

1- Raw data and preprocessing (removing non optimal reads and adapters)

Samps	mRNA	
	Raw reads	High quality reads
ASB-1	23525612	18088064
ASB-2	24800250	19053419
ASB-3	24025104	20827871
ASB-4	25421187	19428806
ASB-5	22825260	20576371

2- De novo Assembly statistics

parameter	value
Number of scaffolds	47.555
Total size scaffolds	45.183.675
Scaffold largest	15.910
Scaffold smallest	100
Number of scaffolds over de 1K nt	14.176 (29,81%)
Number of scaffolds over de 10K nt	18 (0,04%)
Number of scaffolds over de 100K nt	0
Number of scaffolds over de 1M nt	0
Number of scaffolds over de 10M nt	0
Average size scaffolds	950
Average of total scaffolds size	721
N50	1128
L50	11.358
Scaffold %A	21,83
Scaffold %C	28,60
Scaffold %G	28,41
Scaffold %T	21,15
Scaffold %N	0
Scaffold %non-ACGTN	0
Number of scaffolds non-ACGTN nt	0

3- Annotation de novo transcriptome

Datab ase	Sequence	Subject mapping	Species	Score	e- value	Query- from	Query- to	Subject- from	Subjec- t-to	Query frame	Identi- ties	Positi- ves	Query length	Hit length	Align length	Simila- rity	Hsp/Q uery	Hsp/ Hit
nr	Locus_1_Transcript_1/9_Confidence_0.273_Length_878	YER178W	Sacharomyces cerevisiae	1477	0	24	878	4	288	3	285	285	878	420	285	100	97.38	67.86
nr	Locus_1_Transcript_2/9_Confidence_0.455_Length_1025	YER178W	Sacharomyces cerevisiae	1626	0	62	1012	1	317	2	313	313	1025	420	317	98.74	92.78	75.48
nr	Locus_1_Transcript_3/9_Confidence_0.636_Length_1348	YER178W	Sacharomyces cerevisiae	2182	0	62	1321	1	420	2	419	419	1348	420	420	99.76	93.47	100
nr	Locus_1_Transcript_4/9_Confidence_0.545_Length_1339	YER178W	Sacharomyces cerevisiae	2182	0	62	1321	1	420	2	419	419	1339	420	420	99.76	94.1	100
nr	Locus_1_Transcript_5/9_Confidence_0.455_Length_1467	YER178W	Sacharomyces cerevisiae	2182	0	62	1321	1	420	2	419	419	1467	420	420	99.76	85.89	100
nr	Locus_1_Transcript_6/9_Confidence_0.364_Length_1397	YER178W	Sacharomyces cerevisiae	2169	0	1	1251	4	420	1	416	416	1397	420	417	99.76	89.55	99.29
nr	Locus_1_Transcript_7/9_Confidence_0.364_Length_596	YER178W	Sacharomyces cerevisiae	739	3,59E-93	25	450	279	420	1	141	141	596	420	142	99.3	71.48	33.81
nr	Locus_1_Transcript_8/9_Confidence_0.273_Length_572	YER178W	Sacharomyces cerevisiae	739	2,61E-93	1	426	279	420	1	141	141	572	420	142	99.3	74.48	33.81
nr	Locus_1_Transcript_9/9_Confidence_0.091_Length_686	YER178W	Sacharomyces cerevisiae	899	7,07E-117	22	540	248	420	1	172	172	686	420	173	99.42	75.66	41.19
nr	Locus_2_Transcript_1/24_Confidence_0.069_Length_4000	YKL215C	Sacharomyces cerevisiae	6117	0	231	3998	31	1286	-3	1203	1205	4000	1286	1256	95.94	94.2	97.67
nr	Locus_2_Transcript_2/24_Confidence_0.103_Length_4149	YKL215C	Sacharomyces cerevisiae	6279	0	231	4088	1	1286	-2	1233	1235	4149	1286	1286	96.03	92.99	100
nr	Locus_2_Transcript_3/24_Confidence_0.103_Length_4282	YKL215C	Sacharomyces cerevisiae	6229	0	231	4082	3	1286	-3	1224	1228	4282	1286	1284	95.64	89.96	99.84
nr	Locus_2_Transcript_4/24_Confidence_0.069_Length_312	YKL215C	Sacharomyces cerevisiae	152	1,38E-08	2	112	3	39	-3	30	32	312	1286	37	86.49	35.58	2.88
nr	Locus_2_Transcript_5/24_Confidence_0.172_Length_1906	YKL015W	Sacharomyces cerevisiae	147	3,57E-06	497	1393	413	733	2	72	133	1906	979	329	40.43	51.78	33.61

4- Mapping summary

Sample ASB-1

Reads:

Input : 18088064

Mapped : 17509245,95 (96.8% of input)

of these: 1260666 (7.2%) have multiple alignments (3125 have >20)

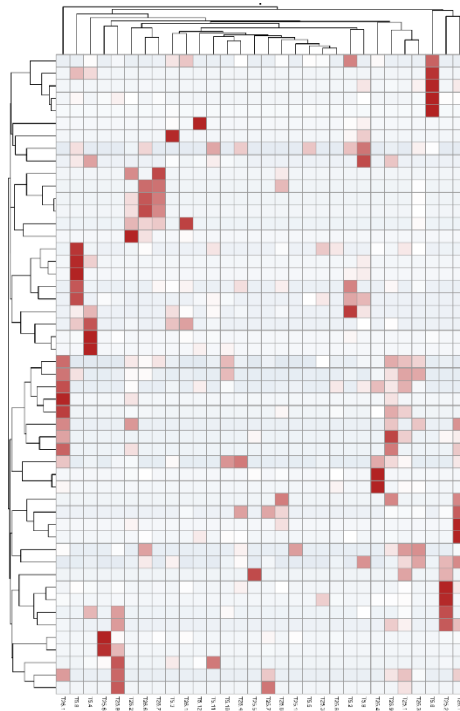
96.8% overall read mapping rate.

5- Gene expression level

	ASB-1	ASB-2	ASB-3	ASB-4	ASB-5	ASB-6	ASB-7	ASB-8	ASB-9
KP93L_(complement(1871..2152))_prot(Q89829.1)_description(Uncharacterized	107,277845	135,982296	129,38487	104,364529	134,240577	103,666592	0	0	374,809814
Q706L_(complement(140119..142239))_prot(Q89581.1)_description(Putative	33,893189	295,538323	284,259873	34,7502292	289,951309	31,2240688	0	449,439256	0
H339R_(136396..137415)_prot(Q65187.1)_description(Protein	207,574705	583,363182	526,105271	214,876519	491,103726	197,640642	0	0	0
DP148R_(164082..164528)_prot(Q65211.1)_description(Protein	266,322899	408,466896	415,717111	273,789684	434,614291	250,899311	0	149,813085	187,404907
I73R_(155210..155431)_prot(P27946.1)_description(Uncharacterized	5163,80439	7254,64248	5909,1514	5506,0187	6216,33927	5228,50554	1526,29067	5543,08416	5434,7423
J328L_(complement(14833..15819))_prot(POC9L7.1)_description(Protein	1002,90115	1707,44883	1706,38818	958,320816	1784,31575	1048,20306	1526,29067	1797,75703	937,024535
A498R_(21945..23441)_prot(Q89777.1)_description(Protein	3004,48787	2749,02641	2812,06583	3048,11592	2876,5838	2904,67685	4578,872	1647,94394	2811,07361
KP177R_(4608..5141)_prot(P23169.1)_description(Envelope	257,824308	289,298217	301,460531	262,092433	280,571144	252,777451	0	449,439256	374,809814
CP312R_(110486..111424)_prot(Q65180.1)_description(Uncharacterized	40066,808	27684,4007	27309,4642	41187,5312	28236,2756	37433,6339	27473,232	24569,346	34295,098
B962L_(complement(75069..77957))_prot(Q89443.1)_description(Putative	55,1059411	361,579438	314,792768	52,3672577	326,01283	51,8500649	0	599,252342	0
L270L_(complement(7280..8092))_prot(P18560.1)_description(Protein	1860,55059	1817,25735	1769,87174	1909,69728	1909,69728	1943,27067	3052,58133	1198,50468	1874,04907
E183L_(complement(145413..145964))_prot(Q65194.1)_description(Envelope	8,49859067	108,161826	89,8717119	9,67655849	100,159313	8,95470072	0	149,813085	0
A179L_(complement(36671..37210))_prot(P42485.1)_description(Apoptosis	1805,03995	2292,1987	2118,7895	1859,23687	1920,6408	2011,28615	3052,58133	1947,57011	1311,83435
DP363R_(165725..166816)_prot(P23164.2)_description(Protein	2777,92624	3377,63036	3294,58229	2844,93666	3536,53048	2712,70417	1526,29067	3745,32714	2623,6687

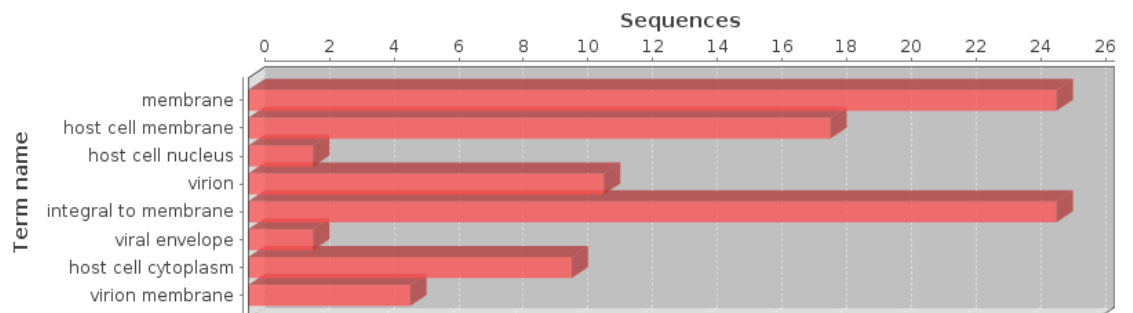
6- Graphical representations

a) Heatmap

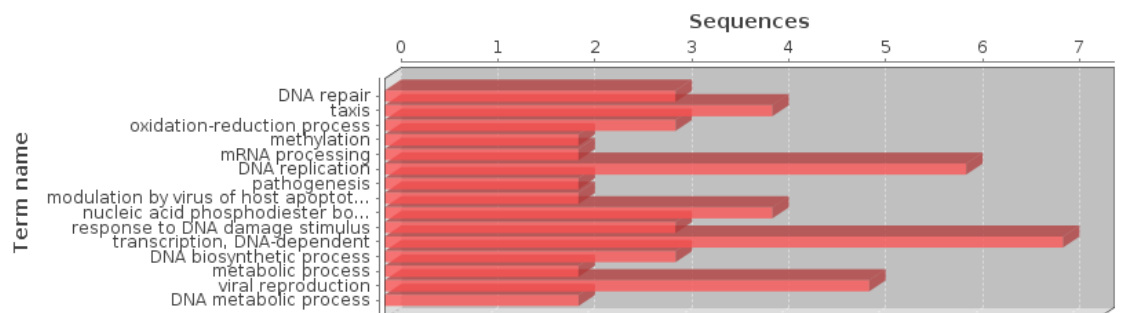


b) Go Categories

Gene Ontology terms distribution (Cellular component, max. level 15)



Gene Ontology terms distribution (Biological process, max. level 15)



Gene Ontology terms distribution (Molecular function, max. level 15)

