

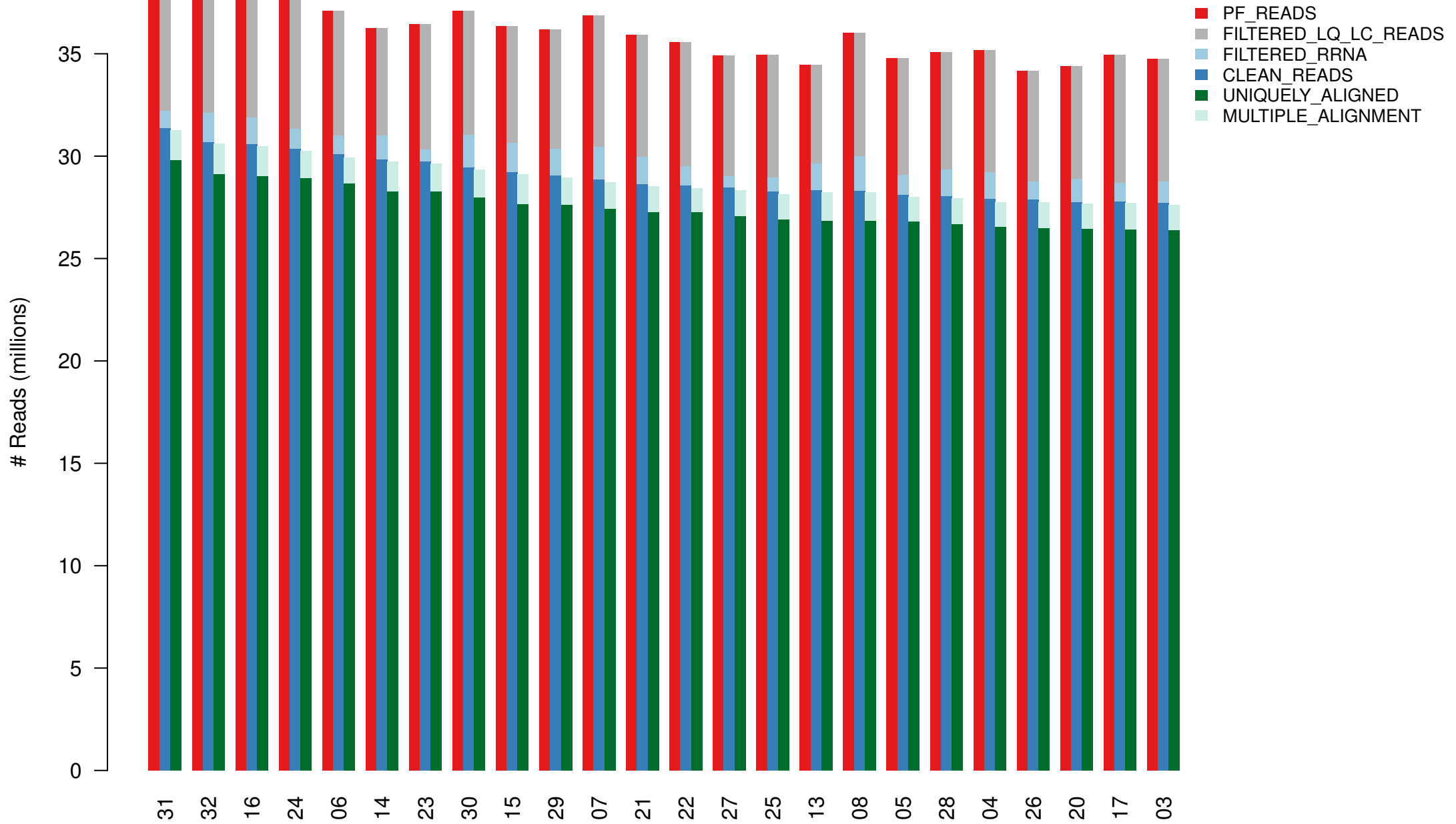
RNA-seq Project QC Report

Project	
Project ID	Project_DSyndrome_CS
Laboratory	
Submitter	
Ref Organism	
Library Created by	
Protocol	
Run Type	
Number of Cycles	

# Alignment Summary

*Homo\_sapiens.GRCh38.98*

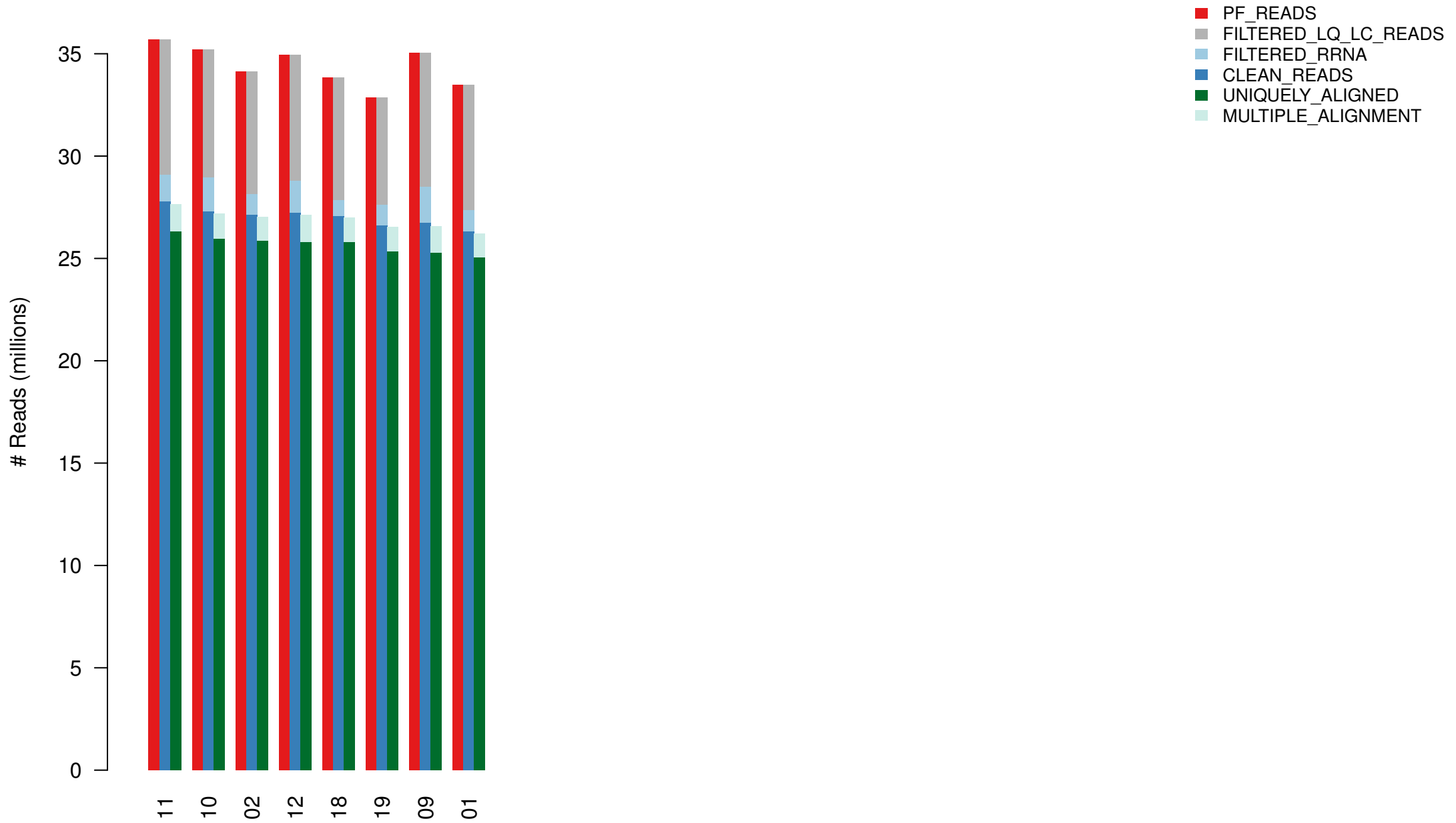
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# Alignment Summary

*Homo\_sapiens.GRCh38.98*

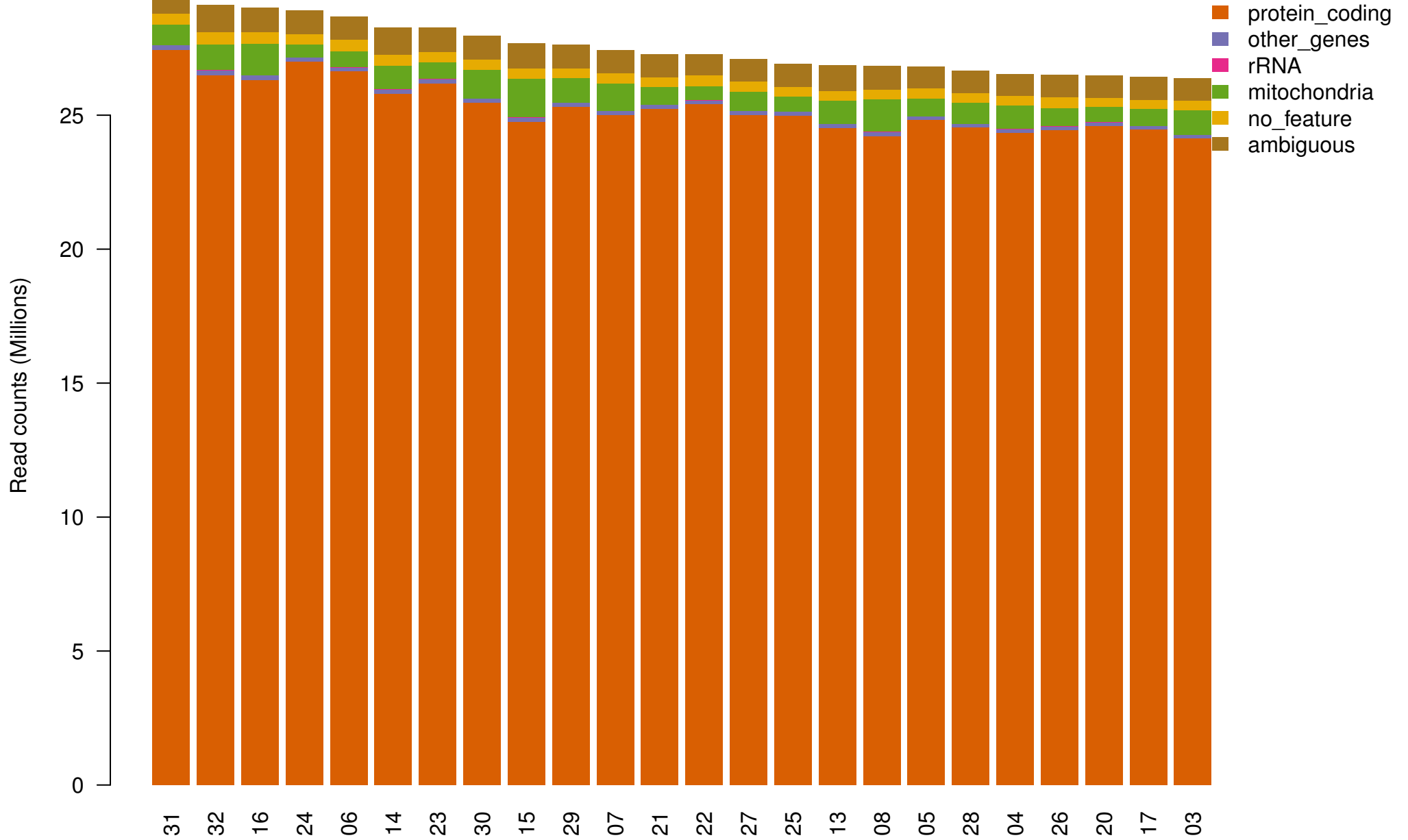
2 / 2



# HTSeq-counts distribution

*Homo\_sapiens.GRCh38.98*

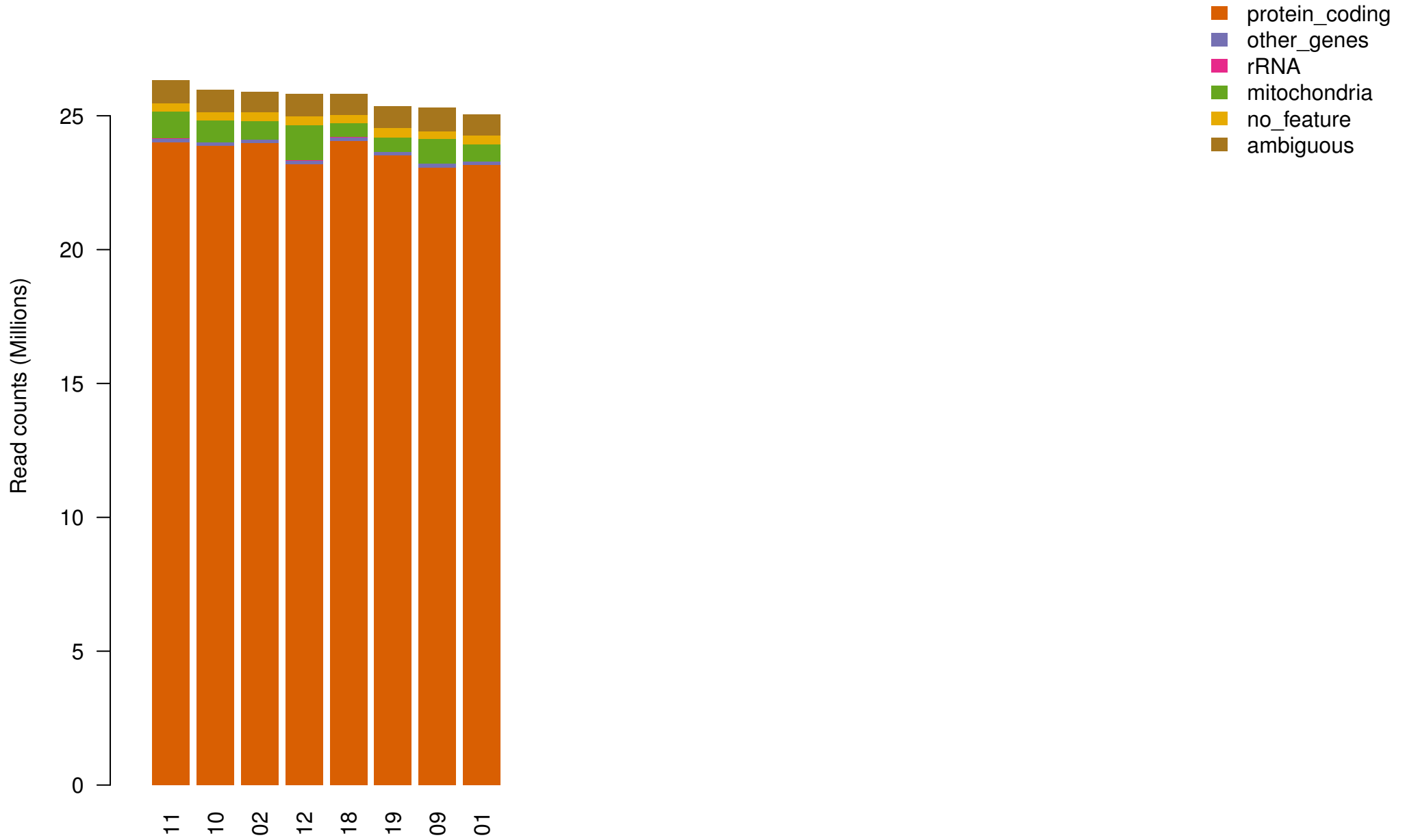
1 / 2



# HTSeq-counts distribution

*Homo\_sapiens.GRCh38.98*

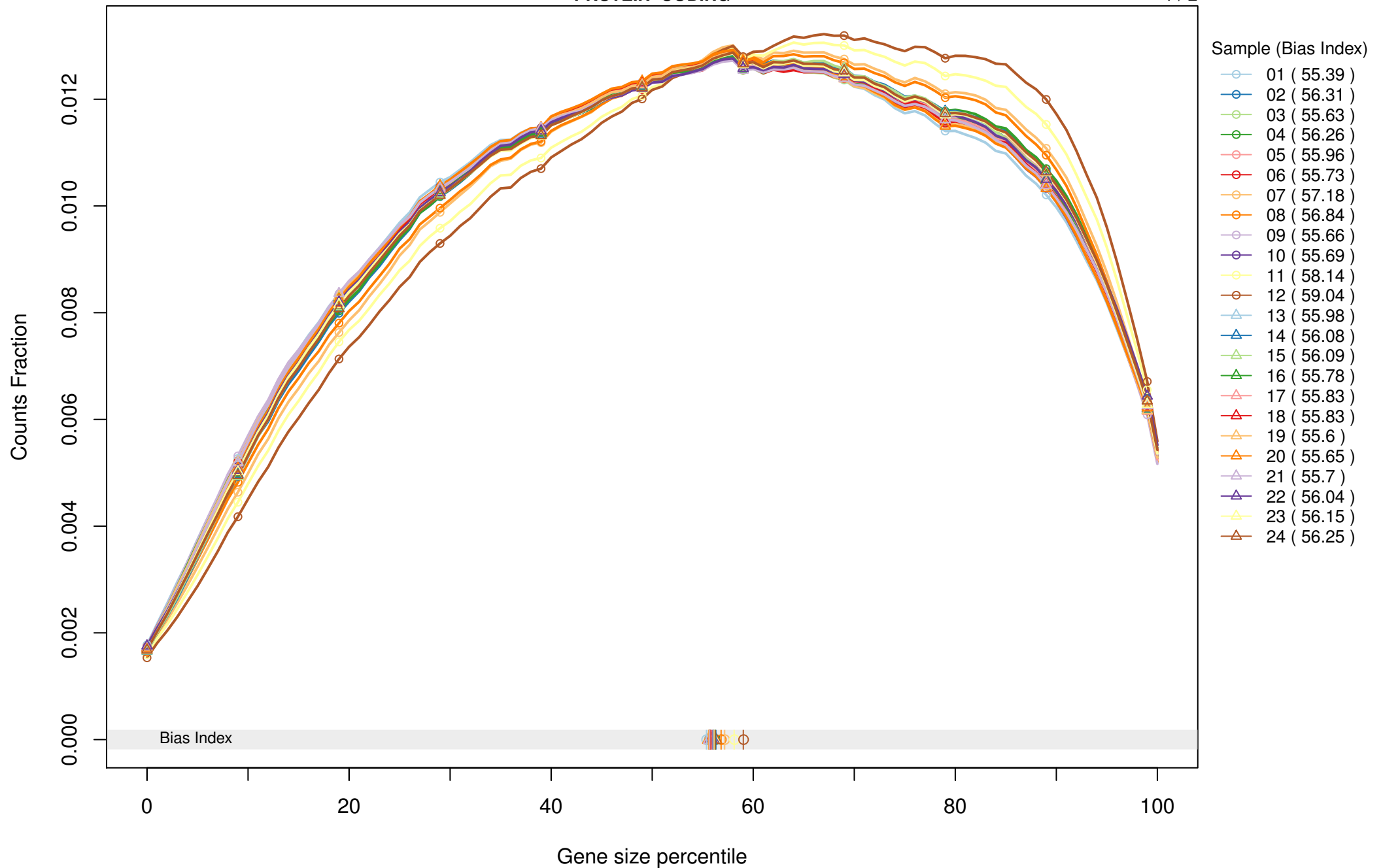
2 / 2



# RSeQC gene body coverage

PROTEIN-CODING

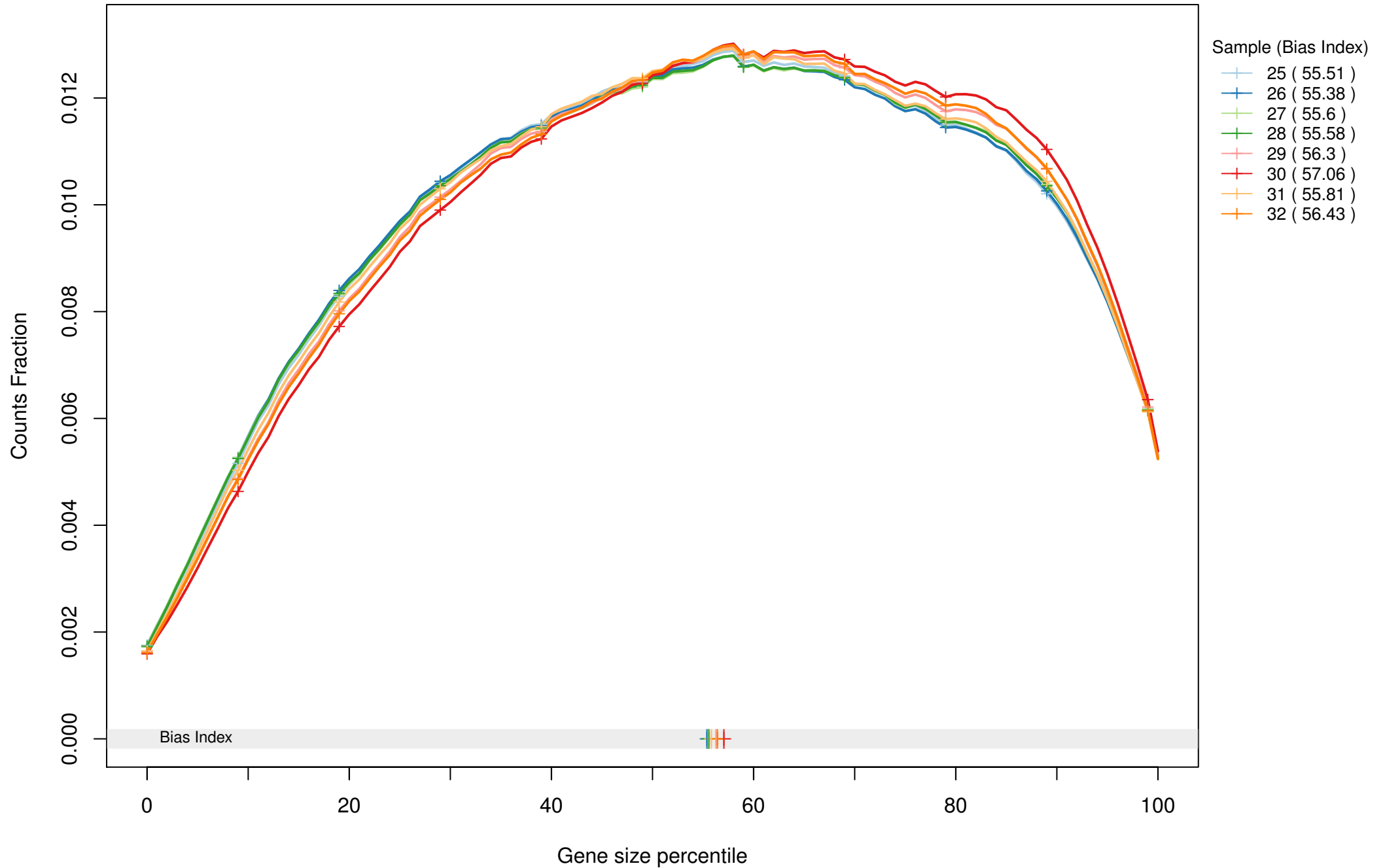
1 / 2



# RSeQC gene body coverage

PROTEIN-CODING

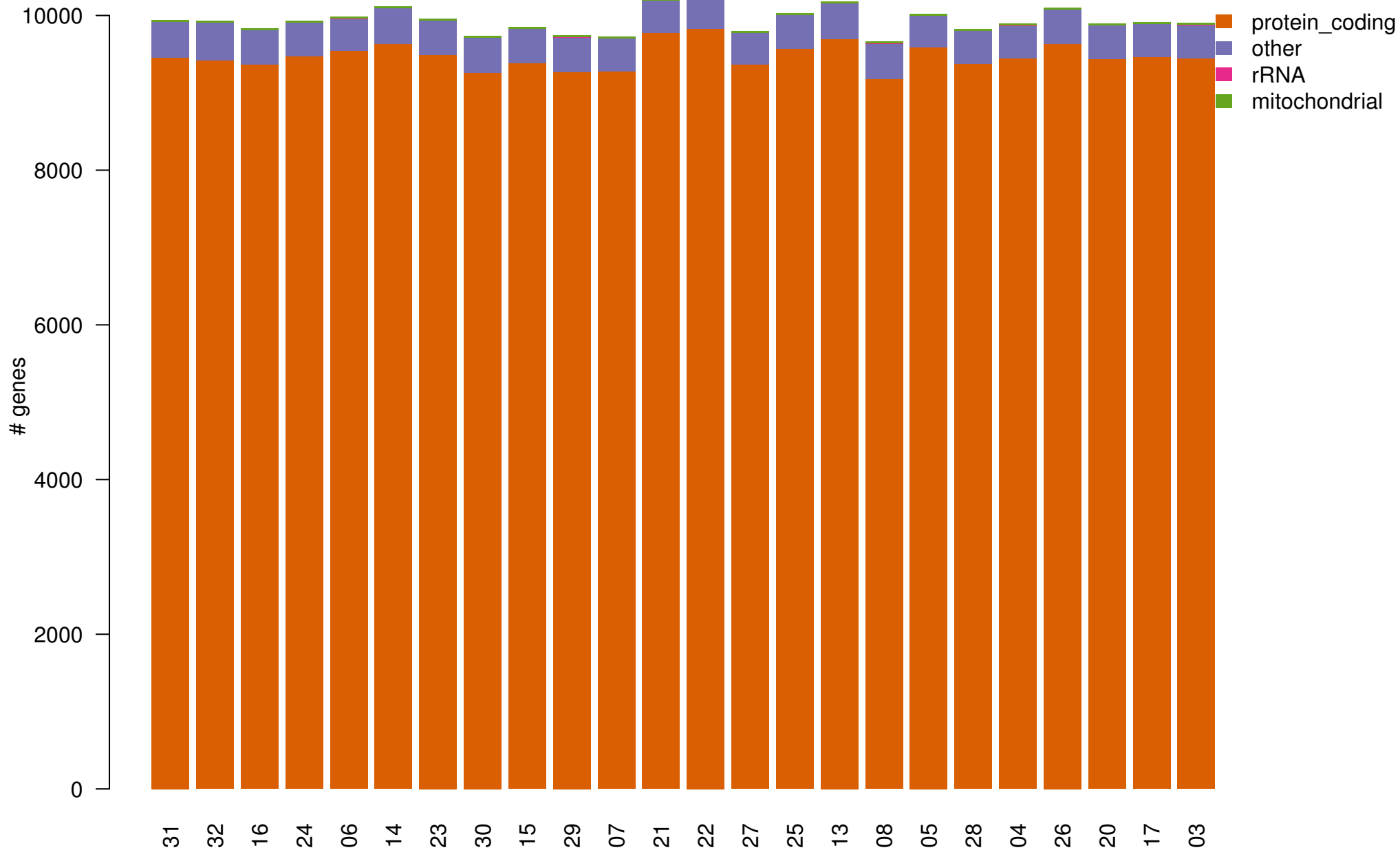
2 / 2



# Expressed genes (RPKM >= 1)

*Homo\_sapiens.GRCh38.98*

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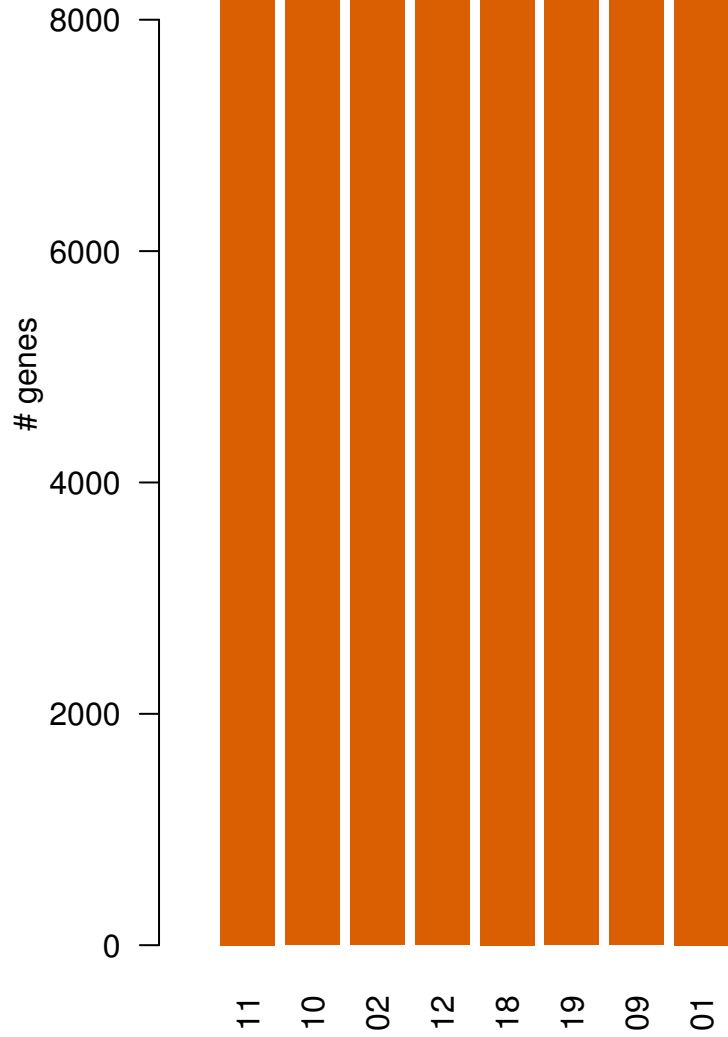


# Expressed genes (RPKM >= 1)

*Homo\_sapiens.GRCh38.98*

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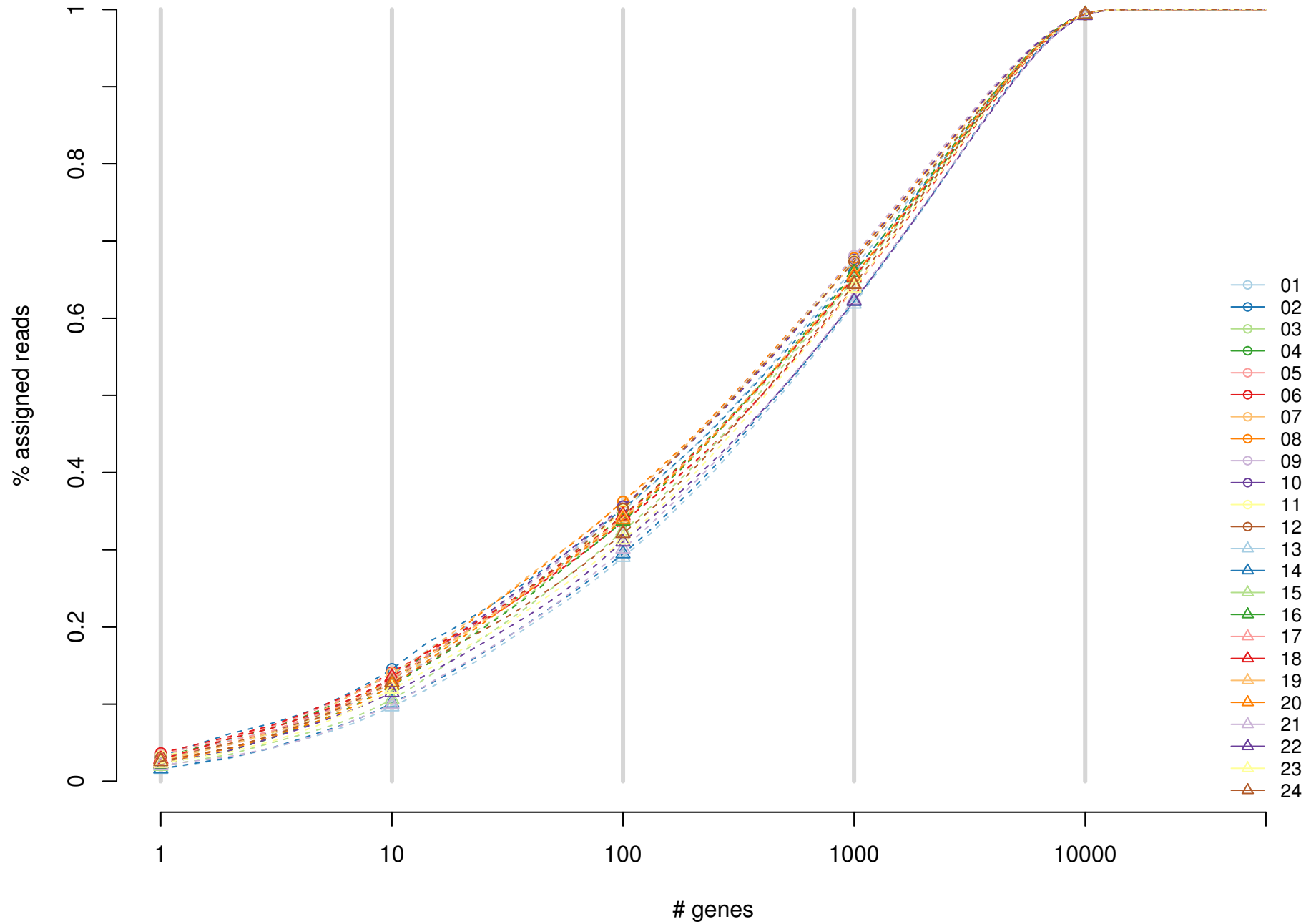
- protein\_coding
- other
- rRNA
- mitochondrial



# Cumulative Gene Diversity

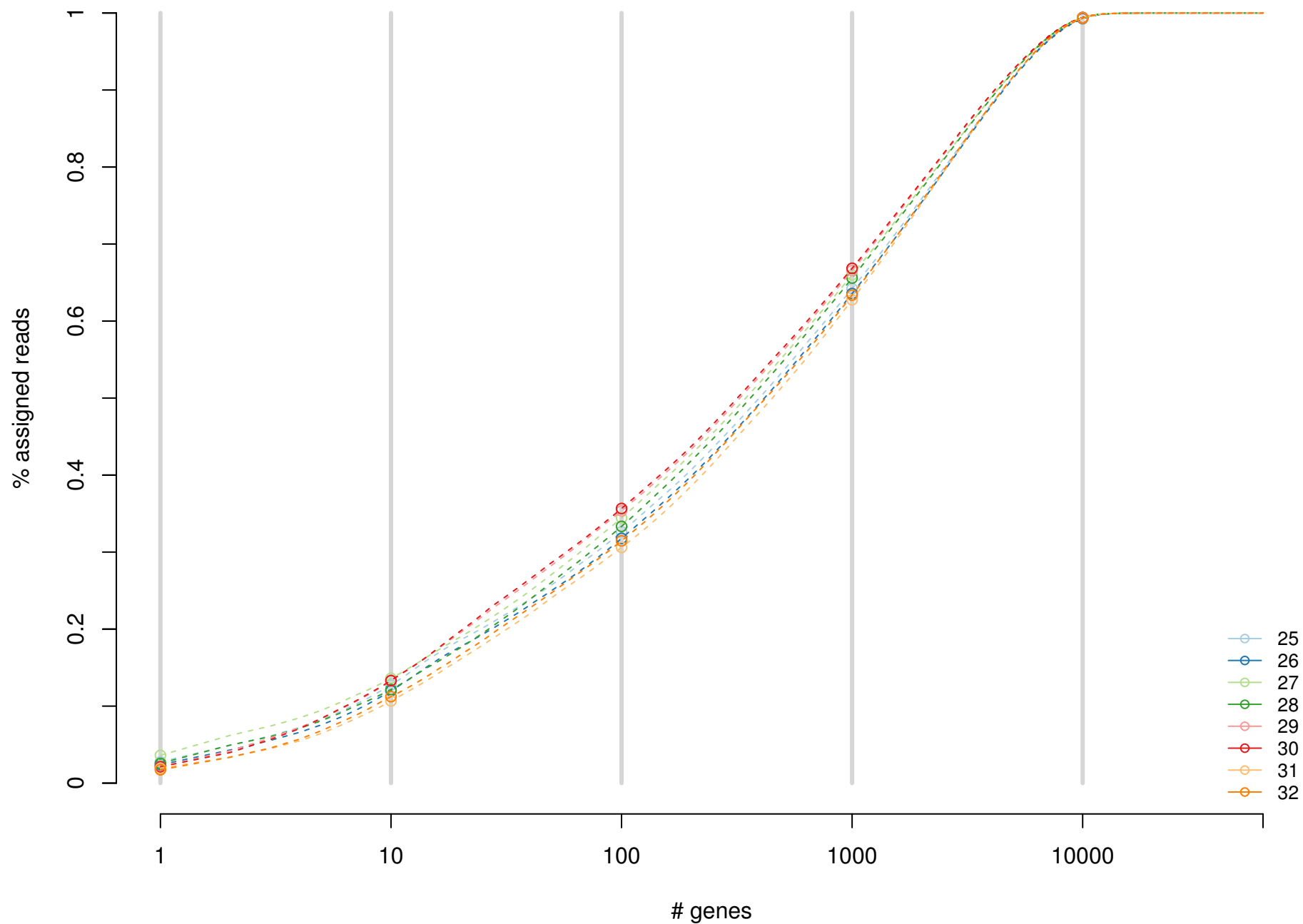
*Homo\_sapiens.GRCh38.98*

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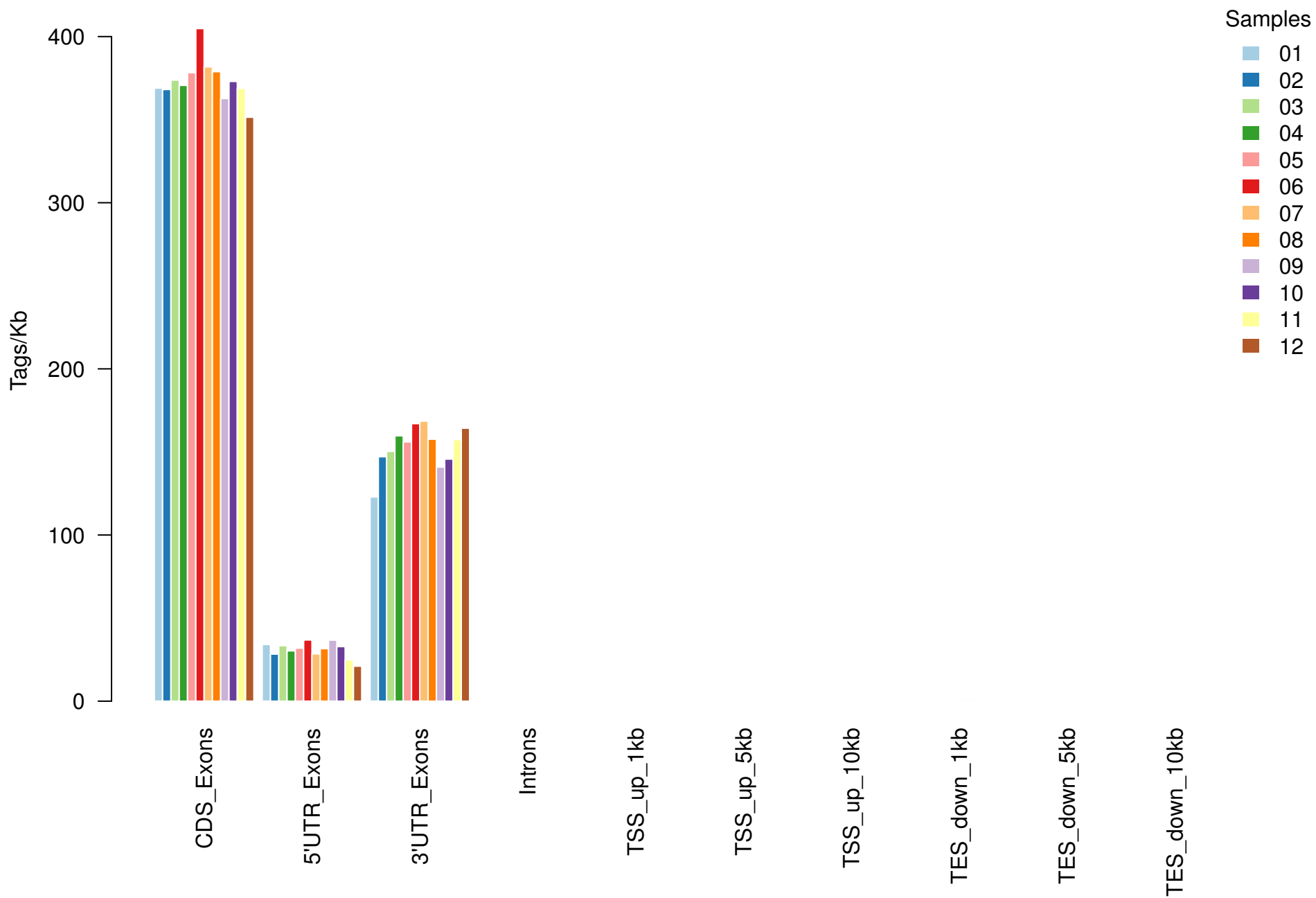


*Homo\_sapiens.GRCh38.98*

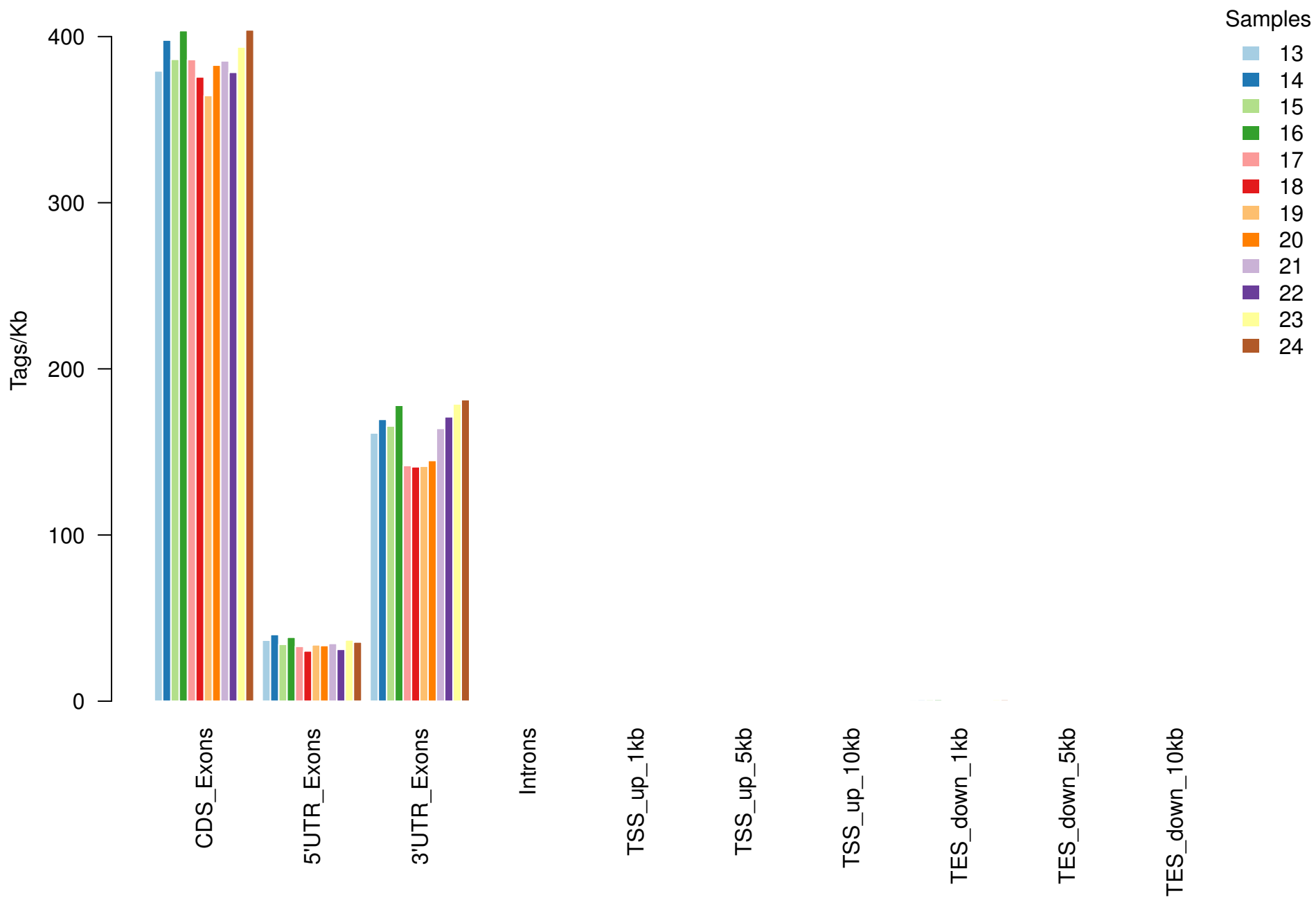
2 / 2



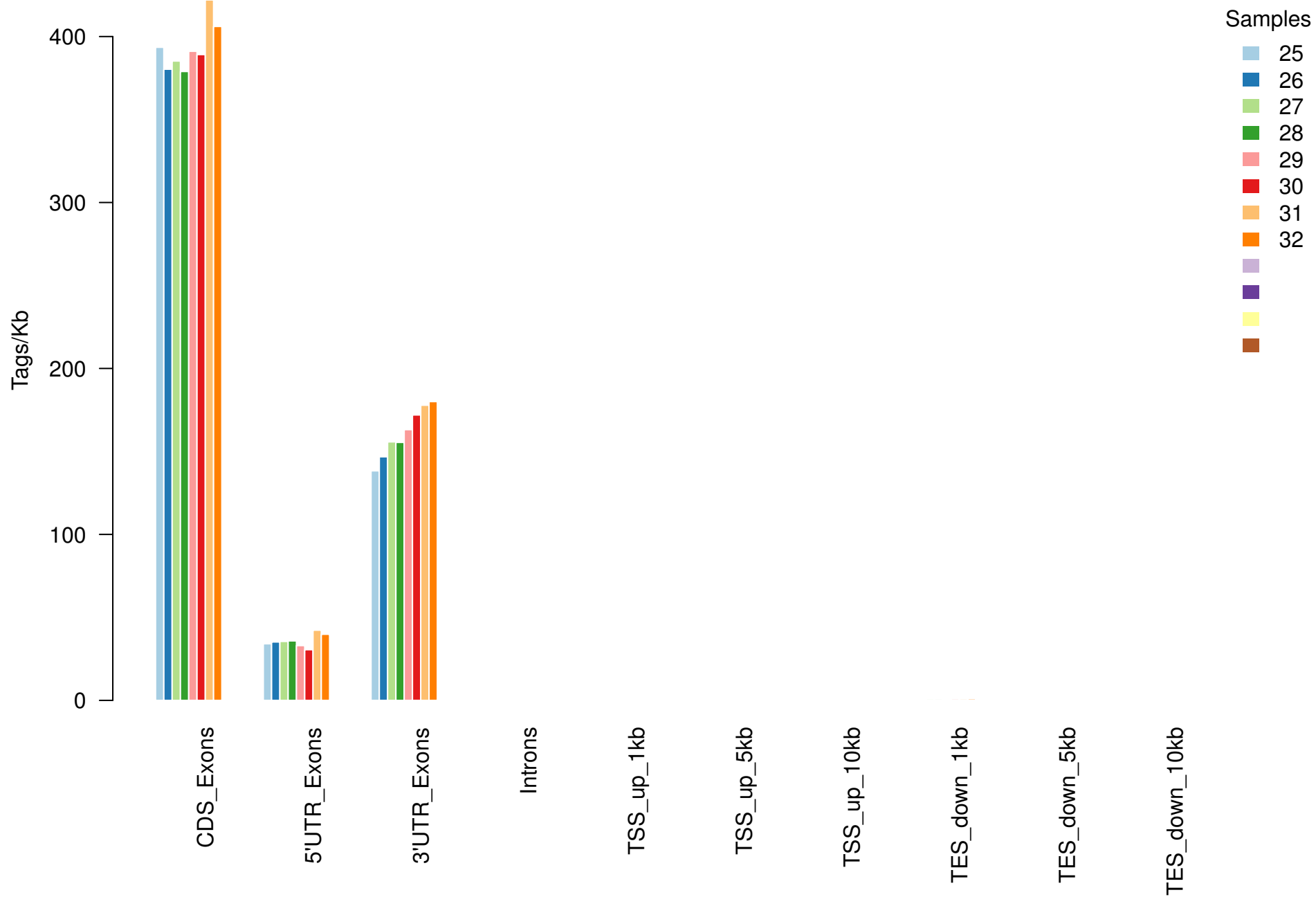
### Reads Density (1/3)



## Reads Density (2/3)



### Reads Density (3/3)

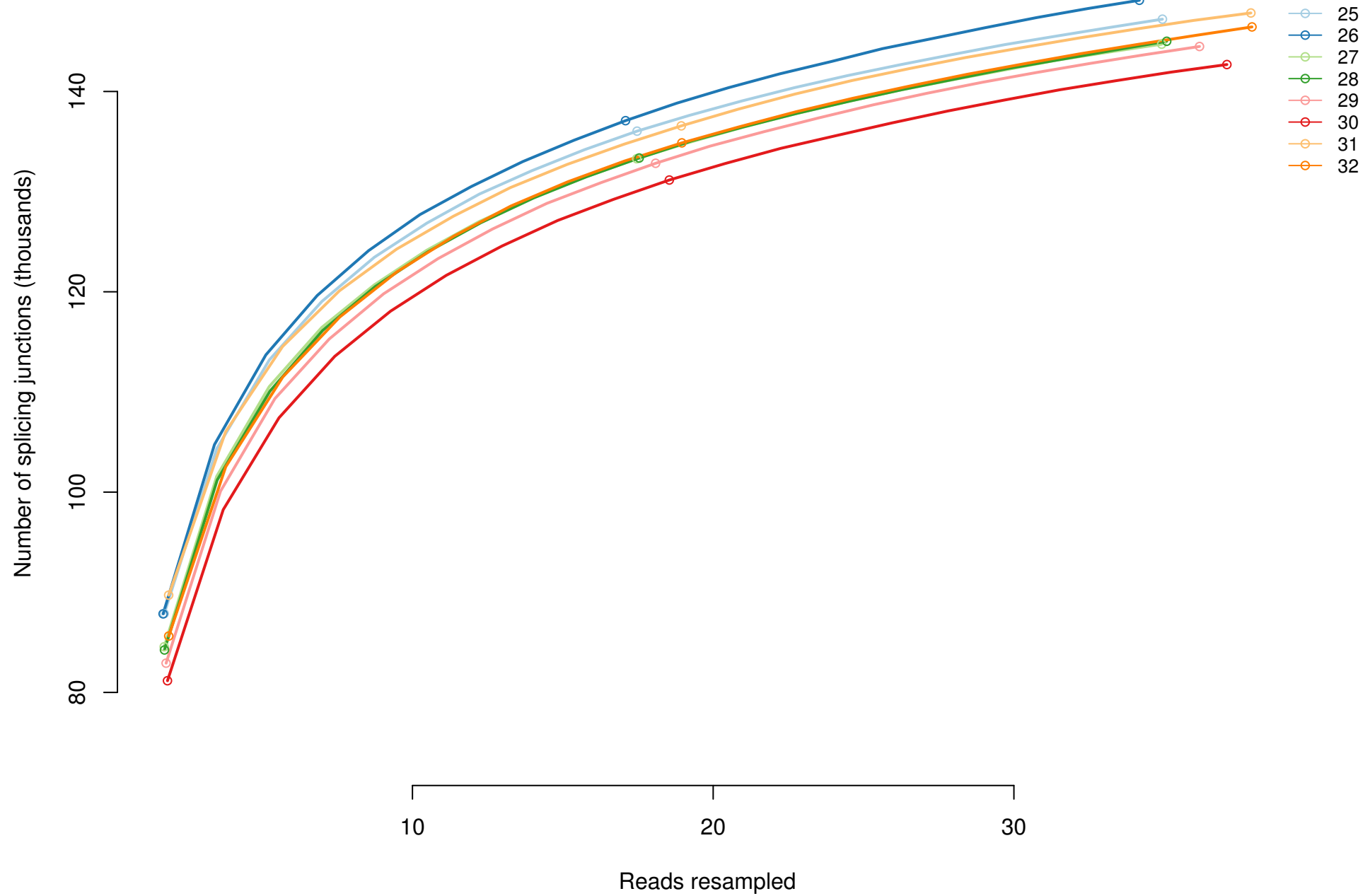


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# Known Splicing Junctions Saturation

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Project alignment metrics (1/3)

METRIC	01	02	03	04	05	06	07	08	09	10	11	12
TOTAL_READS	33486839	34119745	34738879	35168689	34774900	37111215	36871340	36035533	35029947	35206693	35689206	34942970
REMOVED_READS_ALIGNED_TO_rRNA	1013728	996883	1020277	1273774	965702	910197	1593157	1686125	1758717	1629319	1292667	1563826
PF_READS	26344260	27128679	27742328	27923202	28122349	30098580	28873477	28315009	26733538	27301002	27776546	27244942
PF_READS_ALIGNED	26207940	27029901	27599383	27747689	27994605	29920952	28712631	28228342	26577056	27188994	27655320	27129283
PCT_PF_READS_ALIGNED	99.48	99.64	99.48	99.37	99.55	99.41	99.44	99.69	99.41	99.59	99.56	99.58
PF_ALIGNED_BASES	3878557006	4008842001	4088294586	4112218692	4157573826	4433384920	4258403528	4182383424	3929332168	4042331939	4101443209	4031527314
MEAN_READ_LENGTH	148.87	148.83	148.88	149.02	149.18	148.94	149.00	148.72	148.73	149.34	148.99	149.22
READS_ALIGNED_IN_PAIRS	0	0	0	0	0	0	0	0	0	0	0	0
PCT_READS_ALIGNED_IN_PAIRS	0	0	0	0	0	0	0	0	0	0	0	0
STRAND_BALANCE	0.51	0.51	0.50	0.51	0.50	0.51	0.49	0.48	0.49	0.50	0.49	0.48
UNMAPPED_READS	136320	98778	142945	175513	127744	177628	160846	86667	156482	112008	121226	115659
UNPAIRED_READ_DUPLICATES	20195574	20786332	21003163	21113986	21100631	22624110	22511966	22380580	21162325	21151760	22012643	21379957
READ_PAIR_OPTICAL_DUPLICATES	0	0	0	0	0	0	0	0	0	0	0	0
UNIQUELY_ALIGNED	25051231	25882258	26377312	26542675	26807399	28665054	27418542	26844753	25295695	25966273	26331876	25817639
MULTIPLE_ALIGNMENT	1156709	1147643	1222071	1205014	1187206	1255898	1294089	1383589	1281361	1222721	1323444	1311644
READ_ALIGNED_TO_REF_EXONS	23948950	24797445	25188242	25352650	25618813	27389273	26194409	25599325	24133525	24820546	25150215	24653542
NO_FEATURE	311172	326517	365597	381200	388942	424115	377201	353429	288656	314154	327856	331794
AMBIGUOUS	791109	758296	823473	808825	799644	851666	846932	891999	873514	831573	853805	832303
TOO_LOW_AQUAL	0	0	0	0	0	0	0	0	0	0	0	0
NOT_ALIGNED	0	0	0	0	0	0	0	0	0	0	0	0
ALIGNMENT_NOT_UNIQUE	2649591	2625426	2791690	2757727	2721687	2886944	2966517	3178742	2951110	2802341	3057323	3023101
UNMAPPED_READS_ALIGNED_TO_MITOCHONDRIA	5558	3716	7659	9233	5259	6830	9342	5285	7969	4797	5958	7793
UNMAPPED_READS_ALIGNED_TO_MITOCHONDRIA_%	4.08	3.76	5.36	5.26	4.12	3.85	5.81	6.10	5.09	4.28	4.91	6.74
MAPPED_READS_ALIGNED_TO_MITOCHONDRIA	777609	810246	1091105	1030641	788001	717290	1222252	1426379	1079921	940187	1179371	1563022
MAPPED_READS_ALIGNED_TO_MITOCHONDRIA_%	2.97	3.00	3.95	3.71	2.81	2.40	4.26	5.05	4.06	3.46	4.26	5.76
bias_index_50	55.39	56.31	55.63	56.26	55.96	55.73	57.18	56.84	55.66	55.69	58.14	59.04
5over3_cov_ratio	0.63	0.58	0.61	0.58	0.60	0.61	0.53	0.55	0.62	0.61	0.50	0.46

Project alignment metrics (2/3)

METRIC	13	14	15	16	17	18	19	20	21	22	23	24
TOTAL_READS	34449141	36250430	36333007	37982358	34934092	33838466	32868759	34403107	35918588	35558119	36447400	37721633
REMOVED_READS_ALIGNED_TO_rRNA	1292168	1169466	1405461	1295859	892542	772082	991019	1114133	1326159	919808	558704	945163
PF_READS	28332560	29854173	29220394	30581740	27798813	27081728	26633422	27776478	28622989	28574103	29768472	30389666
PF_READS_ALIGNED	28246508	29721650	29128228	30477351	27692938	27000319	26527572	27678971	28534716	28423255	29631502	30236703
PCT_PF_READS_ALIGNED	99.70	99.56	99.68	99.66	99.62	99.70	99.60	99.65	99.69	99.47	99.54	99.50
PF_ALIGNED_BASES	4197727787	4417359323	4321529077	4500471100	4111402126	4018763590	3930577427	4115033708	4241463730	4225733632	4388559597	4481710403
MEAN_READ_LENGTH	149.12	149.26	148.84	148.22	149.10	149.40	148.79	149.22	149.15	149.36	148.62	148.82
READS_ALIGNED_IN_PAIRS	0	0	0	0	0	0	0	0	0	0	0	0
PCT_READS_ALIGNED_IN_PAIRS	0	0	0	0	0	0	0	0	0	0	0	0
STRAND_BALANCE	0.50	0.49	0.48	0.50	0.50	0.51	0.50	0.50	0.50	0.50	0.50	0.51
UNMAPPED_READS	86052	132523	92166	104389	105875	81409	105850	97507	88273	150848	136970	152963
UNPAIRED_READ_DUPLICATES	21775017	22849336	22486882	23555176	21419216	20787604	20258630	21217084	21721831	21320607	22760923	23295016
READ_PAIR_OPTICAL_DUPLICATES	0	0	0	0	0	0	0	0	0	0	0	0
UNIQUELY_ALIGNED	26865647	28283584	27671025	29023027	26412238	25817244	25343834	26471628	27286219	27277928	28281589	28921941
MULTIPLE_ALIGNMENT	1380861	1438066	1457203	1454324	1280700	1183075	1183738	1207343	1248497	1145327	1349913	1314762
READ_ALIGNED_TO_REF_EXONS	25535310	26858656	26365470	27663387	25254657	24731093	24202071	25321212	26046845	26086380	26967286	27636877
NO_FEATURE	377944	411028	383403	447460	311600	313225	342073	327367	377578	411504	406567	394869
AMBIGUOUS	952393	1013900	922152	912180	845981	772926	799690	823049	861796	780044	907736	890195
TOO_LOW_AQUAL	0	0	0	0	0	0	0	0	0	0	0	0
NOT_ALIGNED	0	0	0	0	0	0	0	0	0	0	0	0
ALIGNMENT_NOT_UNIQUE	3176450	3310052	3340062	3343042	2947336	2707929	2717687	2760170	2861323	2618290	3100359	3019497
UNMAPPED_READS_ALIGNED_TO_MITOCHONDRIA	3796	6652	7208	6249	3894	2547	3461	3207	3102	5062	3872	4043
UNMAPPED_READS_ALIGNED_TO_MITOCHONDRIA_%	4.41	5.02	7.82	5.99	3.68	3.13	3.27	3.29	3.51	3.36	2.83	2.64
MAPPED_READS_ALIGNED_TO_MITOCHONDRIA	1012870	1056964	1721762	1412933	777155	622090	643321	683632	783951	637302	732835	560510
MAPPED_READS_ALIGNED_TO_MITOCHONDRIA_%	3.59	3.56	5.91	4.64	2.81	2.30	2.43	2.47	2.75	2.24	2.47	1.85
bias_index_50	55.98	56.08	56.09	55.78	55.83	55.83	55.60	55.65	55.70	56.04	56.15	56.25
5over3_cov_ratio	0.60	0.59	0.59	0.61	0.60	0.60	0.62	0.61	0.61	0.59	0.59	0.58

Project alignment metrics (3/3)

METRIC	25	26	27	28	29	30	31	32
TOTAL_READS	34939047	34172014	34913588	35080848	36172508	37082550	37880124	37916677
REMOVED_READS_ALIGNED_TO_rRNA	656169	878095	547798	1300525	1292476	1589111	834791	1430409
PF_READS	28301082	27877508	28459983	28049056	29053631	29454527	31388993	30702643
PF_READS_ALIGNED	28138531	27739665	28327461	27934817	28952931	29338469	31259470	30601446
PCT_PF_READS_ALIGNED	99.43	99.51	99.53	99.59	99.65	99.61	99.59	99.67
PF_ALIGNED_BASES	4177854703	4113413767	4202521884	4144905408	4299079554	4355621521	4634304083	4523134512
MEAN_READ_LENGTH	149.35	148.99	149.05	148.98	149.05	149.05	148.86	148.32
READS_ALIGNED_IN_PAIRS	0	0	0	0	0	0	0	0
PCT_READS_ALIGNED_IN_PAIRS	0	0	0	0	0	0	0	0
STRAND_BALANCE	0.50	0.50	0.51	0.51	0.49	0.48	0.49	0.49
UNMAPPED_READS	162551	137843	132522	114239	100700	116058	129523	101197
UNPAIRED_READ_DUPLICATES	21642083	20968848	21773886	21439384	22614617	23134127	24096689	23749523
READ_PAIR_OPTICAL_DUPLICATES	0	0	0	0	0	0	0	0
UNIQUELY_ALIGNED	26910458	26500463	27085979	26672864	27621419	27980112	29809024	29111930
MULTIPLE_ALIGNMENT	1228073	1239202	1241482	1261953	1331512	1358357	1450446	1489516
READ_ALIGNED_TO_REF_EXONS	25707149	25273528	25866354	25460725	26381609	26695826	28390388	27647323
NO_FEATURE	349633	385375	396936	375381	364128	389475	419830	458291
AMBIGUOUS	853676	841560	822689	836758	875682	894811	998806	1006316
TOO_LOW_AQUAL	0	0	0	0	0	0	0	0
NOT_ALIGNED	0	0	0	0	0	0	0	0
ALIGNMENT_NOT_UNIQUE	2819002	2848421	2843821	2891437	3055553	3117556	3323969	3423182
UNMAPPED_READS_ALIGNED_TO_MITOCHONDRIA	5552	5793	6078	5820	5082	6842	5285	4515
UNMAPPED_READS_ALIGNED_TO_MITOCHONDRIA_%	3.42	4.20	4.59	5.09	5.05	5.90	4.08	4.46
MAPPED_READS_ALIGNED_TO_MITOCHONDRIA	683504	818727	853357	923030	1072038	1259391	912399	1143210
MAPPED_READS_ALIGNED_TO_MITOCHONDRIA_%	2.43	2.95	3.01	3.30	3.70	4.29	2.92	3.74
bias_index_50	55.51	55.38	55.60	55.58	56.30	57.06	55.81	56.43
5over3_cov_ratio	0.62	0.63	0.62	0.62	0.58	0.54	0.60	0.57