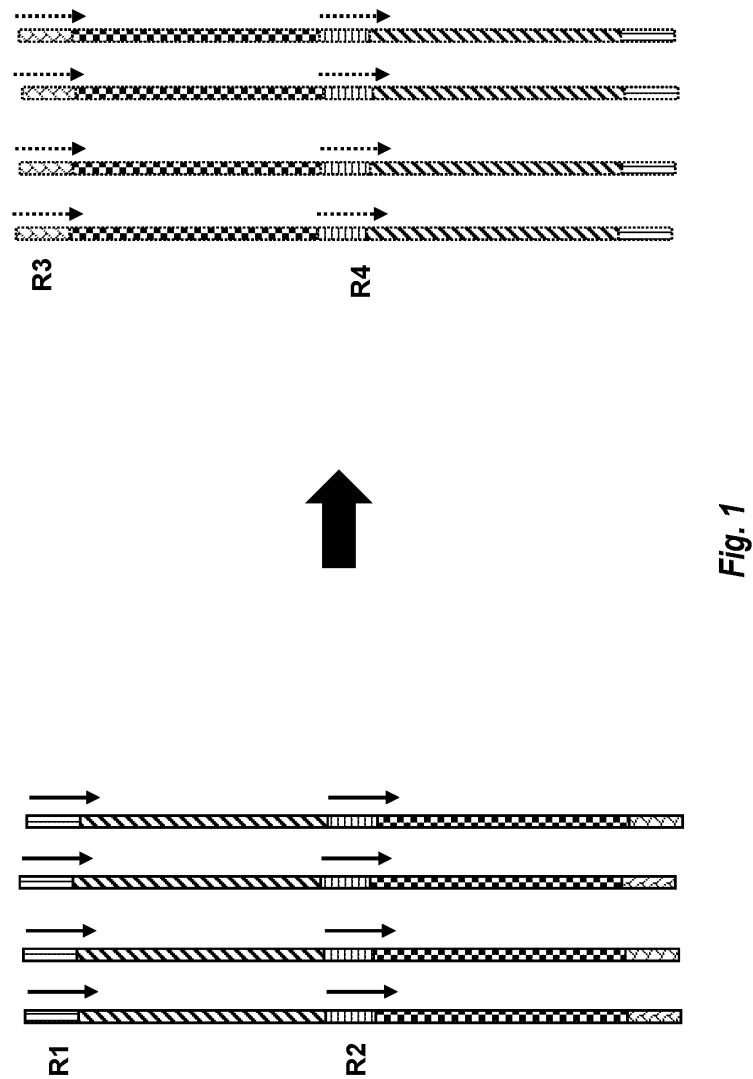




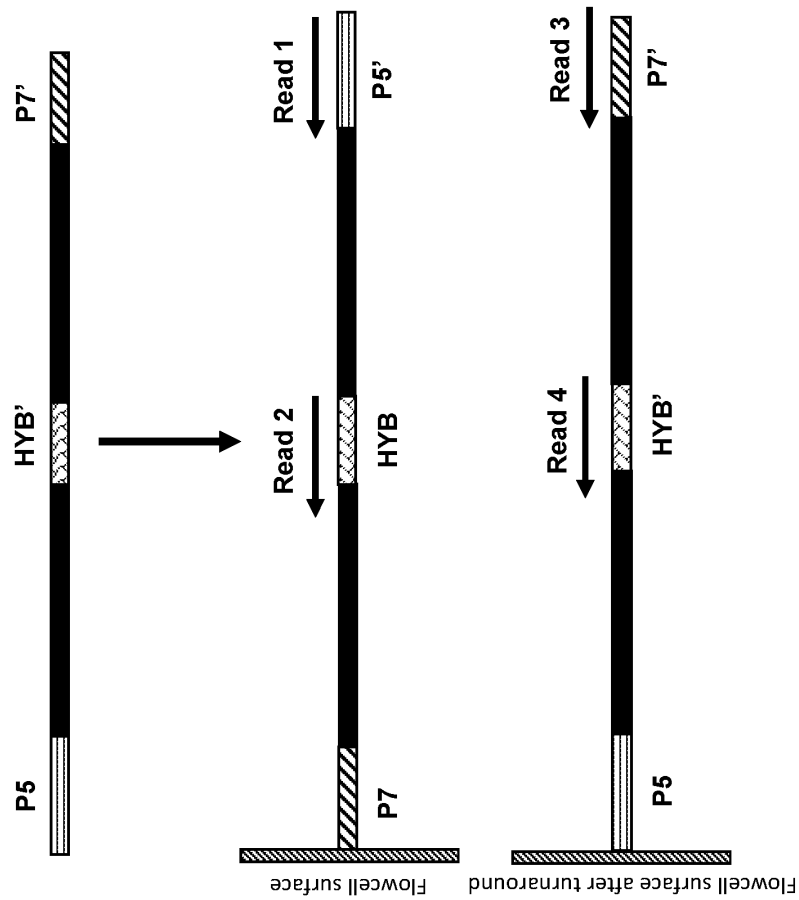


Fig. 2

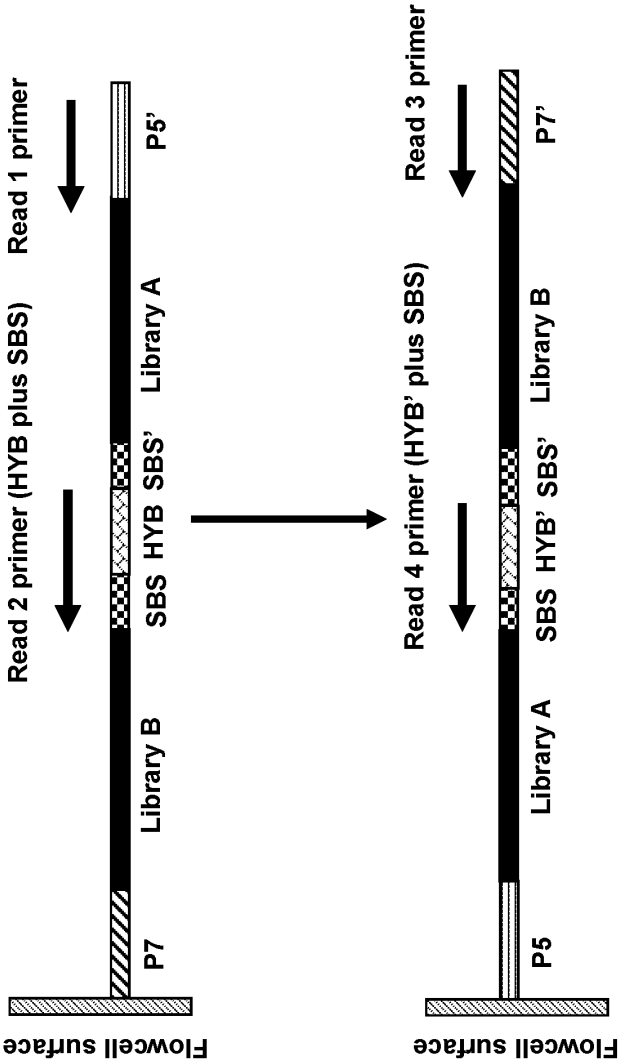


Fig. 3

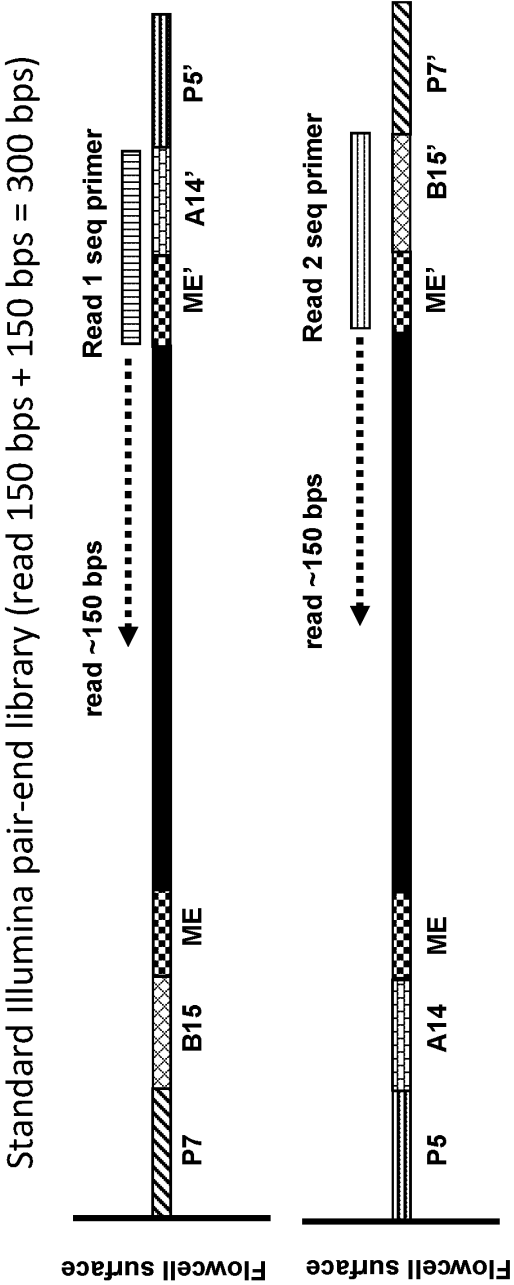


Fig. 4A

New hybrid pair-end library with middle primer (read 150 bps + 150 bps + 150 bps = 600 bps)

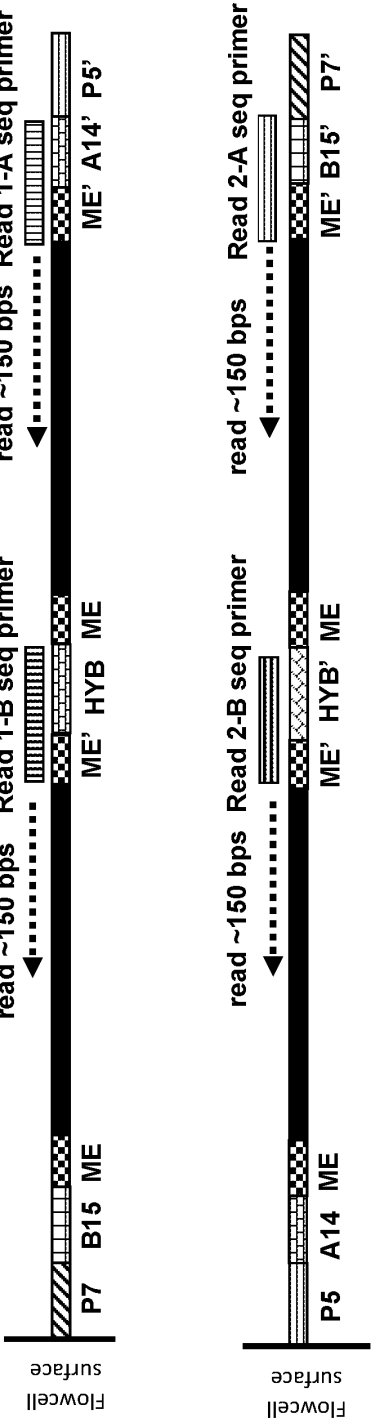
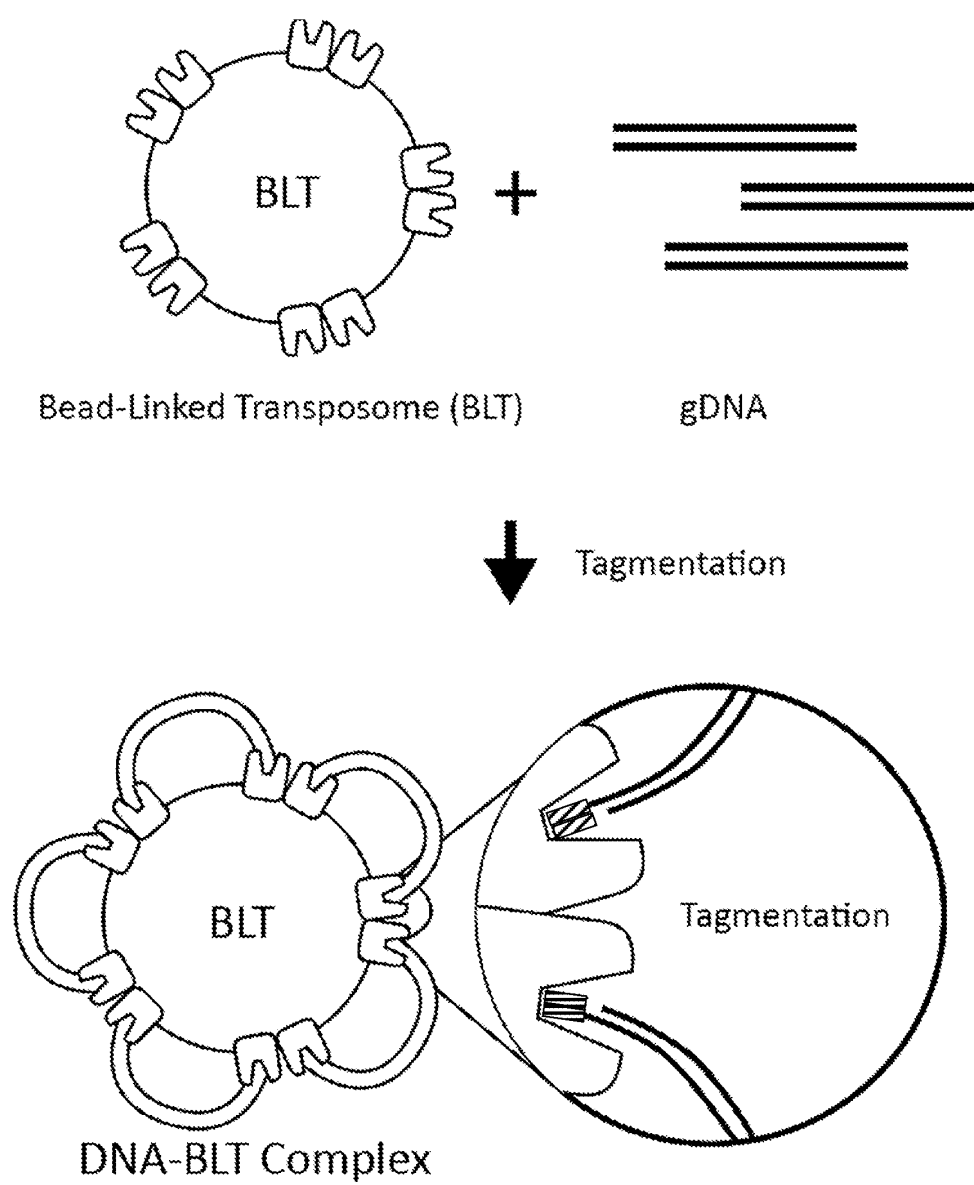
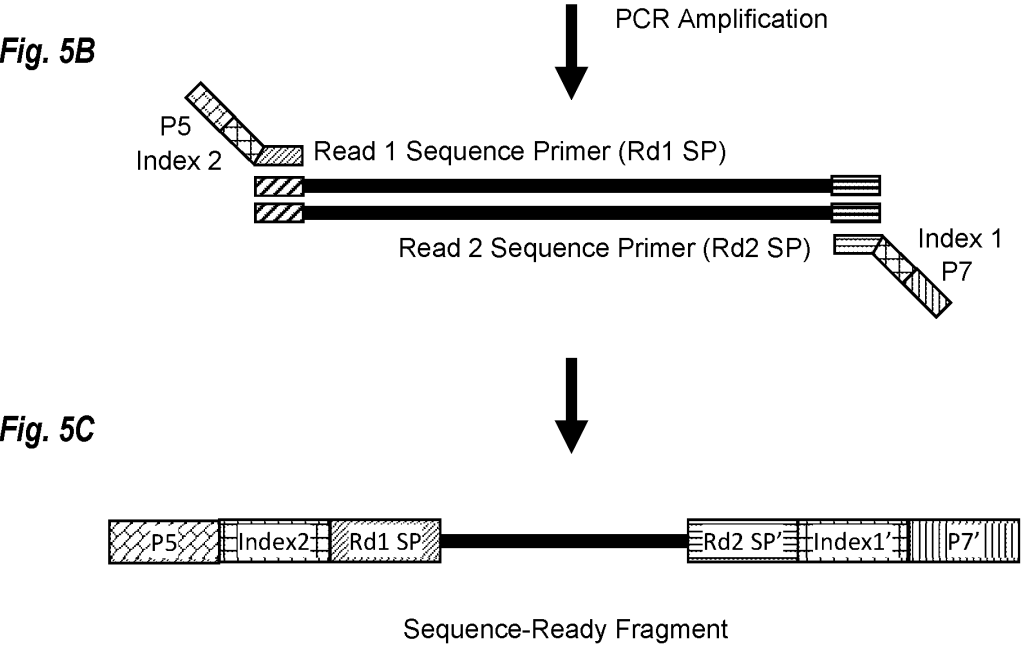


Fig. 4B

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*Fig. 5A*



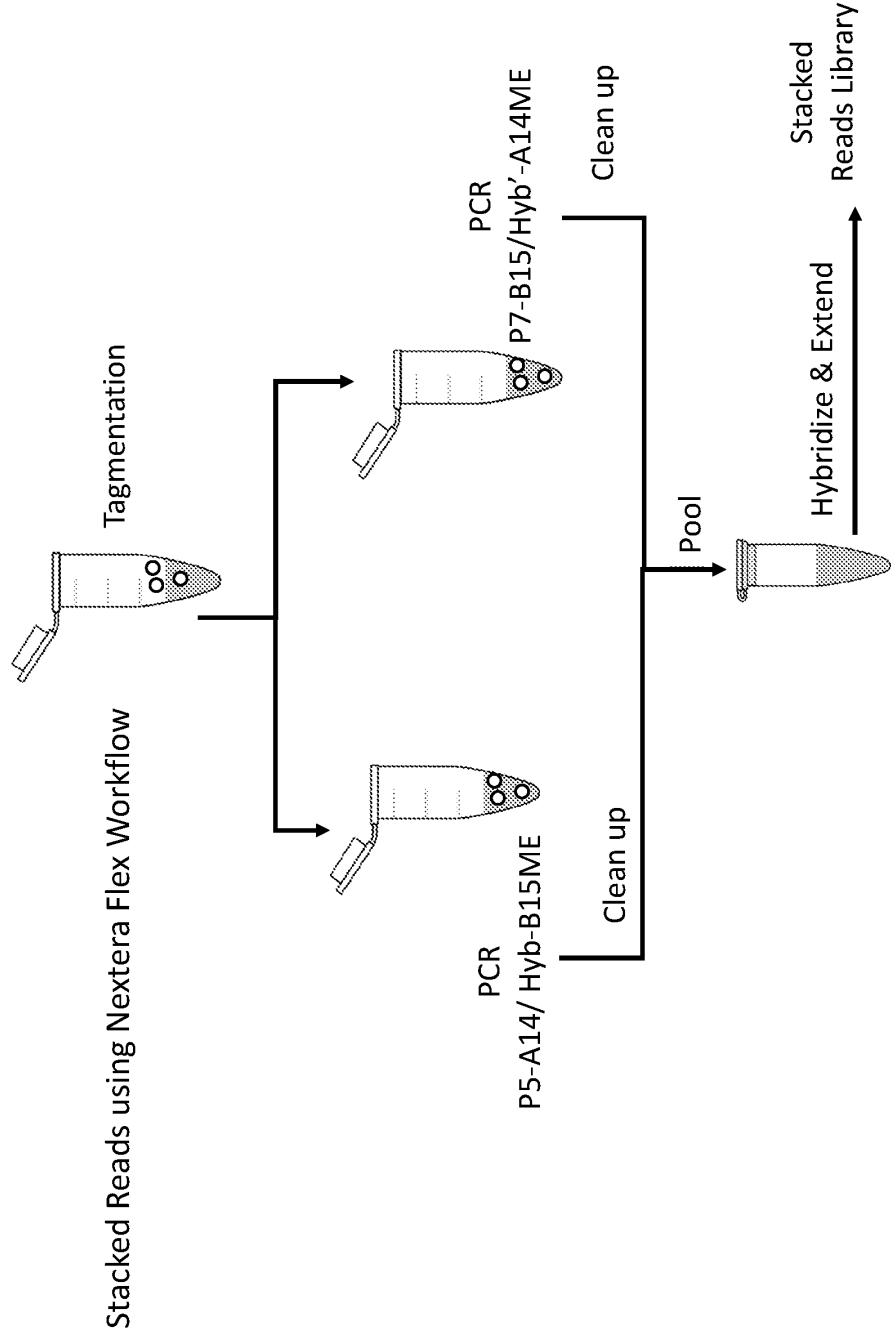


Fig. 6A

Tube1: PCR with P5-A14 & Hyb-B15

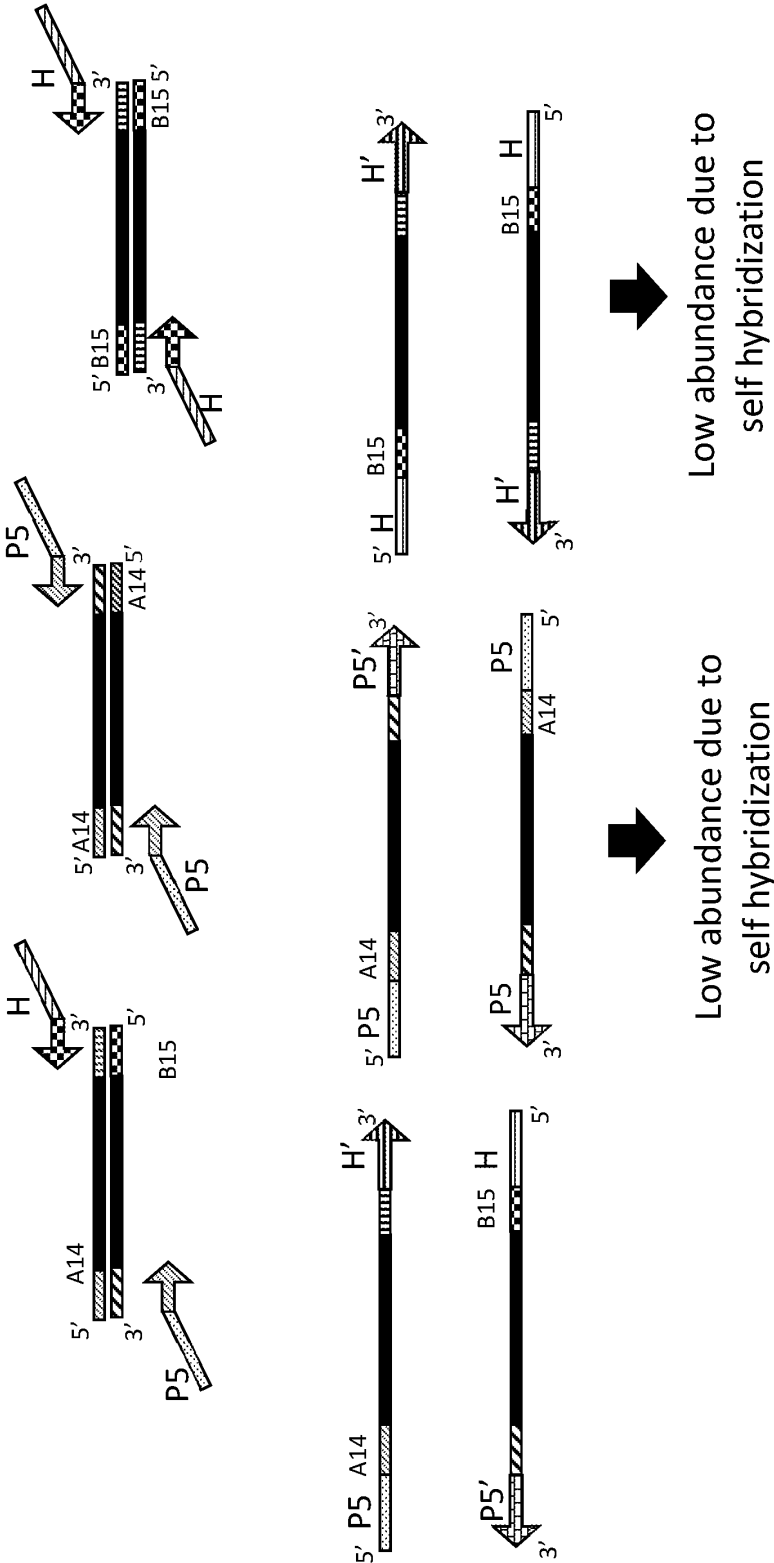


Fig. 6B

Tube2: PCR with P7-B15 & Hyb'-A14

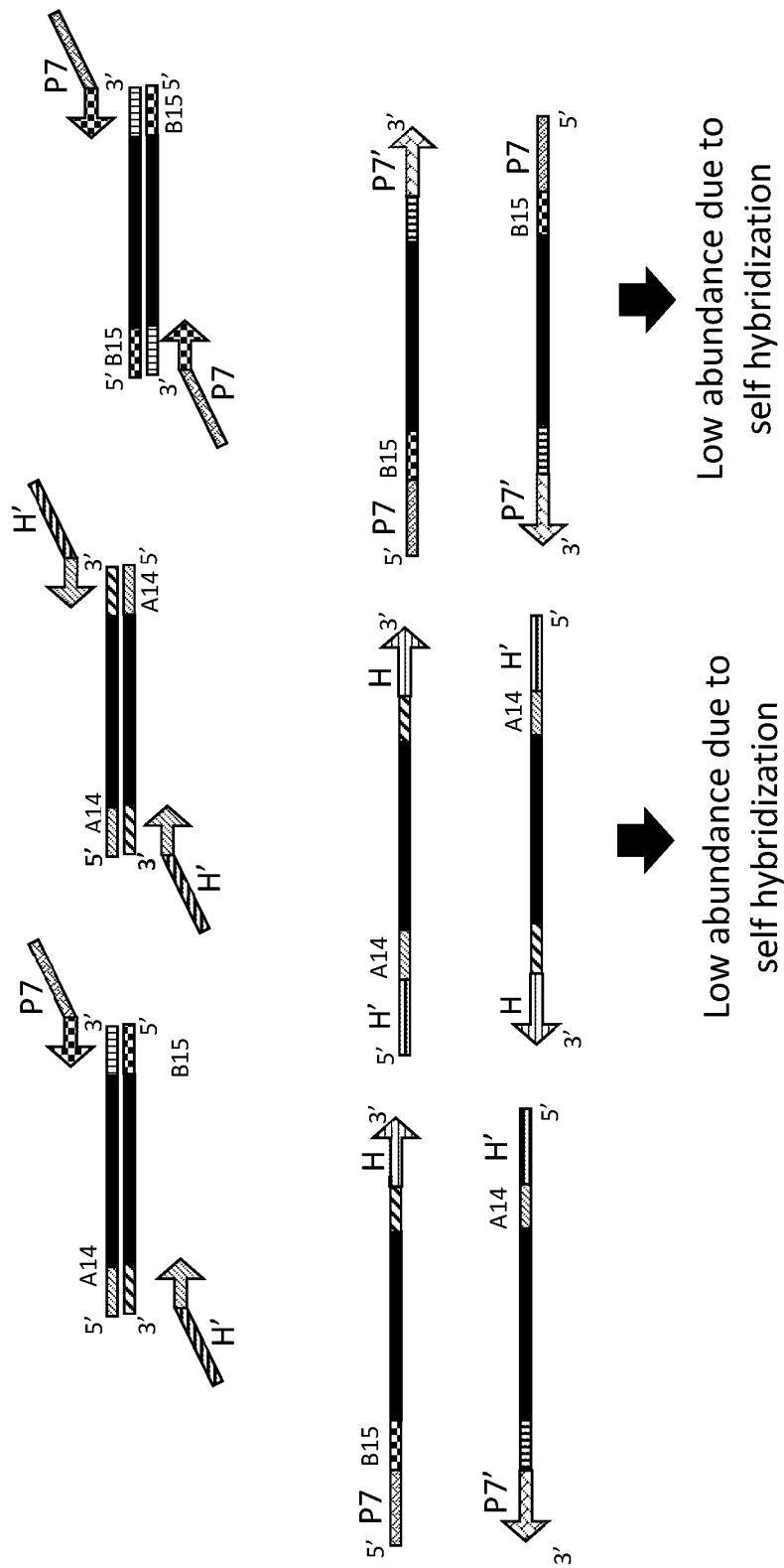


Fig. 6C

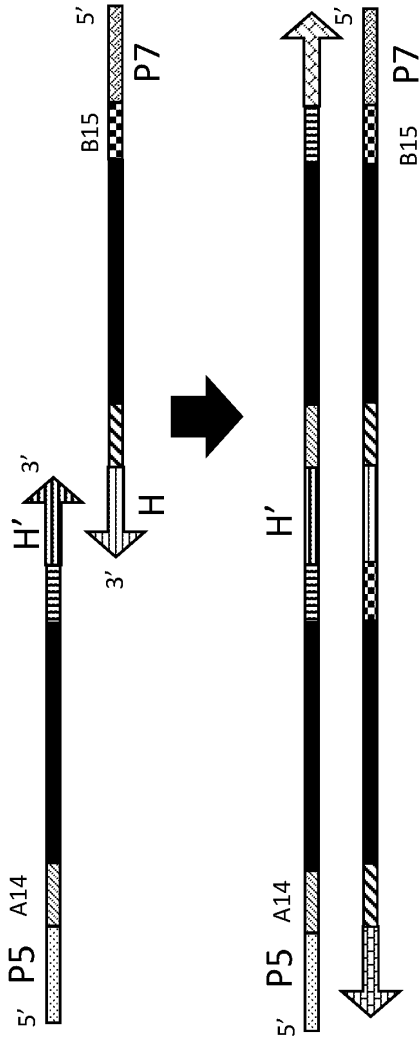


Fig. 6E

Tube 1 Tube 2

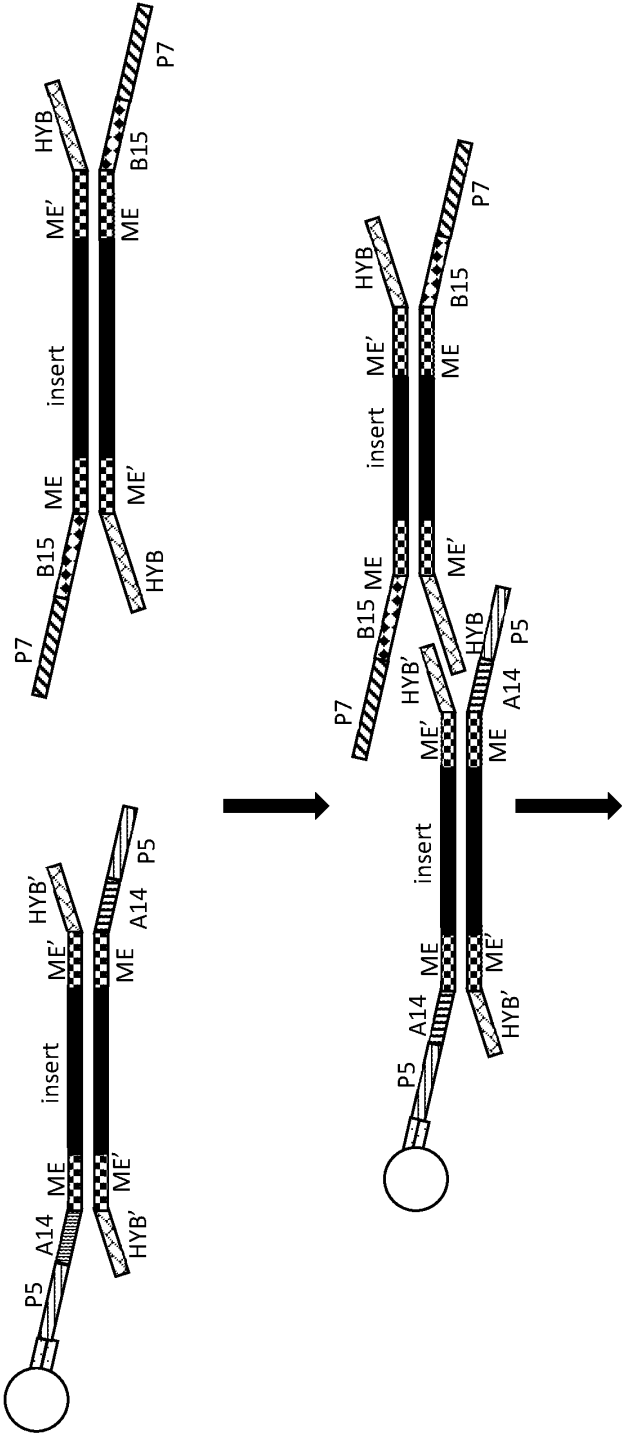


Fig. 7A

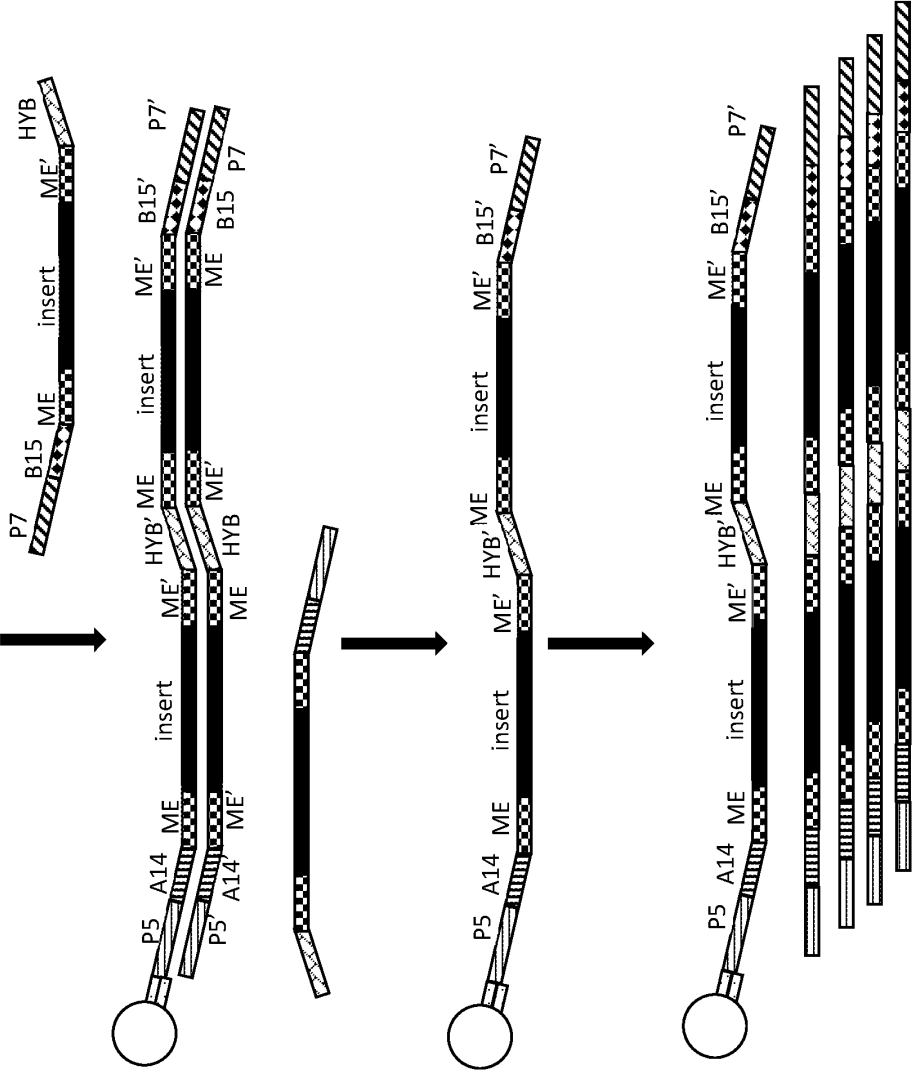


Fig. 7B

Tube 2

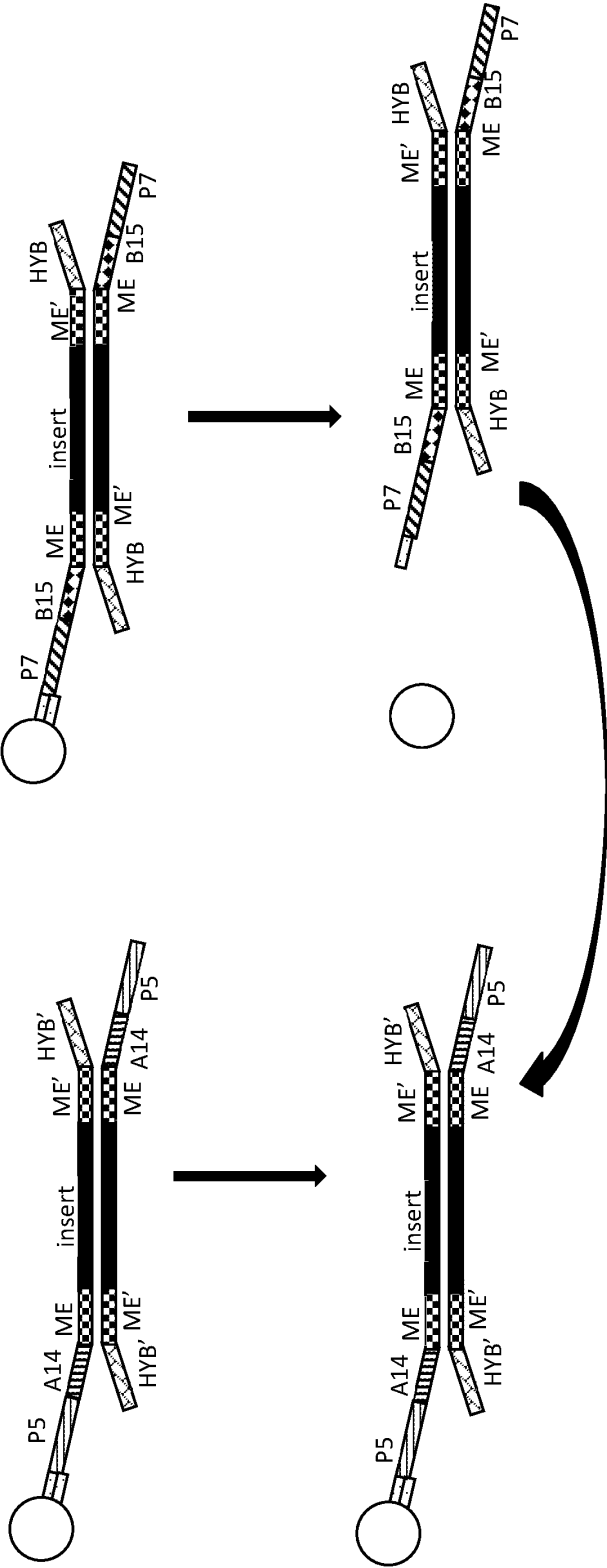


Fig. 8A

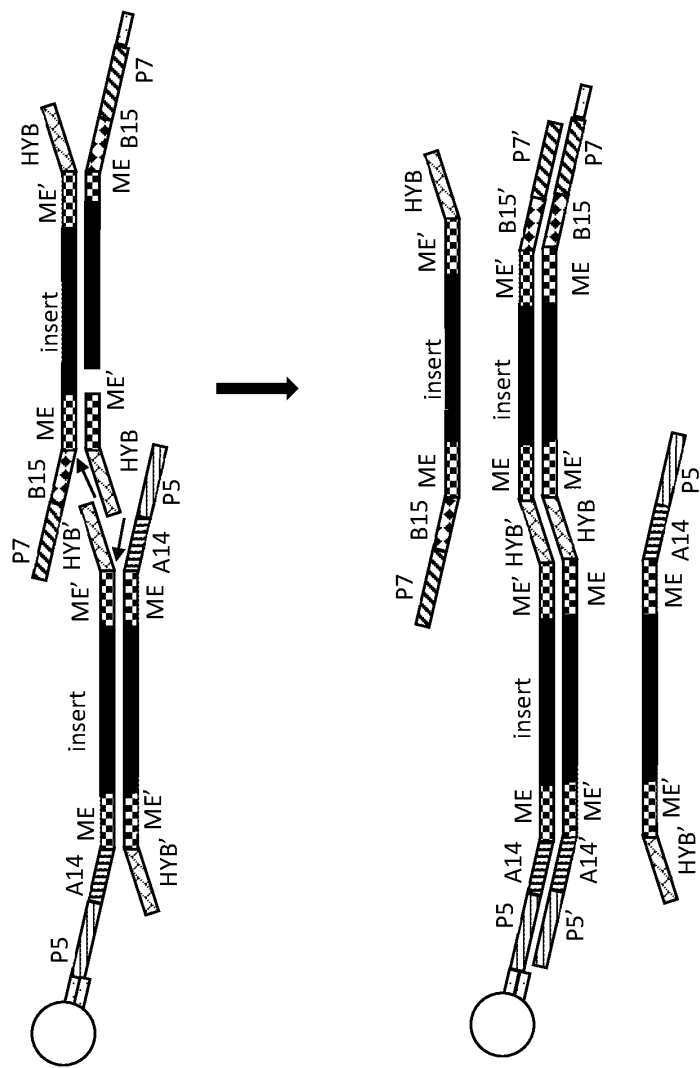


Fig. 8B

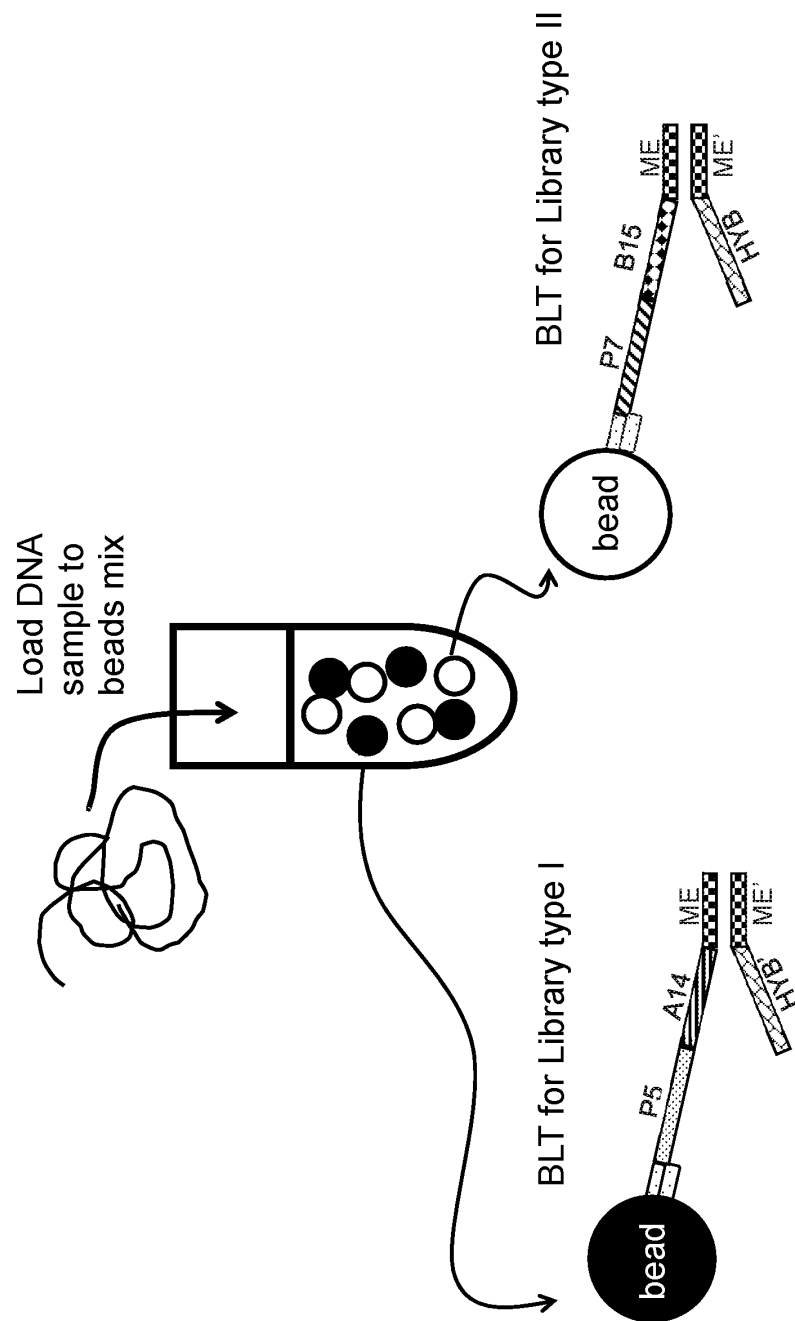
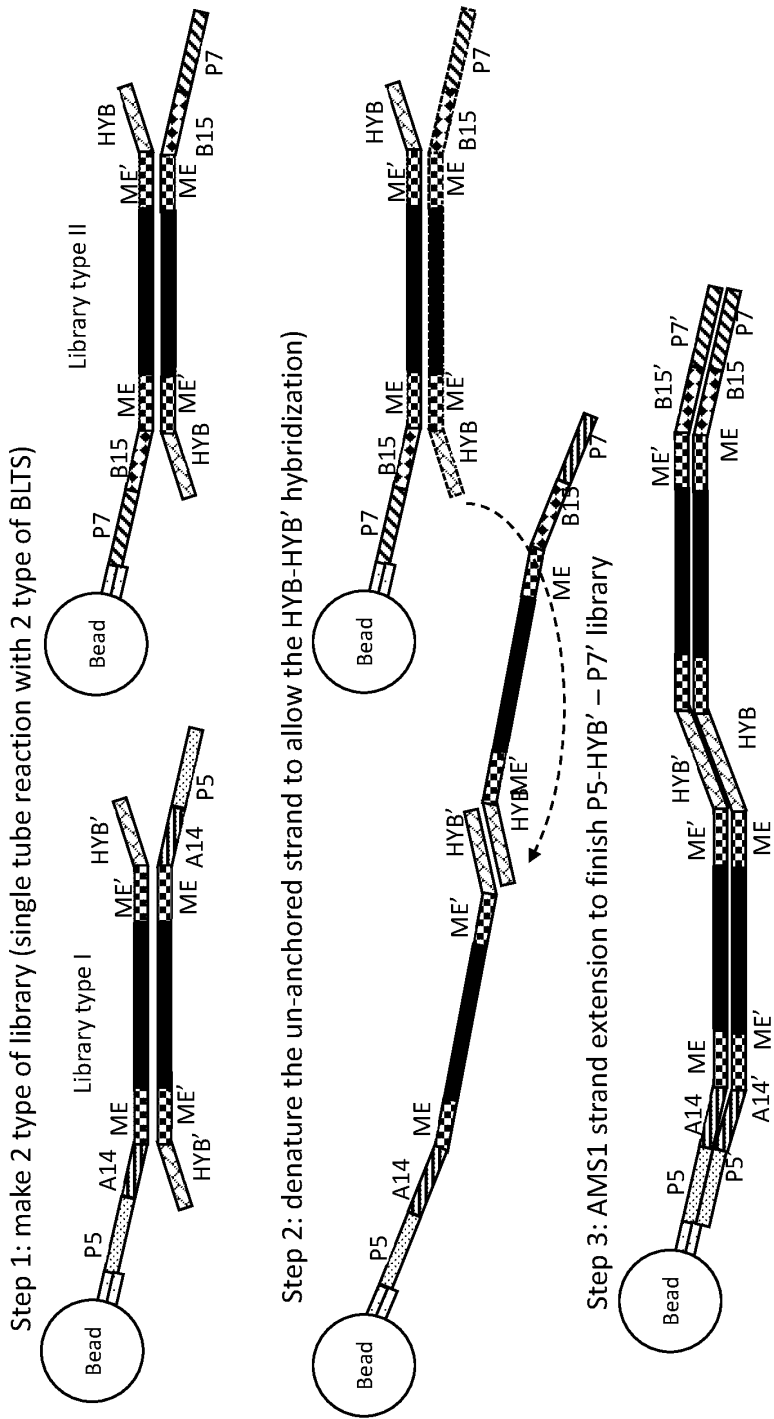
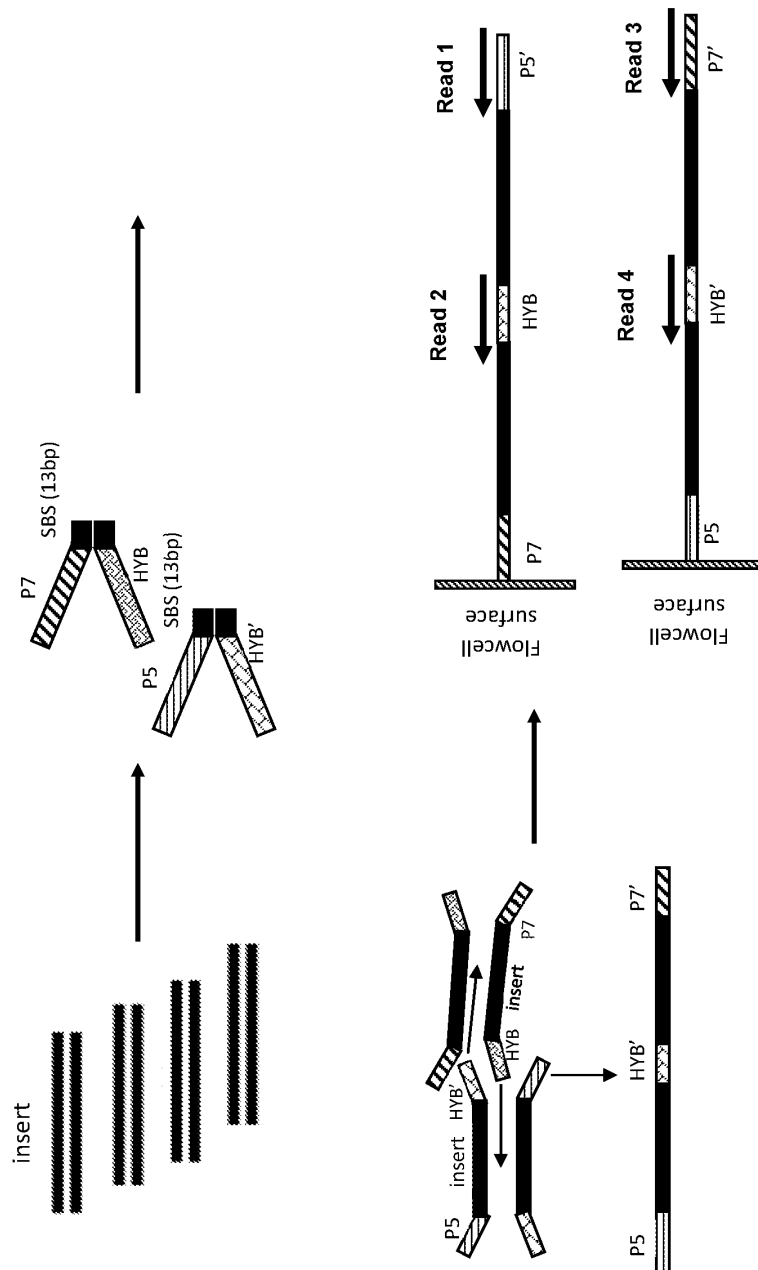


Fig. 9A





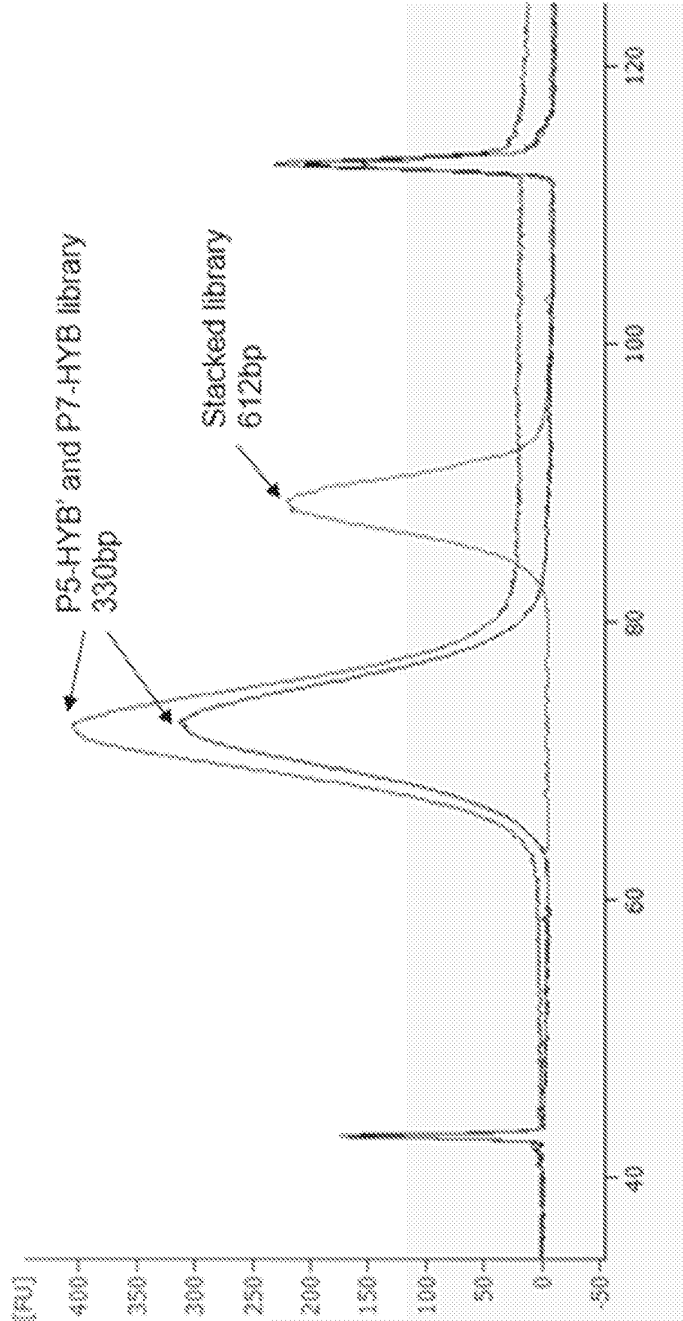


Fig. 11

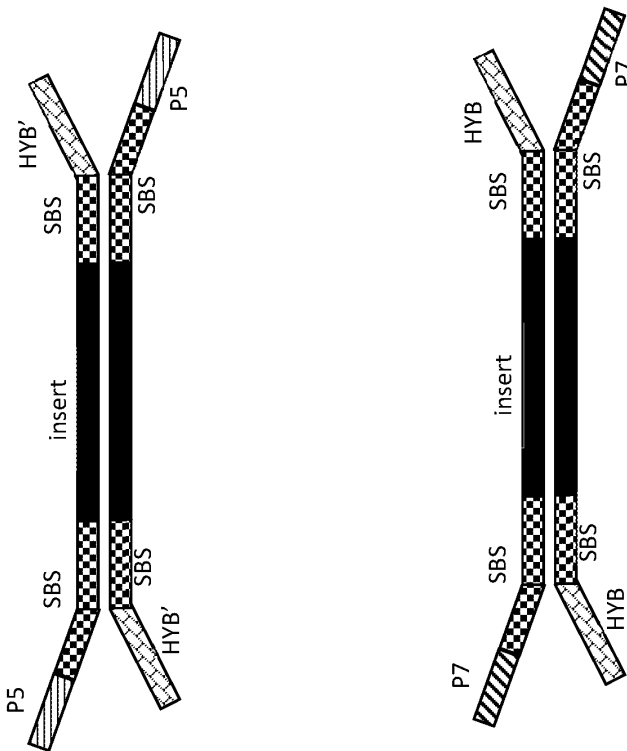


Fig. 12

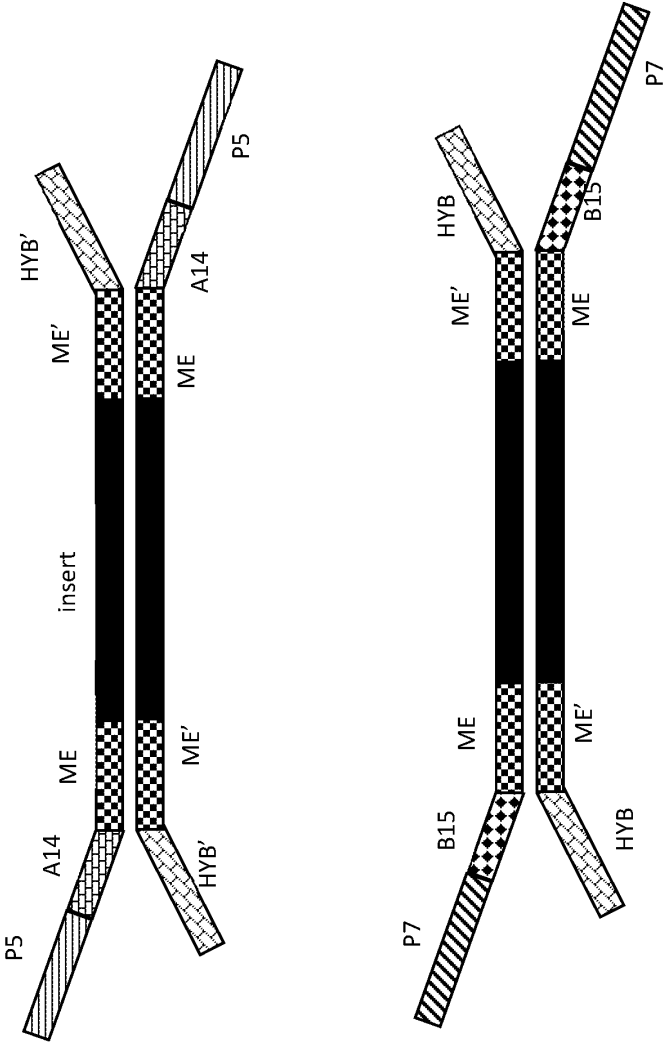


Fig. 13

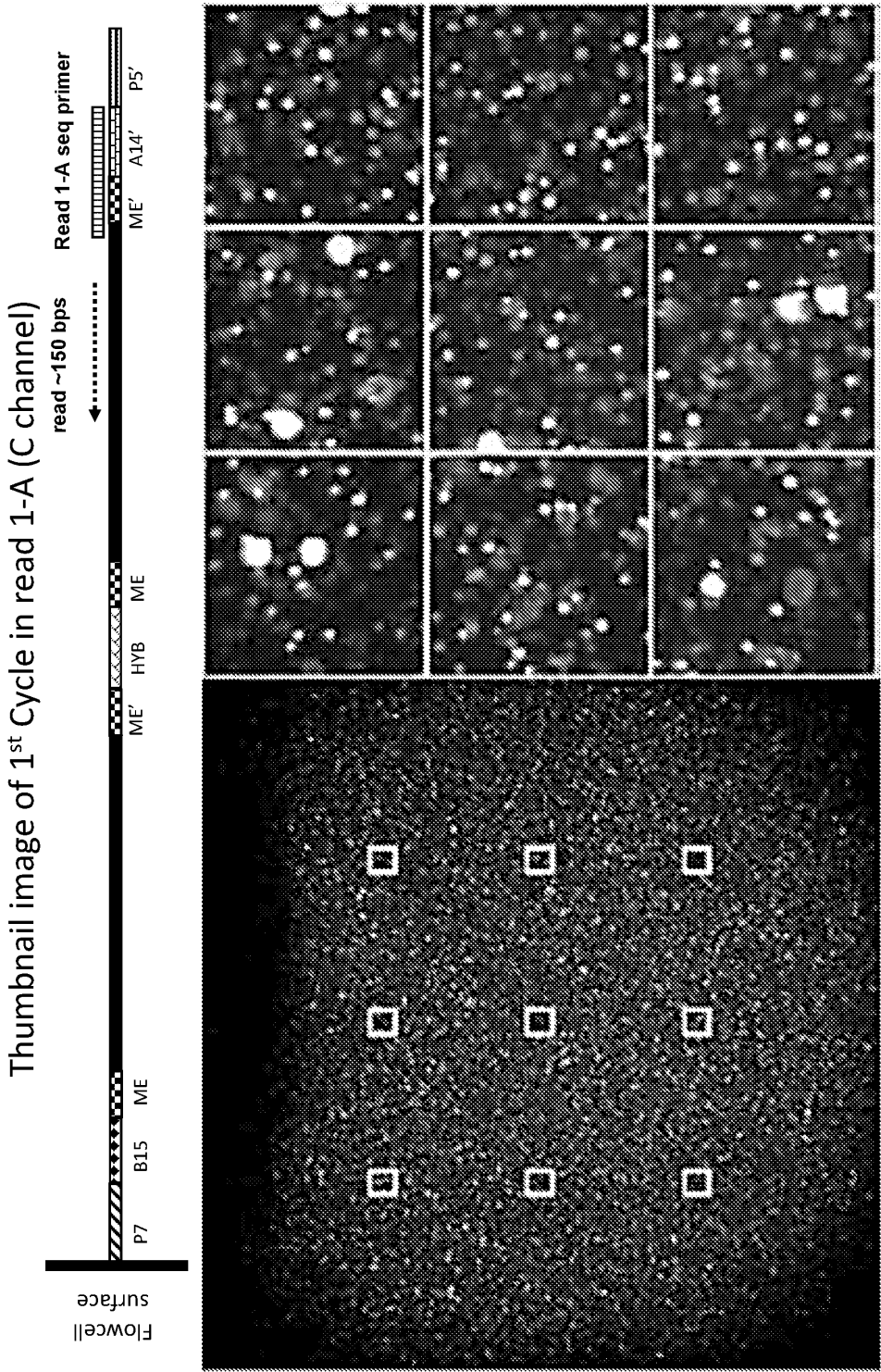


Fig. 14A

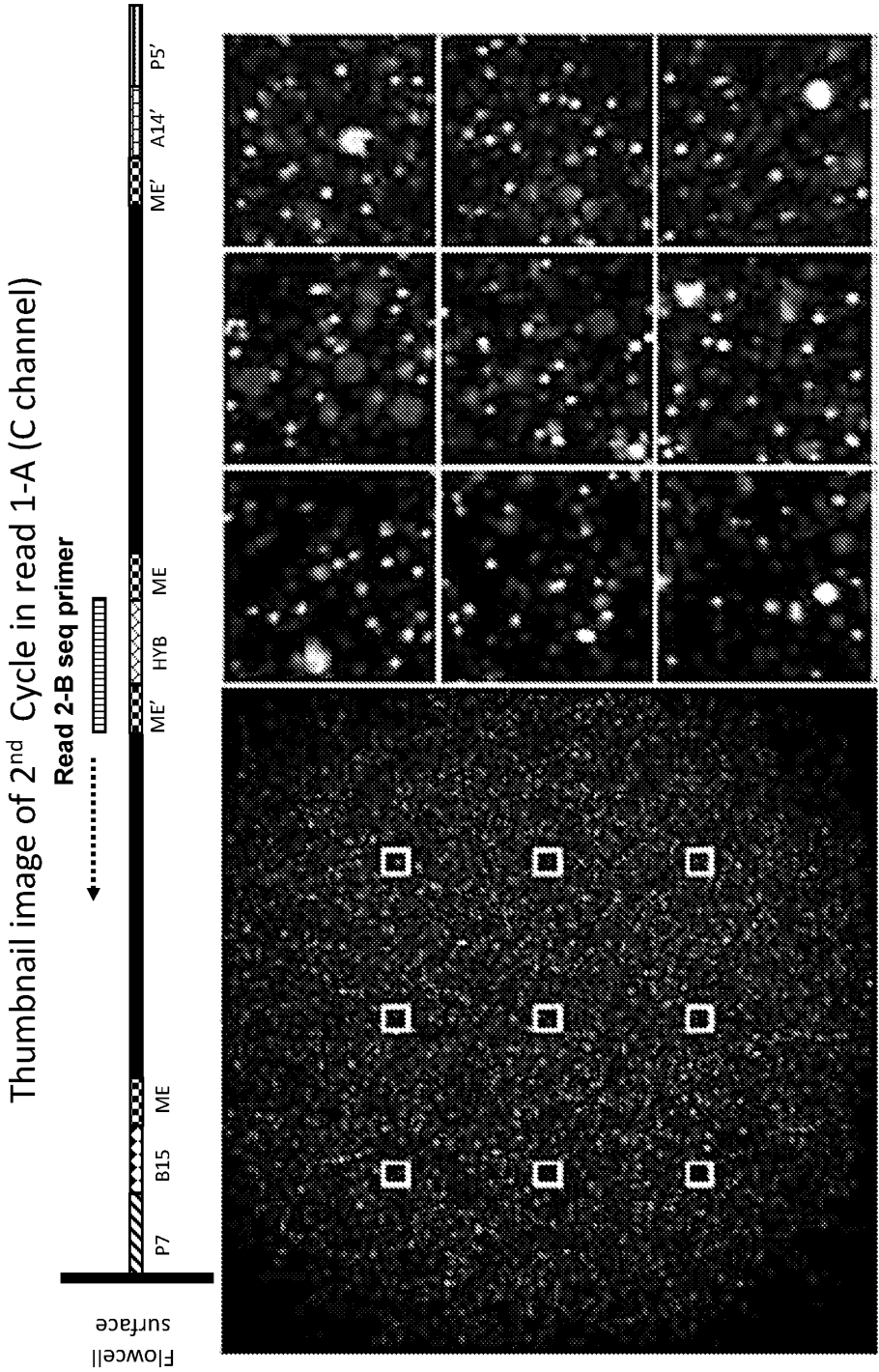


Fig. 14B

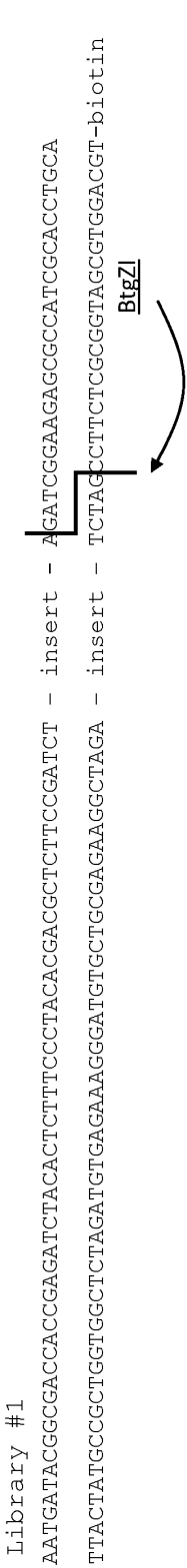


Fig. 15A

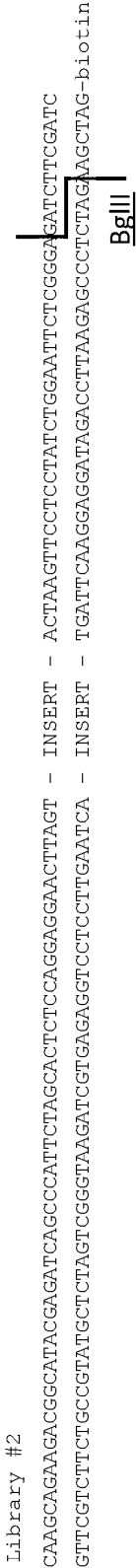


Fig. 15B

Library #1 cut with BtgZI
AATGATACGGCGACCAACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT - insert - A
TTACTATGCCGCTGGTGGCTCTAGATGTGAGAAAGGATGTGCTGCCGAGAAGGCTAGA - insert - TCTAG

Fig. 15C

Library #2 cut with BglII
CAAGCAGAAGACGGCATACGAGATCAGGCCATTTAGCACTCTCCAGGAGGAACCTTAGT - INSERT - ACTAAGTTTCCTCCTATCTGGAATTCTCGGGA
GTTCCGTTCTTCTGCGGTATGCTCTAGTCGGGTAAGATCGTGAGAGGTCCTCCTTGAATCA - INSERT - TGATTCAAGGAGGATAGACCTTTAAGAGCCCTCTAG

Fig. 15D

P5 (SEQ ID NO: 28)

TAATCATAGGGGAGCAACGGGGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT - insert - AGATCTCCCGAGAAATCCAGATAGGAGGAACTTAGT - INSERT - ACTAAGTTTCCTCCTGAGAGTGTCTAGATGGGCTGATCTCGTATGCCGCTCTTCTGCTTG
TTACTATGCCGCTGGTGGCTCTAGATGTGAGAAAGGATGTGCTGCCGAGAAGGCTAGA - insert - TCTAGAGGCTCTTAAGGTCTATCCTCCTTGAATCA - INSERT - TCATTCAAGGAGGACCTCTCAGCATCTTACCCGACTAG**AGCATAGGGGAGCAACGGG**AAC

P7 (SEQ ID NO: 29)

Fig. 15E

Sequence with 4 sequencing primers:

Read 1: ACACTCTTTCCCTACACGACGCTCTTCCGATCT (SEQ ID NO: 32)	Read 2: GATCTCCCGAGAAATCCAGATAGGAGGAACCTTAGT (SEQ ID NO: 33)
Read 3: CAGCCCATTTAGCACTCTCCAGGAGGAACTTAGT (SEQ ID NO: 34)	Read 4: ACTAAGTTTCCTCCTATCTGGAATTCTCGGGAGATCT (SEQ ID NO: 35)

Fig. 15F

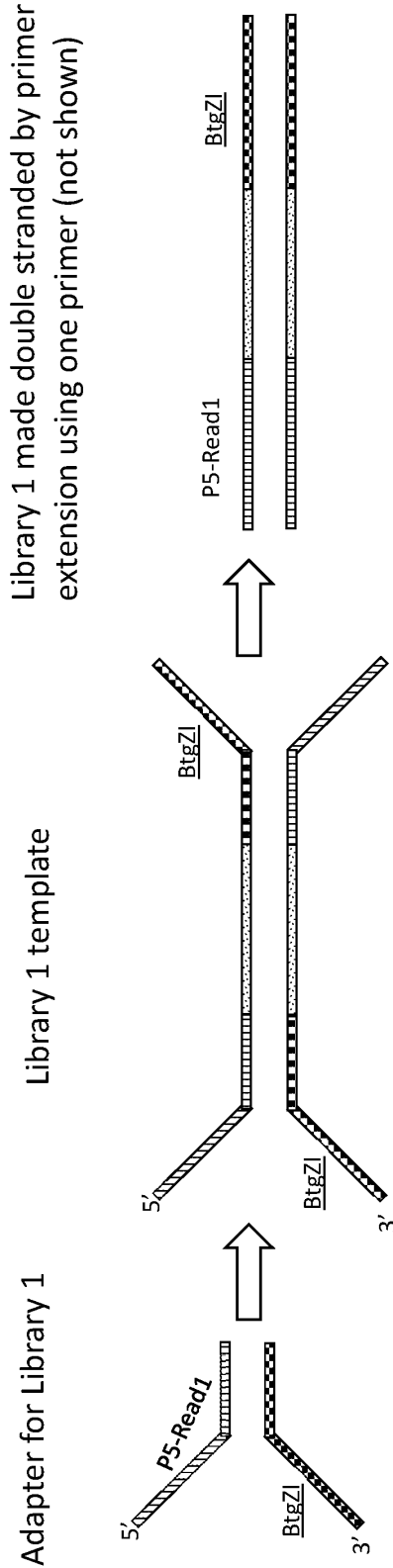


Fig. 16A

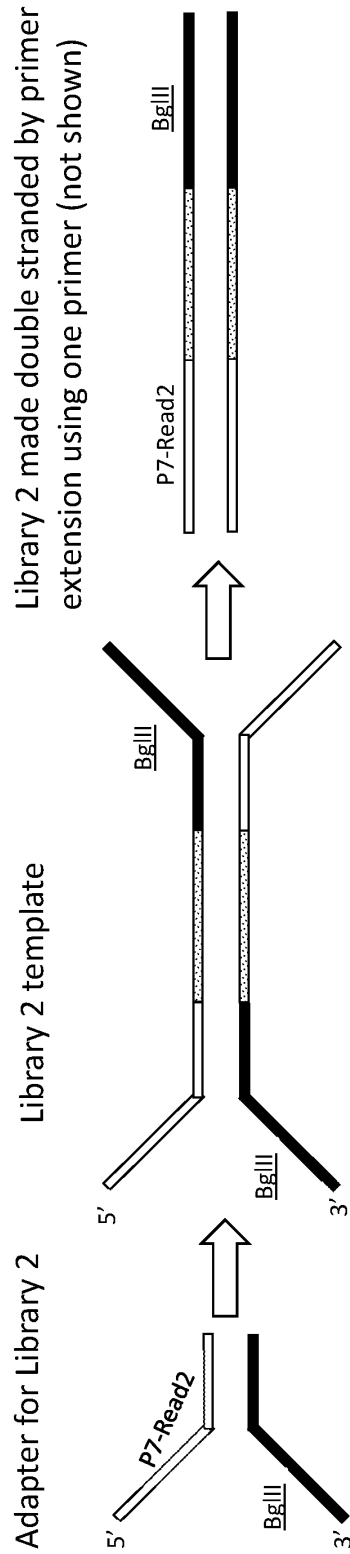


Fig. 16B

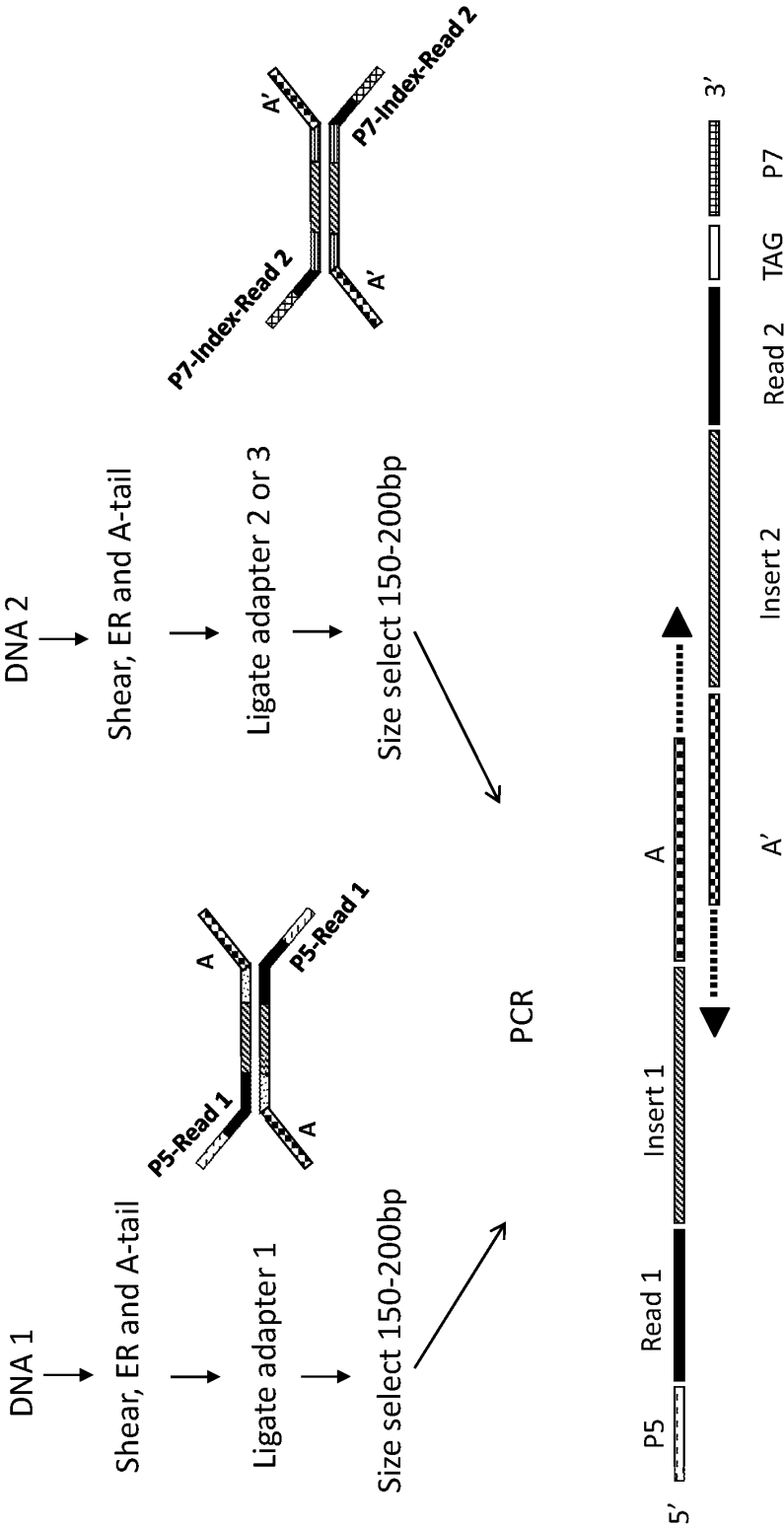


Fig. 17

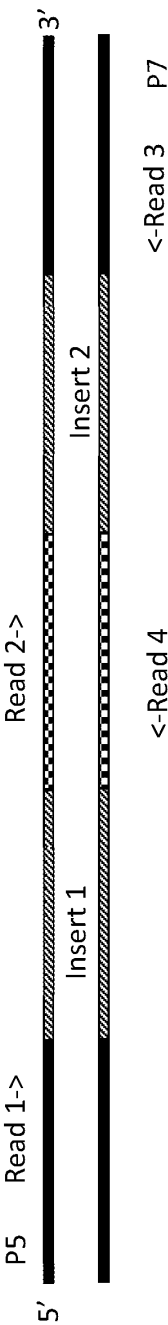


Fig. 18

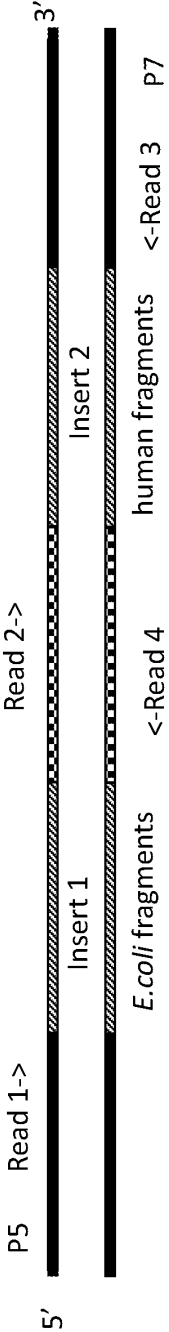


Fig. 19

Read 1

Lane Info		Tile Mean +/- SD for Lane									
Lane	Lane Yield (kbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 20 c (PF)	% PF Clusters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)		
1	74535	112929 +/- 1909	103521 +/- 1620	110 +/- 4	82.05 +/- 11.84	91.67 +/- 0.58	96.63 +/- 0.00	131.46 +/- 3.02	0.37 +/- 0.45		
2	180790	331470 +/- 4245	264313 +/- 4748	105 +/- 3	78.84 +/- 3.27	79.74 +/- 1.27	96.57 +/- 0.00	131.73 +/- 0.62	0.18 +/- 0.06		
3	161603	389111 +/- 10199	236380 +/- 31053	118 +/- 8	76.98 +/- 6.65	60.61 +/- 6.88	0.02 +/- 0.01	0.02 +/- 0.00	0.42 +/- 0.23		
4	141	105856 +/- 2931	281 +/- 81	-34 +/- 74	-126.20 +/- 426.40	0.27 +/- 0.07	100.00 +/- 0.00	602.89 +/- 297.27	67.20 +/- 1.59		
5	74266	149274 +/- 30430	108576 +/- 48786	149 +/- 56	81.12 +/- 50.26	75.49 +/- 35.39	87.26 +/- 29.73	133.72 +/- 62.64	0.89 +/- 1.63		
6	72857	150688 +/- 23208	119047 +/- 37323	104 +/- 27	88.03 +/- 29.08	80.23 +/- 23.71	70.30 +/- 22.05	67.55 +/- 24.57	1.07 +/- 1.94		
7	167435	348612 +/- 12098	273587 +/- 4834	123 +/- 21	89.23 +/- 25.92	78.57 +/- 3.18	79.17 +/- 2.52	77.55 +/- 2.94	0.28 +/- 0.01		
8	146367	372290 +/- 14304	203287 +/- 27183	105 +/- 8	71.64 +/- 7.79	54.43 +/- 5.41	0.07 +/- 0.00	0.07 +/- 0.02	0.38 +/- 0.10		

Fig. 20A

Read 2

Lane Info		Tile Mean +/- SD for Lane									
Lane	Lane Yield (bases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 2 nd (PF)	% PE Clusters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)		
1	60100	110056 +/- 1692	83472 +/- 22759	166 +/- 7	62.45 +/- 13.19	75.87 +/- 20.71	94.96 +/- 4.61	127.22 +/- 10.84	0.59 +/- 0.80		
2	183984	319311 +/- 5128	255534 +/- 4254	159 +/- 3	61.46 +/- 5.09	80.03 +/- 0.88	96.87 +/- 0.00	133.45 +/- 0.49	0.17 +/- 0.00		
3	183126	385959 +/- 4785	234341 +/- 11634	166 +/- 13	58.42 +/- 4.93	65.90 +/- 2.86	0.03 +/- 0.00	0.04 +/- 0.02	0.32 +/- 0.14		
4	21484	106538 +/- 2842	33155 +/- 11462	853 +/- 125	3.09 +/- 0.52	30.98 +/- 10.39	100.00 +/- 0.00	14237.45 +/- 176.79	26.35 +/- 0.99		
5	95	117877 +/- 8020	147 +/- 38	34 +/- 13	123.43 +/- 11.33	0.12 +/- 0.03	0.00 +/- 0.00	0.00 +/- 0.00	0.00 +/- 0.00		
6	85061	143467 +/- 19045	118140 +/- 23639	162 +/- 22	55.07 +/- 6.97	82.54 +/- 13.57	78.54 +/- 19.03	70.96 +/- 18.20	0.66 +/- 0.84		
7	182535	337164 +/- 10287	268865 +/- 6688	168 +/- 22	59.56 +/- 6.41	79.18 +/- 1.99	84.10 +/- 0.53	77.26 +/- 0.93	0.36 +/- 0.03		
8	144640	349421 +/- 31102	200890 +/- 34825	138 +/- 14	62.01 +/- 7.14	57.15 +/- 5.75	0.07 +/- 0.01	0.06 +/- 0.00	0.48 +/- 0.12		

Fig. 20B

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Read 3

Lane Info		Tile Mean +/- SD for Lane							
Lane	Lane Yield (kbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 20 c (PF)	% PF Clusters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)
1	77565	128292 +/- 3448	107730 +/- 2564	101 +/- 4	80.00 +/- 3.71	83.99 +/- 1.31	91.70 +/- 0.92	125.30 +/- 2.92	0.18 +/- 0.32
2	137086	325690 +/- 4443	190397 +/- 11677	90 +/- 6	74.38 +/- 5.47	58.45 +/- 3.34	77.43 +/- 2.05	101.65 +/- 3.67	0.23 +/- 0.06
3	46825	352310 +/- 9555	118247 +/- 32749	91 +/- 5	67.24 +/- 22.74	33.47 +/- 8.78	0.01 +/- 0.00	0.01 +/- 0.00	0.69 +/- 1.06
4	41129	106923 +/- 2213	63470 +/- 6388	-11 +/- 1	1359.16 +/- 225.10	59.37 +/- 5.91	100.00 +/- 0.00	10013.81 +/- 292.49	24.17 +/- 0.58
5	207	24618 +/- 5066	302 +/- 86	46 +/- 10	96.54 +/- 35.88	1.25 +/- 0.38	0.81 +/- 0.62	0.15 +/- 0.13	3.88 +/- 2.96
6	97287	184609 +/- 22759	142332 +/- 26638	101 +/- 12	82.38 +/- 7.15	77.45 +/- 12.42	70.40 +/- 7.61	66.67 +/- 10.90	0.40 +/- 0.46
7	128045	338018 +/- 7625	197600 +/- 14894	100 +/- 7	81.52 +/- 4.94	58.52 +/- 4.98	62.68 +/- 2.54	59.66 +/- 2.90	0.34 +/- 0.08
8	62328	307775 +/- 50441	101844 +/- 41503	77 +/- 9	74.61 +/- 4.23	31.86 +/- 9.32	0.07 +/- 0.02	0.07 +/- 0.02	0.38 +/- 0.20

Fig. 20C

Read 4

Lane Info		Tile Mean +/- SD for Lane									
Lane	Lane Yield (kbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% Intensity after 20 cycles (PF)	% PF Clusters	% Aligns (PF)	Alignment Score (PF)	% Error Rate (PF)		
1	69406	118065 +/- 2047	96388 +/- 2510	118 +/- 5	81.50 +/- 1.84	81.64 +/- 1.10	93.20 +/- 0.60	126.46 +/- 3.98	0.16 +/- 0.08		
2	143999	293042 +/- 4033	198999 +/- 7935	110 +/- 6	75.91 +/- 3.15	68.23 +/- 1.56	86.76 +/- 0.87	116.57 +/- 1.71	0.15 +/- 0.02		
3	122590	531234 +/- 7381	170264 +/- 19950	112 +/- 3	74.34 +/- 3.70	51.31 +/- 5.03	0.01 +/- 0.00	0.01 +/- 0.00	0.15 +/- 0.15		
4	20907	103648 +/- 2548	30567 +/- 20615	18 +/- 3	5144.84 +/- 800.87	29.71 +/- 20.13	99.95 +/- 0.16	33529.50 +/- 43913.11	51.11 +/- 3.32		
5	277	18755 +/- 2204	385 +/- 49	45 +/- 19	95.54 +/- 9.33	2.09 +/- 0.38	0.00 +/- 0.00	0.00 +/- 0.00	0.00 +/- 0.00		
6	86461	165635 +/- 17968	126405 +/- 22234	112 +/- 20	87.22 +/- 16.52	76.36 +/- 10.24	72.90 +/- 10.68	69.62 +/- 14.27	0.38 +/- 0.42		
7	140617	302315 +/- 8847	195302 +/- 11294	118 +/- 9	76.88 +/- 3.27	64.62 +/- 3.62	69.62 +/- 1.73	67.27 +/- 2.00	0.29 +/- 0.01		
8	91034	283247 +/- 42869	126437 +/- 28717	97 +/- 4	71.91 +/- 5.35	44.18 +/- 4.10	0.07 +/- 0.02	0.07 +/- 0.00	0.35 +/- 0.15		

Fig. 20D

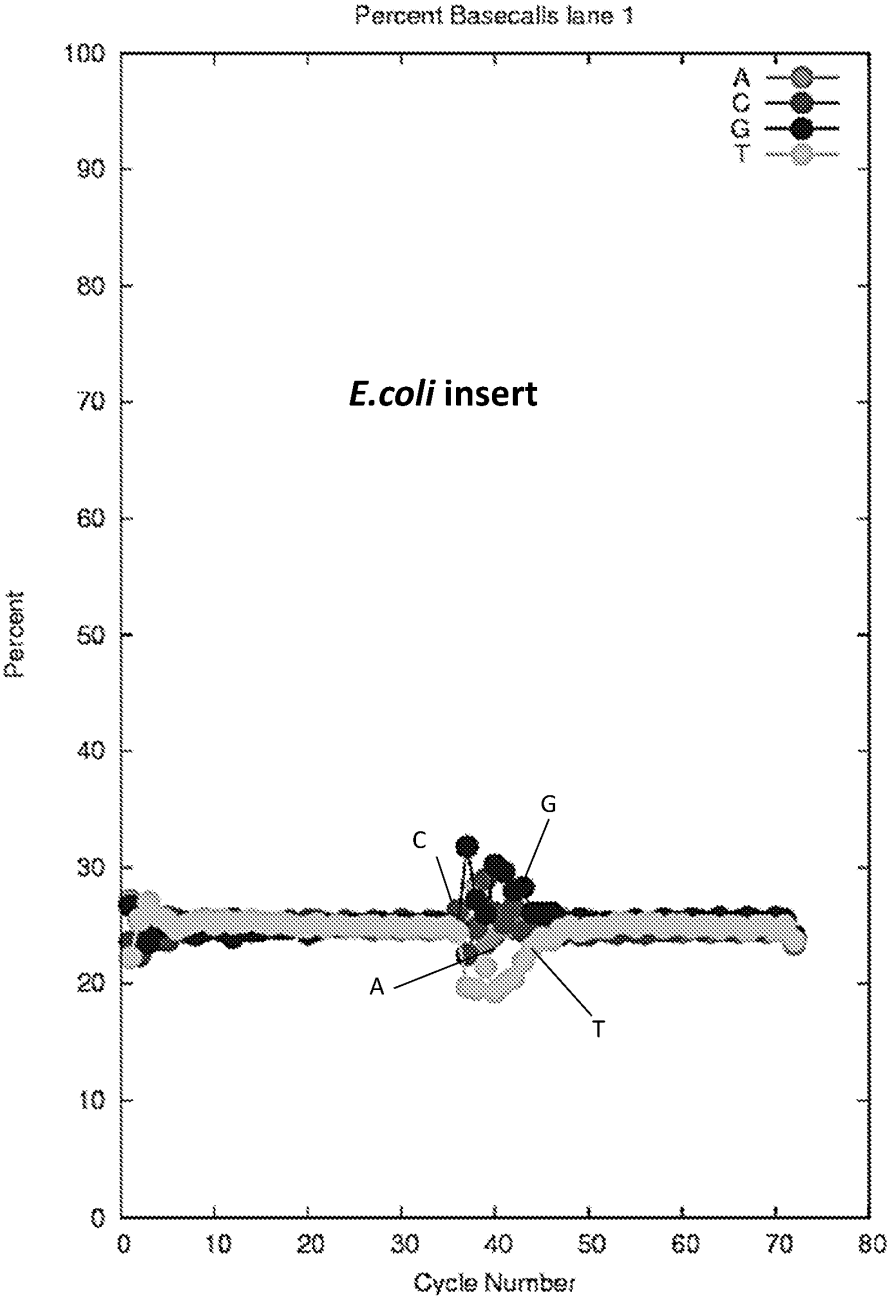


Fig. 21A

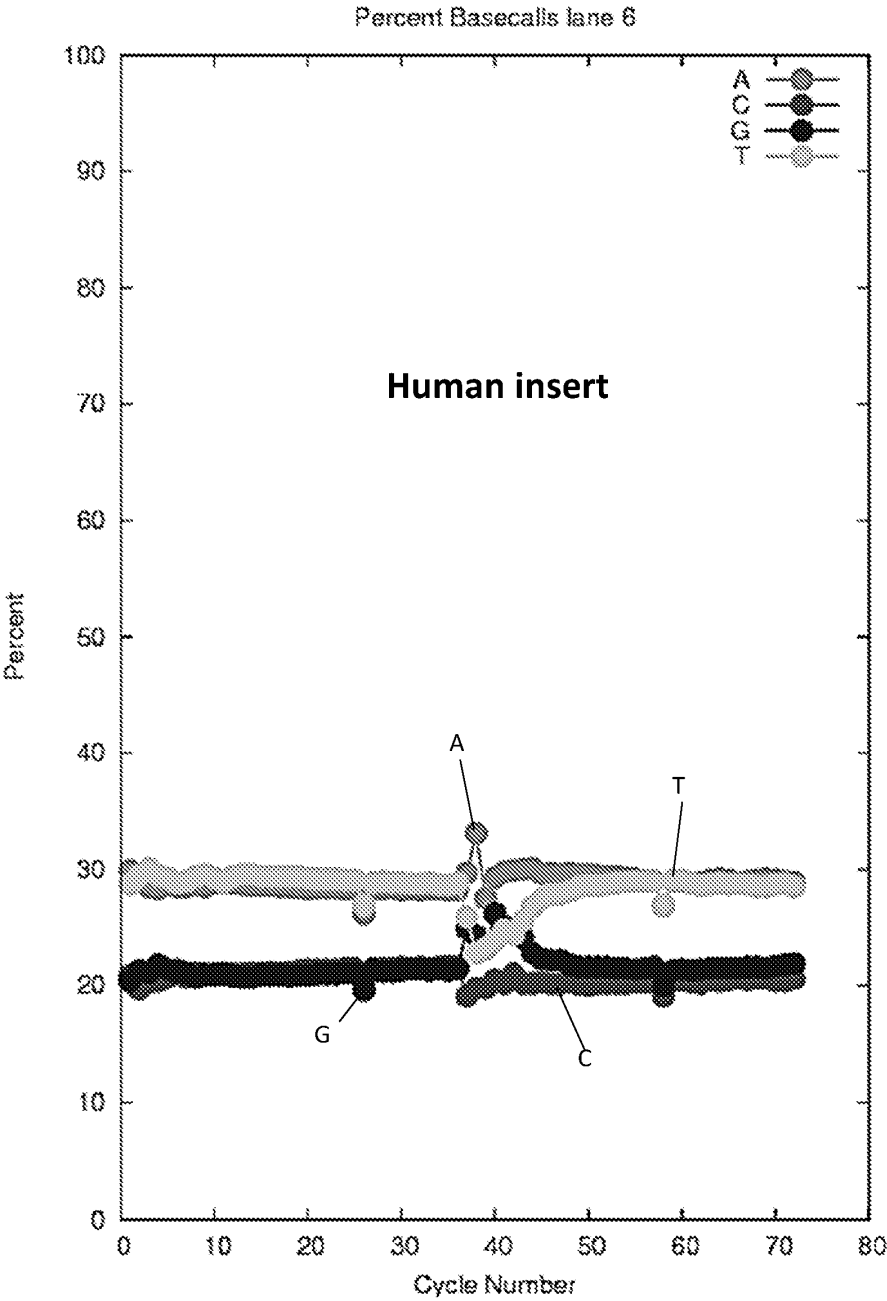


Fig. 21B

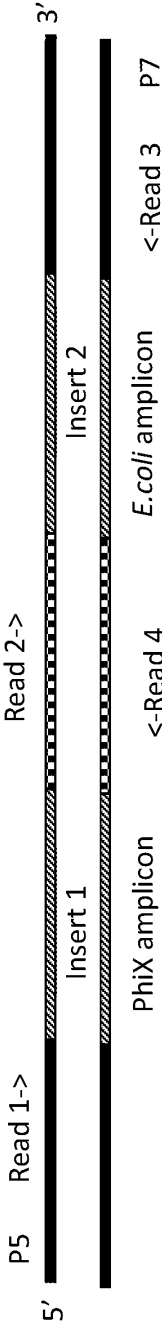


Fig. 22

Read 1

Lane	Lane Yield (kbases)	Clusters (mv)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 20 cycles (PF)	% PF Characters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)
1	37920	57046 +/- 4164	54172 +/- 4521	122 +/- 5	94.33 +/- 3.99	94.93 +/- 0.97	100.00 +/- 0.00	10249.09 +/- 193.35	0.61 +/- 0.08
2	36958	55718 +/- 7501	52798 +/- 7703	127 +/- 5	99.95 +/- 2.84	94.58 +/- 1.49	100.00 +/- 0.23	10077.26 +/- 469.52	0.67 +/- 0.34
3	42864	64285 +/- 3184	61235 +/- 3093	123 +/- 6	101.55 +/- 5.62	95.25 +/- 0.40	100.00 +/- 0.00	10252.58 +/- 146.36	0.53 +/- 0.08
4	41286	62760 +/- 4235	58980 +/- 4274	117 +/- 6	105.66 +/- 5.48	93.94 +/- 0.91	100.00 +/- 0.00	9723.29 +/- 273.11	0.90 +/- 0.32
5	38495	60098 +/- 5630	54993 +/- 4715	122 +/- 8	85.91 +/- 1.99	91.61 +/- 2.74	100.00 +/- 0.18	5694.21 +/- 563.24	0.46 +/- 0.25
6	37669	57976 +/- 9576	53813 +/- 9201	136 +/- 9	81.27 +/- 3.06	92.69 +/- 1.23	100.00 +/- 0.00	10077.70 +/- 452.54	0.57 +/- 0.13
7	35329	54511 +/- 8061	50470 +/- 7911	136 +/- 7	81.70 +/- 3.67	92.45 +/- 1.14	100.00 +/- 0.00	9845.79 +/- 417.49	0.52 +/- 0.05
8	29786	46838 +/- 9525	42552 +/- 9242	148 +/- 16	82.86 +/- 4.64	90.57 +/- 1.97	100.00 +/- 0.17	9162.10 +/- 334.63	0.73 +/- 0.09

Fig. 23A

Read 2

Lane info		Tile Mean +/- SD for Lane							
Lane	Lane Yield (kbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 20 cycles (PF)	% PF Clusters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)
1	39856	57906 +/- 4103	55356 +/- 4272	40 +/- 4	83.89 +/- 4.73	95.55 +/- 0.85	100.00 +/- 0.00	9912.17 +/- 282.44	0.90 +/- 0.34
2	38882	56720 +/- 7175	54003 +/- 7514	40 +/- 4	84.36 +/- 9.82	95.03 +/- 1.73	100.00 +/- 0.19	9759.08 +/- 554.21	0.93 +/- 0.39
3	44651	64824 +/- 2999	62016 +/- 2863	40 +/- 3	83.51 +/- 5.52	95.67 +/- 0.77	100.00 +/- 0.00	10134.23 +/- 210.54	0.81 +/- 0.14
4	42521	64081 +/- 3655	59056 +/- 3907	38 +/- 3	82.25 +/- 5.17	92.12 +/- 1.50	100.00 +/- 0.00	9214.93 +/- 376.06	1.19 +/- 0.33
5	1026	63151 +/- 4506	1425 +/- 966	7 +/- 3	117.60 +/- 11.28	2.29 +/- 1.57	97.90 +/- 8.20	4640427.55 +/- 2722747.85	43.33 +/- 0.46
6	39675	56350 +/- 8713	55104 +/- 8869	50 +/- 5	41.34 +/- 3.34	94.23 +/- 1.76	100.00 +/- 0.00	10338.53 +/- 611.21	0.63 +/- 0.22
7	37365	55351 +/- 7582	51896 +/- 7714	48 +/- 5	41.86 +/- 3.42	93.59 +/- 1.41	100.00 +/- 0.00	10043.72 +/- 508.10	0.68 +/- 0.15
8	31578	48189 +/- 9306	43859 +/- 9172	52 +/- 7	41.09 +/- 5.43	90.76 +/- 1.75	100.00 +/- 0.00	9229.55 +/- 462.89	0.90 +/- 0.29

Fig. 23B

Read 3

Lane Info		Tile Mean +/- SD for Lane								
Lane	Lane Yield (kbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 20 cycles (PF)	% PF Clusters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)	
1	26168	57988 +/- 4059	36345 +/- 17502	21 +/- 9	96.43 +/- 5.21	61.63 +/- 29.07	100.00 +/- 0.00	8218.77 +/- 1250.82	9.49 +/- 4.83	
2	17024	57071 +/- 6625	23644 +/- 17796	12 +/- 4	99.39 +/- 7.20	40.74 +/- 29.50	100.00 +/- 0.00	190151.91 +/- 820690.07	14.81 +/- 14.45	
3	15684	63450 +/- 2382	21784 +/- 13742	9 +/- 1	100.10 +/- 5.78	34.40 +/- 21.62	100.00 +/- 0.00	198800.21 +/- 859823.01	17.88 +/- 17.59	
4	23891	65213 +/- 3211	33182 +/- 21201	15 +/- 7	98.14 +/- 14.95	50.74 +/- 32.05	100.00 +/- 0.00	5706.55 +/- 2881.33	19.49 +/- 19.95	
5	1324	64197 +/- 4244	1839 +/- 891	5 +/- 2	112.74 +/- 6.31	2.90 +/- 1.46	99.77 +/- 0.28	2846203.40 +/- 1164744.36	44.57 +/- 1.07	
6	1311	55995 +/- 6625	1822 +/- 1915	8 +/- 1	112.11 +/- 8.73	5.33 +/- 3.61	99.94 +/- 0.16	2365548.41 +/- 2813698.71	43.84 +/- 17.52	
7	625	55551 +/- 5696	869 +/- 427	9 +/- 1	113.12 +/- 8.65	1.56 +/- 0.68	97.46 +/- 7.41	441173.26 +/- 3039531.40	52.76 +/- 12.15	
8	2396	51193 +/- 9446	3328 +/- 4912	11 +/- 2	95.70 +/- 23.46	6.83 +/- 10.23	99.96 +/- 0.00	1853995.81 +/- 2230640.58	47.64 +/- 23.54	

Fig. 23C

Read 4

Lane Info		Tile Mean +/- SD for Lane									
Lane	Lane Yield (kbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% intensity after 28 cycles (PF)	% PF Clusters	% Align (PF)	Alignment Score (PF)	% Error Rate (PF)		
1	9340	55544 +/- 4509	12973 +/- 3855	10 +/- 1	91.45 +/- 4.87	23.34 +/- 6.36	100.00 +/- 0.09	8056.49 +/- 496.94	7.99 +/- 2.07		
2	13183	55833 +/- 6744	18309 +/- 5632	10 +/- 1	92.37 +/- 5.28	33.09 +/- 9.01	100.00 +/- 0.00	8091.30 +/- 505.65	6.18 +/- 1.76		
3	12498	59007 +/- 4014	17358 +/- 3991	9 +/- 0	94.69 +/- 4.19	29.23 +/- 5.70	100.00 +/- 0.00	8376.86 +/- 580.34	6.59 +/- 2.55		
4	14977	60103 +/- 4523	20802 +/- 5964	9 +/- 1	94.69 +/- 6.39	34.34 +/- 7.23	100.00 +/- 0.00	7551.35 +/- 807.49	8.38 +/- 4.03		
5	14836	60640 +/- 3820	20605 +/- 2816	9 +/- 1	94.62 +/- 5.68	34.04 +/- 4.55	100.00 +/- 0.22	3285.34 +/- 487.97	4.68 +/- 2.52		
6	11815	54940 +/- 7196	16410 +/- 3652	10 +/- 1	81.52 +/- 7.80	30.06 +/- 5.52	100.00 +/- 0.00	8319.21 +/- 705.41	5.08 +/- 1.95		
7	13023	53428 +/- 6036	18088 +/- 2447	10 +/- 1	79.88 +/- 5.90	34.49 +/- 7.50	100.00 +/- 0.00	8204.74 +/- 559.06	3.91 +/- 0.67		
8	12474	48977 +/- 7162	17325 +/- 4317	10 +/- 1	75.67 +/- 6.59	36.42 +/- 11.35	100.00 +/- 0.00	7410.45 +/- 783.98	4.81 +/- 1.55		

Fig. 23D

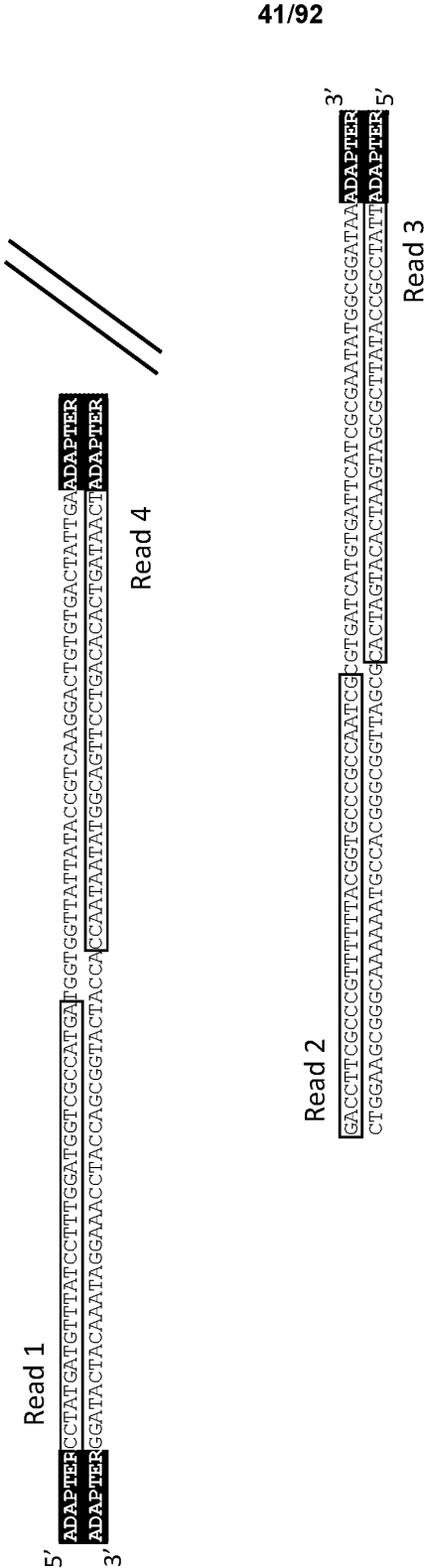


Fig. 24A

Rank	Count	Observed Read 1 sequences
1	39722	CCTATGATGTTTATCCTTTGGATGGTCGCCATGA
2	138	NCTATGATGTTTATCCTTTGGATGGTCGCCATGA
3	116	CCTATGATGTTTATCCTTTGGATGGCCGCCATGA
4	107	CCTATGATGTTTATCCTTTGGATGGTCTCCATGA
5	79	CCTATGATGTTTACCTTTGGATGGTCGCCATGA

Fig. 24B

Rank	Count	Observed Read 2 sequences
1	40882	GACCTTCGCCCGTTTTTACGGTGCCCGCCAAATCG
2	238	GACCTTCGCCCGTTTTTACGGTGCCCGCCACTCG
3	166	GACCTTCGCCCGTTTTTACGGTGCCCGCCAAATCGC
4	122	GGCCTTCGCCCGTTTTTACGGTGCCCGCCAAATCG
5	107	NACCTTCGCCCGTTTTTACGGTGCCCGCCAAATCG

Fig. 24C

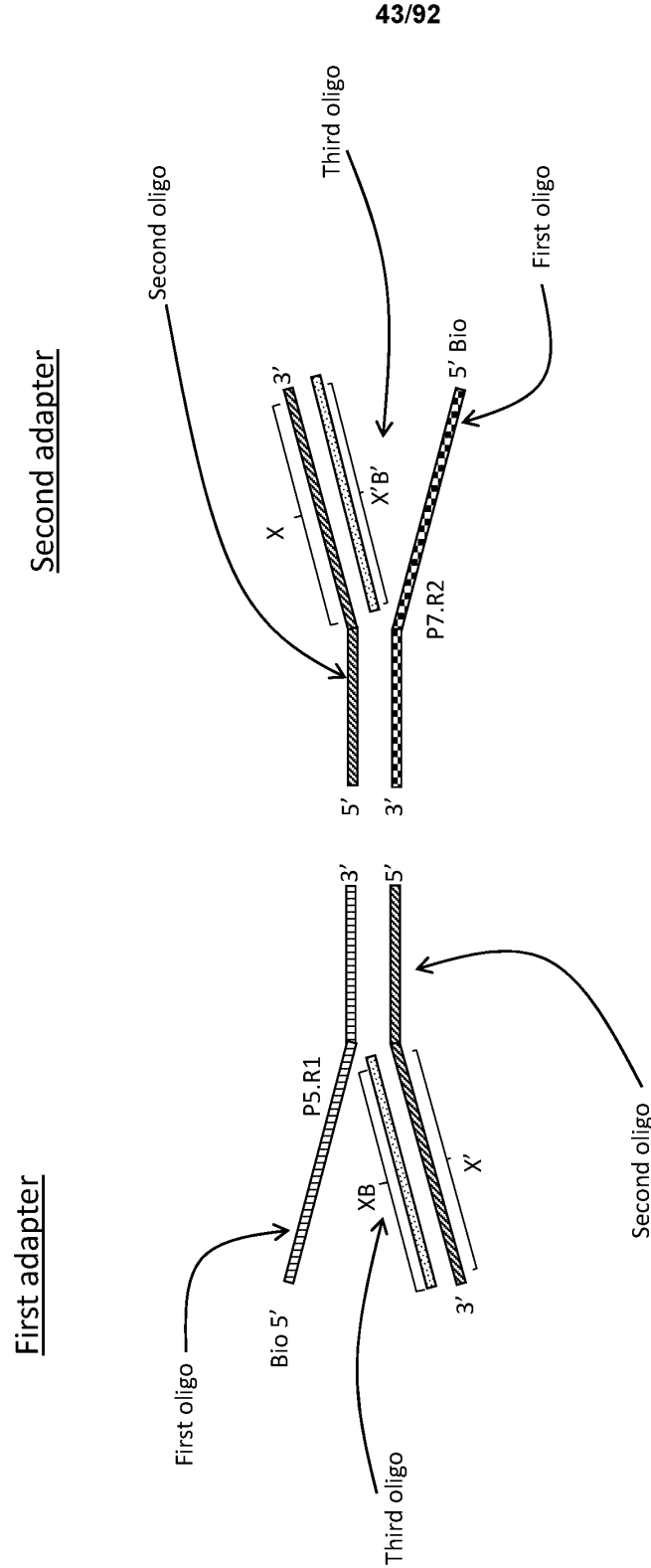


Fig. 25

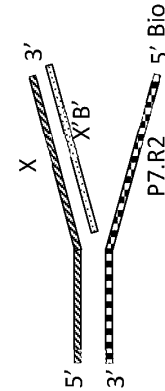


Fig. 26A

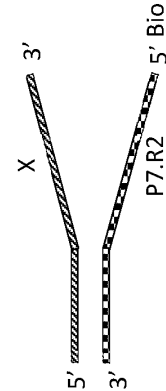


Fig. 26B

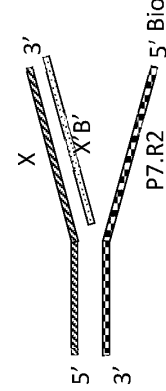
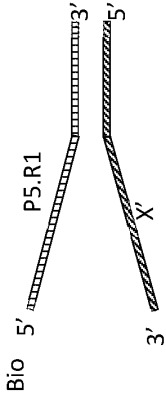
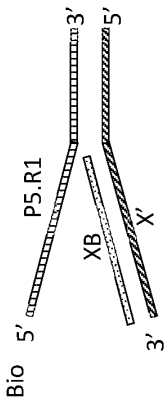
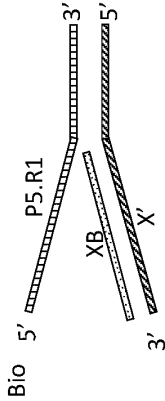


Fig. 26C



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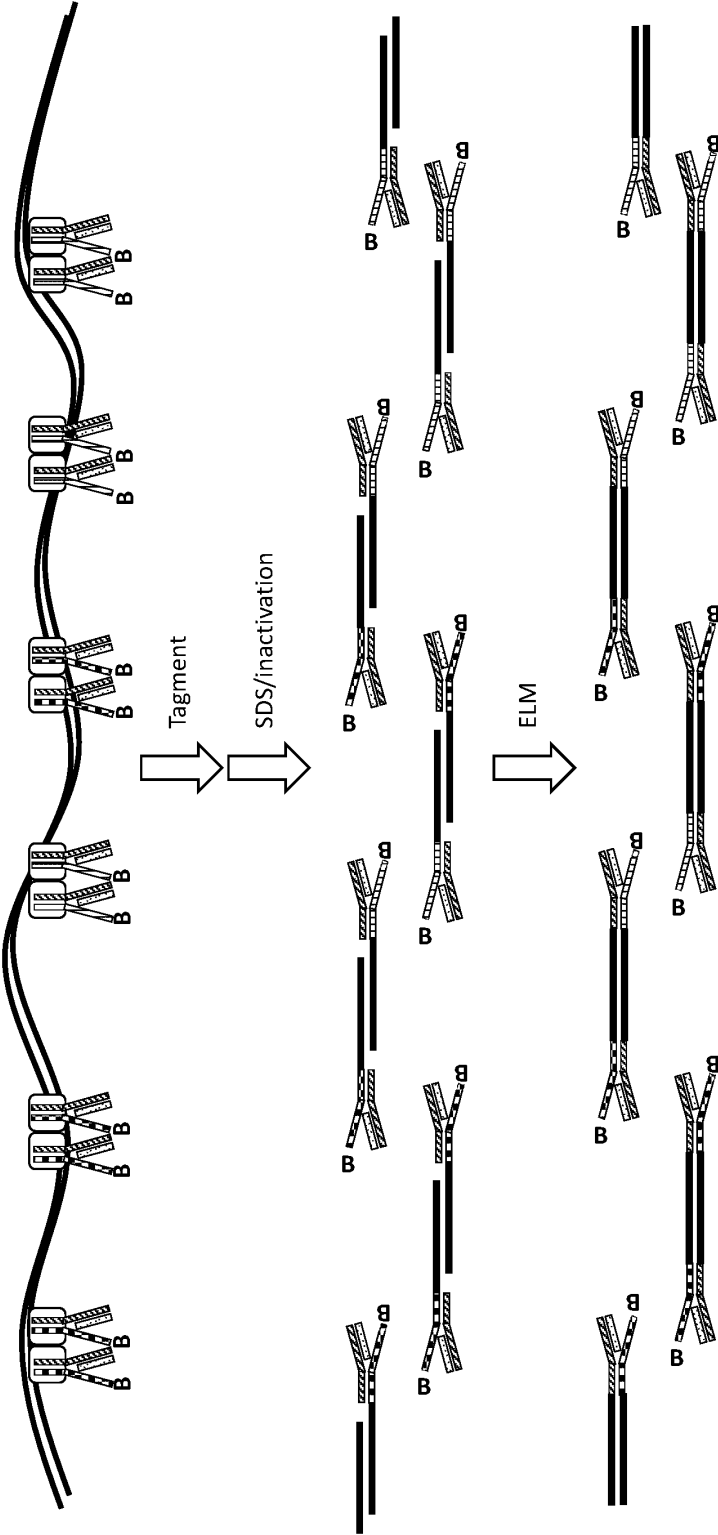


Fig. 26D

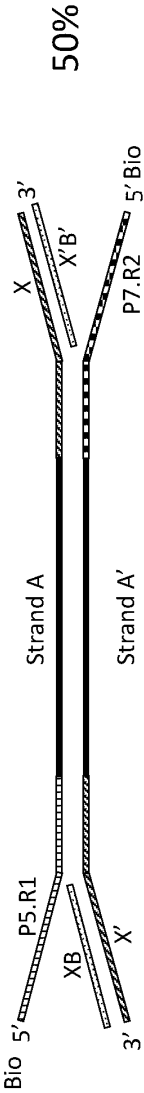


Fig. 27A

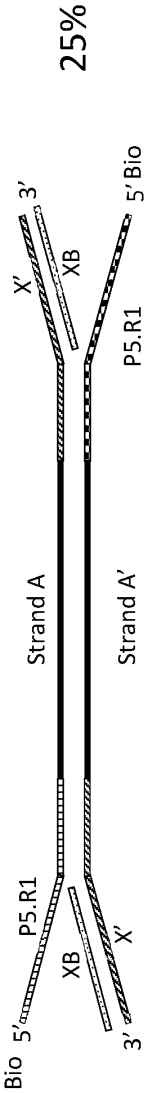


Fig. 27B

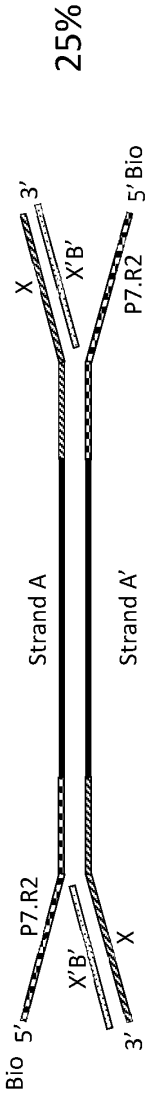


Fig. 27C

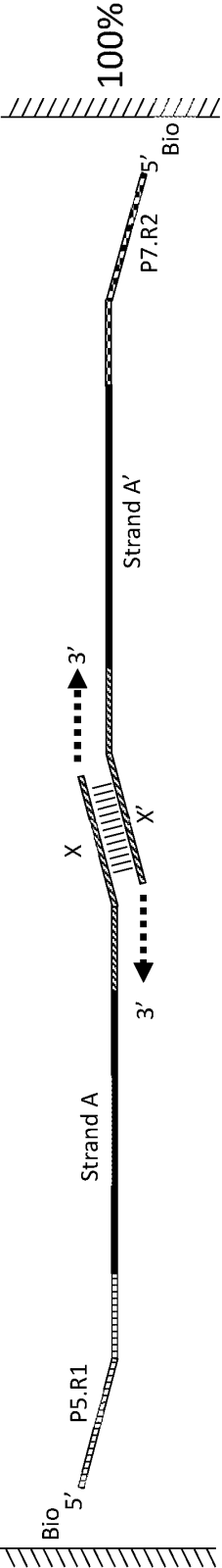


Fig. 28A

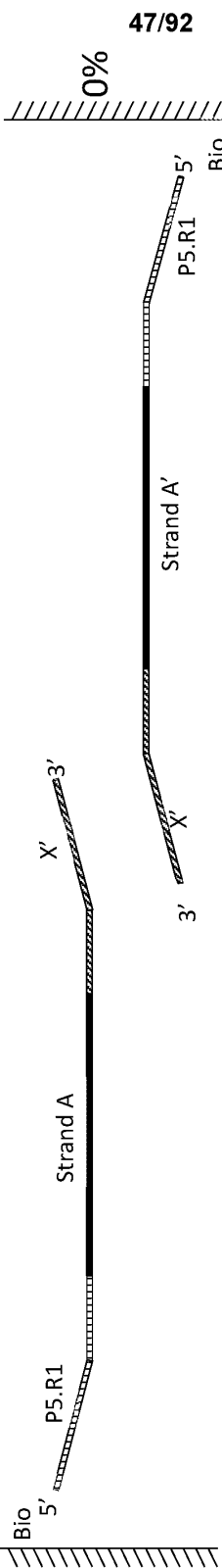


Fig. 28B

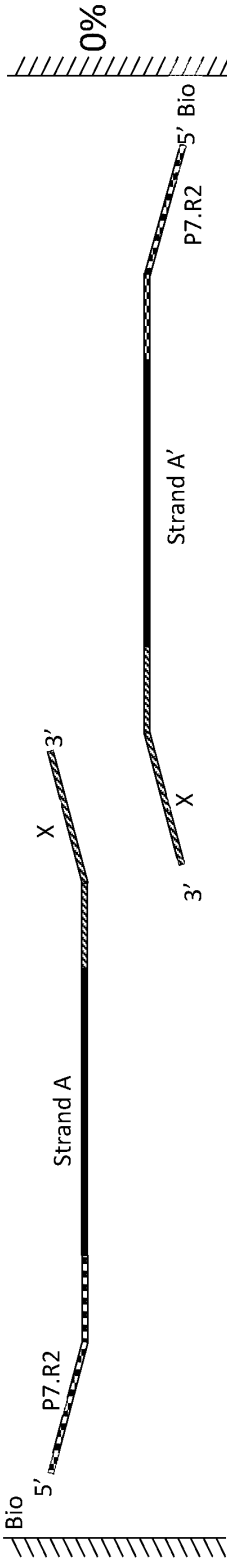


Fig. 28C

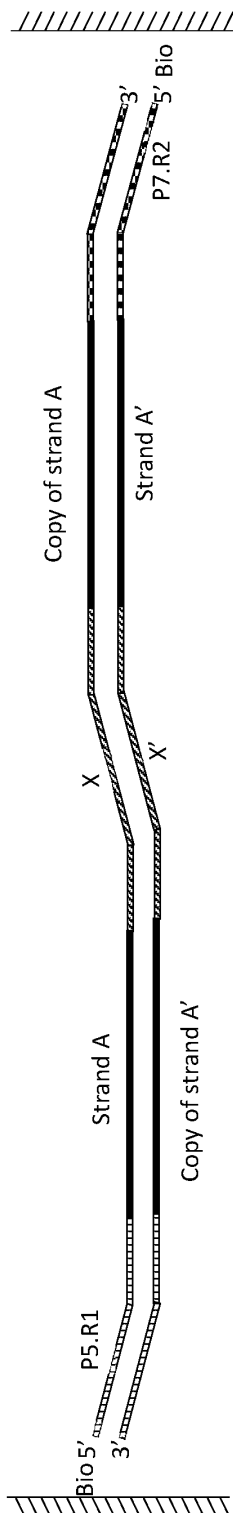


Fig. 29

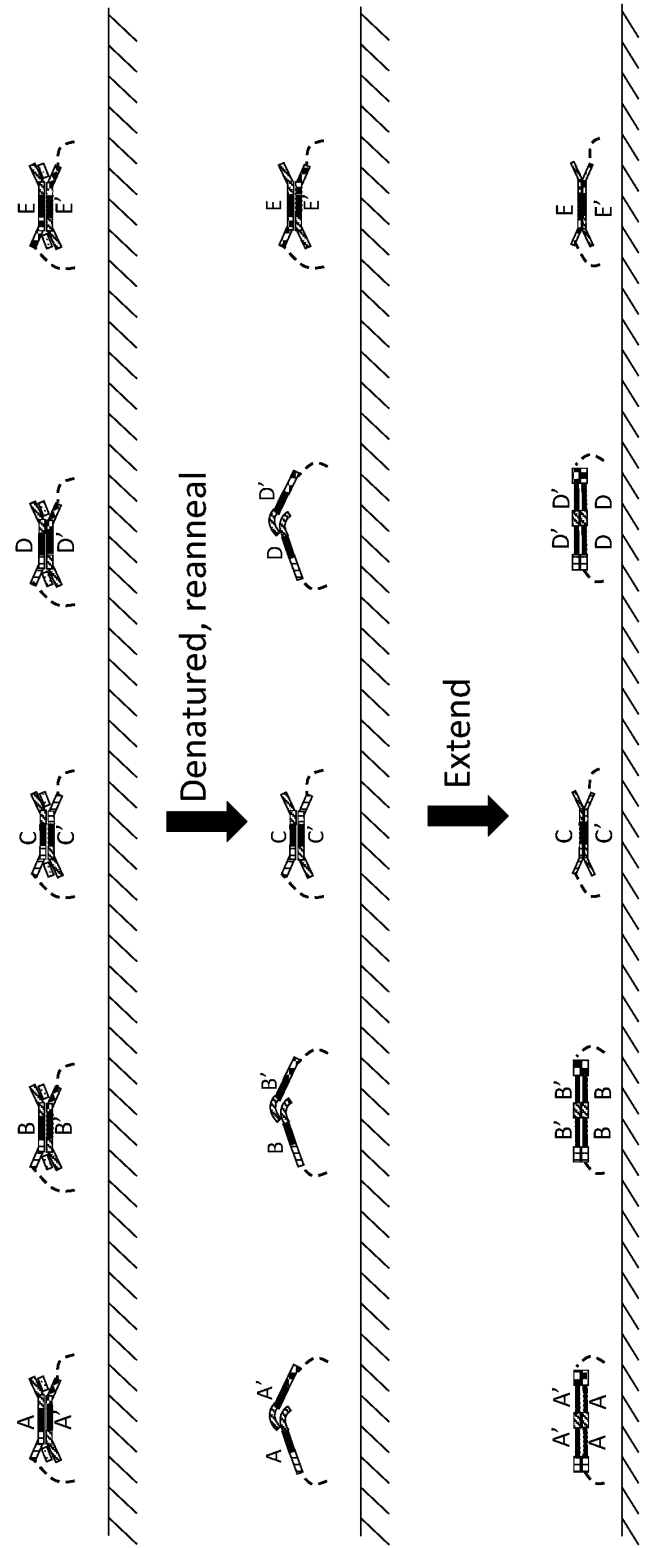


Fig. 30

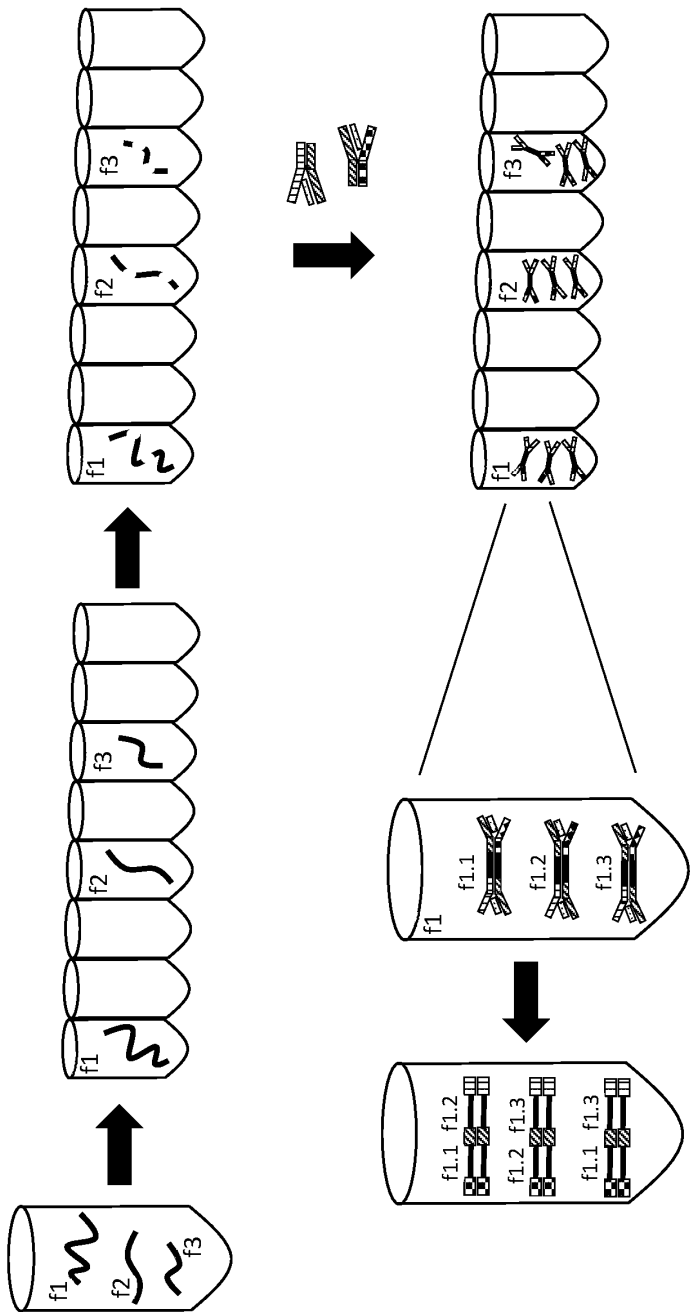


Fig. 31

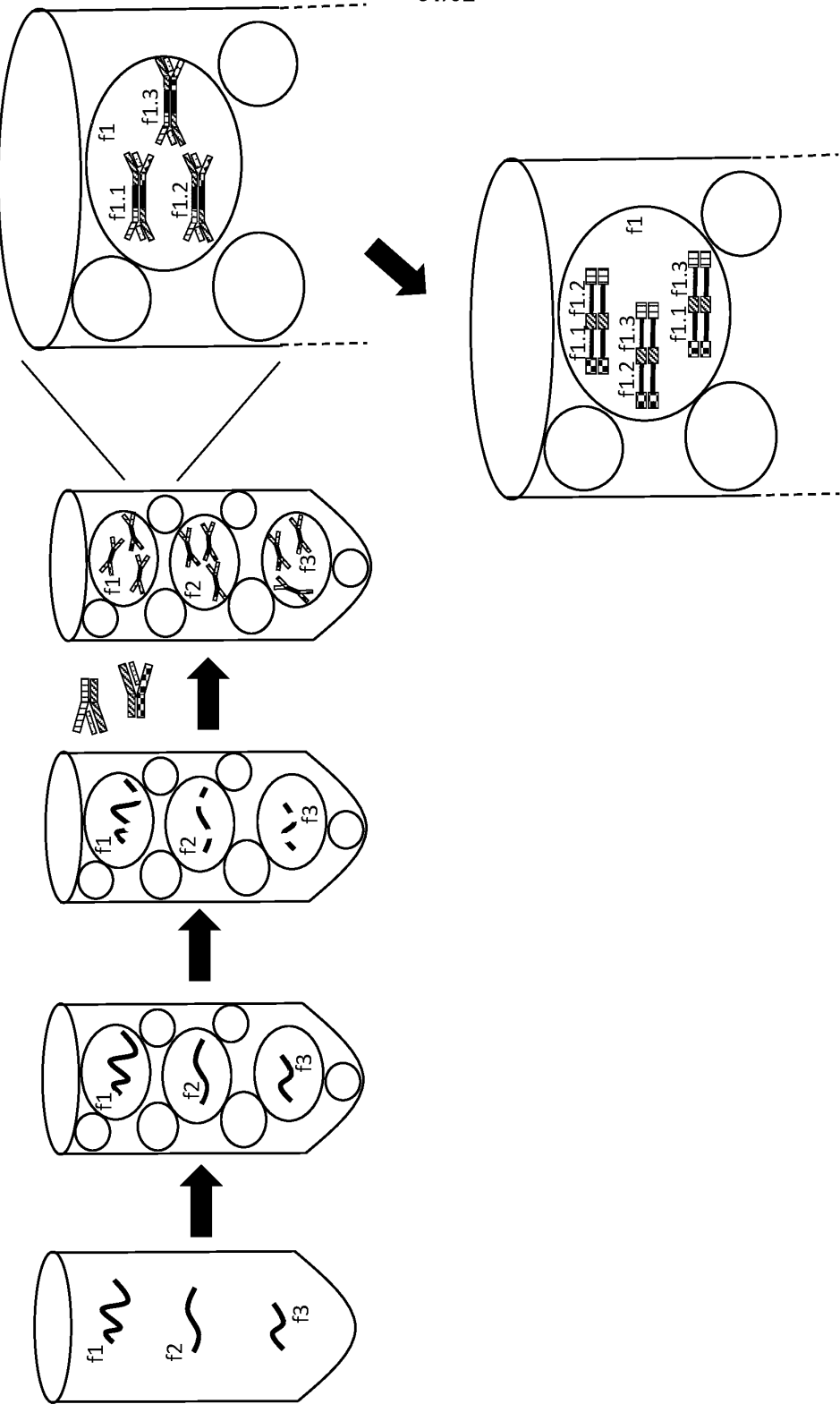


Fig. 32

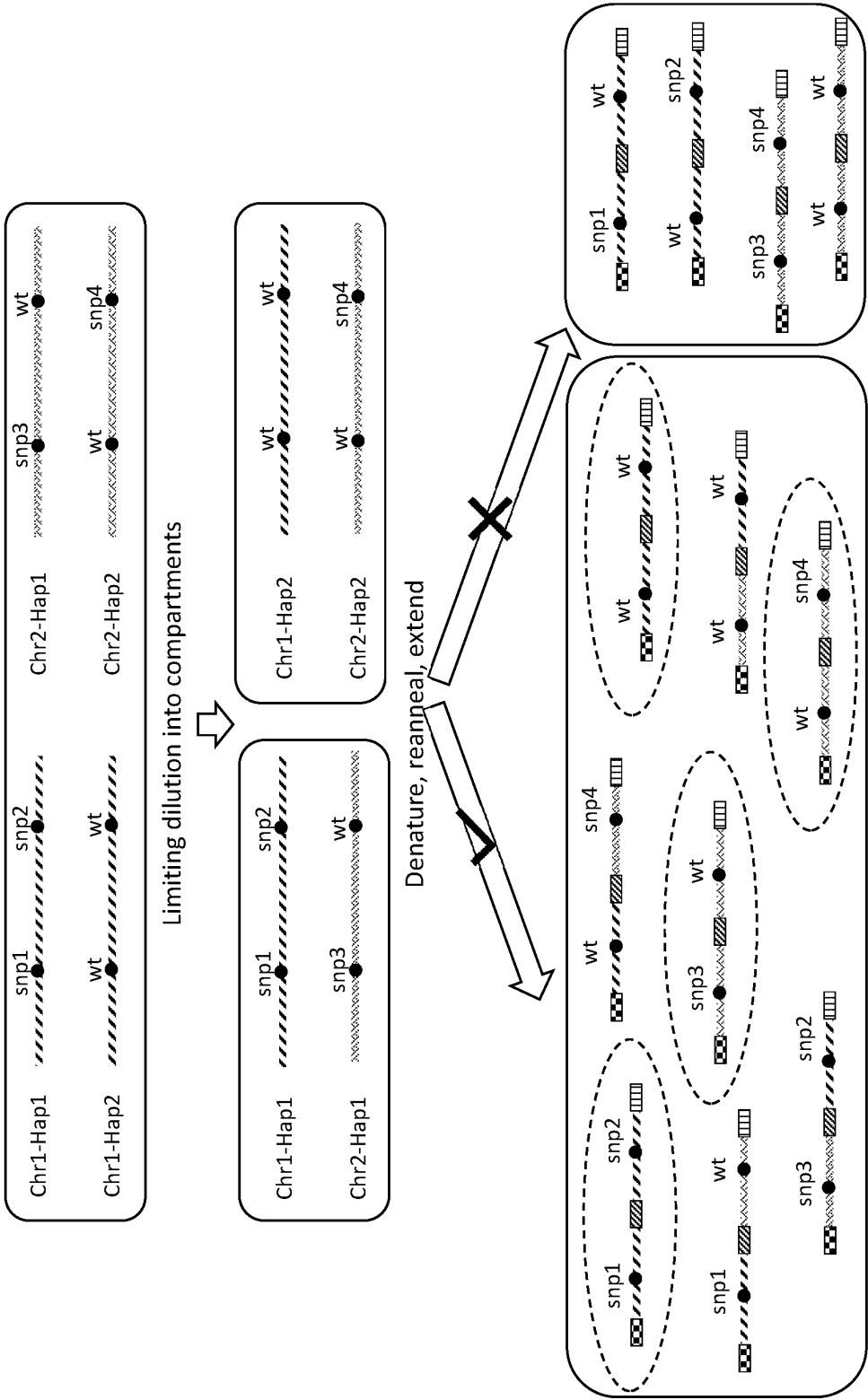


Fig. 33

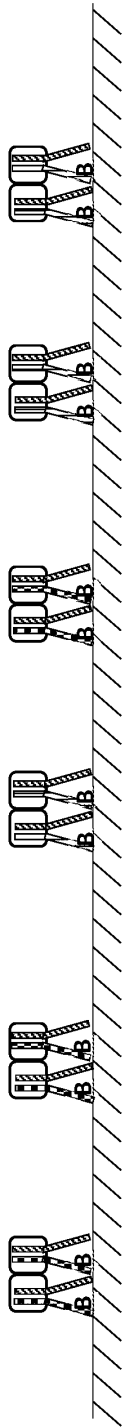


Fig. 35

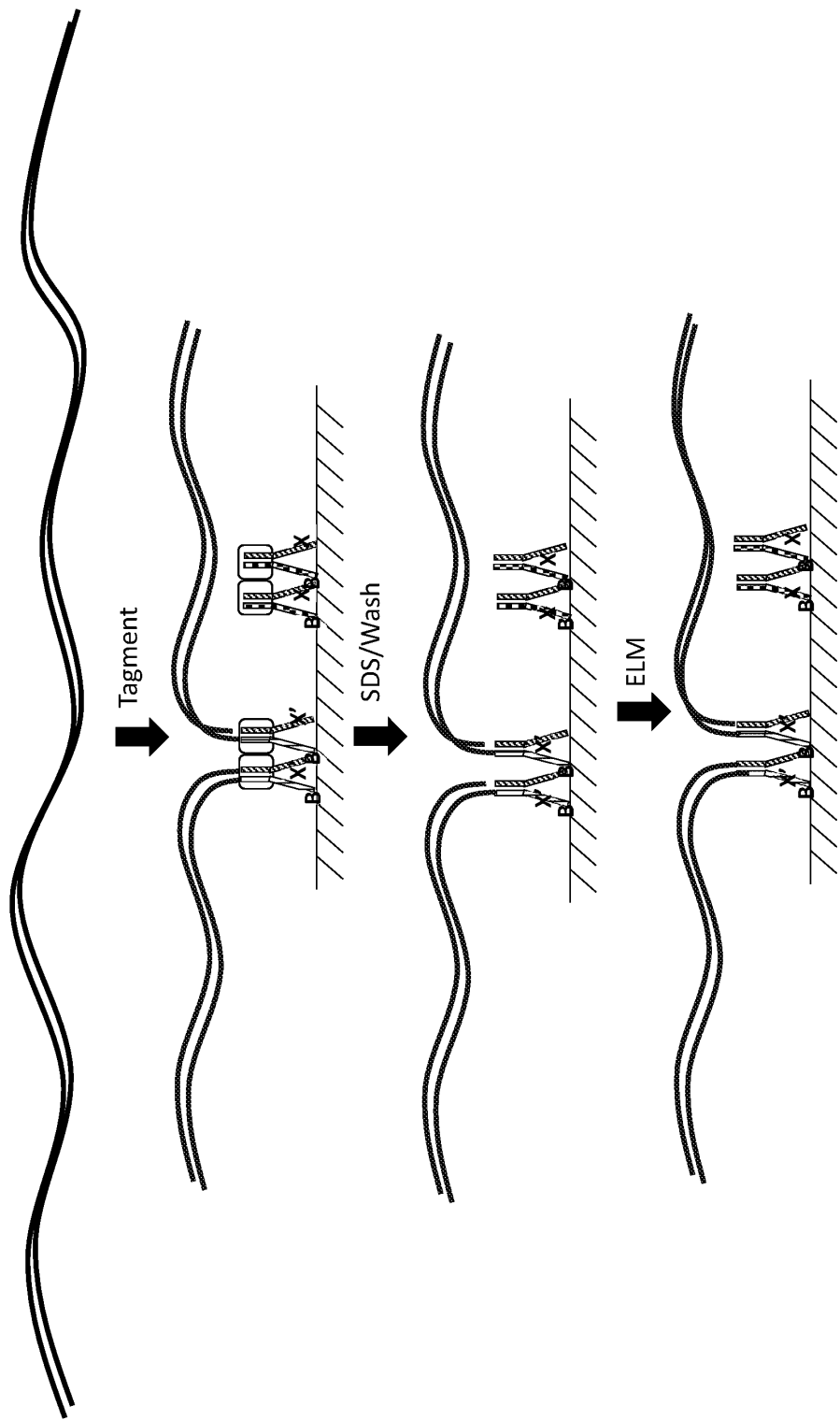


Fig. 36

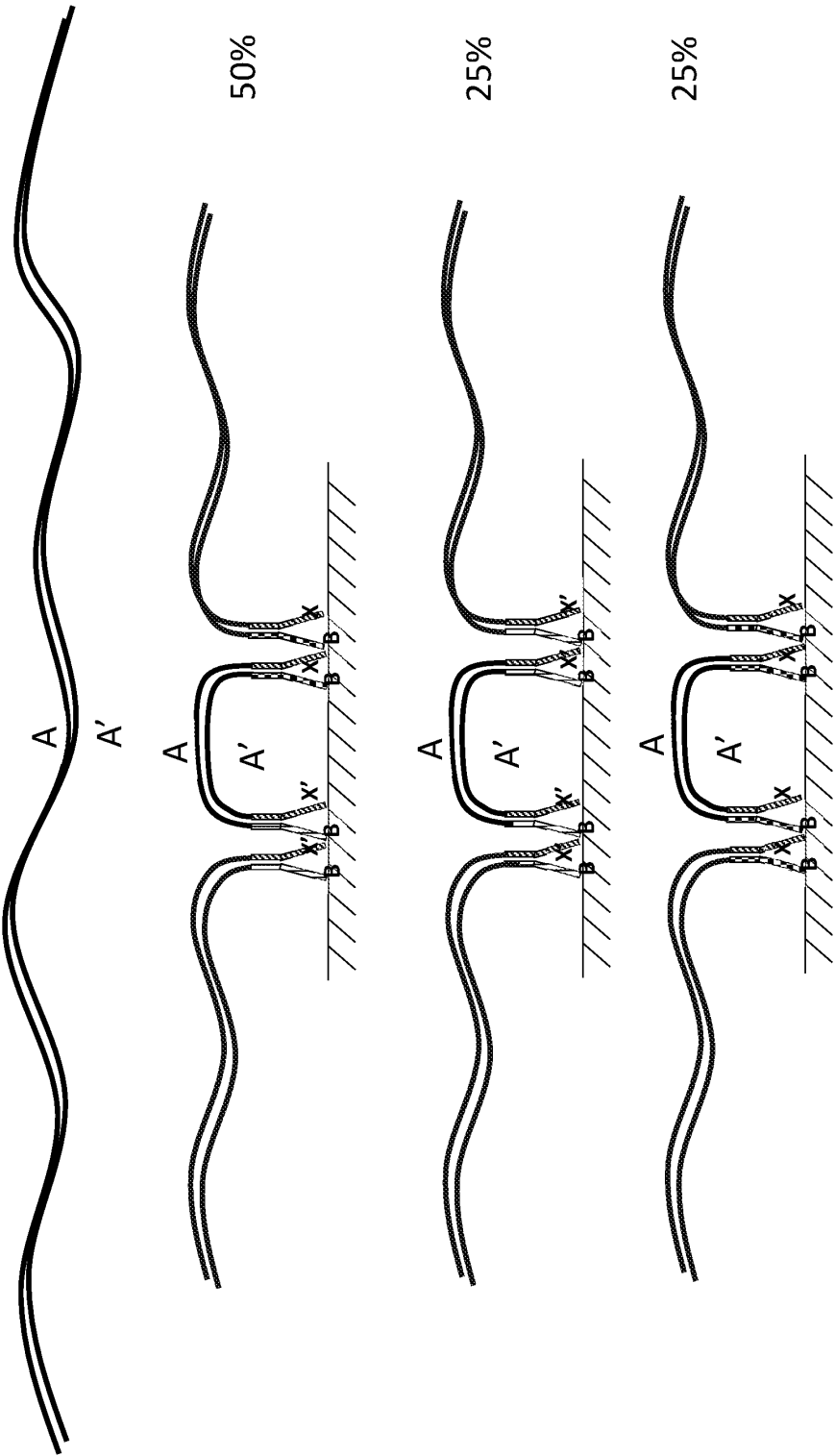


Fig. 37

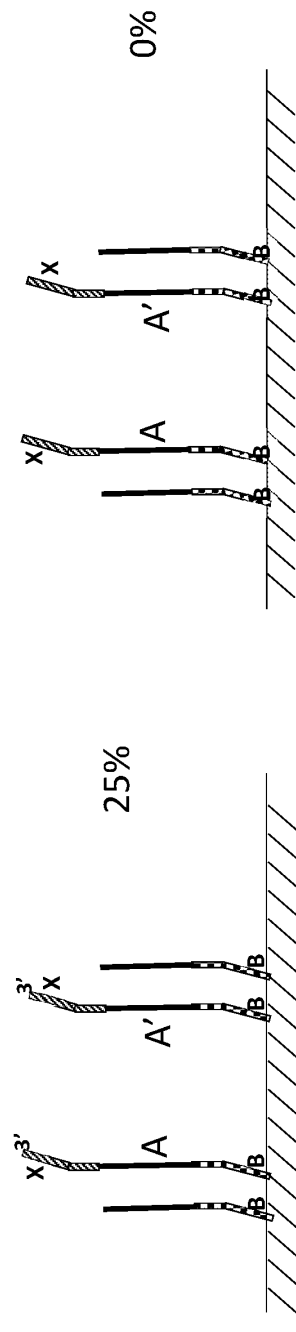
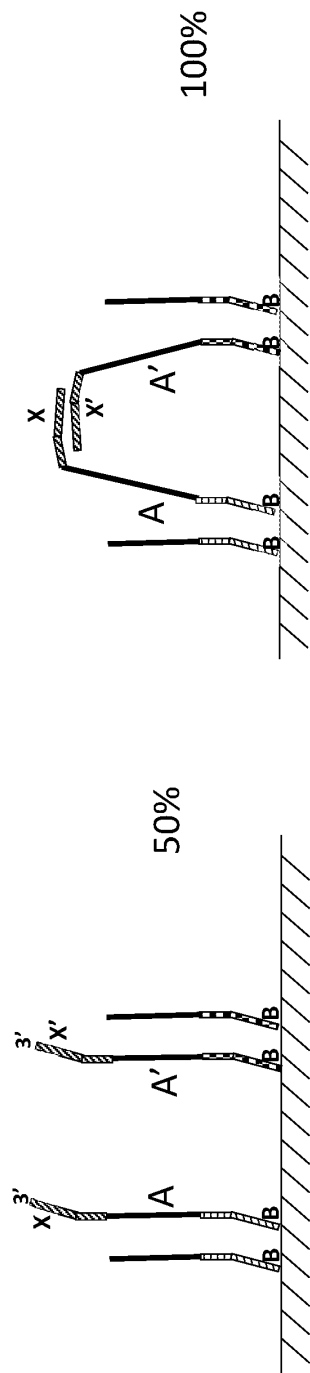


Fig. 38

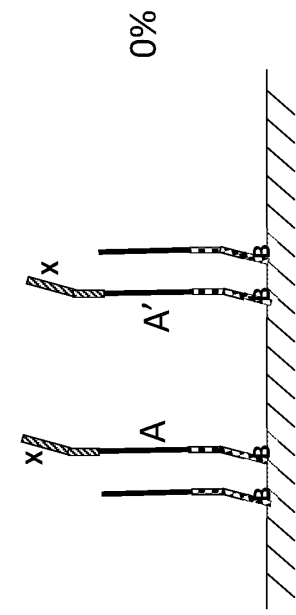
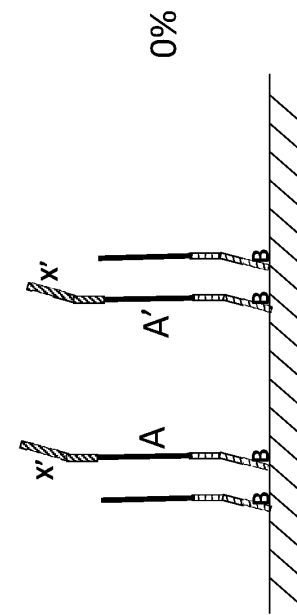
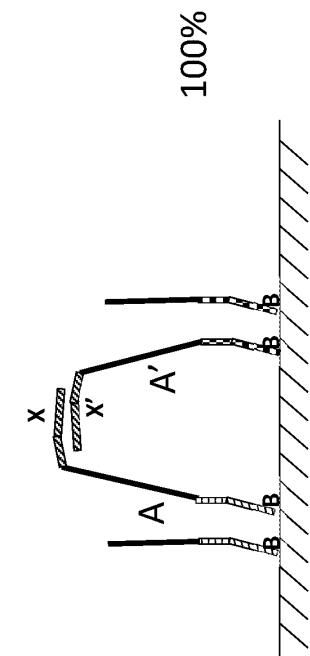


Fig. 39

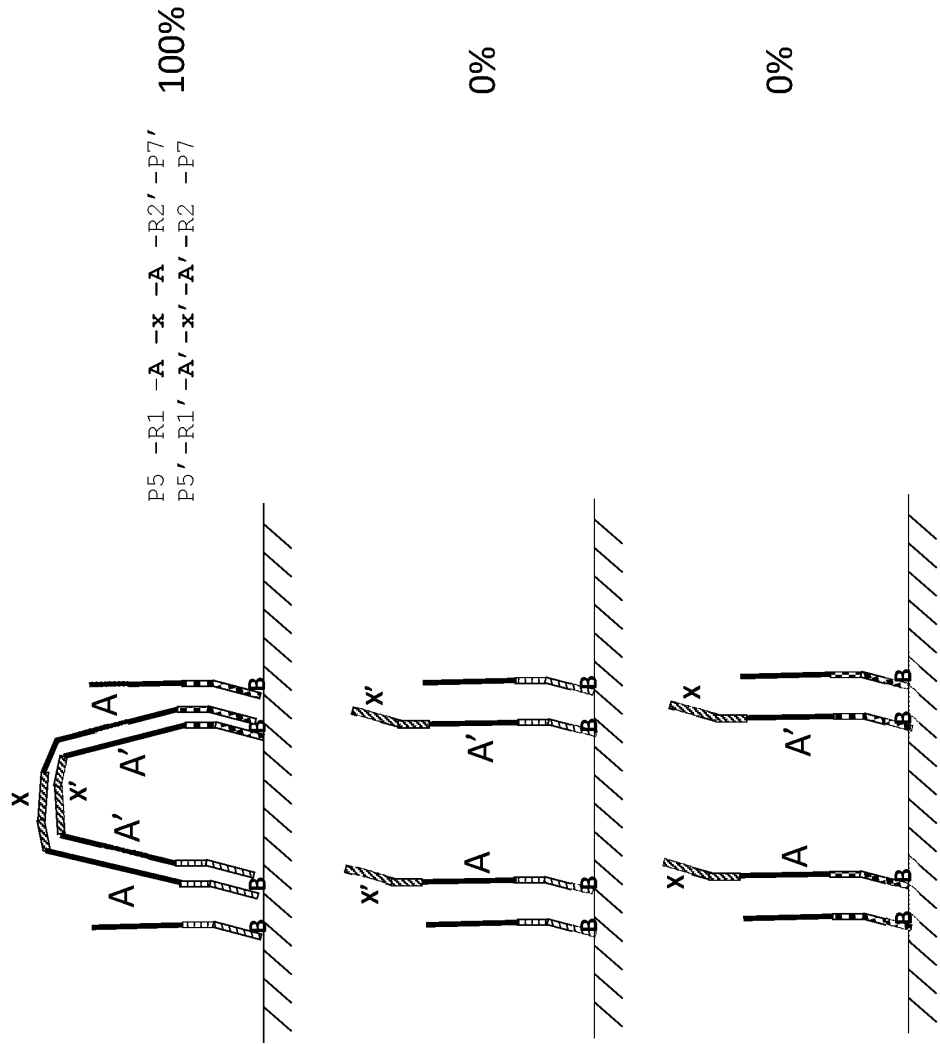


Fig. 40

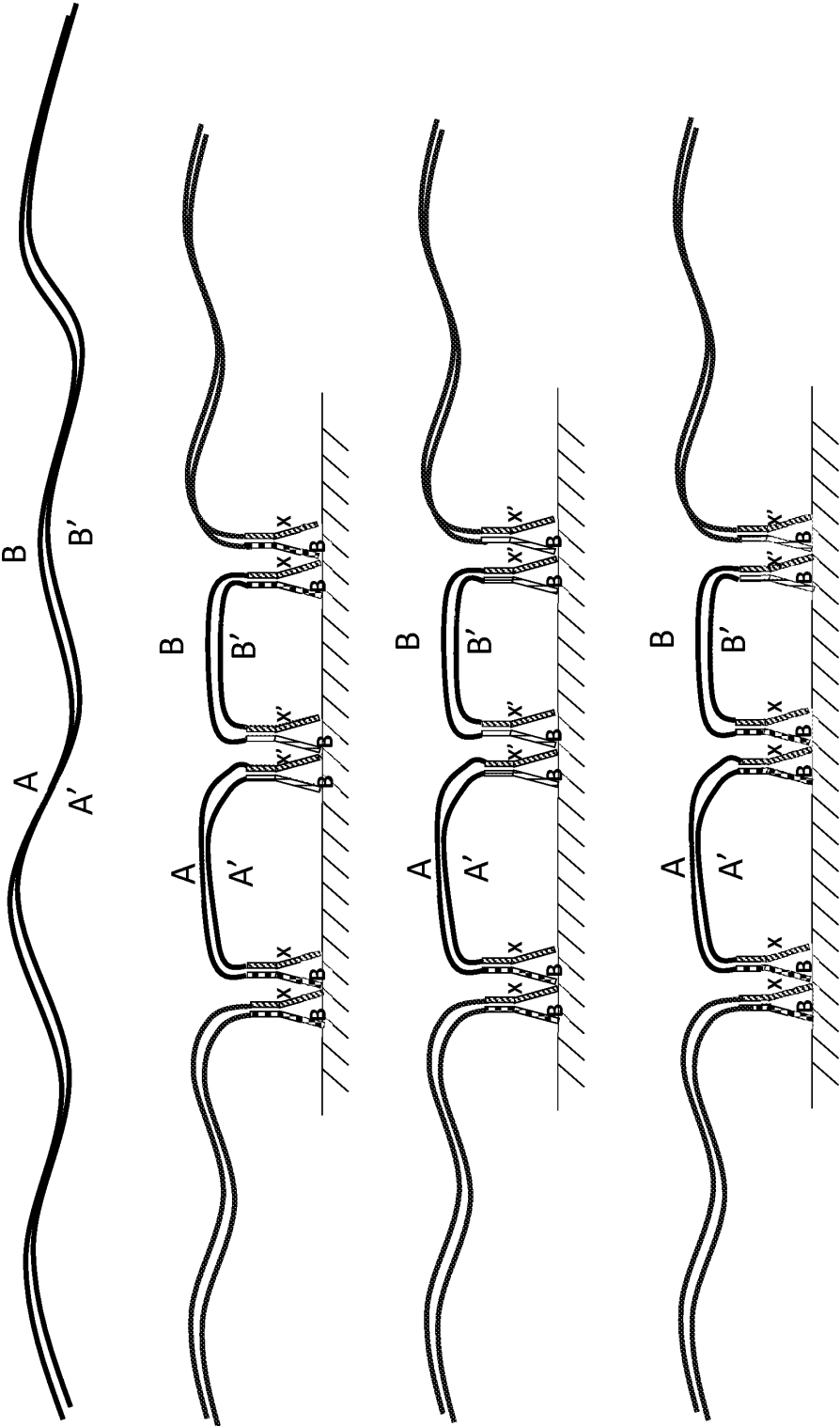


Fig. 41

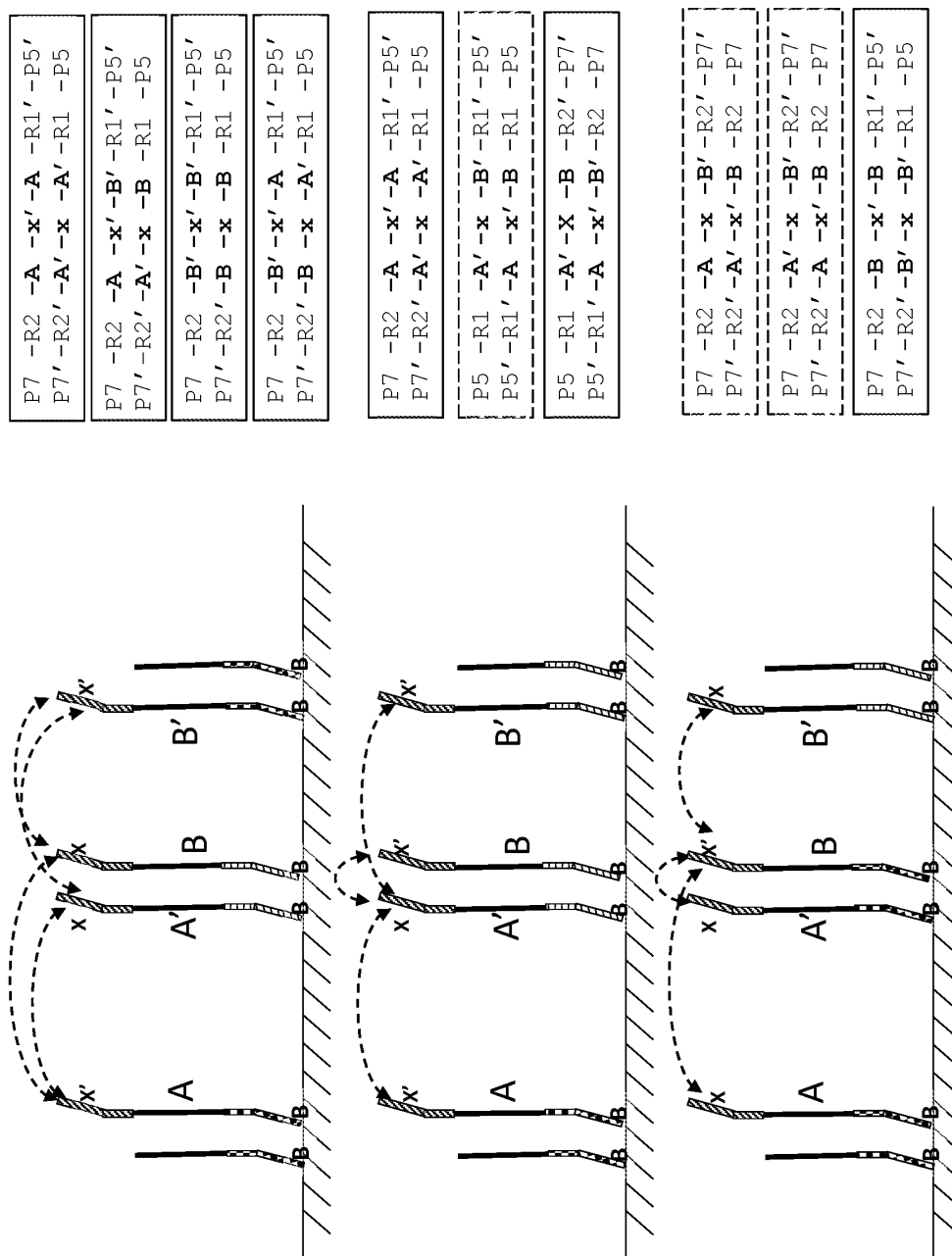


Fig. 42

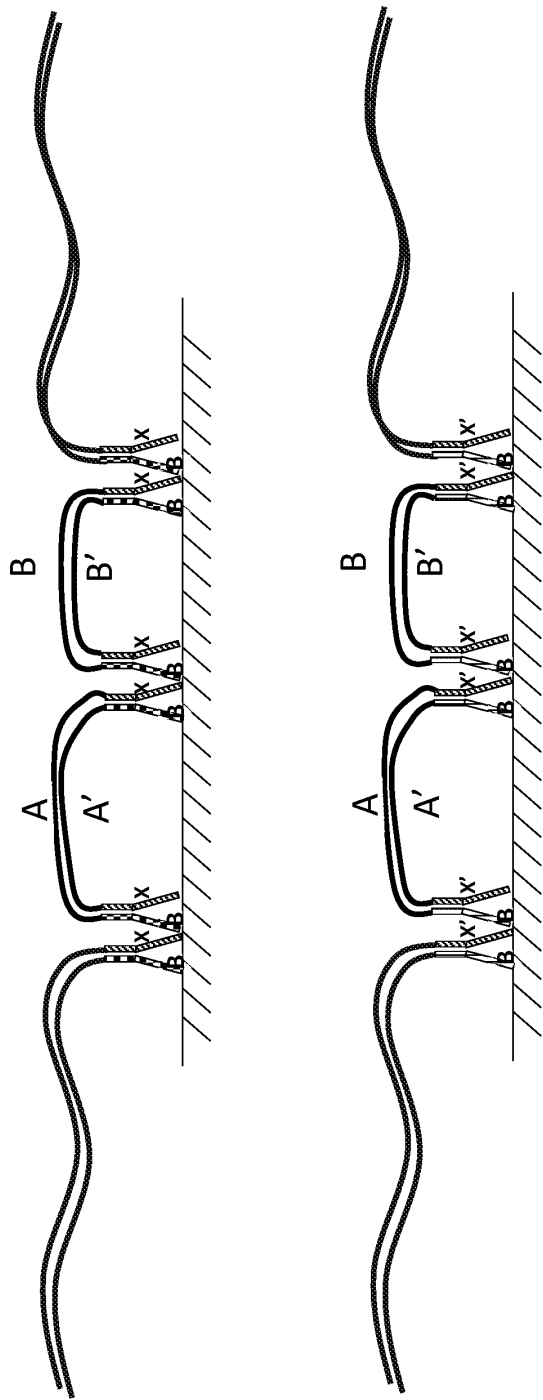


Fig. 43

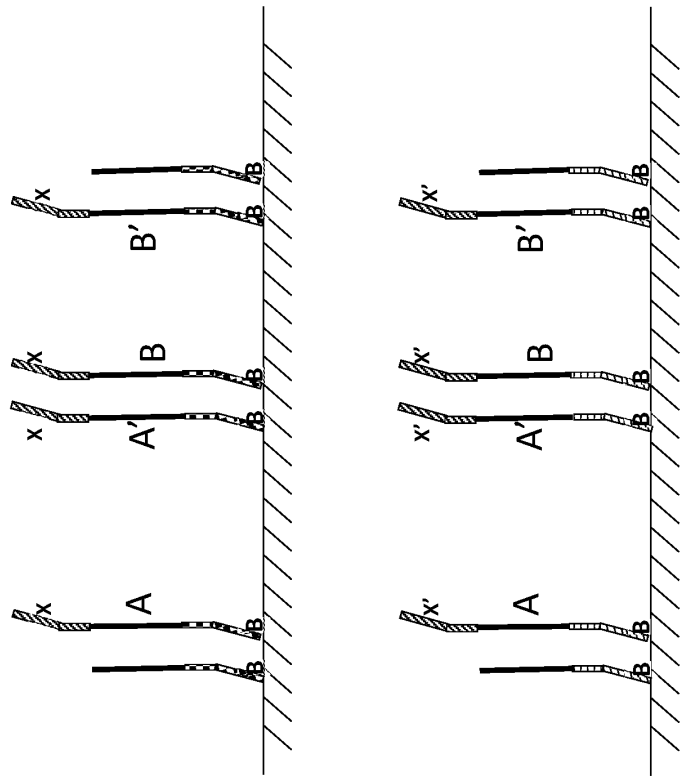


Fig. 44

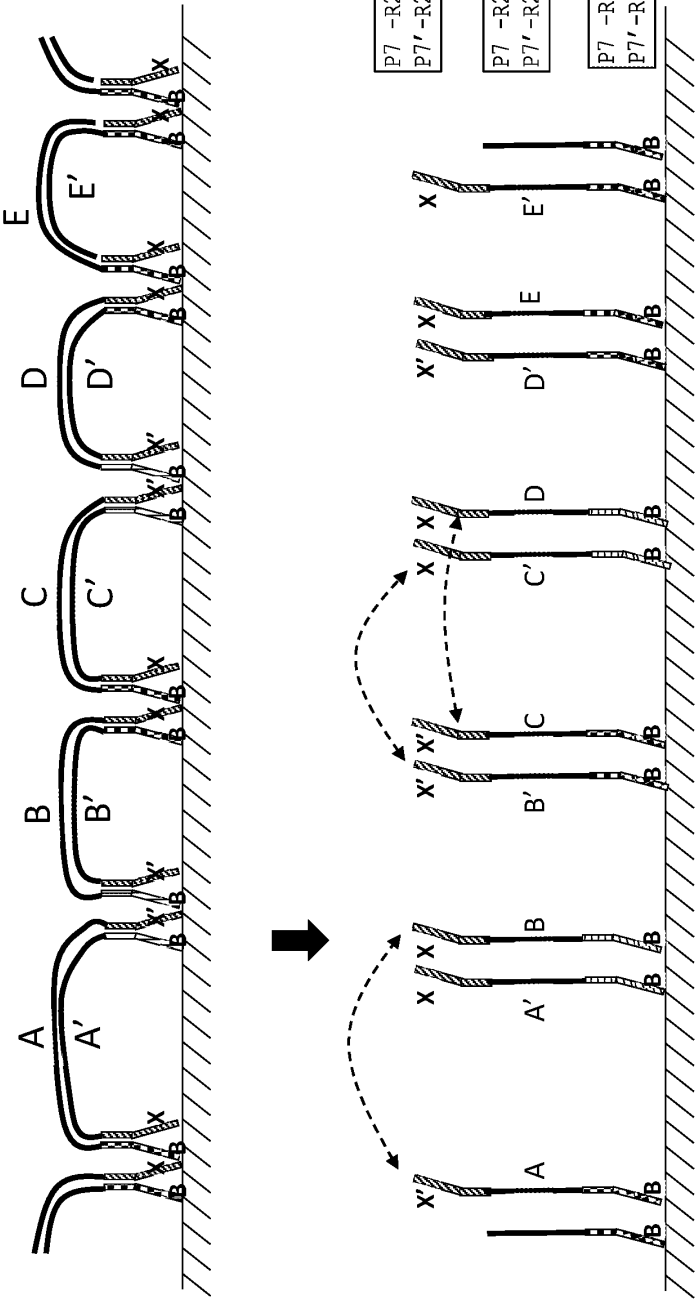
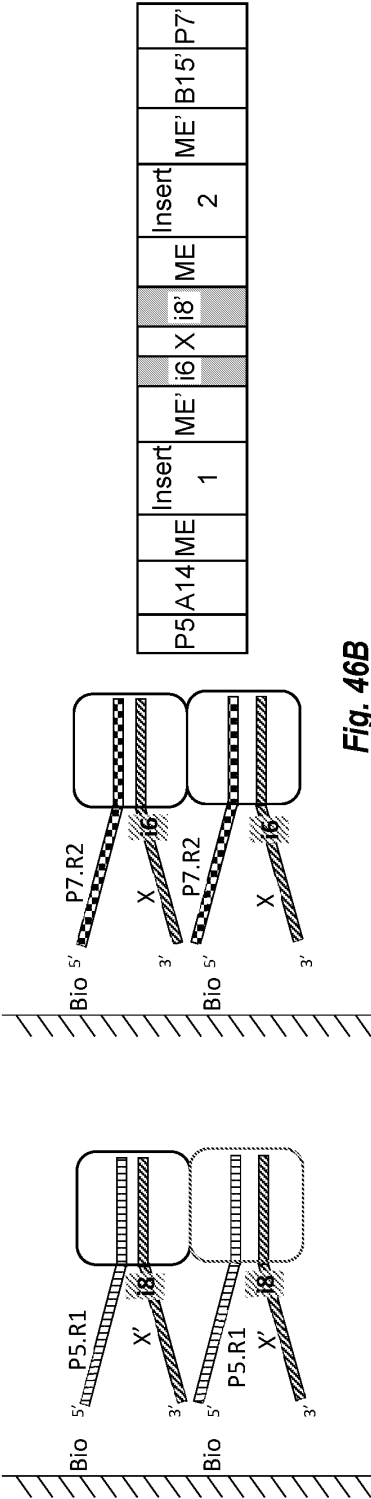
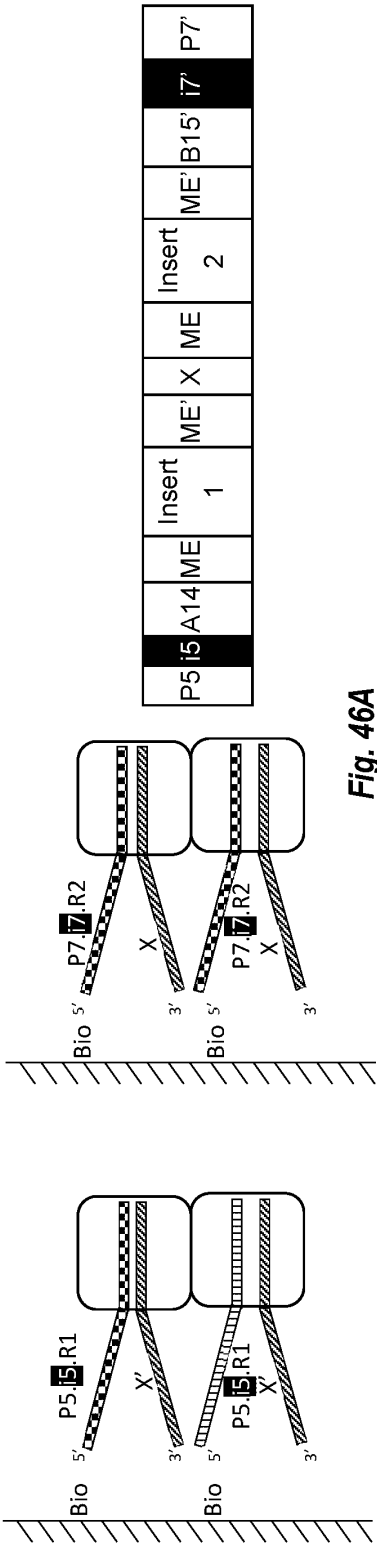


Fig. 45



P5	i5	A14	ME	Insert 1	ME'	i6	X	i8'	ME	Insert 2	ME'	B15'	i7'	P7'
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Fig. 46C

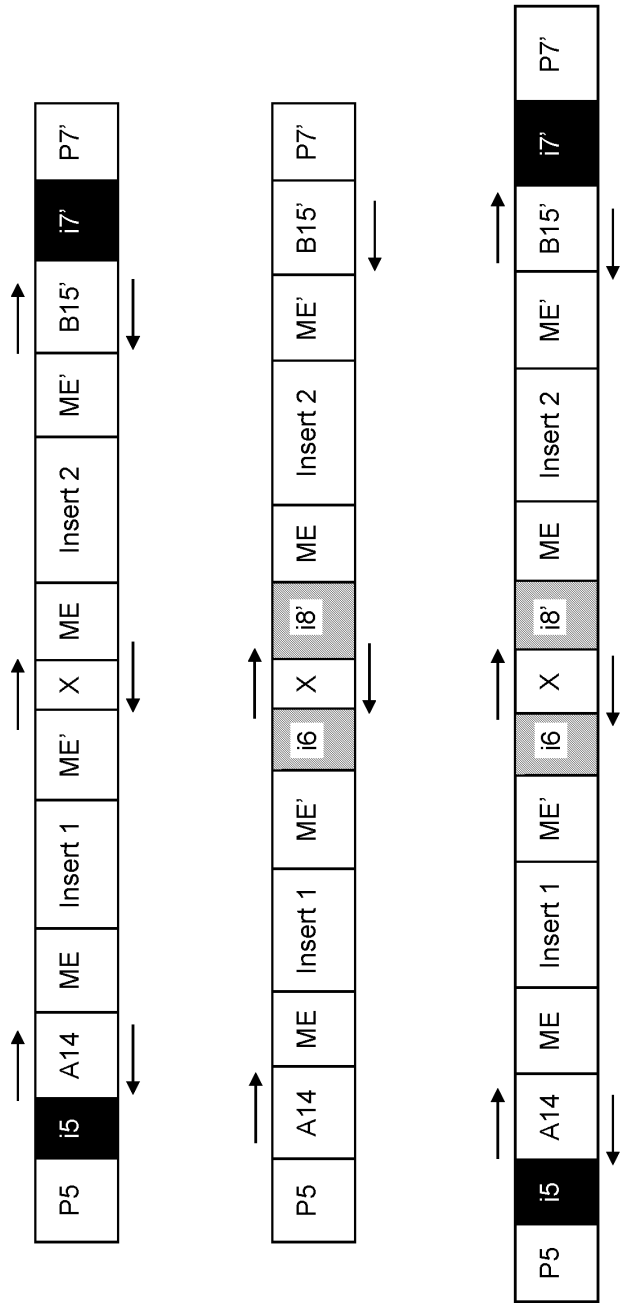
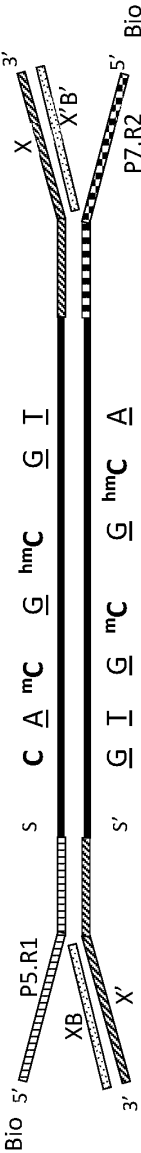


Fig. 47



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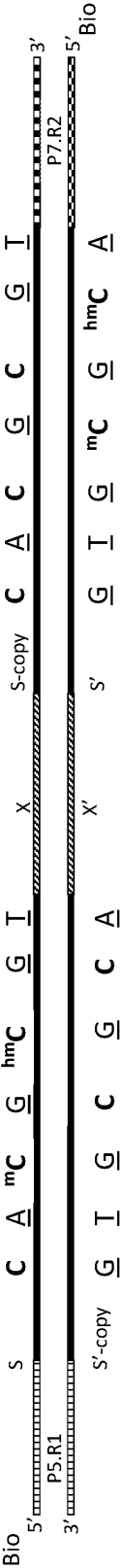
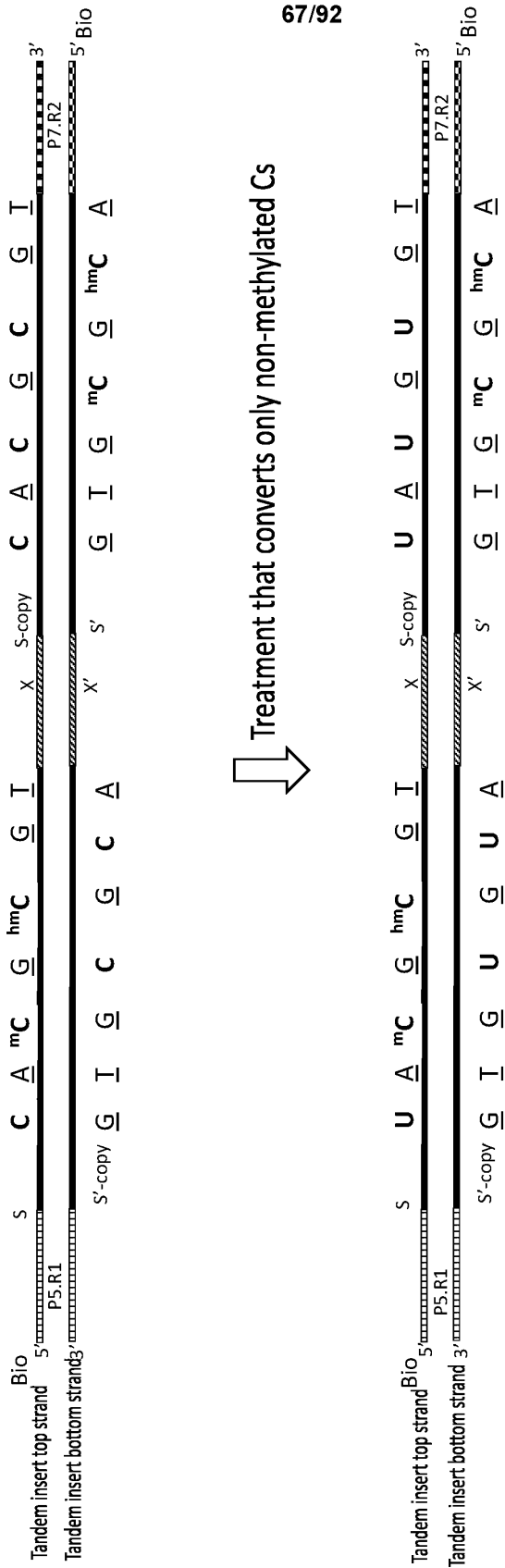
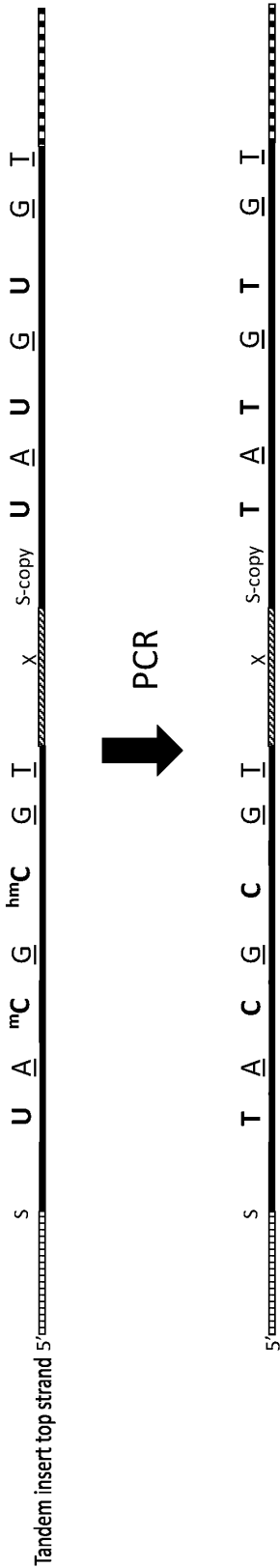


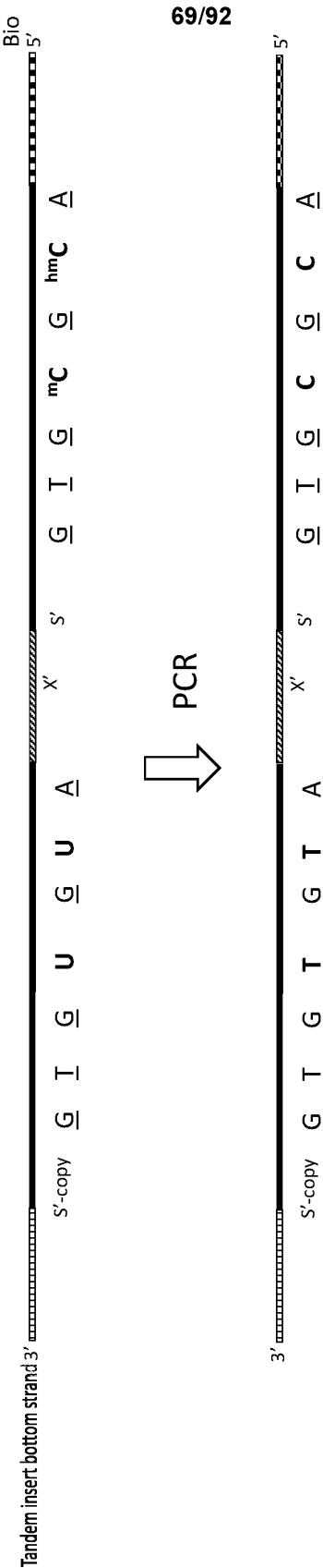
Fig. 48





Each loci is read twice = 5' (T,T) (A,A) (C,T) (G,G) (C,T) (G,G) (T,T) 3'

Fig. 50A



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Each loci is read twice = 3' (G,G) (T,T) (G,G) (T,C) (G,G) (T,C) (A,A) 5'

Fig. 50B

Compare top and bottom strand information

Top strand (original,copy) = 5'

Bottom strand (copy,original) = 3'

(T, T)	(A, A)	(C, T)	(G, G)	(C, T)	(G, G)	(T, T)	(T, T)	3'
(G, G)	(T, T)	(G, G)	(T, C)	(G, G)	(T, C)	(T, C)	(A, A)	5'

Thus, original duplex was =

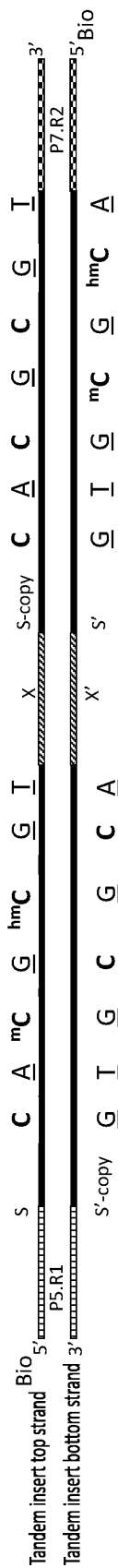
5' C A

3' G T

^x C	G	^x C	G	^x C	G	G	T	3'
			^x C			^x C	A	5'

where ^xC is either ^mC or ^{hm}C

Fig. 50C



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Treatment that converts only methylated C's

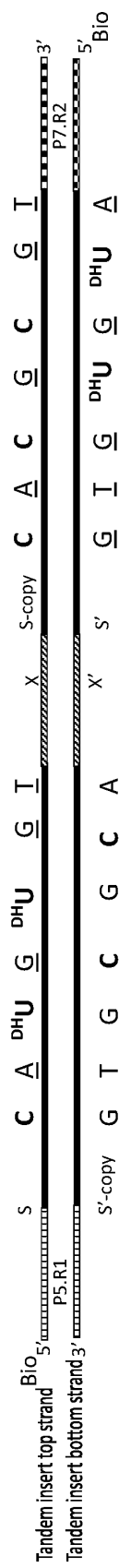
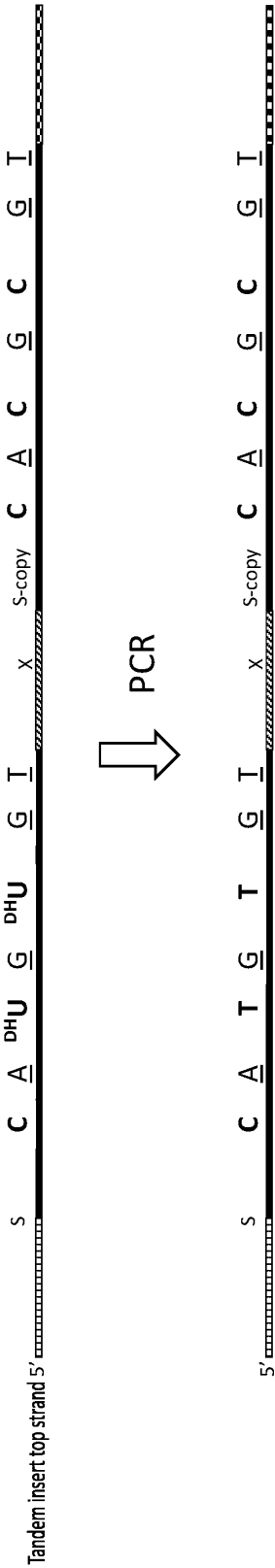
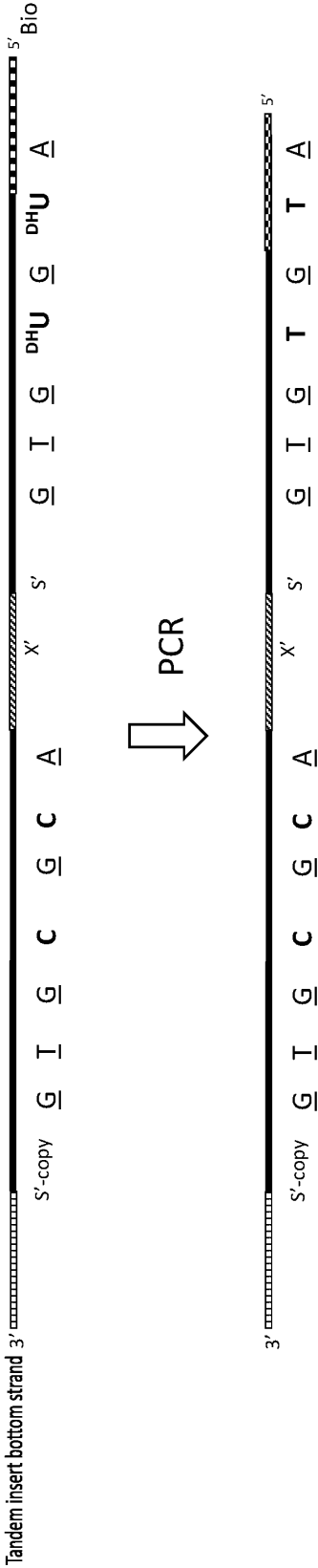


Fig. 51



Each loci is read twice = 5' (C,C) (A,A) (T,C) (G,G) (T,C) (G,G) (T,T) 3'

Fig. 52A



Each loci is read twice = 3' (G,G) (T,T) (G,G) (C,T) (G,G) (C,T) (A,A) 5'

Fig. 52B

Compare top and bottom strand information

Top strand (original,copy)

=

5'

Bottom strand (copy,original)

=

3'

(C,C)	(A,A)	(T,C)	(G,G)	(T,C)	(G,G)	(T,T)	(G,G)	(T,T)	(A,A)
(G,G)	(T,T)	(G,G)	(C,T)	(G,G)	(C,T)	(A,A)	(C,T)	(A,A)	(A,A)

Thus, original duplex was =

5'

3'

A

T

^xC

G

G

G

^xC

G

G

G

^xC

G

G

G

^xC

G

T

A

T

A

3'

5'

where ^xC is either ^mC or ^{hm}C

Fig. 52C

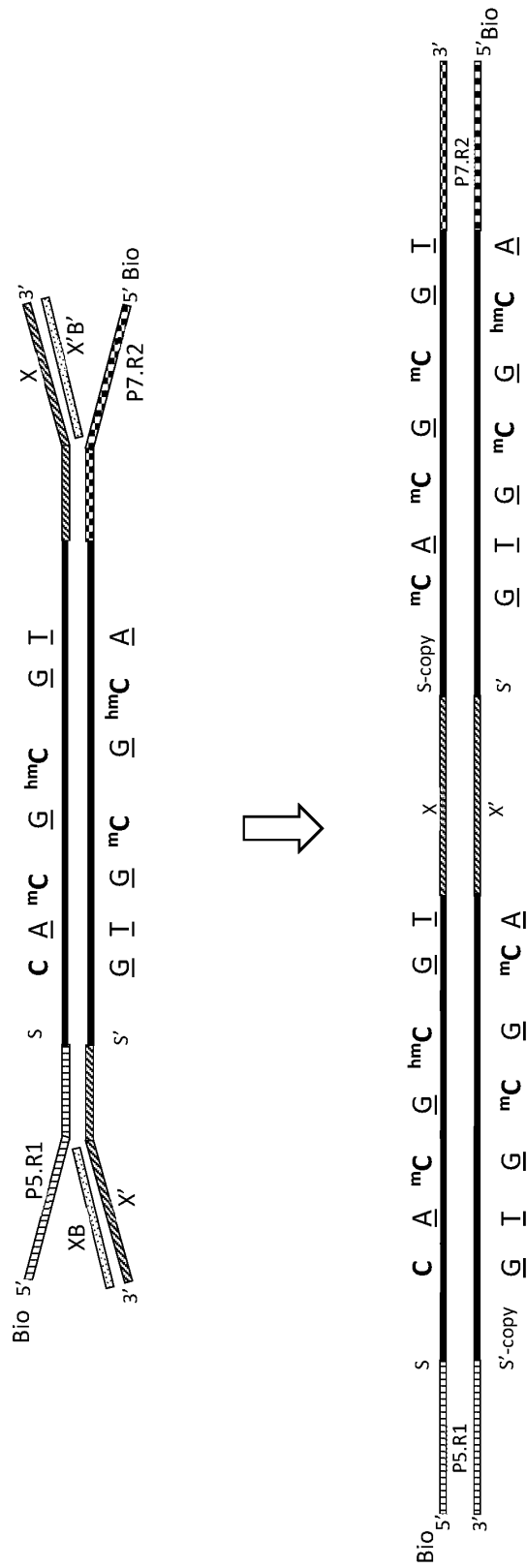
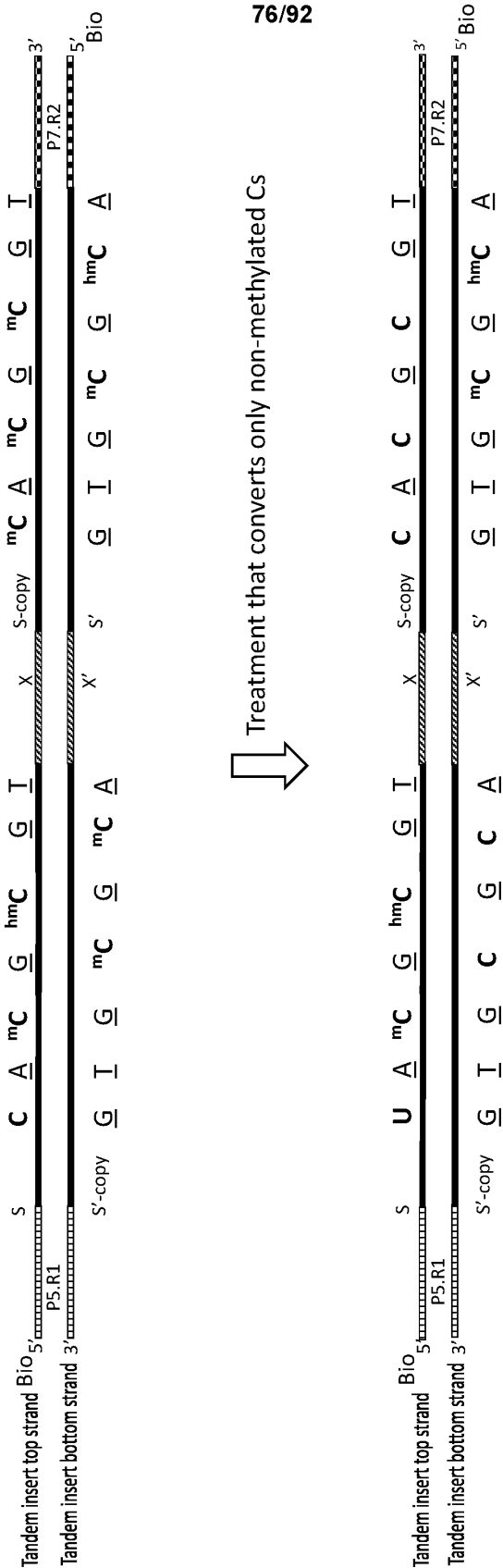
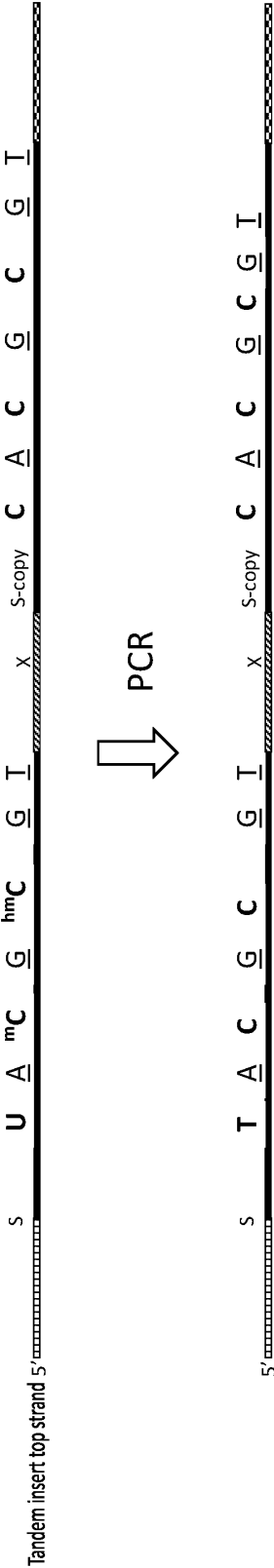


Fig. 53



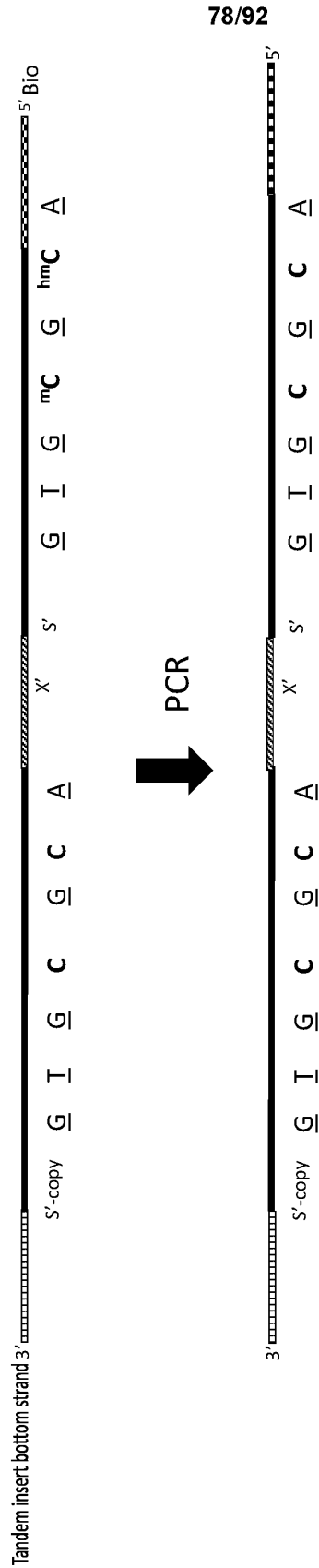
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Fig. 54



Each loci is read twice = 5' (T,C) (A,A) (C,C) (G,G) (C,C) (G,G) (T,T) 3'

Fig. 55A



Each loci is read twice = 3' (G,G) (T,T) (G,G) (C,C) (G,G) (C,C) (A,A) 5'

Fig. 55B

Compare top and bottom strand information

Top strand (original,copy) = 5'

Bottom strand (copy,original) = 3'

(T,C)	(A,A)	(C,C)	(G,G)	(C,C)	(G,G)	(T,T)	(G,G)	(T,T)
(G,G)	(T,T)	(G,G)	(C,C)	(G,G)	(C,C)	(A,A)	(C,C)	(A,A)

5' C A ^xC G

3' G T G

5' 3'

3' 5'

Thus, original duplex was =

5' 3'

3' 5'

G

^xC

G

G

^xC

G

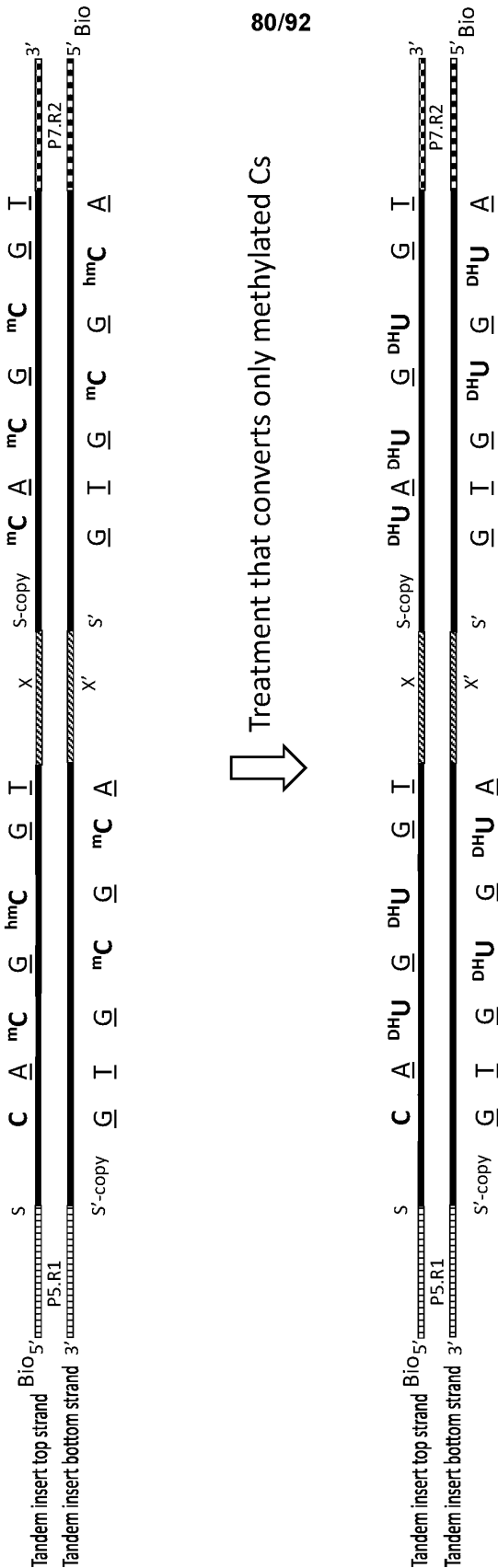
T

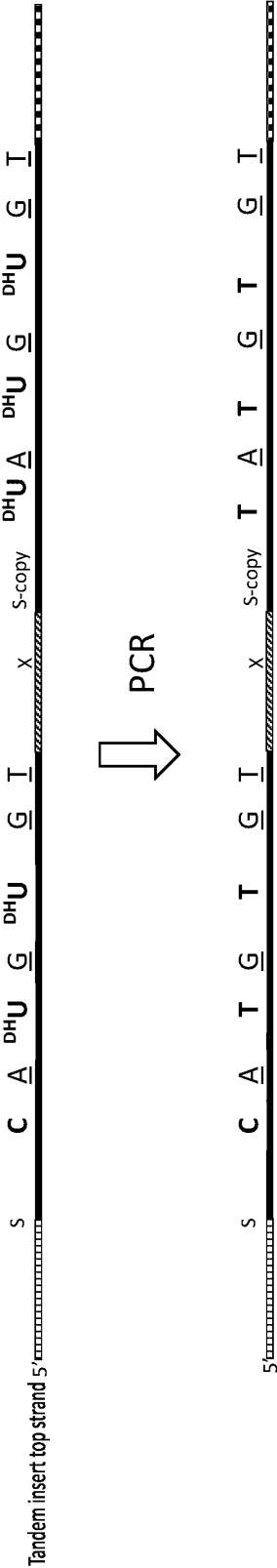
A

A

where ^xC is either ^mC or ^{hm}C

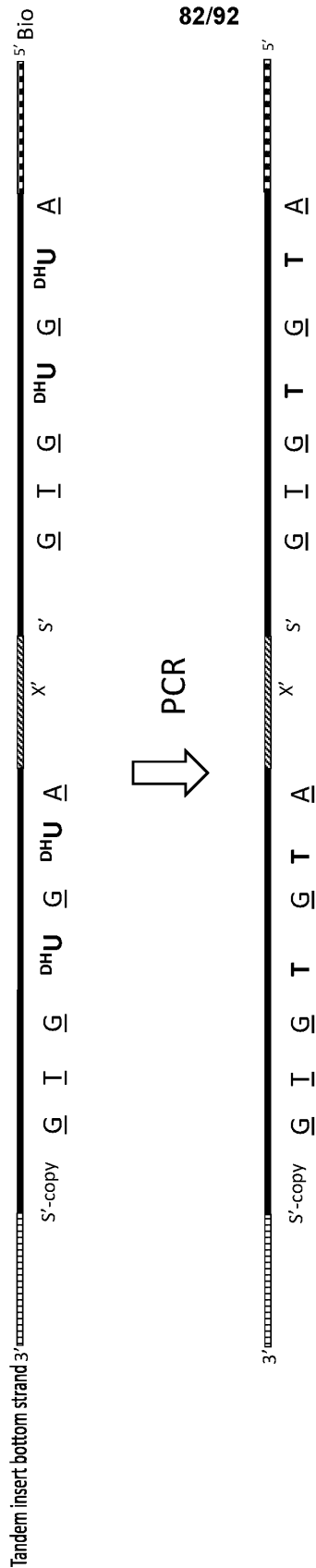
Fig. 55C





Each loci is read twice = 5' (C,T) (A,A) (T,T) (G,G) (T,T) (G,G) (T,T) 3'

Fig 57A



Each loci is read twice = 3' (G,G) (T,T) (G,G) (T,T) (G,G) (T,T) (A,A) 5'

Fig. 57B

Compare top and bottom strand information

Top strand (original,copy) = 5'

Bottom strand (copy,original) = 3'

(C,T)	(A,A)	(T,T)	(G,G)	(T,T)	(G,G)	(T,T)	(T,T)	(G,G)	(T,T)
(G,G)	(T,T)	(G,G)	(T,T)	(G,G)	(T,T)	(G,G)	(T,T)	(T,T)	(A,A)

Thus, original duplex was =

5' C A ^xC G 3'

3' G T G ^xC A 5'

where ^xC is either ^mC or ^{hm}C

Fig. 57C

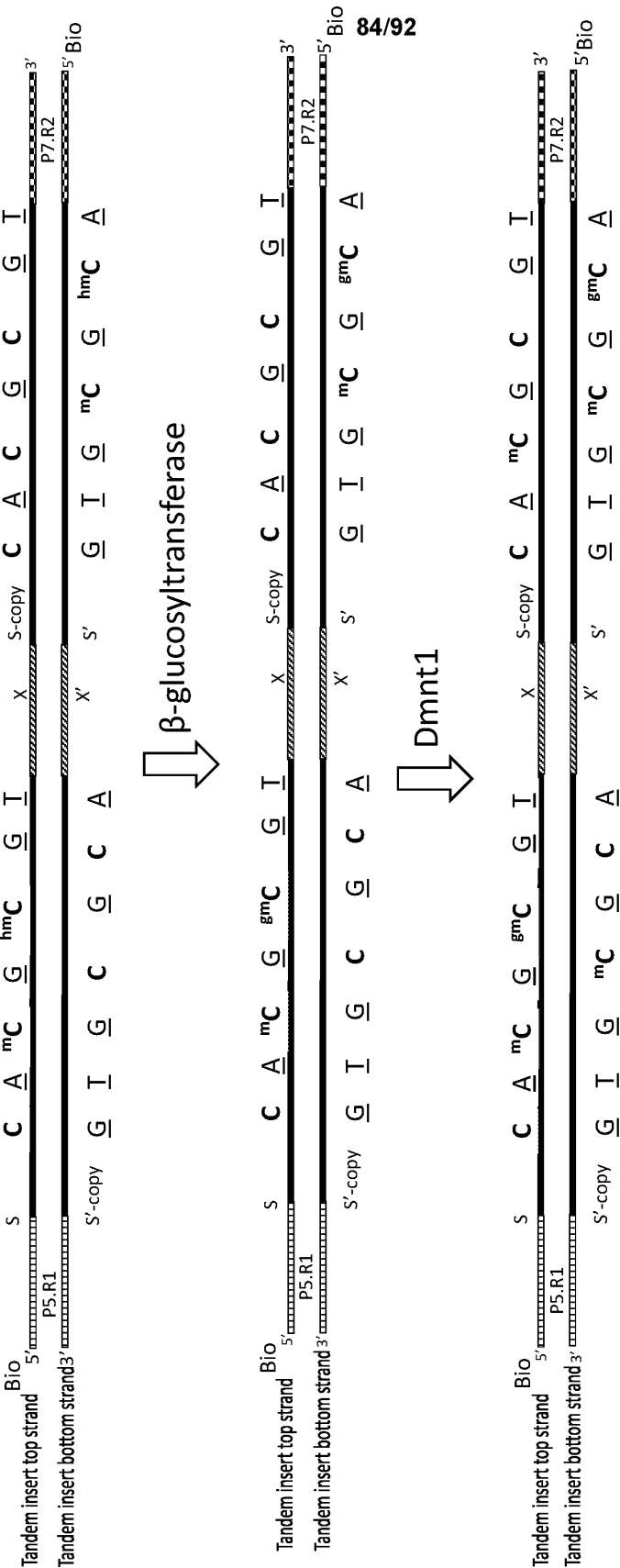


Fig. 58

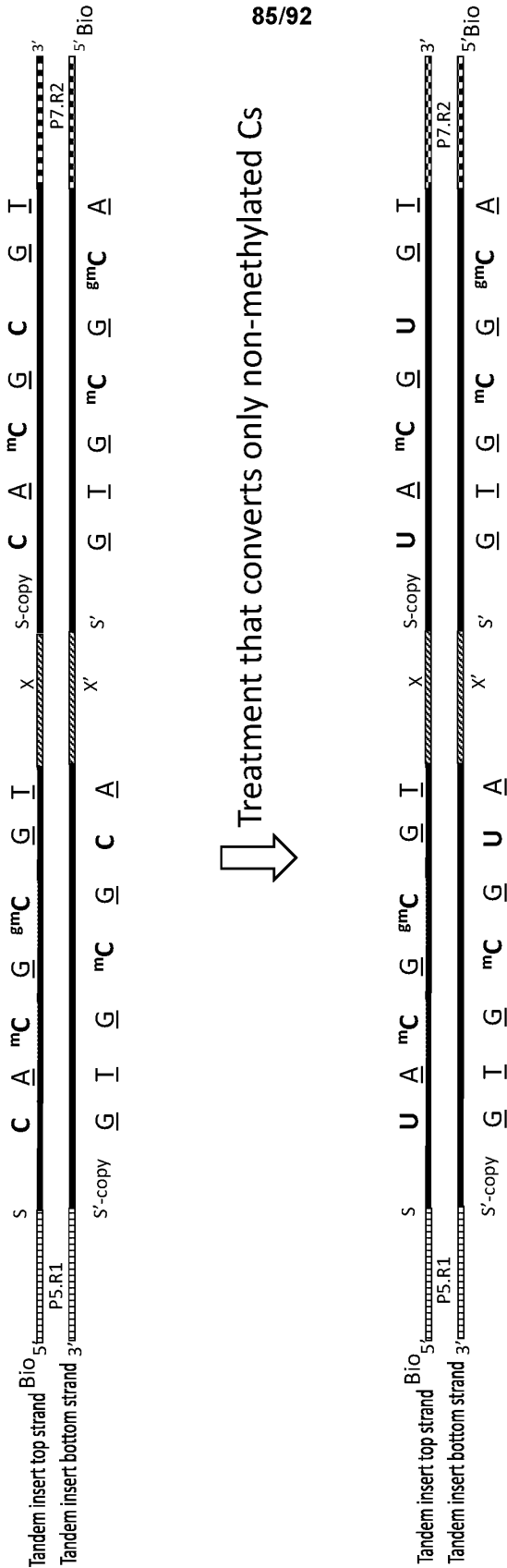
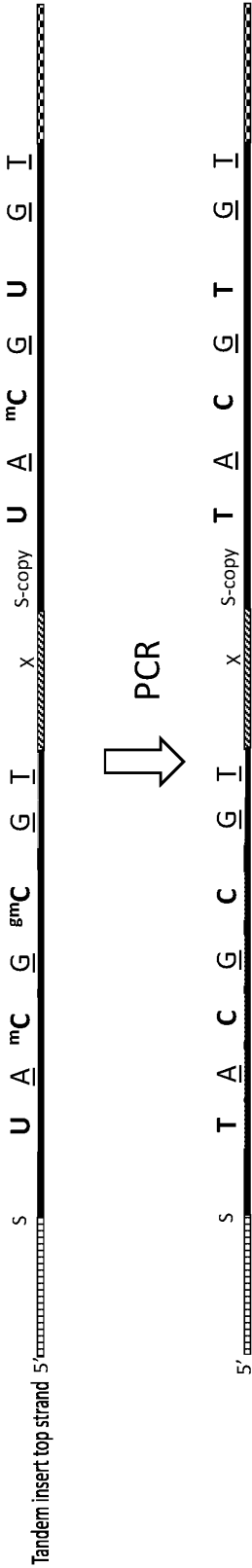
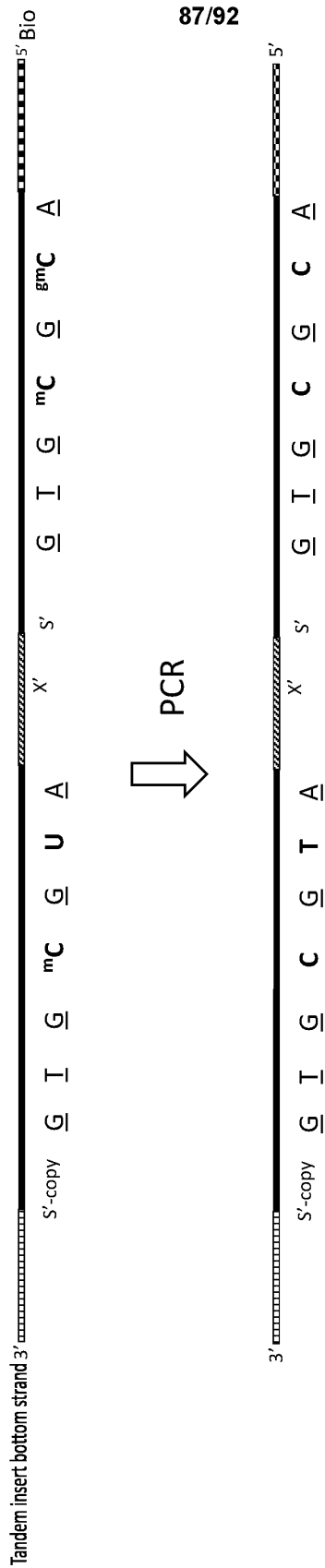


Fig. 59



Each loci is read twice = 5' (T,T) (A,A) (C,C) (G,G) (C,T) (G,G) (T,T) 3'

Fig. 60A



Each loci is read twice = 3' (G,G) (T,T) (G,G) (C,C) (G,G) (T,C) (A,A) 5'

Fig. 60B

Compare top and bottom strand information

Top strand (original,copy) = 5'

Bottom strand (copy,original) = 3'

(T, T)	(A, A)	(C, C)	(G, G)	(C, T)	(G, G)	(T, T)	(G, G)	(T, T)	3'
(G, G)	(T, T)	(G, G)	(C, C)	(G, G)	(C, C)	(T, C)	(A, A)	(A, A)	5'

Thus, original duplex was =

5' C

3' G

A

T

^mC

G

^mC

G

^{hm}C

G

^{hm}C

A

T

A

3'

5'

Fig. 60C

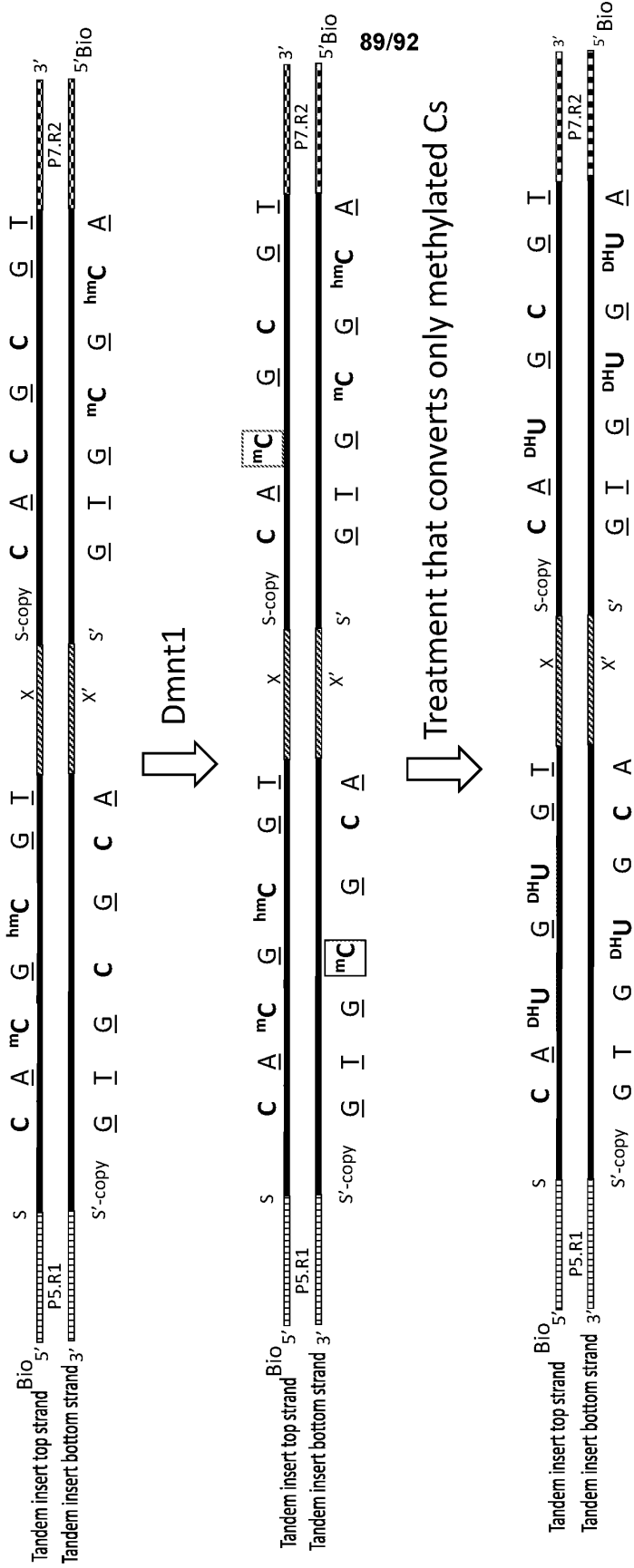
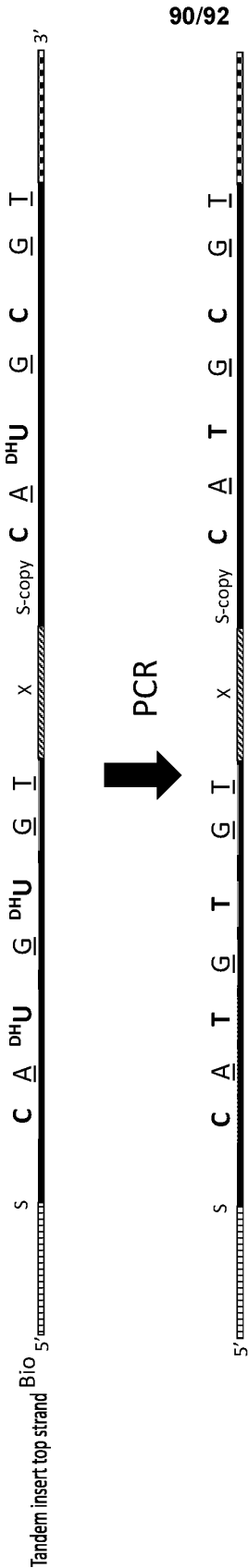
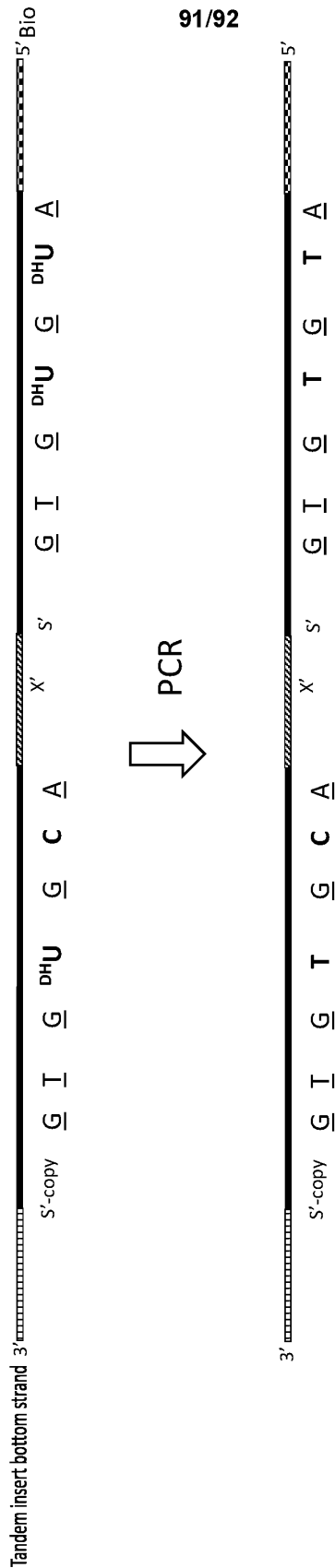


Fig. 61



Each loci is read twice = 5' (C,C) (A,A) (T,T) (G,G) (T,C) (G,G) (T,T) 3'

Fig. 62A



Each loci is read twice = 3' (G,G) (T,T) (G,G) (T,T) (G,G) (C,T) (A,A) 5'

Fig. 62B

