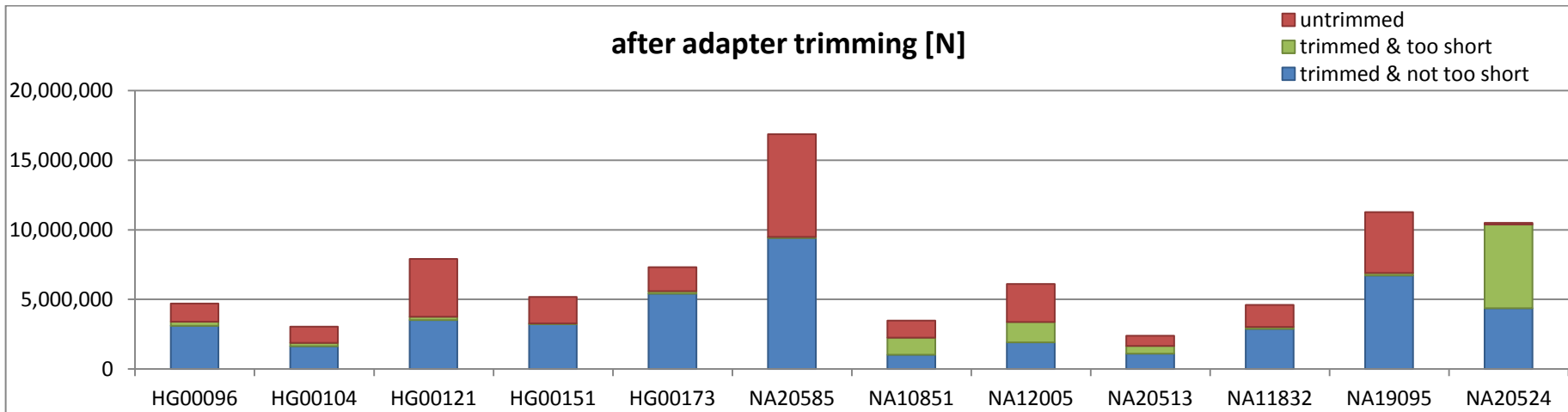
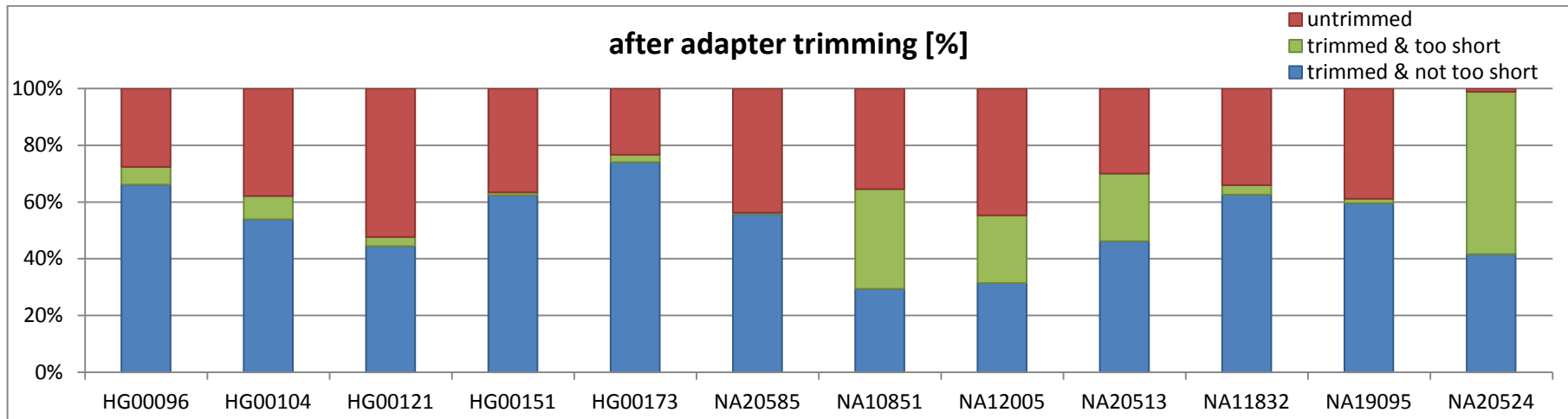


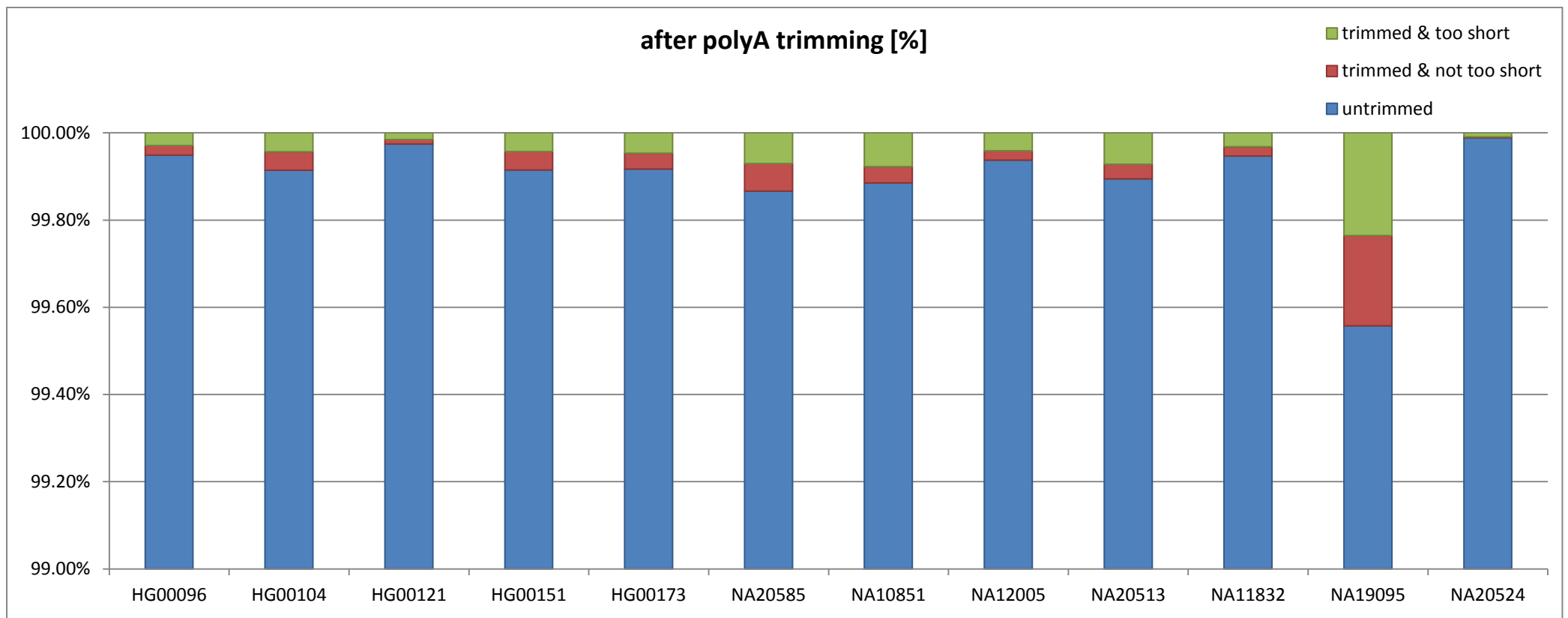
Adapter trimming results

	UNIGE			MPIMG			ICMB			CNAG		
	HG00096	HG00104	HG00121	HG00151	HG00173	NA20585	NA10851	NA12005	NA20513	NA11832	NA19095	NA20524
processed reads	4,701,889	3,040,116	7,903,163	5,178,053	7,314,599	16,878,747	3,489,043	6,113,322	2,384,113	4,599,349	11,285,616	10,507,737
trimmed reads	3,403,870	1,886,837	3,766,515	3,279,014	5,605,865	9,495,349	2,252,054	3,376,492	1,668,359	3,030,773	6,893,775	10,380,069
untrimmed	1,298,019	1,153,279	4,136,648	1,899,039	1,708,734	7,383,398	1,236,989	2,736,830	715,754	1,568,576	4,391,841	127,668
trimmed & too short	293,789	247,112	252,251	48,122	189,733	81,009	1,227,053	1,451,884	567,758	152,607	176,927	6,011,420
trimmed & not too short	3,110,081	1,639,725	3,514,264	3,230,892	5,416,132	9,414,340	1,025,001	1,924,608	1,100,601	2,878,166	6,716,848	4,368,649



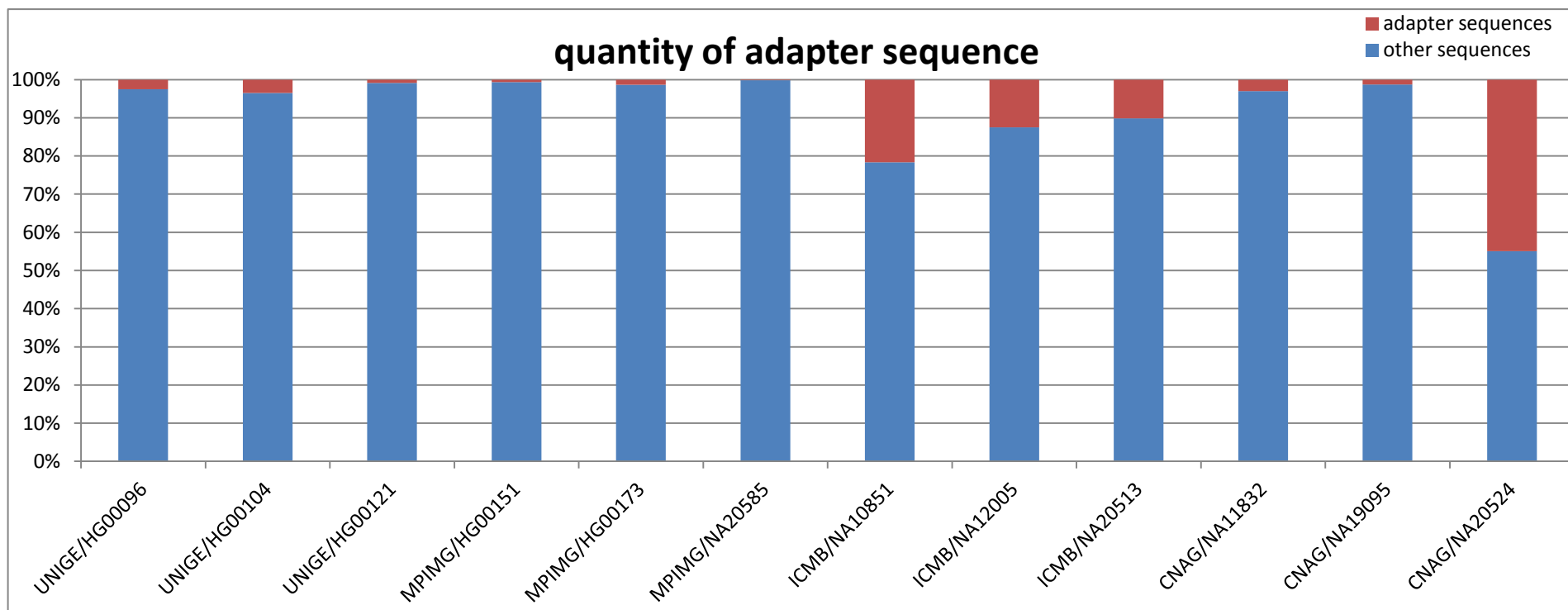
2nd round of trimming to remove polyA tails

	UNIGE			MPIMG			ICMB			CNAG		
	HG00096	HG00104	HG00121	HG00151	HG00173	NA20585	NA10851	NA12005	NA20513	NA11832	NA19095	NA20524
processed reads	3,110,081	1,639,725	3,514,264	3,230,892	5,416,132	9,414,340	1,025,001	1,924,608	1,100,601	2878166	6716848	4368649
trimmed reads	1,578	1,401	896	2,747	4,492	12,596	1,175	1,208	1,162	1,536	29,732	490
trimmed & too short	904	711	538	1,386	2,523	6,631	792	795	789	912	15,829	392
untrimmed	3,108,503	1,638,324	3,513,368	3,228,145	5,411,640	9,401,744	1,023,826	1,923,400	1,099,439	2,876,630	6,687,116	4,368,159
trimmed & not too short	674	690	358	1,361	1,969	5,965	383	413	373	624	13,903	98



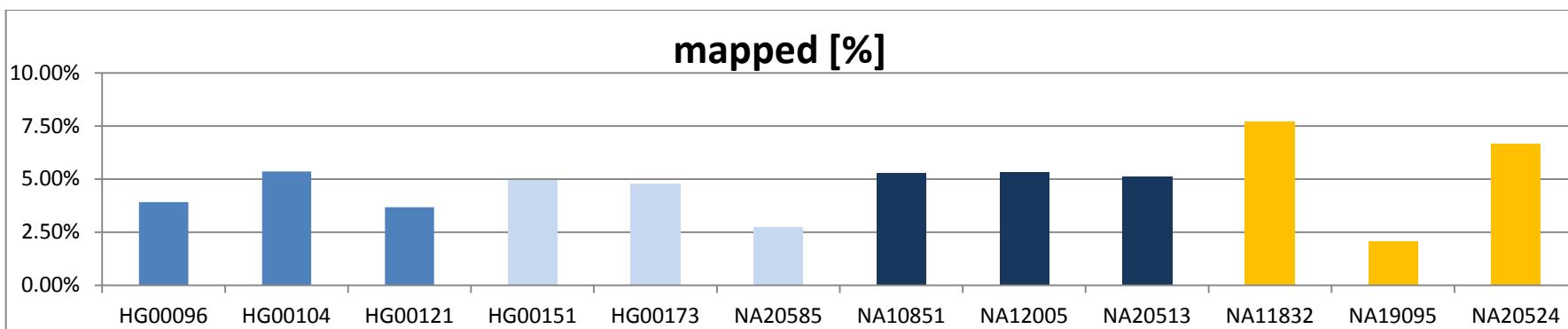
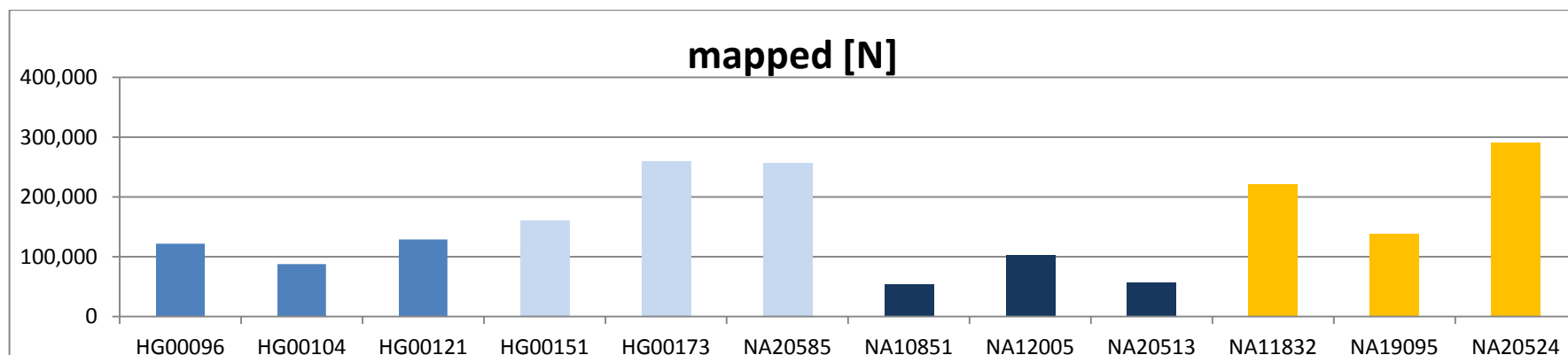
Quantity of adapter sequences

sample	total seqs	other sequences	adapter sequences	[%] of total
UNIGE/HG00096	4,701,889	4,583,735	118,154	2.5129
UNIGE/HG00104	3,040,116	2,934,373	105,743	3.4783
UNIGE/HG00121	7,903,163	7,835,759	67,404	0.8529
MPIMG/HG00151	5,178,053	5,145,138	32,915	0.6357
MPIMG/HG00173	7,314,599	7,217,476	97,123	1.3278
MPIMG/NA20585	16,878,747	16,855,754	22,993	0.1362
ICMB/NA10851	3,489,043	2,733,880	755,163	21.6438
ICMB/NA12005	6,113,322	5,347,236	766,086	12.5314
ICMB/NA20513	2,384,113	2,142,554	241,559	10.132
CNAG/NA11832	4,599,349	4,462,485	136,864	2.9757
CNAG/NA19095	11,285,616	11,145,576	140,040	1.2409
CNAG/NA20524	10,507,737	5,788,999	4,718,738	44.9073



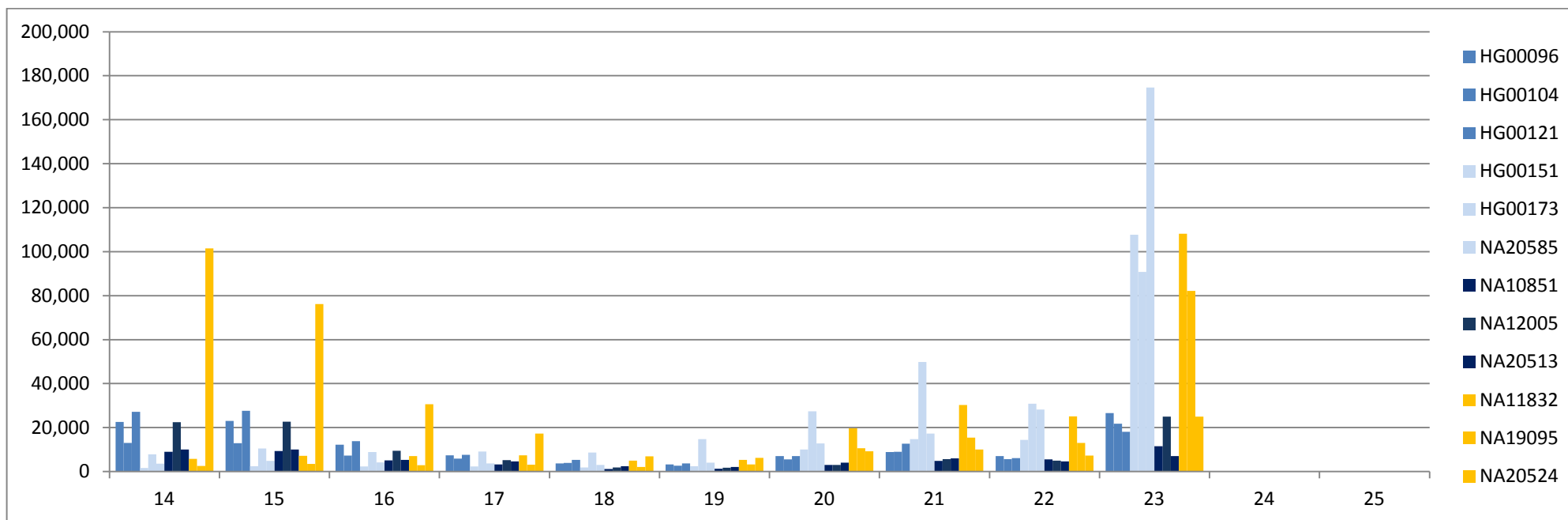
Mapping against miRNA reference

	UNIGE			MPIMG			ICMB			CNAG		
	HG00096	HG00104	HG00121	HG00151	HG00173	NA20585	NA10851	NA12005	NA20513	NA11832	NA19095	NA20524
total fwReads:	3,109,177	1,639,014	3,513,726	3,229,506	5,413,609	9,407,709	1,024,209	1,923,813	1,099,812	2,877,254	6,701,019	4,368,257
mapped [N]	121,714	87,788	129,188	159,806	258,753	256,323	54,035	102,196	56,086	221,130	138,531	290,185
mapped [%]	3.91%	5.36%	3.68%	4.95%	4.78%	2.72%	5.28%	5.31%	5.10%	7.69%	2.07%	6.64%
unmapped [N]	2,987,463	1,551,226	3,384,538	3,069,700	5,154,856	9,151,386	970,174	1,821,617	1,043,726	2,656,124	6,562,488	4,078,072
unmapped [%]	96.09%	94.64%	96.32%	95.05%	95.22%	97.28%	94.72%	94.69%	94.90%	92.31%	97.93%	93.36%
# duplicates:	112,697	81,169	120,541	157,351	252,734	252,433	48,862	93,061	49,622	215,222	135,448	273,691
[%] duplicates:	0.9259	0.9246	0.9331	0.9846	0.9767	0.9848	0.9043	0.9106	0.8847	0.9700	0.98	0.94
avg. CIGAR M length:	18.02	18.61	17.45	22.01	20.7	21.99	18.33	17.76	17.84	21.19	21.62	16.14
avg. CIGAR I length:	0.1	0.09	0.11	0.01	0.03	0.01	0.11	0.12	0.09	0.03	0.02	0.13
avg. CIGAR D length:	0.03	0.02	0.04	0	0.01	0	0.02	0.03	0.03	0.01	0	0.03



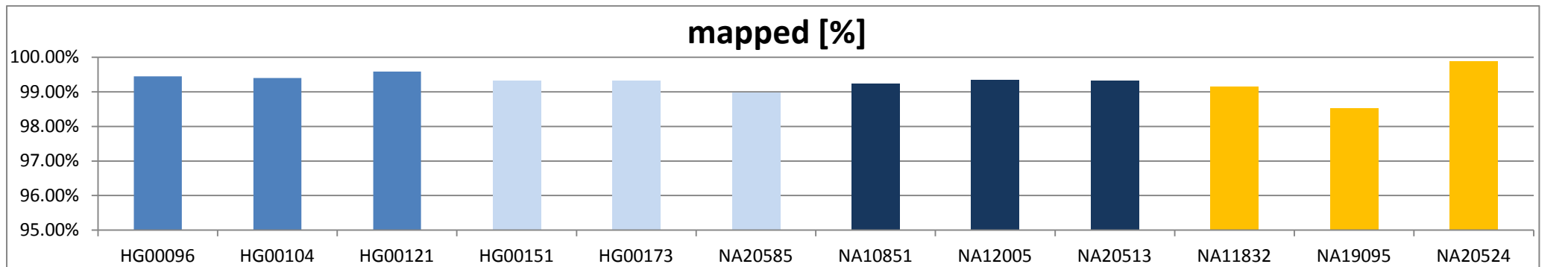
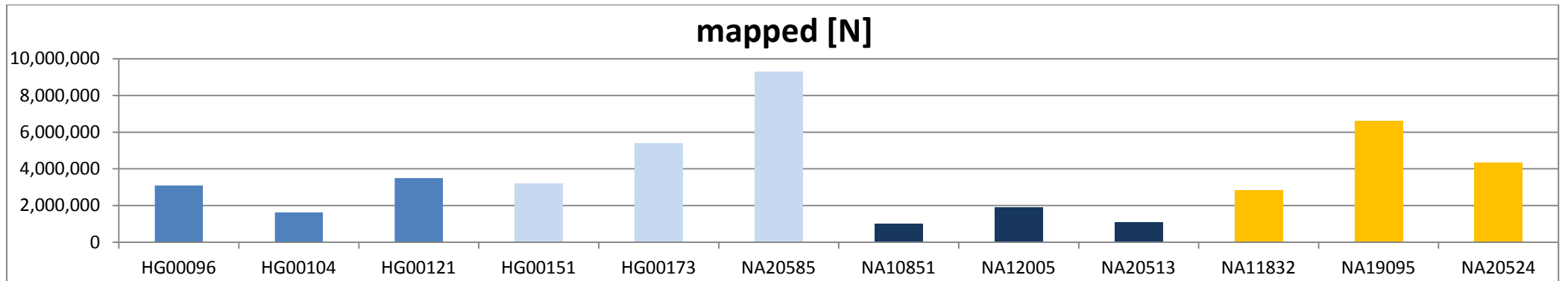
Read length distribution of reads mapped against miRNA reference

read length	UNIGE			MPIMG			ICMB			CNAG		
	HG00096	HG00104	HG00121	HG00151	HG00173	NA20585	NA10851	NA12005	NA20513	NA11832	NA19095	NA20524
14	22,518	13,034	27,199	1,649	7,895	3,599	8,999	22,460	9,993	5,830	2,509	101,445
15	23,014	12,945	27,606	2,451	10,552	4,890	9,375	22,729	9,990	7,155	3,494	76,180
16	12,205	7,278	13,863	2,292	8,871	4,112	5,072	9,460	5,354	7,038	2,865	30,656
17	7,354	5,904	7,595	2,331	9,156	3,681	3,231	5,227	4,635	7,373	3,112	17,291
18	3,694	3,982	5,264	1,833	8,709	3,072	1,196	1,899	2,401	4,936	2,086	6,939
19	3,263	2,669	3,756	2,392	14,756	4,047	1,324	1,797	2,043	5,375	3,245	6,192
20	7,068	5,492	7,082	10,031	27,363	12,741	2,991	2,991	4,105	19,744	10,578	9,197
21	8,897	9,050	12,638	14,724	49,782	17,242	4,805	5,648	5,956	30,316	15,390	10,015
22	7,099	5,673	6,084	14,429	30,805	28,198	5,513	4,984	4,604	25,143	13,060	7,286
23	26,599	21,756	18,092	107,649	90,829	174,693	11,514	24,980	6,997	108,154	82,180	24,982
24	0	4	9	24	34	45	14	21	8	65	12	2
25	0	1	0	1	1	3	1	0	0	1	0	0



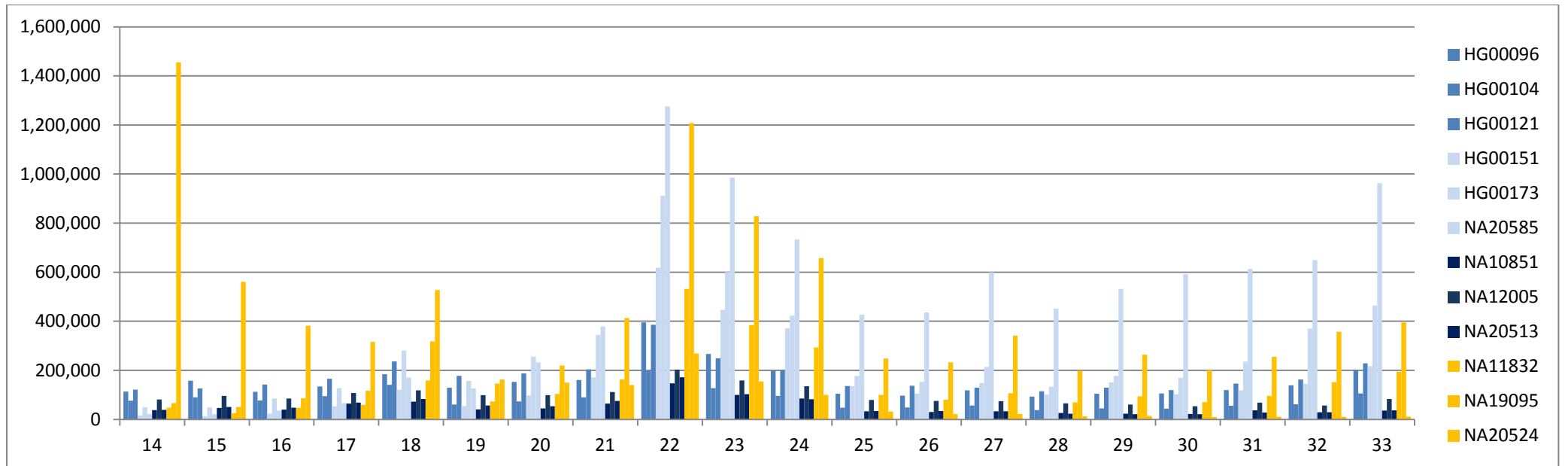
Mapping against genome

	UNIGE			MPIMG			ICMB			CNAG		
	HG00096	HG00104	HG00121	HG00151	HG00173	NA20585	NA10851	NA12005	NA20513	NA11832	NA19095	NA20524
total fwReads:	3,109,177	1,639,014	3,513,726	3,229,506	5,413,609	9,407,709	1,024,209	1,923,813	1,099,812	2,877,254	6,701,019	4,368,257
mapped [N]	3,091,994	1,629,182	3,499,364	3,207,646	5,376,999	9,311,979	1,016,330	1,910,994	1,092,353	2852794	6601693	4363453
mapped [%]	99.45%	99.40%	99.59%	99.32%	99.32%	98.98%	99.23%	99.33%	99.32%	99.15%	98.52%	99.89%
unmapped [N]	17,183	9,832	14,362	21,860	36,610	95,730	7,879	12,819	7,459	24,460	99,326	4,804
unmapped [%]	0.55%	0.60%	0.41%	0.68%	0.68%	1.02%	0.77%	0.67%	0.68%	0.85%	1.48%	0.11%
# duplicates:	2,787,022	1,464,596	3,200,501	2,972,383	5,021,471	8,715,386	894,792	1,664,588	953,261	2655395	6067844	4031573
[%] duplicates:	0.90	0.90	0.91	0.93	0.93	0.94	0.88	0.87	0.87	0.93	0.92	0.92
avg. CIGAR M length:	23.24	22.59	23.33	24.65	24.53	26.24	22.41	22.64	22.09	24.07	24.4	17.13
avg. CIGAR I length:	0	0	0	0	0	0	0	0	0	0	0	0
avg. CIGAR D length:	0	0	0	0	0.01	0.01	0	0	0	0	0.01	0



Read length distribution of reads mapped against the genome

read length	UNIGE			MPIMG			ICMB			CNAG		
	HG00096	HG00104	HG00121	HG00151	HG00173	NA20585	NA10851	NA12005	NA20513	NA11832	NA19095	NA20524
14	113,674	76,484	121,827	16,542	50,212	21,992	38,269	81,369	38,665	48160	66611	1455237
15	157,804	89,648	126,710	12,240	48,759	21,292	46,724	95,442	50,771	25218	50699	560367
16	113,078	76,952	141,766	22,842	85,097	34,989	40,210	85,523	47,824	47281	85915	382080
17	134,230	94,566	165,679	54,150	127,175	66,283	64,448	107,996	68,688	59915	116196	316355
18	184,555	141,159	236,793	120,445	280,332	170,767	72,591	118,375	82,964	159152	317826	526765
19	129,684	60,423	177,320	54,708	156,687	126,441	41,179	99,230	56,760	73067	145539	163082
20	152,493	73,754	186,896	97,412	255,757	232,637	45,038	98,397	53,561	103687	219725	150201
21	160,481	90,084	204,074	171,093	344,358	379,010	64,718	112,108	75,407	162720	412725	140254
22	395,888	198,340	385,747	618,637	911,379	1,275,266	146,797	203,131	171,631	531883	1207721	268825
23	266,448	127,386	249,478	446,158	600,884	986,143	100,022	158,922	102,816	384284	828150	155046
24	198,879	95,891	199,783	371,731	422,534	733,789	84,848	135,237	81,886	293394	657302	100153
25	105,158	47,951	136,068	135,132	177,320	426,933	33,453	78,858	34,129	100012	248521	31741
26	97,344	49,163	137,513	104,435	152,943	435,802	30,206	75,729	33,647	80233	232483	21898
27	118,632	56,989	128,972	147,934	213,585	599,712	32,978	73,835	33,059	107198	341718	22630
28	92,732	38,420	114,157	100,509	133,208	451,056	26,622	65,108	23,296	69576	198064	12810
29	104,804	44,612	129,747	150,707	177,431	532,403	23,293	60,125	21,552	94088	263491	14580
30	105,719	43,571	119,975	103,196	169,301	591,831	21,888	53,310	21,219	70699	200700	9633
31	119,786	55,911	145,529	118,233	235,392	613,774	37,401	68,430	28,349	95852	255514	10049
32	139,104	61,806	162,608	145,082	370,271	649,018	29,580	56,790	29,222	152202	357010	10177
33	201,501	106,072	228,722	216,460	464,374	962,841	36,065	83,079	36,907	194173	395783	11570



Library diversity (1919 mature miRNAs)

UNIGE				MPIMG				ICMB				CNAG			
top 25 miRNAs	HG00096	HG00104	HG00121	top 25 miRNAs	HG00151	HG00173	NA20585	top 25 miRNAs	NA10851	NA12005	NA20513	top 25 miRNAs	NA11832	NA19095	NA20524
hsa-miR-191-5p	29,926	23,017	19,439	hsa-miR-191-5p	113,974	99,915	186,090	hsa-miR-191-5p	12,184	26,443	7,360	hsa-miR-191-5p	113553	86389	29198
hsa-miR-21-3p	1,866	4,635	6,996	hsa-miR-142-5p	3,081	22,052	3,794	hsa-miR-152	1,005	5,058	1,423	hsa-miR-152	830	295	13459
hsa-miR-142-5p	3,287	4,281	6,243	hsa-miR-21-3p	5,914	17,932	3,892	hsa-miR-27b-3p	1,898	2,076	3,568	hsa-miR-27b-3p	13236	8038	5309
hsa-miR-152	3,404	1,205	5,286	hsa-miR-22-3p	4,032	16,575	12,177	hsa-miR-142-5p	1,216	1,232	3,099	hsa-miR-21-3p	11827	6711	1871
hsa-miR-24-2-5p	2,570	4,569	3,057	hsa-miR-148a-3p	464	13,179	412	hsa-miR-122-5p	963	2,544	1,896	hsa-miR-122-5p	413	449	10565
hsa-miR-27b-3p	3,314	3,829	4,388	hsa-miR-27b-3p	7,513	13,174	7,328	hsa-miR-24-2-5p	1,567	1,097	2,199	hsa-miR-22-3p	10075	5560	4184
hsa-miR-122-5p	3,670	2,614	4,173	hsa-miR-29a-3p	1,939	7,905	4,005	hsa-miR-548d-3p	1,294	2,192	852	hsa-miR-548d-3p	1110	281	9417
hsa-miR-22-3p	2,594	3,019	2,682	hsa-miR-155-5p	406	5,189	205	hsa-miR-21-3p	418	1,538	2,132	hsa-miR-24-2-5p	6098	2874	7246
hsa-miR-548d-3p	2,961	1,172	2,260	hsa-miR-19a-3p	1,235	5,116	1,330	hsa-miR-29a-3p	2,080	1,436	1,720	hsa-miR-142-5p	5630	1859	3737
hsa-miR-423-5p	2,105	1,158	1,767	hsa-miR-24-2-5p	2,484	5,074	3,207	hsa-miR-22-3p	1,610	821	1,129	hsa-miR-1295a	425	652	5111
hsa-miR-1273c	771	577	2,030	hsa-miR-423-5p	2,017	3,817	3,673	hsa-miR-30b-5p	1,038	517	1,173	hsa-miR-29a-3p	4667	2647	1700
hsa-miR-101-5p	807	702	1,946	hsa-miR-16-5p	142	2,614	223	hsa-miR-4804-3p	195	1,111	248	hsa-miR-1273c	120	82	4609
hsa-miR-155-5p	1,523	195	469	hsa-miR-320a	942	2,052	1,679	hsa-miR-101-5p	156	1,091	385	hsa-miR-720	948	410	4515
hsa-miR-29c-5p	652	289	1,487	hsa-miR-30b-5p	1,143	1,272	1,896	hsa-miR-4723-3p	706	676	950	hsa-miR-423-5p	4168	2694	3983
hsa-miR-3184-5p	1,374	1,474	1,405	hsa-miR-122-5p	241	1,872	404	hsa-miR-27a-3p	501	944	771	hsa-miR-873-3p	258	121	3753
hsa-miR-29a-3p	1,185	1,094	1,465	hsa-miR-130a-3p	969	1,070	1,630	hsa-miR-1273c	184	907	190	hsa-miR-3184-5p	2771	1072	3433
hsa-miR-499a-5p	1,056	282	1,346	hsa-miR-3184-5p	738	1,456	1,276	hsa-miR-1295a	827	369	336	hsa-miR-4428	71	68	3432
hsa-miR-4634	1,200	166	1,280	hsa-miR-26a-5p	96	1,247	91	hsa-miR-19a-3p	510	816	697	hsa-miR-101-5p	202	52	3042
hsa-miR-4783-5p	367	333	1,177	hsa-miR-1295a	396	1,129	311	hsa-miR-3173-5p	206	738	237	hsa-miR-148a-3p	1100	1277	2928
hsa-miR-1295a	1,155	356	617	hsa-miR-4723-3p	189	1,114	231	hsa-miR-423-5p	707	639	473	hsa-miR-3545-5p	519	303	2658
hsa-miR-3173-5p	378	310	1,116	hsa-miR-152	210	664	1,058	hsa-miR-499a-5p	184	686	139	hsa-miR-19a-3p	2615	847	262
hsa-miR-3545-5p	701	931	1,111	hsa-miR-339-3p	975	719	979	hsa-miR-4783-5p	175	683	206	hsa-miR-30b-5p	2583	538	756
hsa-miR-93-5p	781	214	1,074	hsa-miR-130b-3p	599	867	957	hsa-miR-4745-3p	81	676	79	hsa-miR-4634	211	90	2546
hsa-miR-720	1,040	851	755	hsa-miR-128	662	925	791	hsa-miR-212-5p	406	675	187	hsa-miR-499a-5p	287	99	2367
hsa-miR-19a-3p	614	811	1,031	hsa-miR-548d-3p	134	711	243	hsa-miR-720	457	617	652	hsa-miR-155-5p	1021	385	2082
sum from above	69,301	58,084	74,600		150,495	227,640	237,882		30,568	55,582	32,101		184,738	123,793	132,163
total alignments	121,714	87,788	129,188		159,806	258,753	256,323		54,035	102,196	56,086		221,130	138,531	290,185
[%] of total alignments	56.94%	66.16%	57.75%		94.17%	87.98%	92.81%		56.57%	54.39%	57.24%		83.54%	89.36%	45.54%
undetected miRNAs	59	137	51		694	183	400		263	50	144		181	559	2