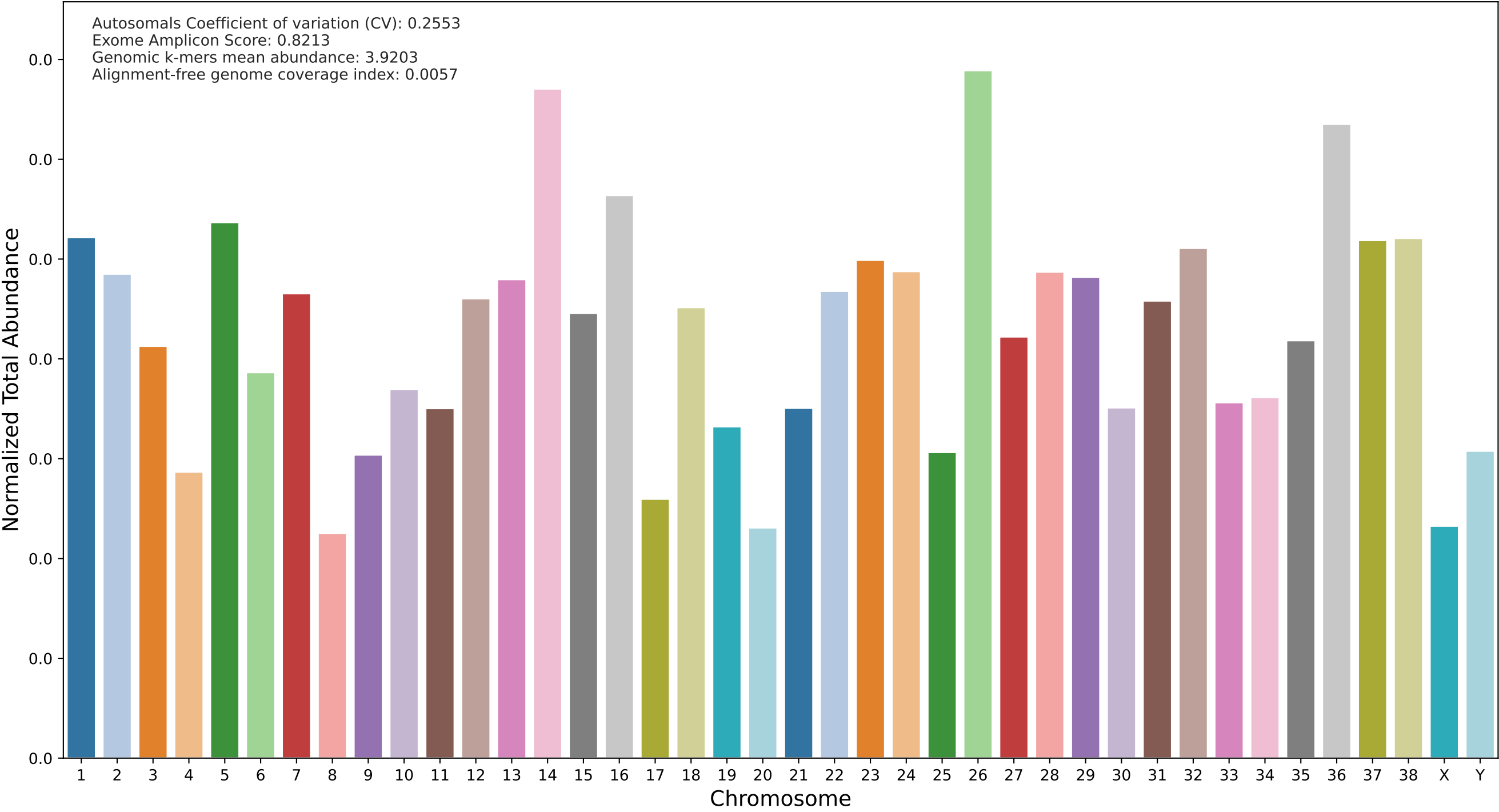
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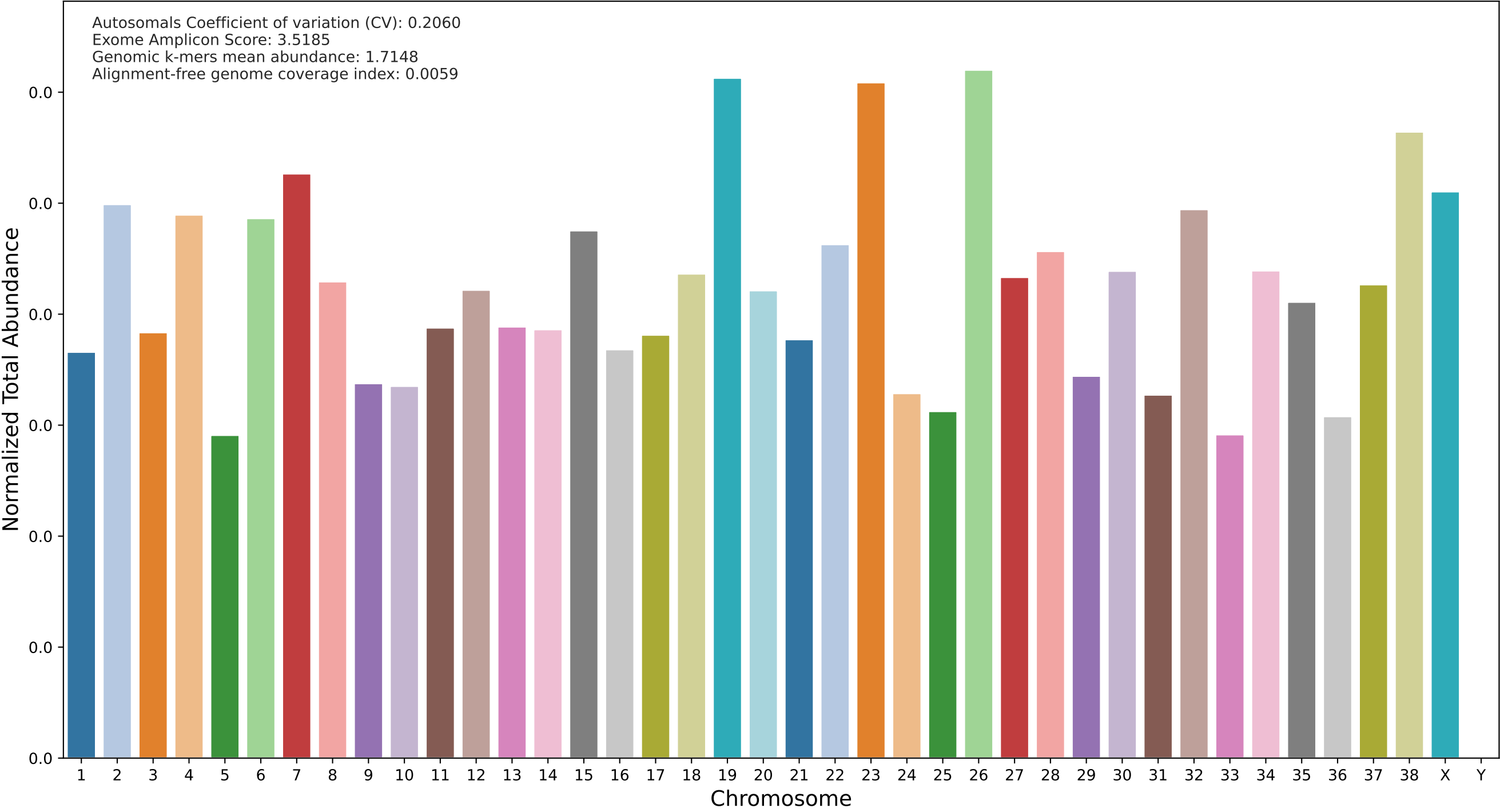
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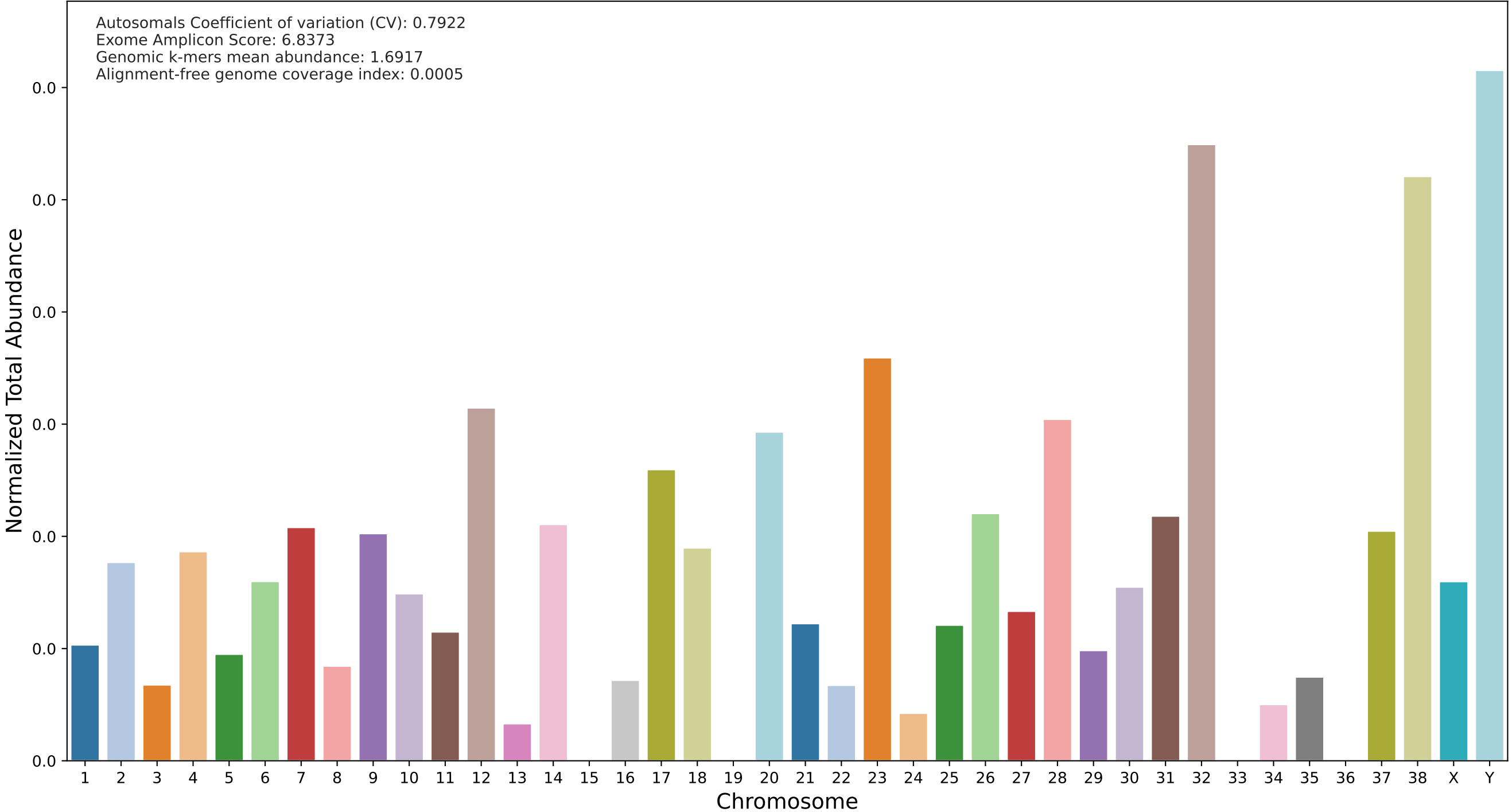
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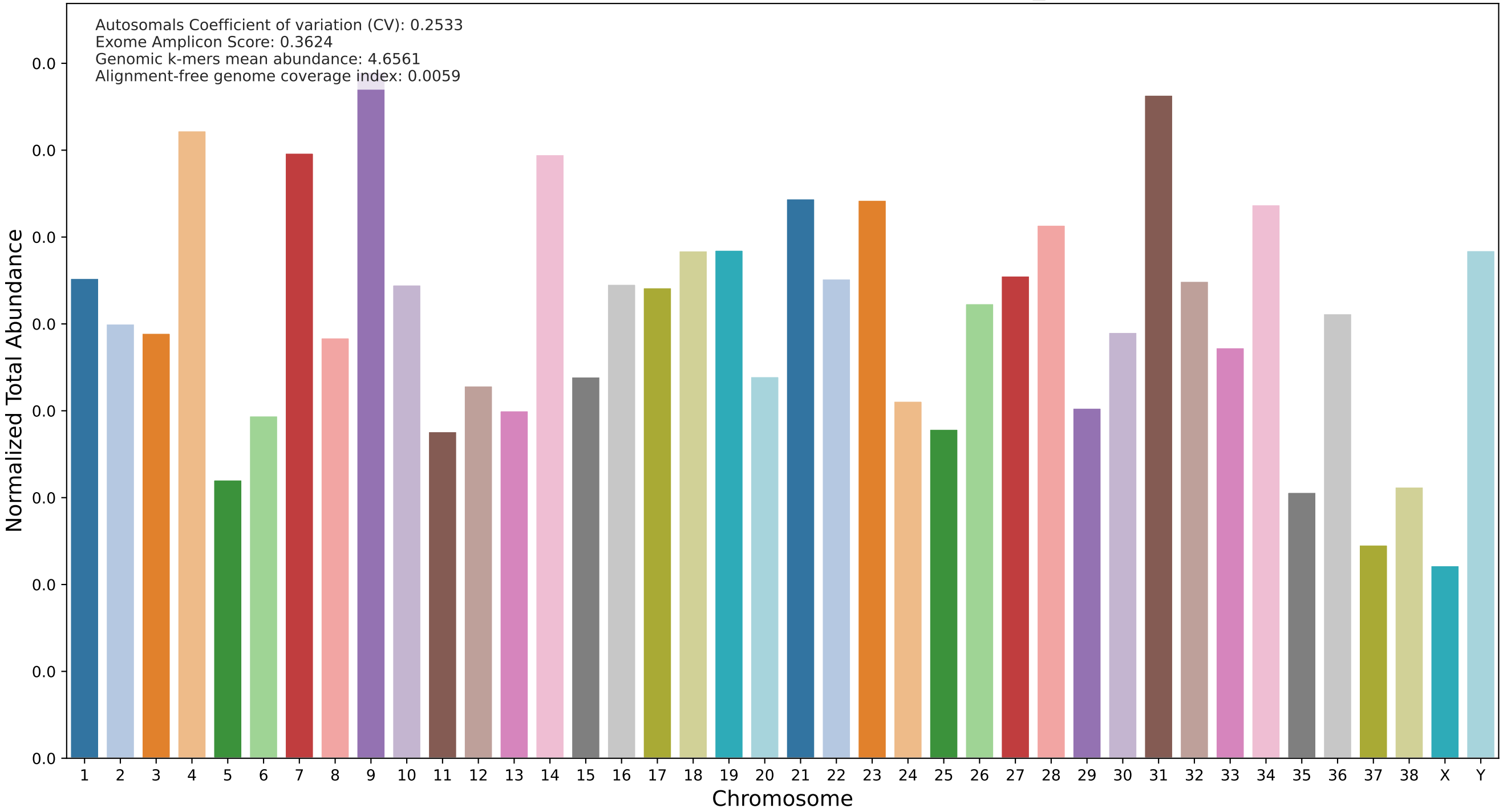
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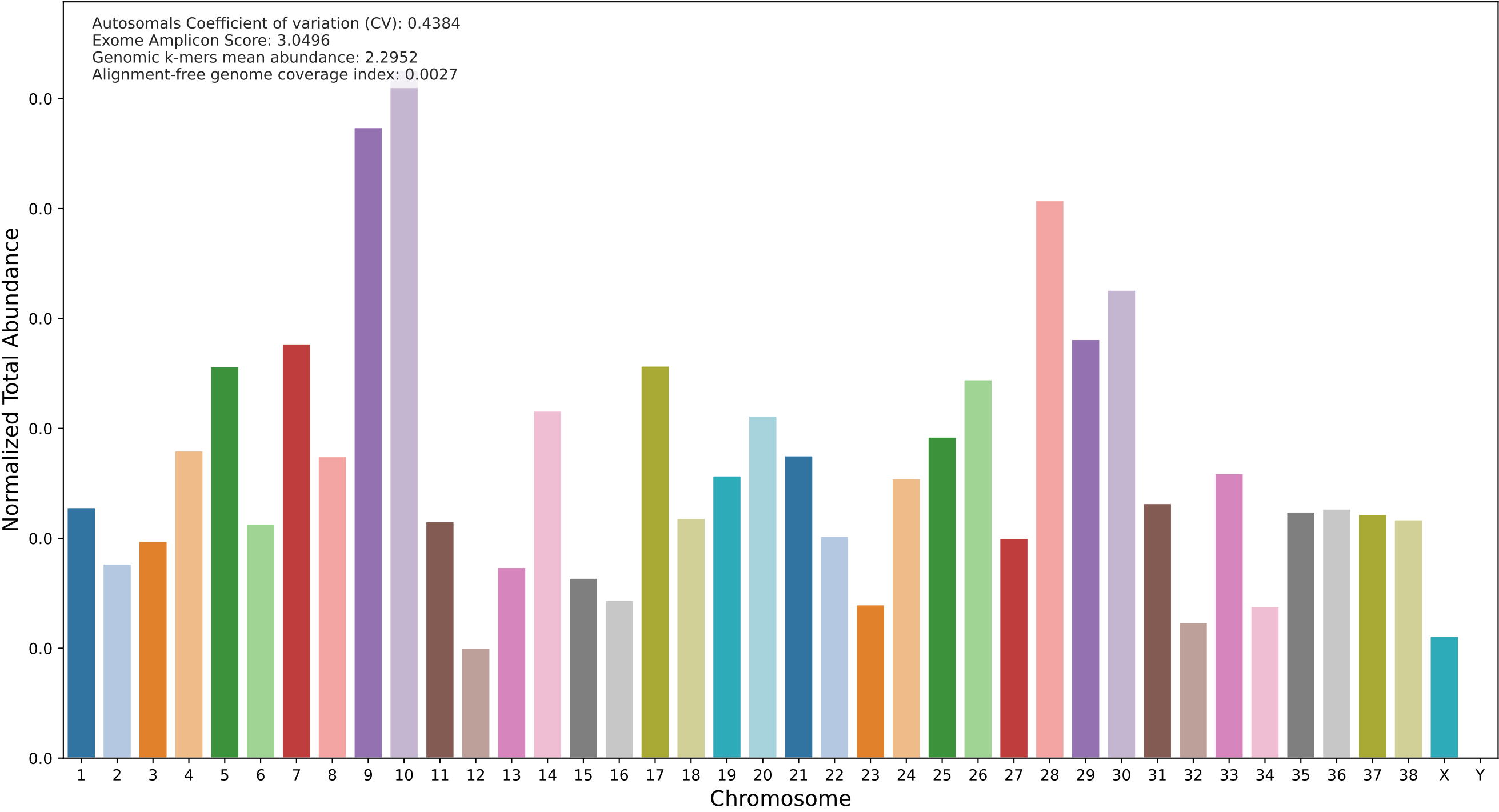
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Normalized Chromosome Abundance - SAMEA7321866_ERX4596792

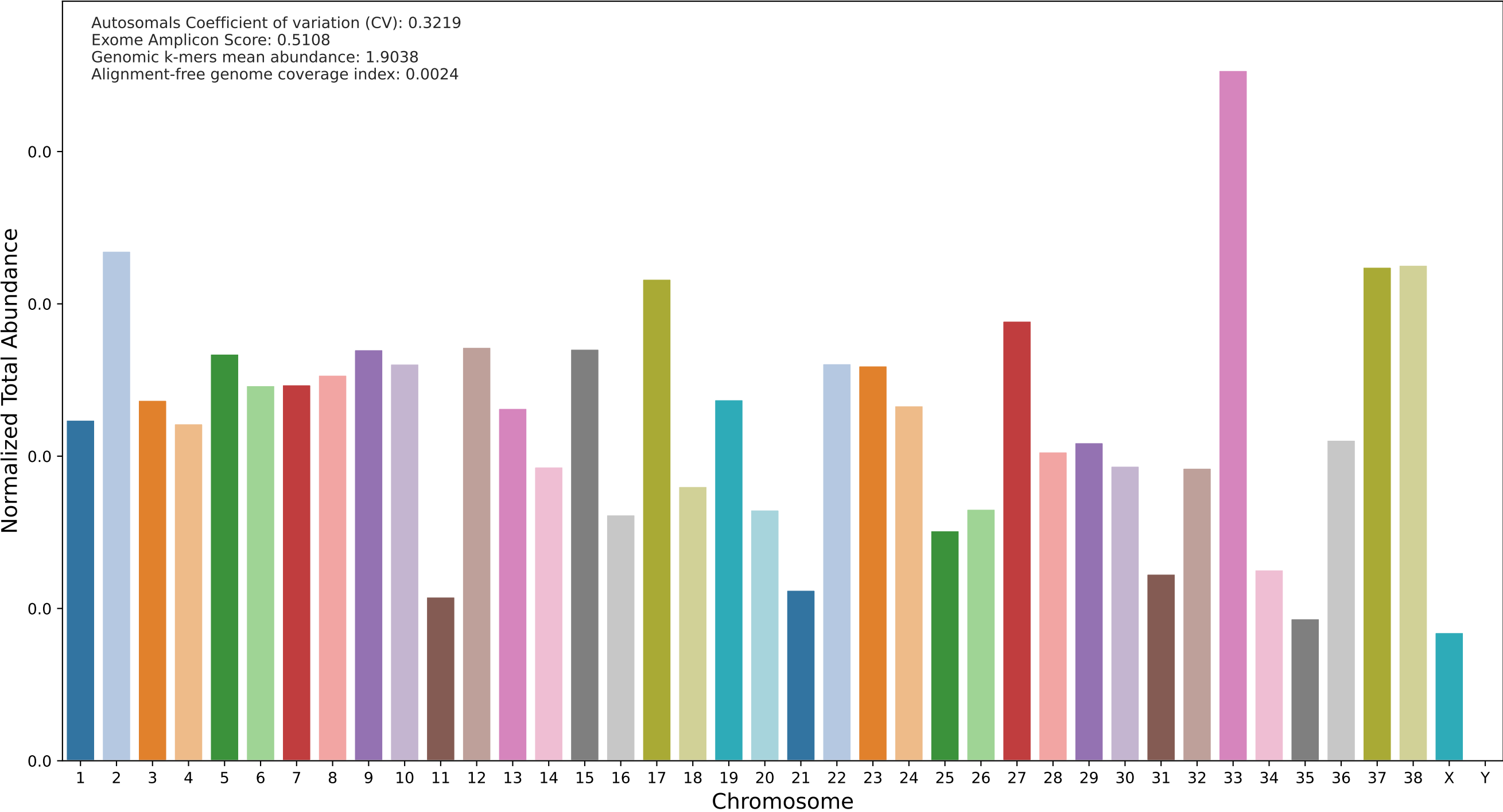


Normalized Chromosome Abundance - SAMN23181555_SRX13148936

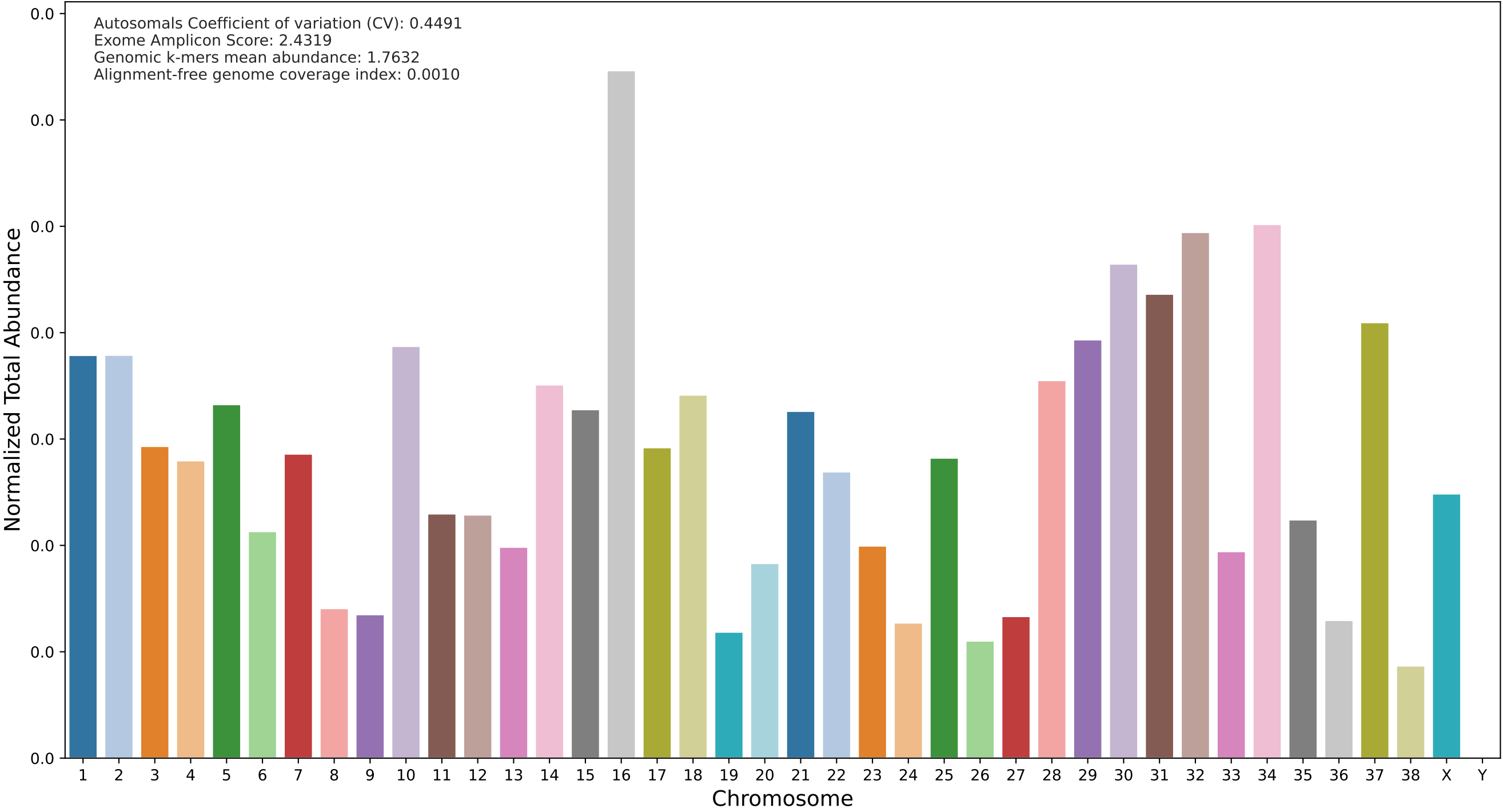


Normalized Chromosome Abundance - SAMN25330626_SRX17765621

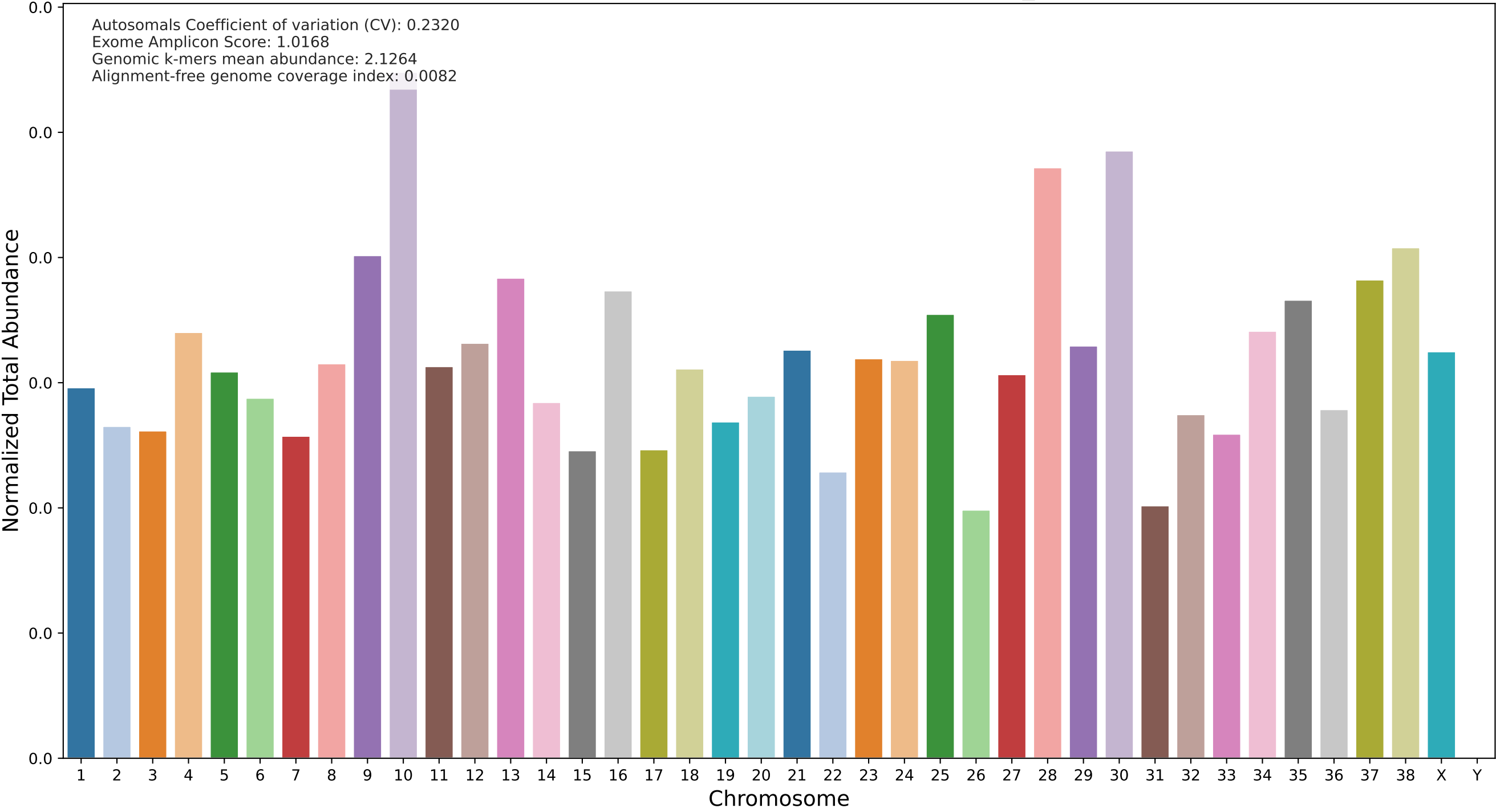
Autosomals Coefficient of variation (CV): 0.3219
Exome Amplicon Score: 0.5108
Genomic k-mers mean abundance: 1.9038
Alignment-free genome coverage index: 0.0024



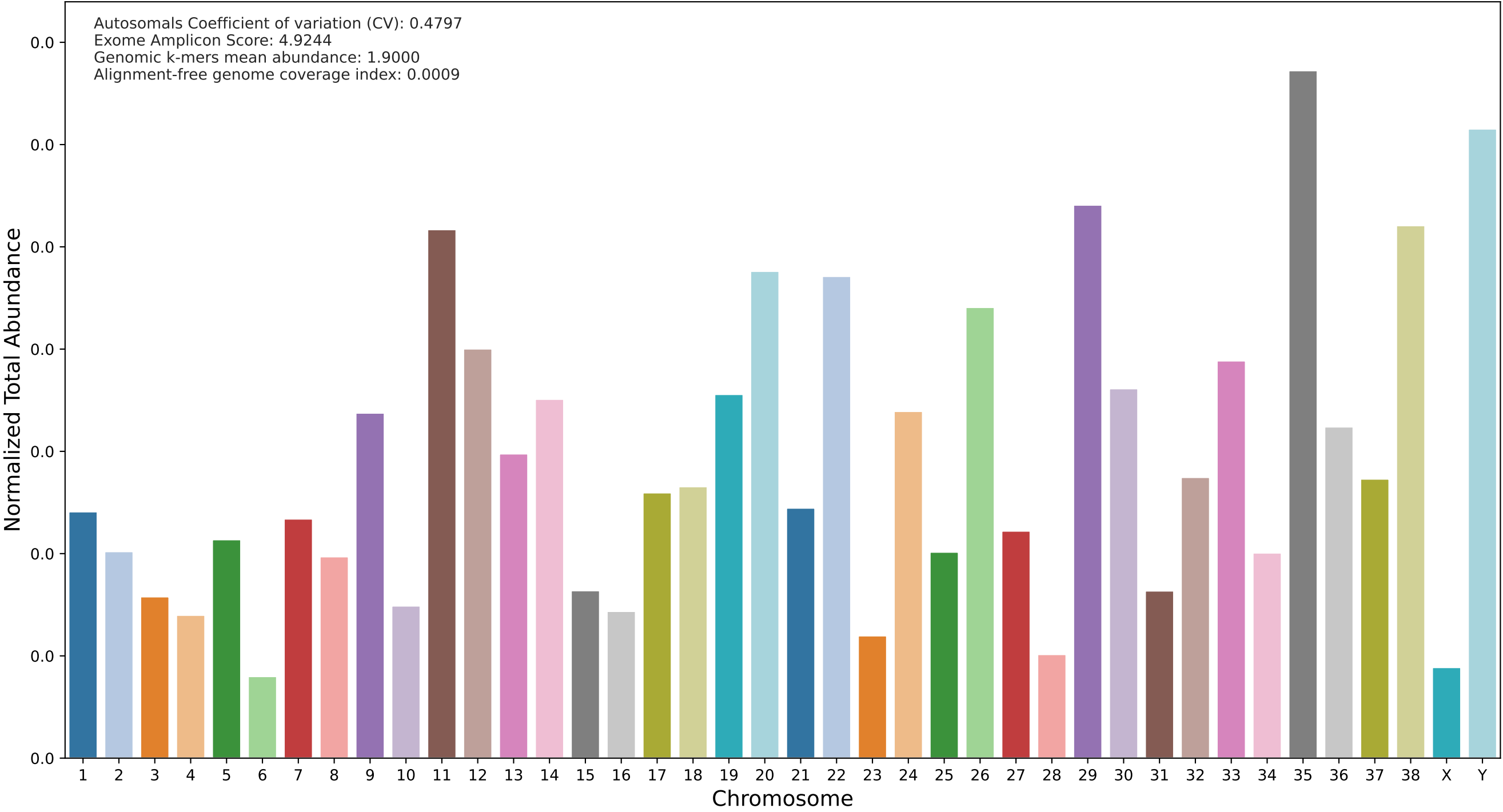
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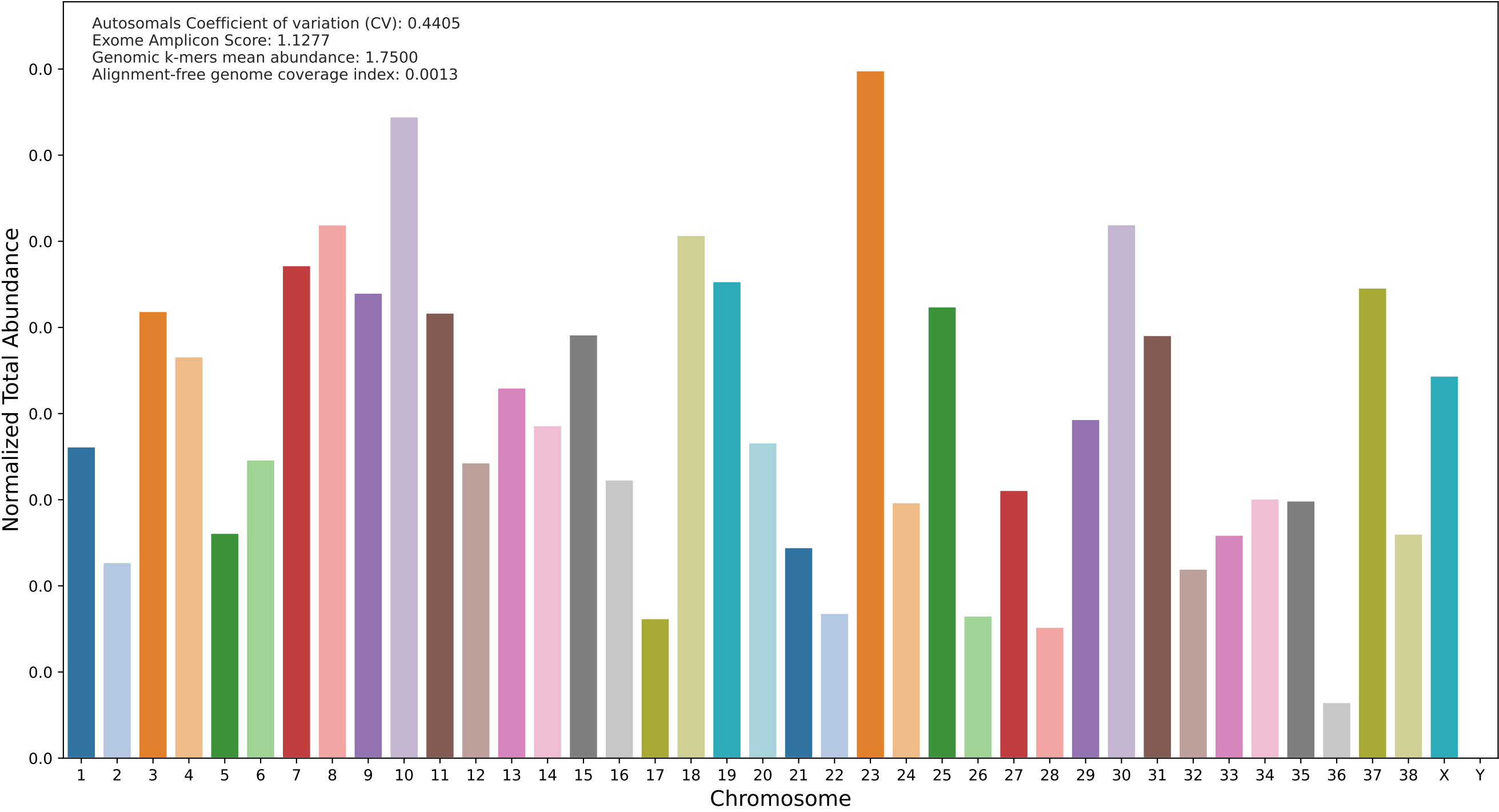
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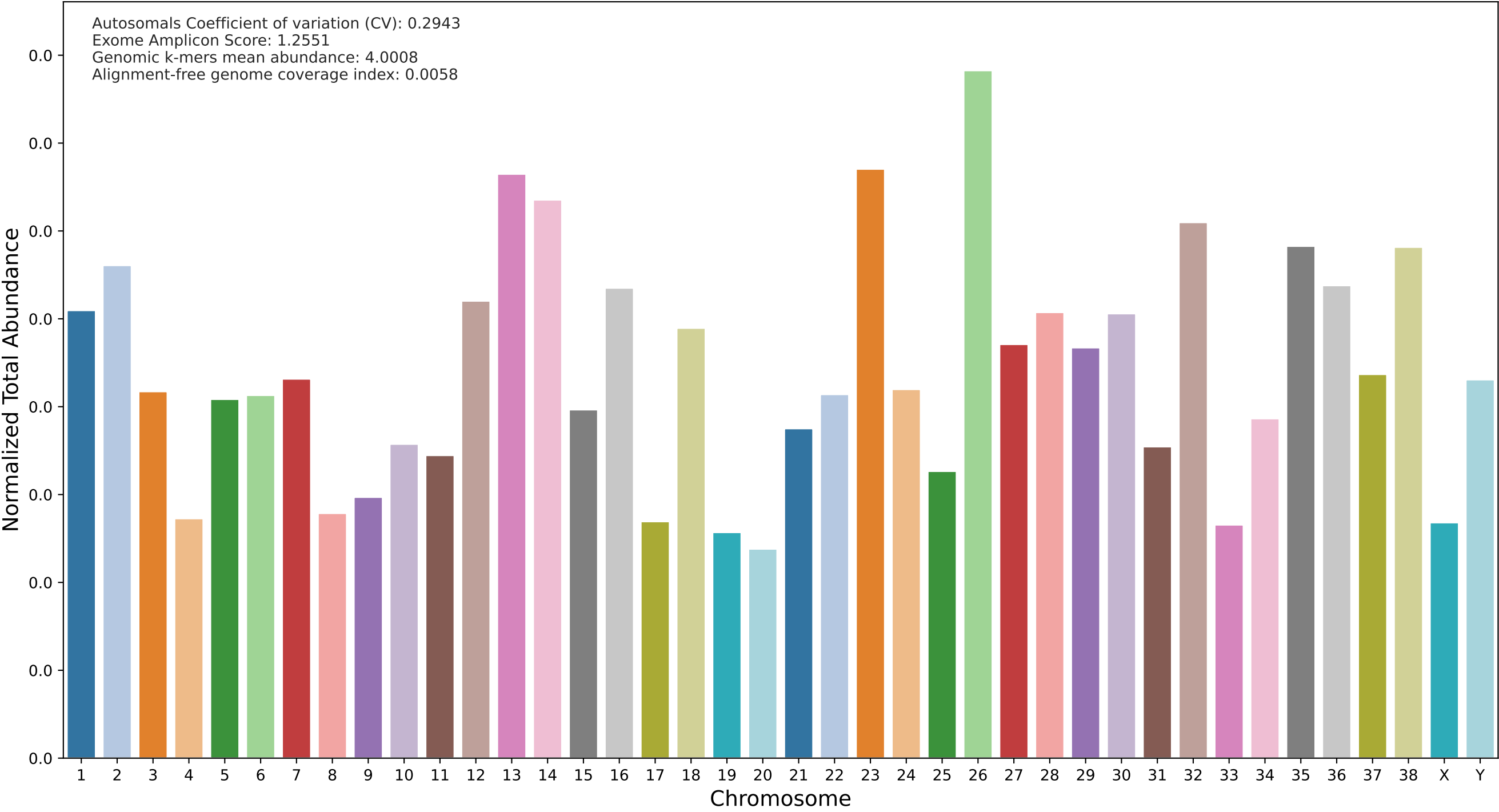
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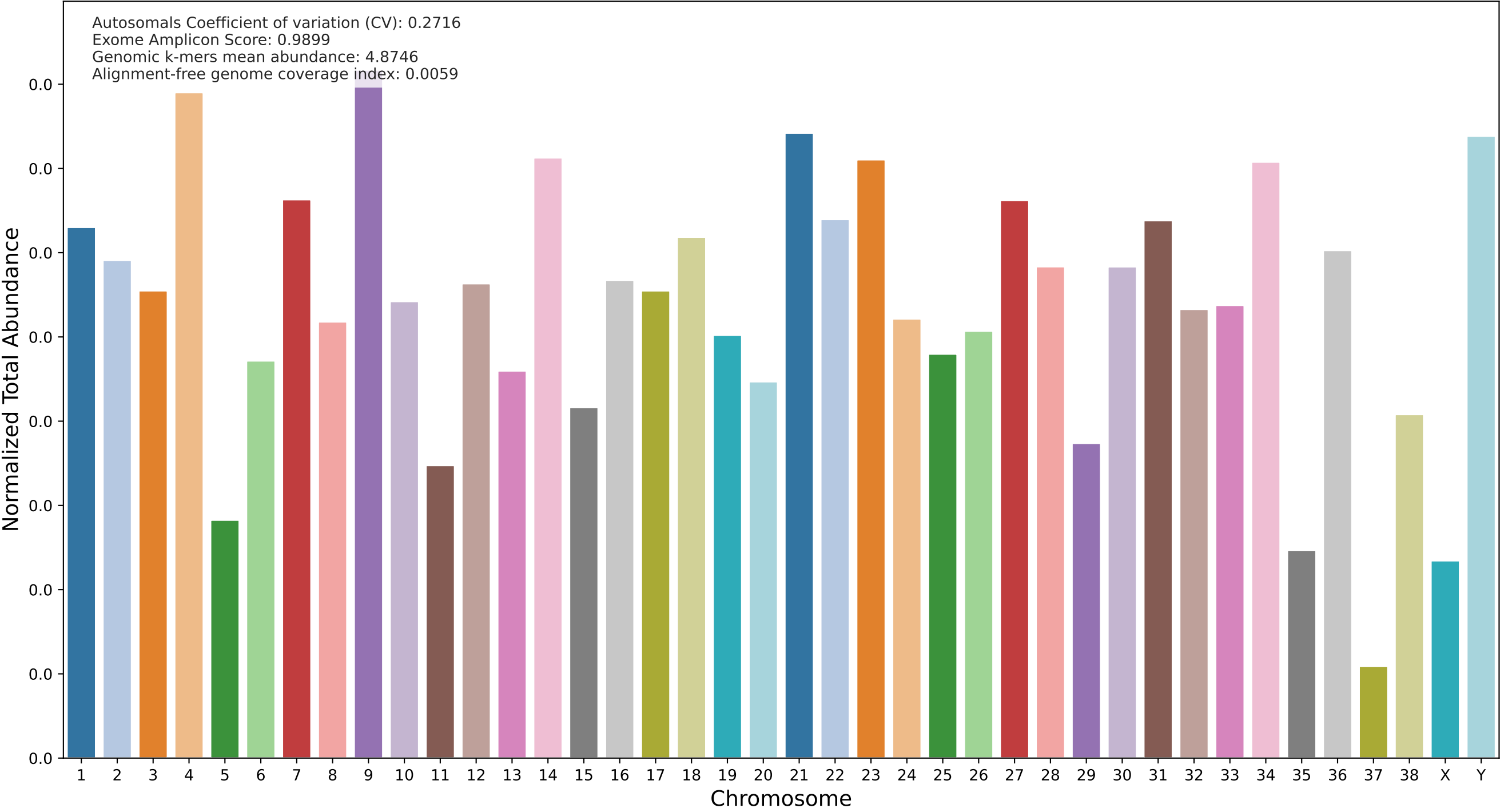
Normalized Chromosome Abundance - SAMN25331889_SRX17765675



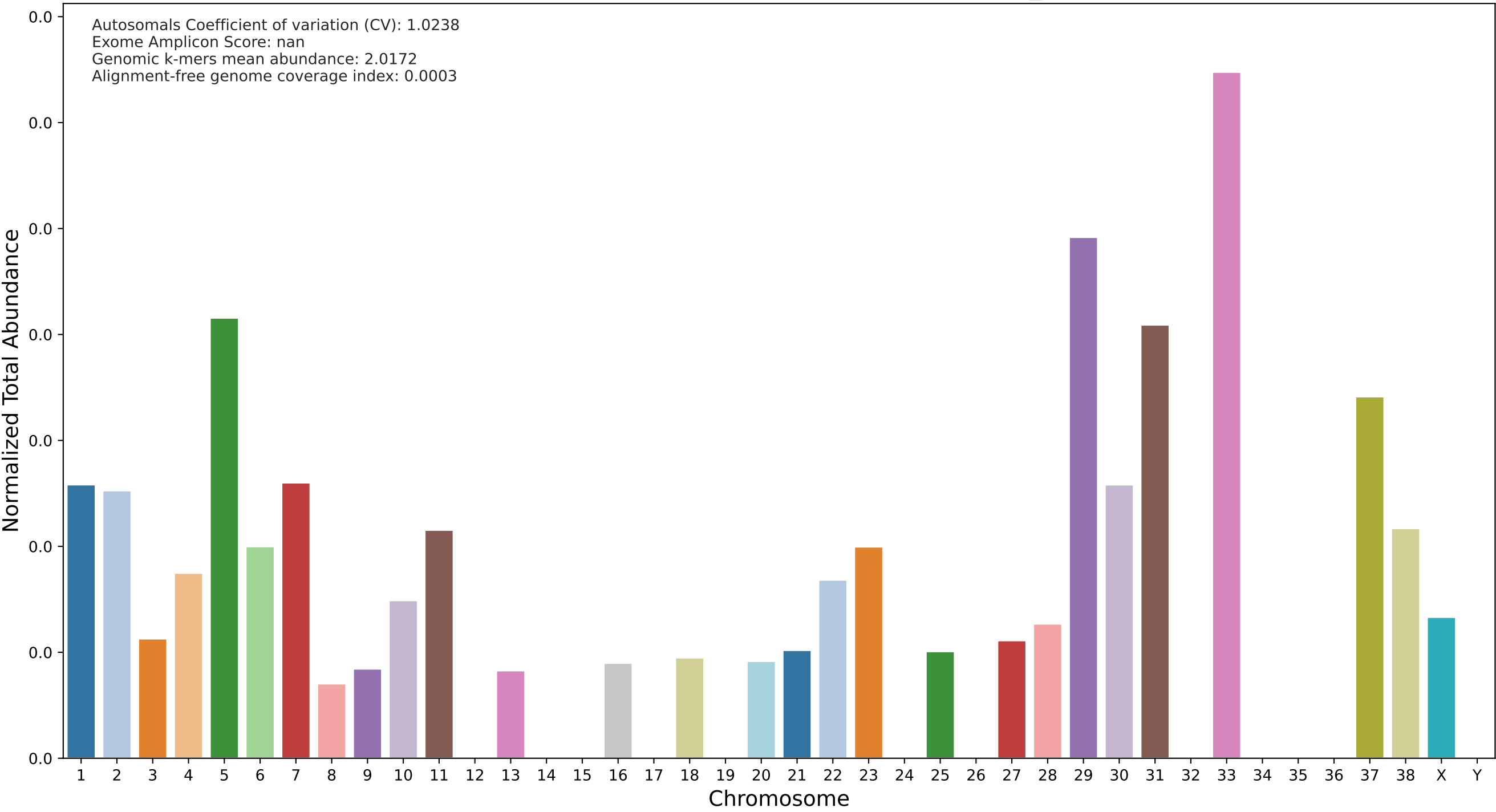
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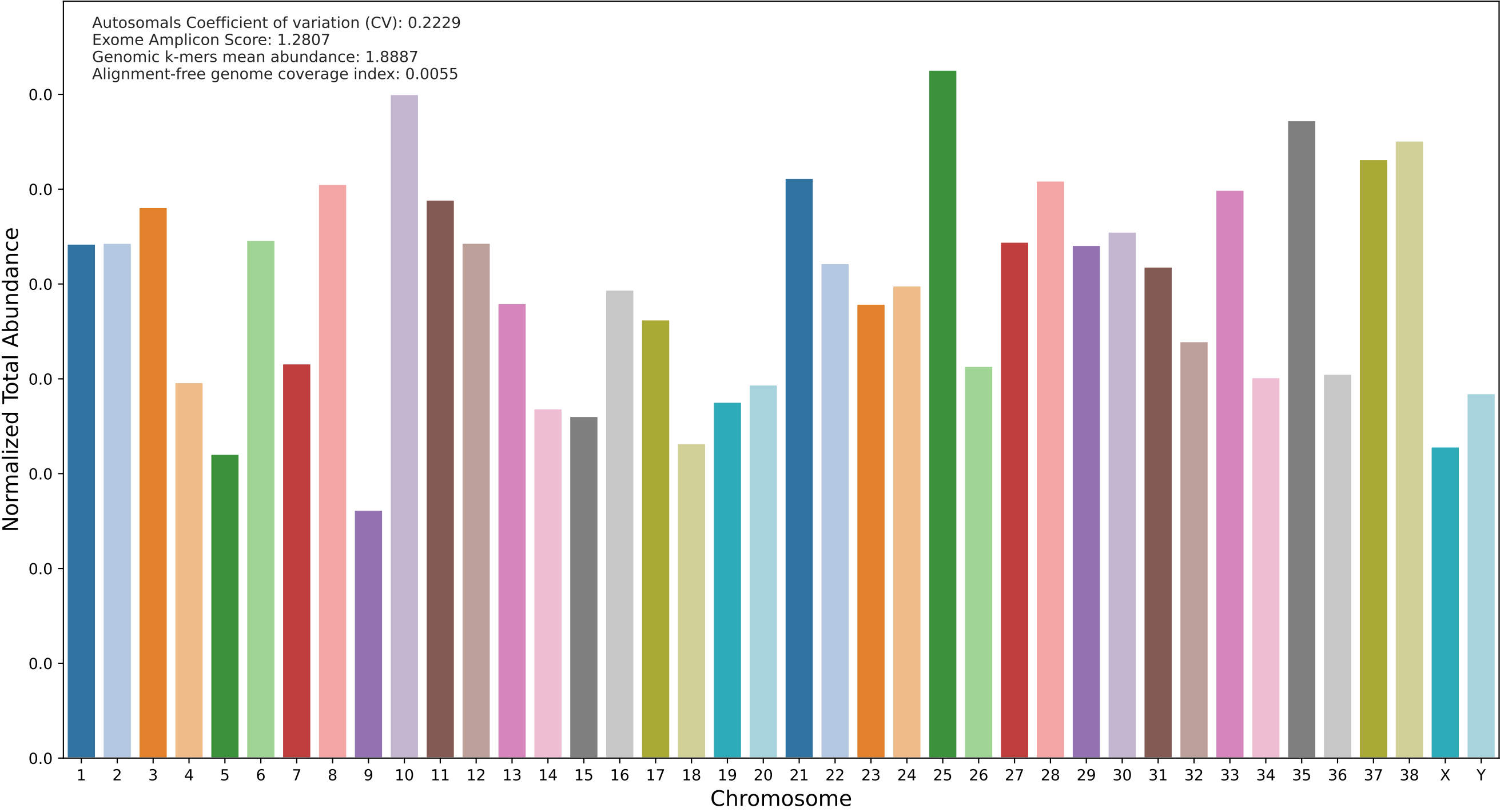
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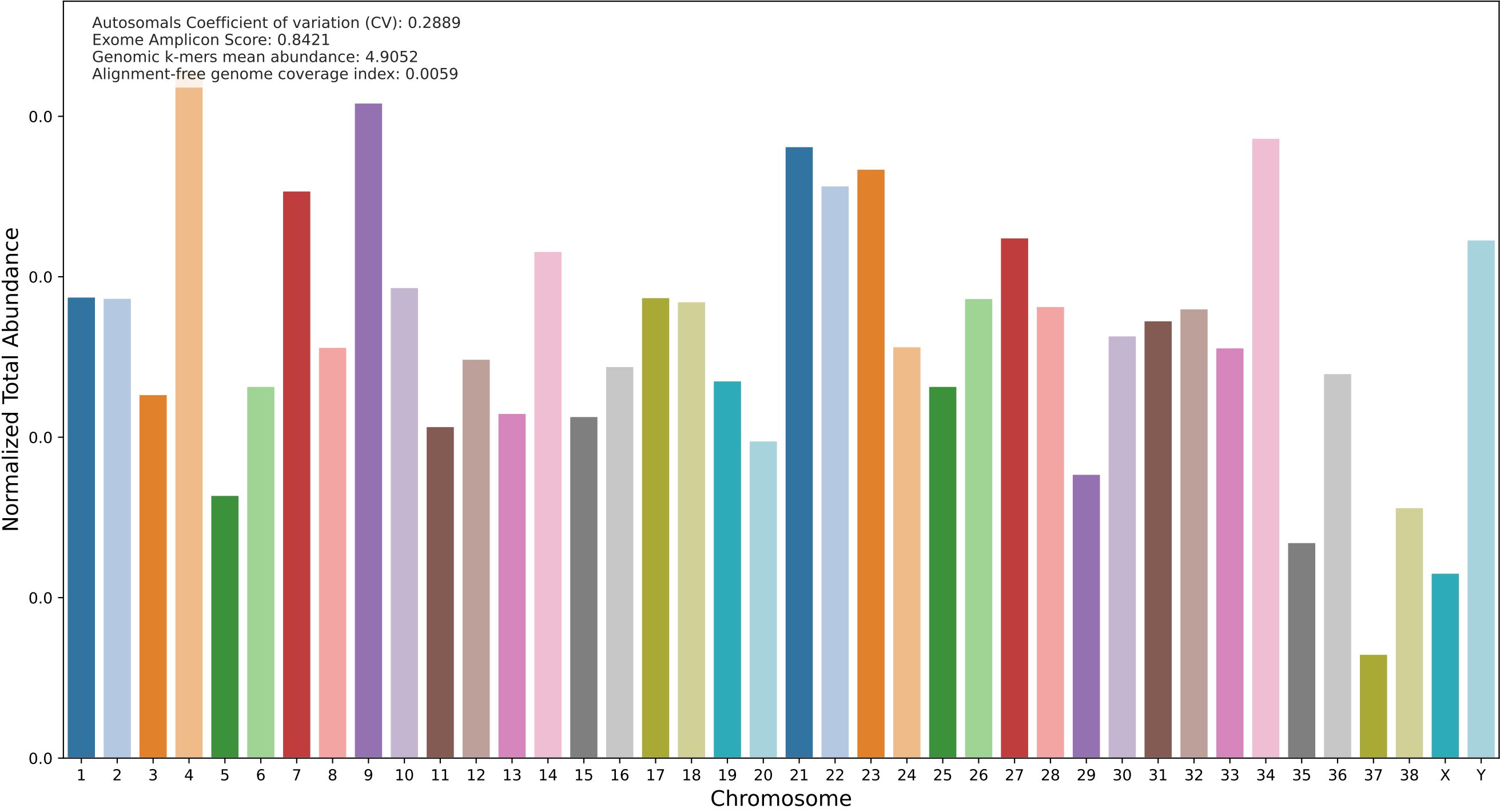
Normalized Chromosome Abundance - SAMEA7321872_ERX4596834



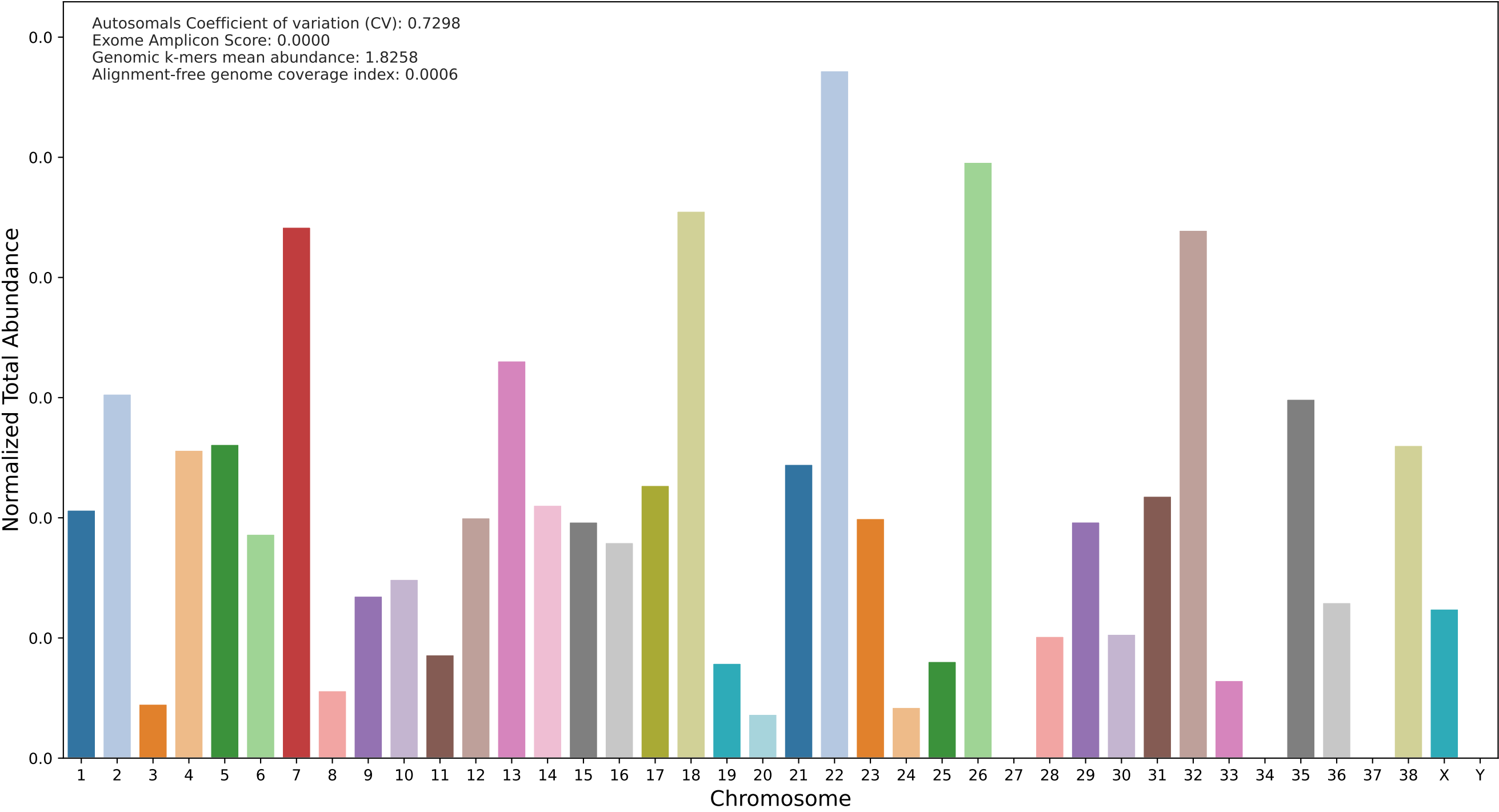
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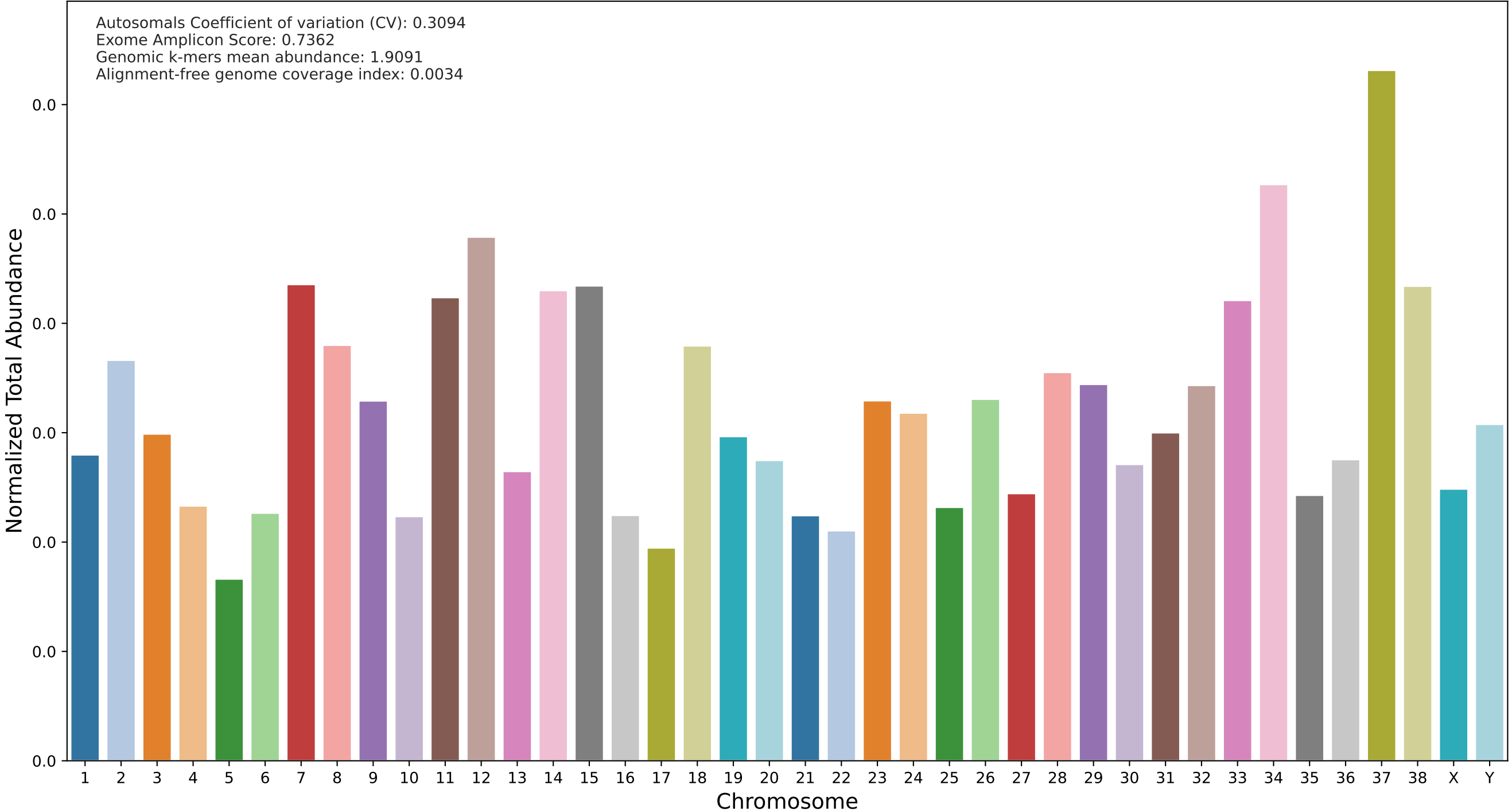
Normalized Chromosome Abundance - SAMEA7321866_ERX4596791



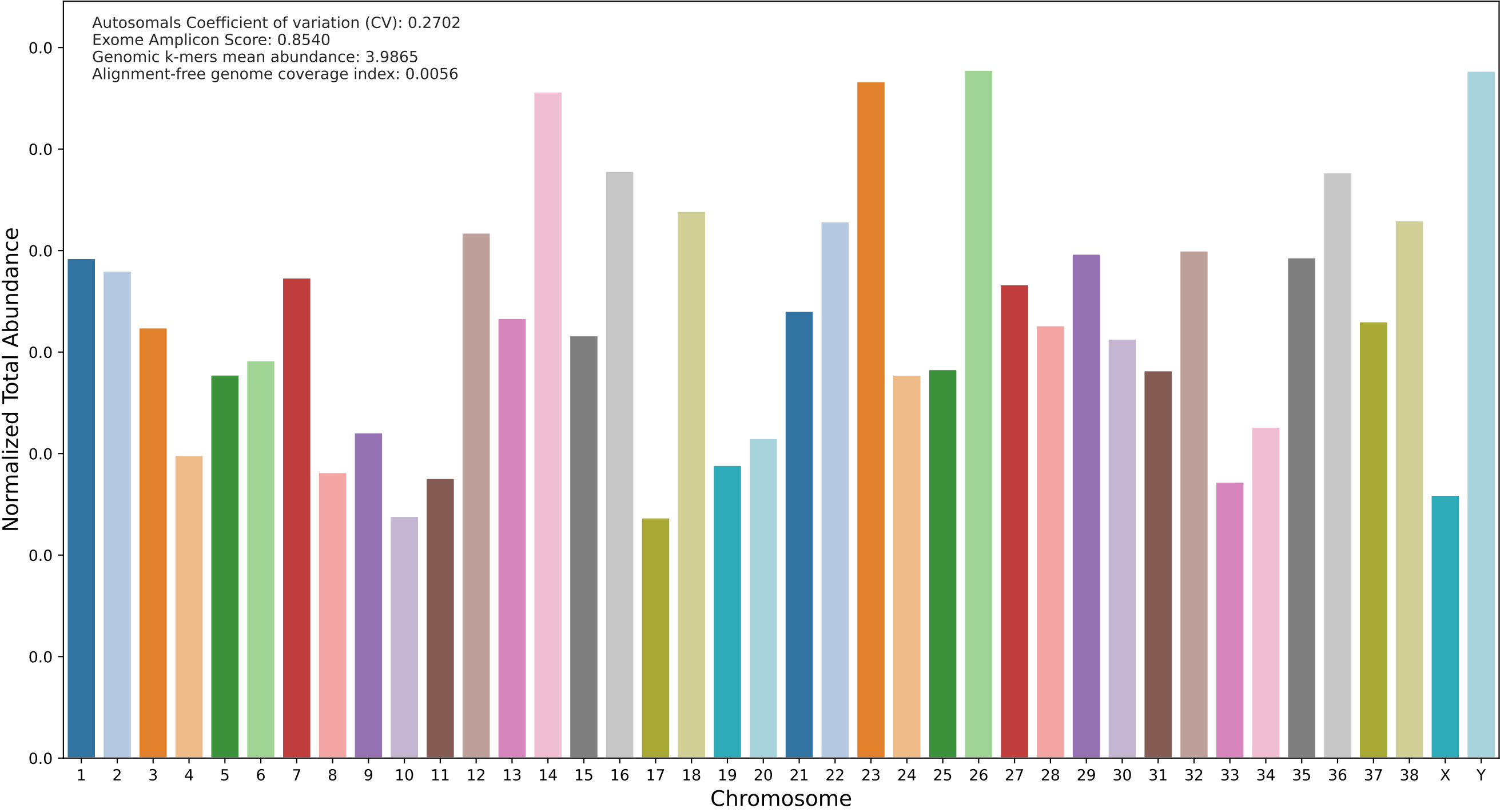
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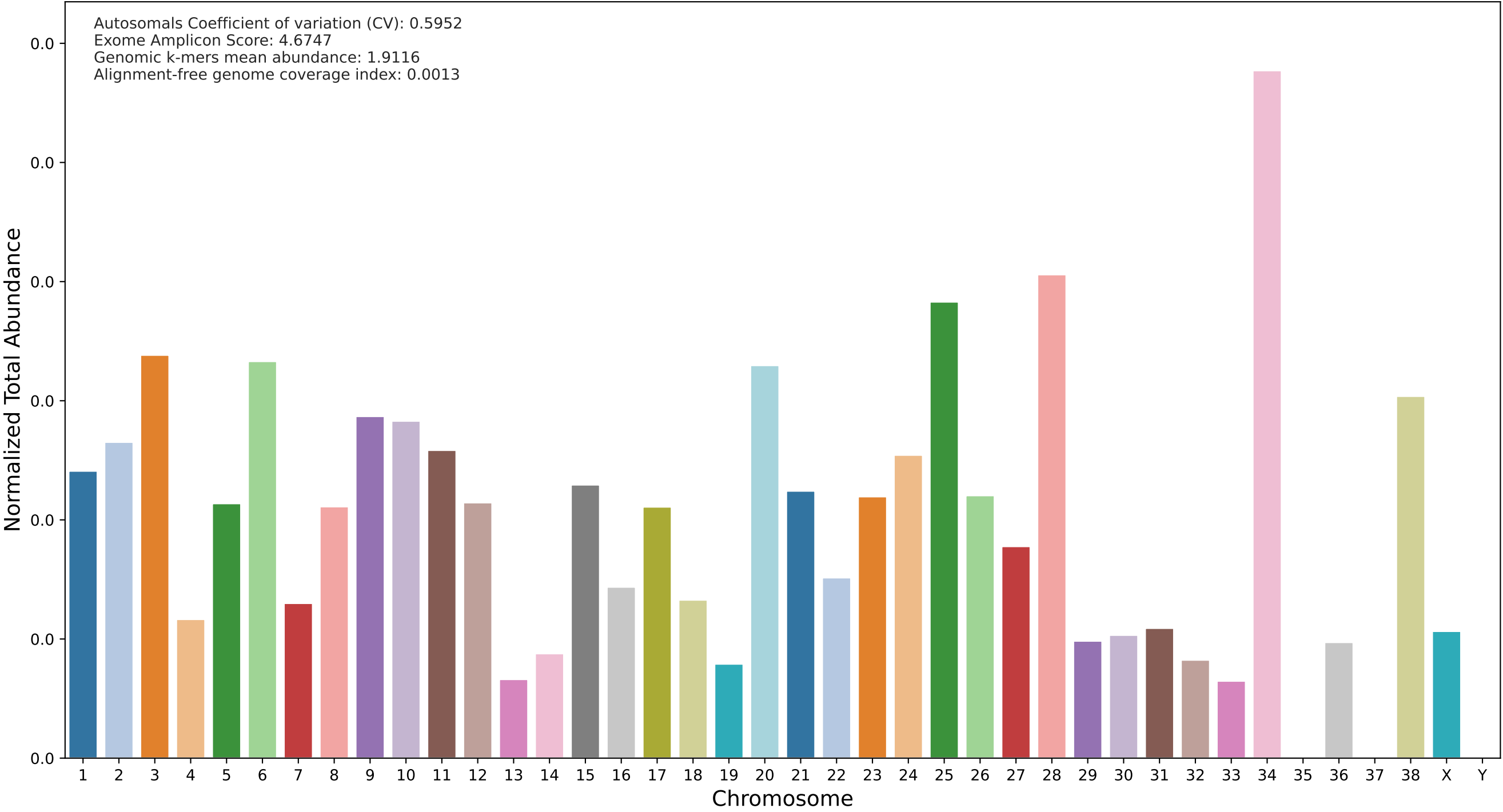
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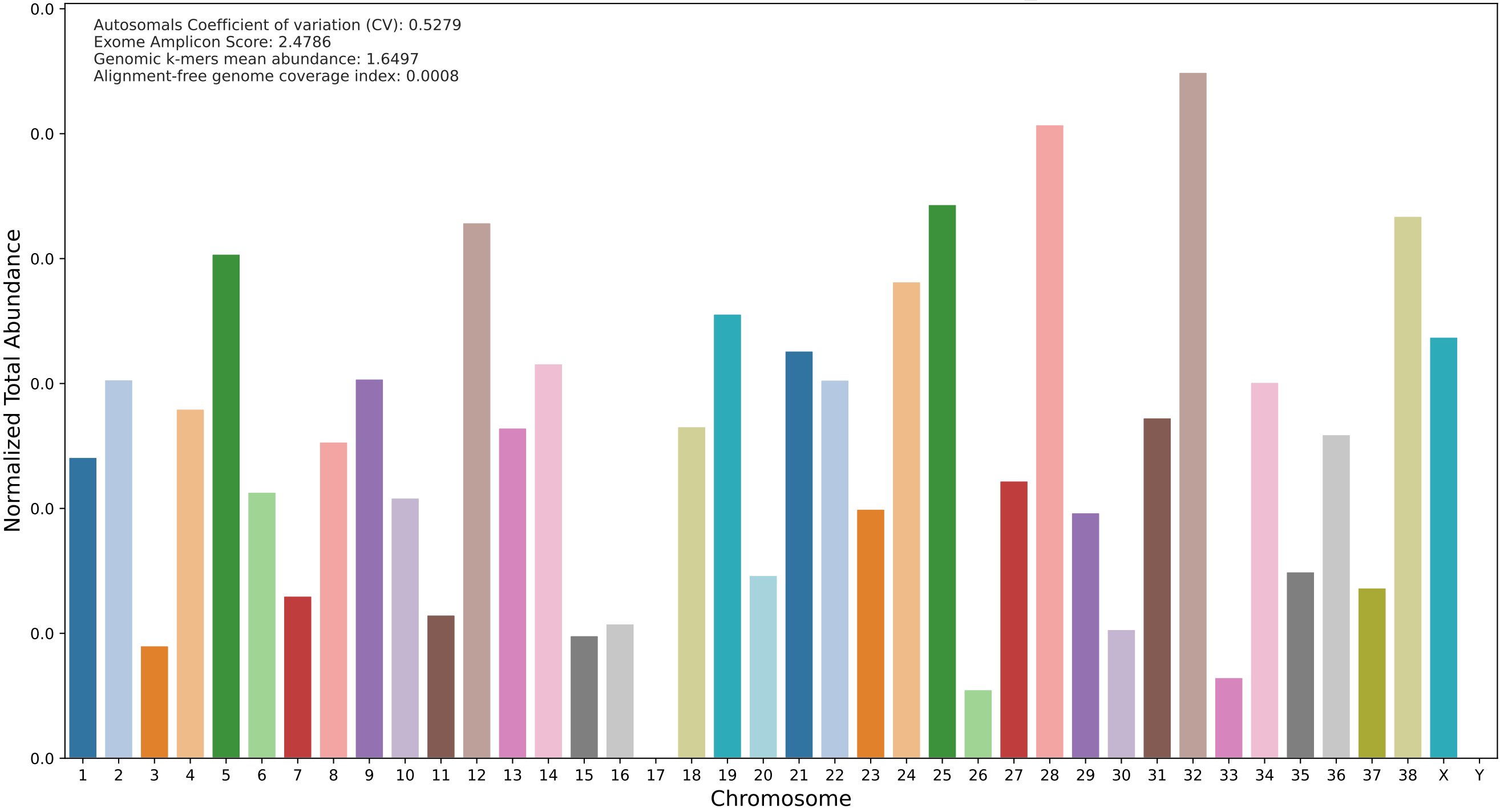
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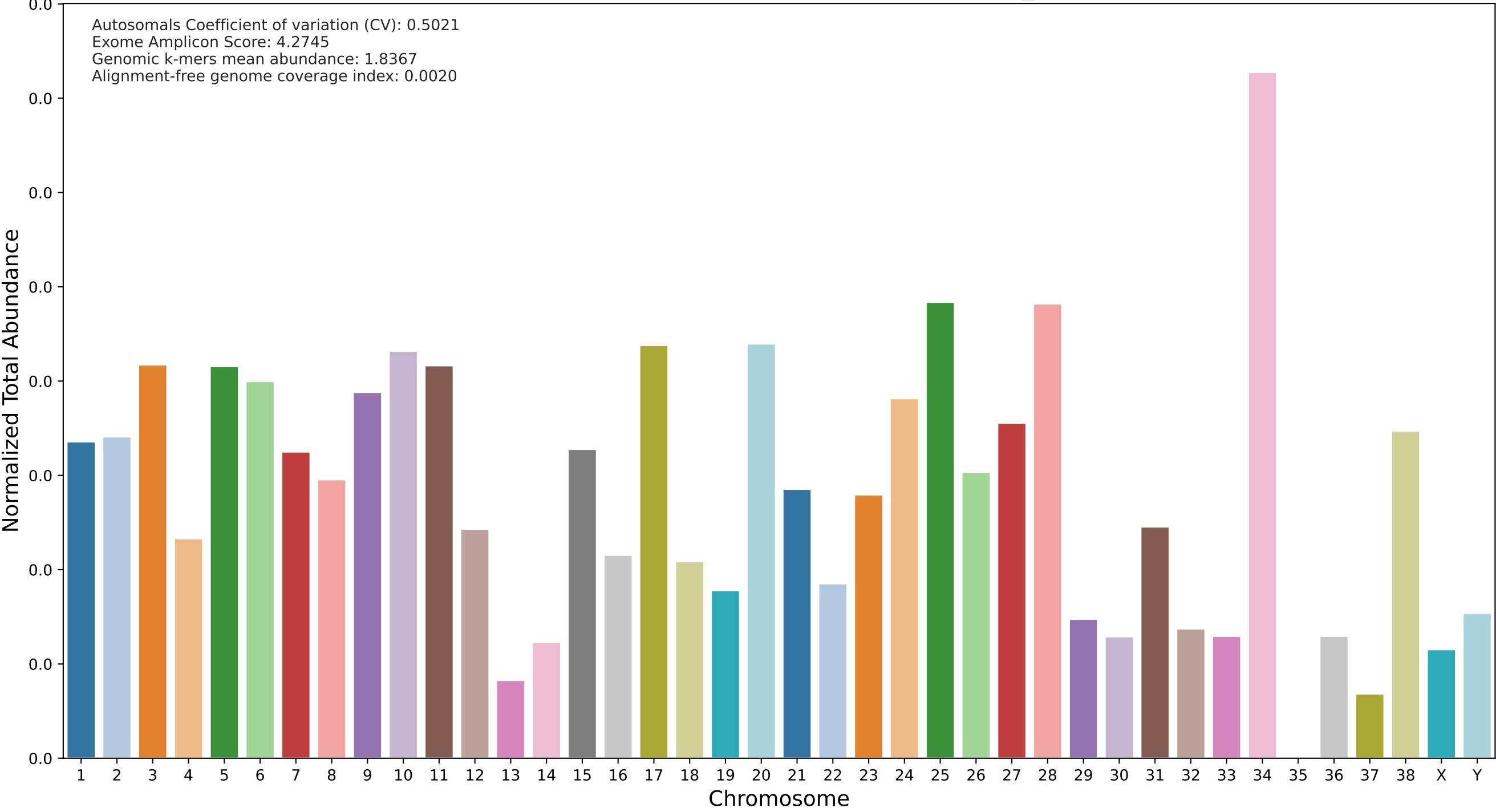
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Normalized Chromosome Abundance - SAMN25331045_SRX17765681



Normalized Chromosome Abundance - SAMN25332674_SRX17765690



Normalized Chromosome Abundance - SAMEA9534563_ERX9169771

