MA graph *Figure 1:* 

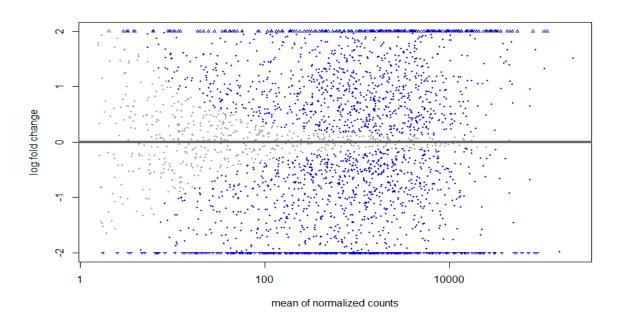
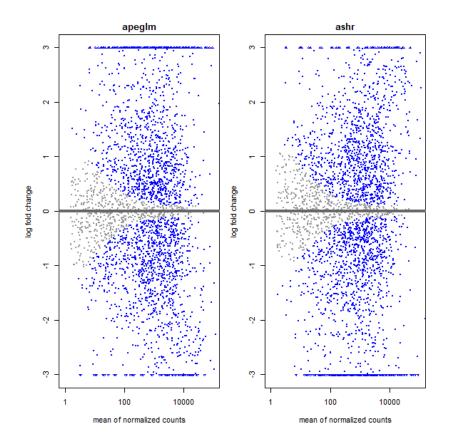


Figure 2: Comparison MA graph of 2 conditions



DESeq Statistics:

### > res

log2 fold change (MLE): condition treated vs reference Wald test p-value: condition treated vs reference DataFrame with 2910 rows and 6 columns

	baseMean	log2FoldChange	1fcse	stat	pvalue	padj
	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>
LBEDEJHI_00011	14.1443	-0.1949939	0.4876625	-0.3998542	6.89264e-01	7.23022e-01
LBEDEJHI_00012	1303.2647	-1.3736049	0.0771384	-17.8070149	6.23475e-71	2.92631e-70
LBEDEJHI_00013	112.8518	0.0097419	0.1848571	0.0526996	9.57971e-01	9.61938e-01
LBEDEJHI_00014	45.4266	-0.9864846	0.2813490	-3.5062669	4.54439e-04	6.70258e-04
LBEDEJHI_00015	3943.7577	1.2770629	0.0674774	18.9257896	6.99336e-80	3.57657e-79
LBEDEJHI_03210	10.71460	0.436995	0.566346	0.771605	0.440349	0.485936
LBEDEJHI_03211	3.35920	-0.526057	0.974545	-0.539797	0.589337	0.628885
LBEDEJHI_03213	20.24168	0.616285	0.426638	1.444514	0.148594	0.178020
LBEDEJHI_03214	14.03588	0.755624	0.487199	1.550957	0.120912	0.146912
LBEDEJHI_03215	3.85548	0.740451	0.999949	0.740489	0.459003	0.504943

### > restFC

log2 fold change (MAP): condition treated vs reference Wald test p-value: condition treated vs reference DataFrame with 2910 rows and 5 columns

Datail and With	2310 1003	and 5 Coramins			
	baseMean	log2FoldChange			
	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>
LBEDEJHI_00011	14.1443	0.15984565	0.4414251	6.89264e-01	7.23022e-01
LBEDEJHI_00012	1303.2647	1.36970451	0.0771293	6.23475e-71	2.92631e-70
LBEDEJHI_00013	112.8518	-0.00921281	0.1818580	9.57971e-01	9.61938e-01
LBEDEJHI_00014	45.4266	0.93683038	0.2779961	4.54439e-04	6.70258e-04
LBEDEJHI_00015	3943.7577	-1.27287872	0.0674638	6.99336e-80	3.57657e-79
LBEDEJHI_03210	10.71460	-0.337256	0.504025	0.440349	0.485936
LBEDEJHI_03211	3.35920	0.280985	0.722948	0.589337	0.628885
LBEDEJHI_03213	20.24168	-0.533378	0.403621	0.148594	0.178020
LBEDEJHI_03214	14.03588	-0.633976	0.457187	0.120912	0.146912
LBEDEJHI_03215	3.85548	-0.390748	0.749017	0.459003	0.504943

## > summary(res)

```
out of 2910 with nonzero total read count
adjusted p-value < 0.1
LFC > 0 (up) : 1166, 40%
LFC < 0 (down) : 1180, 41%
outliers [1] : 0, 0%
low counts [2] : 0, 0%
(mean count < 2)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results
>
> sum(res$padj < 0.1, na.rm=TRUE)
[1] 2346</pre>
```

# > summary(res05)

```
out of 2910 with nonzero total read count
adjusted p-value < 0.05
LFC > 0 (up) : 1128, 39%
LFC < 0 (down) : 1141, 39%
outliers [1] : 0, 0%
low counts [2] : 0, 0%
(mean count < 2)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results
```

### > ressig

log2 fold change (MLE): condition treated vs reference Wald test p-value: condition treated vs reference DataFrame with 2346 rows and 6 columns

	baseMean	log2FoldChange				padj
	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>
LBEDEJHI_00047	1402.31	-4.21063	0.1009782	-41.6984	0	0
LBEDEJHI_00065	3168.11	3.75347	0.0747260	50.2298	0	0
LBEDEJHI_00066	2529.63	4.21174	0.0803574	52.4126	0	0
LBEDEJHI_00067	1790.92	4.94596	0.1093582	45.2272	0	0
LBEDEJHI_00086	7955.15	2.64789	0.0632854	41.8404	0	0
LBEDEJHI_02277	155.71581	-0.274382	0.1540733	-1.78086	0.0749361	0.0931102
LBEDEJHI_00247	150.42166	0.269075	0.1523711	1.76592	0.0774093	0.0961421
LBEDEJHI_02138	9.17169	1.104391	0.6260393	1.76409	0.0777163	0.0964823
LBEDEJHI_00733	8.19710	-1.107921	0.6286560	-1.76237	0.0780076	0.0968027
LBEDEJHI_02450	2661.00424	-0.107691	0.0611548	-1.76095	0.0782467	0.0970579

# > head(assay(vsd), 3)

bh1 bh2 bh3 serum1 serum2 serum3 LBEDEJHI\_00011 8.275147 8.332401 8.349101 8.260404 8.362654 8.390514 LBEDEJHI\_00012 10.181017 10.243772 10.188164 11.280333 11.169068 11.166238 LBEDEJHI\_00013 8.866370 9.030568 8.906162 8.938409 8.915819 8.948777

### > results(dds, contrast=c("condition","reference","treated"))

log2 fold change (MLE): condition reference vs treated Wald test p-value: condition reference vs treated DataFrame with 2910 rows and 6 columns

	baseMean	log2FoldChange	1fcse	stat	pvalue	padj
	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>	<numeric></numeric>
LBEDEJHI_00011	14.1443	0.19499478	0.4876625	0.3998560	6.89263e-01	7.23021e-01
LBEDEJHI_00012	1303.2647	1.37360493	0.0771384	17.8070157	6.23466e-71	2.92627e-70
LBEDEJHI_00013	112.8518	-0.00974167	0.1848571	-0.0526984	9.57972e-01	9.61939e-01
LBEDEJHI_00014	45.4266	0.98648499	0.2813490	3.5062684	4.54437e-04	6.70254e-04
LBEDEJHI_00015	3943.7577	-1.27706285	0.0674774	-18.9257888	6.99347e-80	3.57663e-79
LBEDEJHI_03210	10.71460	-0.436994	0.566346	-0.771603	0.440350	0.485938
LBEDEJHI_03211	3.35920	0.526058	0.974545	0.539799	0.589336	0.628884
LBEDEJHI_03213	20.24168	-0.616285	0.426638	-1.444512	0.148595	0.178020
LBEDEJHI_03214	14.03588	-0.755623	0.487199	-1.550955	0.120912	0.146912
LBEDEJHI_03215	3.85548	-0.740450	0.999949	-0.740487	0.459004	0.504942

0.487199

2.433570

0.552833

0.118762

0.457162

0.144240

0.502965

-0.755623

-0.740450 0.999949

Figure 3: MA graph: Test of log2

14.03588

3.85548

LBEDEJHI\_03214

LBEDEJHI\_03215

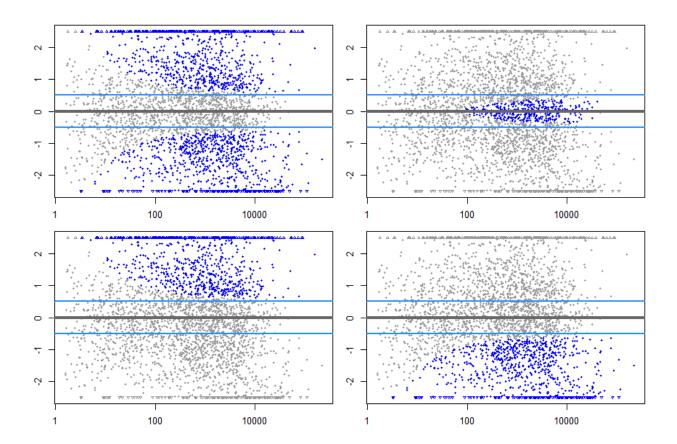


Figure 4: Dispersion Estimation

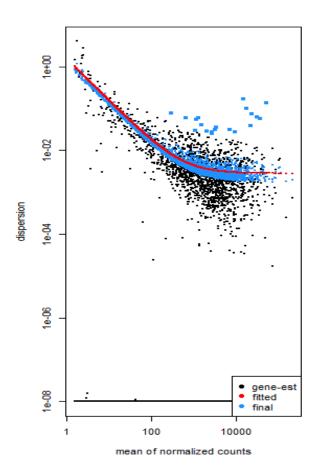


Figure 5: Count of outliers

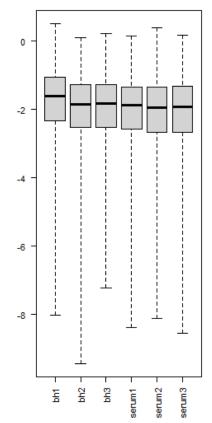


Figure 6:

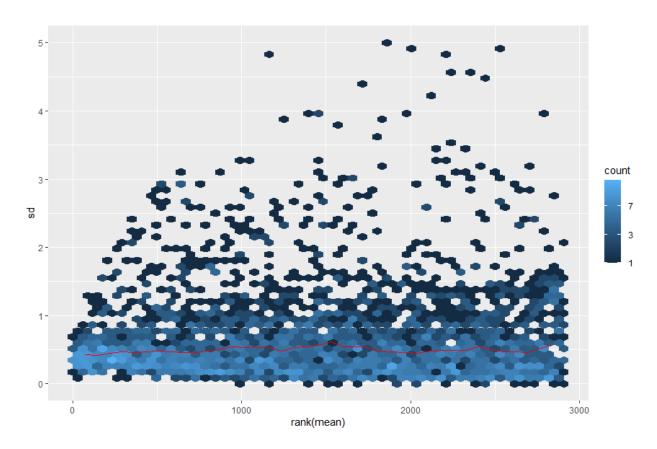


Figure 7: Shrinkage Estimation

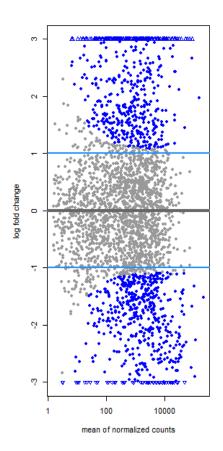


Figure 8: Test of log2

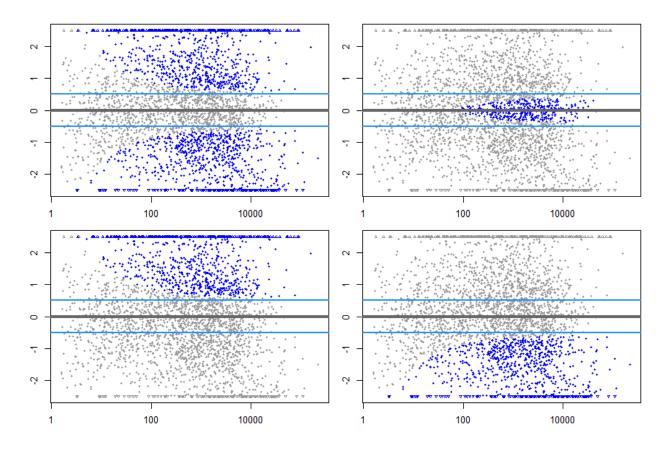


Figure 9:

